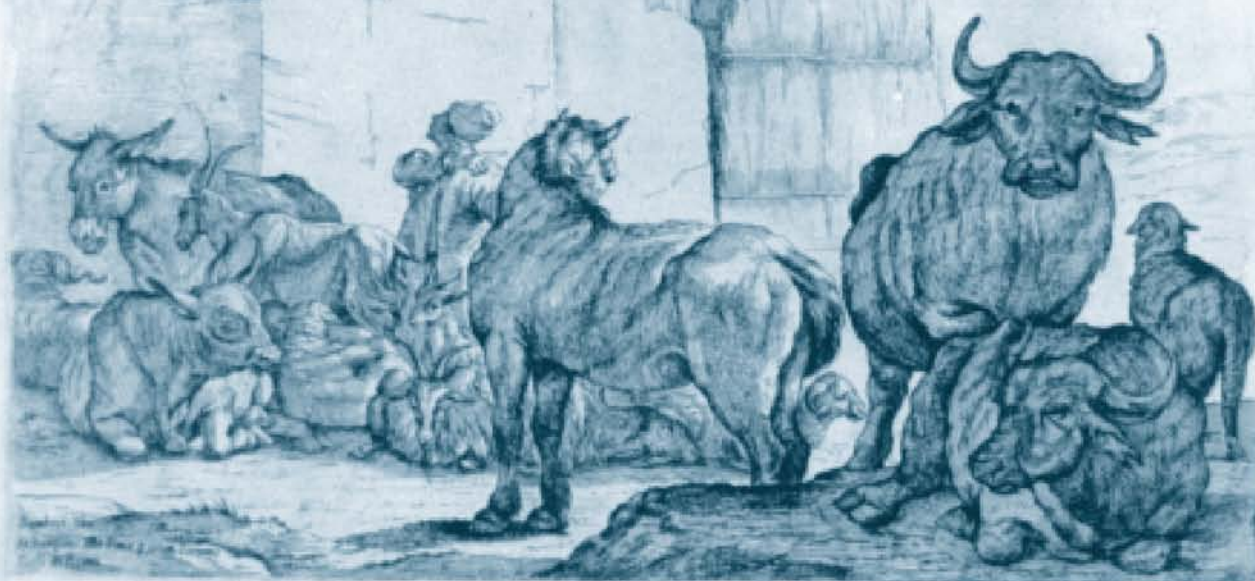


ICAR TECHNICAL SERIES No.13



IDENTIFICATION, BREEDING, PRODUCTION, HEALTH AND RECORDING OF FARM ANIMALS

PROCEEDINGS OF THE 36th ICAR BIENNIAL SESSION
HELD IN NIAGARA FALLS, USA
16-20 JUNE 2008



Pietro Lait di Arlem N. Monfai Bamboccio non solo la struttura del corpo, ma di cui parte inferiore era un po' più lunga della superiore, frons di panno e corno di Cello, ma ancora per la bizzezza di colore Cocco, animali, sugary, Carceri. L'anno 1639. parti d'Italia e la Patria. Abecedario.

EDITORS: J.D. SATTLER
JANUARY 2009

The designations employed and the presentation of material in this publication do not imply the expression of any opinion whatsoever on the part of the Organisation concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries.

All rights reserved. No part of this publication may be reproduced, stored in a retrieval system, or transmitted in any form or by any means, electronic, mechanical, photocopying or otherwise, without the prior permission of the copyright owner. Applications for such permission, with a statement of the purpose and the extent of the reproduction, should be addressed to the Secretary General of ICAR, Via G. Tomassetti 3, 00161 Rome, Italy icar@icar.org

All the manuscripts are published under the responsibility of each Author. ICAR is in no way responsible for the opinion expressed by each Author.

Cover page: 17th century engraving by Pieter Jacobsz van Laer of Haarlem, dit Bamboccio, (1599-1642), representing a livestock farm in the Latium region of Italy

Title of the Series:	ICAR Technical Series
Title of the Volume:	Identification, breeding, production, health and recording of farm animals. Proceedings of the 36 th ICAR Biennial Session held in Niagara Falls, USA, 16-20 June 2008
Date of publishing:	Jan., 2009
Editors:	J.D. Sattler
Publisher:	ICAR, Via G. Tomassetti 3, 1/A, 00161 Rome, Italy
Responsible for ICAR Technical Series:	Cesare Mosconi
ISSN:	1563-2504
ISBN:	92-95014-09-X

The International Committee for Animal Recording (ICAR) wishes to express its appreciation to the *Ministero per le Politiche Agricole e Forestali* and to the *Associazione Italiana Allevatori* for their valuable support of its activities.

In the same series:

- R. Pauw, A. Speedy & J. Mäki-Hokkonen (Eds), Development of animal identification and recording systems for veterinary surveillance and livestock development in countries of Eastern Europe, Finland, 6 June 2006, I.T.S. no. 12
- R. Cardellino, A. Rosati & C. Mosconi (Eds), Current status of genetic resources, recording and production systems in African, Asian and American Camelids, Sousse, Tunisia, 30 May 2004, I.T.S. no. 11
- V. Tancin, S. Mihina & M. Uhrincat (Eds), Physiological and Technical Aspects of Machine Milking, Nitra, Slovak Rep., 26-28 April 2005, I.T.S. no. 10
- R. Pauw, S. Mack & J. Maki-Hokkonen (Eds), Development of Animal Identification and Recording Systems for Developing Countries, Sousse, Tunisia, 29 May 2004, I.T.S. no. 9
- J. Mäki-Hokkonen, J. Boyazoglu, T. Vares & M. Zjalic (Eds), Development of Successful Animal Recording Systems for Transition and Developing Countries, Interlaken, Switzerland, 27 May 2002, I.T.S. no. 8
- A. Rosati, S. Mihina & C. Mosconi (Eds), Physiological and Technical Aspects of Machine Milking, Nitra, Slovak Republic, 26-27 June 2001, I.T.S. no. 7
- H. Simianer, H. Täubert & K. Küttner (Eds), Beef Recording Guidelines: A Synthesis of an ICAR Survey, I.T.S. no. 6
- T. Vares, F. Habe, M. Klopčič & D. Kompan (Eds), The Role of Breeders' Organisations and State in Animal Identification and Recording in CEE Countries, Bled, Slovenia, 15 May 2000, I.T.S. no. 5
- B. Moiola, J. Mäki-Hokkonen, S. Galal & M. Zjalic (Eds), Animal Recording for Improved Breeding and Management Strategies for Buffaloes, Bled (Slovenia) 16-17 May 2000, I.T.S. no. 4.
- S. Galal, J. Boyazoglu & K. Hammond (Eds), Developing Breeding Strategies for Lower Input Animal Production Environments, Bella (Italy) 22-25 September 1999, I.T.S. no. 3.
- T. Vares, M. Zjalic & C. Mosconi (Eds), Cattle Identification and Milk Recording in Central and Eastern European Countries, Warsaw (Poland), 23 August, 1998, I.T.S. no. 2.
- K.R. Trivedi (Ed.), International Workshop on Animal Recording for Smallholders in Developing Countries, Anand (India) 20-23 October 1997, I.T.S. no. 1.

All the above publications can be freely
downloaded from the ICAR web site at: www.icar.org

Sponsors of Niagara Falls Session

Gold Level



FOSS



Silver Level



Bronze Level



AgSource
Cooperative Services
A subsidiary of Cooperative Resource International

Astoria-Pacific
INTERNATIONAL



afimilk
The Heart of the Dairy Farm



Donor & Contributor



ICAR Technical Series no. 13

**Identification, breeding, production,
health and recording of farm animals**

**Proceedings of the 36th ICAR Biennial Session
held in Niagara Falls, USA
16-20 June 2008**

Editor: J.D. Sattler

January 2009

The realisation of this publication has been made possible thanks to the efforts of the Local Organising Committee

Organizing Committee

Jay Mattison
JoDee Sattler
David Harrison
Steven Sievert
Leslie Thoman
Mark Adam
Dani Thom
Jamie Zimmerman
Jere High

George Cudoc
Dan Sheldon
Lee Maassen
Susan Lee
Bruce Dokkebakken
Steve Hershey
Tom DeMuth
Pat Baier

Program Committee

JoDee Sattler
Jay Mattison
Steven Sievert
Neil Petreny
Dan Webb
Jere High
ICAR Staff
Interbull Centre

Dairy Farms

We appreciate these dairy farms sharing their dairy operations.

- Emerling Farms
- Dueppengeisser Dairy Company
- Noblehurst Farms
- Highland Farms
- Reyncrest Dairy
- Lamb Farms
- Offhaus Farms

Volunteers

Randy Perkins
Kathleen Noble
Jack van Almelo
David Rothfuss
Dave Heald
Donna Walker
Katie Allen

and the Chairmen (in alphabetic order) of the Sessions who reviewed the single manuscripts:

Session	Session Chair	Email
AI technologies	Alain Malafosse	alain.malafosse@unceia.fr
Impact of new technologies on performance recording and genetic evaluation	Daniel Abernethy	dabernethy@adhis.com.au
Milk recording	Enrico Santus	enrico.santus@anarb.it
Breed organization services - Data transfer	Erik Rehben	erik.rehben@inst-elevage.asso.fr
Manufacturers showcase	Frank Armitage	FrankA@NMR.co.uk
Beef recording	Japie van der Westhuizen	japie@arc.agric.za
Small dairy species recording	Jean Michel Astruc	astruc@toulouse.inra.fr
New technologies	Kaivo Ilves	kaivo.ilves@jkkkeskus.ee
AI technologies	Laurent Journaux	laurent.journaux@unceia.fr
Alpaca	Marco Antonini	marco.antonini@unicam.it
Management of recording evaluation organizations	Mark Adam	adamm@northstarcooperative.com
ID techniques	Ole Kleis Hansen	OKH@landscentret.dk
Use of molecular genomic tools in animal breeding	Reinhard Reents	reinhard.reents@vit.de
Presentation of Sub-Committees, Working Groups and Task Forces	Uffe Lauritsen	UFL@landscentret.dk

Table of content

ICAR Welcome	1
<i>M. Adam</i>	
Experience with bovine electronic identification in Germany	3
<i>B. Eggers, N. Wirtz, D. Albers & R. Reents</i>	
The importance of recording of AI data for the genetic systems.	
The context of AI from service to genetic progress	11
<i>J. Philipsson & H. Jorjani</i>	
Various systems used to record and process AI data on farms: summary of the ICAR questionnaire	19
<i>L. Journaux & A. Malafosse</i>	
Use of insemination data in cattle breeding; some experiences from Ireland	23
<i>A. Cromie, F. Kearney, R. Evans, D. Berry & D. Wilhelmus</i>	
Valorisation of AI data on farm by AI technicians: French experiences.....	31
<i>A. Malafosse & L. Journaux</i>	
The impact of new technologies on performance recording and genetic evaluation of dairy and beef cattle in Ireland	39
<i>A. Cromie, B. Wickham, S. Coughlan & M. Burke</i>	
Comparison of different models for estimating daily yields from a.m./p.m. milkings in Slovenian dairy scheme	49
<i>J. Jenko, T. Perpar, B. Logar, M. Sadar, B. Ivanovic, J. Jeretina, J. Verbic & P. Podgoršek</i>	
Quality assurance for milking machines and recording devices	59
<i>K. de Koning & P. Huijsmans</i>	
Estimation of fat and protein yields in dairy cattle from one milk sample per day in herds milked twice a day.....	65
<i>M. Trinderup, T. Lykke & U. Sander Nielsen</i>	
Tru-Test electronic Milk Meter – practical field use by AgSource/CRI	73
<i>P. Jandrin</i>	
Supplemental testing on milk recording samples	81
<i>T. Byrem, M. Adam & B. Voisinet</i>	
ICAR guidelines for alpaca shearing management, fibre harvesting and grading	91
<i>M. Antonini</i>	
Genetic improvement programmes of alpaca in Caylloma province - PROMEGE.....	99
<i>C. Pacheco, C. Renieri, M. Antonini, A. Valvonesi, W. Frank & N. Mamani</i>	

Preliminary information on a genetic improvement program on alpacas in Italy	107
<i>A. Valbonesi, G. Berna, A. Briganti, M. Antonini & C. Renieri</i>	
Effect of combining controlled natural mating with artificial insemination on the genetic structure of the flock book of Sardinian breed sheep	113
<i>S. Salaris, S. Casu, P. Fresi & A. Carta</i>	
SIEOL: implementing a global information system for genetic and techno-economic support in dairy sheep in France	123
<i>J.M. Astruc, G. Lagriffoul, E. Morin, F. Barillet, B. Bonaïti & E. Rehben</i>	
Selecting milk composition and mastitis resistance by using a part lactation sampling design in French Manech red faced dairy sheep breed	129
<i>F. Barillet, J.M. Astruc, G. Lagriffoul, X. Aguerre & B. Bonaïti</i>	
Productivity of Slovenian Alpine goat in the conventional and organic farming system.....	137
<i>D. Kompan & M. Kastelic</i>	
Marketing value-added in milk recording products and services	143
<i>P. Baier</i>	
Alternative modelling of body condition score from Walloon Holstein cows to develop management tools	149
<i>C. Bastin, L. Laloux, A. Gillon, C. Bertozzi & N. Gengler</i>	
Development of a milk transport security system	153
<i>C. Thompson, F.A. Payne, B. Luck, J.R. Moore & N. Tabayehnejad</i>	
Integration of quality certification programs into management of milk recording providers in the United States	161
<i>S.J. Sievert</i>	
Estimation of breeding values of total milk yield of Egyptian buffalo under different production systems	167
<i>S.A.M. Abdel-Salam, S. Abou-Bakr, M.A.M. Ibrahim, R.R. Sadek & A.S. Abdel-Aziz</i>	
Automatic systems to identify semen straws: why and how?	173
<i>A. Malafosse & L. Journaux</i>	
Harmonisation of barcode numbers: toward an ICAR recommendation	179
<i>U. Witschi</i>	
Retrofitting genetic-economic indexes to demonstrate responses to selection across two generations of Holsteins	181
<i>H.D. Norman, J.R. Wright & R.H. Miller</i>	
Potential estimation of minerals content in cow milk using mid-infrared spectrometry	187
<i>H. Soyeurt, D. Bruzwier, P. Dardenne, J.-M. Romnee & N. Gengler</i>	

Automated daily analysis of milk components and automated cow behavior meter: developing new applications in the dairy farm.....	191
<i>A. Arazi</i>	
On-farm technologies. Challenges and opportunities for DHI and genetic improvement programs	201
<i>R. Cantin</i>	
Assuring accuracy in milk recording analysis on-farm - Approach on principles for guidelines.....	207
<i>O. Leray</i>	
Impact of new on-farm technologies in dairy cattle breeding	213
<i>F. Miglior, G.R. Wiggans, M.A. Faust & B.J. Van Doormaal</i>	
Evaluation of different visual image analysis methods to estimate of body measurements in cattle	215
<i>A.R. Onal, M. Ozder & T. Sezenler</i>	
Use of the dairy records database to establish benchmarks and estimates for potential economic improvements of individual herds	221
<i>P. Giacomini</i>	
Mobile phone solutions in Finnish milk recording	227
<i>J. Kyntäjä, J. Ilomäki & S. Tommila</i>	
Transition cow index™ in progress	231
<i>R. La Croix & K. Nordlund</i>	
A new approach to perform analysis of milk components incorporating statistical methods adapted in a real time sensor	237
<i>G. Katz & N. Pinsky</i>	
Cow body shape and condition scoring	243
<i>M. Klopčič, A. White, R. Boyce, P. Polak, D. Roberts & I. Halachmi</i>	

Special session on "Presentation of ICAR Sub-Committees, Working Groups and Task Forces"

Report of the ICAR Subcommittee on Animal Identification	255
<i>O.K. Hansen</i>	
Report of the ICAR Sub-Committee on Milk Analysis	261
<i>O. Leray</i>	
Report of the ICAR Task Force for Developing Countries	265
<i>B. Besbes</i>	

Report of the ICAR Task Force on Pig Recording	267
<i>M. Kovac & S. Malovrh</i>	
Report of the ICAR Working Group on Lactation Calculation Methods.....	271
<i>F. Miglior, G. de Jong, Z. Liu, S. Mattalia, L.R. Schaeffer, A. Tondo & P. VanRaden</i>	
Report of the ICAR Working Group on Milk Recording of Sheep	275
<i>J.M. Astruc, F. Barillet, A. Carta, M. Fioretti, E. Gootwine, D. Kompan, F.J. Romberg & E. Ugarte</i>	
Report of the ICAR Working Group on Animal Fibre	283
<i>M. Antonini</i>	
Report of the ICAR Interbeef Working Group	287
<i>B. Wickham</i>	

Workshop on "ICAR Reference Laboratory Network"

Update on ICAR Reference Laboratory Network	291
<i>O. Leray</i>	
ICAR AQA strategy – International anchorage and harmonisation	295
<i>O. Leray</i>	
Interlaboratory reference systems and centralised calibration – Prerequisites and standard procedures	301
<i>O. Leray</i>	
The way to reference systems and centralised calibration for milk recording testing. Present status in Germany	307
<i>C. Baumgartner</i>	
Reference system and centralized calibration for milk recording testing in Argentina	309
<i>R. Castañeda</i>	
Reference system and centralised calibration for milk (payment) testing	315
<i>D. Barbano</i>	

Workshop on "Use of genomic tools in animal breeding"

Bull selection strategies using genomic estimated breeding values	319
<i>L.R. Schaeffer</i>	
Genomic selection in New Zealand and the implications for national genetic evaluation	325
<i>B.L. Harris, D.L. Johnson & R.J. Spelman</i>	
Incorporation of genotype effects into Animal Model Evaluations when only a small fraction of the population has been genotyped	331
<i>E. Baruch & J. I. Weller</i>	
Genomic data and cooperation result in faster progress	341
<i>P.M. VanRaden, C.P. Van Tassell, G.R. Wiggans, T.S. Sonstegard, R.D. Schnabel, J.F. Taylor & F. Schenkel</i>	
Genomic evaluations in the United States and Canada: A collaboration	347
<i>G.R. Wiggans, T.S. Sonstegard, P.M. VanRaden, L.K. Matukumalli, R.D. Schnabel, J.F. Taylor, J.P. Chesnais, F.S. Schenkel & C.P. Van Tassell</i>	
Distribution and location of genetic effects for dairy traits	355
<i>J.B. Cole, P.M. VanRaden, J.R. O'Connell, C.P. Van Tassell, T.S. Sonstegard, R.D. Schnabel, J.F. Taylor & G.R. Wiggans</i>	
Single nucleotide polymorphisms for parentage testing, individual identification, and traceability1	361
<i>B.W. Woodward & T. Van der Lende</i>	

Workshop on "DHI managers"

Herd testing in the USA	371
<i>S.J. Sievert</i>	
Overview of DHI laboratory services in the USA	377
<i>S.J. Sievert</i>	
Serving the diverse production information needs of agriculture	381
<i>J. Zimmerman</i>	
In the right hands, PocketMeter is indispensable	385
<i>B.L. Winters & J.S. Clay</i>	
Using PocketDairy with RFID for herd management	389
<i>P.A. Dukas</i>	

Processing of data discrepancies for U.S. dairy cattle and effect on genetic evaluations	393
<i>G.R. Wiggans & L.L.M. Thornton</i>	
Managing DHI employees in a large-herd environment	399
<i>W.R. Skip Pringle</i>	
Data collection ratings and best prediction of lactation yields	403
<i>J.B. Cole</i>	

Workshop on "Manufacturers' showcase"

Management of individual cows in large herds – a challenge to modern dairy farming	409
<i>N. Pinsky, U. Golan, A. Arazi & G. Katz</i>	
PathoProof™ mastitis PCR assay	415
<i>M.T. Koskinen</i>	

ICAR survey on the situation of cow milk recording in member countries - Reults for the years 2006 and 2007

Table 1. Annual milk production	420
Table 2. Position of milk recording.....	423
Table 3. Costs and financing	427
Table 4.1. Results of milk recording: All breeds together - All recorded cows	430
Table 4.2. Results of milk recording: All breeds together - Cows in herdbook.....	433
Table 4.3. Results of milk recording: Main breeds - All recorded cows	435
Table 4.4. Results of milk recording: Main breeds - Cows in herdbook	446
 Participants to the 36th ICAR Session	 453

ICAR Welcome

M. Adam

*Director of DHI Services, NorthStar Cooperative, Lansing, Michigan, USA
and Past President of National DHIA*

Welcome to the 36th meeting of the International Committee for Animal Recording biennial session held in the United States of America for the first time ever. This historic event is hosted by National DHIA which is an association of 20 DHI affiliates throughout the U.S. that promotes accuracy, credibility, and uniformity of DHI records. National DHIA represents the DHI system on issues involving other National and International organizations and they organize industry activities that benefit members of the association.

We welcome you to Niagara Falls, New York, where you will be partnering with other like-minded organizations from around the globe.

We welcome you to the Niagara area where two friendly neighbors (Canada & the U.S.A.) live and work closely together. The Niagara experience is one of scenic beauty and awesome spectacular water falls. You will experience the majestic roar of the Horseshoe Falls, the mist at your face as you walk under the Bridal Falls and the once-in-a lifetime experience as you view the falls from the catwalk.

Your ICAR planning committee is from the National DHIA staff spearheaded by Jay and Mary Mattison. Their group consists of Steven Seivert, JoDee Sattler, Leslie Thoman, and David Harrison.

Another person that is playing a key role as your host this week is National DHIA president, Dan Sheldon. Dan and his family own and operate a 900 cow dairy in eastern New York. Besides being president of NDHIA he is also a member of several farmer-owned and operated boards of director's organizations which includes Dairy One, the DHI affiliate that operates in 13 northeastern states in the U.S.

Of course we want to thank one of our key industry partners, CanWest DHI, and their general manager, Neil Petreny, who is also the ICAR president for his role in helping us organize this week's events.

Western New York is a large geographical land mass located 6-8 hours to the east of New York City. Western New York is an area that is home to the "Fingers Lakes Region" where seven long narrow lakes create the look of fingers stretched across a land mass. The Finger Lakes area is known for its water sports, hiking trails, scenic beauty, diverse agriculture operations, dairy farms, grape vineyards and the second largest winery area in the U.S. behind California.

Sporting activities in western New York include the Buffalo Sabres professional hockey team, the Buffalo Bills professional American Football team where any given Sunday in the autumn time of the year they play before a sold-out crowd of more than 75 000 people in the Ralph Wilson Stadium located approximately 30 miles from this conference center. Of course, with any pro football team that also means there is the cheerleader squad and in this case, they are known as the Buffalo Jills and they make numerous promotional appearances throughout Western New York.

If food is on your menu, Western New York is the home of buffalo hot wings. They are an addicting little food item that usually comes back to get you the next day when you eat too much the night before.

And if you visit Western New York in the wintertime it is the one of the heaviest areas for snow density in the Continental U.S. On the average, over 10 feet of snow descends on the area as “lake effect” snowstorms are the norm for this region of the country.

Western New York is also home to one of the most prestigious centers for higher education in the world, Cornell University. Cornell is located in Ithaca, New York which is on the south end of Cayuga Lake one of the Finger Lakes. Cornell is one of two private-land grant universities in the U.S. founded in 1865 that has approximately 20 000 students enrolled and a member of the prestigious Ivy League of schools located in the Northeastern U.S.

And of course, Western New York is the home of many dairy farms. From small 20-40 cow Mennonite herds milked in stanchions to large 3-5 000 cow herds that are milked in large parallel or rotary parlors. This week you will be able to witness some of these operations first hand when we tour the countryside.

In the U.S. last year over 186 billion pounds of milk was produced. The top ten states for milk production are in order; California, Wisconsin, New York, Idaho, Pennsylvania, Minnesota, Texas, New Mexico, and Washington. This type of production came from a national dairy herd that numbers 9 153 000 cows. California again leads the way with over 1.8 million cows followed by Wisconsin, New York, Pennsylvania, Idaho, Minnesota, Texas, Michigan, New Mexico and finalizing the top ten is Ohio. Major shifts are taking place within the cow population figures as states like Idaho, New Mexico and Indiana are experiencing huge growth numbers. More detail about the dairy and agricultural industry will follow from several of our key-note speakers this week.

As you spend some time in the U.S. and specifically here at Niagara Falls, you are in the midst of an area that is referred to as the Great Lakes. The Great Lakes are a chain of freshwater lakes located on or within the Canada–United States border. Consisting of Lakes Superior, Michigan, Huron, Erie, and Ontario, they form the largest group of freshwater lakes on Earth that represents over 22% of the freshwater available in the world.

And the best part that I enjoy about the Great Lakes is the fantastic fishing opportunities that it presents! And, if you happen to be out on one of the Great Lakes fishing sometime, you just may have the opportunity to rub shoulders with other people from around the world, that not only enjoy this great sport, they also enjoy the wonderful world of animal recording.

Welcome to the ICAR meetings here in Niagara Falls, New York and I hope your week is fun, educational and entertaining!

Experience with bovine electronic identification in Germany

B. Eggers¹, N. Wirtz¹, D. Albers² & R. Reents¹

¹*Vereinigte Informationssysteme Tierhaltung w.V. (vit), Heideweg 1,
27283 Verden, Germany*

²*Landwirtschaftskammer Niedersachsen, Sarver Straße 39a, 26954
Nordenham, Germany*

Different studies in Germany and Europe investigated in electronic identification systems for animals. The IDEA-project compared different electronic animal identification systems from a technical point of view.

Both, bolus and injectable transponders can be combined with biometric sensors simpler than ear tags. This combination is useful to get information about hyperthermy. Bolus and injectable transponders are preferred by universities and other experimental institutions.

However, farmers and industry prefer electronic ear tags compared with bolus and injectable transponders, because they are easier to handle. In practice, ear tags can be applied by non trained staff. Ear tags are also easier to integrate in practical farming operations.

The number of disappeared electronic ear tags is distinctly lower than the number of lost normal visual ear tags. The involvement of electronic ear tags in automatic identification of animals and in transferring data processes in practical farming is ready to put into practice. The number of disappeared electronic ear tags compared with visual ear tags is lower. So, there are less costs for ordering and replacing lost tags.

Electronic ear tags can be used in practical farming at different places to identify animals. Concerning all costs and savings it seems to be more efficient to use electronic ear tags than normal visual eartags.

Key words: *RFID, Electronic tagging, Electronic identification, Transponder, Bolus, Injectable, Ear tag, Precision farming, Biometric sensors.*

Summary

Introduction

Electronic identification systems can be classified as bolus, injectable transponder or electronic ear tag. All these different systems have to follow an international standard. In the field of animal identification, the international standards are ISO 11784 (Radio frequency identification of animals – Code structure) and ISO 11785 (Radio frequency identification of animals – Technical concept). If people are talking about ISO compatible identification systems, they are talking about systems applying these two standards.

The IDEA project compared different electronic animal identification systems regarding the application, the scanning quality, the withdrawal at abattoir, the number of lost identification systems and the data protection (IDEA, 2002). Table 1 shows that electronic ear tags have a lot of advantages. Only in the number of lost systems, bolus and injectable transponders are more reliable. Because of these reasons electronic ear tags are preferred by farmers and industry, whereas bolus or injectable transponder are preferred by universities and other experimental institutions.

Different processes of identification can be classified, too (Prinkelman and Kern, 1994). At the static process the animal is standing or is moving slowly in a room. It is more or less easy to define the head or rump position of the animal. The scanning distance is around 0.3 to 0.5 m. The scanning speed requirement is low up to middle. At the dynamic identification process the animal is moving, and it is more difficult to define head or rump position. The scanning distance is around 0.5 to 0.9 m. The scanning speed requirement is high, and it is necessary to identify also cows which can achieve a speed of 3 m/s.

The current paper gives an overview about some German studies investigating in electronic cattle identification systems.

Table 1. Comparison between different electronic identification systems (IDEA, 2002, modified).

Feature	Bolus	Injectable transponder	Electronic ear tag
Application	+	+ ¹	++
Scanning (hand held device)	–	+	++
Scanning process control syst.	+/-	+	++
Withdrawal (abattoir)	+	–	++
Lost identification systems	++	++	+
Data protection	+	+	+

+ + Very positive.

+ Positive.

– Negative.

¹Only trained staff

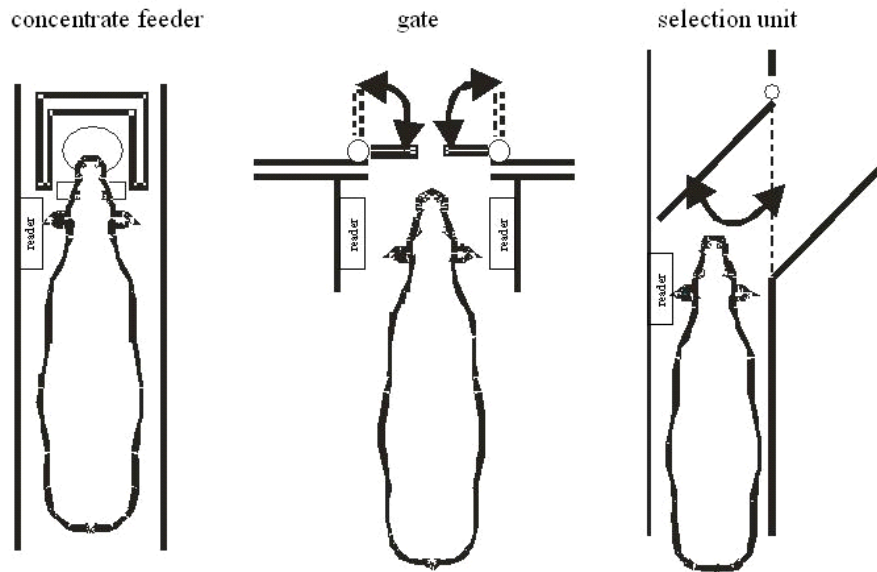


Figure 1. Different processes of animal identification (Prinkermann and Kern, 1994, modified).

Calves were applied with injectable transponders near the ear, ventral to Scutulum. The injectables were equipped with integrated temperature sensors. Between 2 and 11 weeks pp. the temperature measured by the injectable was transferred to a hand reader. At the same time the rectal temperature was measured by hand using a common thermometer.

As second step, the methods were modified: to get more detailed information, a controlled artificial hyperthermy was started (Kamann *et al.*, 1999).

5 calves were applicated with bolus systems, located in the Reticulum. The id systems were equipped with integrated temperature sensors (prototype). Two times a day, in the morning and in the afternoon, the bolus temperature was measured by data transfer to a hand reader. At the same time, the rectal temperature was measured by hand using a common thermometer (Klindtworth *et al.*, 2006).

The first period of the study called ITeK-Rind (innovative technologies in electronic tagging of cattle) dealt with 2 hardware components under experimental conditions. 80 cows and their calves born in the study periode between August 2003 to July 2004 were applicated with electronic ear tags. The animals were weighed at an automatic digital balance. The aim of the study was both to identify the animals and to weigh them automatically. A second hardware component was a hand reader. Here, the aim was to identify the animals automatically and to transfer data messages to the national I&R data base via PDA (birth, arrival, departure, death).

Material and methods - Study 1

Study 2

Study 3

The second period of this study ran from July 2005 to December 2006. The aim of the study was to investigate the management and practicality of several hardware components in parallel operation under practical conditions. 388 animals (cows, heifers and calves) were applicated with electronic ear tags. The hardware components were: a automatic digital balance (see periode 1), a calf feeder, 2 concentrate feeders, a selection unit, and 2 walk through detections (Albers, 2007).

**Results and
discussion -
Study 1**

A correlation of 0.82 between the temperature values messured by the injectable transponder and messured by a common thermometer shows that the automatic messured temperature is a quite good indicator for hyperthermy or hypothermy. But also differences between both methods were found. In average, the transponder temperature was 1 K lower than the rectal temperature. In the second week pp. the difference of 1.5 K was even higher than in the weeks after. A reason was found in the influence of the outside temperature. Because there was not so many tissue between the transponder and the air outside, the temperature messured by the transponder was lower (Kamann *et al.*, 1999).

When a controlled artificial hyperthermy was implemented, a correlation of 0.82 between injectable and rectal temperature was found regarding the increasing and decreasing body temperature (Kamann *et al.* 1999).

Study 2

The correlation of 0.74 between bolus temperature and rectal temperature was also high (Klindtworth *et al.*, 2006). But bolus temperature has to be corrected when animals are drinking water. A former experiment showed the high influence of water intake (Figure 2). The bolus temperarture was reduced when the animal drank a lot of cold water. Because of the application in the Reticulum the bolus temperature was influenced in these cases (Klindtworth, 2004).

Study 3

558 electronic and 796 conventional ear tags were applicated in both periedes. 2 electronic ear tags (0.36%) had a malfunction at a first test before applicating. 5 electronic ear tags (0.9%) and 45 conventional ear tags (5.6%) disappeared during the study.

A combination of a hand reader and a commercial PDA is possible. The data exchange with the national I&R data base worked without any problems. 5 008 readings with the hand reader and 1 180 readings of the automatic digital balance were carried out in the first periode, in both cases 100.0% of all detections worked correctly. When modifying the automatic digital balance as a walk through detection, 98.41% of all detections were successful.

Table 2 describes the result of the second periode. The automatic digital balance, the calf feeder, the concentrate feeders, the selections unit, and the walk through detections worked well with a detection rate of 99.8, 100.0, 100.0, 100.0, and 99.9%, respectively. But the detection rate was reduced at selection unit and walk through detections up to 78.0 and 49.0%, when these devices worked in parallel operation without a synchronisation. In spite of a distance of 12 m between these units (twice the distance as in the manual denoted), the two devices influenced each other's detection. Working in separate operation, the detection rate was high (Albers, 2007).

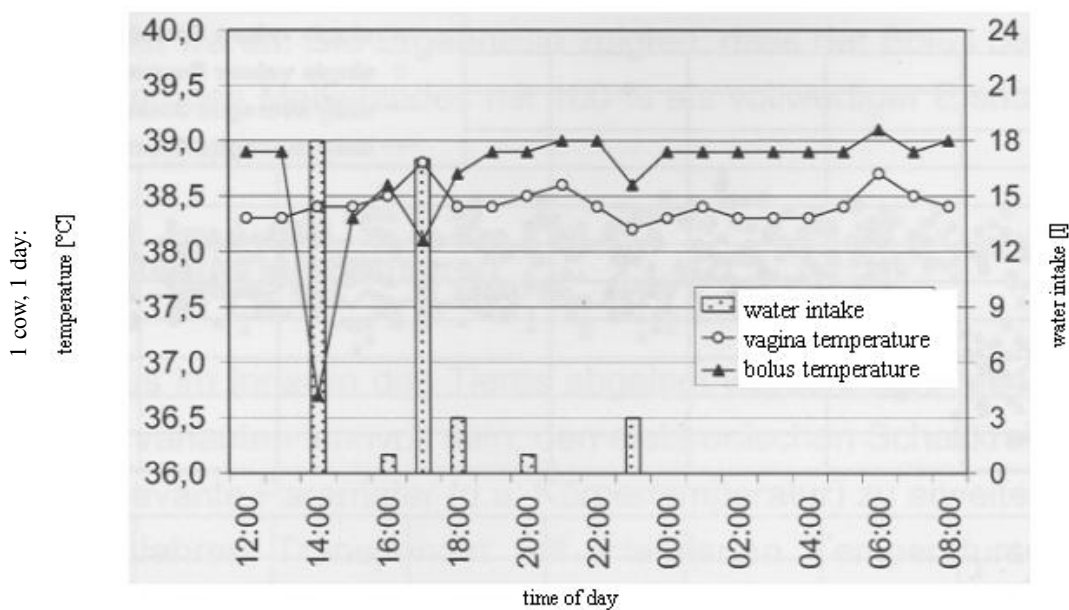


Figure 2. Water intake, bolus temperature and vagina temperature of one representative cow (Klindtworth, 2004).

Table 2. Detection rates in period 2 of study 3.

Unit	No. detection	% detection	Notes
Automatic digital balance	16 332	99.8	Power supply, humidity
Calf feeder	83 808	100.0	Only HDX
Concentrate feeders	202 498	100.0	
Selection unit	34 776	100.0	(78.0% detection rate)
Walk through detection	9 936	99.9	(49.0% detection rate)

Table 3 presents the number of replaced conventional plastic ear tags in the region of Lower Saxony. Between 2001 and 2005 the number of replaced ear tags decreased as well as the ratio between replaced ear tags and applicated ear tags. In 2005 this ratio was 5.65% and as high as the ratio of replaced conventional plastic ear tags of study 3 (5.6%).

Replacing one conventional plastic ear tag with an electronic ear tag, the number of replaced ear tags can be reduced. Study 3 demonstrated that the ratio of replaced ear tags can be reduced from 5.6% to 0.9%. The number of replaced ear tags can be reduced to 58.0% of the two conventional plastic ear tag scenario:

$$0.5 \times T + 0.5 \times [0.056 \times (0.009)^{-1}] \times T = 0.58 \times T$$

where T is the number of replaced ear tags when both tags are conventional).

**Economic aspects
using electronic ear
tags**

Table 3. Replaced plastic ear tags in Lower Saxony between 2001 and 2005.
(http://cdl.niedersachsen.de/blob/images/C25574155_L20.pdf; own results, 2005, not published)

Year	Registered cattle	Applied ear tags	Replaced ear tags	%
2001	2 827 016	5 654 032	679 899	12.03
2002	2 719 416	5 438 832	697 046	12.82
2003	2 661 117	5 322 234	497 065	9.34
2004	2 586 887	5 173 774	347 610	6.72
2005	2 561 585	5 123 170	289 698	5.65

Due to the high labor cost in Germany, it makes sense to reduce the number of replaced ear tags. Additionally, benefits are expected if manual work can be reduced using automatic reader at big cattle collection points like abattoirs or collection stations for animal export. Concerning all costs and savings, it is difficult to calculate the benefits of decreased number of accidents regarding ear tag application.

Conclusion

Electronic identification of bovine animals is possible. Identification with electronic ear tags is easy and reliable. Integration of electronic ear tags and readers into the on-farm production engineering is possible and reliable to operate, but a technical synchronisation of different systems is necessary. Input for administration, farm management and work flow can be reduced using electronic animal identification systems. The integration of electronic ear tags is the next step to automatize the data management on farm and the data exchange between business partners. Concerning all costs and savings, electronic ear tags are not automatically more expensive than plastic ear tags.

Further developments of RFID technologies can lead to get more information about animals. The combination of an identification system and sensoric measurement (temperature, pH, etc.) are interesting both for practical farmer and for experimental barns. At the moment, these combinations can only be carried out using bolus or injectable transponder. But using electronic ear tags is more practicable on farm and on abattoirs.

Furthermore, the continuous data flow between different systems (process control, management software, data bases) makes more standardization of data interfaces, formats and algorithms necessarily, especially on international level.

List of references

Albers, D. 2007. Erfahrungen mit elektronischen Ohrmarken in Niedersachsen – Projekt ITeK-Rind. In: Ministry of Nutrition, Agriculture and Forest (editor), Proceedings of the 1st National Meeting Elektronische Tierkennzeichnung in der Landwirtschaft, Fulda.

IDEA. 2002. Identification électronique des animaux. Joint Recherche Centre of the European Commission. Final report, Version 5.2.

Kamann, B., K. Klindtworth, G. Wendel, W.D. Kraetzel, H. Schön and J. Hartung. 1999. Automatische Gesundheitsüberwachung mit Hilfe von injizierbaren Temperaturtranspondern in der Kälberaufzucht. In: Landtechnik Weihenstephan (editor), Proceedings of the 4th International Meeting Bau Technik und Umwelt in der landwirtschaftlichen Nutztierhaltung, 249-254.

Klindtworth, M. 2004. Von der elektronischen Tierkennzeichnung zum Gesundheitsmanagement. VDI-Max-Eyth-Gesellschaft (editor), VDI-Berichte 1865, 123-138.

Klindtworth, M., H. Kätker, K. Markmann and H. Jürgens. 2006. Untersuchung verschiedener Temperaturmessverfahren beim Kalb. Project thesis, University of Applied Sciences Osnabrück.

Prinkelman, H. and G. Kern. 1994. Einsatzerfahrungen mit injizierbaren Transpondern in der Rinderhaltung. In: KTBL-Arbeitspapier 258, Injektate zur elektronischen Tieridentifizierung, KTBL Darmstadt, 96-100.

The importance of recording of AI data for the genetic systems. The context of AI from service to genetic progress

J. Philipsson¹ & H. Jorjani²

¹*Dept. of Animal Breeding and Genetics, SLU,
P.O. Box 7023, SE-750 07 Uppsala, Sweden*

²*Interbull Centre, SLU,
P.O. Box 7023, SE-750 07 Uppsala, Sweden*

The application of Artificial Insemination (AI) in cattle breeding in the 1940's was primarily done in order to eradicate diseases transmitted through the use of bulls for natural services. AI became an important tool to improve the fertility in dairy cows. However, it was soon realised that AI also was a mean for more wide-spread use of good bulls, thereby contributing to genetic improvement of the cattle stock. The technology status and lack of knowledge at that time on efficient methods for genetic evaluation and selection meant though that genetic improvement in production was marginal, whereas traditional selection for conformation was enhanced. Also fertility of bulls was improved as selection pressure was put on bull's libido and semen quality to get an efficient AI service.

The great importance AI plays in modern breeding programs of today, rely heavily on the following three building blocks:

1. The invention and full use of frozen semen
2. The recording and technical development of data handling through consistently more capable computers
3. Increased knowledge on the genetics of fertility and development of efficient methods for genetic evaluation of fertility

In the following the implications of these developments will be discussed in the context of efficient use of AI data and its opportunities and challenges.

Introduction

AI as a breeding tool changed the breeding program structures globally

The wide-spread use of frozen semen, whereby individual bulls could be used for up to several hundreds of thousands of inseminations, completely changed the structure of breeding programs both nationally and globally. The opportunities to store semen meant that a number of smaller countries collected the semen of individual bulls necessary for use also as a proven bull in a few months time as a young bull, and then the bulls were slaughtered. After progeny test results were obtained semen of only the best bulls were used, while the semen of all the others was thrown away. It was a cost effective breeding program, provided the population was limited. When opportunities opened for export of semen of genetically superior bulls the scene looked different. Both for health control reasons and access to semen of the very best bulls for many farmers the progeny tested bulls had to be kept alive until the progeny tests were known. This so-called lay-off system meant that all young bulls were used to get reasonably accurate progeny tests after which they were layed off until some of them were selected according to their daughter performance for wide-spread use.

Internationally the opportunities for extensive use of individual bulls at a rather cheap price meant that many bulls were used in the same countries all over the world. The “holsteinisation” of the black and white Friesian cattle is the most striking example of globalised use of semen contributing to a total change of a whole breed in just a couple of generations. However, this development took place much faster than the development of genetic tools did to make the most wise selection decisions for breeding programs to be sustainable.

Today the major dairy breeds of the world are kept in more than one country and are served by AI studs marketing their semen not only nationally but also internationally on a highly competitive market. Such a development can only be sustainable if breeding programs include a broad range of economically important traits under various environmental conditions. The knowledge gained in recent decades on the genetics of a number of auxiliary traits important for the functionality of cows has provided new opportunities. These assume though that you have accurate registration of all breeding records to get correct pedigree information, and that you have the ability to compare bulls for all traits across AI studs and nations.

Computerized AI records – basis for genetic studies and fertility improvement

In early days of AI activities they were handled by special AI organizations with technicians responsible for reporting of all inseminations for both administrative reasons and for the needs to follow up the fertility records of individual bulls. Simple measures, such as percentage of Non-Return Rate (NRR) within certain intervals after the insemination, were effectively used to monitor the fertility of AI bulls. Two important developments have followed and which have had dramatic impact on the opportunities for an effective AI service as a basis for not only a continuous improvement of fertility but also for providing the information necessary to automatically construct pedigree records of all recorded animals.

The first development referred to is the integration of AI records with milk-recording information and from other sources of information such as disease records, conformation classifications, slaughter data etc. (Figure 1). The greatest advantage of such an integration of

AI data with the other sources of information is that it can automatically provide the pedigree information needed for genetic studies of all traits recorded, i.e. production, conformation, calving traits, fertility etc. and the genetic evaluations of these traits. Organizations involved in dairy cattle production including AI and milk-recording

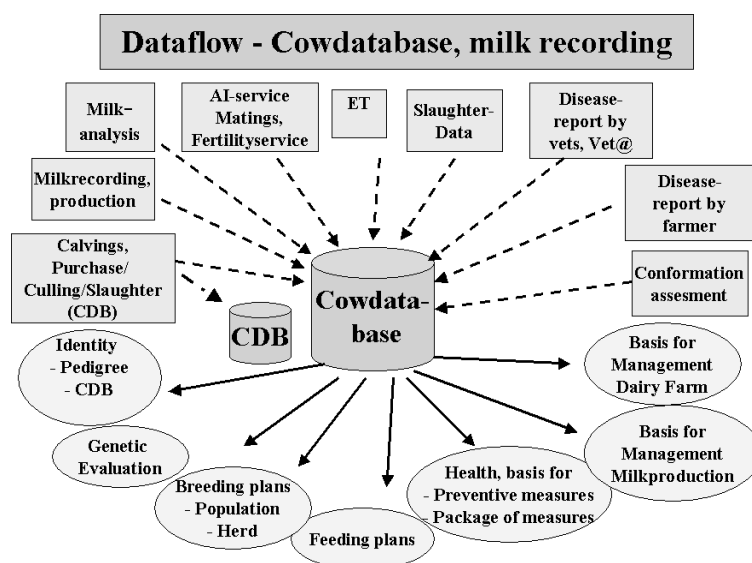


Figure 1. Example of an integrated cow data base including AI records (from Philipsson et al., 2005).

merged in Sweden already in the 1960's enabling both computerization and a successive integration of data from all sources. This development was early followed in the other Scandinavian countries and made genetic studies of cow fertility and its relationships to other traits possible already 2-3 decades ago. Today such integrated cow information systems are available in many countries.

The role of an integrated data base for research and genetic evaluations can be illustrated as in Figure 2 showing the principal relationship between recording schemes delivering relevant animal data and the continuous feed-back from research for improvement of such practical applications as genetic evaluations and use of the results for selection.

The value of an integrated data base containing the information as envisaged above depends on the amount of data and the correctness of the information. In the Swedish case 87% of all dairy cows are recorded and about the same number of animals is

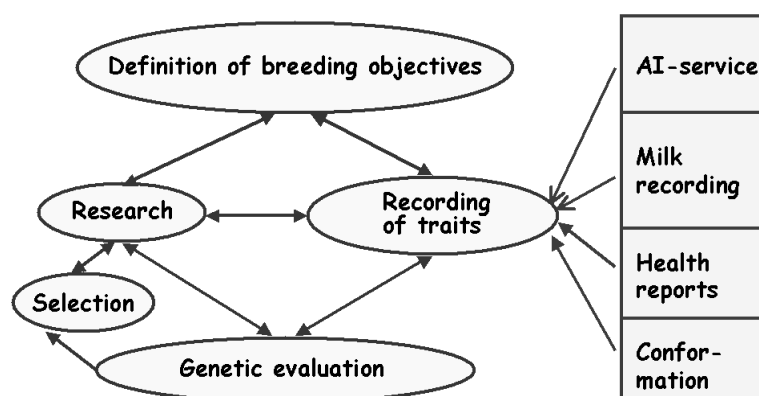


Figure 2. Interactive parts of a breeding programme.

used with AI. Thus, very good opportunities are given for research as well as for efficient application of results for e.g. management at herd and company levels and for genetic evaluations.

The second development refers to the restructuring of the AI organizations leading to fewer inseminations by employed technicians in favour of more do-it-yourself inseminations by the herdsmen. This development easily leads to less accurate or incomplete recording of inseminations, which may seriously hurt the opportunities to monitor individual bull's fertility as well as the completeness of pedigree recording in the herds.

Fertility – a complex of interacting traits...

The interaction of a number of traits at the endocrinology and morphology levels constitute the cow fertility as measured in a pregnancy following successful heat detection and insemination. The complex of fertility traits as can be measured in various ways can be divided into the following three categories:

1. Ability of the virgin heifer to show estrus with visible heat signs
2. Ability of the cow to resume the reproductive cycle post-partum and show visible heat symptoms
3. Ability to become pregnant following insemination

Fertility in virgin heifers and lactating cows must be considered as different traits as it is a difference to show good fertility when the cow is under lactation stress compared when she is not having that stress. Genetic correlations between heifer and cow fertility measures are usually around 0.6-0.7 (Roxström *et al.*, 2001).

Practical measures of fertility used for herd management as well as for genetic evaluation purposes are based on records reported by AI technicians or herdsmen that practice do-it-yourself. Most commonly used is the interval from calving to first insemination (CFI) for the second category, and no. of inseminations (NINS) or NNR as measures of pregnancy rate. Days open (DO) and calving interval (CI) are combinations of these measures, but are restricted to only cows conceiving and which therefore are somewhat selected.

New measures of estrus and heat symptoms include records of pedometers as the activity of cows increase when they are in heat. A more sophisticated method is based on regular measures of progesterone in the milk during a critical period post-partum, whereby the time of ovulation can be more accurately recorded, but at a higher cost (Petersson, 2007).

Some of these measures may not be as easily recorded when certain interventions are practiced such as heat synchronization, having a bull free among heifers in loose-housing systems or on pasture.

... which show low heritability... but large genetic variation among progeny groups!

It is a well-known fact that fertility traits generally show low heritability. In one of the most extensive studies in recent years heritability measures were generally in the range 2-4% (Roxström *et al.*, 2001). This level of heritability has been confirmed in a number of studies comprising different countries and breeds. For international genetic evaluation of female fertility traits more than 150 heritability values are submitted for different breeds and traits, of which 80% have a value of 4% or less (Interbull, 2008). Previously it was thought also that the additive genetic variation in cow fertility was small due to both the low heritability values and the fact that non-additive genetic effects usually are important for the variation in fertility. Thanks

to the availability of AI records integrated with milk recording statistics since the early 1970-ies in Sweden it was possible to show empirically that there was a large variation in fertility measures between large progeny groups within both the Swedish Friesian and the Swedish Red cattle breeds (Philipsson, 1981). In fact it was shown that the additive genetic standard deviation for female fertility (measured as coefficient of variation) amounted to about 7%, compared to the usual 8-10% for milk production. This meant that there was a difference of 15-20% in pregnancy rate among progeny groups.

It is now undisputable that cow fertility is unfavourably correlated with milk production. This was shown already by Janson and Andreasson (1981) on Swedish data and later on confirmed in many studies. In Sweden the correlations are generally of the order 0.3-0.4, which clearly means that fertility will decline as a result of selection for production if not selection pressure is also put on fertility. Similar results have been observed for other countries and breeds and the negative correlations are of the order 0.2-0.5 (VanRaden, 2006; Jorjani, *et al.*, 2007). There is also another relationship of practical importance: cows that in classifications are considered angular or “sharp” have a genetically inferior fertility than other cows according to a study involving data from Sweden, Denmark and USA by Rogers *et al.* (1999). This means that selection according to traditional conformation classifications has led to a further deterioration of cow fertility. Such deterioration is costly. In most dairy populations fertility problems are already the most common reason of culling cows (e.g. Pryce *et al.*, 1997) indicating the necessity to apply methods for direct selection for female fertility.

The availability of fertility records, primarily based on AI records, and accurate pedigree information enabled a genetic evaluation system to be put in place in Sweden already in the mid-seventies. It was gradually improved when the BLUP procedure became available and as a result of the research conducted by Janson (1980) and Roxström (2001). The necessity to consider female fertility as an important sub-trait in the Total Merit Index (TMI), as previously developed by Philipsson *et al.*, (1975) was well demonstrated by Philipsson and Lindhé (2003). An unchanged or slightly improved fertility was shown for the SRB breed along a strong increase in production, whereas a steady decrease of the fertility was noted in the Black and White cattle due to its “holsteinization” and lack of selection for female fertility when choosing bull sires.

Today many countries apply genetic evaluations for their major dairy cattle breeds. In the last two years this development has led to the implementation of international genetic evaluations for fertility by Interbull. In the last routine evaluation (April 2008) data from six breeds originating from 20 countries, comprising up to 5 traits from each country were included in the analyses of in total 50 populations.

As a result of these international evaluations AI bulls can be compared across countries not only for production, conformation, calving traits, mastitis resistance and longevity but now also for a number of female fertility traits. As a side effect it is now also possible to monitor the genetic trends in different traits by breed on a global scale. As an example Figure 3 shows the genetic trend for a number of fertility traits of the Red Dairy Cattle breeds dominated by the Scandinavian red breeds. It is

Unfavourable correlations with production

National and international genetic evaluations for female fertility

The global genetic trend for fertility differs between breeds

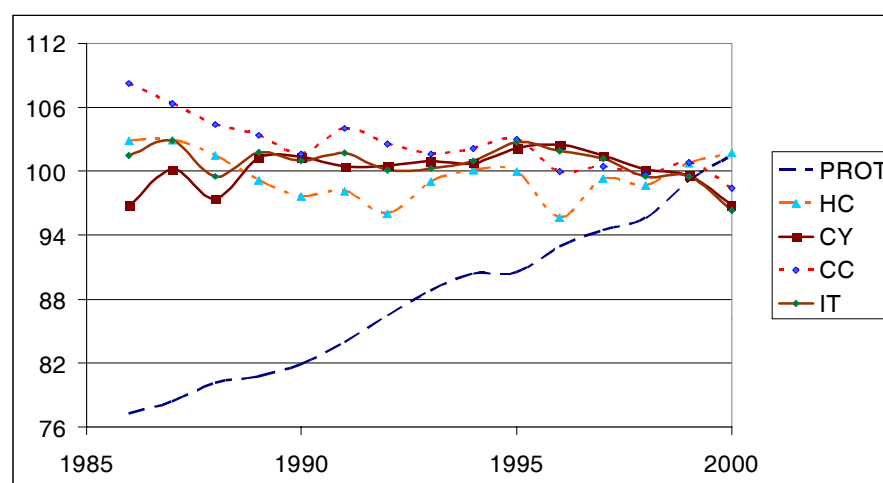


Figure 3. Genetic trends for production and fertility traits of bulls of Red Dairy Cattle populations.

(PROT=Protein, HC=heifer conception, CY=Cow re-cycling ability, CC=Cow conception, IT=Interval traits).

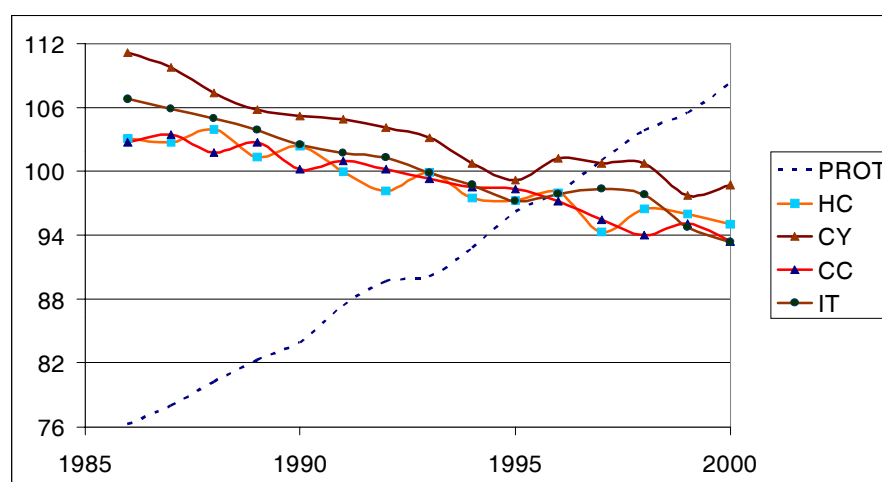


Figure 4. Genetic trends for production and fertility traits of bulls of Holstein populations.

(PROT=Protein, HC=heifer conception, CY=Cow re-cycling ability, CC=Cow conception, IT=Interval traits).

obvious from this figure that fertility traits, measured as heifer's conception (HC), cow's re-cycling ability (CY), cow's conception (CC), and interval traits (IT, days open/calving interval), have been kept rather unchanged over a long period of time. At the same time a strong increase in protein yield (PROT) has taken place.

The trend for the same traits in the Holstein populations (Figure 4) gives a clear indication that fertility has seriously declined during the same period. This is the result of lacking information on breeding values for female fertility when bull sires

have been selected all over the world in this breed. Thus, the decline is a function of the unfavourable correlations with production and with some conformation traits traditionally being selected for.

It is obvious from what has been presented that cow fertility is an important trait that needs to be considered in national breeding programs as well as globally. The negative genetic trend detected for the Holstein breed globally needs to be seriously discussed and acted upon internationally. Such trends should be regularly monitored at both national and global level for all breeds in order to re-evaluate the relative weights of traits in the breeding objectives.

The opportunity to estimate reliable breeding values for female fertility of AI bulls depend heavily on the complete and accurate recording of all breeding events and calving dates. Specific considerations must be devoted to the recordings by herdsmen when they are themselves inseminating the cows. Also handling records from natural services and of synchronized heats may be worth studying in more detail in order to make best use of these and to make sure they are not messing up other information, e.g. expected calving dates, calving intervals etc. Of utmost importance is anyway that the AI service holds such a quality and price that it is the first choice of any farmer, and that these are provided with such information that they understand the needs for correct and complete records for both on-farm statistics to be used for management purposes and for the calculation of both the bull's own fertility and for estimation of breeding values for female fertility.

Female fertility in dairy cattle is made up of a complex of traits that can be indirectly measured from AI and milk-recording statistics. The heritability is low for all fertility traits but the genetic variation is still substantial as demonstrated by large differences among progeny groups in daughter fertility. There is a clearly unfavourable genetic correlation between fertility and production, indicating the needs for direct selection for improved fertility. The application of genetic evaluation systems for female fertility depends on the opportunities for accurate and complete recording of all breeding and calving dates and that all AI records are integrated with all other trait records. Additional methods for heat detection may improve future evaluation systems. The recently applied international genetic evaluations for fertility by Interbull provide new opportunities for selection of AI bulls across countries. Genetic trends in female fertility should be monitored in all breeds at both national and global level.

Interbull. 2008. International Bull Evaluation Service, <www.interbull.org>. Accessed 2008-06-04.

Janson, L. 1980. Studies on fertility traits in Swedish dairy cattle. II. Genetic parameters. *Acta Agric. Scand.* 40, 427-436.

Jansson, L., Andreasson, B. 1981. Studies on fertility traits in Swedish dairy cattle. IV. Genetic and phenotypic correlation between milk yield and fertility. *Acta Agric. Scand.* 31, 313-322.

Future challenges

Conclusions

List of references

Jorjani, H., Jakobsen, J. H., Forabosco, F., Hjerpe, E., Fikse, W.F. 2007. An International Perspective on Breeding for Robustness in Dairy Cattle. 58th Annual meeting of the European Association for Animal Production, Year 2007. Book of Abstracts 1: 4.

Petersson, K.-J. 2007. Milk Progesterone as a Tool to Improve Fertility in Dairy Cows. Doctoral Thesis No. 2007: 46, Swedish University of Agricultural Sciences, Uppsala, Sweden.

Philipsson, J. 1981. Genetic aspects on female fertility in dairy cattle. Livest. Prod. Sci. 8: 307-319.

Philipsson, J., Janson, L., Brännäng, E. 1975. Avelsindex för tjurar med avseende på ekonomiskt betydelsefulla egenskaper. LantbrHögsk. Meddn A 238.

Philipsson, J., Lindhé, B. 2003. Experiences of including reproduction and health traits in Scandinavian dairy cattle breeding programmes. Livest. Prod. Sci. 83: 99-112.

Philipsson, J., Eriksson, J.-Å., Stålhammar, H. 2005. Know-how transfer in animal breeding – the power of integrated cow data bases for farmer's selection of bulls to improve functional traits in dairy cows. EAAP Publication No. 117, 85-95. Wageningen Academic Publishers, The Netherlands.

Pryce, J. E., Veerkamp, R. F., Thompson, R., Hill, W. G., Simm, G. 1997. Genetic aspects of common health disorders and measures of fertility in Holstein Friesian dairy cattle. Anim. Sci. 65, 353-360.

Rogers, G.W., Banos, G., Nielsen, U.S. 1999. Genetic correlations among protein yield, productive life, and type traits from the United States and diseases other than mastitis from Denmark and Sweden. J. Dairy Sci. 82, 1331-1338.

Roxström, A. 2001. Genetic aspects of fertility and longevity in dairy cattle. Doctoral Thesis. Agraria 276. Swedish University of Agricultural Sciences, Uppsala, Sweden.

Roxström, A., Strandberg, E., Berglund, B., Emanuelson, U. & Philipsson, J. 2001. Genetic and environmental correlations among female fertility traits and milk production in different parities of Swedish Red and White dairy cattle. Acta Agric. Scand. 51, 7-14.

VanRaden, P.M. 2006. Fertility traits economics and correlations with other traits. Interbull Bulletin 34, 53-56.

Various systems used to record and process AI data on farms: summary of the ICAR questionnaire

L. Journaux & A. Malafosse

UNCEIA, MNE, 149 Rue de Bercy, 75595 Paris Cedex 12, France

Now days, laptops and PDA are very frequently used by AI technician in farm to record data and transmit them to central databases. This paper describes the situation in different countries and the reasons why AI centres decided to develop these tools.

Key words: *Artificial insemination records, Laptops, Computing equipment, Data exchange.*

The use of laptops computers and personal digital assistant (PDA) had a huge development during the past 20 years. They are now common tools for a large number of tasks including those in artificial insemination.

The ICAR working group on artificial insemination and relevant technologies (WG AI&RT) suggested getting a better view of use of these equipments by AI technician, the exchanges with central or national database and the use of additional technologies to have an identification of straws with an automatic reading. We sent a questionnaire to the major actor of AI in a very large number of countries. We present now the synthesis of the answers. The quite low number of answers is not enough to establish statistics but their variety is a good indicator to describe a large number of situations coming from different continents (Europe, Oceania, and America). Our picture is quite good for AI centres providing technician AI service. It's more difficult to have a good idea of the situation for farmers practicing Do It Yourself or for freelance AI technician.

From all the answers except one, all AI technicians use computing equipment on farm.

The 2 types of equipments (Laptops or PDA) are used. It's difficult to say if one system is more popular than the other one. For example, in France PDA is used about for a third of the services, but this proportion is increasing during the last 5 years. Technicians seems to use only laptop in Finland, and only PDA for Westgen in USA or LIC in New Zealand.

Summary

Introduction

Computing equipment of technicians of AI centers

Table 1. type of equipment of AI technicians (employees or freelance)

Structure	Country	AI activity considered	Nb of technician	Freelance	PDA percent ¹	Laptop Percent ¹
A.N.A.F.I.	Italy	2 500 000	1 000		99	
Swissgenetics	Switzerland	922 033	186		95	
CIAQ	Quebec	57 800	205			100
FABA Service						
Coop	Finland		249			100
ABLN	Portugal	121 690	38		100	
Gencor	Canada		64		98	5
SHIUZ						
Sp. Z o.o.	Poland	537 720	1 595			
West gen	USA		7	1 200	100	
	New Zealand					
LIC	Zealand	3 400 000	900		100	
UNCEIA	France	6 000 000	1 700		35	60
AI Services	North					
NI	Ireland	50 000	30		100	
Genex	USA	2 000 000	400	10	55	25

¹Percent of activity managed with.

Westgen has the specificity to integrate in his own information system the 1 200 freelancers who are working with their own equipment in western Canada.

The motivations to develop the equipment of the AI technicians are by descending interest for the countries:

1. To reduce processing delay.
2. To improve accuracy of data recording for the genetic system (pedigree-fertility EBV etc).
3. To avoid recording errors.
4. To save overhead or processing costs.

Others items like "To launch semen traceability systems", "To improve management (billing booking etc) at client level" or "To develop services to farmers directly by the organisation or on request of other organisations" are evaluated from different way by the different countries. Some of them is considering it as very important and others countries as below average.

Equipment and specific softwares are used:

1. To record and validate AI by checking against a data base (embedded on the device or remote computer)
2. To print AI forms on farm

With a lower frequency it's used to:

1. To store reproduction records of herds.
2. To match AI data with other data stored in the technician data base (calving, movements of straws)

These tools are also used to manage the semen storage and movements for the technician container only.

There is data exchange between technician's computers for all types of data (technical, financial, trade) with the Central data base of the company. In some situations, technician has a direct access to a central database (national or shared with other structures) different from the company data base for technical data. Exchanges are daily.

In all the situations, AI information participates to 3 types of valorisations: validation by the system processing data for genetic purposes (consistence-integrity....), use for genetic evaluation of fertility, use for parentage recording and pedigree printing.

French and The Netherlands are the only two countries using automatic reading at large scale.

In France, the interest of the use of this computing solution is increased by the use of a bare code on the straw to facilitate the identification by automatic reading.

The French AI companies (Semen collecting centres and AI centres) agreed for a common bare code printed on straws consisting of:

- Sire ID (internal ID 5 digits).
- Date (number of days since 1st of January 2002, 4 digits).
- Batch inside collect of semen (1 digit).

This code is 10 digits long and uses the standard 128C.

The reasons to develop this system were to improve semen traceability at the level of the batch and recording accuracy. It's also a tool to improve efficiency of tools recording AI data, to improve evaluation of male fertility by using ejaculates characteristics and to experiment semen processing methods.

Today about in a third of AI the straw with bare code is read automatically. This proportion is increasing quickly because a larger number of AI centres use now on field bare code readers.

The reading results are very good with about 98% of success with all the types of readers.

With this return of experience, Cattle QualiVet - Group (Witschi , 2006) and ICAR WG AI&RT (Malafosse, 2007) decided to propose a recommendation for a standardisation of bare code on straws. The propose is to propose a unique identification of semen collecting centres (SCC) based on NAAB code data base and a code allocated by ICAR for SCC that not participate in the NAAB program. The structure of the bare code will integrate this Identification of SCC and a free part of 10 digits. This proposal is in progress and a recommendation will be proposed to the general assembly of ICAR.

Computing equipment of breeders practicing do it yourself to manage and exchange AI data

It's very difficult to have sound information regarding the equipment of the DIY breeders and the way of management of AI activity.

In every the country, a part of the services of DIY farmers is notified by paper forms. But exchange of data using specific software's or internet portal is in progress.

An additional tool : the automatic reading of the straw

Sending of data is less frequent for farmers than for the AI technicians, generally once a month. Data are generally transmitted to regional data base processing any technical records (parentage, milk recording...) or to herd book data base

The use of this information is exactly the same than for the information coming from AI companies (validation by the system processing data for genetic purposes, use for genetic evaluation of fertility, use for parentage recording and pedigree printing).

Conclusion

It should be worth to improve the description of the situation. New answers to the questionnaire are welcomed and the ICAR WG AI&RT will update the summary and publish it at the ICAR web site.

Computing solution using laptop or PDA is now very frequent for AI technicians. The functionalities are very similar except the adaptation of the specific country's legislation or database organisation.

The next step will be certainly the standardisation of straw identification systems. Bare code is a first good example of the place of ICAR WG AI&RT in this field.

Acknowledgements

For the structures who answered to the ICAR questionnaire:

- A.N.A.F.I. (Italy).
- Swissgenetics (Switzerland).
- CIAQ (Quebec).
- FABA Service Coop (Finland).
- ABLN (Portugal).
- Gencor (Canada).
- SHIUZ Sp. Z o.o. (Poland).
- Westgen (USA).
- New Zealand Animal Evaluation Ltd (New Zealand).
- UNCEIA (France).
- AI Services (North Ireland).

List of reference

Witchi U. 2006, Position of the QualiVet Group Concerning Barcoding of Straws, September 2006, pp. 1.

Malafosse A. 2007, Barcode identification of straws, DRAFT V.1 proposed after the meeting in Dublin on August 22nd, September 2007, pp. 3.

Use of insemination data in cattle breeding; some experiences from Ireland

A. Cromie¹, F. Kearney¹, R. Evans¹, D. Berry² & D. Wilhelmus³

¹*Irish Cattle Breeding Federation,
Highfield House, Bandon, Co. Cork, Ireland*

²*Teagasc, Dairy Production Research Centre,
Moorepark, Fermoy, Co. Cork, Ireland*

³*Wageningen UR, Animal Sciences Group, The Netherlands*

Experiences from Ireland have indicated many potential uses for insemination data in cattle breeding including;

1. Genetic evaluations for traits of economic importance, e.g., gestation length.
2. Better breeding and management advice for farmers, including sire advice facilities and fertility management reports.
3. More accurate invoicing and stock control systems for AI service providers.

These three main benefits, coupled with major improvements in technology for recording insemination data in Ireland, e.g., AI handheld technology and web-based systems of recording, has resulted in the quantity and quality of insemination data available for Irish cattle breeding doubling in the past three years (+115%). Similar improvements are being targeted over the next 3-5 years (currently some 40% of all inseminations on farms are recorded on the cattle breeding database), reflecting the high value placed on insemination data within the Irish cattle breeding industry.

Key words: *Insemination, Technician recording, Data edit, Genetic evaluation.*

Insemination records have many potential uses in dairy and beef cattle breeding. In this paper we give some experiences from Ireland, regarding the role of insemination data in Irish cattle breeding. The paper will be divided in three distinct components;

1. Collection of insemination data.
2. Use of insemination data in ICBF genetic evaluations.
3. Use of insemination data as a support tool in decision making within the Irish cattle breeding industry.

In addition, we will also give some insights into our future plans for the recording and use of insemination data in the Irish dairy and beef breeding programs.

Summary

Introduction

Collection of insemination data

Trends in Recording

The ICBF Cattle Breeding database was first established in January 2002 (ICBF, 2007). Whilst the initial work was largely focused on birth registration and milk recording data, the introduction of new genetic evaluations for gestation length (and calving performance) in 2005, coupled with a desire by AI service providers to move away from manual processing of insemination records, resulted in an increased emphasis in the potential importance of Artificial Insemination (AI) data in Irish cattle breeding.

As a result, the level of AI data recorded in the ICBF database has more than doubled in the past 3 years, from 305,311 insemination records in 2005 to 654,724 records in 2007, an increase of some 115% (Table 1). This figure represents some 40% of all inseminations taking place in Ireland on an annual basis (some 1.5 million inseminations take place annually across 2.2 million dairy and beef cows).

Table 1. Trends in recording of insemination data.

	2005	2006	2007
Technician AI	213 719	291 081	498 073
DIY AI	91 396	137 046	156 651
Total AI	305 115	428 127	654 724

Technician recording of AI data

The main “driver” of this growth has been the introduction of AI handhelds, which are used by technicians, to record AI data on farms. This technology allows the AI technician link directly to the ICBF cattle breeding database (via GPRS), ensuring fast and accurate recording of insemination data on each individual dam (and sire). In addition to providing information for cattle breeding purposes, i.e., the genetic evaluation of gestation length, the new handheld technology also allows ICBF and AI service providers provide many more services to end-users, including;

- *Inbreeding and lethal gene checks.* By having a copy of all animals on the farm, including their ancestry on the handheld, inbreeding and lethal gene checks can be performed on all potential matings.
- *Breeding Advice.* ICBF HerdPlus (see ahead) provides farmers with a sire advice facility, the results of which can be stored on the handheld for use by the technician at the time of AI.
- *Fertility management reports for farmers.* Which provide farmers with valuable benchmark information for their herd e.g., 3 week submission rate reports,
- *Fertility management reports for AI service providers.* Which provide AI service providers with valuable benchmark information for their business e.g., Conception rate reports for AI sires and individual technicians.
- *Semen invoicing and stock control.* Access to “real-time” information on all insemination data allows for much more effective and efficient management of their business by AI service providers.

The other key driver of the growth in recording of AI data has been technology improvements to facilitate easier farmer recording of “Do-it-Yourself” (DIY) AI data. Of the 156,651 farmer recorded inseminations in 2007, 9% were via Animal Event sheets (paper-base recording of AI data by the farmers), 63% were by Animal Events email (electronic recording of AI data by farmers via farm computer packages), and 28% were via electronic recording of AI data by farmers over the ICBF website (www.icbf.com). This last option was only made available to farmers in 2007, and represents an excellent return after only its first full year of operation.

Farmers recording of AI data

Future efforts in the area of data collection will continue to focus on the use of handheld technology (by both technicians and farmers) and web-based recording of insemination data. This year (Spring, 2008) saw a further increase in the number of AI companies and technicians using handheld technology to record insemination data (up from 150 technicians in 2007 to 240 technicians in 2008). Combined these technicians represent some 90% of the total technician inseminations in Ireland. In terms of recorded AI events by farmers, we will continue to improve our web-based systems for recording AI data, as well examine options for direct recording of AI data by farmers via PDA’s (Pocket Digital Applications) and also mobile phones. However, it should be noted that successes in these latter two areas will be completely driven by our ability to provide farmers with valuable management information to help promote the benefits of farmer recording. Without good reports, Irish farmers will see little tangible benefit in recording this data.

Future plans

Currently insemination data is used in 2 key areas;

1. Data edits for genetic evaluations of female fertility, and
2. Genetic evaluation of Gestation Length.

Future work will focus on the role of AI data to evaluate other traits of economic importance for Irish farmers, e.g., Interval traits, and its potential role in sire verification at the time of birth registration.

Use of insemination data in ICBF genetic evaluations

Female fertility is a trait of major economic importance for Irish farmers and represents about 34% of the relative weighting in the dairy Economic Breeding Index (ICBF Annual Report, 2007). Female fertility is evaluated on the basis of daughter calving interval (300-600 days) and survival% with records above 600 days set to missing. Concerns had been expressed by Irish farmers and the breeding industry that the exclusion of these records could result in proofs being biased downwards for lower fertility bulls and cows. By having access to insemination data, ICBF can now establish as to whether an attempt has been made to inseminate the cow and if so, then include this full calving interval record in the evaluation. The net effect of this change has been to introduce a further 3% of records into genetic evaluations for female fertility (Table 2). Test evaluations carried out in November indicated that correlations were generally high (>0.93 across AI sires and cows), with sires having the highest proportion of daughters in the 600-800 bracket, penalized most in the new evaluations. This new edit was therefore introduced into the routine evaluation for female fertility in February 2008.

Data edits for genetic evaluation of female fertility

Table 2. Use of Insemination data to Improve Edits for Genetic Evaluation of CI (Days).

Parity	1	2	3
Old evaluation (Nov 07)	805 762	649 783	502 161
New evaluation (Nov 07)	834 794	671 959	517 301
Difference	+29 032	+22 176	+15 140

Genetic evaluation of gestation length

Due to the seasonal nature of cattle breeding in Ireland (60% of all calves are born during the months of February, March and April - EAAP, 2007), gestation length (both direct and maternal) are traits of major economic importance for Irish farmers. In fact, the economic value of calving interval (one of the objective traits in the dairy EBI) has been evaluated at $\square 11$ /day, for each day over 365 days (www.icbf.com). Genetic evaluation of gestation length was first introduced in February 2005, using a univariate Animal model approach in ASREML (Gilmour, 2007). Some results for AI sires (>40% reliability only) from the last evaluation run (May 2008) are presented in table 3.

To date some 750 000 gestation length records have been collected through the ICBF cattle breeding database (i.e., recording of insemination event and subsequent Animals Events birth registration). Heritability estimates for this trait are some 40% (see table 4 for latest genetic parameter estimates), indicating considerable genetic variation in this trait within the Irish cattle population. For example, the difference between the Limousin and Belgian Blue beef breeds, based on Irish data, is typically 4 days in PTA terms (or 8 days in breeding value terms). In addition, all of the breeds show a within breed difference of at least 4 days (in PTA terms), which is very positive from a breed improvement standpoint. The genetic differences (and breed rankings) are also consistent with the phenotypic data collected on farms (Table 3).

Table 3. Genetic Evaluation of gestation length (Direct) for popular breeds (May 2008).

Breed of AI sire	No. sires evaluated	Phenotypic data		Genetic data (PTA's)	
		Mean	St Dev	Mean	St Dev
Holstein	1 796	281.9	5.6	-1.0	0.98
Friesian	242	281.5	5.4	-1.5	1.07
Limousin	166	289.6	6.2	3.6	0.98
Charolais	153	288.5	6.0	2.3	0.89
Belgian Blue	131	284.6	5.8	-0.3	0.94
Angus	121	283.8	6.1	-0.3	0.87
Hereford	119	286.4	6.0	0.8	0.91
Simmental	95	288.5	5.9	2.3	0.93
Montbéliarde	93	286.9	5.8	1.4	1.03

Future work on the use of insemination data in ICBF genetic evaluations will focus on a number of key areas, including;

Future Plans

Current research work by ICBF, in conjunction with Wageningen UR, is focused on introducing a number of new improvements to how we evaluate gestation length. These include;

Improvements to genetic evaluation of gestation length

1. the inclusion of direct and maternal effects in the genetic evaluation model,
2. breaking 1st and later parity records into 2 separate traits, and
3. including data from other calving traits of economic importance (i.e., calving difficulty and calf mortality) into a single multi-trait evaluation. Initial results (for gestation length only) are summarized in table 4

The above analysis is based on records from some 590 000 records from Holstein Friesian dairy cows, with parameters estimated from a Sire-MGS model, using MIX99 software (Mantysari, 2008). The initial results confirm the high heritability for direct gestation length (~40%), with a high genetic correlation across parities (0.74). The heritabilities for maternal gestation length are also of major interest, given their close biological association with female fertility (especially calving interval). Heritabilities are also high (in this regard), with a correlation across traits on 0.89. Correlations between direct and maternal effects are generally close to zero. We anticipate releasing these new gestation length evaluations to the Irish breeding industry in September 2008, with a view to making them official by the end of the year.

In addition to gestation length, there are a number of other insemination traits that are of interest to ICBF and the Irish breeding industry, including female fertility (especially compactness of calving traits) and male fertility. This work is being undertaken in conjunction with Teagasc, Moorepark (Berry *et al.*, 2007, Evans, *et al.*, 2007 and Twomey *et al.*, 2008). Again initial results are promising, especially for the female fertility traits (Table 5), indicating that these traits could be used as additional predictors of calving interval in future evaluations of female fertility.

Genetic evaluations for other insemination traits of economic importance

The next stage of this work will focus on estimating genetic correlations between insemination traits and calving interval, with a view to selecting appropriate early predictors of female fertility. Again we anticipate having this work completed and implemented by the end of this year.

Table 4. Genetic parameters for gestation length¹.

	GL Days; 1 st Parity (Direct)	GL Days; Later Parity (Direct)	GL Days; 1 st Parity (Maternal)	GL Days; Later Parity (Maternal)
GL Days; 1 st Parity (Direct)	0.36	0.74	0.01	-0.03
GL Days; Later Parity (Direct)		0.44	0.03	-0.24
GL Days; 1 st Parity (Maternal)			0.04	0.89
GL Days; Later Parity (Maternal)				0.08

¹Heritabilities on the diagonal and genetic correlations above the diagonal.

Table 5. Mean and heritability estimates for female fertility traits.

	Parity	Mean (days)	Heritability	St. Error
Calving Interval	1	383	0.047	0.004
	2	382	0.031	0.004
	3	381	0.034	0.005
Calving to 1 st Service	1	75	0.019	0.006
	2	73	0.012	0.006
	3	71	0.021	0.010

Validation of sire births

One additional advantage of having access to insemination data is its potential to validate sires at the point of birth registration (as misidentification of sires can cause biases in genetic evaluations). Initial work by ICBF has indicated that, based on some 57 000 births in January, February and March 2008 (the result of inseminations in April, May and June 2007), the average error rate between the sire identified through the technician recorded insemination event and the sire identified by the farmer at the point of birth registration was 6%.

Of particular interest is the fact that the error rate appears to increase over time (breeding seasons in Ireland typically last about 10-12 weeks), suggesting that as the breeding and calving season progresses, establishing the correct sire becomes more difficult due to a combination of stock bulls (which are often joined with the herd at the end of the fixed AI period) and a certain level of farmer apathy (at the end of a long breeding and calving season). Based on these initial results, we intend to carry out further work, with a view to introducing this check as a component of our routine birth registration process.

Table 6. Validation of sire identification between insemination and birth record¹

Month of Insemination	Number of insemination and birth records*	Number of sire errors	Error rate
Apr	17 341	488	2.8%
May	25 102	1 769	7.0%
Jun	6 192	914	14.8%

¹Number of records within allowable gestation length range of 280-290 days.

Use of insemination data as a support tool in decision making

One of the major benefits of having access to insemination data is its potential role as a support tool for farmers and people involved in the cattle breeding industry. Examples where AI data is currently used to make better breeding and management decisions within Ireland include;

1. Farm fertility management reports.
2. Sire Advice Information.
3. AI management systems.

The ability to benchmark performance is a critical component of profitable dairy and beef farming. Having access to increasing volumes of insemination data has allowed ICBF develop valuable calving and fertility reports for Irish farmers. These are marketed directly to farmers through the ICBF HerdPlus service. An example of one such report is the “Final Fertility Report” (Table 7), which includes herd and National summary information on a range of important calving and fertility traits.

In addition to individual herd fertility reports, ICBF also provides “discussion group” reports, for those farmers involved in Teagasc discussion groups (some 100 groups and 1 500 farmers in total), which allows participating farmers benchmark their herd performance against their group peers as well as National performance data.

*Farm fertility
management reports*

Table 7. Summary of key fertility parameters for ICBF HerdPlus herds¹.

Trait	Mean	St Dev
Calving Date	25/02/2007	11.7 days
Calving Interval	370.5	11.3 days
Total cows calved	84	48
Mating Start Date	20/04/2007	10.4 days
Total Cows Calved and Served	72	40
21 Day Submission Rate (%)	59.8%	15.4%
42 Day Submission Rate (%)	77.5%	12.8%
Pregant to first service (%)	53.9%	16.0%
6 Week Pregnancy Rate (%)	58.4%	15.2%
Overall pregnancy	90.8%	7.8%
Total AI Serves	1.8	0.6
Not in-calf	9.2%	7.8%
Length breeding season	14 Weeks	4 weeks

¹Summary statistics are based on 725 Spring Calving Herds, which received final fertility reports in October 2007.

In addition to fertility management reports, ICBF HerdPlus also offer farmer access to a “Sire Advice” facility, as an additional support tool. Suggested sires are identified for each farmer based on a combination of his defined goals, the genetic merit of his herd, the genetic merit of available AI sires and possibilities for close matings and/or lethal gene combinations. After selecting his preferred sires, these are then allocated to individual animals in the herd in advance of the start of the breeding season. The list of suggested matings are then returned to farmers via either;

1. Breeding charts (for DIY AI users) and/or
2. Directly to handhelds (for users of an AI technician service).

Over 1 700 farmers used the sire advice facility this year (Spring 2008), with the average EBI of bulls selected being equivalent to the average of the top 20 bulls on the ICBF Active Bull List.

Sire advice information

**AI management
information**

As well as providing valuable benchmark tool for farmers, the availability of insemination data can provide AI service providers with valuable benchmark tools for tracking the performance of AI Sires, laboratory procedures and individual AI technicians. Close monitoring of reports on traits such as non-return rates can help to quickly identify potential problems in each of these three key areas.

Future plans

Future work in this area will concentrate on developing further fertility management reports (including group reports), as well distilling the volume of insemination data down to a number of key performance indicators that will help farmers (and AI service providers) during the breeding season. Getting information back to farmers in a quick and efficient manner is a high priority in this regard, with the role of mobile phone technology seen as a key component. In addition, we are currently looking at ways to improve the effectiveness of ICBF Active Bull List, by using information on insemination data to ensure that the bull list always active and up to date for dairy and beef farmers.

**List of
references**

Berry, D.P., Coughlan, S, Evans, R. 2007. European Association of Animal Production, Annual Proceedings, Dublin, August, 2007, <www.icbf.com/publications/files/Sire_fertility_preliminary_analysis.pdf>.

Evans, R, Coughlan, S., Berry, D.P. 2007. European Association of Animal Production, Annual Proceedings, Dublin, August 2007, <www.icbf.com/publications/files/Female_fertility.pdf>.

Gilmour, A.R., Cullis, B.R., Welham, S.J., & Thompson, R. 2007. ASREML Reference Manual. New South Wales Agriculture, Orange, Agricultural Institute, Orange, NSW, Australia.

ICBF Annual Report. 2007. <www.icbf.com/publications/files/Report_May_2008_ver_7.pdf>.

Lidauer, M., Matilainen, K., Mantysaari, E., Strandén, I. 2008. MIX99 Reference Manual, Agrifood Research Finland.

Valorisation of AI data on farm by AI technicians: French experiences

A. Malafosse & L. Journaux

UNCEIA, MNE, 149 Rue de Bercy, 75595 Paris Cedex 12, France

The purpose of this paper is to present initiatives taken in France in term of equipment of AI technicians to improve their capacity of valorisation of recorded AI data and to develop services to farmers. A brief description of collective valorisations of AI data at national level is also presented.

Summary

Key words: Artificial Insemination, AI technicians, Databases, Valorisation.

Artificial Insemination (AI) is organised in France as a service to farmers, provided by AI centres, companies in legal form of AI co-operatives or unions of co-operatives. The goal of this collective organisation is to provide AI service to any farmer whatever it's location on the national territory, the herd size, the breed, along with bull semen fulfilling it's needs according to it's production system. This is like a public service. In France the average number of heads by holding is relative small is the European context: 39 cows, with few small herds and few large herds. Therefore an efficient network of AI technicians, employees of co-operatives, has been set up to render services to any farmer all around the year. In average a herd owner demanding AI service gets 50-60 visits of AI technicians each year (33 1st AI / year /herd). Therefore AI technicians are well considered as essential partners by farmers and are important relay for proposing services. As a consequence, besides AI, AI centres through their technician network, offer a large range of services according to companies' strategy: semen sale, prevision of matting including organisation of progeny testing, oestrus synchronisation and pregnancy diagnosis, infertility monitoring and reproduction improving programmes, sale of feedstuffs. AI technicians are also involved in the embryo transfer programmes offered by AI centres.

Introduction

Semen units are produced by AI companies carrying out selections programmes including progeny-test on behalf of AI centres providing AI services, from bulls either on progeny test either proven with a good reliability. It should be mentioned that changes in regulation and in advanced molecular technologies (implementation of MAS) will have as consequence that bulls without progeny test but with good reliability may be proposed for AI service (major dairy breeds). At the present time

selection programmes are implemented for 16 breeds (1 000 bulls progeny tested) in order to satisfy the needs of the farmers in dairy and beef breeds. AI technicians play an important role in implementing selection programmes: test AI, breeding dam sires, collecting blood samples for various purposes.

Valorisation of AI technician work needs computer equipment

Taking the advantage of the existing network, AI centres have developed some initiatives to enhance efficiency of their technicians. Equipment with laptops computers is a part of this strategy.

Reasons for equipment

The first AI centres that decided to equip AI technicians have several goals.

- Technical reasons:
 - To record accurate AI data including official female identification for any cow (it was a new idea in the eighties), and other items to describe the act. This includes a checking process at farm level to avoid transmitting wrong data in the company's database.
 - To reduce processing delay was also a goal for a better management of companies (figures by bulls and technicians) and reproduction programmes (Non Return Rates).
 - To develop tools for farmers for a better management of reproduction and fertility issue, and then to propose new services.
- Management and commercial issues:
 - To improve administrative management at farmers level (billing, booking)
 - To get a better follow up of clients activity and to propose services
 - To propose AI services for non users.

History of equipment

A reflexion has been developed beginning the eighties to think about the opportunity to build special devices dedicated to AI technicians. But technical development made available micro-computers on the market and then the first attempts took place in mid eighties.

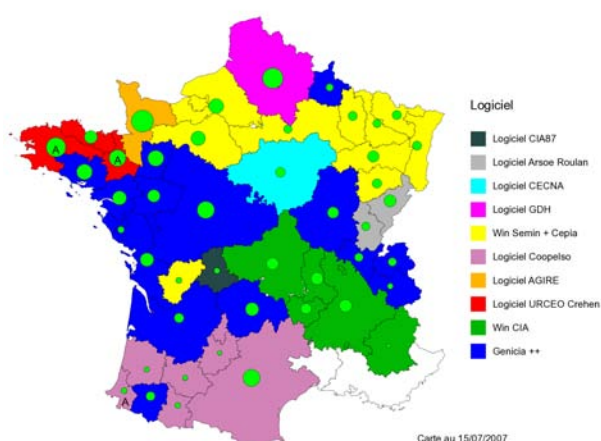
Large developments occurred when lap tops computers with enough capacity and speed became available in the nineties. Beginning the century, PDA became available: a new possibility to equip AI technicians came up.

Then the decision taken by *UNCEIA* to organise systematic reading of bar-codes on semen straws, was a strong sign to generalise equipment of AI technicians.

Today, equipment of AI technicians is on way of generalisation, with various systems and software (*logiciels*) according to companies strategy (see map below, where circles are proportional with AI activity).

Two main strategies to equip AI technicians

The data processing systems of AI centres is organised in taking into account the existence of the National Information System for Genetic Data (*SNIG*) and the National Identification and registration data base (*BDNI*). National system consist in shared software and data bases implemented on 11 computing sites to manage data before transmitting and computing breeding values at *INRA*. There are in these data bases any information coming from the herds on recording schemes (parentage, milk records, type, AI...) and identification of cattle, births and movements of any



herd. Access rights have sorted out between the ministry of agriculture and the professional bodies so that AI centres have access to these data along with their partners.

To facilitate access to any data and to organise services farmers organisations have used the “Minitel” developed by the national phone company (little computer terminal available to any costumer), which is an ancestor of the Internet. This has shaped the organisation of various companies and created an “electronic” culture in some regions of France.

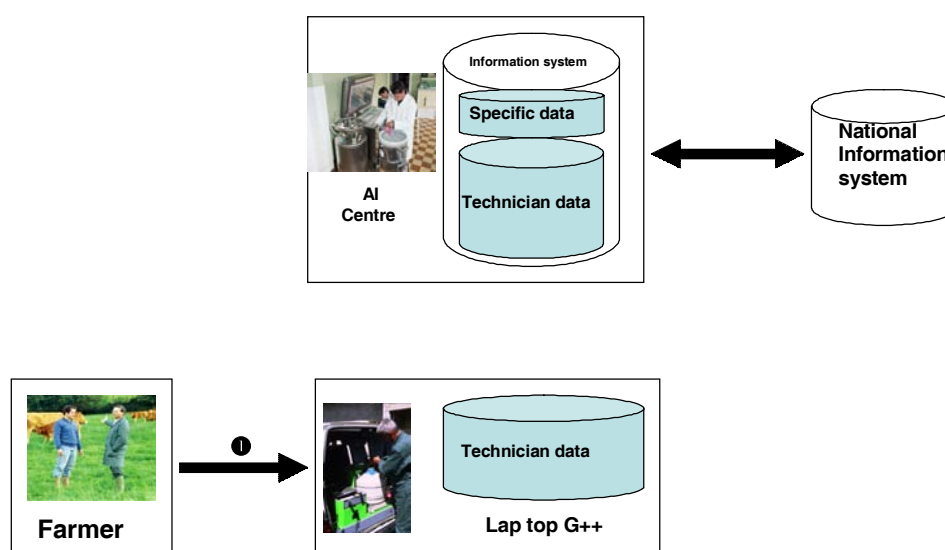
Two main strategies have been developed by AI companies to equip technicians with computers according to the envisaged role and responsibility:

- Maximum responsibility to AI technicians. Then their laptops include a large data base and software to take in charge any potential task (administrative, technique, service). It is described below as the “*bottom up scenario*”.
- To secure AI data recording. Recording AI and billing is prepared at AI centre head quarter and then transmitted to AI technicians that finish recording after work on farm. It is described below as the “*bottom down scenario*”.

- Organisation (see scheme below)
Farmers call AI technician who organise its daily round (1). Data base of AI technicians contains any data useful on farm: client ID, ID of female bred or not bred by AI, reproduction history-calving-AI-oestrus synchronisation-pregnancy diagnoses, ID AI bulls + breeding values, semen stocks, prevision of matting, accounts, invoices, money collecting, for any herds of clients, including DIY farmers, on AI centre area.
If technicians are organised by group, each of them has the same data set. Records of an activity period (day) are sent by a special line from technician home to a central data base (2) that process records and then transmit new data to any technician to refresh their data base (3). This database exchanges continuously with specific data of the AI centre and the National Information System.

Bottom up scenario
(*Genicia ++ on the map*)

- On farm
Procedures are available to AI technicians to choose female to be inseminate and requested bulls by scrolling. Then AI records are validated by consistency of data against laptop database and central data base.
Software executes then billing and booking process, before printing invoices and technical documents: AI form, fertility issues (alerts -abnormal calving-AI intervals, % of cows with 3 AI and more- analysing reproduction records, report and propositions).
Semen storage and movements are automatically recorded for traceability.
- Other
Data recorded for reproduction issues are available for farmers.
Records on oestrus synchronisation and pregnancy diagnosis are processed like AI records. Software takes in charge sales (semen units, feed stuff etc..)



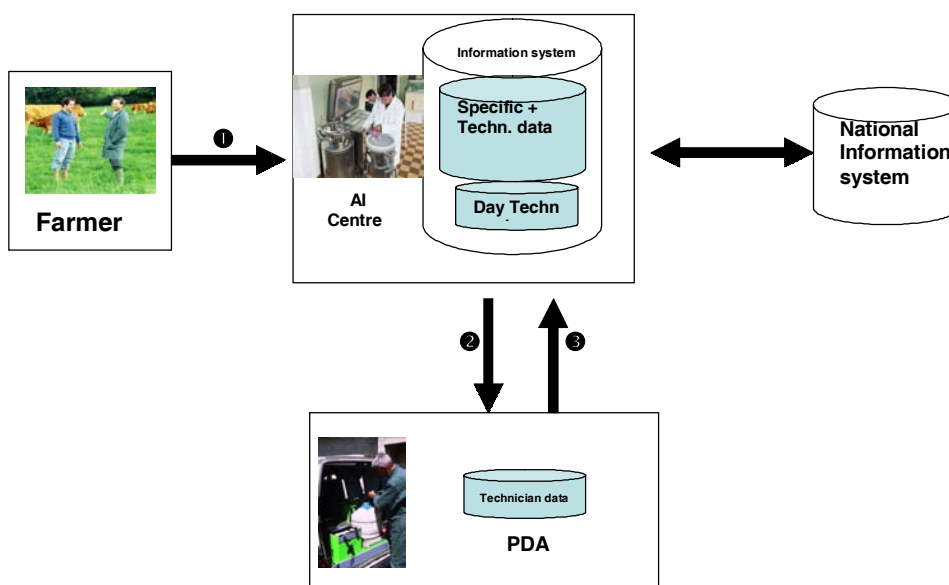
- Integration in data processing systems.
 - AI centre runs a central data base that gets any records mostly overnight. Field technical and booking data are then rapidly available for easy processing programmes.
AI centres transfer specific company's data to technicians –prices-bulls and semen stocks-accounting situation when necessary.
 - The National data processing system transmit to AI centres females ID and movements, calving, some performance data genetic evaluations of bulls and cows. It receives then AI records from AI centre.
- Organisation (see scheme below)
In this scenario demands for service are managed by the AI centre thought the Internet today (*Minitel* in the past). Farmers call the AI centre and are connected to it's database (1).

The AI centre system downloads from its database only data necessary for technician round of the particular day (females ID to be inseminated, pre-allocated semen...) and these data are transferred to the technician's PDA data base (2), which contains clients ID and data common to any farmer, such as bulls ID, price list etc.

Back home AI technicians connect PDA to the AI centre database for validation and up-dating (3).

As in the bottom up scenario, AI centre database exchanges continuously with the National Information System to get ID, performance records, GE...

- On farm AI technician confirms pre-recorded data after AI, by validation and establishes invoice(s), billing and booking being mostly done by company. Then he prints AI forms, other technical documents and invoices. Software records semen movements for traceability.
- Other
Thanks to functions of PDA, AI technicians may sale services and semen to farmers, but reproduction issues are tackled by other technicians of the AI centre.
This database exchanges continuously with specific data of the AI centre and the National Information System.



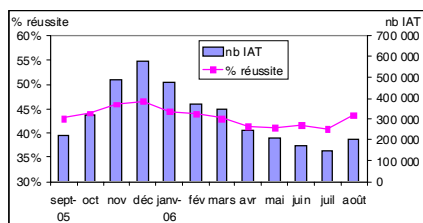
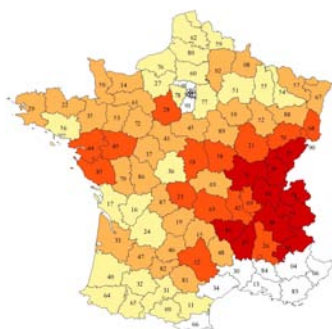
- Integration in data processing systems.
 - AI centre runs a central data base that gets any records overnight. Field technical and booking data are then rapidly available for easy processing programmes.
AI centres transfer specific company's data to technicians –prices-bulls and semen stocks-accounting situation when necessary.
 - The National data processing system transmit to AI centres females ID and movements, calving, some performance data genetic evaluations of bulls and cows. It receives then AI records from AI centres

**Bottom down
scenario (Logiciel
URCEO on the map)**

Collective valorisations

1. Improvement of parentage recording.
Even if there are no systematic figures on it, one may assume that quality and accuracy of AI records have been improved through automatisisation of recording (mainly on female ID). A next step will reach with the bar-code reading of semen straws. Therefore quality of parentage recording mainly based on mating records will improve.
2. National research project on fertility
The systematic and exhaustive transmission of AI data of good quality to the national data base render possible large scale studies on non return rates (NRR). Below is reproduced a summary of such a study on the various differences of NRR on the national territory (best NRR in dark, poorest in light colour). It shows difference between territories, breeds, months, climate, reproduction management and suggests causes for further research project.
3. Genetic evaluation of fertility.
Genetic evaluation on fertility has changed in 2007 in France. Trait on evaluation is then the conception: was AI successful or not? All AI and calving data for cows and heifers are used for the genetic evaluation. The evaluation is carried out with very large set of data: 40 millions of AI records, 90 millions animal ID movements and pedigrees, 90 millions lactations (350 test records). Below is a table presenting distribution of AI records by breed and parity in 2007.

Non return rates : why they differ?



Existing differences: breed, production systems, climate reproduction management, (season linked or not), average age of herds, yield performance...

Conditions +	Conditions -
Montbéliarde High % AI in winter High % AI on heifers Average yield level Few AI with Holstein bulls	Holstein breed Distributed AI over year (many AI in spring) Low replacement rate High yield level AI with Holstein bulls
Genetic make-up? Feeding systems ?	

Breed	AI on cows	AI on heifers	Total animals
Prim Holstein	11 128 315	9 308 126	21 189 286
Montbeliarde	1 883 919	1 602 059	3 182 955
Normand	1 729 154	1 405 035	2 925 477
Abondanc	76 300	55 016	131 355
Pie Rouge	52 591	36 382	88 754
Brune	83 625	61 996	134 492
Tarentaise	32 595	21 934	48 504
Simmmental	80 641	57 495	118 630

The model used is the animal model with a bi-variate evaluation cows/heifers fertility. It should be mentioned that other traits like production are taken into account for the GE.

Thanks to AI processing many effects related to AI records are taken into account: month, day of week of AI, year x technician, interval AI- calving intra x caving rank for cows, calving rank before AI. The other important effects are genetic effect unknown parents (introduced in 2008), Permanent environment, year x herd effect, heifer age, breed of bulls, bull x year, inbreeding % of cow and calf to be born.

As a practical result of the organisation of AI data processing and recording thanks to AI technicians devices, it should be mentioned that in February 2008 all AI records have been registered in the national database 7 days after the day of AI which is a remarkable figure, in full line with the above settled goals.

Generalisation of equipment of AI technicians has many causes such as consolidation of the industry in France, the willingness to trace semen doses as much as possible, the development of tools to provide better services to farmers.

Valorisation of AI data is then a continuous process and a challenge in a more competitive industry.

Conclusion

The impact of new technologies on performance recording and genetic evaluation of dairy and beef cattle in Ireland

A. Cromie, B. Wickham, S. Coughlan & M. Burke

*Irish Cattle Breeding Federation, Highfield House,
Bandon, Co. Cork, Ireland*

New technologies in performance recording have played a critical role in helping develop Irish dairy and beef cattle breeding programs. Fundamental to this has been the establishment of the central cattle breeding database, which allows ICBF quickly expand into new technological opportunities, e.g., EDIY milk recording, Handheld technology and Image data from abattoirs. In addition, a strong emphasis is placed on business partnerships, where the overall goal is to “add value” to information collected on Irish cattle, by linking together systems from across the industry, e.g., marts and abattoirs. The end result of these improvements has been a substantial increase in the quantity and quality of data available for cattle breeding, resulting in increased profitability for Irish farmers and the dairy and beef industries.

Key words: *performance recording, EDIY milk recording, Handheld technology, Carcass image data, Weanling performance, Business partnerships.*

Irish Cattle Breeding Federation (ICBF) commenced operations in 1998, with the objective of achieving the greatest possible genetic improvement in the national cattle herd for the benefit of Irish farmers, the dairy and beef industries and members.

Since its inception, much of ICBF’s work has been focused on improving the quantity and quality of data available for cattle breeding. New technologies have been tapped into and business arrangements established (with both shareholders and industry stakeholders alike), with the overall goal of ensuring that Irish farmers have access to high quality information on which to breed more profitable cattle.

In this paper we identify some of the major data recording developments over the past 10 years, with particular emphasis on “new technologies” for performance recording. These have included;

1. The ICBF Central Cattle Breeding Database.
2. EDIY Milk Recording.

Summary

Introduction

3. Handheld Technology (AI, linear scoring/weight recording and lameness).
4. Carcass image data (from abattoirs).
5. Weanling performance data (from “Farmers Marts”).
6. Web-based recording systems.

In addition, we will discuss the importance of developing strong business partnerships with shareholders and industry stakeholders, as well as give some insights into futures plans for performance recording in Ireland.

The ICBF cattle breeding database

Cattle breeding data in Ireland is recorded in two main databases:

1. The CMMS database (Centralised Movement and Monitoring System) as operated by the Department of Agriculture (DAF) in accordance with relevant EU regulations for animal traceability (www.agriculture.gov.ie).
2. The ICBF Cattle Breeding Database, as operated by the Irish Cattle Breeding Federation on behalf Irish dairy and beef farmers and the wider cattle breeding industry (www.icbf.com). Both databases operate in complete synchrony. This is a major plus for Irish farmers and the cattle breeding industry as information must only be provided once, with data flows allowing data to be shared between all relevant stakeholders.

The ICBF database has been fully operational for dairy, beef, milk recording, beef performance recording, genetic evaluations and herd books since 2005. Some 30 000 herds, with 1.1 million calvings (representing half of the Irish cattle herd) were participating in one or more aspects of the database by the end of 2007 (Table 1). Indeed, the number of herds involved in the ICBF database has more than doubled in the past few months (over 60 000 herds are now involved), with the launch of the new “Animal Welfare, Recording and Breeding Scheme for Suckler Cows” by DAF and the Irish beef industry. A key component of this scheme is the recording of all relevant “Animal Events” data through the ICBF cattle breeding database.

Looking at trends in data recording over the past 6 years (Table 1), indicates a dramatic increase in the quantity and quality of data available for cattle breeding as result of the establishment of the central database. For example the number calving performance events recorded in 2001 (via the National AI progeny test program) was 18 183, compared to 478 234 in 2007, a factor increase of 26.3 times. Similar trends are apparent for other traits, most notably slaughter records, which have increased by a factor of 300 times. Historically these records (including data for milk recording, linear scoring and weight recording) were collected as part of the services provided to Irish farmers through the National progeny test program and/or herdbook/milk recording services. Each of these services had their own separate system resulting in much duplication by farmers and the industry. The establishment of the ICBF database has removed this duplication, at farm level. In addition, the establishment of the shared linkage for CMMS data (with DAF), has resulted in a cattle breeding system that can deliver high levels of quality data for genetic improvement of dairy and beef animals in Ireland.

EDIY milk recording

The level of milk recording in Ireland is somewhat lower than in other developed dairy countries (typically 30% of cows are recorded in Ireland compared to >50% in countries such as UK, Netherlands and the Nordic countries; ICAR, 2008). In an attempt to address these low levels of performance recording, a new milk recording service (EDIY milk recording using the Tru Test electronic meter) was launched to

Table 1. A comparison of the level of performance recording in Ireland (2001 vs. 2007).

Data flows	2001 ¹	2007	Relative increase
Department of Agriculture (DAF)			
- CMMS Births	0	1 111 569	New data
- Slaughter records	2 450	756 911	308.9
ICBF Animal Events/HerdPlus			
- Animal Event Births	0	606 326	New data
- Pedigree birth registrations	85 416	87 832	1.03
- Calving performance	18 183	478 234	26.3
- DIY AI serves	0	156 651	New data
- On-farm linear scoring	9 809	14 362	1.46
- On-farm weight recording	6 039	7 863	1.30
- Farmer mart weight recording	0	159 231	New data
Herdbooks			
- Dairy linear scoring	15 386	23 329	1.52
Milk Recording Organisations			
- Milk recording	336 868	428 170	1.27
AI Companies			
- Technician serves	18 183	498 073	18.8

¹Data recorded via AI progeny test, herdbook& milk recording systems.

dairy farmers in 2006 (after an initial 2-year trial period). Response to the new service has been very positive amongst farmers and industry alike with the percent of cows in milk recording now approaching 40% (Table 2). Furthermore, of the 428,179 cows in milk recording in 2007, some 28% of these were recorded using EDIY, which reflects the value placed in this new service. Recent feedback from farmers and the industry has indicated that the key benefits of the new service have been:

1. A reliable technology (i.e., durable and easy to use).
2. A reduction in cost (due to removal of paper recording and an electronic link to the ICBF database).
3. Better integration between the ICBF database and laboratory systems.

ICBF anticipates rolling additional EDIY cells (currently there are some 20 cells in operation throughout Ireland), over the coming years, with a 5-year goal of having 60% cows in milk recording by 2013.

Table 2. Trends in EDIY milk recording (2004-2007).

	2004	2005	2006	2007
Total dairy cows	1 121 000	1 101 000	1 087 100	1 079 800
Cows in milk recording	381 425	380 196	408 375	428 179
Percent total dairy cows	34.0	34.5	37.6	39.7
Cows in EDIY milk recording	7 231	30198	99562	119890
Percent milk recorded cows in EDIY	1.9	7.9	24.4	28.0

Handheld technology

Handheld technologies are currently being used in 3 areas of ICBF's performance recording business:

1. Technician recording of Artificial Insemination data.
2. Technician recording of linear score and weight recording data on farms.
3. Technician recording of lameness data. Each of these technologies is based on the principle of electronic data capture of performance data and then transfer of this data to the central database via GPRS technology.

Technician recording of AI data

There has been a major increase in the level of insemination data recorded in the ICBF database over the past 3 years (Table 3). The main "driver" of this growth has been the introduction of AI handhelds, which are used by technicians, to record AI data on farms. This technology allows the AI technician link directly to the ICBF cattle breeding database (via GPRS), ensuring fast and accurate recording of insemination data on each individual dam (and sire). In addition to providing information for cattle breeding purposes, i.e., the genetic evaluation of gestation length, the new handheld technology also allows ICBF and AI service providers provide many more services to end-users, including:

1. Inbreeding and lethal gene checks.
2. Sire advice options for farmers.
3. Fertility management reports for farmers and AI service providers.
4. Better semen invoicing and stock control for AI service providers.

Linear scoring and weight recording data

Technician recording of beef linear score and weight recording data was first introduced in 2006. Prior to this date, data was manually recorded and keyed into the database for subsequent reporting and genetic evaluations. The technology used is the same as that for the AI handhelds, with adaptations of the software to cover the range of beef linear and weight recording traits. Some 14 362 beef linear scores and 7 863 weight records were collected via these handheld in 2007 by a total of 8 regionally based technicians. A further adaptation of the software to cover dairy linear scoring has just been completed and tested and is currently being rolled out by Irish Holstein Frisian Association as part of its services to members and to the dairy breeding industry.

Lameness data

In addition to the above traits, work has also been completed on the collection of lameness data on commercial dairy farms by Farm Relief Services (FRS). Again the existing handheld technology will be used, with adaptations to cover the range of lameness traits. Whilst this work is still at trial period it is hoped that that, in the future, the handhelds will become a routine part of the "hoof-care" business, thereby providing ICBF with valuable lameness data, as well as covering the administrative requirements of FRS.

Table 3. Trends in recording of insemination data.

	2005	2006	2007
Technician AI	213 719	291 081	498 073
DIY AI	91 396	137 046	156 651
Total AI	305 115	428 127	654 724

In addition to collecting beef performance data on live animals (e.g., linear score and weight recording data – see above), ICBF also has access to high volumes of carcass data, through its relationship with DAF and the abattoirs (a total of 756 000 records were collected from abattoirs in 2007 – Table 1). This data is reported to DAF (by the abattoirs) for the purpose of EU price reporting and a copy then forwarded onto ICBF (by DAF) for purpose of genetic improvement of carcass traits. The carcass traits received from DAF includes:

1. Cold carcass weight.
2. EUROP scale for conformation and fat score (on a 1-15 basis), with the data then being stored in the cattle breeding database for the provision of breeding and management data for Irish beef farmers.

The latter data (the EUROP scores) is of special interest as it is derived from images collected and stored within the carcass grading machines, rather than from subjective classification by an inspector. ICBF are currently working with Teagasc and the providers of the carcass grading machines to extend the predictive ability of the software to cover carcass cut data, in addition to EUROP grade and score. This would be a major step forward for the Irish beef industry as it would give Irish beef farmer's access to information on the bulls and cows which are breeding animals with high weights (kg) of high value cuts. Initial work in this area (based on dissected data collected in a commercial abattoir) is very positive and indicates significant variation in these traits (Table 4)

Table 4. Genetic parameters for Carcass Cut Data (Pabiou, 2008)¹.

	Carcass kg	Sirloin kg	Fillet kg
Carcass kg	0.59 (0.20)	0.62	0.75
Sirloin kg		0.55 (0.20)	0.75
Fillet kg			0.62 (0.20)

¹Heritabilities on the diagonal and genetic correlation above the diagonal.

A further novel aspect of beef recording systems in Ireland is the presence of farmers marts. There are some 70 marts across the country, trading over 2 million animals per year (usually between the breeder of the animal and owner for subsequent "finishing" to slaughter). A significant "added value" to this activity is the electronic capture of weight and price data. Recent work by ICBF has indicated that there is a high value to this type of information, especially where the sire is known and the weanlings (150-300 days) are being sold as singles, and alongside cohorts from the same herd. Although the loss of data is large (for example of the 159 231 records retrieved from marts in 2007, less than 10 000 made it into genetic evaluations for direct weaning weight), ICBF expects this to become a valuable source of data in the future, due to the advent of the new Suckler Cow Welfare Scheme (referred to earlier) and the introduction of improved recording and reporting technologies within the mart systems.

In addition to significant improvements in field recording of performance data, ICBF has also invested considerable effort and resources into web-based systems for data recording by farmers. A good example of this is insemination data, where opportunities to record AI data by farmers has resulted in a further 41 345 insemination records being recorded in the ICBF database in 2007. Other

Carcass image data (from abattoirs)

Weanling performance data (from farmers marts)

Web-based systems of data capture

traits are now included in the data capture system, e.g., weights and animal health traits. However, success in web-based systems for recording performance data is dependent on having valuable management information to help promote the benefits of farmer recording. Without good reports, Irish farmers will see little tangible benefit in recording this data.

**The benefits of
business
partnerships**

One of the major reasons behind ICBF's success in delivering more data for cattle breeding has been the shared vision that exists within the Irish cattle industry (both shareholders and stakeholders alike) regarding the value of cattle breeding. Complicit in this has been the unique relationship which ICBF shares with the DAF, thus ensuring minimal duplication in data for cattle breeding and maximum "value-add" for Irish farmers and the dairy and beef industries. Many other synergies exist between ICBF and its shareholders and industry stakeholders with a "win-win" approach adopted by ICBF and the relevant business partner (Table 5). In each of the examples, the "win" for ICBF is in getting access to a "new trait" of economic importance for Irish farmers, whilst the "win" for the business partner is usually an improvement in efficiency as a result of using the database to provide services to end-users.

The above partnerships do not include data recorded directly by farmers, or data recorded by ICBF technicians (linear scoring and weight recording of beef cattle). In addition to the above business partnerships, ICBF and the Irish cattle industry are also exploring options for using the cattle breeding database in the provision of "Herd Health" services to farmers, with the database then being used by veterinary practitioners for the routine recording of all relevant events and treatments on cattle farms.

**Impact on
genetic
evaluation of
cattle in Ireland**

The net effect of the above arrangements, coupled with the establishment of the central cattle breeding database and the use of new technology outlined earlier, has been a dramatic increase in the quantity and quality of data available for cattle breeding (Table 1). At this stage, ICBF produces genetic evaluations for some 60 traits, across dairy and beef cattle. These are generated 4 times per year, January, May and August (coinciding with the Interbull dairy runs) and one additional run in November (for dairy and beef cattle). All evaluations are carried out on an across breed basis, allowing dairy and beef farmers the opportunity to select bulls and cows on both a within and across breed basis. Whilst all of the data for each genetic evaluation run is stored in the central cattle breeding database, significant time is required to extract, calculate and then "re-load" proofs for all traits and all animals (including parent averages) back into the database (including the computation economic indexes for an additional 7 traits). Currently the entire process takes some 6 weeks. We are currently examining ways at reducing this time, with the overall goal of having it reduced to 3 weeks.

The across breed nature of ICBF's genetic evaluation systems can perhaps be best appreciated by an examination of Euro-Star proofs for the various breeds present in Ireland (Figure 1). A total of 12 breeds are evaluated, using both pedigree and cross-bred data. The Euro-Star indexes were first made available to Irish farmers in March 2007, and have been very well received (ICBF Annual Report, 2007). The fact that the evaluations exhibit substantial variation on both an across and within

Table 5. Summary of key business partnerships with the Irish dairy and beef industries.

Business partner (including status).	Key data provided	Traits evaluated (based on data)	Benefit for the business partner
DAF (stakeholder)	• Birth registrations, cattle movements and deaths	• Calving Interval (Days), Survival (1st-4th Parity)	• Improving the profitability of Irish dairy and beef farmers and industry
AI Organisations (ICBF shareholder)	• Insemination records	• Gestation length, male and female fertility traits	• Use of database to provide service to users • Greater control of AI business • Real-time recording of data • No paperwork, better accuracy and efficiency
Milk recording organisations (ICBF shareholder)	• Milk performance records	• Mkg, Fkg, Pkg, F%, P%, SCC	• Use of database to provide service to users • Greater efficiency • New and improved reports for farmers
Herdbooks (ICBF shareholder)	• Dairy linear type	• Linear type traits, including body, mammary, feet/legs and overall	• Use of database to provide service to users • Greater efficiency • Real-time recording of data
Abattoirs (Stakeholder)	• Carcass data and price/kg	• Carcass weight, conformation grade, fat score • In the future carcass cut data	• Improving the profitability of Irish dairy and beef farmers and industry • Options for “procurement” service being explored
Farmer marts (Stakeholder)	• Weight data and price/kg (indicator of quality)	• Weaning weight (direct and maternal), Weanling Calf Quality (150 - 300 days) and “Drop calf quality (0-30 days)	• Improving the profitability of Irish dairy and beef farmers and industry • Options for “on-line” catalogue services being explored
Teagasc (Stakeholder)	• Research data	• Range of traits “for the future” including; farmer opinion, lameness, carcass cut data, feed intake/efficiency	• Use of database to build programs (staff and systems) that will increase the future profitability of Irish dairy and beef farmers and industry

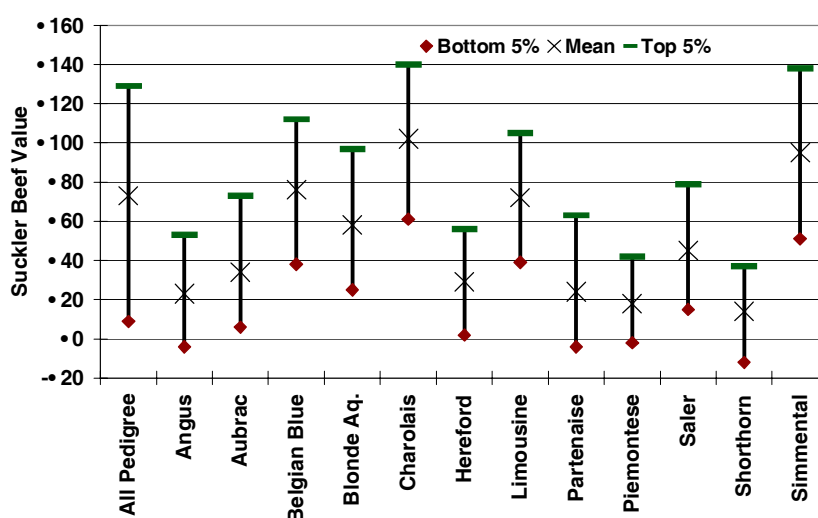


Figure 1. Ranges by breed of uro-Star suckler beef value.

breed basis (typically about 100/calf born in PTA terms) is very positive and demonstrates the benefits of adopting a multi-breed evaluation approach to our cattle improvement systems.

Whilst the uro-Star indexes are relatively new to Irish farmers and the Irish beef industry the dairy Economic Index (EBI), has been in place for a number of years. First launched in February 2002 (ICBF Annual Report, 2007), the index combines information on milk solids (~40% weighting), female fertility traits (~40% weighting) and calving, beef and health traits (~20% weighting). The overall response from farmers and the industry to the index has been hugely positive, as can be demonstrated from a plot of genetic trend for EBI over the past 30 years. Since its

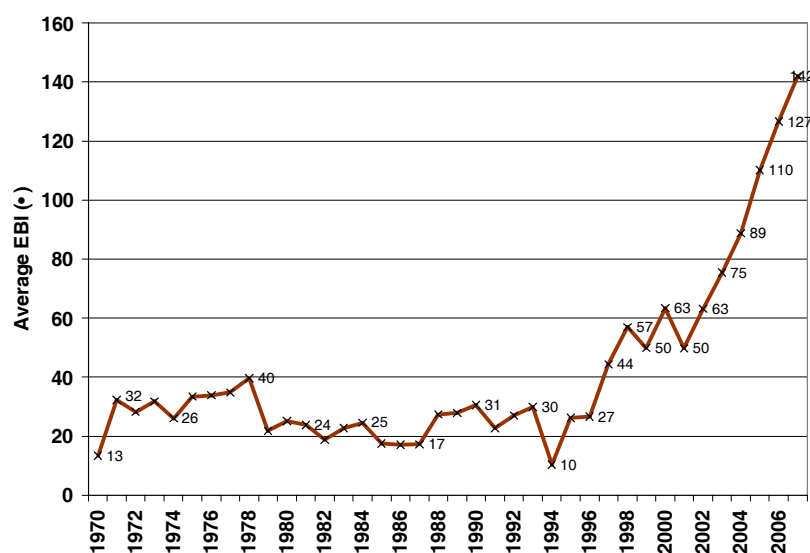


Figure 2. Trend in average EBI of Holstein Friesian bulls registered for use in AI, by year of birth.

inception in 2002, EBI has increased by about 15/year, based on sires being registered for AI use. Our goals over the next few years is to continue this increase and to achieve similar increases within the beef Uro-Star index.

ICBF. 2007. Annual Report, <www.icbf.com/publications/files/Report_May_2008_ver_7.pdf>.

Pabiou, T., Fikse, F., Berry, D. & Cromie, A. 2008. Genetic Parameters for carcass cut data based on commercial and research data (ICAR Annual Proceedings, 2008).

List of references

Comparison of different models for estimating daily yields from a.m./p.m. milkings in Slovenian dairy scheme

J. Jenko, T. Perpar, B. Logar, M. Sadar, B. Ivanovic, J. Jeretina,
J. Verbic & P. Podgoršek

Agricultural institute of Slovenia, Hacquetova 17, 1000 Ljubljana, Slovenia

Evaluation of accuracy and bias for prediction of daily milk yield (DMY), daily fat content (DFC), and daily protein content (DPC) from alternate a.m./p.m. recording scheme was made. The data comprised information on 483 813 test-day records. Five different equations were made from three different models compared on the whole data set or just the upper or the lower quartile of the records. In the first model daily yield or content was included as a dependent variable in regression analysis, whereas in the other two ratio of partial to daily yield or content was dependent variable in regression analysis. The bias on a whole data set was except for one equation, where DPC was underestimated for 0.033%, low. On the upper quartile of data set bias in the underestimation of records was noticed for two equations. In the first equation DMY, DFC, and DPC was on average underestimated for 0.315 kg, 0.196%, and 0.047%, respectively. The third equation on average underestimated DMY, DFC, and DPC for 0.392 kg, 0.211%, and 0.026%, respectively. However the problem with bias at these two equations was also detected in the lower quartile of data set. Here, the records in the first equation for DMY and DFC were on average overestimated for 0.347 kg and 0.170%, respectively and DPC was underestimated for 0.021%. The third equation on average overestimated DMY, DFC, and DPC for 0.329 kg, 0.195%, and 0.023%, respectively. First equation and third equation were both based on the first model. Differences in correlation between estimated and true values were negligible among equations. It was concluded that models where partial to daily yield or content was included as a dependent variable in regression analysis made unbiased estimation, whereas model where daily yield or content was dependent variable in regression analysis made biased estimation with respect to high or low milk yield and fat or protein content.

Key words: Alternating a.m./p.m. scheme, Bias, Milk yield, Fat content, Protein content.

Reliable data from milk recording system are important for herd management and genetic improvement in dairy cattle (Liu *et al.*, 2000). Constant pressure of lowering the cost of dairy recording system forces us into implementation of cheaper methods. When we look for a cheaper alternative of A4 recording scheme (monthly records of

Summary

Introduction

daily milkings) an implementation of AT recording scheme (alternating morning and evening milking records at subsequent visit) is a logical step. Potential benefits from the adoption of AT recording scheme are the following: more herds can be served by one supervisor, recording costs per cow are lower (Everett and Wadell, 1970a; Everett and Wadell, 1970b; Hargrove and Gilbert, 1984), larger number of young bulls can be involved in progeny testing programs per year, rate of genetic gain is increased (Schaeffer and Rennie, 1976), flexibility in scheduling the work of a supervisor is greater and the method disrupts the milking routine less (Cassandro *et al.*, 1995).

There were several studies conducted to investigate the accuracy of AT recording scheme in comparison with A4 recording scheme (Cassandro *et al.*, 1995; DeLorenzo and Wiggans, 1986; Lee and Wardrop, 1984; Liu *et al.*, 2000; Wiggans, 1981). The model proposed by DeLorenzo and Wiggans (1986) has been widely used in many countries. Here daily yield is estimated from one milking by multiplying the yield from the milking by a factor dependent on the length of interval since the last milking. Factors for estimating daily milk yield (DMY) from partial milk yield (PMY) from morning (a.m.) or evening (p.m.) milking adjusted for milking intervals (MI) can be derived through regression analysis of direct (DMY:PMY) or inverse (PMY:DMY) yield ratios on the length of MI. Cassandro *et al.* (1995) showed that inverse adjustment factors have mathematical features that are more favourable than direct factors. The model proposed by Liu *et al.* (2000) estimates daily yield from single milk testing scheme with a multiple regression method. In contrast with DeLorenzo and Wiggans model (1986) they use daily yield instead of direct or inverse yield ratios as the dependent variable in regression analysis. Estimated daily yield is calculated with model where separate regression for every combination of parity, MI, and lactation stage is used. The result is a model with 576 equations for estimating DMY, daily fat yield (DFY), and daily protein yield (DPY).

In March 2004 the AT recording scheme was implemented in Slovenian dairy scheme instead of the ICAR A4 standard reference recording scheme (Sadar *et al.*, 2005). Equations calculated with the model proposed by Klopčič *et al.* (2003) and Klopčič (2004) were used. The main problem observed was systematic underestimation of daily protein content (DPC) (Sadar *et al.*, 2007) and some systematic biases, e.g., underestimation of high daily yields and contents on one hand and overestimation of low daily yields and contents on the other hand (personal communication with breeders). Although Liu *et al.* (2000) warns about some systematic pattern of estimated errors in connection to lactation stage, this problem was also seen in connection to production level. This is quite important for Slovenia where the intensity of milk production differs a lot between farms (Sadar, *et al.*, 2007).

The objectives of this study were to investigate adequacy of official equations proposed for Slovenia and to compare different models for calculation of DMY, daily fat content (DFC), and DPC on the basis of data from single milking.

Milk production data were collected from the database of Slovenian cattle recording scheme (Logar *et al.*, 2005). Combinations of data from regular and supervision dairy recordings carried out from March 2004 through February 2008 were made. With adequate a.m. and p.m. records a calculation of daily yields with regular A4 recording method was made. After screening the records from unreasonable days in milk (DIM) (less than 5 days), MI (less than 540 minutes and more than 870 minutes), more than two times milking per day and problems detected at testing, 483 813 test-day records were used. They were collected from 120 971 lactations of 89 376 cows from 26 046 milk tests in 5 051 herds with all traits recorded in a.m./p.m. or p.m./a.m. milkings. Variables included in the study were: DMY, DPC, DFC, PMY from a.m. or p.m. milking, partial fat content (PFC) from a.m. or p.m. milking, partial protein content (PPC) from a.m. or p.m. milking, MI and DIM.

During the night MI was on average 26 minutes longer compared to daily interval (Table1). This inequality is the main cause of mean difference between a.m. milk yield and p.m. milk yield + 0.40 kg. Slightly higher values for DFC and DPC were observed in p.m. milking. On the other hand DFY and DPY are higher in a.m. milking. The reason is in higher a.m. milk yield in comparison with p.m. milk yield.

Material and methods

Data

Table 1. Descriptive statistics of milk yield and milk composition.

Trait	Number of records	Daily		p.m.		a.m.	
		Mean	Std	Mean	Std	Mean	Std
DMY (kg) ¹	483 813	18.06	7.12	8.83	3.56	9.23	3.76
p.m. : DMY ²	241 914			0.49	0.05		
a.m. : DMY ³	241 899					0.51	0.05
DFY (kg) ⁴	483 813	0.74	0.29	0.37	0.15	0.38	0.16
DFC (%) ⁵	483 813	4.18	0.71	4.22	0.82	4.15	0.82
p.m. : DFY ⁶	241 914			0.49	0.07		
a.m. : DFY ⁷	241 899					0.51	0.07
DPY (kg) ⁸	483 813	0.61	0.22	0.30	0.11	0.31	0.12
DPC (%) ⁹	483 813	3.41	0.38	3.43	0.39	3.40	0.39
p.m. : DPY ¹⁰	241 914			0.49	0.05		
a.m. : DPY ¹¹	241 899					0.51	0.05
MI (min) ¹²	483 813	1436.91	20.57	705.33	44.39	731.55	46.69

¹Daily milk yield.

²Ratio of evening milk yield to daily milk yield

³Ratio of morning milk yield to daily milk yield

⁴Daily fat yield.

⁵Daily fat content.

⁶Ratio of evening fat yield to daily fat yield

⁷Ratio of morning fat yield to daily fat yield

⁸Daily protein yield.

⁹Daily protein content.

¹⁰Ratio of evening protein yield to daily protein yield

¹¹Ratio of morning protein yield to daily protein yield

¹²Milking interval.

Models

In the study, five equations were analysed. They were made on three different models. Model 1 was proposed by Klopčič *et al.* (2003) and Klopčič (2004), Model 2 by DeLorenzo and Wiggans (1986) and an alternative Model 3 which is a combination of Model 1 and Model 2 mentioned previously.

Model 1: The following formula was used for estimating DMY, DFC, and DPC with model proposed by Klopčič *et al.* (2003) and Klopčič (2004):

$$y_i = \mu + b_1 * m_i + b_2 * t_i + e_i \quad (1)$$

where y is an estimated DMY, DFC or DPC for i measurement, μ is the estimated intercept for a.m. or p.m. milking, b_1 and b_2 are the estimated regression coefficient for a.m. or p.m. milking, m_i is the PMY, PFC or PPC, t is the MI in minutes, and e_i is the residual

Model 2: For the model developed by DeLorenzo and Wiggans (1986) the factors proposed by ICAR (2007) were used. Here DMY and DFC estimates are based on measured yield or content and milking frequency. An adjustment factor accounts for differences in the average MI between the preceding milking and the time of measured milking. An additional adjustment is applied to milk yield for the interaction between MI and stage of lactation with mid lactation 158 DIM set to zero. DPY is calculated from the measured percentage and the adjusted milk yield. The MI is divided into 15-minutes classes and formulas for prediction sample day yields and percentages in herds with two milkings are:

$$DMY = FM * PMY + c * (DIM - 158) \quad (2)$$

$$DFC = FF * PFC ; DFY = DMY * DFC ; DPY = DMY * DPC \quad (3)$$

where FM is the factor for milk yield, c is the covariate, and FF is the factor for fat content.

Model 3: A new model which is a combination of DeLorenzo and Wiggans model (1986) and model by Klopčič *et al.* (2003) and Klopčič (2004) was proposed. In this model multiple regression method that calculates factors for estimating DMY, DFY, and DPY is used. Here an inverse ratio of partial to daily yield from a single milking is included as a dependent variable in regression analysis. The formula is applied separately to partial daily yields from a.m. or p.m. milking. For a given trait one formula is to be estimated for calculating daily yield based on partial yield from either a.m. or p.m. milking. There were two proposals of this model tested:

$$y_i = \mu + b_1 * t_i + e_i \quad (4)$$

and

$$y_i = \mu + b_1 * t_i + b_2 * t_i^2 + e_i \quad (5)$$

where y is an estimated factor (inverse ratio of partial to daily yield) for calculation of DMY, DFY, and DPY for i measurement, μ is the estimated intercept for a.m. or p.m. milking, b_1 and b_2 are the estimated regression coefficient for a.m. or p.m. milking, t is the MI in minutes, and e is the residual.

Estimated DMY, DFY, and DPY are calculated with the formulas:

$$DMY = PMY / FM ; \quad DFY = PFY / FF ; \quad DPY = PPY / FP \quad (6)$$

where FM is the estimated factor for milk yield, FF is the estimated factor for fat yield and FP is the estimated factor for protein yield.

Component percentages of fat and protein on a daily basis are then calculated by dividing estimated DFY or DPY by estimated DMY:

$$DFC = (DFY / DMY) * 100 ; \quad DPC = (DPY / DMY) * 100 \quad (7)$$

In the analysis we compare five equations, where the first one (E1) uses the coefficients proposed by Klopčič *et al.* (2003) and Klopčič (2004), and the second one (E2) factors proposed by ICAR (2007) for the model by DeLorenzo and Wiggans (1986). The third (E3), fourth (E4) and fifth (E5) equations have factors calculated on our data set, whereas E3 is based on Model 1 and E4 and E5 on Model 3. Equation E4 is based on MI as linear and E5 as quadratic effect. For the calculation of adjustment factors R statistics package (R Development Core Team, 2008) was used. LM procedure was used for the estimation of coefficients for DMY, DFC, and DPC in Model 1 and factors for DMY, DFY, and DPY in Model 3.

Equations were evaluated on the basis of correlation between the estimated and measured DMY, DFC, and DPC and on the basis of the differences between predicted and true DMY, DFC, and DPC. To study the problem of underestimation of high DMY, DFC, and DPC and overestimation of low DMY, DFC, and DPC upper and lower quartile of records per each trait were analysed.

The accuracy of DMY, DFC, and DPC predicted from analysed equations is shown in Table 2. There is actually no difference in correlation coefficient between the selected equations. Except in the equation E1 for DPC the bias is quite low. In the equation E1 is on average DPC underestimated for 0.033%. This means that equations officially proposed for Slovenia made a systematic bias which on average underestimates the true DPC. From the results shown in Table 2 it cannot be concluded which model estimates the daily milk records better.

The accuracy to predict DMY, DFC, and DPC on the basis of the upper quartile data sets is shown in Table 3. The boundary is set to > 22.4 kg for DMY, > 4.62% for DFC, and > 3.66% for DPC. The correlations for this part of data set are lower compared with the whole data set (Table 2). There are almost no differences in correlation coefficients between equations. However, the differences in bias can be clearly seen. Equations E1 and E3 systematically underestimate DMY, DFC, and DPC. Equation E1 underestimates DMY, DFC, and DPC for 0.315 kg, 0.196%, and 0.047%, respectively. Equation E3 underestimates DMY, DFC, and DPC for 0.392 kg, 0.211%, and 0.026%, respectively. On the other hand, equations E2, E4, and E5 are quite unbiased and make a good estimation of daily yield and composition. The problem of underestimation of high daily yield and contents is solved with Model 2 and Model 3 on which equations E2, E4, and E5 are based.

Results

Table 2. Accuracy and bias of DMY, DFC, and DPC on the whole data set.

Trait	Equation	r ⁴	Bias ⁵	Std ⁶	Min ⁷	Max ⁸
DMY (kg) ¹	E1	0.979	0.044	1.444	-18.31	18.11
	E2	0.980	-0.048	1.445	-19.18	19.05
	E3	0.980	-0.002	1.428	-18.40	18.66
	E4	0.980	-0.002	1.431	-19.14	19.51
	E5	0.980	-0.001	1.431	-19.14	19.50
DFC (%) ²	E1	0.878	-0.006	0.342	-3.43	2.73
	E2	0.879	0.001	0.387	-3.86	3.53
	E3	0.879	0.000	0.340	-3.35	2.57
	E4	0.879	-0.007	0.385	-3.88	3.64
	E5	0.879	-0.003	0.385	-3.88	3.66
DPC (%) ³	E1	0.975	-0.033	0.087	-2.38	1.73
	E2	0.974	0.001	0.089	-2.32	1.83
	E3	0.975	0.000	0.086	-2.32	1.71
	E4	0.975	0.000	0.088	-2.34	1.81
	E5	0.975	0.000	0.088	-2.34	1.81

¹Daily milk yield.

²Daily fat content.

³Daily protein content.

⁴Correlation coefficient between the estimated and measured DMY, DFC, and DPC.

⁵Difference between an estimator's expected value and the true value of the parameter being estimated.

⁶Standard deviation.

⁷Minimum difference between an estimator's expected value and the true value of the parameter being estimated.

⁸Maximum difference between an estimator's expected value and the true value of the parameter being estimated.

Table 3. Accuracy and bias of DMY, DFC, and DPC, on upper 25% records from sample data.

Trait	Equation	r ⁴	Bias ⁵	Std ⁶	Min ⁷	Max ⁸
DMY (kg) ¹	E1	0.923	-0.315	1.867	-18.16	17.63
	E2	0.927	0.080	1.865	-19.18	17.75
	E3	0.925	-0.392	1.836	-18.40	16.91
	E4	0.928	-0.014	1.859	-19.14	17.72
	E5	0.928	-0.011	1.858	-19.14	17.74
DFC (%) ²	E1	0.709	-0.196	0.365	-3.43	2.73
	E2	0.711	-0.002	0.439	-3.86	3.53
	E3	0.710	-0.211	0.356	-3.35	2.57
	E4	0.709	-0.012	0.441	-3.88	3.64
	E5	0.709	-0.007	0.441	-3.88	3.66
DPC (%) ³	E1	0.920	-0.047	0.098	-2.38	1.50
	E2	0.920	0.001	0.101	-2.32	1.60
	E3	0.921	-0.026	0.096	-2.32	1.48
	E4	0.921	0.000	0.100	-2.34	1.58
	E5	0.921	0.000	0.100	-2.34	1.58

^{1, 2, 3, 4, 5, 6, 7, 8}For description see Table 2.

The accuracy of DMY, DFC, and DPC prediction on the basis of the lower quartile data set is shown in Table 4. The boundary is set to < 12.9 kg for DMY, < 3.71% for DFC, and < 3.14% for DPC. Correlation coefficients are lower than in case of the upper quartile (Table 3) indicating that in cows given small amount of milk the accuracy of prediction is lower than in cows with high DMY. Differences in correlation coefficients between equations were small (Table 4), but on the other hand there were considerable differences in bias. Equation E1 overestimates DMY and DFC for 0.347 kg and 0.170%, respectively and underestimates DPC for 0.021%. Equation E3 overestimates DMY, DFC, and DPC for 0.329 kg, 0.195%, and 0.023%, respectively. The bias is much lower in equations E2, E4, and E5 and they seem to be more reliable for prediction of DMY, DFC, and DPC on the lower quartile of data set. As in the upper quartile, here too may be observed that the problem of overestimation of low daily yield and contents is solved with Model 2 and Model 3, on whose equations E2, E4, and E5 are based.

Table 4. Accuracy and bias of DMY, DFC, and DPC on lower 25% records from sample data.

Trait	Equation	r ⁴	Bias ⁵	Std ⁶	Min ⁷	Max ⁸
DMY (kg) ¹	E1	0.892	0.347	1.076	-9.22	9.61
	E2	0.902	-0.024	1.051	-8.90	10.15
	E3	0.897	0.329	1.043	-8.80	9.71
	E4	0.908	0.004	1.017	-8.88	10.16
	E5	0.908	0.003	1.016	-8.88	10.16
DFC (%) ²	E1	0.654	0.170	0.310	-1.72	2.52
	E2	0.653	0.002	0.381	-2.11	3.07
	E3	0.656	0.195	0.302	-1.61	2.52
	E4	0.657	-0.004	0.376	-2.12	3.05
	E5	0.657	-0.000	0.377	-2.11	3.06
DPC (%) ³	E1	0.901	-0.021	0.070	-1.09	1.01
	E2	0.900	0.001	0.072	-1.12	1.09
	E3	0.902	0.023	0.068	-1.03	1.05
	E4	0.902	0.001	0.071	-1.11	1.07
	E5	0.902	0.001	0.071	-1.11	1.07

1, 2, 3, 4, 5, 6, 7, 8 For description see Table 2.

This study showed that bias from DMY, DFC, and DPC which is related to high or low milk yield and fat or protein content can be removed from the model for estimating dairy recordings from a.m./p.m. milkings. The problem can be solved with the Model 2 and Model 3. The problem in the equation E1 made from Model 1 is a systematic underestimation of DPC, which is not seen in any other model. Correlation between estimated and predicted value differs with respect to change in DMY, DFC, and DPC. They are lower for the upper and the lower quartile of records; this means that the accuracy of estimation is not so high for this part of data.

Conclusion

Alternative model which was proposed in this study become an official model for estimating daily yields from a.m./p.m. milkings in Slovenian dairy scheme after the 1st of May 2008. Here, an inverse ratio of partial to daily yield from a single milking is included as a dependent variable in regression analysis with respect to time between milkings.

List of references

Cassandro, M., P. Carnier, L. Gallo, R. Mantovani, B. Contiero, G. Bittante and G.B. Jansen. 1995. Bias and accuracy of single milking testing schemes to estimate daily and lactation milk yield. *J. Dairy Sci.* 78: 2884-2893.

DeLorenzo, M.A. and G.R. Wiggans. 1986. Factors for estimating daily yield of milk, fat, and protein from a single milking for herds milked twice a day. *J. Dairy Sci.* 69: 2386-2394.

Everett, R.W. and L.H. Wadell. 1970a. Sources of variation affecting the difference between morning and evening daily milk production. *J. Dairy Sci.* 53: 1424-1429.

Everett, R.W. and L.H. Wadell. 1970b. Sources of variation affecting ratio factors for estimating total daily milk yield from individual milkings. *J. Dairy Sci.* 53: 1430-1435.

Hargrove, G.L. and G.R. Gilbert, 1984. Differences in morning and evening sample milkings and adjustment to daily weights and percents. *J. Dairy Sci.* 67: 194-200.

Klopcic, M., Š. Malovrh, G. Gorjanc, M. Kovac and J. Osterc. 2003. Prediction of daily milk fat and protein content using alternating (AT) recording scheme. *Czech J. Anim. Sci.* 48: 449-458.

Klopcic, M. 2004. Optimizacija vrednotenja proizvodnosti krav v mlečni usmeritvi [Optimization of milk recording practices in dairy cows]. PhD thesis. University of Ljubljana, Biotechnical faculty, Zootechnical Department, Ljubljana, 171 pp.

ICAR. 2007. ICAR Guidelines approved by the general assembly held in Kuopio, Finland on 9 June 2006. Rome, pp. 475.

Lee, A. J. and J. Wardrop. 1984. Predicting daily milk yield, fat percent, and protein percent from morning or afternoon tests. *J. Dairy Sci.* 67: 351-360.

Liu, Z., R. Reents, F. Reinhardt and K. Kuwan. 2000. Approaches to estimating daily yield from single milk testing schemes and use of a.m.-p.m. records in test-day model genetic evaluation in dairy cattle. *J. Dairy Sci.* 83: 2672-2682.

Logar, B., P. Podgoršek, J. Jeretina, B. Ivanovic and T. Perpar. 2005. On-line available milk-recording data for efficient support of farm management. In: Kuipers, A., M. Klopcic, and T. Cled (Editors), Knowledge transfer in cattle husbandry: new management practices, attitudes and adaptation. Wageningen Academic Publishers, Wageningen, the Netherlands, EAAP Series 117: 227-230.

R Development Core Team. 2008. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL <www.R-project.org>.

Sadar, M., P. Podgoršek, T. Perpar, B. Logar, B. Ivanovic, J. Jeretina, M. Prevolnik. 2005. Rezultati kontrole prireje mleka in mesa Slovenija 2004 [Results of animal recording, Slovenia 2004]. Agricultural institute of Slovenia, Ljubljana, pp. 50.

Sadar, M., A. Biderman, J. Jeretina, B. Logar, T. Perpar, P. Podgoršek and B. Ivanovic. 2007. Rezultati kontrole prireje mleka in mesa Slovenija 2006 [Results of animal recording, Slovenia 2006]. Agricultural institute of Slovenia, Ljubljana, pp. 56.

Schaeffer, L. R. and J. C. Rennie. 1976. AM-PM testing for estimating lactation yields. Can. J. Anim. Sci. 56: 9-15.

Wiggans, G.R. 1981. Methods to estimate milk and fat yields from a.m./p.m. plans. J. Dairy Sci. 64: 1621-1624.

Quality assurance for milking machines and recording devices

K. de Koning¹ & P. Huijsmans²

*¹Animal Sciences Group Wageningen UR, P.O.Box 65,
8200 AD Lelystad Lelystad, The Netherlands*

*²Stichting Kwaliteitszorg Onderhoud Melkinstallaties (KOM),
Dronten, The Netherlands*

Without doubt, the milking machine is one of the most intensively used machines on a dairy farm. A well functioning milking machine is a prerequisite for good udder health and excellent milk quality. Many milking installations are equipped with milk recording devices. Milk recording is a basic prerequisite for management purposes and moreover milk recording is also the basic element of herd improvement and breeding programs. ISO recommendations and ICAR Guide Lines were developed for both milking installations as milk recording organizations to ensure proper construction and functioning. In the Netherlands these standards were implemented in an integrated quality assurance system comprising milking machines, bulk cooling tanks and recording devices. The system has been setup by the national farmers union, the manufacturers of milking machines, the national milk recording organization and moreover has been incorporated in the dairy quality assurance systems of the different dairy industries.

The basic idea is that all checks are conducted by certified technicians of the milking machine dealers. An independent organization KOM, established as result of an agreement between the National Farmers Union, Milking machine manufacturers union and the National Breeding and milk recording organization, is responsible for the quality control. The system guarantees the farmer that the maintenance of his milking machine and the necessary accuracy checks of milk meters and jars are performed well against minimal costs.

Key words: *Quality system, Maintenance, Milking machines, Milk meters, Recorder devices, Accuracy, Calibration.*

In the seventies and early eighties manufacturers and experts from various countries, prepared the first international standards for milking machines which were more or less based on the Dutch system. The most recent ISO standards are from 2007. ISO 3918 describes the vocabulary, ISO 5707 describes the standards for construction

Summary

Introduction

and performance of milking machines and ISO 6690 deals with the testing methods. The standards apply to both new installations, and machines in use, to check the performance of operation periodically. In the same time ICAR developed guide lines for the approval and the use of milk meters and jars for milk recording purposes (ICAR, 1995 -2006). ICAR Guide Lines for milk recording devices are under revision at the moment and an update is expected in mid 2008.

Quality system

In the mid nineties the Dutch national extension service together with the Dutch farmers union and the Dutch organization of milking machine manufacturers, developed plans to start a quality system for milking machine maintenance (KOM). This seemed to be a logical step in the further development of the preventive maintenance system of milking installations developed earlier following the principles of ISO 9000 and HACCP. The quality system was expanded with certification of the technicians, calibration of test equipment and by special courses for machine on time testing. The ultimate goal of course was to guarantee the farmer that the milking machine is working properly, without having a negative effect on milk quality or udder health. Another prerequisite was that the KOM system should fit in to the total quality management system for dairy farms as developed by the Dutch dairy industry and the national farmers union. The KKM system is permissive to the national and EU legislation aspects, and obligatory for all Dutch dairy farmers since 2000. Since 2006 the system is linked to each individual dairy industry. Farmers who want to deliver milk to one of the dairies, have to meet the requirements of the several quality modules. These modules are Medicines, Animal health and welfare, Foodstuff and water, Milking and milk storage, Cleaning and disinfection and Environment and waste products. The module Milking specifies that the milking machine should be tested yearly by a KOM-certified technician.

Institution KOM

The foundation KOM is an independent institution, because quality systems and quality control should be independent from the parties involved. After the start of the KOM organization, also the Dutch breeding and milk recording organizations decided to incorporate the routine accuracy check of electronic milk meters and recorder jars into the KOM responsibilities. This check is necessary for meters used for the official milk recording system as stated by the ICAR rules. The technicians from the manufacturers combine the yearly service on the milking machine and the routine tests on the functioning and accuracy of electronic milk meters and jars. The reason to do so was to reduce the costs for the farmer by combining control systems and maintenance.

The KOM quality assurance system

KOM has developed several activities to control the quality assurance system:

- Registration and evaluation of all test reports made by the technicians including reports on the accuracy of milk meters and jars.
- Annual control and calibration of the test equipment used by technicians.
- Performing random checks on the 'quality of work' of the technician including milk meters and jars.
- Certification of (new) technicians.
- Development of standard test reports (MAR) and tests (based on ISO and/or ICAR).
- Studies on the relation between milking machines and milk quality.
- Development of guide lines for new areas, like automatic milking systems.

During the yearly check on the milking machine, as done by the milking machine technicians, all components are checked and tested. If necessary, repairs are made or devices like pulsators are adjusted to the right value. Vacuum level, reserve capacity, air inlet, air consumption, air leakage and pulsation curves, are measured by using test equipment like airflow meters, vacuum testers and pulsation testers. The test results are recorded in a standard test report, which is equal for all manufacturers. The technician can also write down his comments. A copy of the report is handed over to the farmer, another copy is sent to KOM. The reports are registered per technician and evaluated at random using an evaluation protocol. The evaluation report is discussed with each technician once a year.

Registration of all test reports

At Waiboerhoeve experimental station, the research facility of the Animal Sciences Group of Wageningen UR, a training and test centre was established. This centre has a special test installation suited to test and calibrate vacuum gauges, air flow meters and pulsator test devices (De Koning and Huijsmans, 2001). The centre has also equipment to test other devices used during annual testing and moreover is equipped with almost every approved electronic milk meters available. They are used for training courses, to explain and practice the routine test for milk meters.

Control and calibration of the test equipment in use

KOM performs random checks on farms to evaluate the quality of work by the technicians, both for milking machine maintenance and for the routine test of milk meters. Each technician will get at least one random check per year by one of the KOM-officers. This re-test is carried out as soon as possible after the technician has done the yearly test of the milking installation. It consists of a check on vacuum level, reserve capacity, regulator leakage, the pulsation system partially, cleaning temperature and the presence of the test report. If necessary the whole test will be performed. If the technician is not doing a good job, KOM may decide to withdraw his certificate, so that he is not allowed to do any testing anymore.

Random checks

According to the requirements of KOM and the quality assurance systems of the dairy industry, all technicians should be well qualified and certified. Because there is no general education for this type of work, KOM has set up a special education program for milking machine technicians. The course consists of several modules varying from udder physiology, milking routines, milk quality, Mastitis, machine milking and testing, milk meter routine testing to dialogue techniques with the farmer. For the already more skilled technicians a modified course was developed. Over 350 technicians joined these courses and approximately 85% succeeded and obtained a certificate, so they are allowed to test milking machines within the KOM system. Special courses were designed for those technicians who do regular maintenance of automatic milking systems, which are now in use on over 6% of the Dutch farms.

Certification of the technicians

Results of random checks on milking installations and recording devices

The number and type of milking machine installations and the number of received test reports has changed in the past 25 years as presented in table 1. In the past 4 years the percentage of both rotary parlours as automatic milking systems in The Netherlands was doubled as can be concluded from table 1.

Table 2 presents the results for the random checks performed by KOM in 2007. The objective is to check 2% of all MAR test reports and 5% of the milk meter routine tests. Around 7% of the random checks on milking parlours in 2007 resulted in a remark concerning one or more aspects. Most remarks concerned completeness of data entry, assessments, and test procedures. In a few cases the technician was ordered to repair some things, like pulsation system or air leakages. About 8% of the farms with milk meters had a deviation on the accuracy of one or more milk meters, while 13% of the farms with recorder jars received a comment.

Table 1. Number of farms and type of milking installation in The Netherlands.

Milking system	1983	1993	2003	2007
Bucket milking machines (%)	26.3	5.3	0.8	0.2
Pipe line milking machines (%)	27.3	21.1	14.4	12.6
Herringbone parlours (%)	40.4	62.7	68.6	65.8
Side by side / tandem parlours (%)	5.6	10.1	12.5	13.6
Rotary parlours (%)	0.4	0.6	1.3	2.5
Automatic Milking Systems (%)	0.0	0.04	2.4	5.3
Total number of farms	49 500	35 540	23 595	20 790
Number of MAR test reports	21 000	32 000	25 000	23 000

Table 2. The number of random checks (farms and meters) in 2007 (Huijsmans, 2008).

	Milking parlours	Milk meters		Recorder Jars	
		Farms	Meters	Farms	Meters
Total number	234	118	1 308	106	1 026
Number with comments ¹	16	9	21	14	31
Percent deviation with comments	6.8	7.6	1.6	13.2	3.0

¹There has been a comment due to deviation in the test results, or over the procedure used, the result or on the report itself.

Results of calibrations tests on recording devices

The test results for the calibration (installation) tests are shown in table 3. It is remarkable to see that relatively more meters had to be adjusted during the calibration tests in most recent years.

A correct installation of the recording devices and installation procedure seems to be crucial for correct results of the recording devices in use.

Table 3 Results installation tests on recording devices by KOM technicians (Huijsmans, 2008).

Year	No. meters	Adjustments (number and percent)		Deviating samplers (number and percent)	
2005	6 298	663	10.5	175	2.8
2006	5 691	873	15.3	290	5.1
2007	5 201	1 086	20.8	310	6.0

The fast development and introduction of portable PC's, e-mail services and Internet offer interesting perspectives to improve the quality system. Improving the speed, for example by using digital MAR reports which are send electronically to KOM using Internet, can make a further step. Another interesting aspect is the expected integration of test equipment; so one device is able to measure the different functions of the milking machine and to fill the data into a digital MAR report. New data could be checked for mistakes but could also be compared automatically with the historical data. Moreover working procedures and regulations will be standardized between the neighbouring countries Belgium and Germany.

Annual tests for milk recording devices are quite time consuming due to the fact that most milk meters have to tested in routine test procedures using water. When milk meters are connected to a PC system, statistical data analysis will offer time and money saving alternatives to the current procedures with water tests. For farmers using electronic milk meters connected to a PC system, such an alternative might save costs and will improve the quality of measured data. This is an advantage both for the milk recording organisation as for the farmers.

Future developments

Huijsmans P. 2008. Jaarverslag 2006-2007, Stichting Kwaliteitszorg Onderhoud Melkinstallaties (in Dutch)

ICAR. 1995-2008. The approval and checking of milk recording equipment, ICAR, Sub Committee Meters and Jars, Rome.

ISO 3918. 2007, Milking machine installations – Vocabulary.

ISO 5707. 2007, Milking machine installations – Construction and Performance.

ISO 6690. 2007, Milking machine installations – Mechanical tests.

Koning C. de, P. Huijsmans. 2001. The Dutch Quality System for Milking Machine Maintenance, ICAR Technical Series, no. 7.

List of references

Estimation of fat and protein yields in dairy cattle from one milk sample per day in herds milked twice a day

M. Trinderup, T. Lykke & U. Sander Nielsen

Danish Agricultural Advisory Service, National Centre, Danish Cattle Federation, Udkaersvej 15, Skejby, 8200 Aarhus N., Denmark

A linear regression model was developed to estimate the daily yield of kg fat and protein from milk samples taken either at morning or evening milking in herds milked twice a day. The recommended model includes information on breed, parity, classes of days from calving, milk yield (kg) morning and evening, fat and protein yield (kg) at one milking and time interval between the milkings. The time interval was obtained from the electronic milk meters. A modified model was developed including the milk yield relation morning and evening as a measure of the distance between milkings. This model can be used in herds where the time of the milking is not recorded automatically. The two models were estimated on one half of a dataset that included information on 63 077 cows and tested on the other half of the data. Accuracies for kg protein obtained on the test data were for morning milk samples for the three parities between 0.9910 and 0.9944 for the recommended model and between 0.9909 and 0.9943 for the modified model. For evening samples the accuracies were slightly lower. The accuracies for kg fat were between 0.931 and 0.944 for the three parities and the two models for morning milk samples and slightly larger for evening milk samples. The performance of the two models indicated that a testing scheme with one milk sample per test day can be applied in herds without electronic milk meters if the time interval is substituted with the milk relation. For 4 418 Danish Holstein cows the 305 days yield were calculated using four different sampling methods. If the milk samples were strictly morning or evening samples the accuracies were not as high as if the samples were taken alternately morning and evening throughout the lactation.

Key words: *Testing schemes, Daily yield, One milk sample.*

Danish herds increase and the average herd size at present is 125 cows. The farmers ask for new systems that can reduce the amount of hours and costs used in relation to the milk recording system. To improve the milk recording system the Tru-Test

Summary

Background

electronic milk meters were introduced to herds in Denmark. But doing this the costs were increased from one milk sample per cow per test day to one milk sample per milking per cow per test day.

In Germany and Canada, however, a reduced number of milk samples per milk recording are used to calculate the daily yield of fat and protein. It has been a request from the Danish milk recording organisation to have more knowledge on the possibilities of reducing the number of milk samples.

For a test period from 2003 to 2004 the milk recording was carried out using Tru-Test electronic milk meters in a number of herds. Milk samples were collected and analysed per milking, providing a data set for developing a model to estimate the daily fat and protein yield from one milk sample.

With fewer milk samples we expect to have a lower accuracy of the calculated yield on the test day, but the question is to what extent will this affect the calculated lactation yield?

Some farmers milk the cows three times or more per day, both with traditional milking systems and with automatic milking systems. These procedures cause a new situation, which have to be handled. Up to now a small investigation has been made in relation to the traditional milking three times per day, but more work has to be done to solve the problems in relation to more milkings with irregular distances between milkings.

The purpose of this investigation was to develop a model and estimate the necessary parameters to calculate the daily yield of fat and protein on the basis of one milk sample per day. Given the results from the model it was investigated what the impact of a reduced number of milk samples per test day has on the lactation yield.

Material

The data were collected from June 2003 to July 2004 from 540 herds with two milkings per day. The data included 63 077 cows recorded and in total 478 180 milkings. The model was developed for the three main dairy breeds in Denmark but only results from 38 682 Danish Holstein cows are presented in this paper.

Table 1. Average results for cows of the Danish Holstein dairy breed.

Number: 151.773 "cow test days"					
	38 682 Cows	Mean	Std.	Min.	Max.
Milk, kg	Yield per day	27.01	7.98	2.28	72.30
	Morning	14.84	4.48	1.07	46.49
	Evening	12.16	3.90	1.00	43.81
	Difference a.m. – p.m.		2.68		
Fat, %	Yield per day	4.18	0.69	2.00	7.80
	Morning	3.95	0.75	2.00	8.00
	Evening	4.45	0.80	2.00	8.00
	Difference a.m. – p.m.	0.50			
Protein, %	Yield per day	3.42	0.37	2.12	7.30
	Morning	3.40	0.37	1.66	7.60
	Evening	3.44	0.38	1.59	9.09
	Difference a.m. – p.m.	0.04			
Time interval	p.m. – a.m. milking	13.38	0.78	8.29	17.30
	a.m. – p.m. milking	10.62	0.78	6.71	15.71

Morning milkings were accepted from 3 to 10 a.m. and evening milkings from 2 to 8 p.m. Fat percentages between 2 and 8 and protein percentages larger than 1.5 were accepted. The milking interval from p.m. to a.m. was given from the milking times recorded by the TRU-Test milk meters, while the interval from a.m. to p.m. was found by extracting the p.m.-a.m. interval from 24 hours.

At each milking the milk yield was recorded and a milk sample was obtained. The milk samples were analysed and the fat and protein content was given in percentages. The daily fat and protein percentages were found as the sum of the morning and evening yield in kg divided by the daily milk yield.

Data was divided into two datasets according to herds chosen at random. The model for the daily yield was estimated on the first dataset. The robustness of the model was then tested on the second dataset (the test data).

A third dataset was constructed containing data for the period June 2003 to January 2005 from herds with two milkings per day and 11 test days per year. This dataset included information on the lactations of 4 418 Danish Holstein cows. On these data it was tested what impact a reduced number of milk samples per test day has on the lactation yield.

Schaeffer *et al.* (2000) recommends a model including information on milk yield from both milkings, the fat and protein yield from one milking, milking interval, days in lactation, calving number and calving season to estimate the daily yield of fat and protein. The model has a regression for each of 72 classes.

The Danish model was developed in the same way as the model from Schaeffer. Nine different models were analysed but only the recommended model is presented in this paper.

It is assumed that the fat yield per day (y_{F24}) depends linearly of the fat yield from one milking (y_{F1}). The models that were used to estimate the protein yield per day look like the models used for fat. The only difference was that y_{F24} was substituted by y_{P24} .

$$y_{F24} = \beta_0 + \beta_{1(ijk)} + \beta_{2(ijk)} y_{F1} + \beta_{3(ijk)} y_{M1} + \beta_{4(ijk)} y_{M2} + \beta_{5(ijk)} y_{P1} + \beta_{6(ijk)} t$$

where $i=1$ to 3 (breed), $j=1, 2, 3(+)$ (parity), $k=1$ to 4 (classes of days from calving) and where t is the time interval between the milkings, y_{M1} is the milk yield at the milking where the milk sample is sampled, y_{M2} is the milk yield at the other milking on the test day, y_{P1} is the protein yield (kg) and y_{F1} is the fat yield (kg) measured at milking M1.

The model was estimated for the fat and protein yield expressed both in kg and in percentage.

From the literature it is known that the distance between milkings is important information in the yield calculation. Using the electronic milk meters the starting time for each milking is known, but using other types of equipment it can be missing information. Therefore it was analysed with a modified model what the value was of using the relation between kg milk (morning) and kg milk (evening) to describe the distance between milkings. In the modified model the time interval was substituted with the a.m./p.m. milk yield relation ($m_{AM/PM}$).

Method

As a measure of the robustness of the model the accuracy was calculated on the test data. The accuracy is defined by Schaeffer *et al.* (2000) as

$$\text{Acc} = \text{Var}_{(\text{act})} / (\text{Var}_{(\text{act})} + \text{Var}_{(\text{dif})})$$

where $\text{Var}_{(\text{act})}$ is the variance of the actual 24 hour yield and $\text{Var}_{(\text{dif})}$ is the variance of the difference between the actual and the estimated 24 hour yield. The more accurate the yield is estimated the smaller the variance of the difference and the closer to 1 Acc will be.

Schaeffer *et al.* (2000) found that for a milk sample taken in the morning the accuracy was 0.94 for kg fat and 0.995 for kg protein. A sample taken in the evening had a slightly lower accuracy.

Results

Table 2 shows R^2 -value, the standard deviation of the estimate of the 24 hours' yield (S.D._{y24}) and the standard deviation of the residuals $[(\text{MSE})^{1/2}]$ for the model by estimation of the fat and protein yield per day in kg and percentage.

If R^2 -values for kg fat and protein (Table 2) are compared with R^2 -values for fat and protein expressed as a percentage, lower R^2 -values are achieved for estimation of % fat and protein.

The R^2 -values for estimation of kg fat is highest with the p.m. milk sample. For estimation of kg protein the R^2 is highest with a.m. milk samples. The following results are from the model where fat and protein yield in kg are estimated.

Table 3 shows the results from testing the recommended and the modified model on the test data. The table shows the mean difference between the known 24 hours' yield and the estimated yield defined as $\text{dif} = \text{known} - \text{estimated}$. If the difference is positive, the estimated values on average were lower than the known values and vice versa.

By comparing the accuracy of the recommended model with the modified model, it becomes clear that the modified model is almost as precise as the recommended model. This will as mentioned earlier be an advantage as one milk sample per cow per test day also can be applied in herds where Tru-Test milk meters are not used today without further disadvantages in the shape of manual registration of the starting time of the milking. The standard deviation of the differences (S.D._{Dif}) increases a little, though.

Table 2. R^2 -value, the standard deviation of the estimate of the 24 hours yield (s.d._{y24}) and the residuals $[(\text{MSE})^{1/2}]$.

Milk Sample	Fat			Protein			
	R^2	s.d._{y24}	$(\text{MSE})^{1/2}$	R^2	s.d._{y24}	$(\text{MSE})^{1/2}$	
a.m.	Kg	0.9395	0.3011	0.0765	0.9940	0.2325	0.0181
	%	0.9277	1.0006	0.2797	0.9823	0.4659	0.0625
p.m.	Kg	0.9432	0.3017	0.0741	0.9935	0.2319	0.0188
	%	0.9123	0.9923	0.3081	0.9751	0.4642	0.0743

Table 3. The accuracy for the recommended and the modified model on the test data.

			Recommended model (time interval)			Modified model (a.m./p.m. milk yield relation)		
		Parity	Mean dif.	s.d. _{Dif}	Acc	Mean dif.	s.d. _{Dif}	Acc
Kg fat								
	a.m.	1	0.0035	0.0662	0.9329	0.0043	0.0671	0.9312
		2	0.0042	0.0830	0.9430	0.0058	0.0848	0.9406
		3	0.0023	0.0911	0.9438	0.0037	0.0928	0.9417
	p.m.	1	-0.0028	0.0632	0.9385	-0.0037	0.0637	0.9376
		2	-0.0040	0.0786	0.9485	-0.0054	0.0794	0.9476
		3	-0.0035	0.0860	0.9496	-0.0048	0.0869	0.9485
Kg protein								
	a.m.	1	-0.0007	0.0179	0.9910	-0.0005	0.0180	0.9909
		2	-0.0006	0.0202	0.9938	-0.0003	0.0204	0.9937
		3	-0.0008	0.0206	0.9944	-0.0005	0.0208	0.9943
	p.m.	1	-0.0010	0.0192	0.9897	-0.0009	0.0193	0.9895
		2	-0.0009	0.0207	0.9935	-0.0008	0.0207	0.9935
		3	-0.0012	0.0207	0.9944	-0.0011	0.0208	0.9943

For fat the accuracy is highest with the p.m. samples. For protein the accuracy is highest with the a.m. samples. Therefore, indications are that there in average won't be any difference whether the milk samples are taken out in the evening or in the morning and therefore practical considerations may determine when the samples are taken out.

Using the recommended and the modified model and only one milk sample per test day the daily yield was estimated on the third dataset. From the estimated daily yields the 305 days yields were calculated. To select which milk sample per test day that had to be used to estimate the daily yield four different sampling methods was developed. Table 4 shows the four methods for selecting the milk samples per test day that the 305 days' yields are based on.

Estimation of 305 days' yield

Table 5 shows the accuracy of 305 days' yields in kg fat and kg protein estimated according to the four methods shown in table 4.

Table 4. View of the combinations of time of day when the milk sample is obtained.

Name	Time of day for the milk sample
AM	All samples through the lactation were morning samples
PM	All samples through the lactation were evening samples
AM1PM2	Every second sample was a morning sample and every other sample was an evening sample. The first test day after calving the sample was a morning sample.
AM2PM1	Every second sample was an evening sample and every other sample was a morning sample. The first test day after calving the sample was an evening sample.

Table 5. Accuracy of 305 days yield depending of method of milk sampling.

		Parity	Number	AM	PM	AM1PM2	AM2PM1
Recommended model (time interval)	Fat	1	2 368	0.96	0.94	0.98	0.97
		2	967	0.95	0.93	0.97	0.96
		3	1 083	0.95	0.93	0.97	0.96
	Protein	1	2 368	0.998	0.998	0.998	0.999
		2	967	0.998	0.998	0.999	0.999
		3	1 083	0.999	0.999	0.999	0.999
Modified model (a.m./p.m. milk yield relation)	Fat	1	2 368	0.96	0.94	0.97	0.97
		2	967	0.95	0.93	0.96	0.96
		3	1 083	0.95	0.93	0.96	0.96
	Protein	1	2 368	0.998	0.998	0.998	0.999
		2	967	0.998	0.998	0.999	0.999
		3	1 083	0.999	0.999	0.999	0.999

Table 5 shows that protein is estimated more accurately than fat. The fat yield is estimated most accurately with the recommended model. But where it is not practically possible to register time, the a.m./p.m. milk yield relation can be used. It is almost impossible to see the difference on the accuracy of protein – whether it is the recommended model or the modified model that is used. It applies for both fat and protein that the yield is estimated most accurately if the milk samples are taken out alternate morning and evening.

Differences between the known and the estimated 305 days fat and protein yield are seen in table 6. The estimated yield was determined with the “AM-method” (Table 4) and the recommended model. If the difference is negative, the yield is overestimated and if the difference is positive, the yield is underestimated.

In table 6 it is shown that the differences for fat have a tendency to be negative, because the estimated 305 days fat yield on average was overestimated for all three parities. The differences for protein have a tendency to be positive, because 305 days protein yield was on average underestimated for all three parities.

Table 6. Differences (kg) per parity between known and estimated 305 days yield. The yields were estimated with the recommended model and the AM sampling method.

	Parity	Number yield	Mean known	Mean dif.	S.D.
305 days fat yield (kg)	1	2 368	317	-2.4	11.8
	2	967	359	-2.3	15.2
	3	1 083	376	-2.2	15.6
305 days protein yield (kg)	1	2 368	265	1.3	1.9
	2	967	298	1.0	2.0
	3	1 083	303	0.7	2.0

95 % of the estimates of the fat yield per day will be within the range of 150 grams from the true fat yield per day. 95 % of the estimations of the protein yield per day will be within the range of 35 grams from the true protein yield per day.

There is no sign that the model over- or underestimate certain groups – for example high-performance cows.

The recommended model describes a reasonable correlation between the true yield and the estimated yield for both fat and protein. The calculated accuracies (Acc) are just as high as the accuracies described in the literature. Higher accuracies are obtained using kg fat and kg protein in the model instead of fat and protein percentages.

It has been investigated whether a modification of the recommended model can give the same accuracy. The modification was that the time interval between the individual milkings were replaced by the relation between kg milk a.m. and kg milk p.m. The modified version of the model gives almost the same accuracy as the recommended model.

For both models the accuracy for kg fat was on the highest level with milk samples taken out in the evening. For protein, the models gave the best estimate based on samples taken in the morning. This indicated that the best results are obtained taking the samples out alternate morning and evening.

The analysis to determine the 305 days yield showed that the protein yield could be calculated with great accuracy based on one milk sample per test day. Lower accuracy existed on determination of the fat yield.

The model gave within this material a bit too high estimation of the fat yield in all lactations, but the protein yield was estimated a bit too low. The estimated yields were compared to the calculated true yield.

The breeding values for bulls are not affected from the changed sampling, but in the cows the bias in the estimation of the test day yield of the single cow will affect the breeding values. Thus the selection of bull dams has a bit lower accuracy.

In Denmark it is decided to change the milk recording system in a way, where we use electronic Tru-Test milk meters, and per test day only one milk sample (morning or evening) is analyzed. Results are presented to the farmer as the measured yield in kg milk and the estimated percentages of fat and protein.

Schaeffer, L.R., Jamrozik, J., Van Dorp, R., Kelton, D.F. og Lazenby, D.W. 2000. Estimating daily yields of cows from different milking schemes. *Livestock Production Science*, 65, pp. 219-227.

Conclusion

Implementation

List of references

Tru-Test electronic Milk Meter – practical field use by AgSource/CRI

P. Jandrin

*AgSource Cooperate Services, 135 Enterprise Drive,
Verona, Wisconsin 53593, USA*



Slide 1

AgSource started working with the Tru-Test Electronic Milk Meter in summer of 2005 on trial basis. I was the lead person in field trials, training and working with Tru-Test.

The goals of the trial were, from Tru-Test's side, to see what software changes were needed to get the electronic meters established in the United States. At AgSource our goals were to see how well they worked in different types of parlors and sizes of dairies for durability, ease of use and acceptance by employees and dairymen. In the trial period we also included work with the Wisconsin Livestock Identification Consortium on using RFID tags with the EMMs.



Slide 2

Another one of our main goals was to see if the Tru-Test Data Handler would be able to work with the EMMs and mechanical meters to replace the computer during testing. The Data Handler is very durable, water tight, the menus are very easy to use and the battery lasts for up to 20 hours. It can be used with mechanical meters where the field tech records milk weights, sample numbers and pen numbers or it can be setup to record just samples and pen numbers as with electronic parlor

meters. The Tru-Test Data Handler comes in either a bluetooth model to work with an RFID tag reader or the model which works with the Tru-Test Electronic Milk Meters.

Slide 3



EMMs and Data Handler transfer data to each other via radio frequency. They record the meter id and stall position in the parlor, the milk weights and reads the barcode on the sample vial. They record the pen numbers and CAR codes of any sick cows. The Data Handler alerts you and asks you to verify any duplicate or new cows and allows you to change a previous number if the second cow is the correct number.

The time each cow was milked and how long she took to milk is also recorded along with milk rates per minute to allow you to graph the flow rates of the cows and analyze the wash cycle to make sure each stall is washing properly.

Slide 4



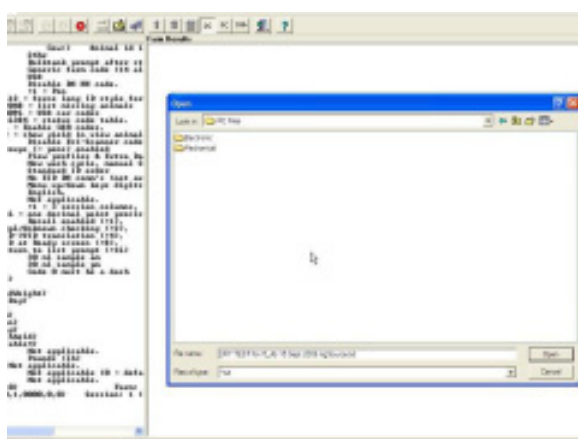
Cow numbers get matched to the meter by entering the cow into the Data Handler and then pressing the Select button on the EMM. Cow numbers can be entered by the whole side of the parlor and then use the Recall menu item to match to the meter or one meter at a time either by stall number or in order cow is milked. When the cow is finished milking the tech presses the Finished Milking button and the cow information is recorded automatically.

CAR codes can be entered cow side. And the field tech and lab save time as the barcoded vials can get placed anywhere in the tray, do not need to have a number on the cap and the lab can run trays in any order. All the information is matched thru the barcode.



Slide 5

The Link program is Tru-Test's program to transfer information between the Data Handler and computer. Information recorded in the Data Handler can also be viewed using the Link program and be sorted either by cow number or sample number. It is very easy to switch between EMMs and mechanical meters by switching the RC file.



Slide 6

RC files tell the Data Handler and EMMs what to do. With mechanical meters if weights and samples are to be recorded or samples only. With the EMMs the RC file tells the meter if you are recording weights only or weights and samples and if you want to store flow profiles and wash information. The RC file also sets the amount of milk put into the vial and can be set for proportionate sampling in 2x herds.



Slide 7

The Select button is used to transfer information between the meter and Data Handler. When the Select light is flashing it means a cow number is needed to be entered or there was an error reading the barcode. Action needs to be taken before taking a sample. If the light is on steady there is a problem with meter, most times this is

Slide 8

when starting the meter before milking or there is problem taking a sample. Action needs to be taken care of right away. The tech just presses the Select button and views the message on the Data Handler.



The Finished milking Release sample button is used to take the sample. When this light is flashing it means the milk flow has stopped or just about stopped. If it is on steady it means the meter is in the process of taking a sample.

Slide 9

Low Battery light comes on when battery is down to 2 hours left on the charge. At full charge the battery lasts for 30 hours.



Slide 10

When the Finished Milking button is pressed the meter agitates the milk and takes the sample.



The meter then fills the vial, empties the flask and is ready for the next cow. This process takes about 10 seconds.



Slide 11

The batteries on the EMM last for 29 hours on a full charge. Each time the meter is turned on the Data Handler will display how much time is left on battery. Up to 10 meters can be charged on one power pack.



Slide 12

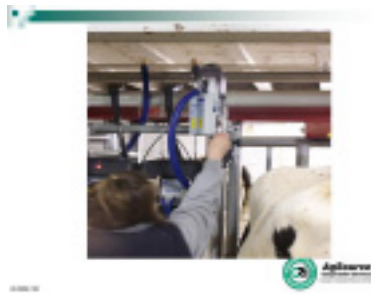
Tru-Test also has portable style chargers. The meters have 2 rivets on the back which are the contact points for charging the battery. Transportation was our biggest obstacle as they are not as easily transported between farms and field techs as other Tru-Test meters. We use plastic tubs deep enough for two layers of meters with 1/8" plywood between and non-slip padding.



Slide 13

The Tru-Test EMMs work very well in flat barn parlors, there is less walking through gates and no passing milk flasks back and forth. We have a 16 stall parlor with 3-4 people milking and they do reattach units on some cows. The field tech with other meters had problems knowing if it was a new cow in the stall or the unit was reattached. With the EMMs the milkers press the End of Milking button when cow is released.

Slide 14



The field tech then just looks for a cow milking and a meter with a full sample vial. The tech then changes the vial and enters the next cow number.

Slide 15



This herd is a 2 sided, 10 stall parlor which samples two milkings. This is the only time you need to make sure the samples are placed in order in the tray as the Data Handler will tell you where the sample is in the tray for the 2nd milking. The meter can also be setup to take a proportionate sample if needed.

Slide 16



When using these meters in a basement parlor we listen for side to be released then go down the whole side and press finished milking buttons. This parlor we have a problem where the equipment dealer did not mount one pipe tight and it keeps turning on us. These meters will compensate for being a bit out of level.

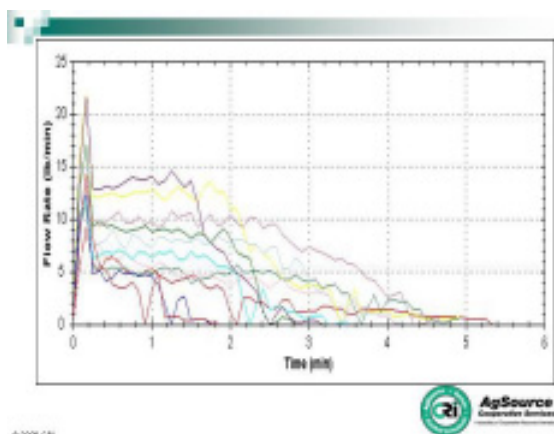


Slide 17

When this herd expanded the parlor the vacuum shutoffs were going to be mounted right on the milkline. When we told the dairyman we needed vacuum 100% of time to agitate the samples and would need to go back to using the pull out meters the dairyman made the dealer mount the vacuum shutoffs on the wall.

In the fall of 2007 Tru-Test came out with new software which changed this. The meters can now be setup to agitate the sample when milk flow slows to 2.2 pounds per minute. They stir the milk for 3 seconds the first time and then 1 second every 10 seconds until the finished milking button is pressed. The meter then fills sample vial and waits for the unit to be put on next cow to empty flask. When the tech hears the side go out they go down the line pressing the finished milking button, changes the vials, go upstairs and enter the cow numbers. Back downstairs, the Data Handler recalls cow numbers in the order they were entered and are matched to the meter by pressing select. The meters empty flasks when vacuum on each unit is turned on.

Slide 18



Slide 19

Flow profiles can be graphed for each cow, for all the cows on each meter, or all the cows in each switch of the parlor. These are used to analyze how well the people milking are prepping cows, how many reattachments are made during the milking, and can be used to check for problems with meters or stalls either during milking or the wash cycle.

We also developed a report in Dairy Comp305 showing milk weights and how many minutes the cow took to milk which is used to speed up milking by marking or segregating slower cows.

Slide 20



Summer 2005

- Trial Program with Tru-Test
 - Get meters established in US
 - Develop software
 - Dairy One, Dairy Comp, DRPCs
- Performance and Durability
 - Different types of dairies
 - Transportation



© 2008 CIB

In summary the trial was very successful for both Tru-Test and AgSource. Tru-Test was able to have the Electronic Milk Meter established in the US. When developing the software they worked with AgSource, Dairy One, Dairy Comp305 and all DRPCs. So the Data Handler files compatible with everyone.

On AgSource's side the meters performed and adapted very well to many different styles of dairies. Our biggest issue to overcome was transportation.

Slide 21



Purchase of Meters

- Repayment
 - Gain Herds
 - Save Labor – sometimes intangible amount
 - Largest Herd – 2x44 Parallel Parlor
 - Smallest Herd – 100 Cow Tie Stall Barn
- 2006 – 50 Meters and 20 Data Handlers
- 2007 – 25 Meters
- 2008 – 100 Meters



© 2008 CIB

When we decided to purchase the meters we looked at repayment of the cost. This came in the form of gain of herds on test and saving labor. We did gain herds and are still continuing to start new herds on test. While also keeping herds from quitting or switching to competition by saving them time and assuring them a higher degree of accuracy.

Saving labor is sometimes an intangible amount. In some parlors we have maintained the same high degree of accuracy with fewer techs while other parlors we have greatly lessened the stress on the techs in the large fast parlors. Tired techs have higher chance of misreading numbers on tags and samples and in our largest parlor we still use 3 techs, but there is the long term benefit of less stress making a happier and healthier employee.

Supplemental testing on milk recording samples

T. Byrem¹, M. Adam² & B. Voisinet¹

¹*Antel BioSystems, Antel BioSystems, Inc.,
3655 Forest Road, Lansing, MI 48910, USA*

²*NorthStar Cooperative, 3655 Forest Road,
Lansing, Michigan 48910, USA*

Milk samples taken from cows by milk recording organizations on periodic test dates are an underutilized resource for both dairy producers and recording organizations. While analysis of fat, protein, and solids continue to be the mainstay of the milk testing laboratory, there are a growing number of supplemental assays that deliver additional information and provide a greater return on investment in the milk recording process. Enzyme-linked immunosorbent assays (ELISA) and polymerase chain reaction (PCR) are two widely used procedures in veterinary research and medicine that have direct applicability to milk recording samples. Compared to traditional blood testing programs for widespread diseases such as Johne's disease, the utilization of the milk recording platform offers dairy producers, veterinarians and animal health regulatory agencies an attractive alternative that greatly reduces the cost and inconvenience of control and surveillance programs. Milk testing programs developed by Antel BioSystems for Johne's, leukosis, bovine viral diarrhoea, and progesterone and successfully implemented by NorthStar DHI are described.

Key words: *Milk testing, Johne's, Leukosis, Bovine viral diarrhoea, Progesterone.*

Traditionally, milk has been viewed as the saleable product of the dairy industry, providing valuable nutrition to consumers and important ingredients to other sectors of the agricultural industry. Even in the milk recording industry, individual cow milk samples obtained on a periodic basis are analyzed for fat, protein, and other solids as they relate to the commercial value of milk and cow performance. As technological advances bring these traditional analyses closer to the farm, the role, or even the existence, of the milk recording industry could be threatened. To answer this threat, supplemental milk testing should be explored to recover more of the inherent value of milk recording by extracting and delivering additional information from milk samples.

Summary

Introduction

Milk, as blood, is an accessible window to the health and metabolic state of the dairy cow and, except for the presence of red blood cells, its composition is basically comparable. Therefore, while blood is typically the sample of choice for diagnostic testing and metabolic analysis, milk samples can satisfy many of the requirements for comprehensive analyses. In the dairy industry, and specifically for milk recording organizations, the major advantage for utilizing milk samples instead of blood samples for additional analysis is that the milk samples are already routinely collected and transported to centralized laboratories. In other words, milk recording organizations invest a considerable portion of their budget on the acquisition and analysis of individual cow samples. The extraction, sale and delivery of additional information from supplemental milk testing can greatly improve the return on this investment.

Johne's disease

Johne's disease (JD) is a wide-spread, chronic digestive disorder in ruminants caused by *Mycobacteria paratuberculosis*. Transmitted primarily to calves through fecal-oral routes, the bacteria colonize leukocytes in intestinal mucosal and lymph tissue, inducing varied immune responses that ultimately interfere with nutrient absorption. Clinically, infected animals are unable to sustain most productive functions and ultimately succumb to malnutrition. An association between bovine JD and human Crohn's disease has led to the development of specific, nationally-sponsored control and eradication programs in many countries.

In the absence of effective treatments and vaccines, Johne's disease is best controlled through a combination of sanitary animal husbandry practices and diagnostic testing to identify and manage infected animals. Current diagnostic tests focus on either the detection of the organism (manure, milk, tissue) or the detection of antibodies (blood, milk). The slow and variable progression of JD dictates serial testing to effectively identify infected animals in a timely fashion, thus milk recording offers a convenient platform to regularly screen dairy animals for infection.

JD milk testing

An enzyme-linked immunosorbent assay (ELISA) was developed to detect the presence of JD antibodies in milk samples. The ELISA was validated against commercially available and USDA-approved testing procedures in herds of varying breed, size and incidence of JD (Figure 1).

Of the individual milk samples from 688 animals in herds considered free of JD, only 4 were found to be positive in the JD milk ELISA. The apparent specificity for milk sample testing was 99.4% and was not different from serum testing where 1/688 (0.15%) samples were positive. In herds suspected of having JD, there were 799 samples with both fecal culture and milk ELISA results. There were 183 samples (22.9%) that were fecal culture positive and 128 (16.0%) that were milk ELISA positive. Of these 183 fecal culture positive animals, 90 (49.2%) were milk ELISA positive and 98 (53.6%) were serum ELISA positive (88% agreement). Clearly, antibodies for JD are in milk and their detection by ELISA is a reliable diagnostic.

Recently, a more sensitive JD milk ELISA has been tested for use in bulk tank samples. As part of the National Animal Health Monitoring Survey (NAHMS) in 2007, the JD bulk milk ELISA was compared to cultured environmental fecal samples to detect the presence of JD at the herd level. Results presented in figure 2 show that the bulk milk ELISA is capable of detecting the majority of infected farms with sufficient specificity to screen herds efficiently and cost effectively.

		Serum Analysis		
		Positive	Negative	Total
Milk Analysis	Positive	0	4	4
	Negative	1	683	684
	Total	1	687	688

		Fecal Analysis		
		Positive	Negative	Total
Milk Analysis	Positive	90	38	128
	Negative	93	578	671
	Total	183	616	799

		Serum Analysis		
		Positive	Negative	Total
Milk Analysis	Positive	83	7	90
	Negative	15	78	93
	Total	98	85	183

Figure 1. Performance of milk ELISA testing for Johne's Disease in individual animals compared to serum and fecal testing.

		HEYENV [#]		
		POS	NEG	Total
Milk-ELISA	POS	199	8	207
	NEG	185	123	308
	Total	384	131	515
Relative Sensitivity		51.80%	SE= 0.025	
Relative Specificity		93.90%	SE= 0.02	

Figure 2. Performance of bulk milk ELISA testing compared to Environmental fecal cultures (HEYENV[#]).

An organism-based bulk milk assay has also been developed using real-time PCR to target the IS900 genetic element as another method of detecting herd-level presence of JD. Figure 3 shows that as few as 50 cells of *M. paratuberculosis* can be quantitatively detected by real-time PCR analysis of spiked milk samples. When applied to the NAHMS 2007 milk samples, the assay was able to detect 40% of the infected farms with similar specificity as the JD bulk milk ELISA (Figure 4). More importantly, the data suggests that 40% of US dairy farms have detectable levels of *M. paratuberculosis* in their bulk tanks, dramatically emphasizing the necessity of effective control and surveillance programs for JD.

Bovine leukosis is caused by a blood-borne retrovirus (BLV) that permanently infects and interferes with the immune system. Transmission occurs through transfer of infected white blood cells from blood or milk to susceptible cattle of any age. Clinical disease is relatively rare however, and the economic impact of BLV is questionable even in herds with prevalence rates greater than seventy percent. In rare cases, infection can result in bovine lymphosarcoma with variable effects dependent on

Enzootic bovine leukosis

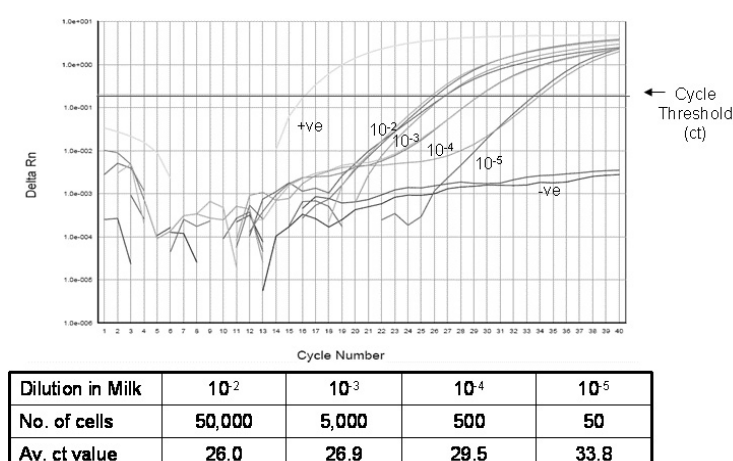


Figure 3. Real-time PCR analysis (IS900) of milk spiked with *Mycobacteria paratuberculosis*.

		HEYENV [#]		Total
		POS	NEG	
Milk-PCR	POS	153	8	161
	NEG	231	123	354
	Total	384	131	515
Relative Sensitivity		39.80%	SE= 0.024	
Relative Specificity		93.90%	SE= 0.02	

Figure 4. Performance of Real-time PCR analysis of bulk milk compared to environmental fecal cultures (HEYENV#).

the anatomical site of tumor formation. The greatest concern for BLV stems from the fact that several countries will not import cattle or germplasm from BLV-infected areas.

There is no treatment or vaccine for BLV. Unlike JD, diagnostic signs of BLV are more readily detectable however, and antibody detection assays have been used successfully to eradicate BLV in several countries. The immune response to BLV infection is rapid with persistent production of high antibody titers to dominant antigens that can be easily used in ELISA format. Once detected, infected animals can be physically isolated, sorted or culled to control transmission. Milk samples obtained through milk recording provide an excellent platform for regular detection and management of BLV.

BLV milk testing

There are several commercial assays available for the detection of antibodies to BLV in milk samples. The sensitivity and specificity of these assays are generally greater than 95% when compared to the serum-based assays (Figure 5), and their utility in control and surveillance programs is unquestionable. There is one problem that must be accounted for when using these assays on milk recording samples; carryover contamination. Because of the large antibody response to BLV infection,

BLV Milk ELISA	Serum ELISA		
		Positive	Negative
	Total		
Positive	89	0	89
Negative	0	87	87
Total	89	87	176

Figure 5. Performance of milk ELISA testing for bovine leukosis in individual animals compared to serum testing.

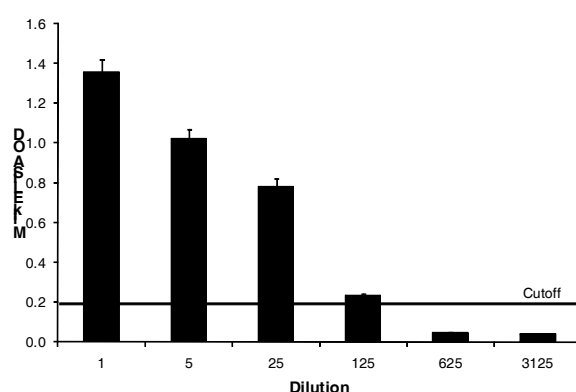


Figure 6. Effect of dilution on the leukosis milk ELISA.

the mixing of milk samples from subsequent cows that occurs during milk collection (through metering devices) and component analysis in the laboratory can lead to false positives. Figure 6 shows positive milk samples can be diluted by as much as 1:125 before the resultant signal is reduced to undetectable levels. Therefore, any carryover contamination beyond 1% will lead to a reduction in the specificity of the assay. This likelihood is negated by minimizing carryover contamination during collection and including a “Suspect” category for milk samples with low antibody titers that would be indicative of a potential carryover effect.

Another prominent viral infection in cattle is BVD. Infection occurs in many epithelia tissues; its predilection to the respiratory system accounts for aerosol-based transmission, its presence in the reproductive system leads to a variety of congenital disorders, and its effects on the digestive system results in death in extreme cases. Thus, the clinical manifestation of BVD infection has a large and consequential economic impact on dairy operations.

The reservoir for the BVD virus is persistently infected animals. When exposed during early gestation, the developing immune system of the fetus may become immunotolerant to the virus, unable to mount an immune response and postnatal, the animal remains persistently infected throughout life. Persistently infected animals act as incubators for new, mutant BVD strains that are not represented in the present generation of vaccines, resulting in new infections and outbreaks even in properly vaccinated herds.

Bovine Viral Diarrhea (BVD)

Testing for BVD is a component of control programs for unvaccinated and vaccinated herds. In unvaccinated herds, the presence of antibody titers suggests previous exposure to and thus, circulating BVD virus. Most BVD infections are acute however, and the immune system effectively clears the virus without complication and thus, diminishes the utility of antibody detection by ELISA. On the other hand, persistently infected animals are unlikely to produce antibody titers and their detection requires antigen (virus) detect tests whether or not vaccination is included in the control program. Since BVD virus is shed in milk, milk recording samples can be used in BVD screening programs for the milking herd; calves are typically screened with blood samples or ear notches in antigen detection assays.

BVD Milk Testing

Pooled samples such as bulk tanks and group samples can be originally screened for BVD virus by PCR to reduce the overall testing requirements and cost to find persistently infected cows. The PCR results presented in figure 7 show the amplification products from the 5' UTR (untranslated region) of the BVD virus and an internal control (β -actin) in the analysis of naturally infected milk samples at various dilutions. While detection is clearly seen at 1:1000, conservatively pool sizes are typically limited to 1:400.

The major advantage of pooling milk recording samples for PCR analysis is that the remaining sample can be stored for immediate, individual sample analysis if required upon a positive pool test. In contrast, if line samples are used for pooled analysis, cow movement and trafficking while waiting on pooled test results can confound individual animal testing if required. For example, if the persistently infected cow is transferred to another group before the test results are returned, individual animal testing in the indicated group would not result in the identification of the persistently infected cow. By using milk recording samples, the individual samples within groups are fixed and easily tracked and accounted for.

A more economical antigen detection test is required for individual milk sample testing within positive pool samples. Figure 8 compares the results of a BVD milk ELISA to traditional testing using serum and/or ear notch samples. There was 100% agreement between the BVD milk ELISA and traditional analysis, indicating that viral shedding in milk is consistent and indicative of persistent BVD infection.

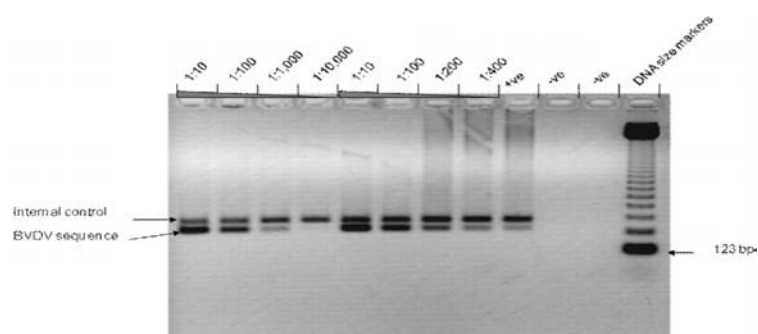


Figure 7. Effect of dilution on PCR analysis of milk for BVD virus.

	Serum / Earnotch ELISA		Total
	Positive	Negative	
BVD Milk ELISA	Positive	0	18
	Negative	386	386
	Total	386	404

Figure 8. Performance of milk ELISA testing for BVD virus in individual animals compared to serum or ear notch testing.

The advantages of the milk testing program described above are best illustrated in Figure 9, which outlines the testing protocol and costs for a 1 000-head dairy. Without a pooling strategy, the cost to screen this herd by individual BVD milk ELISA at US\$6.00 a test would be US\$6 000. By pooling individual samples and using PCR analysis to narrow the scope of testing, the total cost to the dairy producer is reduced to US\$810, including a charge of US\$0.15 per sample for pooling. More significantly however, the dairy producer did not have to incur the cost or effort of drawing blood samples or ear notches from individual cows.

Theriogenologists have analyzed progesterone for many years to research and develop breeding programs for dairy herds. Progesterone is a hormone produced and released into the blood by the corpus luteum (CL) on the ovary. The CL is formed after the follicle has ovulated (estrus) and is maintained for the nine months of gestation if the cow becomes pregnant. If conception fails, the CL regresses after 18 days and progesterone concentration falls, allowing the initiation of another cycle. Thus, progesterone is at low levels for non-cycling cows, and during the 6 days that surround estrus (d 20 to d 4) until the CL is producing sufficient levels of progesterone, which can be measured in both blood and milk.

Progesterone

- 1000-Head Herd (\$0.15/sample to pool)

- 4 PCR X \$40 = \$160

250 Samples	250 Samples	250 Samples	250 Samples

- 5 PCR X \$40 = \$200

50 Samples	50 Samples	50 Samples	50 Samples	50 Samples

- 50 ELISA X \$6 = \$300

Sample Size	Frequency
10	1
20	2
30	3
40	4
50	5
60	4
70	3
80	2
90	1
100	1

- Total $\$810/1000 = \$0.81/\text{Cow}$ ($\$0.50-\$2.50$)

PI Cow

Figure 9. Milk testing protocol for BVD virus using milk recording samples.

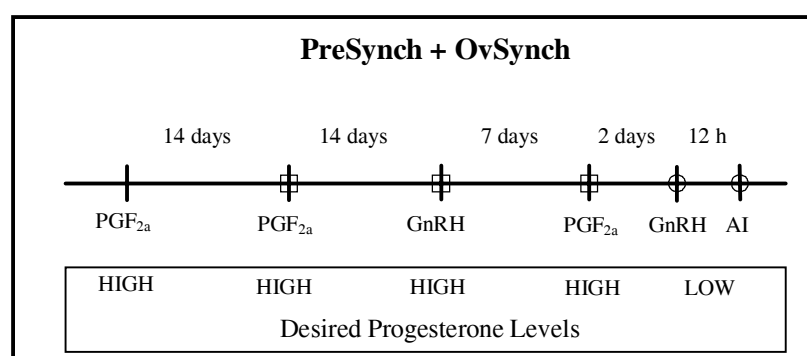


Figure 10. Predicted progesterone levels at critical hormone injection points during estrus synchronization using the PreSynch + OvySynch protocol.

Progesterone testing, along with other factors, can be used as an evaluation tool to assess a herd's breeding program, especially in herd's using synchronization programs for artificial insemination. As an example, Figure 10 details the PreSynch + OvSynch program.

In any synchronization program, cows need to be cycling for the hormone injections to be effective in predicting or timing estrus for AI. Milk samples can be checked for progesterone levels at critical hormone injection points (i%) when the CL is expected to be present on the ovary. At these points, progesterone levels are expected to be high (>5 ng/mL); low or undetectable levels indicate animals in which the synchronization program is failing, either because they are not cycling or they received improper hormone injections. Likewise, milk samples can be checked for progesterone during predicted estrus (E%), when the CL is expected to be absent. At these points progesterone levels should be low (<5 ng/mL); high levels indicate an active CL and very little chance of an ovulation to coincide with the scheduled AI.

Progesterone milk testing

Blood has been the traditional sample for progesterone analysis and is the method of choice for most herds. However, a progesterone milk ELISA has been developed as a convenient alternative to use with milk recording samples. Based on the number of cows required for a worthwhile analysis, the milk testing option is best suited for larger herds that may be inseminating 20-30 cows in any given week. To use milk analysis, a dairy producer identifies cows at critical points (based on their synchronization program) on each milk recording test date for progesterone analysis. A continuous analysis of progesterone data for compliance in each of three lactation groups on successive test dates is shown in figure 11. While noncompliance rates generally average between 20-30% in aggressive yet successful breeding programs, upward trends in noncompliance as shown for the 1st lactation heifers indicate poor responsiveness to the synchronization protocol. As a diagnostic tool, the information is useful for troubleshooting and correcting poor reproductive performance.

Progesterone Non-Compliance

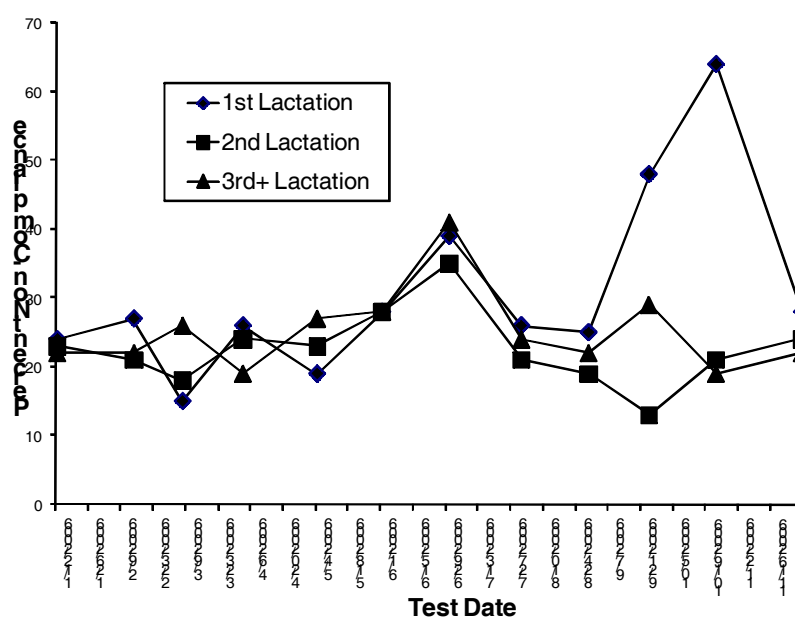


Figure 11. Noncompliance analysis of milk progesterone levels during estrus synchronization.

Thus far, supplemental milk assays for JD, leukosis, BVD and progesterone have proven to be valid and useful tools in the dairy industry. The utility of these testing programs offered through milk recording organizations are attracting the attention of the entire animal health industry, including government regulatory agencies and diagnostic assay manufacturers, which will stimulate the development of additional assays for milk samples in the future. Future assays will not only address other pathogens, hormones and metabolites, but will combine multiple assays in single, high throughput testing procedures (multiplex). How fast these possibilities become reality for milk recording organizations depends on the perceived market. At first glance, the market for diagnosing animal health and metabolism through milk recording might appear limited, but with recent advances in genomic analysis and marker assisted selection, one has to wonder about the future value of additional phenotypes.

Future opportunities

ICAR guidelines for alpaca shearing management, fibre harvesting and grading

M. Antonini

ENEA BAS Via Anguillarese 301, S.M. di Galeria, 00060 Rome, Italy

ICAR opened in the 2007 a Working Group (WG) on Animal for fibre. A Task Force (TF) was established at first on Alpaca fibre production. The WG components represent 6 different countries (Italy, China, Australia, Peru, Argentina and UK) and come from different private and public Organizations (3 University, 3 Research Centre and 3 Private Company). The WG on Alpaca Fibre defined the terms of reference for Alpaca and at the moment two of them have been fixed: the Alpaca identification methods and the guideline of Alpaca fibre harvesting and grading. Present paper describes the second term of reference.

In order to offer a common approach at the Alpaca breeders and at the Alpaca textile processors ICAR suggests a common approach of Alpaca breed management with particular attention at the fibre product management in order to exploit at the best the animal selection development. According to the auto certification methodology yet applied in other advanced fibre animal breeding systems, Alpaca fleece collection critical points have been identified. Through the present procedure, the possible defects that may be found in the end product can be easily individuated and localized the error of management in the previous step of the Alpaca fibre processing chain. Present ICAR Guide Line want to be a concrete support for the first Alpaca selection plans which have been organized in particular in the main producing area as Peru and Bolivia.

Key words: Alpaca, Textile fibre, Shearing, Grading.

ICAR opened in the 2007 a working group on Animal for fibre. A Task Force (TF) was established at first on Alpaca fibre production. The WG components represent 6 different countries (Italy, China, Australia, Peru, Argentina and UK) and come from different private and public Organizations (3 University, 3 Research Centre and 3 Private Company). The WG on Alpaca Fibre defined the terms of reference for Alpaca and at the moment two of them have been fixed: the Alpaca identification methods and the guideline of Alpaca fibre harvesting and grading. Present paper describes the second term of reference.

Summary

Introduction

In 2006 the NGO DESCO (*Centro de Estudios y Promoción del Desarrollo*), Peruvian breeders Group, was the first Alpaca breeder Association jointed at ICAR in the fibre production section. DESCO carried out the first Peruvian Open nucleus selection plan (PROMEGE - *PROgrama de MEjoramiento GENético*) carried on in the Highland of Caylloma Province – Arequipa and TOCCRA Station represents the selection nucleus for the 18.000 Caylloma Province Alpaca population (Gonzales *et al.*, 1998). Index of selection has been defined and recently first improving animal have been produced. In order to offer a common approach at the Alpaca breeders and at the Alpaca textile processors ICAR suggests a common approach for the Animals and fleeces management with particular attention at the fibre product. Present Guide line are defined in harmonized way at the Alpaca fibre recording methods applied in the PROMEGE selection plan defined in cooperation with DESCO, University of Camerino, ENEA and Catholic University of Cordoba, in order to exploit at the best the animal selection development.

Methodology

Alpaca Fleece Collection Critical Control Points (AFCCCCP) have been identified according to the auto-certification methodology currently applied in other advanced fibre animal breeding systems (AWEX 2007).

The application of AFCCCCP utilising simple procedures in animal husbandry, fleece shearing management, fibre harvesting and classification, provides conditions to optimise quality of product for the next step in the processing chain. It will also allow the identification of sources of defects, which are detected in end products and localise the individual system failures and errors in management occurring in previous steps of the chain.

Critical control points

The principal critical control points are organized in 6 distinct steps:

- Standardising alpaca clip preparation.
- Structural needs.
- Preparation for shearing.
- Shearing process.
- Grading and classifying.
- Packaging and transport.

The characteristics, how they are measured, and which define the quality of Alpaca fibre products for the textile industry, are:

- Fineness (fibre average diameter - mm).
- Homogeneity (fibre average diameter Coefficient of Variation - C.V. %).
- Staple length (fibre average length - mm).
- Medullation (- percentage %).
- Impurities (greasy yields and percentage content of vegetable matter - %).
- Colour.

For fleece harvesting arrangements to be considered for animal handling, working environment and equipment are as follows:

- Rest Area for Alpaca before shearing.
- Shearing area.
- Procedures for shearing.
- Grading areas.
- Equipment for grading.
- Packaging and baling area.

The final goals of the correct management of the different steps of the fibre/ fleece shearing, harvesting and grading processes are:

- Optimising the quality and uniformity of raw material and providing confidence for its use by manufacturers.
- maximizing the financial return and profit

These guidelines describe the recommended management of actions during the shearing period and the organization of the different working environments.

Guidelines for shearing

Before the alpaca enter the clip areas the follow actions should be taken into account:

- Keep the alpaca in a rest paddock close to the clip area.
- Keep the alpaca dry.
- Divide the alpaca into different groups of shearing according to, type of Alpaca (Suri and Huacaya), age and sex of animals and the colour of fibre, with emphasis on keeping separate fleeces from the white Alpaca and from the younger animals with the finest fibres.

This is the best way to obtain the most homogeneous lots for colour and quality.

The timing of the shearing period is one decision requiring very great consideration in the alpaca fibre production life. The seasonal shearing period will require to be chosen according to the following aspects:

1. Environmental conditions – when cold and windy after clipping, the Alpaca will require to be housed indoors, kept dry and offered concentrate food for 10 days at least.
2. Reproduction activities – staining is increased in fleece harvested after delivery of the cria and during the breeding season when pregnancy also reduces fleece and fibre yield.
3. Pasture vegetative phase – alpaca need to be clipped before the development of seeds in the pasture. Seeds are the main reason for contamination and depreciation of the fleece and along with other vegetable matter are virtually impossible to remove during the different steps of textile processing (IWTO-19, 2004).

The Pens

In order to reduce contamination in the fleece by extraneous materials, all the farm pens where the alpaca live have to be free of:

- bales, ropes, twines and strings for hay packaging;
- rubbish wastes;
- unused equipment such as old beams or machines;
- wires, barbed wires, old sandpapers, screws, nails, bolts and chains;
- cigarette ends.

The presence of these materials causes major troubles for the textile industry. They greatly reduce the economic value of the end products and even sometimes cause expensive damage to textile processing machinery.

Step 1: Alpaca clip preparation

Step 2: structural needs

The clip shed area

A shed should be utilized only for the alpaca clip. It should be divided physically into three distinct areas:

1. **Alpaca Handling Area.** *Where the Alpaca rest before being brought into the clip area*

This sector has to be totally separate from the other two areas. It is necessary for it to be protected from draughts and rain, to have the floor covered with elevated wooden floorboards and to have suitable ventilation.

2. **Clip Area.** *Where the alpaca undergo the shearing*

The clip area needs to be completely separated from the other two areas and to be covered by wooden floorboard. Careful cleaning needs to be done after shearing finishes for each different Alpaca group separated for fibre fineness and colour and before starting the next group with different fibre characteristics. Finally, all the devices used to immobilize the alpaca have to contain non-contaminating materials (i.e. cotton), in order to avoid contamination especially with synthetic fibres.

3. **Fleece Grading Area.** *Where the single whole fleeces are separated and graded in different fineness categories.*

An appropriate artificial or natural light has to be provided in the fleece grading areas; the grading table has to be constructed of single wood planks separated by spaces to enable the falling-out of impurities. Clean previously used sacks or new sacks have to be available for each fibre category.

Inside the shed area the following important rules of hygiene have to be observed

- Before the shearing: remove all rubbish and carefully wash the shed area when it is empty.
- Provide shearing staff with the equipment to clean the shoes (scrapers, containers with cleansing and / or disinfectant liquid).
- Forbid smoking inside the clip area.
- Forbid eating of food.
- Forbid the grooming of Alpaca feet and especially the cutting of nails.

Step 3: preparation for shearing

Before beginning the actual Alpaca clip, all the hygienic rules above have to be respected. All the alpaca must go without food for at least 4 hours and they must be presented at the shearing according to pre-determined categories (age, sex, colour etc. ...)

Finally the bags, where the shearing and grading fleeces will be collected, will have to be checked inside in order to remove rubbish and contaminant materials.

Step 4: shearing process

The alpaca clip method will have to be performed according to the practice and methods of the local available shearers. Whatever the methods, the shearers will have:

- To be careful to separate firstly the less valuable fleeces fractions (feet and belly parts).
- To keep the fleece as intact as possible, in order to make easier the next fleece grading.

- To avoid absolutely the double-cut during shearing. This causes a great variation in average length of the fleece fibre and results in a heavy depreciation in value of the products.

After shearing, shepherds have to be careful to avoid exposing the alpaca directly to sunlight and currents of cold air in order to prevent sunburn and hypothermia.

The principal grading aim is to offer fibre products in such way that the textile manufacturers do have not to make further selection and cleaning before starting factory processing. The results from good grading and handling practices are the elimination of added unnecessary costs and a better quality end product.

The main actions to carry out in the present step are:

- The fleeces must not be rested on the floor.
- Once sheared, the fleeces have to be put immediately on the grading tables.
- Grading tables have to be cleaned after the grading of each fleece.

The fleeces obtained are classified for:

- Type of fleece.
- Fineness.
- Colour.
- Length.
- Presence of medullated fibre or kemp.
- Stained; special category foreseen for dirty fibres.

Each fibre category has to be identified by suitable codes, which have to be affixed on packaging.

Fineness category¹

Under 20 microns	< 20 µm	(SSF - Super Super Fine)
Between 20,1 and 22 µm	>20,1 µm and < 22 µm	(SF - Super Fine)
Between 22,1 and 24 µm	>22,1 µm and < 24 µm	(F - Fine)
Between 24,1 and 26 µm	>24,1 µm and < 26 µm	(M - Medium)
Between 26,1 and 28 µm	>26,1 µm and < 28 µm	(CM - Coarse Medium)
Between 28,1 and 30 µm	>28,1 µm and < 30 µm	(XCM - Extra Coarse Medium)
Over 30 µm	>30 µm	(C - Coarse)
Stained		(STD - Stained)

¹At the moment the Fineness Categories guide line are referred to Huacaya fleece type .

Step 5: Grading and classification

Alpaca fibre classification proposal

Colour

Type	Code	Range	Sub Code
White	W		
Black	BLK		
		Dark	B - Dk
Brown	B	Self	B - Slf
		Light	B - Lgt
Light Fawn	LF		
		Dark	GR - Dk
Grey (Black)	GR	Self	GR - Slf
		Light	GR - Lgt
		Dark	RN - Dk
Roan (Brown)	RN	Self	RN - Slf
		Light	RN - Lgt
		Dark	PK - Dk
Pink (Light Fawn)	PK	Self	PK - Slf
		Light	PK - Lgt

Length

> 85 mm < 160 mm	A.A.A.
> 40 mm < 85 mm	A.A.
< 40 mm	A.
> 160 mm	O.G.

Medullation

Very heavily medullated fibre should be separated from the fineness category and included in the category (S).

Step 6: Raw material packaging and labelling

There is a number of different packaging methods. Such methods require clean bags which are not stained and which must also not introduce contamination (i.e. plastic from plastic bags)

Generally bags of strong material are preferred, where the fleeces can be well pressed and are easy to store.

Each bag must also have an individual label, which contains two kind of information: one refers to the farms and consists of:

1. Animal code number.
2. Farm name.
3. Farm address.
4. Telephone number.

and one refers to the fibre as follows:

1. Fineness category (code).
2. Color (code).
3. Length (code).
4. Shearing year.
5. The average diameter of fibres when laboratory analyses have been carried out.

Table 1. Label example.

Farm data	Fibre Data
Animal code N.	Type of fleece.....
Farm Name.....	Fineness Category.....
Farm address.....	Colour.....
.....	Length.....
.....	Shearing Year
Telephone N. /	Average diameter.....

The alpaca industry is fundamentally still animal based, the value of animals has become directly related to their fibre diameter. The major demand is currently for fine (and preferably white) fibre. By improving alpaca fibre quality and its preparation, producers will be better able to define common objective of selection. Present guideline will have to attend to the Alpaca breeders in the improvement of the final quality products and in the more accurate animal fibre recording method in the perspective of the organization of genetic selection plan. Present guideline represents the first principal step of ICAR service for alpaca breeders at international level.

ICAR would like to approach the problems of Alpaca fibre heterogeneity due to the great variability in type of fleece and type of fibre in order to supply the best raw material as possible at the end users. Next steps of the ICAR South American Camelid Alpaca fibre Working group will be the objective definition of Huacaya and Suri fibre/type; the definition of the objective and criteria in Alpaca fibre selection program world wide; the contribution to adequate analytical performance quality for Alpaca fibre recording purpose world wide; the development of reference document and standard on methods of Alpaca fibre analysis and quality assurance in laboratories applicable to animal fibre recording.

AWEX. 2007. Code of Practice, preparation of Australian wool clips, the woolclasser: 2007- 2009 Australian Wool Exchange (www.awex.com.au).

Gonzales M. and Renieri C. 1998. Propuesta de un plan de selección de la población de alpacas en la provincia de Caylloma, Arequipa. En Frank E., Renieri C. Y Lauvergne J.J., Actas del Tercer Seminario de Camélidos Sudamericanos Domésticos y primer Seminario Proyecto SUPREME, Universidad Católica de Córdoba, pp. 27-38.

IWTO-19. 2004. Determination of the Wool Base and Vegetable Matter Base of Core Samples of Raw Wool.

Conclusion

List of references

Genetic improvement programmes of alpaca in Caylloma province - PROMEGE

*C. Pacheco¹, C. Renieri², M. Antonini³, A. Valvonesi²,
W. Frank⁴ & N. Mamani¹*

¹Desco Studies Center and Promotion of Development Arequipa, Perú

²Camerino University, Department of Veterinary Science, Matelica, Italy

³ENEA Casaccia, Bistec AGRO, S. Maria di Galeria, Rome, Italy

⁴Catholic University of Cordoba, SUPPRAD Program, Cordoba, Argentina

The breeding program that develops in the Caylloma province, Arequipa Region, Peru, aims to improve qualitatively and quantitatively the production of alpaca fiber. His intervention strategy se basa en un esquema selection of core open, with single-core and 15 multipliers whom have records pedigree and productivity of their animals. The reproductive management of animals kernel is done under the system apareamientos scheduled between males and females in the same race and color but distant in terms of kinship (circular matings), the selection of animals is developed based on qualitative criteria (Fleece type and color) and quantitative (assessment mean diameter fiber, coefficient of variability means of fiber diameters and total weight of the fleece of the first shearing) through which determines their selection indices.

The intensity of selection in the nucleus and herds of planteleros is high, for this reason breeders with purely qualitative selection criteria are not required to keep records of their production or herd animals. The spread and replacement players will take place from the core toward the planteleros, creating a genetic relationship between those with and through the transfer of players and vice versa. Keeping the necessary genetic differential. Also, the relationship between the core and Planteleros a system governed reproductive rate move “circular matings” in which every two years plantelero receive a player from a family genetically diverse and distant from that existing in the core, thus will create a genetic relationship between effective and controlled planteleros inbreeding..

Key word: Genetic improvement, Selection, Index, Core.

This document presents the experience of genetic selection of alpacas in the province of Caylloma in Peru; this objective is driven through a cooperative effort between the Center of Studies and Promotion of Development (DESCO) - Peru, the Department of Environmental Science at the University of Camerino - Italy, the Center for New Technology, Energy and Environment Jan - Italy and Program SUPPRAD of the Catholic University of Cordoba, Argentina.

Summary

Introduction

The PROMEGE (program of genetic improvement) utilizes the selection of the open core of alpacas managed by desco- Center for Development of Alpacas Tocra (CEDAT) which included 15 multipliers (approximately 1 500 animals) and more than 150 of the breeding base of farming families (15 000 animals in total).

The total alpaca population of the Caylloma province is estimated at 200 000 animals, 90% huacaya, 10% suri, 60% of white alpacas, and 40% of color (Gonzales and Renieri, 1998).

The breeding program began in 1985 with the creation of desco's Rural Development Colca Canyon Program and expanded in 1996 with the establishment of the CEDAT. In 1998, a breeding plan was developed, and later, in 2005, started its full operation following the results of two research programs of development financed by the European Union (EU. INCO), SUPREME (1997-2000), DECAMA (2002-2006) enabling the acquirement of the necessary genetic information. PROMEGE is the first breeding program developed to operate in the alpaca and llama populations in the Andean highlands.

PROMEGE

The specified characteristics of the selection objectives are as follows:

1. Qualitative characteristics.
 - Type fleece: Huacaya and Suri.
 - The color of fleece, in this case, the selection is:
 - In favor of white, non-albino.
 - Color fleece (Black, brown, wild, and LF).
 - Against the fleece of two colors and irregular spots.
2. Quantitative Features.
 - Number of fiber produced.
 - Fineness of fiber (diameter).
 - Variability Coefficient of the fiber diameter.

The selection criteria can be summarised as follow:

- Direct observation of animals at birth, by type and color of the fleece.
- Weight of the produced fiber in the first shearing at age one with a confidence interval of ± 2 months (Antonini *et al.*, 2004).
- Average diameter of fiber and the coefficient of variation obtained during the first shearing through a sample on the left side of the alpaca.

Genetic basis of the characteristics

Suri vs. Huacaya

Various theories have been raised concerning the hereditary mechanism of the suri in respect to huacaya (Velasco, 1980; Street Escobar, 1884, Ponzoni *et al.*, 1997, Baychelier, 2000). The analysis of data from a large, private breeding farm in Peru demonstrates information of 588 alpacas (62 families of half paternal brothers) born as a result of the mating between suri x suri and 2 126 alpacas (177 families of half paternal brothers) born as a result of mating between huacaya x huacaya (Renieri *et al.*, 2008, unpublished). Of the animals born into the 21 suri x suri families (of whom was born at least one sample of a huacaya alpaca), four assumptions have been tested for a model of two phenotypes:

1. The hypothesis of a single dominant gene (tested hypotheses, 7 suri: 1 huacaya) and three epistatic scenarios.
2. Double dominant epistasis (15 suri: 1 huacaya).
3. Double recessive epistasis (9 huacaya: 1 suri).
4. Dominant and recessive epistasis (13 suri: 3 huacaya).

Only the hypothesis of a single dominant gene adequately explains the segregation between suri and huacaya ($G_{adj} = 0,347$, $P = 0,556$). Using the modified method Single Jackknife Estimator (MSJE), the frequency of the recessive gene huacaya is estimated at 0.295; while the frequency of the dominant gene for suri is 0.705 (Huet and Murphy, 1980). The heterozygote frequency in the suri population has equally resulted to the entire population at 0.416 and 0.455, with a "carrier" suri/huacaya of 4.780.

The location selection for the suri must be one that seeks to remove heterozygous for the homozygous dominant.

Between 2 126 (1 009 females and 1 117 males) huacaya x huacaya in 177 families of half paternal brothers, 2 123 huacaya and 3 suris were born into three different families. Since the parents belong to several generations of the huacaya line, a classification error by mothers is unlikely to exist. Therefore, this phenomenon is a result of new mutations on gene expression (reverse mutation) of the gametes level lines of the parents. The gene responsible for the synthesis of huacaya and suri would be the result of a recurrent mutation appearing with a constant rate of mutation in each generation. The rate of mutation would be equal to $3 / (2126) = 0.001411101$. The birth of suri as a result of mating between huacaya x huacaya explains why sometimes it is considered recessive. Some authors describe the existence of an intermediate type called chili (anonymous, 1994: C Tuckwel, personal communication and Ponzoni *et al.*, 1997) also described in the llama (Frank *et al.*, 2001).

The favorite colors for selection include the non-albino white and the pigmentation model of black and brown (Renieri *et al.*, 1994 a, b; Renieri, 1995). White signifies the absence of pigmentation. The cells that produce pigments are not found only on the skin of animals fitted with coverage pilífera (melanocytes follicular), but also in the eye, in the inner ear, in the meninges and other internal organs; for clarification, the white is non-albino. This white color is obtained through a mutation which includes the loss of gene function involved in embryonic melanoblasts and the migration of neural crest of the hair follicle in the local development of the animals (Bennet and Lamoreaux 2003). This mutation is identified and cloned in mammals of 22 genes involved in the function (Baxter *et al.*, 2004); however, most mutations associated with white in such loci behave as lethal. In three cases of the reverse for the loci mITF (microphthalmia), C - Kit (Dominant Spottting) and SCF demonstrated the possibility to obtain completely white individuals which may involved these genes within the process.

The black fleece stems from the eumelanina prevalence in the fleece of the animal (Renieri *et al.*, 1991, Renieri *et al.*, 1995; Cecchi *et al.*, 2006). Within the black eumelaninas, a net prevalence of DHI (Dihidroxindo) monomer is present which characterizes the heteropolimero. On the other hand, the prevalence of the opposite acidified form (DHICA) produces the brown eumelaninas. Genetically speaking, the black derives from two origins: 1) a mutation due to the loss of function to Agouti locus which, as a result, behaves like a recessive trait regarding other models of pigmentation, 2) mutations in the gene expression on locus MC1R which is dominant (Lauvergne *et al.*, 1996). These results of data segregation exhibit a

Fleece color

recessive trait in the black alpaca. Nevertheless, it is not possible to exclude the existence of a dominant black. Many mutations are identified in the locus without MC1R function definition (Powell *et al.*, 2007).

The brown represents an eumelanico model with the prevalence of brown eumelaninas due to the presence of brown eumelanosomas (Cozzali *et al.*, 2001); genetically, brown stems from a mutation with loss of function of locus TYRP1 (Brown) alleles while allowing the expression of wild black (Castrignano *et al.*, 2001).

Quantitative characteristics

The quantitative characteristic selection considers the weight of the fleece, the diameter of fleece, and the variability coefficient (VC) of the first shearing. Data of these characteristics have been gathered from 293 male and female alpacas born in Toccra in 2004 and 2005.

The non-genetic factors (type of fleece, age, sex, color fleece) were significant to the analysis of variance, the influence of the birth year on the diameter, as well as a key type of fleece on the variability coefficient of the diameter. The phenotypic correlation is equal to 0.179 between the weight of the fleece and its diameter, 0.091 between the weight of fleece and VC of the diameter, and 0.124 between the diameter and the VC of the diameter. The genetic correlations were equal to 0.230 ($P = 0.001$) between the weight and diameter of fleece, 0.377 ($P = 0.001$) between the weight of fleece and VC of diameter, and 0.324 ($P = 0.001$) between the diameter and VC of diameter; these results are rarely seen in the literature, given the great variability (Frank *et al.*, 2006).

Table 1. Heritability (diagonal), genetic correlation (on the diagonal) and phenotypic correlation of the fleece weight (below the diagonal), of the fineness and of the VC of fineness.

Characteristic	Hair weight	Fineness	VC of Fineness
Hair Weight	0.84	0.230 ¹	0.377 *
Fineness	0.179 *	0.32	0.324 *
VC of Fineness	0.091	0.124	0.46

¹ $P < 0.001$.

Selection method and identification of reproducers

Using the test performance method, alpacas are evaluated for their quantitative characteristics. The basis of genetic parameters of the considered characteristics has proposed a synthetic index estimated with the Multiple Trait model and MTDFREML software (Multiple Trait Derivate Restricted Free Maximum Likelihood), 50% of the fiber diameter, 40% of VC diameter, and 10% of the fleece weight. Of the 293 alpacas born between January-April of 2005, 2006 and 2007, 154 (53%) had positive selection index; the reliability of this estimate varies between 0.503 and 0.783, with an average of 0.733. Of the 154 alpacas with a positive index, 126 hold values higher than average reliability.

The core of Toccra - CEDAT is organized into 14 huacaya alpaca families and 4 suri alpaca families. These families have been created based on their same phenotype and in relation to the degree of its members, ranging from offspring up to first cousins. Each family includes 2 or 3 males and 20-30 females. The 14 huacaya families comprise 9 white families, 3 brown families, and 2 black families while the 4 suri families are white. The reproductive management of the 9 white huacaya families and 4 white suri families was achieved using the “circular mating” scheme (Wright, 1921, 1931; Kimura and Crow, 1963) or circular breeding season, involving the passage of the native family reproducers to distant kinship. Through this mating system, each family reproduces yearly: the male reproducer, the genetically best for mating in the internal core and 2 male breeders transfer to the multipliers. Replacement core reproducers must be done every two years; the females with positive selection index born into each family will be used by substitution, internal family replacement, or transferred to multipliers. The black and brown huacaya families function as a cooperative core with the multipliers due to their limited number.

The multipliers must register phenotype data relating to the fleece weight, fiber diameter, and VC diameter. From this year, the data used will serve to estimate the genetic indexes of the alpacas. The multipliers will receive core breeders which changes every three years. The multipliers will transfer the offspring of breeders to the core or commercial breeders. The value of multiplication must be equal to 5 male breeders per year for every core male received.

Contrary to what is most important within this alpaca genetic improvement program, limitations for the operation do not seem to be environmental in nature (complexity of the Andean environment) or an economic, if not essentially cultural.

A program of genetic improvement requires a well-defined population of where to apply such a program.

The existing alpaca breeds are essential of the primary type, resulting of the first division of the genetic pool assembling the domestication and the effect of genetic drift caused by the shock of conquest (Renieri *et al.*, 2007). The breeds of relatives are classically characterized by a high phenotypic variability of qualitative characteristics (color, type of fleece) and quantitative characteristics (parameter, biometrics, production); the closeness of the selection requires particular impact options within the same population.

An erroneous approach has led to the effects of genetic combination (Incrocio) to those of selection. This particular selection has been highly valued in Peru. From the creation of a Libro Genealogico (L.G.) national allowing the entry of animals belonging to any population stems the idea that a breeder can behave in a manner in any population where it reproduces.

Organization of the core selection in Toccra

Transfer of core reproducers to multipliers

Conclusion

**List of
references**

- Andresen, E.** 1974. The effect of ascertainment by truncate selection on segregation ratios. 1st World Congress Genetic Applied Livestock Production, Madrid, 111-114.
- Anonymous.** 1994. Alpacas Australia, Issue Number I, p. 47.
- Antonini M., Gonzales M.Y. Valbonesi A.,** 2004. Relacion entre la edad y el desarrollo postnatal de los fullicolos pilosos en tres tipos de camelidos sudamericanos domesticos. Livestock Production Science, 90, 241-246.
- Baychelier P.,** 2000. Suri and Huacaya: Two alleles or Two Genes ? Proc. 2000 Australian Alpaca Association National Conf., Camberra, pp. 79-85.
- Baxter L.L., Ling Hou, S.K. Loftus, W.J. Pavan,** 2004. Spotlight on Spotted Mice: A Review of White Spotting Mouse Mutants and Associated Human Pigmentation Disorders. Pigment Cell Research, 17, 215-224.
- Bennett D.C., Lamoreax M.L.,** 2003. The Color Loci of Mice – A Genetic Century. Pigment Cell Research, 16, 333-344.
- Calle Escobar R.,** 1984. Animal Breeding and Animal Production of American Camelids. Ron Henning – Patience, Lima, Peru.
- Castrignanò F., Antonini M., Misiti S., Cristofanelli S., Renieri C.,** 2001. Sequence of tyrosinase related protein-1 (TRP-1) in alpaca. In: Gerken M. and Renieri C. (Eds) "Progress in South American camelids research", EAAP publication No. 105, Wageningen Pers, Wageningen, 2001, 199-206.
- Cozzali C., Dell'Aglio C., Gargiulo A.M., Frank E., Hick M., Ceccarelli P.,** 2001. SUPREME-Project: Pigmentation on South American camelids: II. Morphological features of follicular melanocytes. In: Gerken M. e Renieri C. (Eds): "Progress in South American camelids research", EAAP publication no. 105, Wageningen Pers, Wageningen, 2001, 237-238.
- Frank E. N., Hick M.H.V., Pesarini M., Hick, P.M.L. Hick, Capelli C. I., Ahumada M.R.,** 2001. SUPREME-Project: Classification of fibres of different types of fleeces in Argentine llamas. In: Gerken M. e Renieri C. (Eds): "Progress in South American camelids research", EAAP publ no. 105, Wageningen Pers, Wageningen, 2001, 251.
- Frank E.N., Hick M.V.H., Gauna C.D., Lamas H.E., Renieri C., Antonini M.,** 2006. Phenotypic and genetic description of fibre traits in South American Domestic Camelids (Llamas y Alpacas). Small Ruminant Research, 61, 113-129.
- Gonzales M. y Renieri C.,** 1998. Propuesta de un plan de selección de la población de alpacas en la provincia de Caylloma, Arequipa. En Frank E., Renieri C. Y Lauvergne J.J., Actas del Tercer Seminario de Camélidos Sudamericanos Domésticos y primer Seminario Proyecto SUPREME, Universidad Católica de Córdoba, pp. 27-38.
- Huether C.A. and Murphy E.A.,** 1980. Reduction of bias estimating the frequency of recessive genes. Am. J. Hum. Genet., 32: 212-222.
- Kimura M., Crow C.J.F.,** 1963. On the maximum avoidance of inbreeding. Genet. Res., 4, 399-415.

King R.A. and Oetting W.S., 2006. Oculocutaneous Albinism. In "Genetic Hypomelanoses: Generalized Hypopigmentation". In Nordlung J.J. *et al.* (Eds) The Pigmentary System. Blackwell Publishing, Oxford University Press, pp. 599-621.

Lauvergne J.J., Renieri C., Frank E., 1996. Identification of some allelic series for coat colour in domestic camelids of Argentina. Proc. 2° European Symposium on South American Camelids, Università di Camerino, Italy, 39-50.

Powell A.J., Moss M.J., Tegland Tree L., Roeder B.L., Carleton C.L., Campbell E., Kooyman D.L., 2007. Characterization of MC1R in alpaca (*Lama pacos*) fleece color differentiation. Proc. I Simposium Internacional de Biotecnologia Aplicada en Camelidos Sudamericanos, Huancavelica, Peru, 33-37.

Ponzoni R.W., Hubbard D.J., Kenyoni R.V., Tuckwell C.D., McGregor B.A., Howse A., Carmichael I., Judson G.J., 1997. Phenotypes resulting from huacaya by huacaya, suri by huacaya and suri by suri alpaca crossing. Proc. Intern. Alpaca Industry Sem., pp. 11-13.

Renieri C., 1994 a. Pigmentation in domestic mammals with reference to fine fibre producing species.

EUR. Fine Fibre Network, Occ. Publ. No. 1, 113-136.

Renieri C., 1994 b. The genetic basis of pigmentation in South American Camelids. Proc. Eur. Symp. South American Camelids, M. Gerken & C. Renieri Ed., Univ. di Camerino, 1994, 31-41.

Renieri C., 1995. Biología y genética de las capas de los mamíferos y su extensión a los camelidos. Actas Primer Seminario Internacional de Camelidos Sudamericanos Domesticos, Frank E.N. e C. Renieri Eds, Univ. di Camerino, 69-87.

Renieri C., 2003. Selection for coat colour in alpaca (*Lama pacos*) and llama (*Lama glama*). Proc. III Congreso Mundial sobre Camelids y I Taller Internacional de DECAMA, Potosi, Bolivia, 11-19.

Renieri C., Tralbalza Marinucci M., Martino G., Giordano G., 1991. Preliminary report on quality of hair and coat colour in pigmented alpaca. Proc. IX Italian ASPA, 905-914.

Renieri C., Lauvergne J.J., Antonimi M., Lundie R., 1995. Quantitative determination of melanins in black, brown, grey and red phenotypes of sheep, goat and alpaca. Proc. 9th Int. Wool Textile Res. Conf., II, 580-586

Renieri C., Frank E.N., Rosati A.Y Macias Serrano J.A., 2007. El concepto de raza en zootecnia y su aplicación a la llama y a la alpaca. In Frank E., Antonini M., Toro O. (Eds) South American Camelids Research. Volume II, Wageningen Academic Publisher, in press.

Renieri C., Valbonesi A., La Manna V., Antonimi M., Asparrin M., 2008. Inheritance of Suri and Huacaya type of fleece in alpaca. Italian J. Anim. Sci., submitted.

Sokal R.R., Rohlf F.J., 2003. Biometry. 3rd ed. Freeman WH and Company, New York, 887 p.

Velasco J., 1980. Mejoramiento Genético de Alpacas. Anales III Reunión Científica Annual Soc. Peruana de Prod. Anim., Lima.

Wright S., 1921. Systems of mating. Genetics, 6, 111-178.

Wright S., 1931. Evolution in Mendelian population. Genetics, 16, 97-159.

Preliminary information on a genetic improvement program on alpacas in Italy

A. Valbonesi¹, G. Berna², A. Briganti², M. Antonini³ & C. Renieri¹

¹Department of Environmental Science, University of Camerino, Italy

²ITALPACA Association, Umbertide (PG), Italy

³ENEA CR Casaccia Dept. BAS secondment at the Industrial Liaison Office,
University of Camerino, Italy

Ninety-one alpaca of the huacaya type (42 males and 49 females) from 17 Italian farms, were monitored at first shearing for three fleece traits: fleece weight, fibre diameter and coefficient of variation of fibre diameter. The means and the minimum and maximum values were: 1.69 kg (0.73-3.80 kg) for fleece weight, 22.8 µm (17.3-31.6 µm) for fibre diameter, 26.3% (17.5-44.6 %) for coefficient of variation of fibre diameter. Effect of sex was never observed on any of the three fleece traits. Significant correlation ($r = 0.42$; $P < 0.01$) was detected between fleece weight and fibre diameter. A selection index was given to each animal by summing the estimated breeding values (EBVs) related to the three fleece traits. Each EBV concurred to the selection index in different proportions: 0.10, 0.50, and 0.40 for fleece weight, fibre diameter and coefficient of variation of fibre diameter, respectively. The animals with a positive selection index, showing reliability greater than 0.60 (23 males and 25 females), will be used in a breeding program, with the aim of improving the quality of fibre within the Italian alpaca population. It is concluded that there is good opportunities to improve alpaca fibre quality through selection and breeding focussed to reduce the fibre diameter and the coefficient of variation of fibre diameter.

Key words: Alpaca, Huacaya, Fleece traits, Selection index.

Alpaca breeding in Italy is quite recent; the first Alpaca import is dated at the end of the 1990s. At present, the number of Alpaca in Italy is of 700-800 animals, distributed among approximately 60 alpaca breeders, located in different Italian regions. Most of the Alpaca breeders (50) are members of an association, ITALPACA, established in 2001 as an answer to the growing need for a professional structure specifically dedicated to this new sector. One of the aim of this association was to create and run a national register of alpacas, containing pedigree information on alpaca born and living in Italy. These information are the first step for any genetic improvement programme.

Summary

Introduction

Alpaca are among the best domestic animals for fibre production, being characterized by homogeneously fine, long and soft fleeces, very much in demand by the European textile industry. Of the two types of alpaca, the “huacaya” is the more common among the Italian breeders and is characterized by compact, soft and highly crimped fibres, with blunt-tipped locks which closely resemble those of Merinos sheep. By contrast, the “suri” has straight, less-crimped fibres and locks with a “cork-screw” shape, very similar to those of Angora goat but not as bright.

Fibre diameter is measured in microns (μm) and is the single most important commercial raw fibre

characteristic. Alpaca fibre is currently classed for fineness, as denoted by the Australian

Alpaca Cooperative (www.pir.sa.gov.au/factsheets) into:

1. superfine, less than 20 μm ;
2. fine, 20-24.9 μm ;
3. medium, 25-29.9 μm ;
4. strong, more than 30 μm .

In this context, it is worth bearing in mind that the fibre diameter of 35 μm is the limit value proposed by Wildmann (1954), for distinguishing woolly fibres (undercoat) from coarse ones (outer-coat) in llama fleece. Since the textile industry utilises practically only fibres with diameter smaller than 35 μm , the main goal of the ITALPACA is to develop a genetic improvement program addressed to the production of homogeneously fine fibres from huacaya.

The aim of the present investigation is to supply breeders with information for evaluating alpaca fleece traits. The starting point is understanding the type and the amount of variation found among fleeces and subsequently selecting those animals which could improve quality and quantity of the fibre within the ITALPACA population.

Materials and methods

Throughout two years of investigation (2006-2007), 91 alpaca of huacaya type (42 males and 49 females, belonging to 17 alpaca breeders), devoid of any congenital defects and exhibiting an homogenous coloured fleece (either pigmented or white), were monitored for fleece weight, fibre diameter and coefficient of variation of fibre diameter. The fibre samples were collected from the right mid side of each animal, *i.e.* approximately over the 10th rib, about halfway down the body (Frank, Parisi de Fabro and Mendez, 1989). This body area has been found to be more representative of fleece characteristics than other fleece regions (Martinez, Iniguez and Rodriguez, 1997). The fibres were washed in petroleum ether (pure solution), dried in a stove at 60 °C for 30 min. and the measurements of the diameter were performed on a sample of 150 fibres for each specimen with the aid of a calibrated ocular micrometer mounted on an optical microscope. Sampling was carried out at first shearing, when the animal age ranged from 8 to 14 months old.

Analyses of variance (ANOVA) were performed on the fleece weight, the fibre diameter and the coefficient of variation of fibre diameter. A model I ANOVA was utilised, with sex considered as fixed factor and age as covariate. The relationship among the three fleece traits were calculated by means of the Pearson correlation coefficient. The statistical analyses were performed using the SPSS 12.0 statistical software package (2003).

An estimated breeding value (EBV) was calculated for each trait related to a given animal by means of a software named MTDFREML (Multiple Trait Derivative-Free Restricted Maximum Likelihood) and elaborated by researchers of the "Agricultural Research Service – United States Department of Agriculture". Because of the few animals investigated here (91), we did not feel confident in estimating the hereditability of the three fleece traits on which the EBV are based. Hence, we utilized information from Australian data produced by Ponzoni (2006) as reported in table 1.

Lastly, the individual EBVs were weighted, *i.e.* multiplied by a proper factor, and summed to produce an overall index value, named selection index (SI), for each animal.

Table 2 illustrates the results obtained by the weighing of the fleece and the measurements of the fibres of the 91 huacaya investigated in this study.

These results are similar to those reported in literature for huacaya by other authors (*cfr.*: McGregor and Butler, 2004; Lupton *et al.*, 2006; and references therein). Generally, the mean fibre diameter varies from 20 to 30 μm (with a minimum and a maximum value ranging from 15 up to 50 μm) and a similar range of variation is observed for the percentage values of the C.V. On alpaca fleece, however, there is a strong environmental effect. Fibre diameter and its C.V. appear to be influenced by: farm management, year, age, breed, live weight, colour of fibre, disease, reproduction, and position over the body (McGregor, 1999; Aylan-Parker and McGregor, 2002; McGregor and Butler, 2004). Effect of sex was never observed. Because of the small number of the animals and their distribution throughout 17 different alpaca breeders, it was not possible to carry out any statistical analysis to evaluate the effect of the environmental factors given above. On the contrary, it was possible to estimate the effect of sex. In agreement with data reported by McGregor and Butler (2004), no evidence of a significant difference between male and female resulted from the ANOVA carried out for the three fleece traits ($P=0.08, 0.81, 0.44$, for fleece weight, fibre diameter and coefficient of variation of fibre diameter, respectively). Nevertheless, since all the fibre samples were collected from the same body region of pre-selected animals (healthy, in non-reproductive stage, nearly homogeneous in age) and farm management was largely standardized within the ITALPACA

Results and discussion

Table 1. Hereditability of the fleece traits.

	Clean fleece weight	Fibre diameter	C.V. ¹
Hereditability	0.60	0.60	0.70

¹Coefficient of variation of the fibre diameter.

Tab. 2. Means, standard deviation and maximum and minimum values of the fleece traits

Sex (n)	Fleece weight (kg)				Fibre diameter (μm)				C.V. (%) ¹			
	$\bar{x}$	S.d.	Min.	Max.	$\bar{x}$	S.d.	Min.	Max.	$\bar{x}$	S.d.	Min.	Max.
Male (42)	1.62	0.60	0.73	3.80	22.7	2.8	17.3	29.4	25.7	3.4	17.5	33.5
Female (49)	1.75	0.50	0.96	2.80	22.9	3.6	17.7	31.6	26.8	4.3	18.3	44.6
Total (91)	1.69	0.55	0.73	3.80	22.8	3.0	17.3	31.6	26.3	3.9	17.5	44.6

¹Coefficient of variation of the fibre diameter.

breeders, according to the suggestions given by Berna (2006), we can assume that most of the variability of the fleece traits is due to genetic differences among the animals. If this assumption is true, there is good potential for the improvement of the quality of alpaca fibre through selection and breeding.

An estimated breeding value (EBV) for each trait was calculated for each animal, as a measure of an animal's ability to transmit its genes on to the next generation. These EBVs were properly weighted (Table 3) and then pooled together to obtain an overall selection index for each animal. The weight given to the quantitative trait "fleece weight" was limited to 0.10. This choice was based on the output of a correlation analysis among the three fleece traits as shown in table 4.

In fact, the significant positive correlation between fleece weight and fibre diameter lead us to minimize the influence of the fleece weight on the selection index, to avoid a possible increase of the fibre diameter. Moreover, for textile purpose, the potential benefit is greatest from reducing the fibre diameter and its coefficient of variation.

By considering animals showing a positive selection index with reliability greater than 0.60 (mean, 0.77; s.d., 0.05), it was possible to detect a breeding nucleus consisting of 23 (54.8 %) males and 25 (51.0%) females, distributed among 12 alpaca breeders. These animals will be used in a breeding program, based on exchange of ram within the ITALPACA flocks, in order to improve the quality of the fibre for textile industry.

The validity of this genetic improvement program will be evaluated in the next future, as soon as a new progeny is obtained from these rams and dams. This offspring is expected to exhibit a sensible average decrease in both the fibre diameter and its coefficient of variation.

Acknowledgments

We are very grateful to the members of ITALPACA association for providing the animals, and to Dr. A. Rosati for providing us with the software used for calculating the EBVs. Thanks are also due to Mr. Lebboroni G. (Department of Environmental Sciences, University of Camerino) for his competence and patience in preparing and measuring the fibre samples.

Table 3. Weight assigned to the EBVs of the three fleece traits.

	Fleece weight	Fibre diameter	C.V. ¹
Weight	0.10	0.50	0.40

¹Coefficient of variation of the fibre diameter

Table 4. Pearson correlation coefficient (r).

	Fleece weight	Fibre diameter	C.V. ¹
Fleece weight	1		
Fibre diameter	0.42 ²	1	
C.V.	0.05	0.06	1

¹Coefficient of variation.

²Correlation is significant at the 0.01 level (2-tailed).

**List of
references**

Aylan-Parker, J., McGregor, B.A., 2002. Optimising sampling techniques and estimating sampling variance of fleece quality attributes in alpacas. *Small Rumin. Res.* 44: 53–64.

Berna, G., 2006. *L'Alpaca in Italia: 10 anni di esperienza nell'allevamento dell'alpaca*. M.I.R. (Ed), Firenze, Italy, p 95.

Frank, E.N., Parisi de Fabro, S.G., Mendez T., 1989. Determinacion de variables foliculares en cortes de piel de camelidos sudamericanos y su relacion con las características de vellon. *Rev. Arg. Prod. Anim.* 9, (5): 379-386.

Lupton, C.J., McColl, A., Stobart, R.H., 2006. Fiber characteristic of the Huacaya Alpaca. *Small Rumin. Res.* 64: 211-224.

Martinez, Z., Iniguez, L.C., Rodriguez, T., 1997. Influence of effect on quality traits and relationships between traits of the llama fleece. *Small Rumin. Res.* 24: 203-212.

McGregor, B.A. 1999. The influence of environment, on the quality and production of alpaca fibre. *Proceedings National Conference Australian Alpaca Association*, pp. 88–94. (Australian Alpaca Association: Mitcham, Victoria).

McGregor, B.A., Butler, K.L., 2004. Sources of variation in fibre diameter attributes of Australian alpacas and implications for fleece evaluation and animal selection. *Australian Journal of Agricultural Research* 55: 433-442.

Ponzoni, R.W., 2006. Proposal for the establishment of a breeding nucleus in Australian alpaca. *Australian Alpaca, Further Reading*.

SPSS User's guide. 2003. *Statistics*, version 12.0. Edition 2003. SPSS Inc., Chicago, IL.

Wildmann, A.B., 1954. Fibres from animals of the Genus Llama. In: Wildmann, A.B. (Ed.), *The Microscopy of Animal Textile Fibres*. Wool Ind. Res. Ass., Leeds, pp. 82-99.

Effect of combining controlled natural mating with artificial insemination on the genetic structure of the flock book of Sardinian breed sheep

S. Salaris¹, S. Casu¹, P. Fresi² & A. Carta¹

¹*Dipartimento per la Ricerca nelle Produzioni Animali DIRPA, AGRIS
Sardegna, Sassari, Italy*

²*Associazione Nazionale della Pastorizia, ASSONAPA, Rome, Italy*

The aim of this study was evaluating the effect of combining controlled natural mating with artificial insemination on the genetic structure of the flock book of Sardinian breed sheep. Discussion was focused on the feasibility of a sound genetic evaluation and the strategies to adopt for increasing the efficiency of the selection scheme. Flock and population demographic patterns across years, breeding management and links between contemporary groups were analysed from a dataset including 2 960 169 lactation records from 971 992 ewes in 2 905 flocks from 1986 to 2006. The number of registered flocks, the total female stock and the average flock size increased across years. The average number of mating groups (groups of ewes with a single ram during the reproduction period) per flock was 1.9. The highest incidence of artificial insemination was reached in 2000 with 10% of yearling primiparous born by artificial insemination. Combining the controlled natural mating with artificial insemination led to 68% of connected primiparous contemporary groups and 81% of connected all age classes contemporary groups in the last years.

Key words: *Population demographic patterns, Breeding management, Selected population, Lambing.*

The Sardinian is the largest Italian sheep breed (51% of the national stock) with approximately 3.6 million head, 3.0 of which bred in Sardinia on 12 500 farms, and the rest on the mainland, especially in central Italy (www.istat.it).

In Sardinia the sheep industry is exclusively - the presence of other breeds or crosses with other breeds is negligible - based on the local dairy sheep breed. The typical production pattern is characterised by an out-of-season lambing period. The mating period of mature ewes starts in May and continues until mid-July. Lambings occur in autumn when the grass starts to grow after the summer drought. Lambs are

Summary

Introduction

slaughtered after around 30 days (8-11 kg of live-weight). Yearling primiparous usually lamb between February and March. Milk production is entirely processed into PDO cheeses (Pecorino Romano, Pecorino Sardo and Fiore Sardo). The other important product of the sheep industry is the GPI milk fed lamb named “Agnello di Sardegna”.

The Sardinian scheme is based on a pyramidal management of the purebred population with at the top the registered flocks where artificial insemination (AI), controlled natural mating (NM), official recording and breeding value estimation are carried out to generate genetic progress (Barillet, 1997; Carta and Ugarte, 2003). The genetic progress is then transferred to the base population mainly by natural mating rams. Young rams born from assortative matings between elite rams, used either for NM or AI, and the best dams, are progeny tested every year to select the next generation of elite rams.

The main selection objective is milk yield. Since 1992 breeding values for milk yield have been obtained by Best Linear Unbiased Prediction methodology (Sanna *et al.*, 1994; Carta *et al.*, 1998a). Since 1998 fat and protein content recordings on primiparous ewes have been realized. Till now, dry matter content has not been considered yet as breeding goal due to the lack of a payment system of milk adequate to refund farmers for the potential loss of genetic progress on milk yield. Since 2004, breeding values for teat placement and degree of udder suspension have been estimated (Casu *et al.*, 2006). Scrapie resistance was introduced as breeding goal in 2004 (Salaris *et al.*, 2007).

The main feature of the breeding program is the large application of the controlled natural mating, i.e. grouping ewes with a single ram during the reproduction period (“mating group”). Ewes of a mating group (MG) can be grouped with another ram in the same reproduction season only after a lag of 14 days. This management allows assigning the correct sire of a lamb on the basis of the lambing date. Controlled natural mating is realized either with young rams to progeny test or adult proven rams. The size of MG depends on the sexual aptitude of the ram and the planned lambing period.

AI is usually performed with fresh semen after induced oestrus in June-July. From a genetic point of view, AI is mainly used to create genetic links between flocks either through AI rams or NM rams but born by AI. Moreover, planned matings are realized between elite AI rams and elite dams to generate the new cohort of young rams to introduce in the AI centre.

The aim of this study was evaluating the effect of combining controlled natural mating with artificial insemination on the genetic structure of the flock book. Results will be discussed focusing on the feasibility of a sound genetic evaluation and the strategies to adopt for increasing the efficiency of the selection scheme of the Sardinian sheep breed.

Materials and method

The database used for the genetic evaluation of 2007 managed by the National Association of Breeders (ASSONAPA) was used to extract a dataset including 2 960 000 lactation records from 971 992 ewes in 2 905 flocks from 1986 to 2006.

To analyse flock and population demographic patterns, the following annual parameters were considered: number of registered flocks (FN) with at least 5 milk recorded ewes; number of new registered flocks (FIN); number of flocks coming out of the flock-book (FOUT); total female stock (FS); total number of lactating ewes (LE).

Flock and population demographic patterns

To analyse the breeding management the following annual parameters were considered: number of replacement ewes (NR); number of breeding males (NS); number of mating groups (NMG).

Breeding management

Generally, a ram performs its first service between 15 and 23 months age (on average 18 months). It could be used in further two mating years, before being officially indexed with at least 15 first lactation daughters. According to this, five classes of rams were identified: sampling rams at their first mating year (S1); sampling rams for which the size of previous mating groups was not sufficient to obtain 15 lactating daughters (S2); sampling rams for which the size of previous mating groups was sufficient to obtain 15 lactating daughters (W); proven rams at first mating year (P1); proven rams at successive mating years (P2).

To evaluate the generation interval on the sire-son pathway, the number of mating years of proven rams was considered. This parameter allows to distinguish the effect of proven rams' use duration from the length of their progeny test.

Genetic links between flocks were evaluated considering the AI rate and the exchange of NM rams. With this aim, contemporary group (CG) was defined as the group of ewes in the same flock-year of production, age and lambing season classes. Finally, three CG were defined within flock-year: yearling primiparous, mature ewes lambing before or after December the 15th.

Links between contemporary groups

Two kinds of NM rams producing genetic links were considered: rams born in one flock and used in another one (external rams) and rams with daughters in more than one flock.

To study the genetic connectedness, a database including only records from CG with daughters of at least one sire who had offspring in at least one other CG including daughters of other sires was built. All CG included in this database were considered connected. For each CG, the number of direct links was calculated as the number of other CG with at least one common sire.

An increase of 48% of FN was observed from 1986 to 2006 (Table 1). The highest values were found from 2000 to 2003 whereas in the last four years there was a decreasing of approximately 100 flocks.

Results

On average, 10-11% of FN has been substituted by new registered flocks. An increasing trend of the percentage of flocks sited in the mainland was observed.

Flock and population demographic patterns

The total female stock quadrupled from 1986 to 2006 (Table 1). The annual increasing rate reached its maximum from 1994 to 1999 (11%) whereas it was around 7% in the previous period and 3% in last years. Difference between FS and LE was due to ewes which had first lambing when they were 2 years old. On average this group represented 9% of LE and 36% of first lactations.

On average, every year 31% of newly recorded ewes (LEIN) appeared: 72% of yearling primiparous in already registered flocks and 28% of ewes in FIN. The average percentage of ewes coming out of the flock-book (LEOUT) was 27%: 81% of culled ewes and 19% of ewes in FOUT. Only in 2001 and 2006, LEIN was lower than LEOUT.

The annual average flock size increased from 78 to 209 lactating ewes (Table 1). On the whole, a great variability of flock size was observed across years with an average coefficient of variation of 0.8. Till 1996 the percentage of flocks with less than 100 lactating ewes was more than 50% whereas in the last four years it has been reduced to approximately 25%. The percentage of flocks with more than 300 lactating ewes ranged from 1% in 1986 to 19% in 2006.

Breeding management

AI program started at experimental level in 1986 and it has been applied on large scale since 1995. The rate of replacement ewes born by AI ranged from 3% in the period 1985-1994 to 8% in the period 1995-2000 and 7% in the period 2001-2005 (Table 2). In fact, the highest AI incidence was reached in 2000 with 20 773 AI doses

Table 1. Flock and population demographic patterns across years of the Sardinian breed flock-book: number of registered flocks (FN) and percentage of registered flocks sited in Sardinia (SFN), number of newly registered flocks (FIN), number of flocks coming out of the flock-book (FOUT), total female stock (FS), total number of lactating ewes (LE), new registered ewes (LEIN), registered ewes coming out of the flock-book (LEOUT), average (AFS), standard deviation (SDFS) and maximum (MXFS) flock size.

Production year	FN	SFN (%)	FIN	FOUT	FS	LE	LEIN	LEOUT	AFS	SDFS	MXFS
1986	777	89.1	96	70	67 376	60 544	22 923	16 690	78	59	496
1987	803	87.8	107	76	73 429	67 244	23 286	19 080	84	63	525
1988	834	86.2	124	84	79 955	73 852	25 392	21 005	89	71	562
1989	874	86.3	119	94	86 256	79 202	27 723	23 398	91	72	640
1990	899	85.1	103	91	92 124	84 954	29 483	25 430	94	80	736
1991	911	84.2	75	99	98 001	89 643	31 375	27 784	98	82	828
1992	887	85.0	81	91	100 055	93 194	30 372	27 596	105	86	815
1993	877	84.2	87	74	102 760	93 193	31 164	25 319	106	84	630
1994	890	84.3	114	67	110 325	102 121	32 681	26 612	115	93	990
1995	937	84.2	90	71	123 176	114 254	39 275	31 126	122	104	1 206
1996	956	83.5	148	77	130 935	120 988	39 829	32 363	127	109	1 294
1997	1 027	82.9	188	78	147 271	134 994	49 130	33 895	131	110	1 148
1998	1 137	84.4	148	129	173 556	159 434	60 825	41 474	140	117	1 311
1999	1 156	82.9	130	108	195 680	181 439	63 694	51 210	157	129	1 447
2000	1 178	81.8	137	133	208 648	194 764	64 853	61 729	165	137	1 397
2001	1 182	80.0	142	146	206 620	193 678	59 579	60 812	164	142	1 435
2002	1 178	80.0	127	121	210 337	196 095	65 781	53 495	166	144	1 537
2003	1 184	79.3	125	151	224 235	208 898	67 151	56 526	176	150	1 572
2004	1 158	77.5	110	160	241 047	225 458	72 574	66 466	195	162	1 646
2005	1 108	74.7	104	145	241 919	225 770	70 180	67 011	204	168	1 489
2006	1 067	72.5	119	106	238 021	223 227	62 834	68 473	209	178	2 114

and 10% of replacement ewes born by AI. Since then a decreasing trend of AI spread was observed (in 2005, 2006, 2007 AI programs the number of doses were 15 129, 12 778 and 13 536, respectively).

Around 31% of NR was from unknown sire. This value increased from 24% in 1985-1994, to 35% in 1995-2000 and 41% in 2001-2005. Sixty percent of ewes born from unknown sire was in flocks with less than 3 years of milk recording. Around 27% of FN had all ewes from unknown sire.

The annual NS increased according to the increasing NR (Table 2). The average number of AI breeding sires was 41 in 1985-1994, 142 in 1995-2000 and 149 in 2001-2005 (4%, 9% and 8% of the total breeding males in the 3 periods respectively).

The average NMG per flock was 1.9, with 52% of flocks with only 1 sire, 38% with 2 or 3 sires and 10% with more than 3 sires. The frequencies of MG according to sire classes were: 42% of S1 ram, 20% of S2 ram, 15% of W ram, 10% of P1 ram, 13% of P2 ram (Table 3).

As a result of this distribution of breeding males and the average size of MG, the annual distribution of lactating ewes was: 39% from S1 sire, 17% from S2 sire, 18% from W sire, 11% from P1 sire, 14% from P2 sire.

Table 2. Number of replacement ewes (NR), number of NM replacement ewes (NMNR), number of AI replacement ewes (AINR), number of breeding males (NS), number of NM breeding males (NMNS), number of mating groups (NMG), AI doses, number of flock with only NM breeding males (NMF), number of flocks with NM and AI breeding males (NMAIF) per birth year of the lactating ewes.

Birth year	NR	NMNR	AINR	NS	NMNS	NMG	AI doses ¹	NMF	NMAIF
1985	18 933	18 933		864	864	918		573	
1986	20 103	20 103		903	903	989		602	
1987	22 454	22 269	185	988	979	1 053	1 753	559	62
1988	23 455	23 159	296	1 083	1 059	1 136	2 062	550	68
1989	24 490	23 994	496	1 197	1 164	1 245	3 610	574	88
1990	26 900	26 089	811	1 264	1 223	1 314	4 943	575	108
1991	26 520	25 252	1 268	1 303	1 253	1 341	8 240	565	145
1992	27 227	26 153	1 074	1 204	1 152	1 215	7 304	538	143
1993	27 069	26 011	1 058	1 240	1 169	1 227	5 218	484	181
1994	32 713	30 784	1 929	1 223	1 151	1 212	8 420	491	196
1995	37 917	35 485	2 432	1 327	1 243	1 328	10 895	460	269
1996	41 172	37 784	3 388	1 490	1 361	1 450	16 273	404	349
1997	46 427	42 658	3 769	1 588	1 447	1 540	17 109	442	361
1998	48 449	44 281	4 168	1 703	1 536	1 617	17 468	450	376
1999	49 483	45 024	4 459	1 726	1 571	1 637	19 043	473	384
2000	49 651	44 833	4 818	1 715	1 524	1 606	20 773	437	371
2001	55 481	51 063	4 418	1 731	1 575	1 638	20 519	456	354
2002	54 804	51 166	3 638	1 772	1 607	1 670	18 735	494	309
2003	61 350	56 815	4 535	1 792	1 629	1 700	19 618	479	351
2004	55 746	52 705	3 041	1 887	1 752	1 836	18 594	499	294
2005	53 609	50 788	2 821	1 776	1 631	1 693	18 286	455	290

¹Represents the number of AI doses realized to obtain the replacement born by AI of that birth year.

Rams' age at first mating ranged from 6 months to 11 years. Out of these, 66% was less than two years old. Usually Sardinian rams are mated the first time at approximately 18 months of age and only a small part are mated at on average 6 months. Seventy eight percent of rams older than two years had their first mating in flocks different from the birth one.

The percentage of S1 natural mating rams officially progeny tested was 73%: 41% by the first mating year and 66% by the first two mating years (Table 4). In AI this value was 94%: 68% by the first use year and 92% by the first two use years. Since 2000 the average annual number of indexed rams has been 531. A proven sire was used on average for 2.0 ± 1.3 years (ranging from 1 to 12 years).

Genetic links between contemporary groups

The percentage of flocks interested by AI doubled from 14% in 1985-1994 to 28% in 2001-2005 (Table 2). In the same periods the percentage of NM rams born by AI increased from 2% to 32%, connecting 19% of flocks not directly involved in the AI program.

In regard to the genetic links created by NM rams, the average annual percentage of external S1 rams, i.e. rams born in one flock and used in another one, was: 79% in 1985-1994, 73% in 1995-2000 and 62% in 2000-2005. The average annual percentage of NM rams with daughters in more than one flock was: 30% in 1985-1994, 29% in 1995-2000 and 23% in 2000-2005.

Combining controlled natural mating with AI led to 68% of connected yearling primiparous CG and 81% of connected all age classes CG in the last years (Table 5).

Table 3. Annual number of mating groups (MG) and daughters (D). S1: sampling rams at their first mating year; S2: sampling rams for which the size of previous mating groups was not sufficient to obtain 15 lactating daughters; W: sampling rams for which the size of previous mating groups was sufficient to obtain 15 lactating daughters; P1: rams at first mating year as proven; P2: rams at a successive mating year as proven; MGF: annual number of mating groups per flock.

Period	MG	S1	MGS	S2	MG	W	MGP	P1	MGP	P2	MG	S1	D	S2	D	W	P1	D	P2	D	MGF
1985-1994	1 165	513	246	161	103	142	16	11	19	19	19	1.8									
1995-2000	1 530	617	319	236	156	202	17	15	20	21	21	1.9									
2001-2005	1 707	709	316	276	193	214	17	16	22	22	22	2.1									

Table 4. Annual average number of sampling rams. PT: at first mating; PTF: progeny tested; PTF1: progeny tested by the first mating year; PTF2: progeny tested by the first two mating years. NM: controlled natural mating; AI: artificial insemination.

Period	NM				AI			
	PT	PTF	PTF1	PTF2	PT	PTF	PTF1	PTF2
1985-1994	482	355	192	319	16	14	10	14
1995-2000	589	448	246	398	48	45	35	44
2001-2005	691	484	282	450	49	47	32	46

No CG resulted completely disconnected in the 2007 genetic evaluation (Table 6). More than 80% of yearling primiparous CG not including AI ewes showed from 1 to 5 direct links. Obviously a better result appeared when yearling primiparous CG including also AI ewes were considered. Higher average number of direct links was observed in all age classes CG. It was due to the effect of grouping lactations performed in the same flock-year by ewes of different age classes (2, 3 and 4 years old) so allowing the comparison in the same CG of sires used in different mating years (Carta *et al.*, 1998b).

The 2007 female stock of the selected population was approximately 8% of the whole population. This percentage is below the optimal threshold indicated by Elsen and Mocquot (1974) for dairy sheep. However, the number of milk recorded ewes of Sardinian breed is one of the largest (www.icar.com). Organizational problems and farms' constraints made difficult applying selection tools and limited the number of registered flocks and flock size. In the last decade, efforts made to educate farmers for managing selection tools as well as improvements in milk recording and selection scheme organization have allowed a constant increase in number and size of registered flocks. The average flock size is important to permit an accurate progeny test either in terms of number of daughters per sire or number of compared rams within flocks. Unfortunately, the increase in number of flocks has been coupled with a high rate of coming out flocks so producing negative effects on the genetic structure of the selected population as it will be discussed later.

Discussion

Table 5. Average annual number of contemporary groups (CG) defined for genetic evaluation. TOT: total; KS: with known sire; CN: connected.

CG	Period	TOTCG	KSCG	CNCG
Only	1986-1995	5 447	4 843	3 183
yearling	1996-2001	11 856	10 433	7 878
primiparous	2002-2006	17 311	14 875	11 754
All age classes	1986-1995	16 432	13 887	13 207
	1996-2001	37 087	31 361	30 560
	2002-2006	54 431	45 323	44 313

Table 6. Contemporary groups percentage (%) of 2007 production year per number of direct links classes (DL) with only NM or with NM and AI sires.

Yearling primiparous				All age classes			
NM		NM+AI		NM		NM+AI	
DL	%	DL	%	DL	%	DL	%
1-3	66.6	1-24	9.3	1-4	13.6	1-99	10.1
4-5	16.9	25-99	29.4	5-9	25.2	100-199	11.2
6-10	14.2	100-200	33.6	10-19	25.0	200-499	26.8
11-20	2.3	200-499	26.2	20-49	28.4	500-999	28.8
> 21	0.0	500	1.4	> 50	7.8	> 1 000	23.0

The high percentage of first lambing ewes at 2 years age could be reduced by management techniques. This is important to fast progeny tests and their accuracy.

Like in other dairy sheep breeds, AI was introduced in the breeding scheme mainly to increase genetic links between flocks. The decreasing of AI spreading and fertility rates after 2000 was due mainly to the blue-tongue crisis. Furthermore, the negative economic conjuncture determined by the decrease of milk price and the increase of production costs led farmers to limiting the application of selection tools. Big efforts have been made to come back to the same AI rate of the end of nineties.

The annual turnover of flocks led to a high percentage of ewes with unknown parents with two main negative effects: limited depth of the relationship matrix and low effective size of the selected population. Furthermore, the percentage of ewes without pedigree was high even in the already registered flocks due to a low efficiency of the mating group management.

In fact, the mating group management is one of the most important factors affecting the generation interval and the accuracy of the progeny test. The optimal management of controlled natural mating of sampling rams implies a first use of ram by 18 months of age and a size of the mating group sufficient to produce at least 15 yearling primiparous daughters. For this purpose, it is necessary to reduce the number of rams older than 18 months used at first mating, to size mating groups between 40 to 50 ewes and to apply management techniques able to increase the percentage of primiparous ewes of 1 year age.

Another possible intervention could be trying to limit the habit of using rams in the lag between the first mating year and the indexation year. In fact, this practice limits the number of young sampling rams per year so reducing selection intensity on the male pathways.

The other constraint is the high length of the reproductive life of a proven ram. This is not always due to the high genetic value but somewhat to the farmer's difficulty of buying or internally producing elite males.

Although problems related to the application of controlled natural mating, its combining with artificial insemination allowed reaching a good level of direct genetic connectedness in the selection scheme of the Sardinian breed. On the whole, the number of completely disconnected flocks have had a strong decrease in the last 20 years. However, a more precise evaluation of the genetic connectedness in the registered Sardinia breed population is needed to identify the best strategies for combining AI and controlled natural mating.

Conclusion

Artificial insemination is surely the most important breeding tool to permit sound genetic evaluations of dairy sheep breeds. However its large-scale application encountered strong limitations either in some Western Europe countries or in East Europe and North Africa. In these conditions, the strategy of combining small rates of artificial insemination with controlled natural mating could be effective (Carta, 2008). However, an accurate modelling of the selection scheme is needed to optimise the artificial insemination rates and the genetic impact of the controlled natural mating.

This work was funded by the research program “APQ per la ricerca scientifica e l’innovazione tecnologica, progetto P5a – Attivazione del Centro di biodiversità animale per la valorizzazione del patrimonio animale con riferimento alla produzione e alla ricerca al servizio dell’allevamento” of the Regional Government of Sardinia.

Acknowledgments

Barillet, F. 1997. Genetics of Milk Production. in Genetics of sheep. CAB International, eds L. Piper and A. Ruvinsky. Wallingford, Oxon, UK, 523-564.

Carta, A., S.R. Sanna, A. Rosati, S. Casu. 1998a. Milk yield adjustments for milking length and age-parity-month of lambing interaction in sarda dairy sheep. *Ann. Zootec.* 47 (1):59-66.

Carta, A., S.R. Sanna, S. Casu. 1998b. The use of equivalent mature ewe for the genetic evaluation of Sarda dairy sheep. 6th World Congr. Genet. Appl. Livest. Prod. Armidale, Australia. 24: 173-176.

Carta, A., E. Ugarte. 2003. Breeding goals and new perspectives in dairy sheep programs. Book of abstract of the 54th Annual Meeting of the European Association for Animal Production No 9. Rome, Italy, 31 August – 3 September. Wageningen Academic Publishers.

Carta, A. 2008. Sheep breeding. FABRE TP society meeting. Brussels, 16 April 2008 <www.fabretp.org/content/view/full/92/77/>.

Casu, S., I. Pernazza, A. Carta. 2006. Feasibility of a linear scoring method of udder morphology for the selection scheme of Sardinian sheep. *J. Dairy Sci.* 89: 2200-2209

Elsen, J.M., J.C. Mocquot. 1974. Recherches pour une rationalisation technique et économique des schémas de sélection des bovins et ovins. Bulletin Technique du Département de Génétique Animale, INRA, n. 17, pp. 76-97.

Salaris, S., Sara Casu, A. Carta. 2007. Investigating the relationship between the prion protein locus and udder morphology traits and milk yield in Sardinian sheep. *J. Anim. Sci.* 2007. 85:2840-2845

Sanna, S.R., A. Carta, S. Casu, A.M. Pilla, G. Pagnacco. 1994. Valutazione genetica della razza ovina Sarda: III – Indici ed andamenti genetici ed ambientali. *Zoot. Nutr. Anim.*, 20, pp. 313-318

List of references

SIEOL: implementing a global information system for genetic and techno-economic support in dairy sheep in France

*J.M. Astruc¹, G. Lagriffoul², E. Morin³,
F. Barillet⁴, B. Bonaiti⁵ & E. Rehben⁶*

¹Institut de l'Élevage, INRA-SAGA, 31326 Castanet-Tolosan, France

²Institut de l'Élevage-CNBL, INRA-SAGA, 31326 Castanet-Tolosan, France

³Institut de l'Élevage, 31321 Castanet-Tolosan, France

*⁴INRA-UR631 Station d'Amélioration Génétique des Animaux,
31326 Castanet-Tolosan, France*

*⁵INRA-UR337 Station de Génétique Quantitative et Appliquée,
78350 Jouy-en-Josas, France*

⁶Institut de l'Élevage, 149 rue de Bercy, 75595 Paris Cédex 12, France

With 945 000 ewes in milk recording in 2 660 flocks, the impact of milk recording in dairy sheep is high in France and has permitted the development of efficient breeding schemes in the 5 French local dairy sheep breeds. A new information system called SIEOL has been implemented since 2005 for dairy sheep in France to manage both genetic and techno-economic data. As the previous one, this system is based on a three-levels organization. The local level corresponds to the PC of the field technician, in charge of milk recording, on-farm valorisation and techno-economic advice to the breeders. A regional site, the second level, gathers the data from all milk recording technicians, as well as data from other organizations, such as breed organizations, AI centres, milk analysis labs, dairy plants. These data are replicated to the national central database, the third level, whose main objective is to provide data for genetic evaluations, as well as to receive data from molecular analysis labs. The data model is the same whatever the site. This organization enables a mutualisation of the different valorisations and advice to the breeders, and facilitates therefore the interactions between technicians and breeders.

On the whole, the SIEOL system manages data of 55% of French dairy sheep farms and 65% of the dairy ewes.

After presenting the background and management of the new SIEOL information system, we focus in this paper on the main organisational characteristics of the system and emphasize its multiple-purpose objectives, through genetic evaluations, technical and economic support, and new sanitary purposes.

Key words: Dairy sheep, Information system, Genetics, Techno-economic support.

Summary

Introduction

With 945 000 ewes in milk recording in 2 660 flocks, the impact of milk recording in dairy sheep is high in France and has permitted the development of efficient breeding schemes in the 5 French dairy sheep breeds.

The information system for animal recording and genetic data management, which includes the central and local databases, software to input, check and calculate data, as well as the exchanges between the different databases (central and local), is a key point of the efficiency of a breeding program since it is a requirement to obtain accurate, unbiased and on-time EBVs. In France, each species and production of ruminants has its own specific genetic information system. These systems are, until now, supported in a large part by state subsidies, in the framework of the French Breeding Law. Given the evolution of computing technologies, needs of breeders (new traits, new criteria, new organisation) and genetic evaluation, these information systems must evolve regularly, indeed be totally rebuilt. Over the last 10 years, all genetic information systems for ruminants in France (cattle, dairy sheep, meat sheep, goats) have been reconstructed. This paper focuses on the new dairy sheep information system, whose acronym is SIEOL, meaning Dairy Sheep Information System for Breeders (DSISB). This system gathers 55% of the dairy sheep flocks and 65% of the dairy sheep animals (Table 1).

Table 1. Impact of SIEOL in 2007 in France.

Dairy sheep population in France		SIEOL population	
Dairy sheep flocks	Dairy sheep ewes	Dairy sheep flocks	Dairy sheep ewes
4 820	1 452 000	2 662 (55%)	945 000 (65%)

This paper will successively highlight the background in which this new system has been built (decisions and management, main objectives), the conception of the system and its articulation within the different organisations involved in selection and support in dairy sheep in France. Finally, we will make a focus on the main purposes and specificities of the system, which is opened, beyond the data for genetic evaluation, on an increasing range of data, from techno-economic data to sanitary data.

Background and management of the new SIEOL dairy sheep information system

Historically, 3 successive national genetic information systems for dairy sheep have been implemented in France, since the sixties, with the main purpose of genetic evaluations. The last system operated from 1984 to 2005, including, along its lifetime, major adaptations such as integration of specific simplified design for milk quality recording, management of data from breed and AI organizations, on-farm PC computerization of milk recording. The costs of investment and maintenance of these systems have mainly been supported by Ministry of Agriculture.

Beside the genetic information system, a system had been conceived in the early nineties to produce technical and economic support data (margin on feeding costs, gross margin, analysis of chemical and hygienic quality of milk) for extension service to the breeder. The data, input by field technicians on a PC, through a specific software, or got from economic organizations (milk payment data), were sent to a central database run by the Breeding Institute (Institut de l'Élevage).

In 2000, the field organizations involved in breeding activities for dairy sheep, co-ordinated in the National Committee for Dairy Sheep (CNBL) decided to conceive and develop the so-called SIEOL information system whose main innovations would be:

- Share management of genetic data, techno-economic data, and other data, such as sanitary data, in a same database.
- Same structure of data (same data model) whatever the sites.
- Use of the new technologies of information and communication.

SIEOL is the national information system for genetic and techno-economic uses for dairy sheep in France. The Ministry of Agriculture and the CNBL, full member of the new French Inter-professional organization for genetic improvement of ruminants (FGE), are co-owners of SIEOL. According to the Law, the central database is managed by INRA, which is also in charge of official EBVs. The system was mainly financed both by the Ministry of Agriculture and the organizations involved in the CNBL, through European subsidies or with their own funds. SIEOL was conceived and is administrated by the Breeding Institute. Its development was co-performed by the regional (ARSOE Soual) and national (INRA-CTIG) sites of SIEOL.

The SIEOL information system is based upon a pyramidal organization with 3 levels:

- At the local site, each milk recording operator inputs on-farm data on a laptop (identification and registration, matings and lambings, milk recording), using a SIEOL software (developed in Visual Basic language) to check data and propose on-farm correction (if needed) and valorisation to the breeder.
- The field technicians send all data, through an intranet solution, to a regional site located in the town of Soual (Midi-Pyrénées).
- A national site located at INRA Jouy-en-Josas includes all the data available and needed for genetic evaluations (data from all flocks submitted to milk recording since 1950). The exchanges between the regional and national levels lay on replication from one database server to the other.

The same data model is applied at each site. Whereas the national and regional levels have the whole data, the database of each technician computer includes the data corresponding to the flocks managed by this given technician.

SIEOL is supplied by all the organizations involved in both genetic and techno-economic assessment: milk recording organizations, technical advise organizations, breed organizations, AI organizations, milk analysis laboratories, molecular analysis laboratories, milk plants and inter-professional organizations, INRA for EBVs and research purposes. Each organization may, according to specific access rights, update the database and visualize data through a client x server solution.

Updating of data are authorized, whatever the organization, only through a national software (collection of "functions" written in C language, portable and usable on the different databases and systems: SQL Anywhere and Windows, DB2 and AS400, DB2 and MVS or UNIX) which checks data before updating them and increases therefore security and quality of data.

Organisation of SIEOL

Main purposes of SIEOL

Genetic information system and genetic evaluations

EBVs are the main purpose of the system. According to the Breeding Law, genetic evaluations are conceived and operated by INRA and cast to the field organizations by the Breeding Institute. At each run (3 times a year), SIEOL provides the relevant data for the evaluations, whose issues (EBVs, fixed effects) are fully stored. The computed EBVs to be published are sent back to SIEOL. To face this first goal, a specific evaluation and research information system, including scripts, programs and database, has been established to organize the interface between SIEOL and genetic evaluations (table 2). Scripts and software extract the relevant data from SIEOL, organize and calculate data in operational tables (pedigrees, performances) to be used for evaluations (extension of lactations, editing, other calculations, etc), codify the effects and the animals, launch the evaluation, get back the raw data from the evaluations and organize them in a properly way.

This set of tables and software may be easily used to implement experimental evaluations (in order to test new modellings for example), analyse data, estimate genetic parameters and is thus a useful tool for genetics purposes.

Table 2. Dairy sheep population in SIEOL, genetic evaluation and PrP information system.

	SIEOL	Data included in the evaluations (2008)	Published EBVs in 2008 (active animals and reliability threshold)	PrP molecular data
Sheep (ewes and rams)	4 149 041	4 016 316	8 715 rams and 317 454 ewes	126 748
Lactations	7 511 547	6 414 737		

Techno-economic

SIEOL is the only information system of ruminants in France that combines both genetic data and techno-economic data. Indeed, in dairy sheep in France, the field technician provides a global service to the breeder and is therefore responsible for the collection of all on-farm data, genetic-purpose data (milk recording, inventory, AI and matings, lambings), as well as techno-economic data (data permitting calculation of gross margin or margin on feeding cost). He is also responsible for the valorisation of these data towards the breeders. Since the implementation of SIEOL in 2005, the same system (same database, same software) has included genetic and techno-economic data (table 3), with numerous objectives, such as:

- Facilitating the job of the technician who can import individual data collected for each ewe to generate technical assessment at a flock scale in aggregating individual data, avoiding double input.
- Allowing consistency between all the statements produced to the breeder.
- Economic and genetic data in the same database is a useful tool to rationalize the breeding objectives with an economic background.

Sanitary data

During the last decade, the different sanitary crisis (scrapie, blue-tongue) have been a growing concern in sheep. The SIEOL system has been useful to manage sanitary data in order either to provide advise to the breeder, or to overlook sanitary situation of the flocks.

Table 3. Techno-economic assessments produced by SIEOL in 2007 in France.

Type of assessment	Technical assessment	Techno-economic assessment		Chemical and hygienic assessment
		Margin on feeding cost	Gross margin	
Assessments produced in 2007	1 860	1 683	329	1 687

The strong impact of milk recording in sheep has been used to build a large-scale observatory of culling causes for ewes and rams. This collection of data lays on the knowledge of the breeders, who may give the cause of culling with three degrees of precision: generic group (ex.: mastitis), sub-group (ex.: subclinical mastitis; clear symptoms), precise cause (ex.: somatic cell count; *S.aureus* mastitis). The causes of culling have been defined jointly with veterinarians. In 2007, among the farmers of the Lacaune breeding scheme, almost 25% of the culled ewes had a culling cause. These data may be used as an observatory of sanitary problems and diseases in sheep.

In the framework of the national breeding plan to eradicate scrapie on the basis of the PrP gene selection, PrP genotyping has been set up at a large scale, requiring the record in a specific molecular database available for both meat and dairy sheep (Table 2). This database is connected to SIEOL and enables passing on of checked genotype for selection purposes and computation of genotype predictions on relatives.

The SIEOL system has been set up in 2005 and is now running routinely. The objectives defined for the conception of SIEOL are fully achieved: gathering all relevant data for genetic evaluations, spreading EBVs and molecular information to the breeders and the managers of the breeding schemes, allowing the field technicians to propose adequate valorisation (genetic, technical, economic) to the breeders, permitting collective valorisations (statistic, research, answer to breeders concerns). The main challenge for the future will be to associate and link the SIEOL information system, which concerns 55% of the dairy sheep breeders, to the future tracing system for small ruminants, which will be implemented within the next 2 years. In order to avoid multiple recording of the same data (for example movements of the animals), the relationship between the SIEOL information system and the tracing system must be built. A system such as SIEOL has a lifetime of around 15 years, the condition being that it evolves during its lifetime to take into account new technologies, as well as new data to be managed (new raw data, new selection criteria, new needs from the breeders). This kind of system is expensive to build and maintain, compared to the quite limited population of dairy sheep. Therefore, one of the biggest issues for the future will be to find enough funding to keep the system efficient and at the service of the breeders.

Conclusion

Selecting milk composition and mastitis resistance by using a part lactation sampling design in French Manech red faced dairy sheep breed

F. Barillet¹, J.M. Astruc², G. Lagriffoul², X. Aguerre³ & B. Bonaïti⁴

¹INRA- UR631 Station d'Amélioration Génétique des Animaux,
31326 Castanet-Tolosan, France

²Institut de l'Élevage – INRA-SAGA,
BP52627 - 31326 Castanet-Tolosan Cedex, France

³Centre Départemental d'Élevage Ovin,
Quartier Ahetzia, 64130 Ordiarp, France

⁴INRA- UR337 Station de Génétique Quantitative et Appliquée,
78350 Jouy-en-Josas, France

To face the new challenge of selecting dairy sheep for udder functional traits, it is necessary to implement very simplified designs as part-lactation sampling promoted by ICAR in small dairy ruminants, to reduce dramatically recording costs. Such a design has been applied efficiently in Lacaune dairy sheep breed since 1985 for milk composition and also since 1999 for somatic cell count (SCC) after validation of its relevance for this udder health trait (SCC). Without any verification, such a part-lactation design has been implemented since 2002 in Manech red faced (MRF) breed. Records from 58 378 primiparous MRF dairy ewes were used to estimate genetic parameters for milk traits and SCC in this breed. The heritability estimate of SCC was 0.10 for the lactation mean trait. The genetic correlation between lactation SCC and milk yield was positive (0.21), i.e. antagonistic, as already found in Lacaune dairy sheep, in agreement with the well documented literature in dairy cattle. These results obtained for a medium milk yield level breed reinforce the idea that the genetic relationships between udder health (SCC) and milk yield are comparable between dairy cattle and dairy sheep. The results also confirm that the part-lactation sampling testing is a suitable design both for milk composition and SCC whatever the dairy sheep breed.

Key words: Dairy sheep, Recording design, Simplification, Milk yield, Fat and protein contents, Somatic cell count, Mastitis resistance, Breeding goals.

The emphasis for udder functional traits has resulted from the knowledge established during the last ten years that exclusive selection of dairy sheep on milk traits would lead in the long term to udders more difficult to milk by machine and also more susceptible to mastitis (Barillet, 2007). The French dairy sheep Lacaune

Summary

Introduction

breed has the oldest and most efficient breeding scheme based on an extensive use of AI since the 1980s. It is therefore not surprising that the Lacaune breeders have chosen new breeding objectives in 2005 giving the same relative weights to milk production traits (milk yield and composition) and udder functional traits (udder scoring for milkability and somatic cell count (SCC) for mastitis resistance). The example of the Lacaune breed shows that a part-lactation sampling design allows efficient selection both on milk composition (fat and protein contents) and mastitis resistance (SCC), while reducing dramatically the number of test days involved in a qualitative recording compared to the A4 testing. Thus without no more verification this recording strategy has also been applied since 2002 for the second French dairy sheep breed, the Manech red faced (MRF) breed, to face its new breeding goals.

The objective of the present study is to analyse the MRF data to verify that such a design is suitable to MRF, i.e. to any breed, given that the MRF breed is a medium milk yield breed compared to the Lacaune dairy sheep belonging to the high milk yield level breeds. Regarding the MRF breed, the present study is the first step towards an evolution of its breeding goals.

Materials and methods

Data

The MRF breeding programme became fully efficient for milk yield in the 1990's exhibiting an annual genetic gain close to 4 litres, i.e. 2.2 % of the population mean (Astruc *et al.*, 2002). Therefore the recording of milk composition (fat and protein contents) became a priority at the beginning of the 2000's. To face the question and reduce dramatically the recording cost, a part-lactation sampling design in first lactation has been implemented as already practised in France in Lacaune breed, i.e. only two to four times during the first 4 test days of each ewe at the morning milking (Barillet, 1997). Moreover, it was assumed that such a part-lactation sampling

Table 1. Characteristics of the data.

Characteristics	
Breed	Manech red faced
Study period	2002-2007
Animals in data (first lactation for milk traits and SCC)	58 378
Animals in pedigree	118 313
Number of flocks (flock x year)	258 (1221)
Mean $\pm$ standard deviation of the traits	
Lactation number	First lactation
Length of milking period	132d $\pm$ 42
d (after a 30-d suckling period)	
Milk yield, litre (lactation basis ¹)	149.2l $\pm$ 63.1
Equivalent mature milk yield corrected for length of milking period, litre... (lactation basis ¹)	217.2l $\pm$ 65.8
Fat yield, g (part lactation sampling ²)	1 3096g $\pm$ 3 820
Protein yield, g (part lactation sampling ²)	1 0333g $\pm$ 3 073
Fat content, g.l ⁻¹ (part lactation sampling ²)	61.1g/l $\pm$ 8.8
Protein content, g.l ⁻¹ (part lactation sampling ²)	47.8g/l $\pm$ 3.9
Lactation SCS (LSCS) arithmetic mean of SCS ⁽²⁾	3.36 $\pm$ 1.38

¹Monthly recording design at the morning milking (AC method) with 4.4 test days on average per first lactation.

²Part lactation sampling with 2.8 test days on average at the morning milking within the first 4 test days for milk yield of each ewe.

design was also relevant in MRF breed for SCC as previously demonstrated in Lacaune breed (Barillet *et al.*, 2001; Rupp *et al.*, 2003). The years 2002-2007 were needed to generate enough data on milk composition and SCC in the MRF nucleus flocks, and were simultaneously made profitable to intensify the PrP selection: from 2001 to 2005, the ARR allelic frequencies at the PrP gene in the MRF nucleus flocks increased from 0.19 to 0.50, while it reached 0.74 for the AI rams born in 2004 (Barillet, 2007). Under these conditions, after data editing, 58,378 MRF ewes, recorded in first lactation for milk composition and SCC between 2002 and 2007, were included in the analysis (Table 1).

These primiparous MRF ewes were recorded on average with 4.4 test days for milk yield per first lactation and, due to the part lactation sampling design, with 2.8 test days on average for milk composition (fat and protein contents) and SCC, at the morning milking only, since all these recordings were carried out in the framework of the AC method as described in ICAR rules for dairy sheep (Table 1).

A cell count lactation mean (LSCS) was computed as the arithmetic mean of test-day somatic cell score (SCS) as proposed by Wiggans and Shook (1987), SCS being defined in a classical way through a logarithmic transformation

$$SCS = \log_2(SCC/100\,000) + 3$$

to account for the highly skewed distribution of SCC. Genetic parameters for milk production traits and LSCS were estimated using a REML method applied to an animal model on the 58,378 MRF ewes with data in first lactation and 118 313 animals in pedigree traced up to 4 generations of ancestors for the ewes with records (Table 1). The fixed effects corresponded to those applied in the calculation of the official EBV for each trait (Astruc *et al.*, 2002): for milk traits considered on a lactation basis, the model included the fixed effects of flock x year x parity, age and month at lambing within parity and year, for milk yield the lambing-first test-day interval within year and parity, for fat and protein yields or contents the effect of qualitative recorded category defined with the number of test-days x average lactation stage at recording.

Genetic parameters are presented in table 2. They follow the well known patterns for milk traits (Barillet, 1997 and 2007), given the part-sampling design for fat and protein contents. Indeed, fat (FC) and protein (PC) contents determined from a part lactation sampling (2.8 test days at the morning milking versus 4.4 on average for milk yield – Table 1) are, as expected, less heritable (0.28 and 0.51 respectively for FC and PC) than the homologous genetic parameters when using the A4 method (heritabilities in the range of 0.60 for FC and 0.55 for PC). We can notice that the decrease of heritability is really limited for part lactation sampling PC, in agreement with previous Lacaune results. Nevertheless heritabilities of FC and PC with such a part-lactation sampling design remain high enough, and at least comparable to those of fat or protein yields (0.28 to 0.30), which is suitable for selection purposes, since the breeding scheme is designed for milk, fat or protein yields. Moreover heritabilities of yields based on such a part lactation sampling are quite identical to the heritabilities of yields when recorded on a A4 basis. Furthermore the genetic antagonism between milk yield (MY) and FC or PC (-0.39 and -0.44 respectively) is the same whatever the design (A4 or part lactation sampling) in MRF breed as already shown in Lacaune breed (Barillet, 1997 and 2007).

Estimation of genetic parameters

Results and discussion

Table 2. Genetic parameters: heritabilities¹ on diagonal, genetic correlations² above and environmental correlations under the diagonal.

Trait	MY	FY	PY	FC	PC	LSCS	Trait	σ ³	σ ⁴
Milk yield (MY)	0.33	0.87	0.92	-0.39	-0.44	0.21	MY	51 l	30 l
Fat yield (FY)	0.84	0.28	0.91	0.10	-0.16	0.25	FY	3161 g	1662 g
Protein yield (PY)	0.96	0.82	0.30	-0.16	-0.06	0.25	PY	2352 g	1277 g
Fat content (FC)	-0.17	0.34	-0.16	0.28	0.60	0.07	FC	7.8 g.l ⁻¹	4.1 g.l ⁻¹
Protein content (PC)	-0.34	-0.20	-0.04	0.16	0.51	0.07	PC	3.6 g.l ⁻¹	2.6 g.l ⁻¹
LSCS (LSCS)	-0.26	-0.16	-0.17	0.16	0.38	0.10	LSCS	1.31	0.42

¹Standards errors between 0.01 and 0.02

²Standards errors between 0.01 and 0.03

³Phenotypic standard deviation

⁴Genetic standard deviation

On the other hand, the present results (Table 2) regarding the cell count mean (LSCS) confirm, in MRF breed as in Lacaune breed (Barillet *et al.*, 2001), that the genetic parameters are quite similar for part-lactation or total lactation sampling of SCC: a moderate heritability (0.10) of LSCS whatever the sampling design and a genetic antagonism between LSCS and milk yield (0.21) or fat (0.25) or protein yields (0.25). Thus the balance between cost and genetic efficiency is clearly in favour of the part lactation design both for milk composition (FC and PC) and SCC (LSCS). Such SCC results for MRF breed are in agreement with all the homologous results obtained in Lacaune dairy sheep breed between 2001 and 2007 (Table 3) and with the abundant literature in dairy cattle. As reported in dairy cattle reviews (Mrode and Swanson, 1996; Detilleux, 2002; Rupp and Boichard, 2003), heritability estimates of single SCC range from 0.05 to 0.14 for monthly test-day and increase on average up to 0.15 for lactation mean (LSCS) with a range 0.10-0.20. Moreover, in dairy cattle, the genetic antagonism between SCC and milk production traits is well documented (Mrode and Swanson, 1996; Rupp and Boichard, 2003): genetic correlation between SCC and milk yield is equal on average to 0.14, with a range 0.10-0.20 in cattle.

In dairy sheep, contrary to cattle, the lactation incidence of clinical mastitis (CM) is low and around 5 %, while the prevalence of subclinical mastitis (resulting mainly from bacterial infections whose reservoir is generally in the udder or teats) ranges from 10 to 50 % or more (Bergonnier *et al.*, 2003; Berthelot *et al.*, 2006). Thus, in dairy sheep, considering SCC only appears as a sound approach for selecting mastitis resistance. Assessment of the suitability of SCC for udder health in dairy sheep is under way in an experiment based on SCC divergently selected Lacaune dairy sheep lines in an INRA experimental flock (La Fage): first results show a clear decrease of CM and udder infections caused by mammary pathogens (measured by repeated bacteriological tests during the lactation) for the low SCC line (Rupp *et al.*, 2006). Since SCC is a suitable tool for selecting resistant dairy sheep, it is therefore important to overcome the present inconsistency regarding SCC genetic parameters in this species. In dairy sheep, heritability estimates of single SCC range between 0.04 and 0.14 for monthly test-day and between 0.10 and 0.18 for lactation measures (Table 3), which is in agreement with homologous dairy cattle results. But genetic relationships of udder health (SCC) with milk yield (or fat or protein yields) are quite inconsistent in dairy sheep, ranging from antagonistic (Mavrogenis *et al.*, 1999; Barillet *et al.*, 2001; Rupp *et al.*, 2003; Barillet, 2007; Riggio *et al.*, 2007) to favourable (El-Saied *et al.*, 1998; Othmane *et al.*, 2001; Serrano *et al.*, 2003; Hamann *et al.*, 2004; Legarra and Ugarte, 2005). When looking at these results (Table 3), we

Table 3. Estimates of genetic parameters for milk yield (MY) and somatic cell score (SCS) in dairy sheep.

Breed (authors and year)	Data	Heritabilities		Genetic correlation MY- SCS
		MY	SCS	
Chios (Mavrogenis <i>et al.</i> , 1999)	1 457 ewes/1 457 lactations first lactation (test day model)	0.26	0.18	0.20
Churra (El-Saied <i>et al.</i> , 1998)	2 379 ewes/3 231 lactations all lactations (lactation model)	0.24	0.12	- 0.15
Lacaune (Barillet <i>et al.</i> , 2001)	5 272 ewes/5 272 lactations first lactation (lactation model) first lactation (test day model)	0.34 0.24	0.15 0.08	0.11 0.04
Churra (Othmane <i>et al.</i> , 2001)	1 111 ewes/1 962 lactations all lactations (lactation model)	0.26	0.11	- 0.17
Lacaune (Rupp <i>et al.</i> , 2003)	94 474 ewes/139 973 lactations lactations 1 and 2 (if 1 known) (lactation model)	0.28	0.13	0.18
Manchega (Serrano <i>et al.</i> , 2003)	28 694 ewes/36 873 lactations 3 lactations (lactation model)	0.27	0.12	- 0.12
East-Friesian (Hamann <i>et al.</i> , 2004)	1 108 ewes/1 746 lactations all lactations (test day model)	0.15	0.16	- 0.08
Latxa (Legarra and Ugarte, 2005)	6 165 ewes/9 805 lactations all lactations (lactation model)	0.21	0.13	-0.29
Lacaune (Barillet, 2007)	121 283 ewes /121283 lactations first lactation (lactation model)	0.32	0.15	0.15
Valle del Belice (Riggio <i>et al.</i> , 2007)	2 277 ewes/13 066 test-days first lactation (test day model)	0.14	0.14	0.16

can notice that authors studying only first lactations or two first lactations only if the first one was also available in the data (Rupp *et al.*, 2003) found antagonistic relationships between SCC and milk yield (Table 3) as in dairy cattle. On the contrary all the analysis estimating favourable relationships between SCC and milk yield were based on data including all lactations (Table 3). Moreover these studies were usually based on a few years of experimental recording with more records in multiparous lactations than in first lactations. Thus data editing did not exclude a later parity if the previous one was unknown in the data. Therefore culling on milk yield or udder health over lactations not taken into account in these studies could explain favourable and thus probably biased association found in these analysis. The contradictory results in Latxa breed (Legarra and Ugarte, 2005) and Manech red faced breed (this paper), these 2 breeds belonging to the same medium milk yield Pyrenean population, reinforce the present interpretation: the genetic correlation between SCS and milk yield was estimated as favourable in Latxa breed (- 0.29 with 9805 multiparous lactations) and as antagonistic in Manech red faced breed (+0.21 with 58 378 first lactations in the present results). Under these conditions, we incline to consider unfortunately as more likely that in dairy sheep as in dairy cattle the genetic relationship between udder health (SCC) and milk production traits is antagonistic, and that udder health will be deteriorated when selecting only production traits.

Conclusion

Genetic improvement of udder functional traits has become a new challenge in dairy sheep, since there is now evidence that selection on milk traits only will lead in the long term to udders more difficult to milk by machine and more susceptible to mastitis. The present results obtained in MRF breed, first confirm the genetic trends described above specially for mastitis susceptibility, second validate the part-lactation sampling design as a suitable tool both for milk composition (FC and PC) and udder health (SCC) whatever the breed. Thus including udder scoring and SCC in the breeding goals, at the moment on a quantitative genetic basis, is a new challenge applied in France for the Lacaune breed since 2005 and in progress for other breeds such as MRF breed. Moreover windows opened by molecular genetics will be profitable for udder functional traits as it is already the case for the PrP gene for scrapie resistance (Barillet, 2007).

Finally the promotion of the part-lactation sampling design by the ICAR dairy sheep group appears as a sound strategy to reduce dramatically the recording cost in small dairy ruminants while facing new objectives related to udder functional traits. On the other hand this strategy of reducing the qualitative tests to decrease the recording costs in small ruminants needs to maintain a high accuracy of each individual test day as presently defined in ICAR requirements regarding manual or electronic milk recording devices and analytical quality analysis of sheep milk in laboratories.

List of References

- Astruc, J.M., Barillet, F., Barbat, A., Clément, V., Boichard, D.** 2002. Genetic evaluation of dairy sheep in France. In: Proceedings of the Seventh World Congress. Genet. Appl. Livest. Prod., Montpellier, France, CD-ROM communication 01-45.
- Barillet, F.** 1997. Genetics of Milk Production, Chap 20. in: I. Piper and A. Ruvinsky (Eds), CAB International, The Genetics of Sheep, pp. 539-564.
- Barillet, F., Rupp, R., Mignon-Grasteau, S., Astruc J. M., Jacquin M.** 2001. Genetic analysis for mastitis resistance and milk somatic cell score in French Lacaune dairy sheep. Genet. Sel. Evol. 33: 297-415.
- Barillet, F.** 2007. Genetic improvement for dairy production in sheep and goats, chapter of the special issue entitled "The outlook of quantitative and molecular genetics. Application in improving sheep and goats", D. Notter, R. L. Baker and N. Cokett (Eds), Small Ruminant Research, 70 (2007) 60-75.
- Bergonier, D., de Cremoux, R., Rupp, R., Lagriffoul, G., Berthelot, X.** 2003. Mastitis of dairy small ruminants. Vet. Res. 34, 689-716.
- Berthelot X., Lagriffoul G., Concordet D., Barillet F., Bergonier D.** 2006. Physiological and pathological thresholds of somatic cell counts in ewe milk. Small Ruminant Research 62: 27-31.
- Detilleux, J.C.** 2002. Genetic factors affecting susceptibility of dairy cows to udder pathogens. Vet Immunol Immunopathol. 88 (3-4): 103-110.
- El Saied U.M., Carriero J.A., De La Fuente L.F., San Primitivo F.** 1998. Genetic parameters of lactation cell counts and milk and protein yields in dairy ewes. J. Dairy Sci. 82: 639-644.

Haman H., Horstick A., Wessels A., Distl O., 2004. Estimation of genetic parameters for test day milk production, somatic cell score and litter size at birth in East Friesian ewes. *Livest. Prod. Sci.* 87: 153-160.

Legarra A., Ugarte E. 2005. Genetic parameters of udder traits, somatic cell score and milk yield in Latxa sheep *J. Dairy Sci.* 88: 2238-2245.

Mavrogenis, A.P., Koumas, A., Gavrielidis, G. 1999. The inheritance of somatic cell counts in Chios sheep. In: *Proceedings of the Sixth International Symposium on Milking of Small Ruminants*, vol. 95, Athens, Greece, EAAP Publication, pp. 389-392.

Mrode, R.A., Swanson, G.J.T. 1996. Genetic and statistical properties of somatic cell count and its suitability as an indirect means of reducing the incidence of mastitis in dairy cattle. *Anim. Breed. Abstr.* 64 (11), 847-857.

Othmane M.H., Carriedo J.A., San Primitivo F., de la Fuente J.A. 2002. Genetic parameters for lactation traits of milking ewes: protein content and composition, fat, somatic cells and individual laboratory cheese yield. *Genet. Sel. Evol.* 34: 581-596.

Riggio, V., Finocchiario, R., Kaam, J.B.C.H.M. van., Portolano, B., Bovenhuis, H. 2007. Parameters for milk somatic cell score and relationships with production traits in primiparous dairy sheep. *J. Dairy Sci.* 90: 1998-2003.

Rupp R., Boichard D. 2003. Genetics of resistance to mastitis in dairy cattle. *Vet. Res.* 34: 671-688.

Rupp R., Lagriffoul G., Astruc J.M., Barillet F. 2003. Genetic parameters for milk somatic cell scores and relationships with production traits in French Lacaune dairy sheep *J. Dairy Sci.* 86: 1476-1481.

Rupp R., Bergonier D., Dion S., Hygonenq M.C., Aurel M.R., Foulon E., Foucras G. 2006. Effects of SCC-based selection for mastitis resistance: first results from a divergent selection experiment in sheep. *Proc. 8th World Congres. Genet. Appl. Livest. Prod.*, Belo-Horizonte, 13-18 August 2006, Brazil. CD-ROM communication 15-16.

Serrano M., Perez-Guzman M.D., Montoro V., Jurado J.J. 2003. Genetic analysis of somatic cell count and milk traits in Manchega ewes: Mean lactation and test-day approaches *Livest. Prod. Sci.* 84: 1-10.

Wiggans G.R., Shook G.E. 1987. A lactation measure of somatic cell count *J. Dairy Sci.* 77: 2666-2672.

Productivity of Slovenian Alpine goat in the conventional and organic farming system

D. Kompan & M. Kastelic

University of Ljubljana, Biotechnical Faculty, Domzale, Slovenia

Milk production and milk composition of dairy goats in organic and conventional farming were studied in Slovenian Alpine goat population. The conventional farming shows a tendency to higher production, but the differences between both production systems are due to high variability not statistically significant. The preorganic productivity of both groups was also studied. The group, which was later included in organic production produced less also in preorganic period. Mostly, farms with low production intensity in preorganic period accepted the organic production. It has been established that production was in both groups on a low level, therefore a special selection program for organic farming in Slovenia is not necessary.

Key words: *Milk recording, Lactation, Variability, Production traits, Milk composition*

Goat production can be considered as a valuable part of sustainable farming system. Furthermore, integration of livestock can increase economic and environmental benefits as well as diversity, thereby making important contributions to the farm's sustainability. Goats may fit well into the biological and economic niches in a farm operation that otherwise go untapped. They can well be incorporated into the existing grazing operations with donkeys or horses.

Goats can also be used for the control of weeds and bush to help utilize a pasture's diversity, as long as they are not allowed to overgraze. To produce milk, meat, and fiber livestock uses grass and other plants that cannot be included to human diet. In a balanced agro-ecosystem, both animals and plants are thriving successfully. Livestock eats the excess plant materials, and animal wastes provide nutrients for the plants. Grazed pastures need less fertilizer than those that are hayed. The primary goal of controlled grazing is to use livestock as a tool to manage forage growth. Animals use up very few of the nutrients from the plants they eat; most minerals are returned in animal wastes and can be considered as part of a natural cycling of nutrients. If wastes are evenly distributed throughout the grazing area and biological agents such as earthworms, dung beetles, and soil bacteria are active, the system should be relatively stable.

Summary

Introduction

Many organizations have adopted goal statements that focus on achieving a sustainable future. While these vary widely in specific wording, they show a surprising degree of convergence around several key ideas:

- *Whole-systems thinking*: the integration of social, environmental, and economic forces, also known as the triple bottom-line;
- *Long term thinking*: understanding the consequences of actions over time, and preserving choices and opportunities for future generations;
- *Recognizing limits*: an acknowledgement that people, economies, and the entire life depend on healthy functioning ecosystems; and
- *Improved livelihoods*: a better “quality of life,” both today and for future generations.

The principles were created to provide a framework to guide ecology toward sustainable solutions with interdependence between ecological, economic and social factors in achieving sustainability.

Environmental, economic and social goals can be compatible, and interrelated in such a way that one goal cannot be effectively pursued if at the expense of another. In other words, the availability of natural resources and a clean and healthy environment are essential to our production capability, and conversely, our ability to address environmental and social issues often depends on a strong and vibrant economy.

The productivity of dairy goat reared in organic farming was not very widely studied. Some studies were done on dairy cattle and conclusions are maybe applicable also on dairy goats. Results are different from case to case. Nauta *et al.* (2006) found the production of 6 440 kg of milk per cow and lactation in organic and 7 156 kg milk in conventional management in the same geographic area. Farms which are in the phase of conversion from conventional to organic farming had an average production of 6 622 kg per cow and lactation. It is interesting that the average preorganic production was lower (6 991 kg/cow and lactation) than on the conventional farms. After the farms started to convert to organic management, the percentage of proteins dropped. The diet on organic farms is based on fiber forages, but the percentage of fat is a little lower on organic farms. The total production of fat and proteins per cow and lactation in conventional production was larger mostly because of larger milk production and not because of different milk composition. Toledo *et al* (2002) did not find the differences between the milk composition in conventional and organic farming in Swedish conditions. Small differences in milk production and composition were found also in the study of Kristensen and Kristensen (1998) in Danish conditions. Dual purpose dairy cattle produced only 115 kg more energy corrected milk (ECM) in lactation. In the other study in Danish conditions (Kristensen and Mogensen, 2000) the difference between the two production systems was much larger - 7,043 in conventional comparing to 6 627 kg ECM in organic production. Rosati and Aumaitre (2004) compared two French farms. The difference was much larger: the conventional farm produced 7,260 and organic only 5 130 liters of milk per cow and lactation in primiparous Holstein cows. In extensive production (without concentrates) cows produced only 5 030 kg of milk per lactation. When 8 kg of concentrate was daily supplemented in first 24 weeks of lactation the production of milk was 6 664 kg (Sehested *et al.*, 2002). The difference between the two production systems was also relatively large in Norway; 4 854 in year 1994, 4 791 in year 1995 and 4 554 kg per cow per lactation in year 1996 in organic production comparing to 6 212, 6 014 and 6 040 for every year respectively in conventional production (Reksen *et al.*, 1999). It can be concluded that the productivity of animals in organic farming is mostly determined by the management of every single farm.

The aim of this study is to find out the differences between two production systems and if the special selection program for the organic farming is necessary.

In Slovenia milk recording of goats using A4 method was practiced in the years 1996 to 2002. The AT4 method has been used since 2003. Till the year 2000 there were no officially recognised organic goat farms in Slovenia. The selection procedure and the selection criteria do not differ between the organic and conventional farming system. Our research focuses on goat farms that have been included in selection programme since 1999 or before. In 2002 the rural development programme was initiated, followed by the subsidies offered to certain kinds of sustainable agriculture, among them the ecological farming and subsidies programme for the separate measures of agricultural policy, only some ten or twenty goat farmers decided for it, mostly in 2003 and 2004 when the subsidies substantially increased, especially for organic farming.

In 2007 milk yield and milk composition were compared between the flocks of Alpine goats in organic and in conventional farming system. Another comparative study was conducted in 1999 when flock results were compared between those that stayed in the conventional system, and those that were later changed to organic farming. Data processing included lactations lasting over 199 days. The following statistical model was used:

$$Y_{ijklm} = T_i + F_{ij} + L_k + b(\bar{x} - x_{ijklm}) + e_{ijklm} \quad (1)$$

where:

- Y_{ijklm} = ijklm-th observation of studied trait;
- T_i = i-th farming (conventional, organic);
- F_{ij} = j-th farm (flock) nested in breed I;
- L_k = k-th lactation;
- b = regression coefficient
- x_{ijklm} = ijklm-th observation of lactation length
- e_{ijklm} = residual for observation ijklm.

MEANS and GLM procedures of SAS/STAT programme were used for the statistical evaluation.

The number of observations, the average values, standard deviations and coefficients of variability for organic and conventional production systems in years 2007 and 1999 are presented in Table 1. Apparently, the farmers with poor production results decided for organic farming. Before the change, milk yield on farms in 1999 was 515 kg (SD=228.6 CV=44.2, lactation 253 days), while milk yield results on farms that did not change to organic farming was 542 kg (SD=185.4 CV=34.2, lactation 247 days) The situation on almost the same farms in 2007 was as follows: milk yield on conventional farms was 574 kg (SD=180, CV=31.5, lactation 243 days), compared to organic farms, where milk yield was 502.5kg (SD=267, CV=53.1, days in lactation 244) (Table 1). Higher variability of the results was observed on organic farms. Presumably, this is the result of different production systems.

Analysis of variance for production traits such as milk yield and milk composition on Slovene Alpine goat farms in years 2007 and 1999 are presented in table 2. Determination coefficients (R^2) are higher for milk yield and other traits closely

Material and methods

Results and discussion

related to it, as well as for the total fat, protein and lactose content. Variability of milk components was not well described with the model used in this case, as the determination coefficient was about 0.2, with the exception of fat percentage, which was just slightly above 0.3.

The major variability source was a flock, which had a statistically significant effect on all the studied traits. The lactation number had an impact on milk yield, and on produced quantities of milk components. Milk content was generally not affected by the successive lactation. The same stands for the lactation length.

Different farming system (organic, conventional) statistically significantly affected only the percentage of fat and dry matter in 2007. It is interesting that between farms that changed later to organic farming, and those that stayed in conventional system, the difference was evident already in preorganic period in the year 1999. In the same year a difference between both production systems was present also in milk fat rate and milk fat content. In the conventional system a noticeable tendency for higher productivity was observed (Table 1), but the variability was so high that the

Table 1. Number of lactations (n), average values, standard deviations (SD) and coefficients of variability (CV) for production traits in conventional and organic farming for goats in year 2007 and for the same flocks in year 1999

	Conventional				Organic			
	No.	Mean	SD	CV (%)	No.	Mean	SD	CV (%)
<i>Year 1999</i>								
Lactation (days)	287	252.9	24.7	9.77	131	246.6	33.4	13.53
Total milk (kg)	287	541.7	185.4	34.22	131	514.6	228.6	44.42
Milked milk (kg)	287	419.0	170.0	40.56	131	395.0	215.7	54.61
Fat (kg)	285	16.59	5.59	33.68	130	15.80	6.77	42.83
Fat (%)	285	3.10	0.46	14.88	130	3.15	0.51	16.25
Proteins(kg)	285	15.08	5.04	33.41	130	14.67	6.61	45.03
Proteins (%)	285	2.80	0.25	9.02	130	2.84	0.30	10.49
Lactose (kg)	285	22.86	7.83	34.24	130	21.14	9.93	46.96
Lactose (%)	285	4.23	0.23	5.37	130	4.06	0.31	7.71
Dry matter (%)	285	10.13	0.66	6.51	130	10.05	0.83	8.29
<i>Year 2007</i>								
Lactation (days)	240	242.9	19.7	8.11	250	243.7	23.9	9.82
Total milk (kg)	240	574.0	180.9	31.52	250	502.5	267.0	53.13
Milked milk (kg)	240	464.2	178.4	38.43	250	402.5	267.0	66.33
Fat (kg)	239	18.54	6.06	32.68	246	13.82	7.61	55.09
Fat (%)	239	3.26	0.56	17.17	246	2.77	0.58	21.02
Proteins(kg)	239	17.17	5.60	32.61	246	14.69	7.88	53.63
Proteins (%)	239	3.00	0.36	11.96	246	2.94	0.38	13.00
Lactose (kg)	239	24.87	8.19	32.92	246	21.19	11.90	56.17
Lactose (%)	239	4.31	0.39	9.08	246	4.19	0.43	10.25
Dry matter (%)	239	10.58	1.08	10.20	246	9.90	1.13	11.39

Table 2. Analysis of variance for productivity and milk composition of Slovenian Alpine goat according to model (1) in years 2007 and 1999.

	Model			T _i			F _{ij}			L _k			b(X ₁ X _{ijklm})		
	DF	DF		mod.	err.	F ratio.	P	R ²	DF	P	DF	P	DF	P	b
Year 1999															
Total milk (kg)	21	396	38.60	<0.0001	0.6717	1	0.4968	12	<0.0001	7	<0.0001	1	<0.0001	2.75	
Milked milk (kg)	21	396	39.92	<0.0001	0.6792	1	0.8698	12	<0.0001	7	<0.0001	1	<0.0001	2.33	
Fat (kg)	21	393	28.50	<0.0001	0.6036	1	0.3815	12	<0.0001	7	<0.0001	1	<0.0001	0.077	
Fat (%)	21	393	8.85	<0.0001	0.3211	1	0.2514	12	<0.0001	7	0.0948	1	0.1894	-0.0013	
Proteins(kg)	21	393	40.66	<0.0001	0.6848	1	0.2128	12	<0.0001	7	<0.0001	1	<0.0001	0.079	
Proteins (%)	21	393	5.69	<0.0001	0.2332	1	0.3376	12	<0.0001	7	0.0002	1	0.7611	0.0002	
Lactose (kg)	21	393	38.47	<0.0001	0.6728	1	0.7038	12	<0.0001	7	<0.0001	1	<0.0001	0.113	
Lactose (%)	21	393	4.29	<0.0001	0.1866	1	<0.0001	12	0.0002	7	0.4672	1	0.6746	-0.0003	
Dry matter (%)	21	393	3.32	<0.0001	0.1506	1	0.0172	12	0.0002	7	0.0109	1	0.4081	-0.0014	
Year 2007															
Total milk (kg)	22	467	52.92	<0.0001	0.7137	1	0.2600	13	<0.0001	7	<0.0001	1	<0.0001	1.76	
Milked milk (kg)	22	467	54.69	<0.0001	0.7204	1	0.8099	13	<0.0001	7	<0.0001	1	<0.0001	1.63	
Fat (kg)	22	462	44.30	<0.0001	0.6784	1	<0.0001	13	<0.0001	7	<0.0001	1	<0.0001	0.058	
Fat (%)	22	462	12.61	<0.0001	0.3751	1	<0.0001	13	<0.0001	7	0.0009	1	0.4220	0.0011	
Proteins(kg)	22	462	49.41	<0.0001	0.7017	1	0.3104	13	<0.0001	7	<0.0001	1	<0.0001	0.056	
Proteins (%)	22	462	4.98	<0.0001	0.1917	1	0.7176	13	<0.0001	7	0.3208	1	0.0830	0.0017	
Lactose (kg)	22	462	50.99	<0.0001	0.7083	1	0.0838	13	<0.0001	7	<0.0001	1	<0.0001	0.078	
Lactose (%)	22	462	3.43	<0.0001	0.1404	1	0.0048	13	0.0002	7	0.4375	1	0.0616	0.0021	
Dry matter (%)	22	462	5.07	<0.0001	0.1944	1	0.0003	13	0.0001	7	0.0885	1	0.1001	0.0049	

differences were not statistically significant. High variability and lower average values on organic farms were most probably caused by not so well balanced animal nutrition and by poor health condition in the flocks in organic system, mostly due to parasites. These may not be treated preventively. The parasites have to be diagnosed prior to treatment. Because the analyses represent additional costs, farmers usually avoid it as long as possible.

Interestingly, the farms which later changed to organic system had on average lower production results already in 1999. This may be the result of production conditions or might be even more probably caused by producers. The change to organic system was performed mostly by producers who already had poor production results beforehand. The entry to organic system made the production method »formal«, although it had been practiced previously, but not formally yet.

Conclusions

Milk recording results, as well as the composition of milk indicate that some traits such as milk yield and milk fat content are lower in organic farming system compared to the conventional one, although in most parameters the differences are not significant. Apparently, even the conventional systems have low input (lower quantities of concentrates). It is evident that mostly those farms with relatively extensive production decided to change to organic farming. According to our results we can conclude that the recording methods and breeding goals can be the same for both production systems. Therefore, the differentiation of selection index is not necessary. To our opinion, better management is required regarding nutrition and parasite control on organic farms. Proper management could improve the production economy.

List of references

- Kristensen, T., Mogensen, L.** 2000. Danish organic dairy cattle production systems – feeding and feed efficiency. In: Ecological animal husbandry in the Nordic countries. Hermansen, J.E., Lund, V., Thuen, E. (Eds). Tjele, Danish Research centre for organic agriculture.
- Kristensen, T., Kristensen E.S.** 1998. Analysis and simulation modelling of the production in Danish organic and conventional dairy herds. *Livestock Prod. Sci.* 54, 55-65.
- Nauta, W.J., Veerkamp, R.F., Brascamp, E.W., Bovenhuis, H.** 2006. Genotype by Environment interaction for milk production traits between organic and conventional dairy cattle production in The Netherlands. *J. Dairy Sci.* 89, 2729-2737.
- Reksen, O., Tverdal, A., Ropstad, E.** 1999. A comparative study of reproductive performance in organic and conventional dairy husbandry. *J. Dairy. Sci.* 82, 2605-2610.
- Rosati, A. Aumitre, A.** 2004. Organic dairy farming in Europe. *Livestock Prod. Sci.* 30, 41-51.
- Sehested, J. Kristensen, T., Sørgaard, K.** 2003. Effect of concentrate supplementation level on production, health and efficiency in an organic dairy herd. *Livestock Production Science* 80, 153-165.
- Toledo, P., Andren, A., Björck, L.** 2002. Composition of raw milk from sustainable production systems. *Int. Dairy J.* 12, 75-80.

Marketing value-added in milk recording products and services

P. Baier

*AgSource Cooperative Services, 135 Enterprise Drive, Verona, Wisconsin
53593 USA; a subsidiary of Cooperative Resources International,
Shawano, Wisconsin, USA*

Value-added marketing is a business philosophy that embraces the objective of developing and delivering higher-valued services to the customer, and selling those services to the customer on that basis. It is fundamentally opposite of commodity based marketing with high levels of price sensitivity and reliance upon personal relationships. In the past four years AgSource Cooperative Services and Cooperative Resources International (CRI) have adopted a value-added marketing approach which has placed equal value on products and the people necessary to deliver them. It has resulted in a significant improvement in results. In the twelve months ending in May 2004 AgSource had over 360 000 fewer individual cow recordings than in the previous twelve months. In April 2008 its annualized increase was 370 000 recordings resulting in a much stronger foundation for future success, particularly in an increasingly competitive but shrinking domestic market.

Key words: *recording industry, Value-added, Information.*

In the past twenty years much of the milk recording industry has been evolving from a structure with, in a given country or region, a single provider and exclusive service rights to a much more competitive and open market. This process is in various stages in different areas, but moving from monopolies to open markets is an evolutionary process. Historically, milk recording service providers have frequently been non-profit and/or government-based organizations, perhaps with subsidy, and consequently the price of services has generally been kept low to farmers. While this can be viewed as positive for the customer, it becomes a limitation if the insufficient profit generated by low prices results in less investment in product and service improvements. Perhaps even more limiting, the customer will equate price with value. Ironically, if less investment is made in products and services and customers perceive lower value, utilization declines, and lower volumes are applied against the high fixed costs associated with the milk recording business. This then forces prices higher, instead of lower, with even more pressure from declining demand. This could be described as the death spiral for a business or an industry.

Summary

Introduction

In the last four years AgSource and CRI have made significant investments in converting to a value-added business philosophy. That philosophy can be described as proactively looking for ways to enhance, augment, or enlarge our bundled package for the customer. It is about always seeking ways to create meaningful value and to exceed customer expectations and making our products and services so important to the customer that they cannot afford to replace us, without price being an issue.

The three-dimensional bundle of value

Value-added salespeople sell three things: the company, the product, and themselves. This can be referred to as the three dimensional bundle of value. In our experience, it has absolute application to milk recording organizations evolving from exclusive providers that may have received some form of external support to a competitive market fully funded by service revenue.

Company

It is easy to underestimate the fundamental impact the image of an organization or brand can have on marketplace success. In reality, little success can be expected from improvement in products and services without the foundation of a strong organization and positive brand image. By strong we mean reliable, trustworthy and with a history of commitment to quality service. We believe our structure as a member-owned and directed cooperative is positive in the marketplace, and our references here to members and customers is largely interchangeable. We were fortunate to have a positive reputation at AgSource and CRI before engaging in our conversion to a value-added organization. Without it, our challenge would have been much more difficult.

In spite of a firm foundation to build from, we did find the need to sell the value of AgSource/CRI in the broader sense, rather than relying on products and people. For example, we found that many of our customers had a relationship with and loyalty to their local field technician, but very little was applied to the organization that employed them. While this was positive in member retention when we faced competitive challenges, it could be a major limitation when we experienced employee turnover. We realized we needed to make the customer more reliant on our organization without decreasing their loyalty to the individual. This challenge is ongoing, but we feel we have made progress by involving more and different personnel in providing service, particularly to larger herds. We have employed a more focused brand strategy, and we have broadened our product and service offering. These steps have had a positive impact on making the customer feel more reliant upon AgSource and CRI as a whole, rather than just on the person regularly involved in service on the farm.

This concept also extends to the need to increase reliance on the organization for service rather than on external factors. For example, we cannot rely on breed programs or the dairy cattle breeding industry to sell or create demand for our services. While useful, they do very little to increase recognition of the value of the outstanding management information we provide. If we sell our programs to a new herd primarily on the basis it will allow them to receive progeny testing incentives or participate in breed recognition programs, we have made ourselves reliant on those programs, and potentially victims of them if changes outside our control are made. The potential that genomic evaluations may reduce the need for progeny testing is a current case in point. It is our responsibility to create recognition of value in what we do. To deliver real value means absolutely nothing in the marketplace if it is not recognized by the customer.

Product

An organization cannot sell value that does not exist. The marketplace does an excellent job in the long run of sifting products and services that are not worth the price. In our organization we were fortunate again to have a strong foundation. However, we needed to apply more effort to differentiate ourselves from the competition, and to better coordinate market release of new products and services.

An important piece of value added marketing is the need to create differentiation within the industry. We cannot be offering the exact same products with the exact same look. There may be similarities and some parts of delivered product may overlap, but the entire package cannot be the same. This results in a commodity-based industry where price is the primary driver of a buying decision.

At AgSource we have adopted a strong commitment to new product development and enhancement. It is our goal to introduce at least one major new product or enhancement each year. Product releases are coordinate with field training, advertising, industry and member education, and marketing incentives.

- Our 2006 introduction of the Fresh Cow Summary and List, including the patented Transition Cow Index® was the most successful rollout of a new management option in AgSource's history. Members, with nearly a third of all the cows we record, chose to receive and pay for information that had not been previously made available. This option added value to our milk recording services at all levels: on-farm data collection, laboratory analysis, and the dairy records processing database. The information could not be provided without all three components.
- Earlier this year we introduced significant upgrades to our Udder Health Management package, including herd summary and individual cow reports related to milk quality and udder health. All members received these reports at no additional charge for the first three months and then chose to continue or discontinue receiving the report beginning in April. Although it is still too early to produce final retention numbers, initial results indicate we may see as much as a ten percent increase in utilization of these optional reports even though the improved products are sold at a higher price. Again, this is information that adds value to our field and laboratory services. Because much of it would be difficult to replicate on an on-farm system, it also adds value to the dairy records database.
- Our latest new product offering is the Profit Opportunity AnalyzerSM. This report benchmarks performance for our 5 000 herds in seven critical areas of management, applies economic values, and estimates for a herd what areas of management may carry the greatest opportunity for improved profitability. Valuable information that is once again only available from AgSource, reliant on a large database, and a product that adds value to our complete milk recording and laboratory service.

Another area of product differentiation that adds value is our increased offering of supply products in conjunction with our regular field service. While most of these products – milking gloves, ID tags, calf coats, etc. ... are available from other suppliers, we make it more convenient for our members to order them from us as part of their regular service. This becomes one more reason for them to stay with AgSource when offered competitive options, and adds value to our regular herd test. Our average annual growth in sale of farm supplies by our field staff has been 28% in the past three years.

People

If there is a “most critical” component to our three dimensional bundle of value it would have to be people. Changing attitudes, performance and perceptions of our own people has been our greatest challenge, but also our most rewarding achievement. Clearly, the most effective way to create recognized value is for us to sell our real value through a well trained field staff that believes in and understands the value and can explain it to our members. Making the necessary progress in this area has required a three-pronged approach: information, motivation, and separation.

- Information means training, expertise, and the confidence that it creates. It requires organizational and employee commitment. It is not enough to introduce new or improved products. An educated and effective field staff is required to ensure these products increase the value of our services to their members.

AgSource has significantly increased the required training and resources applied to field staff education. We have expanded training on product knowledge, have implemented required programs on selling and the importance of the value-added approach, and developed several new tools in the form of video and on-line programs to deliver this information. Time spent in small groups sharing experiences and information adds to the knowledge base of the local team. We have significantly upgraded the expectations of our field staff to be more than good service technicians. Dairy producers today expect sales people to know more about their products and how to use them. To deliver value we must exceed those expectations.

- Motivation is a combination of rewards and recognition that inspires achievement and performance. At its base level, it is the pride of being part of a successful organization committed to meeting the needs of its members. However, personal rewards and recognition are also important.

Compensation for on-farm milk recording services is a challenge, and our observations suggest there is tremendous variability in how field service personnel are paid by various organizations. We claim no special insights, and acknowledge the challenges associated with field compensation and changing the methods within it. We do believe, however, in the axiom that “what gets rewarded and recognized is what gets done.” We have made ongoing adjustments in how, and how much, we compensate our field staff and have increased the portion of their total compensation tied to the production of revenue. When introducing new products and services we have simultaneously implemented incentives tied to the successful sale of those specific items.

Recognition may be as important as compensation as a motivating tool. We have increased the opportunities to recognize our field staff for sales and service at the organizational and regional level. Monthly newsletters identify top performers in several areas of sales and service. Region managers are encouraged to more frequently recognize their staff in front of their peers. Many times we reward employees with organizational apparel for them or to give to their customers in order to increase brand awareness in the marketplace.

- Separation has been used sparingly, but is important. For employees who fail to adopt an attitude conducive to delivering and selling added-value, or who fundamentally do not believe in the importance of the products and services

we offer, we have found that they are happier and frequently more successful in another profession. Separation may be voluntary or involuntary and we are fortunate that most employees from whom we have separated have recognized themselves that they would not be able to meet our expectations and made the decision to resign or retire. These separations have the added benefit of sending the message to other employees that we do expect more. We highly value our people and commit tremendous resources to training and personal development. The time required to develop a person who may not wish to grow can be very counterproductive.

Attitude and a fundamental belief in the organization, the product, and its value to customer profitability are critical to the success of a value-added salesperson. One of the primary ways we measure effectiveness of our program is the percentage of active herds and cows actually tested in a month. Before adopting value-added sales approaches, our field staff would frequently respond to an objection related to price or inconvenience of the milk recording process by offering to skip a monthly test or to extend testing intervals. A value-added salesperson responds by emphasizing the importance of regular and complete information from a monthly test. Figure 1 shows the increase in annualized percentage of active cows tested since December 2003. The change from 89.4% to 92.7% on 600,000 active AgSource cows equates to approximately 237 600 additional individual cow recordings per year.

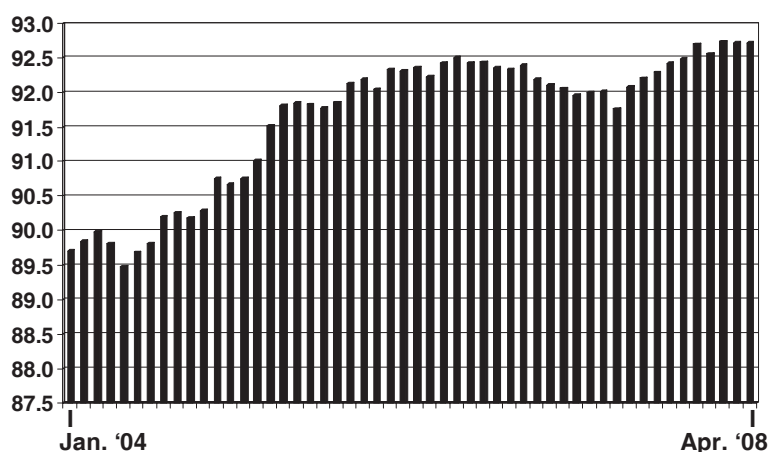


Figure 1. Monthly annualised percent cow tested (Jan. 2004 - April 2008).

Since committing to the philosophy of value-added marketing AgSource and CRI have experienced positive and measurable results. Although some of our recent success can be attributed to strong dairy prices and stable cow numbers in our primary market areas, the growth shown in Figure 2 could not have been achieved without the steps described in this presentation. Since 2004 our programs have increased substantially. As of April 2008, our gain in individual cow recordings the previous twelve months was 369 778 more than in the twelve months ending April 2007. Steady improvement has been achieved since initiating value-added marketing programs.

Conclusion

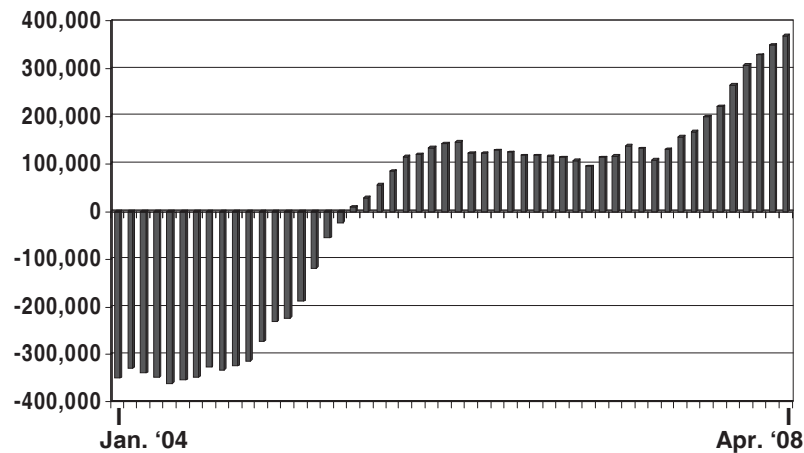


Figure 2. Monthly annualised change in total cow recordings (Jan. 2004 - April 2008).

Value-added marketing is a philosophy that has strong application to providers of milk recording services. It requires commitment from the organization at all levels, from the board of directors, management, and service employees. Milk recording organizations must continue to evolve to maintain their relevance and meet the needs of dairy producers. To be successful, we must continue to increase the value of our specific services, be less reliant on external programs, and increase producer recognition of value.

List of references

Reilly, Thomas P. 2003. Value-Added Selling: how to sell more profitably, confidently, and professionally by competing on value, not price. McGraw Hill.

Alternative modelling of body condition score from Walloon Holstein cows to develop management tools

C. Bastin¹, L. Laloux², A. Gillon¹, C. Bertozzi² & N. Gengler^{1,3}

¹Animal Science Unit, Gembloux Agricultural University,
Gembloux, Belgium

²Research and Development Department, Walloon Breeding Association,
Ciney, Belgium

³National Fund for Scientific Research, Brussels, Belgium

The objective of this study was to formulate and test an alternative modelling for body condition score (BCS) in order to develop management tools for dairy farmers based on performance recording data. This modelling allowed the prediction of a BCS value for each day in milk of a given cow and would contribute to the development of decision making indicators, (e.g. the prediction of BCS loss at early stage of lactation). The model especially included two herd effects (a random herd x test-day and a fixed herd x month period effects). Results indicated that the overall fit of the model was good. Moreover, the ability of the model to predict future or missing records was tested and indicated satisfying correlations between observation and prediction (from 0.57 to 0.67) considering the structure of data (two years of recording only). Based on these results the tested model can allow the use of BCS for management purposes and permits the development of decision making indicators for dairy farmers.

Key words: *Body condition score, Test-day model, Prediction.*

For a few years, the Walloon Breeding Association, in collaboration with the Gembloux Agricultural University, has increased the use of performance recording data for management purposes. For instance, an adaptation of the lactation yield computation method was performed and allowed the development of management tools regarding peak yield, persistency as well as total lactation yields. Usefulness of these developments were also presented in other studies (VanBebber *et al.*, 1999; Koivula *et al.*, 2007) which showed the interest of using predictions or solutions in order to advice dairy farmers.

Moreover, since April 2006, body condition score (BCS) is monthly recorded in 76 dairy herds of the Walloon Region of Belgium. In fact, BCS is a valuable indicator of the stored energy reserves of dairy cows and it is linked to the energy balance

Summary

Introduction

status as well as the production, the fertility and the health traits. In addition to the development of a genetic evaluation for this trait (Bastin *et al.*, 2007), the objective of this recording is to develop and offer management tools to dairy farmers. Currently, BCS results are monthly sent to each farmer as a "Herd BCS balance sheet". It allows him to point, across time, the groups of cows which are not in the range of desirable scores according to their parity or lactation stages. Nevertheless, this "Herd BCS balance sheet" is developed based on observed values. Modelling this data in a management goal could provide more interpretable information, e.g. predicting the BCS loss at the early stage of lactation.

The objective of this study was to model BCS for predicting a BCS value for each day of the lactation in order to develop later decision-making indicators for dairy farmers.

Material and methods

Data used in this study were BCS measurements monthly collected by milk recording agents between the 1st April 2006 and the 31st March 2008 in the Walloon Region of Belgium. Records before 5 days in milk (DIM) and after DIM 365 were eliminated for the estimation of variance components. The data set represented 54 955 BCS values from 5 123 cows. BCS of dairy cows was evaluated based on a nine-point scale (with unit increments), with scoring of 1 representing an emaciated cow to 9 for obese cow.

The model was developed in order to allow the prediction of BCS value for each day of the lactation of a given cow. To achieve this objective, the classical fixed herd x test-day effect was replaced by the sum of two herd effects: a fixed herd x test-month period effect and random herd test-day effect. This approach allowed to define a herd effect for each day of the lactation and was first presented by Mayeres *et al.* (2004) for production traits. Besides these two herd effects, the single trait multi-lactation test-day model finally used in this study included four fixed effects: stage of lactation expressed as classes of 5 DIM; milk recorder combined with classes of 14 DIM; age at calving expressed in months; state of the cow: lactating or dried. Three random regression effects were also defined: permanent environment within lactation, permanent environment across lactation and additive genetic effect. Regression curves were modelled using Legendre polynomials of order two.

Covariance components were obtained using AI-REML (Mizstal, 2007). Solving was done using adapted BLUPF90 (Mizstal, 2007) programs which provided prediction errors (PE = prediction – observation). Standard deviation of the prediction error and correlation between observed and predicted values were computed considering three different cases. Firstly, the adjustment of the model was studied by examining data collected from 1st April 2006 to 29th February 2008 and used for solving the model. Secondly, accuracy of prediction for missing records was estimated by solving the same model as previously described but considering that the data collected on March 2007 were missing. Finally, BCS values for March 2008 were predicted and compared with the observed value of BCS in order to assess the ability of our model to predict future test-day records.

Results and discussion

Regarding the adjustment of the model, Table 1 indicated that the overall fit of the model was good. The average PE was very close to 0 and the correlation between predicted and observed BCS ranged from 0.88 to 0.91 for all lactations.

For the prediction of missing or future records, the fit of the model was satisfying according to the structure of BCS data (only 2 years of recording). The average PE was negative in both cases, indicating that BCS values were systematically

underestimated. The range of PE standard deviation was limited and lower than one unit of BCS (around 0.95 for prediction of missing values and around 0.80 for future values). Table 1 also indicated that the PE was globally closer to 0 and the correlation was lower for the prediction of missing records than for the prediction of future records. It indicated that the average error is lower for the prediction of missing values but its distribution is larger.

No equivalent studies were found for the prediction of future BCS test-days records. Moreover, for information only, previous researches using test-model to predict fat, protein and milk yields for future test-day records indicated ranges of correlations between observation for the test-day n and prediction for the test-day $n+1$ from more or less 0.70 to 0.90 according to the study, the trait and the number of the test-day predicted (Macciota *et al.*, 2002, Mayeres *et al.*, 2004; Vasconcelos *et al.*, 2004).

Figure 1 illustrates the purpose of the developed model and gives an example of the BCS values observed and predicted across the lactation for a randomly chosen cow in the 7th parity. In this particular case, the modelling allowed the prediction of the

Table 1. Adjustment and predictive ability of the model for missing and future records.

	Lactation	Average PE	Standard deviation of PE	Correlation
Adjustment on data from 1 st April 2006 to 29 th February 2008	1	0.00	0.47	0.88
	2	0.00	0.46	0.91
	?3	0.00	0.49	0.91
Predictability for missing records from March 2007	1	-0.34	0.78	0.64
	2	-0.42	0.84	0.58
	?3	-0.41	0.81	0.67
Predictability for future records of March 2008	1	-0.13	0.92	0.57
	2	-0.06	0.98	0.54
	?3	-0.10	0.92	0.67

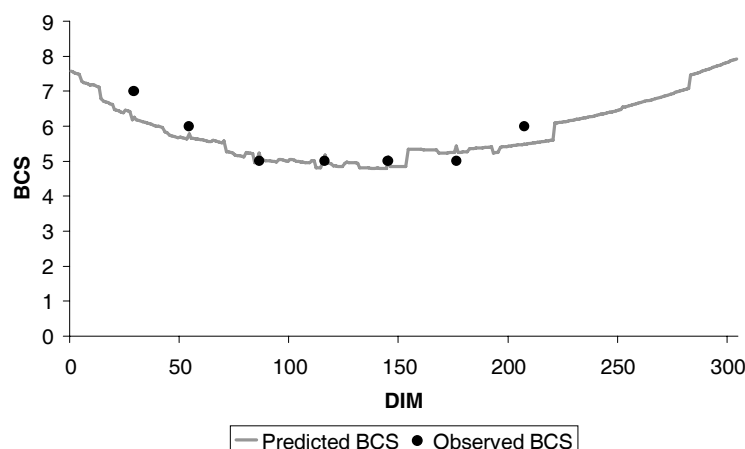


Figure 1. Prediction of a BCS value for each DIM, example of a given cow in 7th lactation.

Conclusions and perspectives

BCS value of this cow at the end of its lactation. Currently too fat cows at drying are a recurrent problem in Walloon dairy herds, this prediction could help the farmer to pay attention to such cows before they are dried of.

Acknowledgments

This study was the first step toward the development of management tool for dairy farmers based on BCS data and focused on the definition and the test of an alternative modelling of this data. Even if prediction of future or missing BCS records was not perfect, the adjustment of the model was good. Based on these results, some parameters could be estimated. For example, the loss of BCS at the early stage of lactation could be estimated even if records at this time are not available. BCS values at critical point of the lactation (peak yield, calving, drying) would also be valuable. These preliminary results seem to be encouraging for the use of BCS information for management purposes and the development of decision making indicators for dairy farmers.

List of references

The authors gratefully acknowledge the financial support of the Ministry Agriculture of Walloon Region of Belgium (MRW-DGA) (Namur, Belgium). Nicolas Gengler, who is Research Associate of the National Fund for Scientific Research (Brussels, Belgium) acknowledge his support. Additional support was provided through grants 2.4507.02F (2) and F.4552.05 of the National Fund for Scientific Research. The authors gratefully thank manuscript review by Elodie Bay and Hélène Soyeurt (Gembloux Agricultural University, Belgium).

Bastin C., L. Laloux, A. Gillon, C. Bertozzi, S. Vanderick and N. Gengler. 2007. First results of body condition score modelling for Walloon Holstein Cows. *Interbull Bulletin*. 37,170-174.

Koivula M., J.I. Nousiainen, J. Nousiainen and E.A. Mäntysaari. 2007. Use of herd solutions from a random regression test-day model for diagnostic dairy herd management. *J. Dairy Sci.* 90,2563-2568.

Macciotta N.P.P., D. Vicario, G. Pulina and A. Cappio-Borlino. 2002. Test day and lactation yield predictions in Italian Simmental cows by ARMA methods. *J. Dairy. Sci.* 85,3107-3114.

Mayeres P., J. Stoll, J. Bormann, R. Reents and N. Gengler. 2004. Prediction of daily milk, fat, and protein production by a random regression test-day model. *J. Dairy Sci.* 87,1925-1933.

Misztal I. 2007. BLUPF90 family programs. University of Georgia. <<http://nce.ads.uga.edu/~ignacy/numpub/blupf90>>.

Van Bebber J., N. Reinsch, W. Junge and E. Kalm. 1999. Monitoring Daily Milk Yields with a Recursive Test-Day Repeatability Model (Kalman Filter). *J. Dairy Sci.* 82, 2421-2429.

Vasconcelos J., A. Martins, M. F. Petim-Batista, J. Colaço, R.W. Blake and J. Carnevalheira. 2004. Prediction of daily and lactation yields of milk, fat, and protein using an autoregressive repeatability test day model. *J. Dairy. Sci.* 87,2591-2498.

Development of a milk transport security system

C. Thompson¹, F.A. Payne², B. Luck², J.R. Moore³ & N. Tabayehnejad²

¹Regulatory Services, University of Kentucky, Lexington, KY, USA

²Department of Biosystems and Agricultural Engineering, University of Kentucky, Lexington, KY, USA

³Applied Physics Institute, Western Kentucky University, Bowling Green, KY, USA

The United States Department of Homeland Security (DHS) has targeted bulk food contamination as a focus for attention because it poses a high consequence health threat to our society. The current manual methods used for monitoring milk during transport are cumbersome, paper intensive and prone to errors. The bulk milk transportation sector necessitates a security enhancement that will reduce recording errors and enable normal transport activities to occur while providing security against unauthorized access. A robust security system coupled with improved recordkeeping would provide the opportunity for security breaches to be investigated more quickly and more thoroughly. The goal of this research was to develop a milk transport security system to meet these demands, demonstrate it and transfer the technology to the public.

A milk transport security system was designed and consists of a security monitoring system (SMS) located on the milk transport tank, a handheld device (computer), and a remote data server. The SMS controls access to the milk during transport, automatically collects security data and transmits it to the handheld device. The handheld device is used by the milk hauler/sampler to collect the milk data. Both the milk data and security data are transmitted by the handheld device using cell phone communication to a data server where access is provided to data users.

The SMS was mounted on a milk transport tank and used to pick up milk during four days of operation with delivery to a dairy processor. The results to date indicate that the SMS was effective for securing the milk transport tank and recording the security data and the handheld device was effective for collecting the milk data and transmitting both the milk data and security data to a data server.

Key words: Recording, Monitoring, Physically store, System design, Security Monitoring System,

The Bioterrorism Act of 2002 (Food and Drug Administration 2002) addresses threat assessments, technologies and procedures for securing food processing and manufacturing facilities and modes of transportation. The development of security systems to prevent potential adulteration of foods, while still enabling routine food

Summary

Introduction

production and transportation activities to occur, is stated as essential. Key elements of the Bioterrorism Act focus on protection against adulteration of food and maintenance and inspection of records for foods.

In the US, food safety and defense of Grade A milk is under the purview of the Food and Drug Administration (FDA). Manufacturing grade (Grade B) dairy production is regulated by the United States Department of Agriculture (USDA). FDA has identified milk as a heightened food security concern and a priority in terms of national security (Food and Drug Administration 2004). Bulk milk's large batch size, high degree of accessibility, thorough mixing during processing, rapid turnaround at retail and rapid consumption after purchase by consumers are consistent features of a high-risk food. Together, the FDA and USDA comprehensively monitor dairy food safety.

The bulk milk transportation industry lacks a uniform, formal security policy. Loaded and unloaded trucks and/or tankers are regularly left unattended and may be parked overnight in unsecure and unsupervised areas. Many of these unattended, unsecure locations are secluded and may include dairy farms, remote transfer points, hauling company property and hauler residences.

Bulk milk transporters currently use voluntary seal programs to secure milk during transport. The seal programs generally utilize plastic, numbered seals on tanker openings. Not all seals are tamper evident. Seal number identifiers are recorded as they are applied to openings. As seals are broken during routine transportation activities, seal numbers are accumulated. Some companies require that broken seals be maintained. These sealing systems are problematic in that they are prone to record keeping errors and maintaining broken seals are burdensome (it is not uncommon to have numerous broken seals for a single load of milk).

Additionally, current bulk milk records are primarily handwritten. The level of detail associated with records maintained on bulk milk manifests, bills of lading, etc. for each load of milk is inconsistent and prone to inaccuracies (Department of Transportation, 2004). The maintenance of records is critical to provide for adequate trace-back of food and agricultural products when potential adulteration occurs. Most farms have a handwritten record in the milk house known as a "barn card". Furthermore, haulers typically maintain bulk milk manifests or load tickets. Pertinent information relating to each dairy farm is maintained within these records. Similar to the seal information, these records are error prone and legibility is often a concern. Recording mistakes, mathematical errors and misplaced tickets are commonplace (Department of Transportation, 2004).

The objective of this project was to develop a milk transport security system (MTSS) that will provide assurance that the milk, milk samples, milk data and security data are securely transported between the dairy farm and dairy processor, demonstrate the security system at two milk plants and multiple dairy farms, and deliver the technology to the national community through collaborations, technical conferences, publications and standards.

Materials and methods

System design

An analysis of the system was conducted and a set of critical functional design requirements were established for the milk transport security system which were to:

1. Provide "secure transport" of milk.
2. Operate within the current milk transport infrastructure.
3. Physically store the milk and security data with the milk transport tank.
4. Provide redundant storage of milk and security data to meet the operational and security needs of the dairy industry.

The design of the milk transport security system incorporated all of the critical design requirements to assure the secure transport of bulk milk, milk samples, milk data and security data between locations and specifically between dairy farms, transfer stations, receiving stations and dairy processors. It includes three processor subsystems: a security monitoring system (SMS) installed on the milk transport tank, a handheld device, and a data server. Figure 1 shows the components of the SMS and their location on a typical milk transport tank. Figure 2 graphically illustrates the three processor subsystems used to collect the milk and security data and transmit it to the data server. These three subsystems were designed to work together to meet the functional design requirements for the milk transport security system.

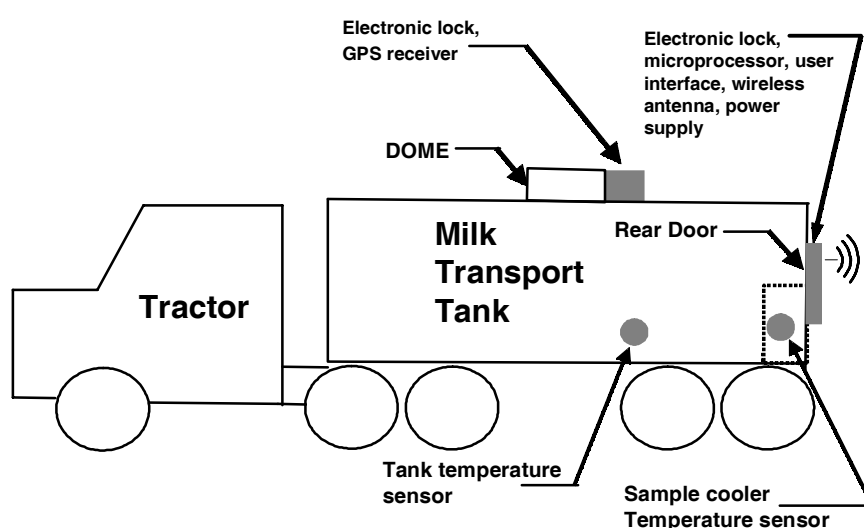


Figure 1. The Security Monitoring System (SMS).

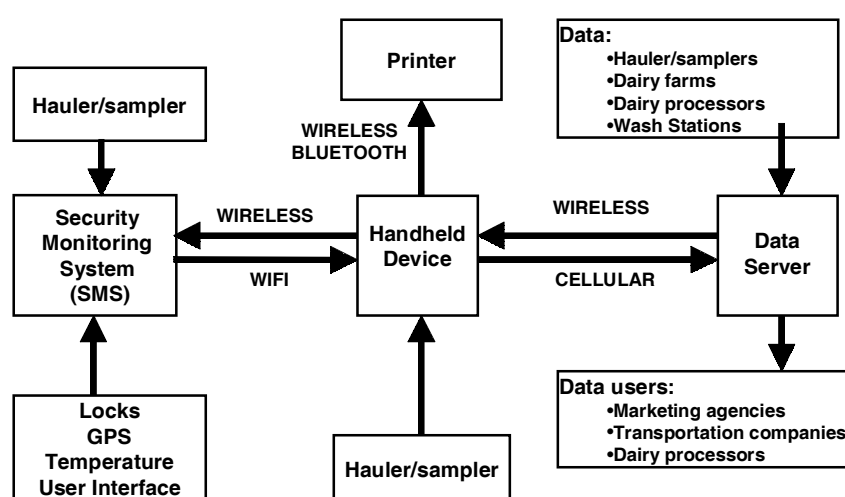


Figure 2. Milk transport security system design and communication diagram.

Provide “secure transport” of milk

Security of the milk transport tank is assured by

1. Identification of authorized personnel who may access the vessel to load, unload, sample milk, wash/ sanitize or adjust/ inspect equipment.
2. Locking access ports and monitoring their status.
3. Recording the reason for access.
4. Monitoring the geographic location of the milk transport tank and e) recording all data for traceability.

The system was designed to meet the following functional requirements:

1. Only authorized persons are given pass codes to the handheld device.
2. The combination of physical locks and electronic monitoring of the locks provide a constant assurance of the security of the milk transport tank even when not observed by a qualified employee. Securing the vessel means locking it so that access cannot be obtained without “breaking the lock”. Locking the milk transport tank provides the level of security sought for transport of milk and is similar to security levels implemented in milk processing plants.
3. The data is collected throughout a security session which typically encompasses the time from initiation of washing/ sanitizing the milk transport tank to the end of unloading of the milk at the plant and the security data is stored.
4. A “reason code” is used for tank access.
5. A GPS (Global Positioning System) unit is installed on the milk transport tank.
6. The milk and security data are stored on a server for future traceability.

Operate within the current milk transport infrastructure

The system must operate within the existing bulk milk transport infrastructure, operate with electronically instrumented and non-instrumented dairy farms, operate for dairy farms that direct-load a milk transport tank, operate for multiple dairy record keeping systems, provide versatility to allow the bulk milk hauler/ sampler to perform routine activities if any part of the milk transport security system malfunctions, maintain security in the event of a system failure (power loss, mechanical, electrical, software malfunction) and accommodate the potential future requirement that herd data be collected.

The system was designed to meet the following functional requirements:

1. Bar codes are used to identify the farms thus no farm power is required for non-instrumented dairy farms.
2. A digital entry key pad is included in the design for unloading events when a handheld device is not available or if it malfunctions.
3. Wireless WiFi communication was included as part of the system for collection of herd data from farm based PC.
4. A database structure was developed to accommodate flexibility for the entire system.

Physically store the milk and security data with the milk transport tank

Loaded tankers are regularly connected to and moved by multiple tractors. This practice emphasizes the importance of a system that provides tanker-based data collection/ storage. For example: a hauler/ sampler may perform the farm pickups using one handheld device. The hauler/ sampler may drop the full tanker trailer of milk at a location. Another driver may connect to the tanker with another tractor to pull the milk across country. Additionally, this driver may or may not have a

handheld device. The tanker of milk may be pulled by multiple drivers across country. Maintaining the physical association of milk and the data is a basic premise for a successful system.

Meeting this function requires that the data collection be tank-based and contain sufficient auxiliary power for up to 100 hours. Milk tankers are required to be washed and sanitized prior to each use. The sanitization cycle is valid from the time of sanitization for up to 96 hours until the first milk is loaded onto the tanker. Additionally, tankers are regularly separated from tractors (the power source) and stored without use for varied amounts of time. For these reasons, the tanker based portion of the system must maintain sufficient auxiliary power for up to 100 hours. If a tanker is stored dormant for an extended period, this auxiliary power will allow continual monitoring of the tanker security. The 100 hour time period will be sufficient because tankers remaining dormant past this period will need to be connected to a tractor (a power source) and moved to a facility for a new wash and sanitization cycle (due to the 96 hour requirement). This movement will subsequently result in a new "security session".

The system was designed to meet the following functional requirements:

1. The Security Monitoring System (SMS) will contain auxiliary power sufficient to power the system for 100 hours. The design of the power system has not been specified.
2. The SMS collects security data and stores it in a data file on the SMS.
3. The handheld device combines the security and milk data and stores this in a data file on the SMS.

The loss of data will result in the loss of a load of milk, disrupting the marketing of farm milk and detrimentally impacting dairy producers. The dairy industry will not implement any data system which has potential to lose the data collected.

Data redundancy is critical because multiple hauler/samplers may be involved in farm pickup processes and because multiple drivers may be involved in the transport of a tanker. Additionally, data redundancy provides backup in the event of a handheld device failure during the milk pickup or transport process or if the handheld device does not accompany the load from one driver to the next.

The system was designed to meet the following functional requirements:

1. SMS data is stored in a "log" and "security data" file on the SMS and maintained for 60 days.
2. Security data is transmitted to the handheld device and stored for up to 60 days.
3. Milk data is stored on the handheld device.
4. Milk data and security data are combined into a "Security Session" data file and stored on the SMS for up to 60 days, on the handheld device for up to 60 days, and on the server for an undetermined period of time.

Provide redundant storage of milk and security data to meet the operational and security needs of the dairy industry

Results and discussion

System design

The SMS electronics included electronic locks for the hatch and back door, a temperature sensor on the milk transport tank wall and another in the milk sample cooler, a GPS receiver, Wi-Fi antenna, digital user interface keypad, Liquid Crystal Display (LCD) screen, and a data storage unit. Figure 3 shows the rear access of the milk transportation tank along with the keypad, Wi-Fi antenna, LCD screen and electronic lock. Figure 4 shows the top dome access to the milk transport tank and the GPS receiver, dome electronic lock and also specifies other critical components of the modified dome assembly. Three on-board electronics nodes were linked with a Controller Area Network (CAN bus). The CAN bus has the ruggedness and bandwidth to work well in this application. The SMS processor monitors and stores the status of the locks, GPS, and temperature sensors on one minute intervals or upon an event i.e. when a lock is opened or when other events as defined occur. The temperature sensors monitor the milk in the transport tank and the sample cooler. The tank temperature has the potential to record the tank temperature during the wash cycle thus verifying a proper wash.

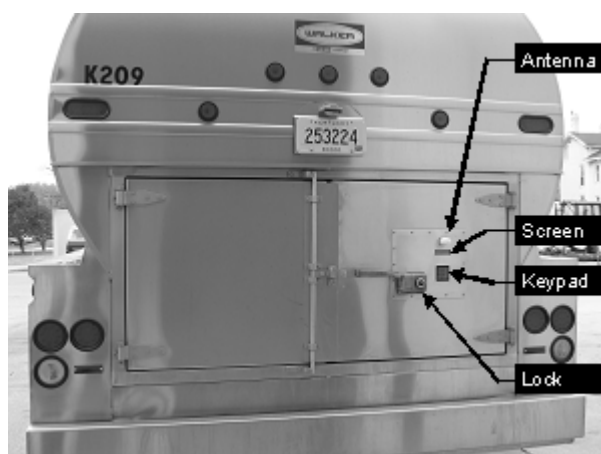


Figure 3. Rear access port of the Security Monitoring System (SMS).

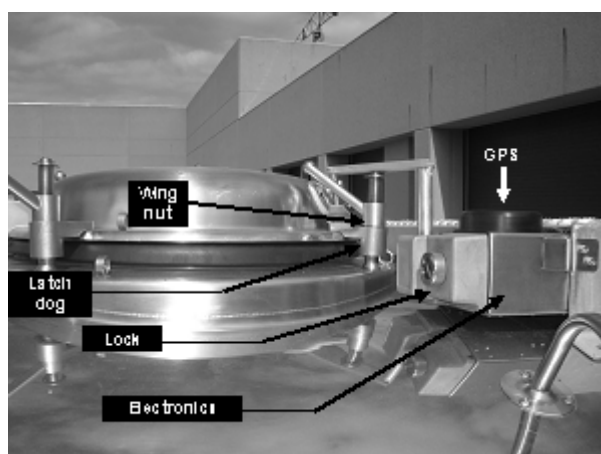


Figure 4. Top dome of the Security Monitoring System (SMS).

The handheld device (CN3, Intermec, Everett, WA) utilized three modes of communication (Bluetooth, Wi-Fi, and Cellular) and possessed an alphanumeric keypad, barcode reader and touch screen. The device is constructed in a rugged, water-proof case and is suitable for this application. Bluetooth was used to communicate with the label printer, which was always within close proximity. WiFi (802.11 standard) had a range of 100 m and was used to communicate to the SMS.

The data server contained the information attributes of the dairy farms, milk transportation companies and their transportation tanks and tractors, receiving stations at dairy processors and wash stations. This information was stored as tables with associations as required. A database structure for storage and retrieval was developed as part of this system. The system was developed to permit only authorized personnel to access any of the access ports. If any of the access ports are accessed, the SMS will record the reason for access, monitor the geographic location using GPS, and record all security data.

A prototype was first demonstrated on a commercial milk truck in September 2007. System testing began in October 2007 with the pickup of milk on a regular route for delivery to a processor. The objective of the system tests was to confirm the function of the SMS, handheld unit and data server as well as the associated hardware and programming. The focus of the initial tests were to unlock the locks using wireless communication, collect the milk data using barcodes for farm identification, print milk sample labels and print a milk ticket from data transmitted to the data server.

The results were positive with the milk being successfully picked up on all days. The wireless technology proved to functionally work throughout testing. The handheld device initially communicated milk data to the server. The milk data was uploaded to the server after each farm pick-up through cellular communication and the system secured milk during transport. There were a multitude of interrelating issues regarding the data structure, sequence of events, data storage on the SMS and general programming that have required a continuous effort to improve robustness. The focus on robustness continued through February when a robustness test showed that the complete system functioned flawlessly on six consecutive simulated pickups.

System testing resumed during February 2008 with the goal of demonstrating the system robustness, printing milk tickets at the dairy processor from data in the data server, and quantifying the amount of data being transmitted over the cell phones. Quantification of the hardware design for a commercial phase will also be an objective of the testing in 2008.

The system validation and a gradual development and verification of software enhancements and web based software input and output programs are expected to continue through 2008 including the development of traceability programs. Continued prototype field testing will include collecting milk on multiple routes with deliveries to multiple processors.

1. A system analysis of milk transport security requirements was conducted.
2. A set of critical functional requirements were developed.
3. A prototype system was designed and developed to implement the critical design requirements.

System tests

Conclusions

4. The system tested in the fall of 2007 and demonstrated the functional performance of the system.
5. Development work will continue during 2008 to further develop and implement enhancements including web base data input and output programming.

Acknowledgments

This research was supported by a grant “A Wireless Electronic Monitoring System for Securing Milk between the Dairy and Milk Plant” from the Department of Homeland Security through the National Institute for Hometown Security. Close collaboration with Alan Wilson Trucking, Bluegrass Tank and Equipment, Dairy Farmers of America-Mideast Council, Kentucky Milk Safety Branch, Slayback Milk Transport, Southern Belle Dairy, Starr Stainless, and Winchester Farms Dairy has ensured that anomalies associated with any one particular segment was addressed.

List of references

Department of Transportation. 2004. “Security of Milk Transport in the United States Project”, U. S. Department of Transportation Report Number DOT-VNTSC-TSWG-04-01, May 2004.

Food and Drug Administration. 2004. “Security Surveillance Assignment for Periods of Increased Risk, Executive Summary”. Internal report dated 9/08/04 v2.

Food and Drug Administration. 2002. “The Bioterrorism Act of 2002”. www.fda.gov/oc/bioterrorism/Bioact.html.

Integration of quality certification programs into management of milk recording providers in the United States

S.J. Sievert

Quality Certification Services, Inc., a subsidiary of National Dairy Herd Information Association, Verona, Wisconsin, USA

Quality certification programs are an essential component of the milk recording industry in the United States, ensuring the accuracy of the data submitted to genetic evaluation programs, management programs and compliance with Uniform Operating Procedures and a Code of Ethics by all participants. Quality certification programs are offered for all segments of the recording industry, with standards of performance for field service providers, meter calibration centers and their technicians, milk analysis laboratories, and data processing centers. These integrated programs are neutral with respect to size, business structure, and/or geography and provide opportunity for all participants to provide input and direction to the program. While the primary focus of these programs are compliance, a review of the top quartile of field service providers demonstrates that these programs serve as a framework for the management of certain day-to-day operations, providing a foundation for success and growth without limiting local business decisions and program applications.

Summary

Key words: Milk recording industry, Quality certification program, Standards, Field Service Providers

The milk recording industry in the United States has experienced significant changes over the past two decades. Traditionally, milk recording organizations were organized as non-profit entities, often working with land-grant universities as part of the Cooperative Extension Service. These organizations served defined territories (usually state lines) and were supported by resources and staff as needed to serve the dairies in their trade area.

At present, the milk recording industry is markedly different. While certain regions of the country are still served by traditional milk recording organizations, other geographic regions are now served by organizations that no longer resemble the former. The organizations currently providing milk recording services to dairies include sole proprietorships, privately held corporations, cooperatives and federated (either partially or fully) associations. These organizations no longer operate within a defined trade area; but rather compete in an open-market climate.

Background

In addition, the meter centers and laboratories providing services to the recording industry have seen similar changes in business structure, trade area and competition. All data generated from the various components of the recording entity are processed at one of four dairy records processing centers prior to submission to the Genetic Evaluation Program (GEP). Like the field service, meter center and laboratory entities, these processing centers have diverse business structures and compete in an open-market environment. One of the challenges in this open-market climate is to maintain standards among competing organizations. The dairy industry in the United States has long realized the need for a quality certification program to ensure that the minimum standards of services are maintained and to assure the accuracy of data flowing between milk recording industry entities and flowing to the Animal Improvement Programs Laboratory (AIPL) and Interbull.

Scope of the quality certification program

The quality certification program in the United States' milk recording industry is currently administered by Quality Certification Services, Inc. (QCS) and audits participating entities on a routine basis to assure compliance with all aspects of the current auditing guidelines as approved by the dairy industry. It is important to note that these guidelines are business-structure neutral and do not exist to determine if an entity should be in business – rather to certify that the entity is operating within compliance. In addition, there is a mechanism for all participating entities to contribute to the content of the guidelines on a regular basis. Furthermore, the Purebred Dairy Cattle Association (dairy breed associations) and National Association of Animal Breeders (artificial insemination organizations bull studs) have representation and input as well, ensuring that the guidelines are fluid, current and best serve the needs of the milk recording industry.

Summary data from the audit activity of QCS during 2007 is presented in table 1. During 2007, cows on recording programs in the United States reached their highest level since 1998. It should be noted that though the number of herds on recording programs has declined (following a similar trend in the total number of dairy herds in the United States); the perceived value of participation in a recording program is evident. The range of size and scope of the certified field service providers operating

Table 1. Summary statistics from QCS, 2007 auditing of milk recording entities.

Parameter	Value	Min.	Max.
Herds on recording programs	23 005		
Cows on recording programs	4 414 821		
Field service providers	27		
Meter centers	46		
Meter technicians	91		
Laboratories	49		
Dairy records processing centers	4 (5 Distinct Processing Platforms)		
Cows tested by field service providers	4 414 821	10 412	784 214
Certified field technicians	3 018	6	196
Certified portable meters (ICAR approved)	108 139	164	10 814
Certified electronic meters (ICAR approved)	66 022	0	3 987
Milk samples analyzed monthly (2-year average)	4 700 000		12 000

within the United States is significant. The business structure and scope of each of these providers is a local management decision and is not influenced or audited by QCS. Rather the auditing guidelines are applied to each provider on an equal basis, providing the framework for an independent audit not influenced by the size, business structure or any other external factor related to an individual field service provider. Similar principles are in place for meter center, laboratory and processing center providers.

The Auditing Guidelines administered by QCS provide minimum standards for compliance and subsequent certification by each provider operating within the milk recording industry. These minimum standards have been developed and approved by all participants, and are subject to review on an annual basis. In addition, procedures are in place to allow for new entrants to the system, ensuring that new entrants are held to the same standard of compliance without providing any barrier to entry.

Table 2 summarizes the auditing schedule of all providers for compliance and certification. All certified providers are audited regularly, ensuring accuracy of data flowing within the system and entering the GEP. From the outside, this schedule may appear aggressive, but it should be noted that the frequency of these audits was determined and approved by the participants. Furthermore, the auditing program allows for flexibility in scheduling to meet the needs of both parties and minimizes the intrusion on the day-to-day operations of the each cooperating entity.

The auditing guidelines administered by QCS encompass the minimum standards to attain or retain certification by an entity in the milk recording system. While all certified providers meet these requirements, many of the field service providers operating in the milk recording system in the United States have chosen to exceed the minimum requirements as part of their operations.

As previously mentioned, the changes in the last decades within the United States milk recording industry have placed participants in direct competition with each other and have reduced the level of government/university support and expertise available to the industry. As the management of each of these organizations looks to

Application of minimum standards

Going beyond the minimum standards

Table 2. Current auditing frequency of milk recording entities.

Parameter	Frequency	Comments
Field Service Providers	Annually	Alternating on and off-site
Meter Centers – Facilities	Biennially	All audits on-site
Meter Technicians – Procedures	Biennially	All audits on-site
Meter Technicians – Training School	Once every 5 years	
Laboratories – Facilities/Procedures	Biennially	All audits on-site
Laboratories – Samples Unknown	Monthly	
Dairy Records Processing Centers	Annually	All audits off-site
DRPC – File Transfer Accuracy	Monthly	

position their organization within the recording industry, many have realized the value of an independent certification program to aid in establishing the basis for many of the fundamental aspects of their business.

Table 3 summarizes some of the key minimum standards attained by all field service providers (n=27), along with the activities of the top quartile (n=7) of these providers with respect to each of these standards. The top quartile was identified as those providers who regularly exceed the minimum standards in all areas. It should be noted that many of the certified providers exceed the minimum requirements in one or more areas of service and their commitment to the quality certification program is recognized as well, though not summarized in this paper.

As table 3 demonstrates, the top quartile of field service providers range in the size and scope of their operations. Though not specifically listed in the table, these providers operate in diverse areas of the country with respect to geography, herd size, business structure and trends of growth or decline in cow numbers in their trade area. Similar comparisons can be made when comparing the operations of laboratories with respect to going beyond the minimum standards of compliance, though they are not summarized in this paper. When evaluating these organizations, three main characteristics of each of these providers surface. These characteristics are: commitment of management at the local level; commitment to the quality certification process and use of the auditor(s) as a resource.

Commitment of management team at the local level

Strength of the management team at the field service level is paramount in an open-market milk recording industry. While there is a broad range of experiences and education levels within the management teams of our field service providers, the most successful have a focus on serving their customers or members. This focus is often demonstrated by investment in employees with training and support, responsiveness to needs of the customers by service and attention to detail, and a vision of business growth through marketing of value-added services to their dairies.

Table 3. Minimum standards and application by top quartile of field service providers.

Standard	Total	Minimum	Top Quartile (n=7)
Number of herds serviced	23 005		145 to 4 425
Number of cows serviced	4 414 821		110 000 to 559 685
Growth (no. cows, 2007 to 2008)	4.04 %		8.92 %
Initial training of field technicians		3 herds	7 herds to 20 herds
Active field technicians	3 018		15 to 196 Technicians
Field technician training meetings		1x/year	2x to 12x/year
Number of portable meters	108 139		930 to 10 814
Frequency of portable meter calibration		Annually	1 to 4 times/year
Number of electronic meters	66 022		72 to 3 987 meters
Frequency of electronic meter calibration		Annually	1 to 12 times/year
Evaluation of bulk tank/test day deviations		Report values	In-depth investigation and follow-up

A common trait among the managers in the top quartile of field service providers, along with many others operating in the system, is a commitment to the quality certification process. These managers not only realize the process is needed for their organization as an audit of their performance relative to the minimum standards, but also realize that it is an important investment in the totality of the milk recording system. The importance of a nationwide system builds value in the programs marketed locally by the affiliate and allows for the benchmarking of an individual's performance relative to standards.

Another key understanding by these management teams is that the quality certification process provides the framework for certain aspects of the management of the operation. Each of the standards in the guidelines has been identified as an important contributing factor to the accuracy of the data and/or operations of the milk recording entity. Activities at the local provider level that include or address these standards as part of the day to day business operations not only meet compliance needs but build value into the cooperating milk recording entity's service. Furthermore, while the standards identified in the guidelines are the minimum of performance, there is intrinsic value for performance and accuracy in going beyond the minimum. For example, the auditing guidelines require an annual calibration of milk meters. Yet, realizing many of the portable meters in service today are being used 300-400 hours monthly, an annual calibration may not be frequent enough. These providers have moved to calibrating meters two to four times yearly, finding that 5%-6% of the meters brought in for the interim calibration are in need of repair or routine maintenance. The net result from exceeding the minimum standards is a gain for all parties – the dairy potentially receiving more accurate data, the field service provider with a valuable marketing tool, and the industry as a whole with improved accuracy and reliability.

One of the key characteristics of successful managers, regardless of the industry served, is surrounding themselves with good people. The milk recording industry is no different, and the managers of many of the field service providers view the interaction with the quality certification auditor as a resource – not just a compliance effort or paperwork audit. Whether it is ideas for program or database management, instrument or equipment operation, or training and marketing, the auditor(s) has become an invaluable resource for many entities. While the main focus of each audit is compliance with the auditing guidelines, the coupling of a review of past actions with a forward view of operational compliance and needs builds value at both the local provider and at the national level.

An active Quality Certification program not only serves the United States dairy industry by assuring the accuracy of data flowing to the GEP and to the dairy, but can also serve as an essential component for the management of a local milk recording provider. The Quality Certification program in the United States is neutral on many fronts – business structure, size, geography or other external factors – and provides a basis for compliance by all entities with the recording industry. When coupling this certification program with managers of local providers who realize the value of the program and the resources that can be harvested locally, the entire dairy information industry is stronger at the local, national and global levels.

Commitment to the quality certification process

Use of the quality certification auditor(s) as a resource

Conclusion

Estimation of breeding values of total milk yield of Egyptian buffalo under different production systems

S.A.M. Abdel-Salam, S. Abou-Bakr, M.A.M. Ibrahim,
R.R. Sadek & A.S. Abdel-Aziz

Department of Animal Production,
Faculty of Agriculture, Cairo University, Giza, Egypt

A total of 3 526 lactation records of 2 179 buffaloes in 51 herds at 8 governorates under four production systems was recorded by the Cattle Information System/Egypt (CISE) of Cairo University, Faculty of Agriculture during the period from 1990 to 2006, the records were used to estimate genetic and non-genetic parameters of total milk yield of recorded Egyptian buffaloes. The highest least squares means of total milk yield was 2 044 kg milk in Fayoum governorate, while the lowest was 1 444 kg milk in Ismailia governorate. The least squares means of total milk yield of commercial, experimental, flying and small holder production systems was 1 844, 1 328, 1 993 and 1 770 kg, respectively. The least squares means of total milk yield of buffaloes in first six parities ranged from 1579 kg for first parity to 1808 kg for sixth parities. The heritability estimate of total milk yield ranged from 0.05 to 0.25 in the different production systems. The repeatability estimate of total milk yield ranged from 0.07 to 0.38 in the different production systems. The maximum and minimum estimates of breeding values of total milk yield for commercial, experimental, flying and small holder production systems were 368 to -377, 297 to -302, 190 to -290 and 96 to -76, respectively.

Key words: Total milk yield, Egyptian buffalo, Heritability, Repeatability, Breeding value.

The contribution of buffalo to total milk production in Egypt is around 70 per cent (Khalil *et al.*, 1992). FAO (1990) noted that Egyptian buffaloes contribute to about 5 and 14% of the world buffalo's milk and meat, respectively. Information about the phenotypic and genetic parameters of various economic traits is essential for the selection of higher productivity and efficient production systems. The formulation of breeding plans and genetic improvement necessitates defining and analyzing the production systems of Egyptian buffaloes. The main aim of selection in animal breeding is to improve targeted desirable traits. Breeding values of individual animals represent the best criteria for identifying selected animals.

Summary

Introduction

There are different types of production systems to raising buffaloes in Egypt. The first system is the traditional crop/livestock system (small holders) which is traditionally integrated with the dominating agricultural system. It contains about 96% of the cattle and buffalo population and produces about 70% of the total domestic milk output. The second system is the intensive production system which contains large commercial farms. Commercial farms contain about 4% of the total cattle and buffalo population but produce about 30% of the marketable milk. The third system raising buffalo called flying system. In this system, buffaloes are put under very intensive feeding regimes to produce high-fat milk. The fourth production system is experimental farms which keep the buffalo for educational training and research purposes.

Materials and methods

Data

This study was carried out using milk production records of buffalo herds recorded by the Cattle Information System/Egypt (CISE) of Cairo University, Faculty of Agriculture during the period from 1990 to 2006, which were used to estimate genetic and non-genetic parameters of total milk yield of recorded Egyptian buffaloes.

The data comprised 3 526 lactation records of 2 179 buffaloes in 51 herds at 8 governorates under four production systems were used. The 8 governorates were Elbehera, Baniswif, Fayoum, Giza, Ismalia, Kaliobia, Elminia and Sharkia. The four production systems were commercial, experimental, flying and small holder herds. Parities included the first six lactations.

This study was focused on calculating estimates of heritability, breeding values and the least squares means of total milk yield of Egyptian buffaloes under different production systems.

Statistical analysis

The following fixed model was used to estimate the least squares means of total milk yield of buffaloes in different governorates, production systems and parities; using the General Linear Model (GLM) procedure (SAS, 2001).

$$Y_{ijklm} = \mu + G_i + S_j + P_k + YS_l + e_{ijklm}$$

where:

Y_{ijklm} = observation of total milk yield;

μ = overall mean;

G_i = fixed effect of governorate i , ($i=8$);

S_j = fixed effect of production system j , ($j=4$);

P_k = fixed effect of parity k , ($k=6$ parities);

YS_l = fixed effect of year-season of calving l , ($l=32$) and

e_{ijklm} = random residual effect.

The following repeatability animal model was used to estimate heritability, repeatability and breeding values using the Derivative-Free Restricted Maximum Likelihood (DF-REML) procedure (Meyer 2000).

$$Y_{ijklm} = \mu + A_i + P_j + YS_k + H_l + e_{ijklm}$$

where:

Y_{ijklm} = observation of total milk yield;

μ = overall mean;

A_i = additive genetic random effect of the individual i ;
 P_j = fixed effect of parity j , ($j=6$ parities);
 YS_k = fixed effect of year-season of calving k , ($k=32$);
 H_l = fixed effect of herd l , ($l=51$) and
 e_{ijklm} = random residual effect.

The least squares means of total milk yield of recorded buffalo ranged from 2 044 kg milk in Fayoum governorate to 1 444 kg milk in Ismalia governorate (Table 1). The difference in total milk yield between governorates is due mainly to the environment, management and prevailing production systems.

Table 2 shows the least squares means of total milk yield in different production systems used to raise Egyptian buffaloes. The highest production was 1 993 kg milk yield for flying herds which raise very highly producing buffaloes. The flying herds use good management and high quality feed to produce more milk. This system is usually located outskirt cities. Also, the lactation period was the longest (326 day). While the least squares means of total milk yield of buffalo under commercial herds was 1 844 kg milk yield. These commercial herds have high producing animals, good management, and nutrition system and use machine milking.

Small holdings present the dominant production system in Egypt as contains about 95% of the total number of buffaloes in Egypt. The least squares means of total milk yield of buffaloes located under this system was 1 770 kg which is lower than the average milk yield of all buffalo herds (1 884 kg). The buffaloes raised under this system usually receive special attention from the farmer although family

Results and discussion

Table 1. Least squares means(X) of total milk yield (kg) and their standard error (SE) of buffaloes in eight governorates.

Governorate	No. of records	X (kg) ¹	SE
Fayoum	334	2044 ^b	36
Giza	1496	1873 ^c	21
Elminia	318	1846 ^{ce}	36
Kaliobia	385	1767 ^{ef}	35
Baniswif	229	1652 ^a	41
Sharkia	46	1639 ^{af}	77
Behera	660	1603 ^a	27
Ismalia	58	1444 ^d	68

¹Means followed by different letters differ significantly ($P<0.01$).

Table 2. Least squares means (X) of total milk yield (kg) and their standard error (SE) and average Lactation period (LP) in days of buffaloes under different production systems.

Production systems	No. of records	X (kg) ¹	SE	LP, day
Commercial	1 340	1844 ^a	25	293
Experimental	472	1328 ^b	34	255
Flying	307	1993 ^c	37	326
Small holders	1 407	1770 ^d	26	319

¹Means followed by different letters differ significantly ($P<0.01$).

management practice used. Buffaloes located under experimental herds had the lowest milk production (1 328 kg). The differences between least squares means of total milk yield in different production systems was highly significant ($P<0.01$). Galal and Elbeltagy, (2006) observed the same characteristics of different buffalo's production system in Egypt.

Table 3 shows the least squares means of total milk yield of buffalo in different parities. Under different production systems the number of parities of Egyptian buffaloes ranged from 1 to 6 parities. The total milk yield increases gradually from the first to the sixth parity. The least squares mean of total milk yield of second parity was higher than the first parity by 8% and different significantly ($P<0.0001$). No significant differences between total milk yield of both second and third parities ($P=0.92$). Slight increase about 62, 77 and 90 kg in total milk yield from the second to the fourth, fifth and sixth parities, respectively, and different significantly ($P<0.05$). The differences between total milk yield of fourth, fifth and sixth parities was not significant ($P>0.05$). Similar results observed by Badran *et al.*, (2002).

The estimates of heritability and repeatability of total milk yield of Egyptian buffaloes are presented in table 4. The heritability estimate of total milk yield for all buffalo herds was 0.17. The highest heritability estimates of total milk yield were 0.25 and 0.24 for buffalo under experimental and commercial herds in respectively. Heritability estimate of total milk yield for buffaloes recorded in the flying herds was 0.19. The lowest heritability estimate of total milk yield for buffaloes recorded in small holder herds was 0.05. The low value of heritability was may be due to that the low input environment in these herds might suppress genetic variedicty among individuals. These results are in agreement with those reported by (Abdel-Aziz and Badran, 2000) and (Mourad and Mohamed, 1995) which showed that heritability estimates ranged between 0.03 and 0.20 for total milk yield. Metry *et al.*, (1994)

Table 3. Least squares means (X) of total milk yield (kg) and their standard error (SE) of buffaloes for different parities.

Parity	No. of records	X (kg) ¹	SE
1	347	1579 ^a	34
2	383	1718 ^b	33
3	590	1722 ^b	29
4	677	1780 ^c	28
5	593	1795 ^c	28
6	936	1808 ^c	27

¹Means followed by different letters differ significantly ($P<0.01$).

Table 4. Estimates of heritability (h^2) and repeatability (r) of total milk yield for all buffalo herds and under different production systems.

Item	h^2	R
All buffalo herds	0.17	0.30
Commercial herds	0.24	0.26
Experimental herds	0.25	0.38
Flying herds	0.19	0.20
Small holder herds	0.05	0.07

Table 5. Maximum and minimum estimates of breeding values of total milk yield (kg) for all buffalo herds and different production systems.

Item	Max.	Min.
All buffalo herds	322	-305
Commercial herds	368	-377
Experimental herds	297	-302
flying herds	190	-290
Small holder herds	96	-76

showed that the heritability estimate of experimental herds was 0.28. The same trend was observed in the estimates of repeatability for total milk yield. The low repeatability estimate is a good indicator to high changes of temporary environmental effect from record to record on the same individual (Bourdon, 1997). Metry *et al.*, (1994) and Mourad and Mohamed, (1995) and Mourad *et al.* (1991) obtained similar estimate of repeatability for experimental herds.

Table 5 showed the maximum and minimum estimates of breeding values of total milk yield for all buffalo herds and different production systems. The highest breeding value of total milk yield found in commercial herds. Commercial herds have high producing buffaloes. Also, experimental herds had a good producing. Flying herds utilize a high producing and highly genetic buffaloes for once lactation and then slighting them which led to low breeding value estimates of total milk yield (190 kg) under this production system. The lowest estimate of breeding value for total milk yield was observed in small holder herds (96 kg).

Abdel-Aziz, M and A. E. Badran. 2000. Effect of data imbalance and small herd size on the heritability estimated by different methods (a case study of milk yield in a buffalo herd). Alexandria Journal of Agricultural Research. 45(3):1.

Badran, A.E., A. El-Barbary, A. E. Mahdy and G.M. Assar. 2002. Genetic and non-genetic factors affecting the lifetime production traits in Egyptian buffaloes. Buffalo Journal. 18(2):235.

Bourdon, R.M. 1997. Understanding Animal Breeding. Prentice Hall, Upper Saddle River, New Jersey 07458, USA.

FAO. 1990. Production yearbook, Rome, Italy, FAO, pp. 420. (no. 49).

Galal, S. and A. Elbeltagy. 2006. Achievement of research in the field of buffalo production in Egypt. WAAP Book of the Year 2006: 177.

Khalil, M.H., Afifi, E.A., Bedeir, L.H. and Zedidan, S.M. 1992. Genetic analysis of lactation traits in Egyptian buffaloes. Anim. Prod. 92: 155-172.

Metry, G.H., J.C. Wilk, R.E. McDowell and H.A. El-Rigalaty. 1994. Factors affecting the performance of Egyptian buffalo. Annals of Agricultural Science, Moshtohor, 32: 827.

Meyer, K. 2000. DFREML (Derivative – Free Restricted Maximum Likelihood) package. Version 3.1á <<http://agbu.une.edu.au/~kmeyer/>>.

List of references

Mourad, K.A., M.M. Mohamed and A.S. Khattab. 1991. Genetic parameters for milk production traits in a closed herd of Egyptian buffaloes. *Egyptian Journal of Animal Production*. 28: 11.

Mourad, K.A. and M.M. Mohamed. 1995. Genetic and phenotypic aspects of milk yield traits and reproductive performance of Egyptian buffaloes. *Egyptian Journal of Animal Production*. 32: 125.

SAS Procedures Guide. 2001. Version 8.2, 2001. SAS Inst., Inc., Cary, NC.

Automatic systems to identify semen straws: why and how?

A. Malafosse & L. Journaux

UNCEIA, Union nationale des coopératives d'élevage et d'insémination animale, 149, Rue de Bercy, 75595 Paris, France

The purpose of this paper is to introduce the presentations at the 2nd session on AI technologies of the special session programme of ICAR, Nigara Falls 19 June 2008, on the topic of automatic identification of bovine semen straws. It presents the general problematic and challenges to be overcome to achieve this goal: why and how to invest in those technologies, what benefits are expected, what is the consequence on the organisation of the AI industry?

Key words: Identification, Semen straws, Automatic reading.

The idea of implementation automatic system to identify semen straws is not a new one. Before implementation, IA industry should a first equipped AI technician with computers and organise it self to support this project. Looking back the history of AI it's relative new and the systematic use of computers is becoming common just during the last years. Automatic reading is then a new step in the industry.

Automatic identification means that straws are read with automatic readers, whatever the identification system, or the reading devices, without hand recording. By "hand recording" it means paper forms, laptops or PDA. Straws are supposed to be deep-frozen to discuss the problematic in this paper, but general concepts apply also to fresh semen units.

Identification of semen straws means any information printed on straws. Identification data are defined either by the Authorities or by professional agreement. ICAR has adopted an international recommendation for identification of semen straws and edited in its guidelines.

Important items commonly recorded are:

- Semen collection or processing centre code.
- Breed.
- Identification of the bull (id or hb number, name).
- Collection code: date where the semen batch was collected.

Summary

Introduction

General definitions

Formats, order of data are usually defined at national level but not at international level, where general recommendations are given, such as maximum length of codes, the possible formats etc.

By semen batch it means the set of semen units obtained after processing from one or several ejaculate(s) on collected from a particular bull on a particular day. Batches may be split in sub-batches of part of ejaculate having undergone the same process. Very often the terms “ejaculate” or “semen batch” do have the same signification in the context of our problematic.

Goals for automatic straw identification

Hand recording of data identification on semen straws is daily done. Nevertheless many technician managers of AI centres wish to improve this process because:

- It's subject to recording mistakes (even when using electronic devices).
- It's time consuming, on farm when using papers and provides administrative constraints.
- A limited number of data on identification is collected.

The idea to implement automatic reading is to overcome these difficulties. The expected goals are:

- *To insure accurate identification of any semen unit* produced in Semen Collecting Centres from bulls to AI. Then accuracy of AI records will improve, allowing a better accuracy of parentage recording and then a better accuracy of genetic evaluation for any trait but especially for male fertility.
- *To take into account the information of semen batches.* Identification of semen refers on batches and for this reason date of collection is recorded: on a specific day there is a unique batch of semen produced for a specific bull. In add, a code allows to identify a specific treatment of this particular batch(or a part of it), (semen processing, extenders, semen sexing ...).
 - It's then a useful tool to have a better management of semen production because results of processing may be assessed by a limited number of AI bull by bull (example progeny testing) and then extended to the all bull's semen production.
 - It has been proven that the fertility of bulls varies from ejaculate to ejaculate. Taking into account batch semen information, it will improve male fertility.
- *To trace any semen doses all along the movement* chain from bull to semen use (AI) or destruction. The new sanitary requirements in Europe render responsible any operators (Collection or distribution centre) of the dissemination of diseases transmitted by bull semen if it's proven that there has been a failure in the quality system. If collecting centres are in a forbidden or restricted area due to disease outbreak, any distributed semen must be collected. Need for traceability is becoming crucial.

The summary of the questionnaire sent to world wide AI organisations to prepare this session made evident that those goals are shared by most of the AI organisations having or not a project of equipment for automatic reading.

In order to get accurate straw identification, it's necessary that there is continuous identification from the bull to straws ready to be stored in a nitrogen container. The way is optimal when bull's identification is automatically read from tag or chips and matched with identification tags prepared in advance on various devices used to collect, process semen and then filling straws. At the end of the process bull's identification and ejaculate references are printed on straws.

In many countries, regulation provisions impose that straws must enter a quarantine period and then distributed if analyses results prove that the bull is safe from legal diseases.

After a quarantine period, batches of semen are distributed and introduced in semen storage centres of the distribution centres. The same batch may be distributed to several distribution centres and there are movements of semen between storage centres, nationally or internationally. Commonly, national or international health regulation requires that bull identification and semen batch identification must accompany the movement from the semen collection centre to storage centres by paper forms or electronic files. There are usually physical controls when doses arrive to destination to a storage centre, but when units are distributed to another storage centres or to technicians or to farmers depots the track of batches are lost because the transmitted information refers just to bull identification and number of units. To get full traceability of semen doses it should be necessary to have tools able to record automatically straws movements. Otherwise the unique solution is to organise physical controls of any container where semen doses of one particular bull subject to veterinarian problems have been stored. This is not always possible.

Figure 1, below, presents semen flow with authorized and forbidden movements in the French situation. Similar diagrams should be sketch for other countries, especially in Europe.

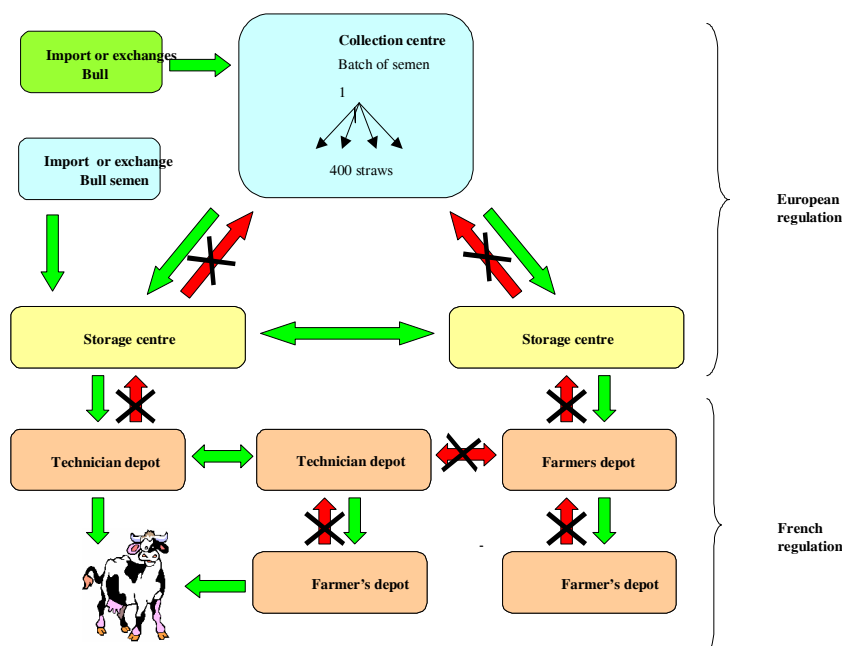


Figure 1. Semen flow from production to AI.

Artificial insemination

After insemination, technicians of companies providing AI services fill in systematically paper forms or record AI on their laptop or PDA. This is not systematically done by farmers. AI recorded data refer *inter alia* to technical information such as bull and semen batch (not always done), cow identification, herd, date and technician code. If semen identification is automatically read from straw before service and recorded in the technician computer, then the accuracy of bull identification recording is tremendously improved. It's also possible to record at the same time other information according to the capacity and the sophistication of the automatic reading system. Until now only semen batch reference are recorded by this way. It could be mentioned that automatic reading of cow identification is not practiced in AI context.

Constraints

Systems implemented to read automatically semen straw must match a set of constraints

Characteristics of semen straws

Semen straws are little cylindrical containers (0.5 ml) with few space to print readable information and deep-stored in nitrogen (-196°C). The tag or automatic system used for automatic reading must be printed or imbedded in / on each straw and must resist to storage conditions. When deep-frozen straws are removed from containers, it appears condensation that makes difficult reading. Straw must then be cleaned but damages to the frozen cells may occur, which is an inconvenience if straws must be transferred again into the container.

Practicability

Systems must be practicable at laboratory level of the collecting centre where straws are produced and at technician level where there are read in other words simple and affordable in order to not increase too much production costs.

- Codes must be easily allocated within the process of production.
- Technicians in charge of semen movements in laboratory or in storage centres may use easily the system.
- Automatic reading by technician devices is used to record bull's identification for AI recording; the code read must automatically refer to the AI bulls registered in the technician computer data base.
- Reading at farm level must be quick, accurate- with few failures in reading-and not compulsory because a percent of straws will never be coded or read.

Organisation

- Equipments. Labs must be equipped with systems identifying semen straws. AI technicians, have to be compulsory equipped with computers, the reading system being complementary
- Implementation of automatic reading systems is more possible in the situations where AI companies are providing technician service to farmers and decide of the investment in those technologies.
- Coding of information

It must be decided the kind of information that must be coded for automatic reading, having in mind that the code will refer to a unique batch of semen. The wishes of AI managers is to put as much information as possible to be close to the regulatory requirements (Bull ID, breed, date of collection, code number of the collecting centre).

Unfortunately the current systems do admit a limited number of digits. Then codes for automatic reading must be cross-referenced with other files. When there are discussions on this topic, mainly at national level, two decisions have to be made at first:

1. To define the length of the code.
2. To define the code structure and there are two ways: either it's a non significant number or it's a significant number.
 - Non-significant means that the code has to be cross referenced in the technician data base with the information of any batch of semen possible to be used.
 - Significant means that the structure of the code refers to the most important items: bull's code, date of collection.

Each system has advantages or disadvantages as mentioned in table 1.

The table shows that there is no ideal solution and that choices must be done by the AI industry itself in accordance with its organisation and independently of the manufacturers.

Table 1. Advantages and disadvantages of non-significant-significant code structure.

System	Advantages	Disadvantages
Non significant code	• No need to define code structure • Codes are practically unlimited and don't have to be changed over the time • Code may refer to a large number of items	• Management of cross reference files • Data base must be referenced with any batch of semen susceptible to be used. • Adapted to situations where collection centres and distribution centres are more or less integrated and where majority of semen is issued from few (one) AI companies.
Significant code	• No need to store references of any batch of semen in the data base • Fits well with AI industry practices: codes for bull are commonly used for many purposes, technician data bases contain this code • Date of collection is easy to define • Easy to implement when there are many semen movements between independent AI companies	• Code structure must be defined at least at national level • Code list of bulls may be accessible to any stake holder of the AI industry. • Codes of bulls or dates are not unlimited. • Well adapted to countries having a strong national organisation on AI.

3. Current technological possibilities.

The number of technological possibilities is limited today: bare code systems are implemented on large scale in France and in the Netherlands, and many other organisations or countries are thinking about this. But technology offers new developments that may be of interest for the AI industry: RFID chips, magnet ink etc.

Discussion

Costs/benefits

It's difficult to assess balance between costs and benefits for such equipment because benefits are indirectly connect with the investment. If the system avoids dissemination of diseases in farms the benefits are huge but impossible to calculate. There are certainly benefits in increasing accuracy of breeding values but again difficult to assess. Indirect benefits come from the better management and better organisation of AI companies (semen traceability, better knowledge of technician stocks etc) to implement systems.

Then the costs may be considered as insurance for the AI industry. A rough calculation for the French situation comes up with an extra expense of 0.1 % of the service costs (0.5% of the administrative costs).If should also be added the cost of data processing and organisation to support the project.

Exhaustively of recording

It will be impossible to record any AI with automatic systems because AI companies producing semen are interested in such system only if they also provide AI service or if their clients request labelling straws for automatic reading.

Farmers and free lance operators will not use automatic system to record straw identification: the challenge for those populations is to get any record of AI with good accuracy

Nevertheless it's interesting to develop this service because it improves quality of service and image besides the technical advantages mentioned above. Exhaustively is not requested to launch the projects.

International harmonisation

As the international trade increases from year to year it will be necessary to harmonise the coding system accordingly to the technologies in order to get full benefits of the automatic reading.

The AI working group of ICAR made some proposals in this respect. This is to be discuss by the AI industry before it becomes a standard after adoption by the general assembly.

Conclusion

Automatic reading of semen straws is already developed by some countries. It is no more a project and not yet a common way of working in the AI industry

Harmonisation of barcode numbers: toward an ICAR recommendation

U. Witschi

Swissgenetics, Meienfeldweg, Zollikofen, Switzerland

Correct and reliable identification of semen is an important element for traceability and sanitary security of these products for international trade and their use in breeding programs world-wide.

Furthermore the technique, how the straw is identified, affects every step of the marketing and selling process. With regards to sanitary security most countries have set up regulations on how semen-straws should be labeled. Article 3.2.1.10, paragraph 3 in Appendix 3.2.1 of the OIE Terrestrial Animal Health Code refers to the ICAR (International Committee of Animal Recording) standards for labeling semen straws. Current state is, that the required information is printed on the straw with no barcode. This means, that this information can be read by eye, but cannot be handled electronically. International trade volume with semen is still growing. Sales process could be made more efficient by introducing a system which allows the straw identification to be read and handled electronically.

To address this topic the EU-QualiVet group has proposed a system to identify semen straws by barcode, remaining within the frame set by the legislation and offering a maximum of flexibility for semen processing and trading companies. French trials have shown that the technical problems of printing and reading barcodes on semen straws have been solved. Key factors to make the barcode readable and useable worldwide are: the use of one uniform coding system (Code 128C), the unique identification of the processing AI Centres and that the information on how to interpret the barcode is easily available. The recommendation of the QualiVet group is shown in table 1.

Table 1. QualiVet recommendation for the coded information.

Digits	No. of digits	Description
1-3	3	Identify the AIC (sufficient to specify all the World's aics)
4-5	2	The production year
6-10	5	The processed batch

This proposal has been submitted to the International Committee for Animal Recording (ICAR).

To avoid parallel and inconsistent systems, negotiations are continuing with the National Association of Animal Breeders (NAAB) in order to harmonize the AI-Centres Identification with the NAAB stud code system. The required flexibility can be achieved with the obligation, that the code must begin with the centre identification (in the U.S. already given by the NAAB bull code). The rest can remain undefined as long as somewhere the information about the content of the barcode by AI centre is available and easily accessible. ICAR would host a web site which provides this information. Coordinated action is needed to assure that the advantages and benefits for international trade are realized.

Retrofitting genetic-economic indexes to demonstrate responses to selection across two generations of Holsteins

H.D. Norman, J.R. Wright & R.H. Miller

*Animal Improvement Programs Laboratory, Agricultural Research Service,
United States Department of Agriculture, Beltsville, MD, USA*

Three U.S. genetic-economic indexes for dairy cattle were retrofitted to demonstrate the progress that would have been made for currently evaluated traits if selection had been based on those indexes across 2 generations. Holstein bulls were categorized by quintile for each index, and 25 cow groups were formed based on sire and maternal grandsire quintiles. Data included records from 1 756 805 cows in 26 106 herds for yield traits, productive life, pregnancy rate, and somatic cell score; 692 656 cows in 9 967 herds for calving ease; and 270 564 cows in 4 534 herds for stillbirths. For each index, least-square differences between the 25 cow groups were examined for 8 first-parity traits (milk, fat and protein yields; productive life; somatic cell score; pregnancy rate; calving difficulty; and stillbirth) that had been standardized to mature equivalence. Analysis was on a within-herd basis with cow birth year in the model. When cow groups were combined by selection intensity (low, medium and high), the highly selected group based on the 2006 net merit index had an advantage of 219 kg more milk, 21 kg more fat, 11 kg more protein, 6.3 months longer productive life, 0.21 lower somatic cell score, 1.2 percentage units higher pregnancy rate, 0.19 lower calving difficulty score and 5 percentage units lower stillbirth rate over the group with low selection intensity. Corresponding differences for the 1976 index, which included only milk, fat and protein yields, were larger for yield traits but were less favorable for other traits. The 1994 net merit index had differences intermediate to the 1976 and 2006 indexes. Selection based on the 2006 net merit index should provide phenotypic improvement for all traits included in the index and result in a dairy population that performs more satisfactorily for a number of health and fitness traits.

Key words: *Genetic-economic indexes, Selection, Yield, Fitness, Health.*

Throughout most of the 20th century, considerable emphasis in dairy cattle populations was directed towards yield traits (volume and component percentages). A consequence was some decline in other traits with a negative genetic relationship with milk yield. A large decline in cow fertility and a small increase in somatic cell score were particularly unfortunate.

Summary

Introduction

With more comprehensive data recording, genetic evaluations for health and fitness traits were developed. To address the growing list of evaluated traits on which breeding decisions could be made, genetic-economic indexes were developed to combine estimates of genetic merit for various traits so that breeders could base selection decisions on a single trait. Choosing parents of the next generation based on such indexes helps produce cows with fewer functional deficiencies and thus a greater capacity for efficient performance over a longer herd life. Most countries that evaluate several traits update their genetic-economic indexes periodically, either when genetic evaluations for new traits become available or when economic values to weight the traits are no longer appropriate (International Bull Evaluation Service, 2008).

The U.S. Department of Agriculture (USDA) has used 6 major genetic-economic indexes (Table 1) since the first “predicted difference dollars” index was introduced in 1971 (Norman and Dickinson, 1971). The economic weights used in USDA’s current net merit index (VanRaden and Multi-State Project S-1008, 2006) were expected to lead to genetic improvement for all 10 traits included if selection decisions were directed exclusively toward net merit. Breeding values per decade are predicted to increase by 486 kg for milk yield, 34 kg for fat yield, 24 kg for protein yield, 6.0 months for productive life, 0.80 for udder composite, 0.60 for feet/legs composite, 1.4 percentage units for daughter pregnancy rate and \$25 for calving ability and to decrease by 0.34 for somatic cell score and 0.80 for body size (smaller body size now is considered to be an asset). Based on June 2006 economic weights and genetic and phenotypic parameters for U.S. Holsteins, Cunningham and Täubert (2007) reported that an index with only yield traits overstated economic gain from selection by 4.4%, an index with yield and type traits understated gain by 1.7% and an index with yield, type, health, and fertility traits had an improvement of 3.4% in economic gain.

The objective of this study was to retrofit 3 USDA genetic-economic indexes that have been used over the last 37 years to demonstrate the progress that would have been made for currently evaluated traits if the alternative indexes had been the basis for selection decisions across 2 generations.

Materials and methods

The 1976 milk-fat-protein dollars (MFP\$76) and 1994 and 2006 net merit indexes (NM94 and NM06, respectively) were used to categorize artificial-insemination Holstein bulls with ≥ 35 daughters into quintiles (1 = low, ... 5 = high). For each index, 25 cow groups were formed based on sire and maternal grandsire (MGS) quintiles. For example, group₁₁ contained cows with both sire and MGS in the lowest quintile, where the first subscript refers to sire quintile and the second subscript refers to MGS quintile. Only cows with birth dates from 1993 through 1999 and calving dates from 1995 through 2005 were included. Cows that changed herds or had missing lactation records within their first 5 parities were excluded as were those in herds with < 5 cows. Data included records from 1 756 805 cows in 26 106 herds for yield traits, productive life, pregnancy rate, and somatic cell score; 692 656 cows in 9 967 herds for calving ease; and 270 564 cows in 4 534 herds for stillbirths.

For each index, least-square differences between the 25 cow groups were examined for 8 first-parity traits (milk, fat and protein yields; productive life; somatic cell score; pregnancy rate; calving difficulty; and stillbirth) that had been standardized to mature equivalence. Analysis was on a within-herd basis with cow birth year in the model.

Table 1. Relative emphasis (%) on traits included in U.S. Department of Agriculture genetic-economic indexes for dairy cattle and year introduced¹.

Trait	Predicted difference dollars, 1971	Milk-fat protein, 1976	Net merit			
			1994	2000	2003	2006
Milk yield	52	27	6	5	0	0
Fat yield	48	46	25	21	22	23
Protein yield	...	27	43	36	33	23
Productive life	...	...	20	14	11	17
Somatic cell score	...	...	-6	-9	-9	-9
Udder composite	...	...	...	7	7	6
Feet/legs composite	...	...	...	4	4	3
Body size composite	...	...	...	-4	-3	-4
Daughter pregnancy rate	...	...	...	...	7	9
Service sire calving difficulty	...	...	...	...	-2	...
Daughter calving difficulty	...	...	...	...	-2	...
Calving ability index ²	...	...	...	...	...	6

¹Source: VanRaden and Multi-State Project S-10082, 2006.

²Includes calving difficulty and stillbirth for both service sire and daughter.

Because 600 least-squares means (25 cow groups $\times$ 8 traits $\times$ 3 indexes) were generated, only results for low (group₁₁ + group₁₂), medium (group₃₂ + group₃₃ + group₃₄) and high (group₅₄ + group₅₅) levels of selection intensity are presented (Table 2). For NM06, the highly selected group over 2 generations had an advantage of 219 kg more milk, 21 kg more fat, 11 kg more protein, 6.3 months longer productive life, 0.21 lower somatic cell score, 1.2 percentage units higher pregnancy rate, 0.19 lower calving difficulty score and 5 percentage units lower stillbirth rate over the group with low selection intensity. Least-square means for the group with medium selection intensity were intermediate to means for the groups with high and low selection intensities for all traits. Although the differences for milk, fat and protein yields were low (and, therefore, disappointing), favorable differences were evident for the other traits.

When selection was based on MFP\$76, which placed emphasis only on milk, fat and protein yields, differences in least-squares means between the high and low selection intensity groups were impressive for yield traits (1 127 kg more milk, 50 kg

Results and discussion

more fat and 37 kg more protein) and considerably higher than corresponding NM06 differences. However, MFP\$76 differences for other traits (2.1 months longer productive life, 0.12 higher somatic cell score, 1.4 percentage units lower daughter pregnancy rate, 0.06 lower calving difficulty score and 0.9 percentage units lower stillbirth rate) were less favorable than NM06 differences. Although selection on MFP\$76 increased productive life, larger increases were realized by selection on net merit indexes, which include productive life directly in the index. The increase in somatic cell score and decrease in pregnancy rate likely are due to the negative genetic correlation between milk yield and those traits.

Table 2. Least-square means for first-parity traits standardized to mature equivalence for cows selected for 2 generations based on the 1976 milk-fat-protein dollars (MFP\$76), 1994 net merit (NM94) or 2006 net merit (NM06 index) by selection intensity.

Trait	Index	Selection intensity ¹			Difference between high and low selection intensity
		Low	Medium	High	
Milk (kg)	MFP\$76	10 443	11 053	11 570	1 127
	NM94	10 443	11 012	11 417	973
	NM06	10 961	11 083	11 180	219
Fat (kg)	MFP\$76	374	400	424	50
	NM94	384	400	411	27
	NM06	391	401	411	21
Protein (kg)	MFP\$76	299	319	336	37
	NM94	304	318	328	24
	NM06	314	320	325	11
Productive life (mo)	MFP\$76	29.8	30.7	31.9	2.1
	NM94	27.8	29.9	33.6	5.8
	NM06	27.9	30.5	34.2	6.3
Somatic cell score	MFP\$76	2.83	2.91	2.95	0.12
	NM94	2.99	2.92	2.86	-0.13
	NM06	3.03	2.91	2.82	-0.21
Pregnancy rate (%)	MFP\$76	29.5	28.5	28.1	-1.4
	NM94	28.7	28.3	28.7	0.0
	NM06	27.9	28.3	29.1	1.2
Calving difficulty (1-5 scale)	MFP\$76	1.76	1.75	1.70	-0.06
	NM94	1.81	1.75	1.68	-0.13
	NM06	1.85	1.72	1.66	-0.19
Stillbirth (%)	MFP\$76	12.1	11.6	11.3	-0.9
	NM94	14.5	13.3	11.2	-3.3
	NM06	13.6	11.9	9.0	-4.6

¹Selection intensity based on sire and maternal grandsire quintiles for 25 cow groups: low = group₁₁ + group₁₂, medium = group₃₂ + group₃₃ + group₃₄ and high = group₅₄ + group₅₅, where first subscript refers to sire quintile and second subscript refers to maternal grandsire quintile.

Selection on NM94, which includes yield traits, productive life and somatic cell score, resulted in differences that were intermediate to those from selection on MFP\$76 and NM06. Relative trait emphasis (Table 1) and assigned economic values affected whether the NM94 difference was closer to the MFP\$76 or NM06 difference for individual traits. The NM94 milk yield difference was closer to the MFP\$76 difference, but the NM94 differences for fat yield, somatic cell score and stillbirth were closer to NM06 differences. The NM94 differences for protein yield, pregnancy rate and calving difficulty were almost exactly intermediate to differences for the other indexes.

First-parity least-squares means for cows that had sires and MGS selected based on NM06 demonstrate that selection based on the current USDA genetic-economic index for dairy cattle should provide phenotypic improvement for all traits included in the index. Such selection will result in a dairy population that performs more satisfactorily for a number of health and fitness traits. Some of the expected improvements are large enough that they will be noticeable to producers in a single generation (e.g., increases in productive life and pregnancy rate and declines in somatic cell score and stillbirths). Future concern by consumers about animal welfare issues should be reduced substantially through the use of a comprehensive composite index that includes health and fitness traits even though progress for yield traits will be slowed. Profit from selection on NM06 was greater than from selection on indexes with fewer traits or on individual traits.

Manuscript review and improvement by P.M. VanRaden and S.M. Hubbard of the Animal Improvement Programs Laboratory (Beltsville, MD) are appreciated.

Cunningham, E.P. & H. Täubert, 2007. For measuring the impact of change in selection indexes, old ways are best. *INTERBULL Bull.* 37: 21–25.

International Bull Evaluation Service, 2008. Description of GES as applied in member countries, <www-interbull.slu.se/national_ges_info2/framesida-ges.htm>.

Norman, H.D. & F.N. Dickinson, 1971. An economic index for determining the relative value of milk and fat in Predicted Differences of bulls and Cow Index values of cows. *USDA-Dairy Herd Impr. Ltr.* 47(1), ARS-44-223.

VanRaden, P.M. & Multi-State Project S-1008, 2006. Net merit as a measure of lifetime profit: 2006 revision. AIPL Research Report NM\$3, <<http://aipl.arsusda.gov/reference/nmcalc.htm>>.

Conclusions

Acknowledgments

List of references

Potential estimation of minerals content in cow milk using mid-infrared spectrometry

H. Soyeurt¹, D. Bruwier¹, P. Dardenne², J.-M. Romnee² & N. Gengler^{1,3}

¹Gembloux Agricultural University,
Animal Science, B-5030 Gembloux, Belgium

²Walloon Agricultural Research Center, Quality Department,
B-5030 Gembloux, Belgium

³National Fund for Scientific Research, B-1000 Brussels, Belgium

Mineral contents in milk influence the human and animal health. The variation of sodium (Na) could also be a good indicator of mastitis and are related to the milk fever. A low intake of calcium (Ca) promotes the osteoporosis in human. Consequently, knowing regularly the mineral contents in milk could be interesting. Unfortunately, the common chemical analyses used to measure the concentrations of mineral in milk are expensive. The aim of this study was to develop some calibration equations to predict the contents of mineral directly in bovine milk using mid-infrared (MIR) spectrometry. Using a principal components approach, 70 samples were chosen based on their spectral variability from the 1 609 collected milk samples. A total of 14 samples were considered as outliers. So, 57 samples were analyzed by inductively coupled plasma atomic emission spectrometry (ICP-AES) to estimate the reference concentrations of minerals. Based on these values and the corresponding spectra, 3 calibration equations were built permitting to predict the contents of Ca, Na and phosphorus (P). To assess the accuracy of the developed equations, a full cross-validation was applied. In the same way, the RPD ratio corresponding to the ratio of the standard deviation to the standard error of cross-validation was estimated. The best accuracy was observed for the calibration equations estimating the contents of Ca ($R^2_{cv}=0.82$, $RPD=2.35$) and P ($R^2_{cv}=0.77$, $RPD=2.06$). In conclusion, the MIR spectrometry seemed to be a good alternative method to predict the contents of Ca and P in bovine milk.

Key words: Calcium, Sodium, Phosphorus, Cow milk, Mid-infrared.

The contents of mineral are important for the human and animal health. The contents of calcium (Ca) are related to the osteoporosis in human (Nordin, 1997). The variation in the content of sodium (Na) in milk is related to the milk fever (El-Amrousi and Hofmann, 1970), alkalosis (Nicpon and Hejlasz, 1985) and could be a good indicator of mastitis (Waldner *et al.*, 2001).

Summary

Introduction

In Belgium, some recent dairy products are enriched in Ca to prevent the osteoporosis due to a low intake of this mineral per day. This process of production requires regular analyses of milk to quantify the contents of Ca. In the same way, if we want to detect the presence of mastitis, it is essential to realize also a regular check of the mineral contents in bovine milk. However, the common chemical analyses [e.g., inductively coupled plasma atomic emission spectrometry (ICP-AES)] are expensive.

Mid-infrared (MIR) is an electromagnetic radiation located from 1 000 to 5 000 cm^{-1} . The fundamental absorptions of molecular vibrations occurred in this region confer a high sensitivity to the chemical environment (Belton, 1997). This method is also fast and cheap. Finally, this method has already used by many milk laboratories to measure the content of major milk components as the percentages of fat, protein, urea or lactose. This last advantage is the most interesting if we want to implement largely and routinely the measures of minerals in milk.

The aim of this study was to develop the calibration equations for the measurement of Ca, Na and phosphorus (P) directly in bovine milk using MIR spectrometry.

Material and method

A total of 1 609 milk samples were collected twice during one year (Mars 2005 - May 2006) from 475 cows in 8 herds. These cows belonged to 6 dairy breeds: dual purpose Belgian Blue, Holstein Friesian, Jersey, Montbeliarde, Normande, and non-Holstein Meuse-Rhine-Yssel type Red and White. According to the ICAR rules, milk sample contained 50% of morning milk and 50% of evening milk. One part of these samples was analyzed by MIR spectrometry (Foss MilkoScan FT6000) at the Walloon milk committee (Battice, Belgium) and the generated spectra files were recorded. The second part of these samples was conserved at -26°C waiting the reference chemical analysis. This large number of samples covered a large variation of milk composition.

Seventy samples were used for the calibration procedure. They were chosen from their spectral variability using a principal component approach. The mineral contents were measured 6 times using ICP-AES without previous mineralization of milk. Nine samples showed a bad conservation and were not analyzed and 4 were considered as outliers from PCA results. The final data set contained 57 milk samples. From the reference concentrations of mineral obtained by ICP-AES and the corresponding spectral data, 3 calibration equations were built by partial least squares regressions using a specific program for multivariate calibration (WINISI III, <www.winisi.com>). No previous pre-treatment was used on spectral data. To assess the accuracy of the developed calibration equations, a full cross-validation was used. Different statistical parameters were estimated: the standard error of calibration (SEC), the calibration coefficient of determination (R^2_c), the standard error of cross-validation (SECV), and the cross-validation coefficient of determination (R^2_{cv}). The RPD ratio corresponding to the ratio of the standard deviation to SECV were also estimated to assess the accuracy of the developed equations.

Results and discussion

Table 1 shows the descriptive statistics of the 57 analyzed milk samples as well as the statistical parameters estimated for the developed equations. If the RPD value is superior to 2, the result given by the calibration equation can be considered as a good indicator of the studied trait. The RPD value was superior to 2 for the calibration equations, which predicted the contents of Ca and P in bovine milk.

Table 1. Descriptive statistics.

mg/l of milk	No.	Mean	SD	SEC	R ² c	SECV	R ² cv	RPD
Na	57	431.39	102.10	41.11	0.84	57.31	0.69	1.78
Ca	57	1 251.58	157.44	48.87	0.90	66.98	0.82	2.35
P	57	1 071.02	107.03	29.42	0.92	51.87	0.77	2.06

Guéguen and Pointillart (2000) indicated that 65% of Ca is bonded to the casein. Consequently, the prediction of Ca by MIR spectrometry could not give more information than a correlation between the protein content and the Ca. So, the correlations between the known milk components such as the percentages of fat, protein, urea and lactose in milk and the predicted mineral contents were calculated to assess the pertinence of this prediction of minerals by MIR spectrometry. The correlation between the protein percentage and the Ca content equal to 0.21 was largely inferior to the correlation estimated from the calibration (0.95) (Rc) and the correlation estimated from the cross-validation (0.90) (Rcv). The other estimated correlations were also inferior to Rc and Rcv. The same observations can be done for P. However, the content of Na seems to be better predicted based on the correlation between the percentage of lactose and Na. So, this calibration seems to be not really interesting for a potential use.

Table 2. Correlations between the mineral contents measured by ICP-AES and the known milk components.

	Ca	P	% fat	% protein	% lactose	Urea
Na (mg/l of milk)	-0.25	-0.08	-0.49	0.33	-0.76	0.46
Ca (mg/l of milk)		0.58	0.52	0.21	0.19	-0.37
P (mg/l of milk)			0.38	0.56	-0.02	0.14
%fat (g/dl of milk)				0.29	-0.41	0.39
%protein (g/dl of milk)					0.19	-0.12
%lactose (g/dl of milk)						-0.33

Even if the developed calibration equations need the addition of more analyzed samples, the MIR spectrometry seems to be a fast method to predict the contents of minerals directly on milk samples. The calibration equations, which predicted the contents of Ca and P, showed the best accuracy. The implementation of these equations in milk laboratories could offer interesting industrial (e.g., nutritional quality) and management applications (e.g., animal selection).

Conclusions

List of references

- Belton, P.S.**, 1997. Spectroscopic approaches to the measurement of food quality. *Pure & Appl. Chem.* 69(1): 47-50.
- El-Amrousi, S., and W. Hofmann.** 1970. Untersuchungen über das Festliegen der Rinder. 3. Mitteilung: Der Gehalt der Milch gesunder und festliegender kühe an Natrium, Kalium, Kalzium und anorganischem Phosphor. *Dtsch. Tierärztl. Wschr.* 77: 403-407.
- Guéguen, L., and A. Pointillard.** 2000. The bioavailability of dietary calcium. *J. Am. Coll. Cah. Nutr. Diet* 19: 119-136.
- Nicpon, J., and Z. Hejlasz.** 1985. Effect of experimental rumen acidosis on mammary gland function and on some physiochemical properties of milk. *Dtsch. Tierärztl. Wschr.* 92:275-278.
- Nordin, B. E. C.** 1997. Calcium in health and disease. *FNA/ANA* 20: 13-26.
- Waldner, D. N., S. R. Stokes, E. R. Jordan, and M. L. Looper.** 2001. Managing milk composition: normal sources of variation. Division of Agricultural Sciences and Natural Ressources. Oklahoma State University.

Automated daily analysis of milk components and automated cow behavior meter: developing new applications in the dairy farm

A. Arazi

S.A.E. Afikim, Kibbutz Afikim, 15148, Israel

Summary

Two new sensors, an on-line milk analyzer (Afilab™) and a behavior meter (Pedomer+™) were developed in S.A.E. Afikim. The results of applicative research carried out by S.A.E. Afikim Application team and researchers of the Volcani Center (Israel), are presently described.

A controlled large scaled field trial was carried out in an Israeli commercial dairy herd, milking 800 cows from May/07 through July/07. Daily milk components of the milk analyzer were compared to reference laboratory.

Daily calculated variations of fat and protein in bulk milk between the analyzer and the laboratory were -0.05% to +0.28% and 0.01% to 0.05% respectively. The agreements between the estimated payment returns under Israeli economy corrected milk formulas were -1.1% to 0.0% and allow for a daily follow up of dairy returns. Variations of the estimated daily dry matter intake calculated by the NRC 2001 formula revealed differences of 1.8 Mcal/day and 15 gr protein/day per cow between the analyzer and the laboratory results. Prediction of NEB/ketosis is possible with diverse sensitivity and specificity values depending on the fat: protein ratio cutoffs. The results of the retrospective analysis suggest that further research and interaction with other Afimilk sensors will improve the results.

Applied studies for uses of the behavioral meter showed that behavioral data collected and analyzed may be used as a useful tool for evaluation and detection of stressful situation (e.g. heat stress, noise disturbance, bedding condition). Derived applications would be monitoring housing management, influence of alteration in farm routine or facilities and prediction of calving time.

The author believes that the new sensors will improve management of the commercial dairy herds while further research will allow more practical application and better understanding of the complex dairy cows behavior.

Key words: Milk analyzer, Behavior meter, Lying behavior, Animal welfare, Milk components.

Introduction

The structure of the milk industry is going through extensive changes in the last decades. The number of farms is dropping, while the average number of animals in each farm is increasing sharply. As a consequence, monitoring and control of production, fertility, animal health and welfare cannot depend anymore on familiarity of the individual cow. Since the basic production unit in the dairy is still the individual cow, an efficient and precise monitoring approach for dairy farms is required. Familiarity is replaced by an analysis of an ensemble of data which will avail addressing of the individual cow within a large herd. This data must be accurate, reliable and accessible. These requirements dictate automated data collection.

However, though the cow is being addressed individually in terms of health and reproduction in the modern dairy it is not yet being fully implemented in terms of management. One of the reasons is lack of information about the individual cow and another reason may be the lack of means to exploit this information if and when it is provided. Gathering accurate data is not enough anymore. The emerging of new technologies avails new data in higher resolution than ever before. Firms developing new technologies are now required to conduct research to supply applications for advanced use of their newly acquired data.

Two new additional sensors were developed by S.A.E. Afikim, a milk analyzer (Afilab™) and a behavior meter (Pedomer+™). These sensors are already installed and used in several commercial and research farms. This work summarizes some results of applied research that has been recently performed, by S.A.E. Afikim Application team and researchers of the Institute of Agricultural Engineering, Agricultural Research Organization - The Volcani Center in aim to study and develop meaningful applications for the two newly sensors.

Milk analyzer (Afilab™)

The Afilab™ is a newly device that performs real time analysis of milk solids (fat, protein and lactose) and gives indication of blood and SCC. The technology is based on light scattering off matter, therefore it does not interfere with the milk flow through the pipe nor does it change the milk in any way. The concept is to amplify the laboratory performing periodically (milk test) to the milk line, in each stall at each milking. The data concerning milk components of any individual cow is now available in every milking and during the milking. This resolution shows great differences between and during milking sessions.

Materials and methods

Large filed study was performed by S.A.E. Afikim Application Team in a commercial dairy farm milking 800 cows thrice daily from May/07 to July/07 (Shkulnik *et al.*, 2008, unpublished data).

Milk components (e.g. % fat, % protein, % lactose, SCC) data as measured by the analyzer were recorded for each cow in every milking, as a reference (gold standard) milk samples were collected from each cow once a week (on a regular day) during noon milking, and was analysed for the same components with laboratory equipment (Combi MilkoScan™, Foss Analytical A/S, DK-3400, Hillerød, Denmark). Blood samples from each cow in the fresh cows group (cows up to 21 days postpartum) were collected three times a week and B-hydroxybutyrate (BHBA) levels (mmol/liter) were measured as a reference for negative energy balance (NEB)/ketosis status. The statistic analysis was performed by statistical software (JMP® 6, SAS Institue Inc., NC 27513-2414, USA).

The described applications are based on the results of this study (only part of the results is presented).

Control of nutritional status of groups and herds – for efficient economical dairy farm, ration evaluation is essential. Eicher stated that the calculated ration is generally easy evaluated. However evaluating the ration that is actually fed and ingested is problematic and general assumptions and approximations have to be made. Eicher summarized “If milk components are utilized in conjunction with herd health program it allows for rapid detection of nutritional changes which may result in metabolic and/or reproduction problems” (Eicher, 2004).

The analyzer data that could be presented at all levels (individual cow, group or herd) and emphasizes any exception, which may lead for an early detection of nutritional problems (e.g. fat, protein or fat/protein ratio decrease or increase).

Comparison analyzer fat and protein percentage with the milk test day of the whole herd revealed differences of -0.05-0.28% and 0.01-0.05% respectively.

Individual feeding – gathering the data daily and individually allow performing an individual feeding program that could be analyzed and corrected if needed, this is particularly important when supplement of additional concentrate feeding is needed (e.g. pasture management and fresh cows or other non homogenous groups).

For example - Using the NRC 2001 formula for predicting dry matter intake of individual lactating cow:

$$[DMI(kg/d) = (0.372 * FCM^{0.75} + 0.0968 * BW) * (1 - e^{-0.192 * (w_{ol} + 3.67)})]$$

the newly data now available by the analyzer, together with already existing data (milk production and BW) enables precise calculation of individual cow requirements.

When fat and protein were added to the formula (of an average virtual milking cow) there were differences of 1.8 Mcal/day and 15 gr protein/day per cow between the analyzer and the laboratory (Combi MilkoScan™, Foss) results.

Predictions (diagnosis) of metabolic diseases – the correlation between metabolic diseases, as ketosis and Sub Acute Ruminant Acidosis (SARA), with milk component is well-known.

Fat:Protein ratio (FPR) was suggested as potential indicator for energy balance (EB) (Grieve *et al.* 1986), and FPR of 1.35-1.5 was found in different studies as indication for negative EB (Heuer *et al.*, 1999 on the studies of Driksen *et al.*, 1997; Geishauser *et al.*, 1997; Hamann and Kromer, 1997 and Heuer and Pflug, 1993). Friggens and co. argued that automated sampling and inline milk analysis may improve accuracy of EB determination (Friggens *et al.*, 2007).

The agreement between BHBA blood levels with FPR in milk was tested, various cut offs were examined, and some of the results are presented in table 1.

It is clear from the data displayed in table 1. that sensitivity and specificity values depend on chosen fat/protein ratio cut offs and allows farm manager to dictate his cut off.

Derived applications

Table 1. Analyzer FPR versus BHBA (mmole/L) in blood (n=345).

FPR	BHBA>1.4 (31.3%*)			BHBA>2.0 (9.3%) ¹		
	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)
>1.2	59.3	56.1	57.1	75.0	54.0	55.9
>1.4	33.3	82.7	67.2	53.1	80.8	78.3
>1.6	11.1	92.4	67.0	25.0	93.0	86.7
>1.8	2.8	98.3	68.4	9.4	98.7	90.4

¹% of cases with BHBA above threshold (1.4 or 2.0)

The addition of second variable, change in daily milk yield (ΔMY), into the model improved the results (data is not presented). Further sophisticated multivariable models will be developed and have to be tested in the near future.

SARA is defined as extended periods of depressed ruminal pH below 5.5–5.6. (Instead of 6.0 and 6.4) and is a common in modern dairy herds (Nordlund *et al.* 2004 on the study of Garrett *et al.*, 1997). The diagnosis is based on primary symptoms (reduced or erratic feed intake, reduced rumination, mild diarrhea, foamy feces), ruminal fluid Ph and production records (e.g. depressed milk-fat content). Nordlund and co. reported that Holstein herds with more than 10% of the cows are with milk fat 2.5 or less are suspected for SARA (Nordlund *et al.*, 2004), while Tomaszewski and Cannon, suggested that rumen acidosis is presented when FPR<1.0 (Tomaszewski and Cannon, 1993). This application could not be tested in the study, because this particular farm did not suffer from SARA at this specific period. This issue has to be evaluated in the future.

Follow ups dairies' milk payment – in most countries payment for milk is affected by amount of fat and protein and the level of Somatic Cells Count (SCC). The information is given today by DHI or private milk laboratories and is done periodically or not at all. This routine does not allow daily follow up on the milk income.

Monthly economy corrected milk (ECM) calculated by analyzer compared to calculations based on milk test day using the Israeli formula, of three months showed differences of -1.1%-0.0%. These results enable good follow ups for the farmer in real time.

Retrospective analysis – using the analyzer data (fat and protein) to evaluate the influence of some risk factors (as EB status) on production parameters was done with retrospective analysis model (Model Nir) and was found satisfactory.

Applications under research and development

Early Detection of mastitis – mastitis affects the milk quality and the productivity of the cows, and it has a great impact in the dairy farm (economically and labor's work). Early detection of mastitis (clinical or sub clinical) and rapid treatment have the potential to prevent milk production loss (quantity and quality) and to save labor time and efforts.

Many studies described the correlation between milk components and udder health (Bansal *et al.*, 2005; Leitner *et al.*, 2004; Ogola *et al.*, 2007; Nielsen *et al.*, 2005; and Pyorala, 2003). Pyorala suggested lactose and electrical conductivity of the milk as two of the most promising parameters for monitoring subclinical mastitis (Pyorala, 2003).

Our observations in some commercial dairy farms, which already have the analyzer installed, support these studies. Thus, a field study must be done in order to perform a statistical validation and to develop an application based on the analyzer data.

Application derived from interaction with other sensors – interaction of analyzer's data with information acquired from other sensors including; milk meter (milk production, milk flow, milk conductivity), weight scale (changes of body weight), and pedometers (cow's activity, lying behavior) open new horizons for developing new applications and improving established applications.

The Pedometer+™ is a new leg tag that continuously records activity (steps/hour), lying time and lying bouts. It is based on a 3 dimensional sensor which detects the position of the animal leg. The concept is to determine the routine behavior of the animal (at individual, group and herd levels) and to pinpoint the deviation from the daily routine as a potential indication for welfare, health, fertility, production and stressful events.

Animal welfare and comfort is an emerging issue in modern agriculture driven by consumers and animal organizations. Poor welfare usually leads to greater susceptibility to disease (Broom and Corke, 2002). Weary and Tucker suggested that standing and lying behavior may be a suitable approach when cow comfort is assayed (Weary and Tucker, 2003). Moreover in aim to maintain good health and welfare and high levels of productivity, it is essential that dairy cows have enough time to lie down and rest (Tucker *et al.*, 2004). Furthermore blood flow to the mammary gland is increased by 24-28% when cows lay down (Cook 2003 on the studies of Metcalf *et al.*, 1992 and Rulquin and Caudal, 1992), and this may improve nutrients delivery to the udder and hence increase milk yield (Cook, 2003)

The data presented is based on two studies done by groups leaded by Maltz E., from the Agricultural Research Organization - The Volcani Center, and observations that had been performed in commercial farm equipped with the pedometer+™.

Study 1 – Lying behavior of dairy cows under different housing systems – the study was performed in a commercial dairy farm milking 550-600 cows thrice daily. In a first trial, lying behavior of 12 multiparous was recorded in a roofed no-stalls barn, under comfortable thermal conditions. In a second trial, lying patterns of 16 first-calvers cows were monitored in two adjacent barns: a no-stall completely roofed barn (8 cows) and a free-stall completely roofed barn (8 cows). In the third trial, change-over of 4 cows from each group of second trial was done. Activity and performance were monitored by Afifarm management system (S.A.E. Afikim, Israel). Significant differences were evaluated using Student T-tests, unpaired – between groups, paired – between periods and treatments of the same cows (Livshin *et al.*, 2005)

Behavior meter (Pedomer+)

Materials and methods

Study 2 – Detecting calving time of dairy cows by analyzing activity and feeding behavior – fourteen cows prior calving were allocated each 5 kg concentrates a day that were allowed in 5 equal portions of 1 kg in each of 5 even feeding windows, using computer controlled self feeders. Activity and feeding behavior were recorded and analyzed for the last 7 days prior calving. Activity variables that were measured included number of steps, number of lying bouts and accumulating lying time. The data of each day was compared to those of the previous day and differences were analyzed by paired t-test for significance. Analysis was performed for day time (06:00 – 19:00), night time (09:00 – 06:00) and diurnally.

Derivative application

Cow welfare and comfort assessment – in the result of study 1 and from observations in commercial farms, the lying behavior has a constant pattern during the day, the longest lying periods are during the night hours, and the shortest are at noon time (Table 2). It was found that there is only a 20% range of differences, between individuals in daily lying time, while in activity it can get higher that 100% (Livshin *et al.*, 2005). Therefore it was concluded that lying behavior could be considered as a relatively stable parameter, and that any changes from the routine may indicate a stressful situation. We observed sharply changes in lying behavior of the whole herd in response to heat stress and to noisy disturbance (data not presented).

In study 1 the lying behavior was found to be a powerful tool that indicates differences in cow comfort in two different housing systems (Table 3) and therefore may be used as a tool for evaluation of housing management, and influence of alteration in farm routine or facilities.

Table 2. Lying time (mean $\pm$ SD) in between milking diurnal intervals of 8 cows in no stalls barn and in free stall barn (From Livshin *et al.*, 2005).

Time interval	Lying Time (min)	
	No stall barn	Free stall barn
04:30-12:30	157 $\pm$ 42 (29.4) ¹	120 $\pm$ 43 (28.1)
12:30-20:30	118 $\pm$ 50 (22.1)	108 $\pm$ 49 (25.3)
20:30-04:30	258 $\pm$ 51 (48.4)	199 $\pm$ 50 (46.6)

¹% from daily lying time.

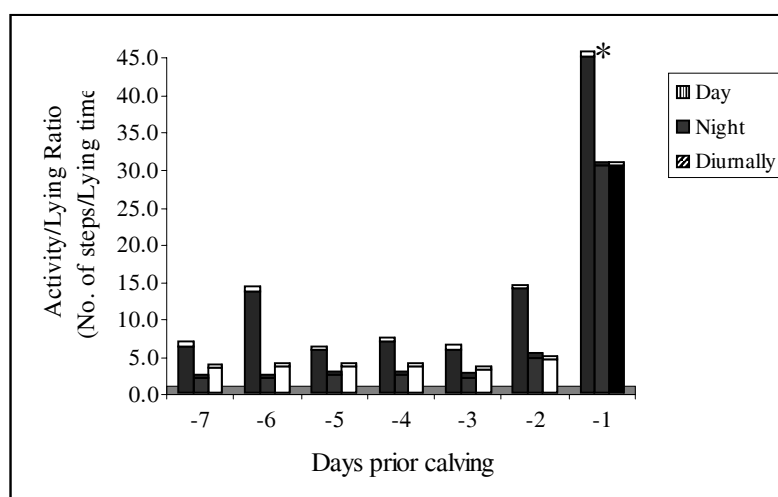
Table 3. Cows lying time (mean $\pm$ SD) in between-milkings diurnal intervals of two groups of four cows that were transferred from one type of barn (period 1) to the other type (period 2). (From Livshin *et al.*, 2005).

Time interval	Period 1		Period 2	
	No stall	Free stall	No stall	Free stall
04:30-12:30	153 $\pm$ 41 ^{1a}	120 $\pm$ 39 ¹	178 $\pm$ 55 ^a	126 $\pm$ 55
12:30-20:30	110 $\pm$ 45 ¹	113 $\pm$ 48 ¹	148 $\pm$ 46 ^a	78 $\pm$ 43
20:30-04:30	254 $\pm$ 51 ^{1a}	180 $\pm$ 56 ¹	259 $\pm$ 58 ^a	200 $\pm$ 75

¹Significant difference ($P < 0.01$, paired t-test) in lying behaviour of the same cows when transferred from one barn to the other in different periods.

^aSignificant difference ($P < 0.01$, unpaired t-test) in lying behaviour between groups (4 cows) inhabiting different barns within period.

Detecting calving time of dairy cows – the results of study 2 (Figure 1) demonstrated that cow's behavior changes prior calving, the activity of the cows increases and the lying time decreases significantly one day prior to calving. The results showed that calving time can be predicted by measuring these parameters, and therefore may help to plan the daily routine in the farm, and attend to expected difficult calving. In an earlier study it was found that the most sensitive parameter is Activity/Lying ratio (number of steps/lying time) (Maltz and Antler, 2007).



* $P < 0.01$ day -1 compared to day -2

Figure 1. Activity/Lying ratio in the last 7 days prior to calving, during day time (06:00-19:00), night time (19:00-06:00) and diurnally (Maltz and Antler, personal communication).

Heat detection in unfavorable condition – cows in heat are usually restless, and tend to increase activity and decrease lying time. In some management condition (e.g. tie stalls) the cows do not have the option to show high activity and hence heat could not be detected via regular pedometers. We believe that monitoring lying behavior changes will enable heat detection in such unfavorable condition. Studies regarding this issue will be conducted in the near future.

Applications under research and development

Define the best density of milk cows in barns – with the growing demand for milk all over the world, dairy farms are increasing the number of milking cows and hence the density of cows in barns. This overcrowded will induce penalties such as increase in SCC and decrease in ECM (Nir (Markusfeld), personal communication). We are now conducting a research in aim to test the possibility to determine the best density for each barn with the aid of lying and activity behavior and milk production.

Discussion

Efficient management of modern dairy farm requires rapid and accurate data collection and an easy way to exploit this information. Gathering accurate data is not enough anymore, and companies developing new technologies are required to conduct applied research for the use of this new data. Applied research has been conducted in order to develop applications for new acquired data; Data supplied by on-line milk analyzer and behavior meter, developed by S.A.E. Afikim, and some derived applications were presented. Some applications are ready for use e.g. follow ups dairies' milk payment, control of nutritional status of groups and herds, individual feeding, predictions (diagnosis) of metabolic diseases, retrospective analysis, cow welfare and comfort assessment and detecting calving time of dairy cows. While others e.g. early detection of mastitis, heat detection in unfavorable condition, definition of optimal density of milking cows in barns still have to be tested and to be proven.

However, our goal is to develop models consisting of a multivariable integration and analysis of data collected from all sources.

List of references

Bansal B.K., Hamann J., Grabowski N.T. and K.B. Singh, 2005. Variation in the composition of selected milk fraction samples from healthy and mastitic quarters, and its significance for mastitis diagnosis. *J. Dairy Sci.* 72, 144-152.

Broom D.M. and M.J. Corke, 2002. Effects of disease on farm animal welfare. *Acta. Vet. Bron.* 71, 133-136.

Cook N.B., 2003. The influence of cow comfort on lameness and production. Proceeding of 16th annual full symposium on recent advanced in Clinical Vet. Med. U.C. Davis, 61-70.

Eicher R., 2004. Evaluation of the metabolic and nutritional situation in dairy herds: Diagnostic use of milk components. 23th World Buiatrics Congress, Québec, Canda.

Friggens N.C., Ridder C. and P. Løvendahl, 2007. On use of milk composition measures to predict the energy balance of dairy cows. *J. Dairy Sci.* 90, 5433-5467.

Grieve D.G., Korver S., Rijpkmea Y.S. and G. Hof, 1986. Relationship between milk composition and some nutritional parameters in early lactation. *Liv. Prod. Sci.* 14, 239-254.

Heuer, C., Schukken, H. and P. Dobbelaar, 1999. Postpartum body condition score and results from the first test day milk as predictors of disease, fertility, yield, and culling in commercial dairy herds. *J. Dairy Sci.* 82, 295-304.

Litner G., Merin U. and N. Silanikove, 2004. Changes in milk composition as affected by subclinical mastitis in goat. *J. Dairy Sci.* 87, 1719-1726.

Livshin, N., Antler A., Zion, B., Stojanovski, G., Bunevski, G. and E. Maltz, 2005. Lying behaviour of dairy cows under different housing systems and physiological conditions. Proc. Implementation of Precision Agriculture, 2nd ECPLF, Uppsala, Sweden, pp. 305-311

Maltz, E. and A. Antler, 2007. A practical way to detect approaching calving of the dairy cow by a behaviour sensor. Proc. Precision livestock farming '07, Edited by: S. Cox, Wageningen Academic Publishers, pp. 141-146

Nielsen t., Larsen M., Bjerring M. and K.L. Ingvarsen, 2005. Quarter health, interval, and samplin time during milking affect the concentration of milk constituents. J. Dairy Sci. 88, 3186-3200.

Nordlund K.V., Cook N.B. and G.R. Oetzel, 2004. Investigation strategies for laminitis problems herds. J. Dairy Sci. 87 E27-E35.

Ogola H., Shitandi A. and J. Nauna, 2007. Effect of mastitis on raw milk compositional quality. 8, 327-342.

Pyörälä S, 2003. Indicators of inflammation in the diagnosis of mastitis. Vet. Res. 34, 567-578.

Schcolnik T., Flexer H. and Nir (Markusfeld) O. 2008, unpublished data.

Tomaszewski M.A. and T.J. Cannon, 1993 Using records for large herd management. Western Large Herd Management Conference, Las Vegas Nevada, USA. pp 137-140.

Tucker C.B, Weary D.M., Jeffrey Rushen J., and A. M. de Passillé, 2004. Designing Better Environments for Dairy Cattle to Rest. Advances in Dairy Technology 16, 39-53

Weary, D.M. and C.B. Tucker, 2003. The scince of cow comfort. Proceeding of the joint meeting of the Ontario Agri. Business Association and the Ontario Association of Bovine Practitioners, Guelph, Ontario.

On-farm technologies. Challenges and opportunities for DHI and genetic improvement programs

R. Cantin

CanWest DHI, Guelph, Ontario, Canada

As dairy herd sizes increase so will the trend to increase use of automation and technology at the farm level. For milk recording (DHI) organizations and for genetic improvement (GI) programs, these trends will create opportunities but also challenges. Those opportunities and challenges can be addressed through effective business like strategies. Furthermore, a good understanding of the dairy herd of the future will be required for DHI and GI programs to be successful.

Key words: Strategy, Herd management software, Customers, Value added laboratory services, Quality, Genetic improvement.

Trends of increasing herd sizes and use of on farm technologies are occurring worldwide. Some of the technologies such as herd management software, electronic identification, electronic meters and robotic milking systems have been in use for decades. Emerging technologies such as cow side somatic cell count and component monitoring are being actively developed. Down the road it is conceivable that disease screening or pregnancy diagnosis will be possible cow side through automated milk sample collection and analysis.

The adoption of on farm analytical technologies and automation technologies will no doubt continue in the future.

For DHI and GI programs, the increased use of on farm technologies provides many opportunities. The obvious one is for access to more data. Farms with automated ID systems, electronic milk metering devices and current/future cow side analytical technologies can be a valuable source of data for industry programs, particularly GI programs.

Summary

Introduction

Opportunities

Through automation there is the possibility for improved quantity of data. Furthermore, accuracy and quality of cow information can be improved versus manual collection systems. Additionally, since labour is a significant component of DHI data collection, reduced cost for DHI services is possible through the automation of the collection process at the farm. Possibly, data on new traits could be collected routinely through the on farm technology systems (ex. lameness).

Finally, if data generated by the on farm technologies can be electronically and easily provided to DHI organizations, then data collection costs (ie. DHI fees) would be lowered and therefore more farms would participate in DHI and GI programs.

Challenges

Often, the belief is that DHI organizations just need to build an 'electronic pipeline' for data exchange. DHI staff would not even be required to go to the farm. Herds could just upload their on farm data to the central database, for use in industry programs. Unfortunately it is not that simple.

Even after decades of commercialization, significant data quality issues accompany on farm automated animal ID and electronic metering devices. Between read errors, ID reuse/misuse and metering equipment failure, a significant amount of data quality and completeness issues are common. These issues usually lead to the need for extensive data editing and outright discarding of data.

On the surface the principle of building an 'electronic pipeline' to exchange data between thousands of farms in the field and a central processing centre is appealing. However the cost to program and manage these data interfaces are significant, not to mention the practicality of keeping up with numerous on farm software manufacturers and DHI version updates.

However the biggest challenge is in the fact that if dairy farmers' herd management information needs are being met by their on farm technologies, will they enroll on DHI services or even allow the use of their data for industry programs, even at no charge? The issue of 'perceived value' is not new, but as the use of on farm technology grows, so will the issue for DHI and GI programs. Dairy producers will increasingly ask... 'What value do I get from central processing of my farm data?'

Strategy and key issues

For both DHI and GI programs, strategies can be developed to increase the perceived value of their services and to maintain relevance, even in the face of increased on farm technology adoption.

DHI - Milk recording

For profit culture and principles. It is imperative that DHI organizations operate in a 'for profit' culture. Most DHIs have originated from government run programs and many are still today, either formally or in the way they operate. Regardless of the legal entity (government, not for profit...etc) it is important that a business culture be present across the organization. Dairy producers are business owners and are operating in a business environment – so should DHIs.

It is important for DHIs to have a business plan and to apply sound business principles such as:

- Define the business you are in.
- Define the customer.
- Identify, leverage core competencies.

- Utilize economies of scale.
- Adopt appropriate technologies.
- Invest in innovative and new products.
- Identify key deliverable.
- Etc...

Without an effective business approach, DHI organizations will fail.

Be in the Herd Management Software business. Ultimately, all of the data from the on farm technologies resides in the herd management software of the farm (ie. Cow database). DHIs have experience and expertise in information management. Traditionally, software suppliers provide little data and herd management support and expertise – this is a strength of DHI which should be exploited.

Strategically, DHIs should be providing/selling herd management software, be the technical support for the customer and assist with on farm data management. This service is high value for dairy producers (larger ones in particular), and provides the opportunity for a common platform that makes data exchange between the farm, DHI and farm advisors, practical and cost effective (Figure 1).

Flexibility in service. The days of one size fits all are long gone. Most DHIs have adapted to that principle. With the advent of new on farm technologies, it will be important for DHIs to continue to be flexible and tailor the service offering based on changing customer needs.

Value added services. As more of the traditional milk recording services are being met by on farm technologies (ex. milk weights info), DHIs will be required to provide improved services to maintain value and relevance to the customer. Examples of such services are:

- 'Quality Control' for on farm data collection (ex. milk meters verification)
- Benchmarking services
- Records management for regulatory requirements
- Herdbook registrations assistance
- Forage, soil analysis services
- Feed management software
- Etc...

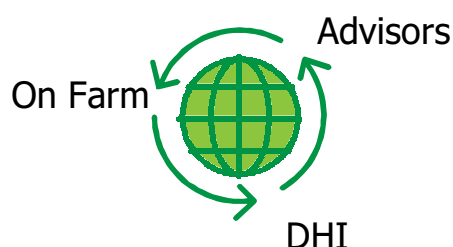


Figure 1. Common platform between the farm, DHI and Advisors makes electronic data exchange practical and cost effective.

Many opportunities exist to provide value added services. These should be proactively pursued.

View advisors as customers. Developing a pipeline of data for advisors (veterinarians, nutritionists) is as important, if not more, than the pipeline of data for industry programs. Advisors have the ability to tremendously increase the value of DHI services, through the use of the DHI information at the farm level.

By providing meaningful information and services to advisors (ex. herd management software), DHI then becomes indispensable to them and their advisory services. It not only increases the value of DHI at the farm but also enhances the profitability of the dairy industry through improved advisory services. Advisors should be viewed as a specific market segment for DHI services.

Value added laboratory services. The development of new analytical technologies is not limited to on farm applications. Much research and development is being done from a traditional central laboratory perspective. Opportunities currently exist for value added lab services (ex. disease screening) using the routinely collected DHI sample. No doubt additional opportunities will emerge. DHIs must proactively search and implement those opportunities.

Pursuit of service quality and value. DHIs are service organizations and as such must pursue service quality and excellence. Many DHIs are also not for profit, producer owned organizations operating under low cost principles. At the end of the day, dairy producers will judge relevance based on value and quality, not low cost. DHIs must be cautious of constant cost cutting and the lowering of the bar on service quality.

Sales and marketing principles. The dairy industry, like most agricultural industries is still very much a people business and professional sales and marketing matters to dairy producers. The days of dairy producers initiating the discussions regarding the need for milk recording services are over. DHI organizations need to proactively implement and practice field sales and marketing principles.

By following the principles outlined, DHI in the province of Ontario (Canada) has been able to grow the market share of herds on milk recording, simultaneous to the increased use of on farm technologies (Figure 2).

Genetic Improvement (GI)

For GI, certain strategies can also be implemented to help optimize the effectiveness of programs in light of the increased use of on farm technologies.

Data quality. With the possibly very large amount of data that can be generated from on farm technologies, GI programs will need to carefully understand and differentiate the quality of data and account for the variability.

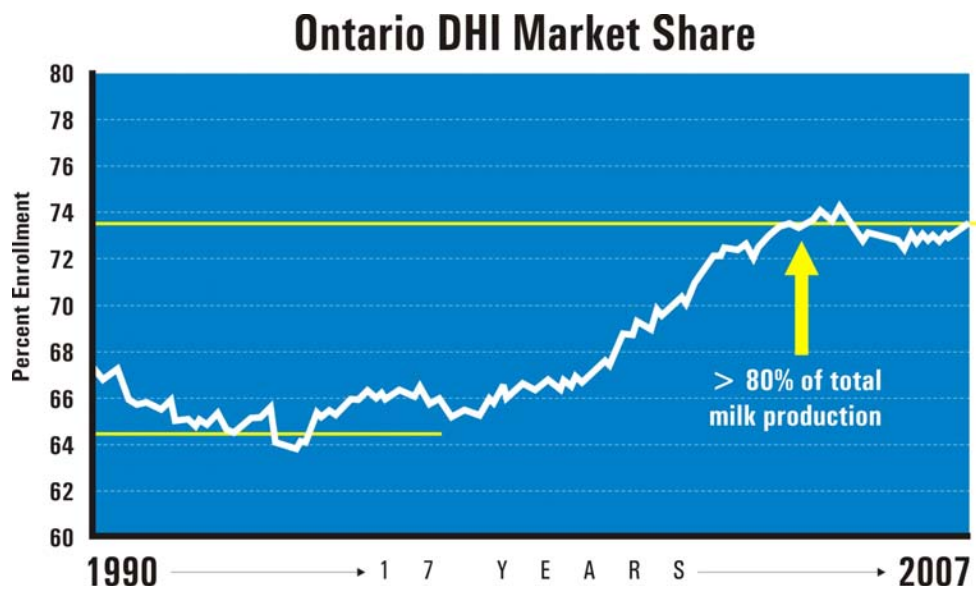


Figure 2. Percent of herds enrolled on milk recording in the province of Ontario, Canada.

GI as Research and Development. The Artificial Insemination industry should consider their Progeny Testing program as their 'Research and Development' (R and D) division, and as such, like any other company, should manage it based on strong business principles. Benefits could be gained by concentrating efforts on the farms providing the best return on investment ie) quality data.

Concept of data farms. The idea of dairy producers being paid for their data is not new. It has been raised by dairy producers in the past... how much are you willing to pay for my data? GI should consider 'high tech' farms as specialized data providers and approach them with a business transaction in mind ie) we buy data, do you want to sell?

Too many traits? Even with new technologies, GI industry should be cautious about adding too many traits to improvement models. Often new traits have low economic impact, low heritability and therefore require a large amount of data collection for effective improvement. Dairy producers already complain about data collection 'fatigue', so the industry must proceed cautiously on new traits.

Technology to it's advantage. The development of new technologies is not limited to on farm applications. Much development has occurred in the field of sexed semen and genomics just to name two. No doubt additional opportunities will emerge. GI must proactively search and implement those opportunities to its advantage.

Technology and the herd of the future

Things will continue to change. A decline in herd numbers and an increase in average herd size will continue to be a fact of the dairy industry worldwide. Large operations will be the common practice. With that, the adoption of automation and technology at the farm will continue. As DHI and GI organizations plan for the future, we need to consider certain practical key issues surrounding these trends. These may appear self evident, but are often overlooked.

Dairy farms are independent businesses and making money is and will be the priority. Additionally, on a dairy farm time is money (Thomson, 2007). When asked what is the one thing they wish they had more of, dairy farmers never reply 'more data'! Invariably, what they wish for is more financial resources, time, quality of life and reliable, quality labour.

One of the key issues with some of the technology at the farm is that it does not always result in greater profits or time savings (Thomson, 2007). In some cases, because of the high cost (capital and maintenance) as well as being impractical (i.e. the parlour cannot be stopped while I wait for repairs to be made on some of the components), some of the technology options have a poor cost benefit or are simply not implemented. For example, many large farms have opted not to invest in auto parlour ID and electronic metering devices. They simply do not see a return on investment.

For many years, larger herds have been telling us that they really are not concerned about information on individual animals, since they manage by groups. Their data need is for groups of animals (focusing on early lactation) and on identifying problem cows. In addition they require data on how well their equipment and employees are performing (Thomson, 2007). They are not interested in information on the well performing animals. These trends are directly opposite to the GI approach of identifying superior performers and using them as the basis for future improvements.

No doubt that time savings, labour and quality of life considerations will play a key role in the adoption of future technologies. Technologies and automation that provide benefits in these areas will have the greatest chance of success.

Conclusion

As average dairy herd sizes increase so will the trend to increase use of automation and technology at the farm level. For DHI organizations and for GI programs, these trends will create opportunities but also challenges. Those opportunities and challenges can be addressed through effective business like strategies.

A good understanding of the dairy herd of the future will be required for DHI and GI programs to be successful. The large commercial herds of the future will question the value of having their herd information sent to DHI and GI databases. DHI organizations and GI programs have gone through significant changes and adaptation in the past and will be required to continue to do so in order to remain relevant to dairy producers.

List of references

Thomson, R., 2007. American Dairy Science Association symposium, San Antonio, Texas, USA.

Assuring accuracy in milk recording analysis on-farm - Approach on principles for guidelines

O. Leray

Actilait/Cecalait, Poligny, France

Until these last years milk recording analysis has been performed in specialised milk testing laboratories equipped with automated indirect method for rapid testing. Those laboratories have implemented quality control and quality assurance so as to provide confidence to result users thus entering accreditation or certification processes. The last decade has shown the advent of portable analytical devices and analytical modules devoted to direct in-line/on-flow analysis which can be either transported or implemented to the farm. As a consequence the new situation for milk recording could become that of many independent analytical units spread over the region beside the former laboratory of the area that should be accounted and managed in an harmonisation system of milk recording data. To achieve this, appropriate guidelines are needed.

Key words: *On-farm, At-line, In-line, Milk recording, Analysis, Accuracy, Uncertainty.*

During the last decade a number of portable analytical devices have been commercialised for possible utilisation on the farm that can be either used by the farmers or by external technicians whereas analytical modules specifically devoted to direct in-line/on-flow analysis for installation on the milking system in the farm have been developed and are proposed nowadays. If analysis de-localised on the farm is being developed at the first extent for the benefit of farmers in milk management production, use by/for official genetic milk recording for the relevant criteria must be envisaged and care be taken that at-farm analytical devices can respond to the needs for both individual and collective interests.

An analytical quality assurance (AQA) frame has been designed by ICAR for milk analysis in laboratories and defines general recommendations to be followed by organisation to get ICAR approval or certification for that part. In the forthcoming situation where official milk recording data will be obtained from different analytical systems in different conditions, ICAR should complement the existing AQA system so that comparable quality and precision of recording data be assured in every analytical systems and easy correspondence can be made. Hence a frame is needed as well as a safeguard for quality to users, as a practical tool to manufacturers who

Summary

Introduction. A new situation in milk recording analysis

can find adequate technical indications or targets. It should be defined by ICAR through adequate guidelines dealing with the respective aspects related to milk recording analysis.

Issues about on-farm analysis and outlines of guidelines

As being located at farm, analytical devices can hardly be kept separated from milk quantity measurement and sampling – also because they can be tightly associated in an in-line real time measurement – , no more from animal identification since they can be part of integrated systems. Although made at first for farm milk production management, collected data are also expected to be exported and used for collective purposes or connected to other external systems making necessary compatible records under standard formats.

Since increasing milk testing number is the major objective of analysing milk on the farm, It is also to adapt the methods of lactation calculation with more production measurement than presently applied. Specific recommendations are also needed with regard to possible implementations on automated milking system (AMS) so to cope with representative milking.

Devices developed for use on the farm are designed to support tougher conditions of use than at the laboratory with regard to temperature, humidity, shocks, etc, that should be reflected in the general structure of the instrument and technological choices. Also lower prices than for laboratory instruments are requested to make such system economically reliable thus it can be expected less sophisticated technical solutions. This may result in lower precision performance so as to gain in robustness and stability. Such lower analytical performance can be found acceptable since more analyses can be performed and be used to reduce estimate uncertainty by averaging the point being that no systematic bias can be admitted. So need is first to define what overall accuracy limits can be accepted for milk and composition measurement.

The frame to draw should provide proper elements for ICAR agreement including on-farm measurement system validation and minimum quality control and quality assurance procedures necessary to provide sufficient quality in milk recording data. Similarly as classical former devices the on-farm analytical devices should be accounted in a quality assurance system for milk production and genetic evaluation through compliance with international ICAR guidelines.

Therefore guidelines will define :

1. Various possible situations with on-farm analysis.
2. Acceptable limits for precision and accuracy of on-farm analytical devices.
3. Conditions to fulfil for evaluation and ICAR approval.
4. Conditions and check limits for quality control.
5. Compatibility with existing system (identification, data record/transfer, lactation calculation).

Definitions on on-farm milk analyser

Different categories of on-farm analysers are distinguished with regard to main characteristics and relevant recommendations needed. Beside and to complete the general term of on-farm milk analyser - analytical device or system installed on the farm that is used either to detect or quantify various components or characteristics in milk - it is defined:

- **At-line milk analysers.** Analytical device installed beside a production line and used once the whole of a representative sample is obtained. In a farm such devices are likely to be located near the milking place but not exclusively. They can have similar characteristics as those used in laboratories and in extreme cases be an element of an on-farm laboratory. The number of analysers is independent of the milking place number but relates to the number of sample to analyse. They can also be called off-line analysers
- **In-line milk analyser.** Analytical device installed in the production line (i.e. milk pipeline). Analysis may be run during the milking process (real time) or at the end on a representative aliquot sample (differed time). There is necessarily one instrument per milking place. They can also be called on-line analysers

The major objective is to establish consistence and correspondence between different measuring systems with regard to measurement uncertainty that enables comparison within time and space. Analytical quality monitoring is based on not exceeding (upper) limits for measurement accuracy therefore this is to establish limits of accuracy for milk composition analysis that provide sufficient precision for the benefit of both parties, milk producers, to manage day-to-day milk production, and milk recording organisations, to maintain a suitable precision in estimating genetic indicator.

Bases and conditions of equivalence in milk recording analysis

Choice is made for the principle that the accuracy of the analytical device must allow to measure significant production changes day after day. Composition information of interest is that outside the regular natural variation related to normal physiological and milking conditions. Therefore it cannot be larger than the natural day-to-day fluctuation of the measured criteria to achieve statistical significance. Fat concentration variation is used (as the most reactive/fluctuating milk component) to establish the equivalence ratio used to calculate maximum limits for precision and accuracy statistical from that stated for laboratory analysers. The latter calculated values serve to establishing limits for the evaluation of new milk analysers and quality control in routine testing.

Defining maximum limits of accuracy for composition measurements

The choice of a upper limit value for the natural day-to-day (or between day) variation of fat content was made from literature (Allen Young, Utah State University) and a convergent validation with data from Denmark (Tove Asmusen (Lattec) and Peter Lovendahl, Aarhus University, 2004). The latter shows the day-to-day variation of fat concentration lies within the stated limits for every sampling (morning, evening and 24 hours) and are independent of the fat level (Figures 1 and 2). Moreover the limit appears especially suitable in the example in that the so defined maximum confidence belts do not overlap and allow to differentiate significantly morning and evening measurements.

The regular natural day-to-day variation as expressed through the standard deviation s_{BDC} has its maximum acceptable limits defined as $Ls_{BDC} = 0.25 \text{ g/100g}$ making a maximum 95% range $\pm 2.L\sigma_{BDC} = \pm 0.5 \text{ g/100g}$.

The calculation of the maximum analytical accuracy derives from the composition of the error of the concentration estimate C of the individual milk described as

$C = T + e_{BDC} + e_s + e_A$ (composition result = true value + between day composition error + sampling error + analytical error) which results in the breakdown of the variance as

$$\sigma_C^2 = \sigma_{BDC}^2 + \sigma_S^2 + \sigma_A^2 \quad (1)$$

The maximum acceptable analytical error $L\sigma_A$ is deduced from the statement that the error of measurement at farm must be lower or equal to the error resulting from day-to-day variation

$$\sigma_{FS}^2 + \sigma_{FA}^2 \leq \sigma_{BDC}^2 \Leftrightarrow \sigma_{FA} \leq (\sigma_{BDC}^2 - \sigma_{FS}^2)^{1/2}$$

where

σ_{BDC} = between days standard deviation of concentration.

σ_{FA} = the standard deviation of analytical measurement at farm.

σ_{FS} = the standard deviation of sampling at farm.

Therefore, with L defining the standard maximum limits

$$L\sigma_{FA} \leq (L\sigma_{BDC}^2 - L\sigma_{FS}^2)^{1/2} \quad (2)$$

thus giving, from the sampling limits $L\sigma_{LS} = L\sigma_{FS} = 0.103$ g/100 g of ICAR guidelines, respectively $L\sigma_{FA} = 0.22$ g/100 g for at-line measurements and $L\sigma_{FA} = 0.25$ g/100 g for in-line measurements (with $\sigma_{FS} = 0 \Rightarrow L\sigma_{FA} \leq L\sigma_{BDC}$).

Standard limits for instrument evaluation and quality control

With analytical systems fulfilling different maximum limits of analytical accuracy, consistency and equivalence can only be established through the reducing of variance of the mean estimate which is achieved through repeated recording/sampling. For exact analytical equivalence at limits, the ratio of respective recording number is related to the ratio of maximum limits of analytical accuracy for fat. However it is the same for all the milk component measured.

Thus the correspondence is made through a multiplying factor called equivalence factor

$FE = L\sigma_{FA}/L\sigma_{LA}$ which is applied to all the standard limits used for analyser evaluation and quality control. For at-line analysers it is obtained $FE=2.2$ rounded down to 2 and for in-line analysers $FE=2.5$.

At the end this allows to differentiate three classes of analytical devices for milk recording with different precision and accuracy requirements and different level of agreement for use:

Category 1: Laboratory milk analyser	$FE=1$
Category 2: On-farm milk analyser at-line	$FE=2$
Category 3: On-farm milk analyser in-line	$FE=2.5$

Provided analysers are identically calibrated, the recording/sampling number N_e needed to reach equivalent analytical accuracy as for one sample analysed in the laboratory is given by $N_e = FE^2$ making N_e equal to 4 for at-line analysers and 6 for in-line analysers where analysers meet respective maximum limits.

Cow 480 : Fat% morning and evening

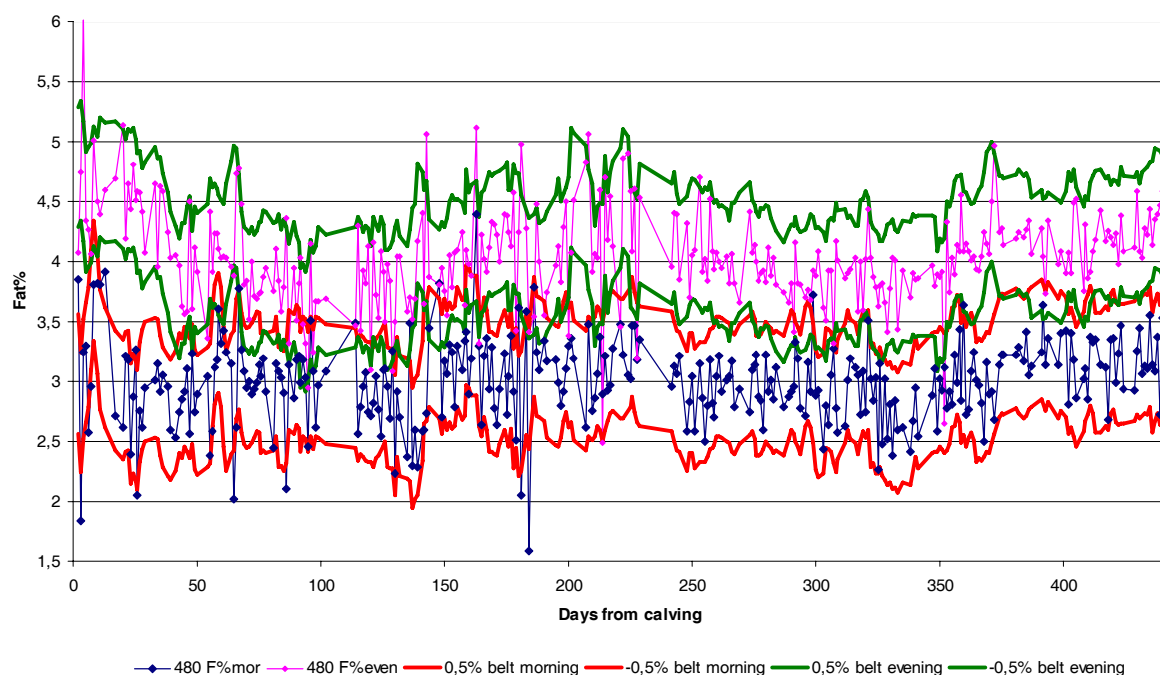


Figure 1. Example of suitability of a $\pm 0,5$ % fat belt as limits of natural between day variation of fat concentration, from data of T. Asmussen (Lattec) and P. Lovendahl (Aarhus University), 2004.

Fat day-to-day variation - Cow 809

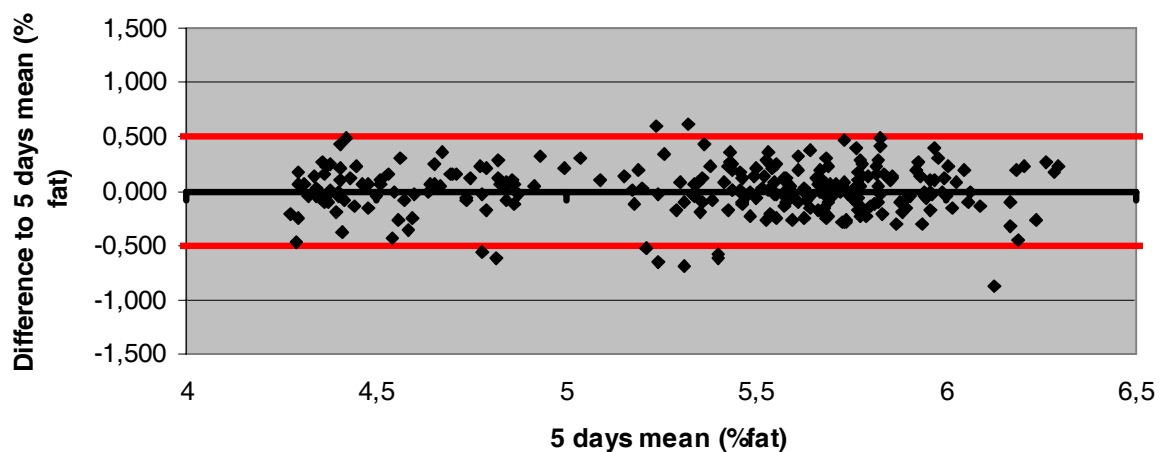


Figure 2. Suitability of a $\pm 0,5$ % fat belt as limits of natural between day variation of fat concentration with 24 hours samples (morning+evening)/2 (from data of Peter Lovendahl, Aarhus University, Denmark, 2004)

Accuracy equivalence for milk recording performance

The larger uncertainty provided by less accurate analytical data in on-farm analysis is expected to be compensated by repeating record sampling. However record replication reduces also the part of error related to the day-to-day variation beside the measurement error (i.e. sampling and analysis).

From equations (1) applied to on-farm and in-laboratory situation and constraint (2), then equivalence number $N = n_{FA}/n_{LA}$, as the ratio of respective records numbers on-farm and in-lab, is calculated by

$$N \geq (2 \cdot L\sigma_{BDC}^2) / (L\sigma_{BDC}^2 + L\sigma_{LS}^2 + L\sigma_{LA}^2)$$

Thus with analytical devices fulfilling the limits stated, $N=2$ records on-farm is sufficient to provide uncertainty of the result average equivalent to one with laboratory, and throughout a lactation, the equivalence total record number is given by multiplying the usual total number by 1.5.

Conclusion

Rules are being defined through adequate recommendation in guidelines to respond to the need of the new situation of on-farm analysis. The principle and the rational for establishing consistency and equivalence between different analytical systems (in-lab/on-farm) in milk recording, have been drawn. They provide keys of correspondence between systems in relation with suitable limits for precision and accuracy indicators used in milk analyser evaluation and quality control and, through this, allows to distinguish three classes of analysers. Thanks to these tools milk recording schemes can estimate the degree of equivalence of dairy genetic data from different systems or adjust genetic evaluation designs with regard to record numbers.

List of references

Asmussen T., Lowendahl P., 2004. Private communication of daily milk recording raw data from Institute of Animal Science. Aarhus University, Denmark. Unpublished.

Young A. Variations in Milk Fat Composition: Why do my milk processor and DHIA tests not always agree? Utah State University, 4815 Old Main Hill, Logan UT 84322-4815, USA.

Impact of new on-farm technologies in dairy cattle breeding

F. Miglior¹, G.R. Wiggans², M.A. Faust³ & B.J. Van Doormaal²

¹Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada, Sherbrooke, QC, J1M 1Z3 Canada

²Canadian Dairy Network, 660 Speedvale Avenue West, Guelph, ON, N1K 1E5 Canada

³Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, USA

⁴ABS Global, Deforest, WI, 53532 USA

Current trends of the dairy industry are quite similar worldwide. Consolidation is occurring as the number of herds decrease and the herd size increases. A general increase of automation is also observed at the farm level. An increasing number of farmers have invested in computerized electronic milking systems or in automatic milking systems (robots). Both technologies record milk weights for every animal, every day, every milking. Additionally, they can record milk temperature and conductivity. In-line analysis technology may also be available soon at the farm level.

S.A.E. Afikim from Israel has unveiled Afilab™, an on-line real time milk analyzer. It provides fat, protein, lactose contents and also indications of classes of SCC. Additionally, it monitors for blood in the milk. The Israeli company states that a combination of above parameters serves as indicators for nutrition and health management of dairy farm. At the same time, Lattec, a 50:50 partnership of FOSS and DeLaval, has unveiled the Herd Navigator™. The Danish company reports that the on-farm milk analyzer provides information for udder health, nutrition, and reproduction cycle monitoring, through the analysis results from LDH (enzyme for early detection of clinical mastitis), urea and BHB (a ketone body), and progesterone, respectively. Thus, information on fat, protein, SCC, lactose, MUN, progesterone, ketosis and mastitis indicators may be available on a daily basis for each cow in the herd. In 2006, Miglior *et al.* (2006) surveyed ICAR member organizations and they reported that most countries (53%) had less than 10% of electronic milk meter farms. However, three large dairy countries, namely Denmark, Great Britain and The Netherlands were among those with at least 30% of farms with the automated technology. The same survey by Miglior *et al.* (2006) reports that 11% of organizations worldwide have at least 2% of robotic farms over the total number of farms. Among this group, Denmark had the highest percentage (10%) followed by Sweden (4%), The Netherlands (3.5%) and Luxembourg (2%).

Many dairy farms invest in automatic data collection to make appropriate management decisions in real time. Stored data can also be transferred electronically to DHI organizations for further processing in order to provide data back to the farmer or to provide input data for genetic evaluation units. Given the availability

of this technology, it is easier now to access more milk weight data than was available previously with traditional milk recording 8 to 10 times per year. With automatic data collection the producer will improve the management of the farm, via the use of more accurate data, more indicators, and greater quality control. Can automatic data collection help genetic improvement? As stated before some trends are clearly observable:

1. more traits are recorded;
2. increasing number of larger herds;
3. larger investment to improve equipment for electronic recording.

Additionally, there is an increased worldwide competition among AI organizations. There is a strong demand for increased data accuracy and comprehensiveness, especially for traits with low heritability.

The needs of genetic improvement programs include a continued participation of producers, maintained or improved data quality and adaptation to change. The benefits to genetic improvement from automatic data collection are threefold: improved accuracy, reduced cost and a larger number of economically important traits. However, there are some tradeoffs in adding traits to genetic evaluations and to selection objectives. Most of those new traits may have low heritability, and it may be difficult to estimate the relative economic value. Furthermore, when too many traits are included in a selection index there could be the risk of dissipating the selection differential. Additionally, new electronic devices will also include recording errors.

As summarized before, on-farm data should provide added value to genetic evaluations. Thus, producers may be compensated for data in the future. Currently, AI organizations may pay for progeny-test daughters few incentives bundled with DHI or type classification programs. A new system may be managed by AI organizations directly, connecting to on-farm computers. Then, data quality could be monitored by AI organizations, and the farm will be regarded as data vendor. Thus, producers could market own data to AI organizations and be compensated based on quality collection. Then, a cooperation among producers, DHI and AI Organizations is needed in order to establish mechanism for equitable resolution of competing interests.

Measures of data quality are also needed. Milk weights could be compared with data from milk shipped. With the advent of genomics, parentage verification will be more common, and it will help to improve the accuracy of animal identification and parentage. However, new protocols to avoid electronic ID misreads will have to be put in place by the manufacturers. Within-herd heritability could be used to measure data quality in large herds; a low value of within-herd heritability could identify herds that lack data quality. Next year genomic evaluations will be available in some countries. The advent of genomics will bring higher accuracy of animal EBV and new opportunities for farmers. A dairy producer may then use genomics to genotype the new born females and/or heifers for parentage verification and for early animal evaluation, which will help to keep only those animals carrying the right combination of genetic markers.

In conclusion, automatic data collection is growing and if properly monitored will increase data quantity and quality. Automatic data collection will impact genetic programs with the availability of more traits, higher accuracy of inputs for genetic evaluations, and tighter connection to the sources of data.

Evaluation of different visual image analysis methods to estimate of body measurements in cattle

A.R. Onal¹, M. Ozder¹ & T. Sezenler²

¹Namik Kemal University, Faculty of Agriculture,
Dept. of Animal Sci., 59030, Tekirdag, Turkey

²Marmara Animal Research Institute, 10220,
Bandirma, Turkey

Body measurements of the animal using for evaluation of individual identification, structural capacity, relationship with yield levels, morphological type and determination of breed characteristics. In generally this measures obtaining by traditional tools. Difficulties on holding some big animals like water buffaloes and cows or half domestic and wild animals may cause some mistakes on collecting and evaluating data. Many researchers specified that using of traditional tools for measuring these kind of animals carry out suspicious results. By the developing computer based technology, using of Visual Image Analysis technology gained in animal science especially for estimating of body measurements and live weight, quality of products etc. The possibilities of use, working principles, advantage and disadvantage of methods which used for estimating of body measurements in cattle by Visual Image Analysis evaluated with the literatures in this study. The researches showed that Visual Image Analysis method absolutely can be use for estimating of body measurements in cattle and other species.

Key words: *Morphometric parameters, Animal breeding, Visual Image Analysis, laser telemeter, laser pointer.*

Morphometric parameters are used for a most important selection criteria in animal breeding. Body measurements of the animal can use for evaluation of individual identification, structural capacity, relationship with yield levels, morphological type and determination of breed characteristics. Also, these measurements have moderate and high heritable (Tien and Tripathi, 1990; Velea *et al.*, 1991). These characteristics give idea about growth levels of animals. Hence it can be use for culling which animal do not reach wanted levels in wanted time periods.

Summary

Introduction

Desired of improvement in animal breeding by morphologic evaluation; the method which using for measure and evaluation of morphologic characters must be practical, fast, objective and comparable also used perfect technology and data processing.

In many researches about determination of body measurements of animals; Lydtin's Stick, Duerst's goniometer and tape measure have been used as a measure tools (Figure 1) (Nilipour and Butcher, 1997). But many researchers specified that using of traditional tools for measuring semi domestic and wild animal as cattle and water buffaloes, carry out suspicious results (Soysal and Kok, 1997; Sekerden and Tapki, 2003).

Digital image analysis and image processing have been used for mainly for determination of morphometric parameters, evaluation and classification of the products in animal science (Mc Donald and Chen, 1990; Gerrard *et al.*, 1996; Li *et al.*, 1997; Cebeci and Bek, 1994; Van der Sluis, 1991).

Many researchers have used to both traditional and digital image process method for estimating of body measures in Holstein and crossbreeds of Holstein and other cattle breed and have described that digital image processing is more suitable, exceptional, fast and economical method (Ozder *et al.*, 2007; Barbera, 1990; Balestra *et al.*, 1994; Negretti *et al.*, 1997; Barbera *et al.*, 1995).

Patterson (1990); Zehender (1996); Pargas *et al.*, (1997) and Trenkle and Liams, (1999) have been used digital image processing method for animal morphometric evaluation and specified this method give possibilities to measuring of animal confirmation; objective, fast and exceptional.

The differences between Visual Image Analysis methods in generally by changing of reference point. Four different methods for Visual Image Analysis were evaluated in this study.

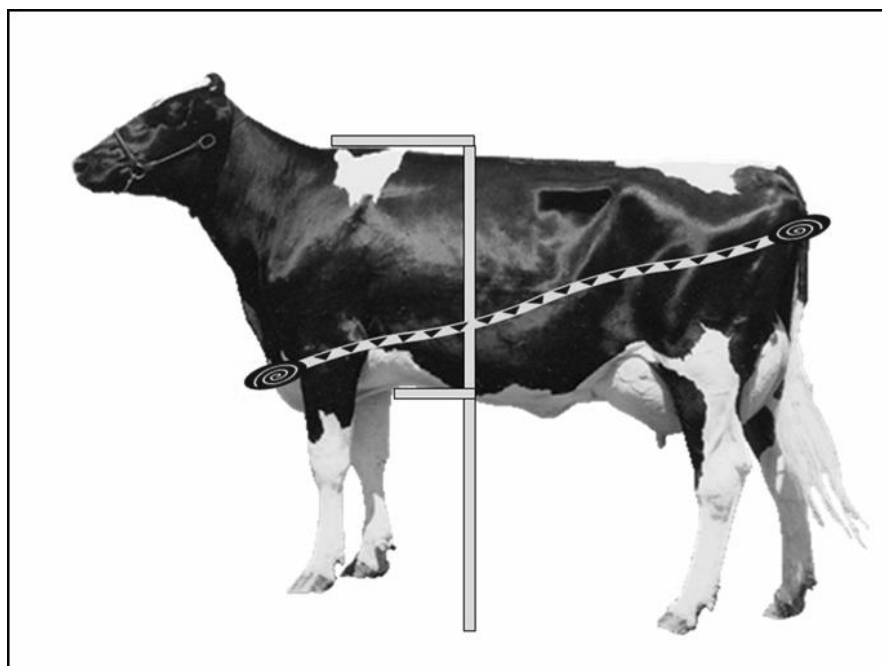


Figure 1. Measuring by traditional tools.

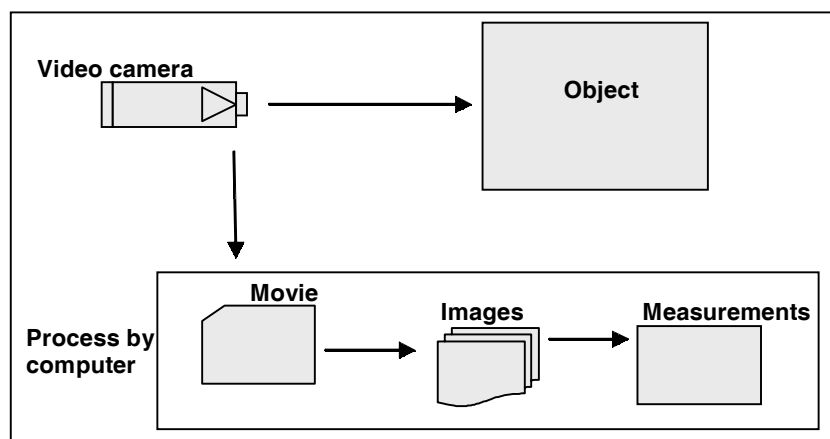


Figure 2. Details of recording scene

The recording is in same procedures for all methods (Figure 2). The visual images getting by video camera and transfer to computer. The digital images captured from movie by an image process software. Body measurements obtaining from images by using of reference points on body surface.

Four different methods has been detailed with their advantage and disadvantage on the below.

A scale which has 20 centimeters diameter and divided per centimeter by colors has been put on body of animals with a view to reference points to help for determinate real measures by computer (Figure 3). This method can be used for domestic herd mostly. Due to the scale should be on surface of animal in this method, it could not be successful for measuring animal as semi-domestic and wild animals.

Methods and differences

Method 1. Using of a constant scale as a reference point

A constant object which is in the same line or as near as the body surface of animal can use as a reference points. Almost the real measurements of the object must be known before. For example banister of cage or any constant object in way where animal to pass (Figure 4). For successfully working of this method animals must be in free stall, cage or animal should pass in gate when recording done, otherwise it could not be obtaining a reference point on image. Due to working of this method is not successfully for semi-domestic and wild animals.

Method 2. Using of constant object as a reference point

The distance between focus of camera and animal is obtaining by the laserteleometer in this method (Figure 5). Inconvenience of this method is calibration is changing for each camera. Cause of that spatial calibration should be make for which camera will use in record before recording. The most important advantage of this method is give possibilities to obtaining of body measurements of semi-domestic and wild animals or animals in pasture.

Method 3. Using of laserteleometer as a reference point

Method 4. Using of the laser pointers as a reference points

Two laser pointers fitted as parallel to the video camera. Distance between two laser pointer must be fixed for example at 35 cm. The distance between two laser pointers should be calibrate in leave point from laser pointers and arrive point as the surface of the animal. Laser wavelength and power were must be chosen in standard ranges for animal rights which described in international rules (Figure 6). The advantages of this method are also similar as a described in *Method 3*. The Inconvenience of this method, diameters of light points changes as larger than leave point by the distance. Due to by long distances resolution of light points decrease.

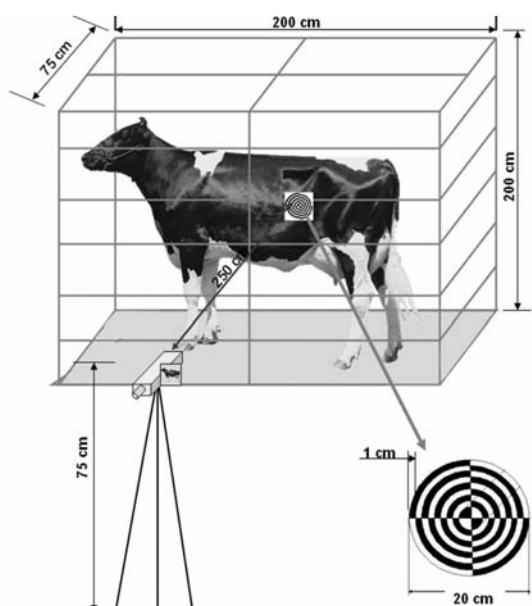


Figure 3. Using of a constant scale as a reference point.

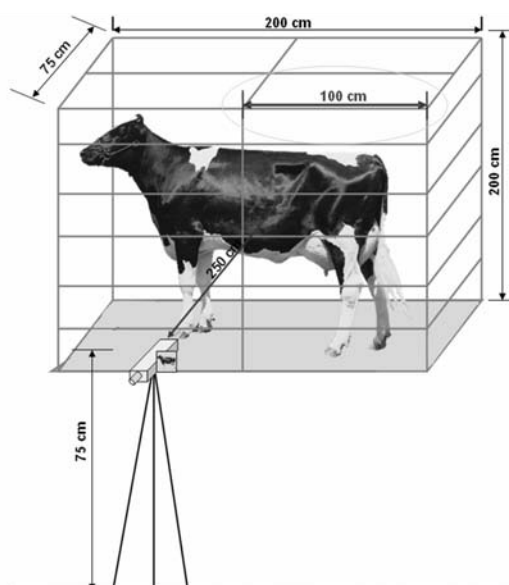


Figure 4. Using of constant object as a reference point.

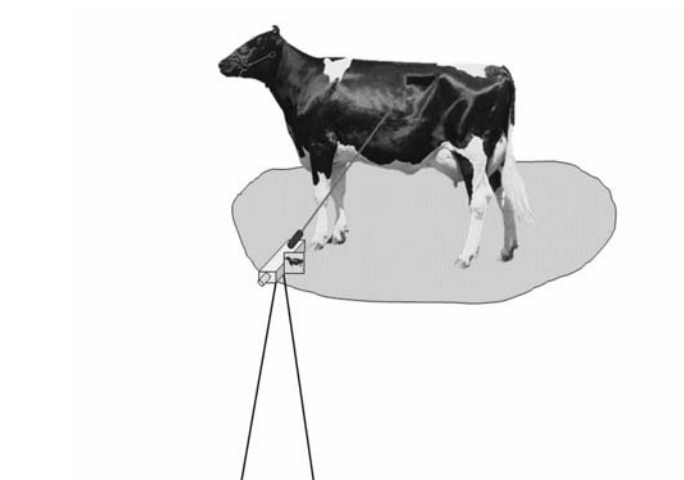


Figure 5. Using of laser telemeter as a reference point.



Figure 6. Using of the laser pointers as a reference points.

The possibilities of using Visual Image Analysis, methods and their differences explained in this study. Each method have advantages and disadvantage to each another. The researches showed that Visual Image Analysis method absolutely can be use for estimating of body measurements in cattle and other species. Also using of the Visual Image Analysis is most practical, fast, and give objective and comparable results.

Results

List of references

- Barbera, S.** 1990. Ann.Fac.Sci.Agr.Univ. Torino Vol.XVI: 101.
- Cebeci, Z. and Y. Bek.** 1994. Yapagi örneklerinin Kalite Kontrolünde Görüntü Isleme Sistemi Kullanimi Üzerine Bir Arastirma. Tarimda Bilgisayar Uygulamalari Sempozyumu 5-7 Ekim 1994. E.Ü.Ziraat Fakültesi-Izmir. S: 1-7.
- Gerrard, D.E., Gao, X. and Tan, J.** 1996. Beef marbling and colour score determination by image processing. J.of Food Sci., 61(1): 145-148.
- McDonald, T. and Chen, Y.R.** 1990. Separating connected muscle tissues in images of beef carcass rib eyes. Transcations of the ASAE, 33(6): 2059-2065.
- Nilipour, A.H. and Butcher, C.D.** 1997. Data collection is important in poultry integrations. Misset World Poultry, 13 (8): 19-20.
- Ozder, M., Dogaroglu, O.K., Tuna, Y.T. and Onal, A.R.** 2007. Utilizing Possibility Of Image Process Technology On The Estimation Of Live Weight And Various Body Measurements Of Slaughtery Cattles. 3rd Joint Meeting of the Network of Universities and Research Institutions of Animal Science of the South Eastern European Countries, Thessaloniki 10-12 February 2007.
- Sekerden, O. and I.Tapki.** 2003. Hatay Ili Anadolu Mandalarinin Köy sartlarinda Büyüme Özellikleri. A. Ü. Ziraat Fakültesi Dergisi. 2003-Erzurum. S: 51-55. Cilt 34, Sayi: 1.
- Soysal, M.I. and S. Kök.** 1997. Bazi Vücut Ölçülerine göre Çesitli Ergin Manda Populasyonlari Arasi Genetik Uzakliklarin Tesbiti. Trakya Bölgesi II.Hayvancilik Sempozyumu. 9-10 Ocak 1997 – Tekirdag S: 103-109.
- Tien, N.Q. and Tripathi, V.N.** 1990. Genetic Parameters of body weight at different ages and first lactation traits in Murrah buffalo heifers. Indian Vet. J., 67(9): 821-825
- Trenkle, A. and C.Liams.** 1999. Use of a Digital Camera to Collect Carcass Data from Experimental Cattle. Beef Research Report-Iowa State University.
- Van der Sluis, W.** 1991. A camera and PC can now replace the quality inspector. Misset World Poultry, 7 (10): 29.
- Velea, C., Bud, I., Muresan, G., David, V., Vomir, M., Cristea, C. and Elisei, L.** 1991. The main milk traits of Romanian buffaloes breed. In Proceedings, Third World Buffalo Congress, Varna, Bulgaria, May 1991, Vol: II, Sofia, Bulgaria, Agric. Academy, 494-499.

Use of the dairy records database to establish benchmarks and estimates for potential economic improvements of individual herds

P. Giacomini

AgSource Cooperative Services, a subsidiary of Cooperative Resources International, Verona, Wisconsin, USA; Shawano, Wisconsin, USA

Use in herd management is the primary reason dairy producers acquire milk recording services. The value of production data for grouping, culling, mating and other decisions has long been the traditional application of the information. Secondary uses of the dairy records database in genetic selection and measurements have also resulted in considerable value to the producer as well as the dairy industry. Publication of high herds and cows for production, as well as average levels for various management attributes has allowed some comparative analysis by individual herds. However, relative position to the high or the average has been more difficult to ascertain, and extension of economic values to those differences have, when available, frequently been outside services provided by milk recording organizations.

The Profit Opportunity AnalyzerSM™ (POA) has been developed to estimate the major areas of potential economic improvement in dairy herd management. The POA takes seven major herd management areas and, when applying user-defined economic values, establishes percentile rankings for individual herds in each of these categories. Relative performance levels are established from use of over 5 000 herds in the AgSource/CRI dairy records database. POA is size neutral and economic potential is measured against the 80th percentile for cohort herds in each individual management category. Level of potential is graphically summarized to illustrate areas of most and least significance allowing the producer to focus on the broadest opportunities to enhance overall herd profitability.

Key words: *Herd management, Economic improvement, Performance recording, Reproduction, Udder health, Genetics, Production.*

Applying dairy records' databases to benchmark herd performance has been achieved to varying degrees. Traditional lists of high herds and cows set standards of performance allow producers to recognize what is possible with excellent

Summary

Introduction

management. Publishing averages for various management measures allows a herd manager to assess performance against the mean. However, these mechanisms are limiting in failing to allow the herd to more precisely, other than above or below average, measure their position against others. Additionally, there have been few attempts to place a financial value on milk recording data to allow for an economic assessment of performance. Some highly sophisticated systems have been developed to establish benchmarks and quantify economic potential. While these systems have been very flexible they have resulted in less standardization, had limited use of graphics, and consequently made education and training to support interpretation and application of results more challenging.

AgSource has attempted to address this need in development of the Profit Opportunity Analyzer™. POA allows users to input basic parameters specific to their situation then reports are presented in standard formats using several graphs and tables. It identifies opportunity for potential economic gain against the 80th percentile of contemporary herds by breed and size in the AgSource records database in each of seven major areas of dairy herd management. Top performance is measured in each of the seven areas rather than overall. This allows the herd manager or consultant to quickly identify what area should receive primary management attention. Results are summarized in graphic form on the first page of the report (Figure 1). Although additional profit may be available from improvement beyond the 80th percentile, this report assumes that at extremely high levels of performance net returns begin to diminish relative to what could be achieved if resources were applied to an area where performance is not as comparatively outstanding.

The POA is designed to be a very broad and standardized evaluation of economic potential. While “Profit” is used in the name, the economic gain from a given management area may come from increased revenue, reduced expense, or a combination of both. The product is not intended to delve into the specific issues that may or may not affect individual herd performance. Rather, it serves as an unbiased analytical tool for identifying operational areas with the most economic opportunity from improvement. Currently, POA benchmarks are being produced only for Holstein herds, although Jersey products are near release and other breed comparisons will be developed.

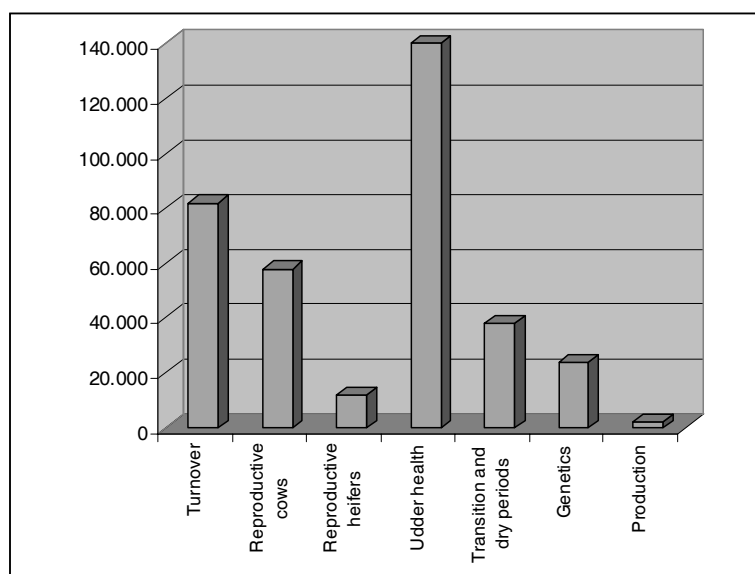


Figure 1. Sample graph profit opportunity summary.

Very little information not already included on the milk recording database is needed to produce a POA. When requesting the product, a simple input form is provided by the herd operator or consultant with the following herd-specific values:

- Net milk price per hundredweight.
- Replacement value per animal.
- Cull cow value per animal.
- Calf value (estimated value per calf at 3 weeks of age).
- Annual Interest Rate (current rate of borrowed capital).

Additional information necessary to evaluate and benchmark herd performance is available from the AgSource records database.

Single page reports are produced for each of the seven major management fields. In each, they are headed by a summary of the herd's position relative to the 80th percentile for their cohort group, and the economic value of the difference between the two positions. Most areas are accompanied by a graph showing trends the previous year or two. These graphs are valuable because, in some cases, the management changes needed to generate improvement may already have been made during the course of the year. But, because the estimate uses a full year of performance in the benchmark, the benefit may not fully show in the analysis. Likewise, deterioration during the past year may suggest even greater opportunity than expressed in the summary. However, the trend line should give an indication of what lag time exists in the data.

The value of improved management of herd turnover is expressed through calculation of turnover the previous year, excluding sales for dairy purposes, and incidence of death loss. This data is coupled with the cow values submitted by the herd, and benchmarked against the top performers of the cohort group. It is accompanied by a bar graph showing early lactation turnover by period across the previous year. Turnover in the first 60 days in milk is an indicator of future annual turnover. Total profit opportunity is reported from the total of the two areas.

The profit opportunity for milking herd reproduction uses herd Pregnancy Rate (percent pregnancies vs. cows eligible to be bred after a 55 day voluntary wait period) as the primary output to assess performance. In applying the economic opportunity against the targeted standard all five of the variable inputs are used as the model calculates impact on milk production as well as the value of surplus (or purchased) replacements, calves, etc. Assuming the herd manager replaces open cows at 318 days in milk with a fresh cow, lower Pregnancy Rates affect the value of replacement costs far more than milk volume. If all breeding dates and pregnancy confirmations are not available on the database, Average Days in Milk can be used as the primary benchmark of reproduction. This is less accurate but can still be used for a broad assessment.

Age at first calving is used as the primary management attribute associated with heifer reproductive management. For Holsteins, the optimum calving age is between 23 and 25 months. Average rearing costs are considered as is the impact on first

Input required

Management fields

Turnover

Reproduction - milking herd

Reproduction-heifers

lactation milk production from a younger or older calving age. The difference between feed savings (reduced rearing costs) of the heifer and production loss during the subsequent lactation is the value of reducing the number of heifers calving at less than 23 months. Loss from heifers freshening older than 25 months is entirely extra rearing costs for the heifer. An accompanying bar graph shows distribution of first calving ages in months during the previous year.

Udder health

Udder health management profit opportunities are measured in terms of milk production losses as well as the value of premiums paid for higher milk quality. Milk losses are calculated for two groups – first lactation and second and greater lactations – by valuing the difference in milk production impact between the herd level and 80th percentile lactation linear somatic cell score (LSCR). The value of somatic cell count (SCC) premiums is estimated using typical adjustments in regional milk markets. The analyzed herd's premium or deduction is made against the premium obtained by herds at the 80th percentile. An associated graph shows the herd level weighted SCC average for the previous two years in addition to the average LSCR for the two lactation groups during the same period.

Transition and dry period

Transition management looks at performance with the herd's Transition Cow Index® and management of the length of dry period. TCI™ is a unique measure of transition cow performance developed at the University of Wisconsin-Madison and licensed to AgSource. Each pound of TCI between herd performance and the 80th percentile equates to 1.27 pounds of additional milk in the subsequent lactation, which is then applied to milk price to establish economic value. Additionally, each pound increase in TCI would be expected to contribute to a decrease in herd turnover. For dry period length, adjustments are made based on the estimated economic impact of excessively short (less than 30 days) or long (over 70 days). A herd TCI graph for the past year is provided which shows the trend in transition cow management.

Genetics

USDA-ARS Animal Improvement Program Laboratory values for Lifetime Net Merit (NM\$) are used to calculate the profit opportunity associated with improved genetics. The milking herd average NM\$ is compared to those in the 80th percentile. As NM\$ is a lifetime estimate, the value is divided by the annual herd turnover percentage to convert it to an annual impact. The herd input milk price is divided by current milk price used for NM\$ to adjust for real value of genetic opportunities. USDA average NM\$ is used if sire is not identified. Clearly, there will be a time lag associated with mating decisions reflected by sires of the milking herd and current service sire selection. A graph associated with this section shows the trend in NM\$ for second and greater lactations cows, first lactation cows, and service sires used for the previous two years. This gives additional information on potential genetic progress from more recent sire selection decisions.

Production

Impact from increased production is simply the difference between rolling herd average (RHA) for milk and that of 80th percentile contemporary herds multiplied times the herd input milk price and the number of cows in the herd. An associated graph shows the two year trend in RHA for the herd and 305 day age standardized milk production for two separate lactation groups.

One additional graph related to increased milk production is included in the POA. This pie chart shows the total opportunity for increasing per cow milk production from the individual herd management areas. Opportunities to increase milk production as a result of improvements in the individual management areas will total the herd-level potential shown in the Production area. Turnover is not included because, in the economic model, reducing high turnover more frequently lowered production while increasing overall profitability. Production increases not specifically attributable to the other individual areas are categorized as “nutrition and management.” If a herd already exceeds the 80th percentile in a given area, the production increase potential is shown as zero. A sample chart is shown as figure 2.

POA is produced either as printed copy or a Portable Document Format (PDF) to allow for electronic distribution to the end user for printing and review. Detail on methodology and calculations are included in every report to allow individual users (producers or consultants) to understand and adjust for herd-specific differences that may be affected by the broad assumptions used in the report.

In test and trial, and since product release, hundreds of POAs have been produced and no herd has yet been identified to be so well managed that it has no opportunity for improved performance in multiple areas of herd management. The greatest value seems to be immediately identified for herds universally regarded as extremely well managed but, at high levels of production and/or profitability, may have failed to recognize their relative opportunity in one or more key areas to make further improvement. One tactic used to illustrate the diversity of management opportunities across herds has been to produce summary graphs for multiple herds included in training groups, without individual identification. In that way, the herd owner is able to recognize their herd but can contrast their opportunities with the unidentified peers. This clearly illustrates operational diversity and the variability of opportunities across herds.

Marketing of POA was initiated in early 2008 and is primarily targeted at organizations and consultants providing services to members of the cooperative. AgSource provides comprehensive training to these organizations and individuals

Marketing and distribution

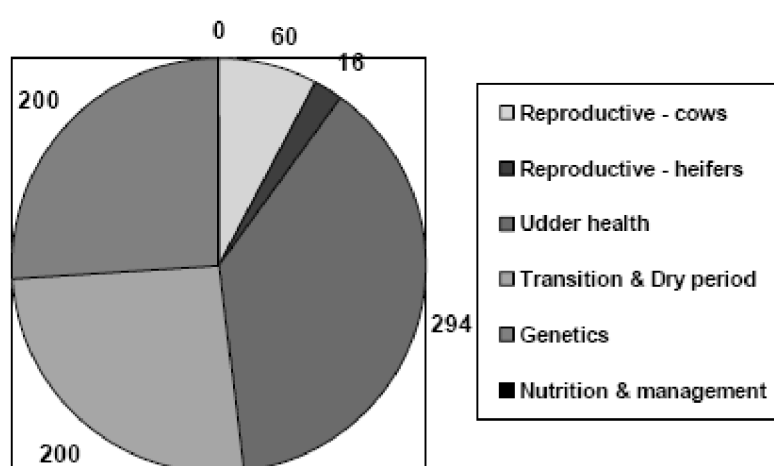


Figure 2. Sample graph opportunities for raising per cow production.

Mobile phone solutions in Finnish milk recording

J. Kyntäjä¹, J. Ilomäki² & S. Tommila²

*¹ProAgria Association of Rural Advisory Centres, Urheilutie 6,
01370 Vantaa, Finland*

*²ProAgria Agricultural Data Processing Centre, Urheilutie 6,
01370 Vantaa, Finland*

ProAgria presents to its customers a mobile phone service for electronic data capture directly in the cowshed. The solution is based on a very simple web page whereby the cows are chosen and milk yields entered. It allows the use of electronic data capture irrespective of the milking and recording technology used. This solution is supported by a web page for checking the data and correcting errors, as well as a text message service to remind the farmer of the testing.

Key words: Milk recording, Mobile phone.

In Finland, farmers have for decades been responsible for testing their own animals, and nowadays approximately 97 % of the ProAgria customer farms have a do-it-yourself milk recording scheme. More than 90 % of them also own the recording equipment utilised in this. Taking into account the existing situation and the fairly long distances in the country, attempts in launching expensive electronic milk meters have not proven successful. Yet there is a great demand for easier milk recording, and also a need for a quicker data transfer. There are also a number of farmers who sometimes fail to test in time to have official records.

Mobile phone technology turns out to be the key to these problems. Most new mobile phones are capable of taking an internet connection, and almost all Finnish dairy farms are within reach of a mobile network. By creating a possibility to enter data to the database directly from the cowshed by mobile phone, we can offer to every milk recording customer a paperless and more modern way to test. We can also remind them of the recording and its details by and SMS scheme where the time of the next message depends on previously input data in the database.

Summary

Introduction

Technical approach

Currently there are two main approaches to design and implement mobile software which has to communicate with a central system. First, one could create *installable software* for specific mobile phone or mobile phone platform (for example, the Series X- platform or Microsoft Mobile Windows operating systems) and create an endpoint to the server which needs to be contacted. In the second scenario, one could create a *web application designed specifically for mobile devices*. In this section we first discuss the benefits and drawback of both approaches and then represent the selected one in more detail.

Installable software for specific mobile phone operating system has several advantages. The software can take advantage of the phone's special abilities. The user interface for instance is dramatically different in for example Apple's iPhone and Nokia's N-series as both have their own ways to handle user input, providing navigation between and within programs etc. If a software was designed and implemented for specific phone model and application framework, it could integrate fully with other applications in that environment. It is also quite often possible to save data in the phone itself which allows the program to operate even when Internet connection is not active. This allows offline working scenarios, which are critical in some cases.

The drawbacks for installable mobile software are evident. If the customers have a variety of different mobile phones from different manufactures, then a service provider would have to create the software for many different platforms and with different programming languages and architectures. The development and maintenance costs could be huge, as well as it could be very difficult to spread new versions of the software. In addition, one would have to create a separate server-side endpoint which would handle the data transfer between the main IT system and the mobile phone. Even a minor change to this endpoint could make the earlier phone software installations obsolete and therefore cause a lot of additional work.

Web application designed for mobile application provides different benefits and drawbacks than installable software. First of all, when basic web controls are used, the software will work well with variety of different mobile phones. If you have a mobile phone which can connect to the Internet and which has a basic web browser, then you most likely are able to use the software. No installations, no extra memory or processing capability requirements. The web server which runs the application would contain all the necessary business critical rules, do validation to user input etc. The software also could be used with a normal computer as the service is actually a very simple web application. In addition, for service provider the maintenance of the software is a lot easier as the improvements installed to the web server are immediately available for every customer.

The drawbacks of a web application are quite intuitive. First of all, you cannot use the software if the Internet connection is not active. This means that offline operations are quite limited and usually non-existent. In addition, if connection failures occur, in worst cases some of the data that user typed in could be lost. A web application is usually unable to store data on the user's device or phone, mainly due to security reasons. This causes problems as there is no local storage for user preferences, or for earlier, unsent inputs. However, most of these issues can be addressed by using special software design patterns and using server-side data storages.

The number of potential users for ProAgria's mobile services is great and the farmers a large number of different mobile phones. There is no single application framework to build on and no single programming language and environment to use. This reality practically dictated that the second approach, the web-based application designed specifically for mobile software was our choice. The system was

implemented with Microsoft .NET 3.5 –framework under which the ASP.NET –web programming section has special routines and controls for mobile phone –based application development. As the input abilities with a mobile phone a quite challenging (usually you have only numeric keyboard), the amount of written text was reduced to minimum and faster controls like dropdown -lists were used.

The following picture (Figure 1) sums up the technical framework and solutions. The users connect to the Internet with their mobile phones or devices and the endpoint is a plain web application running on a Microsoft IIS –based web server. This web server uses services from business logic servers which contain the software components meant for calculation and validation purposes.

The backbone of the system is a central Microsoft SQL Server 2005 database which contains all the necessary data for successful interaction with the actual application and integration to other systems and application on data level.

It was established at an early stage that the practical mobile solution will have to be very simple and very easy to use. Yet in the first pilot version, there was e.g. a question about test milking date which in practical testing caused some misunderstanding and errors. The test milking date can easily be deduced from the

The practical solution

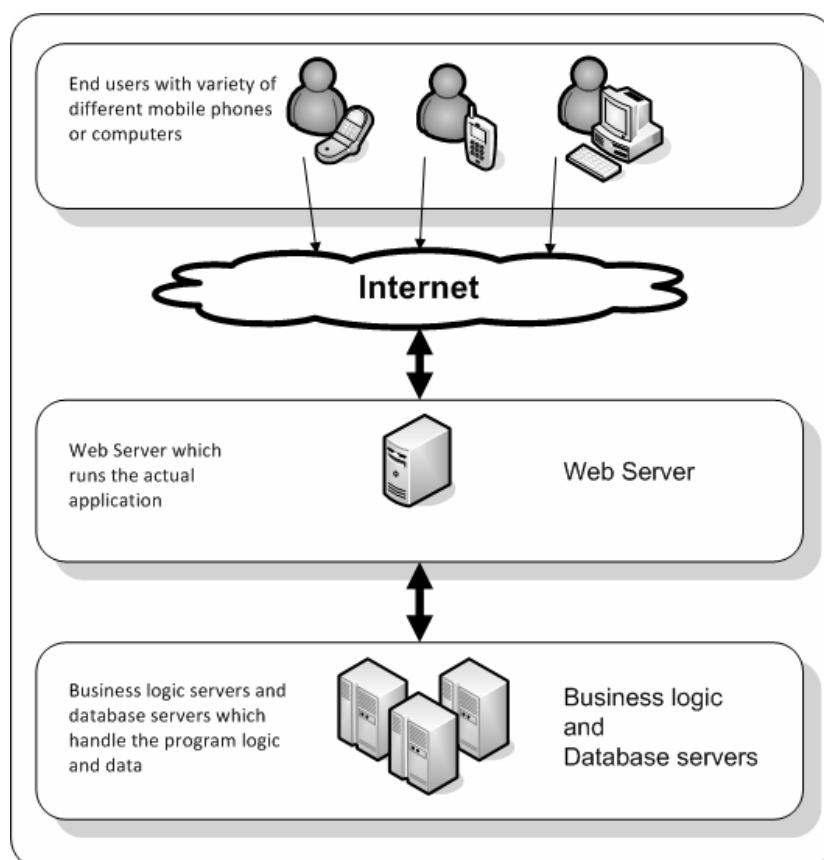


Figure 1. Web-based application architecture

time when the first set of data comes in. It is also crucial that all data goes to the database immediately, so nothing is lost if the phone is lost or suffers breakdown during milking.

The solution used only asks for user (and herd) identification, and then goes on to ask if this very milking is sampled. After that, it produces a list of cows that are in the herd and are not reported to be dry or to already have a recorded milk yield within the last 4 hours. As the milking progresses, cows are chosen from the list and milk yields assigned to each one. Cows thus disappear from the herd list, and the milking ends either when there are no cows left on the list, or when the farmer reports the milking finished. Upon doing that, he receives a list of reported yields. He can correct the data on the ProAgrid website whenever necessary.

Another minor addition to this solution is the ProYield Reminder service that sends four kinds of SMS-s to the farmers who order the service. At 28 days, it reminds him of the necessity to test, as well as whether and how to take samples. At 40 days, it reminds him again that if he will not test now he is going to have unofficial results, and if he already has tested, then he should report it. At 60 days, it reminds the farmer again that if no data comes into the database, there will be no further reminders. In the end of November, it recalls the number of test milkings necessary before the end of the year in order to have official records.

These solutions are entering the market in summer 2008. We believe them to make our milk recording database more real-time by making electronic data capture easier.

Transition cow index™ in progress¹

R. La Croix¹ & K. Nordlund²

¹VP Product Services & Development, AgSource Cooperative Services,
135 Enterprise Drive, Verona, Wisconsin 53593 USA; a subsidiary of
Cooperative Resources International, Shawano, Wisconsin, USA

²School of Veterinary Medicine, University of Wisconsin, 2015 Linden
Drive, Madison, Wisconsin, USA

A tool called Transition Cow Index (TCI™) was released to dairy producers early in the year of 2006. Fourteen factors from the historical Dairy Herd Improvement Association (DHIA) record of each individual cow are used to project her milk yield and projection at her first test date, a date that frequently overlaps with fresh cow disease periods. Deviations from her expected milk yield are calculated and used at the herd level to evaluate the overall effectiveness of transition cow management programs. TCI has been marketed as part of a product entitled Fresh Cow Summary that also includes first test fat to protein ratio (FPR) as a measure of the risk for metabolic disorders, dry cow and heifer udder infection summary as a measurement of udder health, and the trend of cows leaving the herd in the first 60 DIM as a measure of early lactation culling. These four reports provide very objective fresh cow performance monitors to dairy herd managers and their consultants. TCI offers dairy managers and consultants an objective tool to benchmark current programs and monitor the effectiveness of interventions.

Key words; *Transition, Metabolic disorders, Benchmark.*

The transition period, generally defined as the last three weeks of the dry period through the first month after parturition, is recognized as a critical period in the management of dairy cattle herds. Management practices during the transition period can determine health and/or disease events, which in turn, have a substantial influence on performance. The better the transition performance of a dairy cow, the greater her overall health and productivity in the current lactation. Monitoring the transition performance of milk-producing animals is of great importance to evaluating transition program management practices (Nordlund and Cook, 2004).

Summary

Introduction

¹Transition Cow Index. Patent Pending 2006. Wisconsin Alumni Research Foundation

TCI satisfies these needs by accurately predicting an individual cow's early lactation milk performance, and compares this to her actual milk performance which is heavily influenced by health and/or disease in the transition period. The prediction of the individual cow's milk performance is based upon objective measures of her own individual previous lactation performance and current state.

The prediction component of TCI was developed using DHIA data from approximately 500 000 cows in over 4 000 herds and was accessed from AgSource, Inc., a Wisconsin DHIA service. Factors utilized in the model to calculate the expected first test projection include days in milk at first test, previous 305 day milk, days in milk in prior lactation, start of current lactation as calving or abortion, start of prior lactation as calving or abortion, month of calving, SCC linear score at last test of prior lactation, days dry, daily milking frequency current lactation, milking frequency prior lactation, parity number, breed, BST use at herd level, and interaction between BST use and prior 305 day milk. The TCI therefore provides a method for utilizing this prediction to calculate a monitor of transition performance of individuals. At the herd level, summarization of individual cow TCI values can be used to benchmark and monitor transition programs in order to better manage both individuals and herds for optimal health and productivity.

Using TCI to benchmark herd transition programs

TCI values were calculated for all cows and herds in the AgSource record system. Herd average TCI scores for all cows over a one-year period of time are presented in figure 1 as a histogram. Because the predicted first test value used in the TCI calculation represents the average performance of cows with similar histories (age, prior production, days dry, prior SCC, etc.), it is not surprising that the median herd average TCI value is near zero. However, the range indicates that herd level

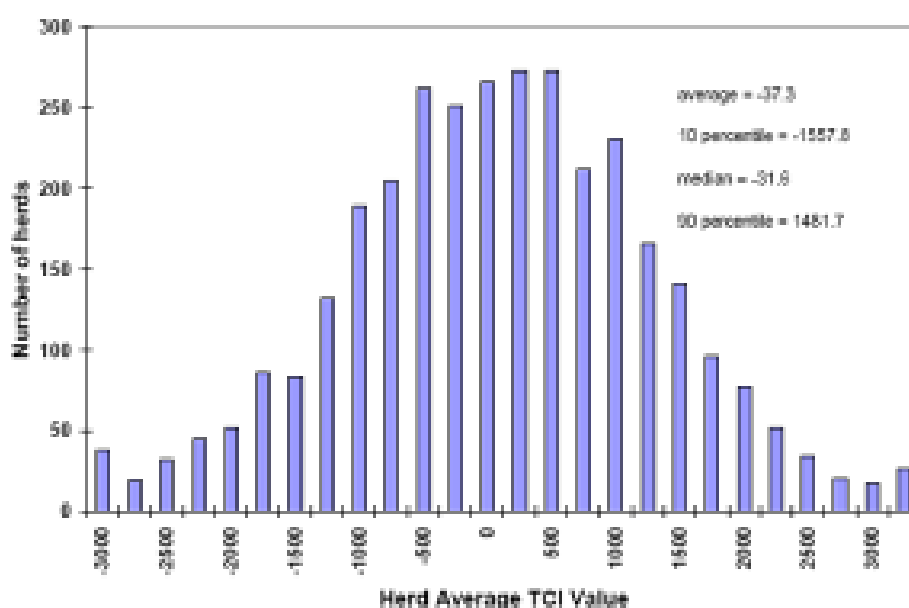


Figure 1. Histogram of herd average TCI values of AgSource dairy herds.

transition programs have an effect of more than 7 000 lbs on first test projections. Benchmarks are expressed as TCI levels for the 90th percentile, average, and 10th percentile levels (Nordlund, 2006).

The effectiveness of individual herd transition programs can be benchmarked relative to the rest of the industry. The ability to identify truly superior transition cow management programs is valuable to people who study the issue, and it can be helpful in motivating change to improve transition management on commercial dairies.

A graph developed to monitor transition management programs over time is shown in figure 2. Each dot on the scatterplot represents single cow and shows her TCI value above her most recent calving date. Individual cows with TCI's greater than $\pm 6\,000$ lbs are not shown on the graph, but are included in the summary calculations (Nordlund, 2006).

Because the TCI index attempts to quantify the herd transition management program, it is important to not overlook individual cows that fail. In the system that has been developed with AgSource, all cows that have a first test milk recorded are included in the TCI calculations and graph for 365 days. This includes cows that are culled from the herd or that die after the first test date. It also includes cows where milk was measured, but were given a "condition affecting record" (CAR) code. For example, if a fresh cow is sick with mastitis, dairy managers can code that test date with a CAR code and that (usually low) milk weight is not used in the cow's lactation record. However, that milk weight is used to compute the TCI value.

Use of TCI to monitor herd transition management programs

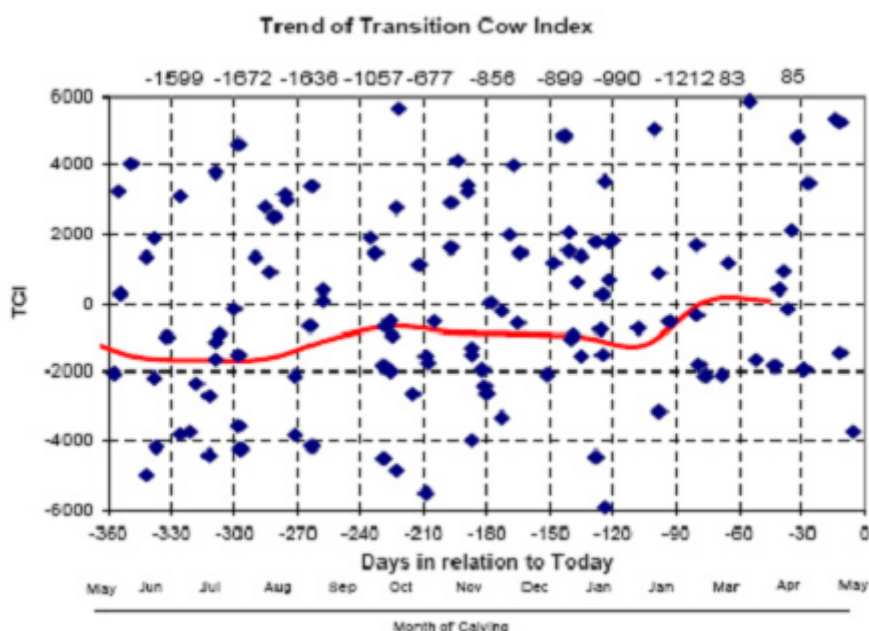


Figure 2. Transition Cow Index graph showing herd trend over the past year.

The line that runs through the middle of the graph represents a rolling average TCI value and above the graph are TCI averages for 90 day intervals. In herds of greater than 250 cows, the calculated value represents all calvings over the prior 30 days. The line and value serve as ongoing monitors of transition cow management for the specific dairy. In the example shown in Figure 2, the dramatic increase in TCI shown by cows calving in January was associated with modifications of the fresh cow pen and included enlargement of the freestalls from 45 inches wide to 50 inches and an increase from 22 inches feedbunk space per cow to 27 inches.

Continued research

Continued research with TCI has led to modifications that were introduced to AgSource's Fresh Cow Management Report in November 2007. One result is that the herd average TCI scores went up by about 700 lbs. The average transition management program now has a TCI score of about zero, not a minus 700.

The modifications are due to more cows in the database used to develop the equations. The original equations were developed using cow records available at the time. However, production from cows with Condition Affecting Records (CAR) codes on their first test date and also cows that did not complete a 305-day lactation were not included. Using available records, the average TCI score was zero. However, cows with CAR codes and cows culled before completing their lactations tended to have below average first tests. As TCI was applied to all cows, the addition of the poorer first tests resulted in an industry average TCI of about minus 700 pounds. The availability of additional data has allowed for an improved set of equations and an industry average of about zero (Nordlund, 2007).

Economic impact of TCI

With almost two years of TCI data, the impact of improved transition management on survival and subsequent milk production can be measured. In terms of survival, a cow with a TCI of zero has a 63% chance of calving again. This was pleasing to find because the industry average annual culling rate is 37%, which means that 63% survive. The likelihood of a cow with a TCI of 10 000 calving again is 86%, while a TCI of -10 000 is associated with 32% likelihood of survival. Stated another way, an additional 1 000 pounds TCI increases the likelihood of surviving to start a new lactation by 2.7%.

Increasing TCI is also associated with increased milk production for the entire lactation. Using cumulative milk produced during the lactation, each additional pound of TCI is associated with 1.27 pounds of additional milk. Cumulative milk is the total milk produced in the lactation, regardless of length. For example, a cow may produce 1 000 pounds of cumulative milk before being culled at 30 days. These data provide the basis for estimating the economic impact of TCI scores. At the herd level, increasing the average TCI score by 1 000 pounds is associated with an increase of 1 270 pounds of milk while at the same time lowering the turnover rate 2.7%. Converted into dollars using recent prices, a thousand pounds change in your herd's TCI is worth approximately \$250 per cow per year.

The spread between better and poorer herd average TCI scores is about 4 000 lbs, meaning there is an opportunity of almost \$1 000 per cow per year for some herds from improving transition cow management. If your herd average TCI score is zero, taking the steps to reach an average score of 2 000 would yield approximately \$500 extra income per cow per year. Potential income at this level will cover the costs of improved transition cow care (Nordlund, 2007).

There is much to learn about managing transition cow programs and TCI provides a tool for that research to continue. Preliminary information suggests that the primary risk factors are very different in freestall herds compared to tiestall or stanchion housed herds. In a recent study in freestall herds with more than 300 cows, the most important management factors for improving herd average TCI scores were provision of approximately 30 inches of bunk space per cow in both the prefresh and fresh cow pens, screening programs based upon appetite and attitude of the fresh cows, social stability or no pen moves in the period 3-10 days before calving, and larger size stalls (at least 48 inches wide) and sand or deep loose bedded stalls after calving. In general, dairy managers achieve higher TCI scores in tiestall and stanchion herds than in larger freestall herds. In tiestall barns, most managers typically provide almost 48 inches of bunk space for fresh cows, can easily identify fresh cows with problems very early, and limit pen moves that result in cows continually establishing their social order rather than eating. However, weaknesses in tiestall herds are commonly found in prefresh nutrition and prefresh housing. In addition, it is uncommon to find stall surfaces as comfortable as sand in tiestall barns. In the next few years, with the use of TCI, dairy producers served by AgSource have an opportunity to identify the most important transition management practices, make the changes needed and move their fresh cow health and performance ahead of the rest of the industry (Nordlund, 2007).

Key management factors that affect TCI

The technology transfer agency of the University of Wisconsin, WARF¹, has applied for a patent on TCI. WARF has licensed TCI to AgSource, the Wisconsin based DHIA service and will also be licensing the technology to other dairy record services. AgSource has released TCI as part of a new Fresh Cow Summary that also includes first test fat to protein ratio (FPR) as a measure of the risk for metabolic disorders, dry cow and heifer udder infection summary as a measurement of udder health, and the trend of cows leaving the herd in the first 60 DIM as a measure of early lactation culling. These four reports provide very objective fresh cow performance monitors to dairy herd managers and their consultants.

Distribution of TCI by milk recording organizations

AgSource has been successful in marketing the TCI product Fresh Cow Summary by;

- Training Field Staff and key Influencers.
- Providing financial incentives to stakeholders to sell the product.
- Providing written materials describing how to interpret and use TCI data.
- Focusing on larger herds as primary market.
- Providing a three month no-charge trial period to all customers to allow them to integrate TCI into their management system.

Thirty percent of dairy herds larger than 100 cows have adopted TCI as a management tool; larger herds show adoption levels as high as 62%.

¹Wisconsin Alumni Research Foundation, Madison, Wisconsin; patent applied for, TCI inventors Kenneth Nordlund, Thomas Bennett, Garrett Oetzel, Murray Clayton, and Nigel Cook.

**List of
references**

Nordlund Kenneth V, Cook Nigel B. 2004. Using herd records to monitor transition cow survival, productivity, and health. *Vet Clin North Am Food Anim* 20: 627-649.

Nordlund, Kenneth V. 2006. University of Wisconsin-Madison School of Veterinary Medicine, "TCI Basics," Presentation to "Evaluating and Improving Transition Cow Management" Seminars in five Wisconsin locations, February and March 2006.

Nordlund Kenneth V. 2006. 39th Proceedings American Association Bovine Practitioners. St. Paul, MN. Sept. 20-24, pp. 139-143.

Nordlund, Kenneth V. 2007. Transition Cow Index Turns Two years Old! Fact sheet.

Østergaard S., Gröhn Y.T. 1999. Effects of Disease on Test Day Milk Yield and Body Weight of Dairy Cows from Danish Research Herds. *J Dairy Sci.* 82: 1188-1201, 1999.

Rajala P.J., Gröhn Y.T. 1998. Effects of Dystocia, Retained Placenta, and Metritis on Milk Yield in Dairy Cows. *J. Dairy Sci* 81: 3172-3181.

Reneau J.K. 1986. Dairy Herd Performance Evaluation: Mastitis Monitors. *Proc Am Assoc Bov Prac* 18: 38-49.

SAS Institute. 2001. User's Guide. Statistics, Version 8.2 Ed. SAS Inst., Inc., Cary, NC, USA.

Wiggans G.R., Powell R.L. 1980. Projection factors for milk and fat lactation records. *USDA Dairy Herd Improvement Letter* 56: 1.

Wiggans G.R., Dickinson F.N. 1985. Standardization of NCDHIP dairy cattle lactation records. National Cooperative Dairy Herd Improvement Program Handbook, Fact Sheet G-2. National DHIA, Columbus, OH, USA, 1-7.

A new approach to perform analysis of milk components incorporating statistical methods adapted in a real time sensor

G. Katz & N. Pinsky

Afimilk (S.A.E. Afikim), Kibbutz Afikim, 15148, Israel

New sensors emerging from technological breakthroughs avail higher resolution of data. A configuration for on-line real time acquisition of milk components is presented. Within this apparatus, a new developed milk analyser is installed at each milking stall. Acquisition of milk components such as fat, protein and lactose is performed in the same automated configuration that milk weight is acquired by milk meters and at the same time resolution. Means to address the value of the new acquired data are offered.

Summary

Key words: *On line milk analysis, Milk meter, Automated data collection system.*

The basic production unit of the dairy industry is the cow. Management of the dairy farm requires monitoring a heterogeneous collection of basic production units. The key for managing heterogeneous ensembles lies in making decisions based on the collection and evaluation of different observables regarding the individuals which constitute the ensemble. Modern dairy farming evolves around data and the means to collect it. Manual observation and recording is gradually being replaced by automated collection and recording of data that is available with new emerging technologies.

Introduction

Milk recording is a main element for monitoring production. It involves measuring the milk weight and its components. Currently, milk weight recording is automated and performed by electronic milk meters. However milk components recording is still performed manually.

This paper presents new technology for automated milk components analysis and recording.

In this approach, on-line milk analysers (Afilab™) developed in S.A.E. Afikim and A.R.O (Figure 1), are installed in the parlour at every milking stall. The system records milk composition of every cow in real time during the milking session.

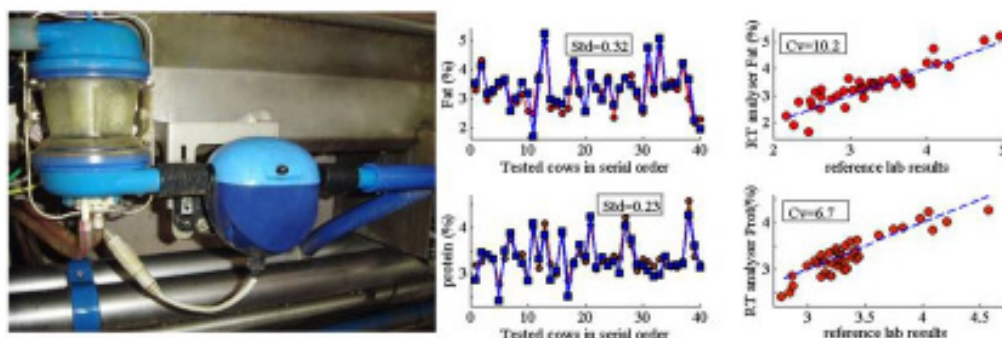


Figure 1. The real time milk analyser installed in the parlour on the milk-pipe following the milk meter (left panel). A comparison between the RT analyser and the reference lab is presented (middle and right panels). Top: protein. Bottom: fat. Middle panel: y axes represent component concentration, X axes represent cow's milk sample, the line represent RT analyser results and the reference lab results. Right panel: X-axes represent lab results, Y-axes represent RT analyser result.

The advantages of this new milk analyser are:

- Free flow.
- Non-interfering measurement.
- Continuous real time acquisition of milk components.
- Data is acquired automatically for the individual cow during its milking.

The evolution of milk recording began with the Dairy Herd Improvement (DHI) in the USA as data recording source for herd management in 1920's. It was followed by the proportional mechanical flow milk meters in the early 1960's and the electronic milk meters in the late 1970's. The last essential step of the identification and PC data collection was introduced in the 1980's.

The new on line milk analyser is another step in the progress of in-parlour milk automated recording scheme. The new sensor presented couples the "lab" to the milking parlour allowing daily real time automated measurements of milk components at each stall.

Multiple sampling compared to periodic sampling

Currently, analysis of milk components is not performed daily. A periodic test is conducted manually at intervals of 4-6 weeks. On a periodic test day, milk samples are collected from every individual in the herd and sent to a chemistry lab for analysis.

An "In-parlour at every stall" sensor is required to be robust, low cost and easy to maintain. These demands impose some tradeoffs. The main one lies in the accuracy of the sensor which is inferior to that of the lab. Its strength arises from two major advantages it has over the current method: automated collection of the measured data and the frequentness of the measurements.

Automated data recording is objective, accurate, consistent, effortless and accessible. Therefore, these two advantages of the sensor compensate for the trade-offs derived from its robustness.

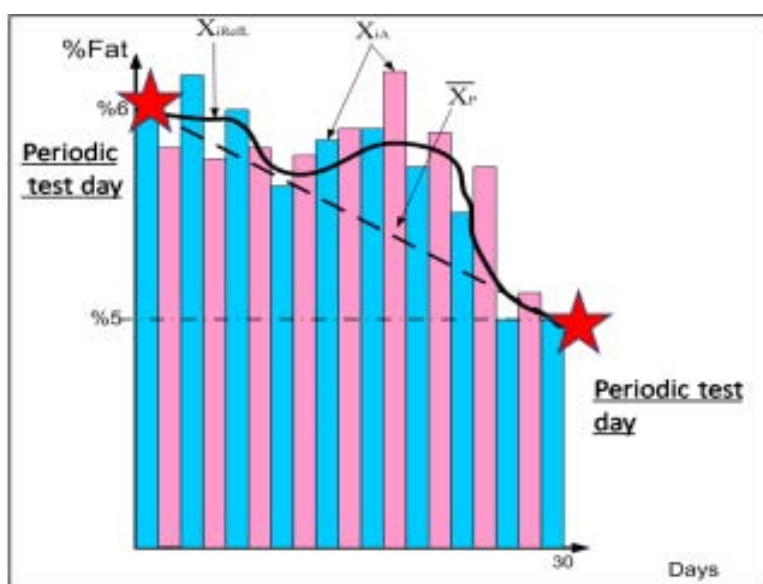


Figure 2. An illustration of the multi-sampling approach compared to the periodic test day. X-axes represent time, Y- axes represent fat concentration. Each bar represents a daily analysis performed by the RT analyser. The stars connected by the dashed line represent the periodic test day analysis. The full line represents the real fat value. The true picture is given by integrating over the continuous line representing the true fat value at each day. The sum of the bars and the integral of the dashed line represent multiple sampling and periodic test days' approaches, respectively.

A mean to compare low accuracy multiple sampling to single high accuracy sampling is required. The concept of such a comparison is illustrated in figure 2. The compared is the average milk fat of a cow for a duration of 30 days.

The following equations are offered to derive the accuracy needed from a device performing multiple measurements to match a device performing a single accurate measurement:

- σ_T^2 - the general total variance of any measurement system
- σ_p^2 - the average of all the cows variances in that period of time
- σ_L^2 - the variance of the lab accuracy
- σ_c^2 - the total variance between cows
- σ_A^2 - the total variance of the RT analyzer and n - the number of multiple measurements (number of milkings) of the RT analyzer.

Assuming all variables are independent, eq a. describes the total variance of an evaluation of a periodic test (the way it is performed today)

$$a. \sigma_T^2 = \sigma_C^2 + \sigma_P^2 + \sigma_L^2$$

If we neglect the error of the lab, eq b. describes the total variance of the suggested system with the multiple measurements of the RT analyzer:

$$b. \sigma_T^2 = \sigma_C^2 + \frac{\sigma_P^2 + \sigma_A^2}{n}$$

From the equality of a. and b. we can subtract from both of the equations .
equation c is derived from the equality of b. and a.

$$c. \sigma_P^2 = \frac{\sigma_P^2 + \sigma_A^2}{n}$$

is extracted from equation c and determines the variance to be permitted for a number of n multiple measurement of the new method with respect to a single measurement.

$$d. \sigma_A^2 = (n-1) \cdot \sigma_P^2$$

In this approach, the required accuracy from multiple measurements to properly address the current periodic measurement is dictated by:

- Duration between test days.
- Total variance between samples of the individual.
- The average variance of all samples for a given duration.

The variance of the measuring system must be smaller than the variance of the measured ensemble in the given time.

In a research reported here (Maltz, 2007), an attempt was made to determine the required accuracy from a multiple measurement system to properly represent a single measurement system. In this research (A.R.O farm Israel 2006, 88 Holstein cows), milk samples from three daily milking sessions these cows were sent to the reference lab for a duration of 10 days.

Figure 3 demonstrates the maximal fluctuations in fat concentrations during this period of time for all the cows. The mean standard deviation of all 88 cows was 0.57% for fat and 0.36% for protein. The mean peak-to-peak fluctuations per cow of this herd for that duration was 2.16 % for Fat and 1.55% for protein.

Evaluation and maintenance

This new apparatus for milk analysis differs from the current methods. Means to evaluate its performance should be determined to assure the value of the data acquired in this method is not inferior to the current method.

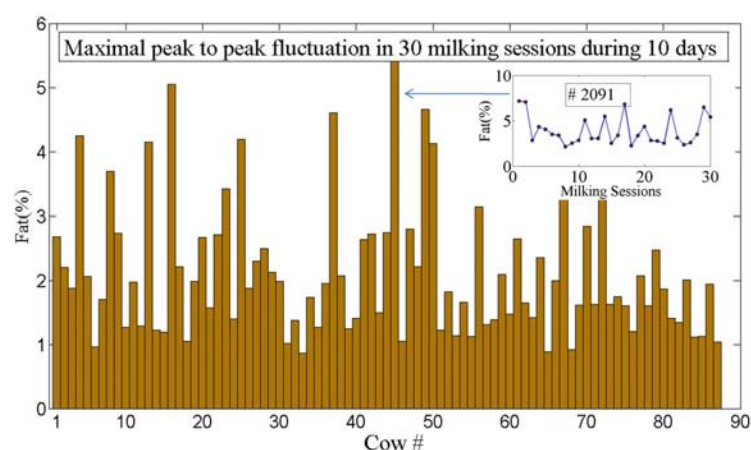


Figure 3. The maximal fat(%) fluctuations per cow over 30 milking sessions in 10 consecutive days. Y axes - fat(%) X-axes - Cows. Insert: the fat(%) fluctuations over 30 milking sessions for cow2091(emphasized by arrow). X-axes milking session, Y-axes: fat concentration.

A pragmatic viable approach is needed for evaluation, maintenance, surveillance and control of the global system for real time in parlour milk analysis. This approach should consider a multiple-sensor system (as opposed to the current method the sensor is not a stand-alone analytic device but part of an automated data collection system) like the milk meter and fat sampler (see configuration in figure 4.).

The following principles are offered for such a framework:

- Analyzing devices are coupled to ICAR approved milk meters and ID.
- Statistical ensemble for the evaluation of a single device should be large enough to represent normal dispersion.
- Evaluation of concentration analysis of RT devices should be a comparison to ICAR approved Lab test.
- Sample for comparison should represent directly the cow's milk. (Not from an ICAR approved fat sampler).
- The main evaluation parameters should be based on average deviation and variance of errors (similar to evaluation of fat samplers and milk meters).
- Required accuracy of device should be derived from the natural fluctuations of milk components concentration between different cows at a defined duration.
- The evaluation of the global system is acquired by performing the same evaluation as that of one device on the herd.

Within the above principles, figure 4 demonstrates evaluation of the milk analysis of the total parlour as it shows the mean error of 10 milking sessions for each cow with respect to the reference lab. This mean error represents the error of the total system and includes the natural variance between the different analysers since cows are not designated to permanent stalls.

Since the analysis method is based on multiple sensors it enjoys the advantage of the system conducting checking over its self. This allows more flexible calibration and validation requirements. This principle is demonstrated in figure 5 (Left panel). A malfunction at a single stall is detected when all the cows that are being milked at that stall have a large deviation from their three days running average.

When the deviation from average occurs for a single cow at a stall or for the total herd (Right panel) then there would be no malfunction in the analysis but a real change in the milk butterfat is detected.

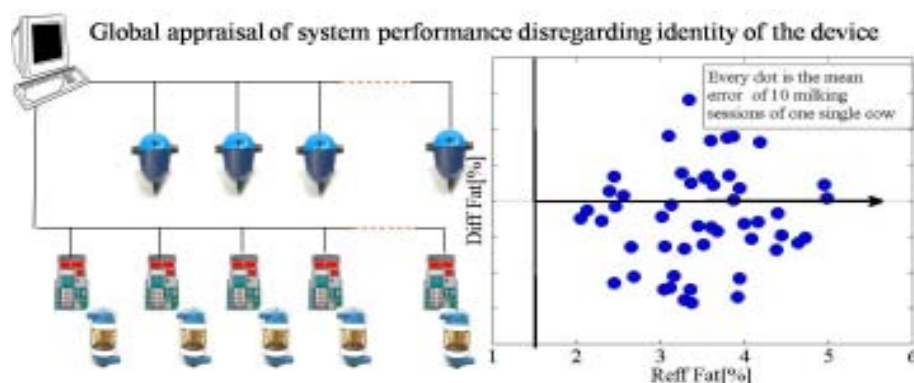


Figure 4. Left - The configuration of an automated in-parlour milk weight and analysis system including ID, milk meters and RT milk analysers at each stall linked to a central computer.

Right - An example for evaluation of total parlour performance (the configuration on the left). The fat analysis mean error of the system. Mean error over ten consecutive milking sessions for each of the individuals comprising the herd.

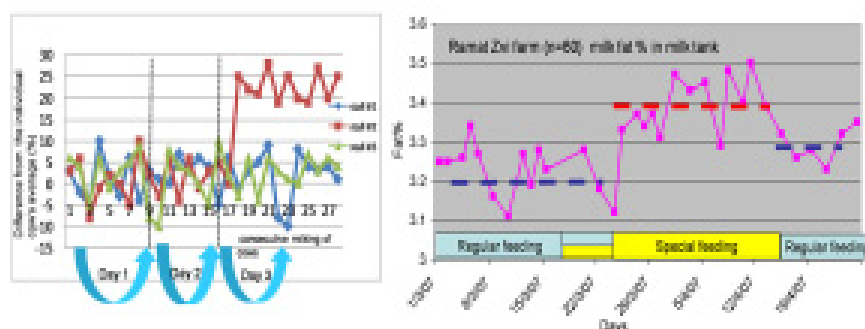


Figure 5. Left panel - follow up in time of the deviation from the fat average of cows at three different stalls shows a malfunction of the device at stall 2 at day 3 (X-axes days and cows, Y- axes the difference of each cow from its running three day average). Right panel - fat (%) (over a year) in the milk tank as calculated by the RT analysers- shows real changes of fat (%) for the herd due to change of feed.

Conclusion

The approach presented here for milk analysis evolves from the automated milk recording approach employing electronic milk meter identification and PC data collection.

Addressing this new approach for milk analysis should be different then the protocol used for the current method. The data of interest collected by the system is milk analysis of the individual cow and since this is a multi-sensor system the evaluation should be made upon the performance of the total system and not a single sensor. The guiding principles to address it should evolve from the guiding principles used to address the milk meter and fat sampler since it employs the same configuration.

The high resolution of the data acquired may in the future contribute much more applications than the traditional uses for milk components periodic analysis. This is due to the fact that a low resolution motion picture may unravel a story that cannot be observed in a high resolution snapshot.

References

Maltz, E. 2007. Private communication.

Cow body shape and condition scoring

M. Klopčič¹, A. White², R. Boyce², P. Polak³,
D. Roberts⁴ & I. Halachmi⁵

¹University of Ljubljana, Biotechnical Faculty, Depart. of Animal Science,
1230 Domžale, Slovenia

²IceRobotics Ltd., Logan Building, Roslin BioCentre, Roslin,
Midlothian EH25 9TT, Scotland, UK

³Research Institute for Animal Production,
Slovak Agricultural Research Center, 949 92 Nitra, Slovakia

⁴Scottish Agricultural College, Dairy Research Centre,
Crichton Royal Farm, Dumfries DG1 4SZ, Scotland, UK

⁵Institute of Agricultural Engineering, Agricultural Research Organization,
Volcani Center, Bet Dagan 50250, Israel

A feasibility study on the introduction of body-shape parameter that may lead, in the future, to the development of automatic monitoring of cow body reserves on live animals is described. The hypothesis tested in this study was that 'if a cow is fatter, her body shape is more likely round and therefore the parabola may fit better to the shape of a fat cow rather a thin cow'. About two hundred Holstein-Friesian cows were monitored by means of thermal camera, ultrasound and manual body condition scoring (BCS). An image-processing model was designed and implemented. The model calculates the parameter of cow body shape. The model outputs were validated against two reference measurements (1) the thickness of fat and muscle layers using ultrasound and (2) manual BCS. The correlation found in this study between the thermal camera and the fat and muscle thickness was 0.47. The thermal camera overcomes some of the drawbacks of a regular camera. The hooks and the trailhead nadirs of a thin cow diverge from the round shape drawn by the parabola. Further research is needed in order to reach full automatic, accurate, body conditioning scoring.

Key words: Dairy cows, Body conditioning scoring (BCS), Thermal camera, Image processing.

Body condition scoring (BCS) is a technique to estimate an animal's body energy reserves, i.e. estimating fatness or thinness of cows according to a five-point scale (Edmondson *et al.*, 1989). In dairy herds, BCS is probably the most useful management

Summary

Introduction

tool available to dairy producers for assessing the nutritional status of cows. Additionally, there are nutritional, health, reproductive, and environmental decisions made by the dairy producer that have a major impact on changes in body reserves for both individual cows and groups of cows. In high-yielding dairy cows, the peak of daily feed intake usually occurs after the peak of milk output. This state is commonly known as negative energy balance and is negatively associated with a range of health traits (Gillund *et al.*, 2001) and fertility (Dechow *et al.*, 2002). Body condition influences productivity, reproduction, health and longevity (Heinrichs and Ishler 2004). However, the current method of measuring BCS is manual and subjective. The values depend on the individual who performs the measurements; sometimes, the same individual might score the same cow differently, depending on the previous cows seen (Schröder & Staufenbiel, 2006). BCS is a time-consuming task especially on large farms and requires trained labour (Leroy *et al.*, 2005; Pompe *et al.*, 2005). Therefore the development of a device for automatic, objective monitoring of body condition scoring is of interest.

A number of feasibility studies have already been conducted into the automation of BCS, including those by Coffey *et al.* (2003), Leroy *et al.* (2005), Pompe *et al.* (2005), Ferguson *et al.*, (2006), and Bewley *et al.*, (2007, 2008). Coffey *et al.* (2003) examined the feasibility of automating BCS using structured red laser light to create light lines across the tail-head areas of a cow. After software enhancement of the resulting images, body shape curves were extracted after and were identified using image editing software and a mouse to isolate the lines. Leroy *et al.* (2005) used a digital camera, positioned 1.5-2 m from the rear of the cow, to obtain a silhouette image of the cow from the tail to the legs. The contours of nineteen predefined points, corresponding to visual features were incorporated to determine the overall contour of each animal from which a BCS was calculated. Pompe *et al.* (2005) used a black and white charge coupled device (CCD) camera and a line laser to collect a series of images from the rear of a cow. A 3 dimensional analysis of the images provided an outline of the left pin, left hook, and tailhead. Ferguson *et al.* (2006) investigated the ability to assign a body condition score (BCS) to a dairy cow from digital photographs or videos. Bewley (2008) used a digital camera placed above a stationary weighting station.

The literature reports the developments of an objective method for BCS by using ultrasound (Mizrach *et al.*, 1999; Williams, 2002). Mizrach *et al.* (1999) used a method for the measurement of subdermal fat thickness in dairy cows by digitizing cross-sections of ultrasonic scans. Williams (2002) describes ultrasound applications as a non-invasive method for estimating fat and muscle accretion and body composition in live cattle. Keren & Olson (2007) used thermal imaging software for cattle grazing on a winter range. Sharony (2003) described the application of a digital camera for the purpose of BCS (not thermal camera and using a different algorithm). Kriesel and McQuilkin (2005) described the high potential for applications of digital camera (not thermal) for the dimensional measurement of livestock, but not for BCS. As yet, none of the above scientists or practitioners has reached the point of a low-cost commercial device capable of working in every farm. Therefore the aim of the study was to advance the development of automatic and objective monitoring of cow body reserves. The hypothesis tested in this study was that 'if a cow is fatter, her body shape is more likely to be rounded and therefore a parabola may fit better to the cow shape. The hooks and the trailhead nadirs of a skinny cow diverge from the round shape drawn by the parabola'.

Data were collected at the Scottish Agricultural College Crichton Royal Farm in Dumfries, Scotland, UK, September 2007. The study involved 186 cows; the nutrition, selection strategy and management are described in detail by Pryce *et al.* (2001).

The reference numbers for body reserve were:

1. the thicknesses of the muscles and fat layers, and
2. manually observed body condition scoring.

The thicknesses of the muscles and fat layers was measured using the ultrasound device, Sonovet 2000 (Medison, Korea), linear probe PB-MYL 2-5/1 170 mm, 2-5 MHz, 96 elements. The Sonogram of the longissimus dorsi muscle (LDM) was carried out from the 12th and the 13th vertebrae. The thickness of the fat is the distance between the dorsal fascia of LDM and the ventral layer skin. The converting factor from the thicknesses of the fat and muscle layers (in millimetre, so called Tot_mm) on the 1-5 BCS scale was:

$$\text{Ultrasound scoring} = 5 * [\log(\text{Tot\_mm}) - 3.6] \quad (\text{Eq. 1})$$

where:

Tot_mm was the thickness of the fat and muscle layers (in millimetre, not pixels); 5 and the 3.6 normalized the ultrasound units into the 1-5 BCS scale; the log function depressed the large variation found in the our ultrasound measurements in the large values.

The manual BCS was obtained from two different technicians according to a five-point scale (Edmondson *et al.*, 1989). BCS was measured manually in the same week as measurement by ultrasound and by thermal camera.

A thermal camera (FLIR systems®, model InfraCAMSD™, detector type: focal plane array 120 x 120 pixels, spectral range 7.5 to 13 µm) was linked to the barn ceiling above the cow body weighing scale, at the exit of the milking parlour. The cow identification was done electronically (RFID); the antenna being built into the weighing scale.

The video from the camera was divided into frames by using 'Serif movie plus 4'. The frames were manually observed in order to select the best frame from each cow. Identified frames, those that were associated with cow number and fitted to the cow timing on the scale, were fed into Matlab software for image processing analysis (Anonymous, 2005).

The size of the frames were 787 x 576 pixels, 1.3 MB BMP files. Figure 1 presents the raw thermal images of two typical cows, a fat cow and a thin cow. The images were read using Matlab's 'imread' function then degenerated to grey (using the 'rgb2gray' function). The black cursors that indicate the temperature points of measurement were erased by using the 'roifill' function. The place where the cow was expected to be found was cropped from the original picture to a specified rectangle (Matlab's 'imcrop' function). 'Imcontour' found that unique cow individual boundary and 'polyfit' fitted a parabola to the boundary of each individual cow.

The visual difference between fat and thin cows is presented in figure 2. It can be seen (Figure 2) that in a fat cow, only the tailhead diverge from the rounded shape of the fitted parabola, while many deviations can be noticed in a thin cow. The converting factor from 'distance from parabola' to 1-5 BCS scale was:

Materials and methods

$$TBCS = 5 * 9 * (1./MAE) \quad (Eq. 2.)$$

where:

TBCS stands for thermal BCS.

9 is the best fit ever reached in our herd (i.e. only the tailhead diverges from the parabola shape),

5 normalized the model output into 1-5 BCS scale.

The distance between the fitted parabola and the cow contour was expressed in MAE (mean absolute error) units. If a cow is thin, her body shape is less round and therefore her MAE is larger.

The Image processing is presented by Halachmi *et al.* (2008). The process is almost automatically executed. The selection of the best frame for each cow requires further programming.

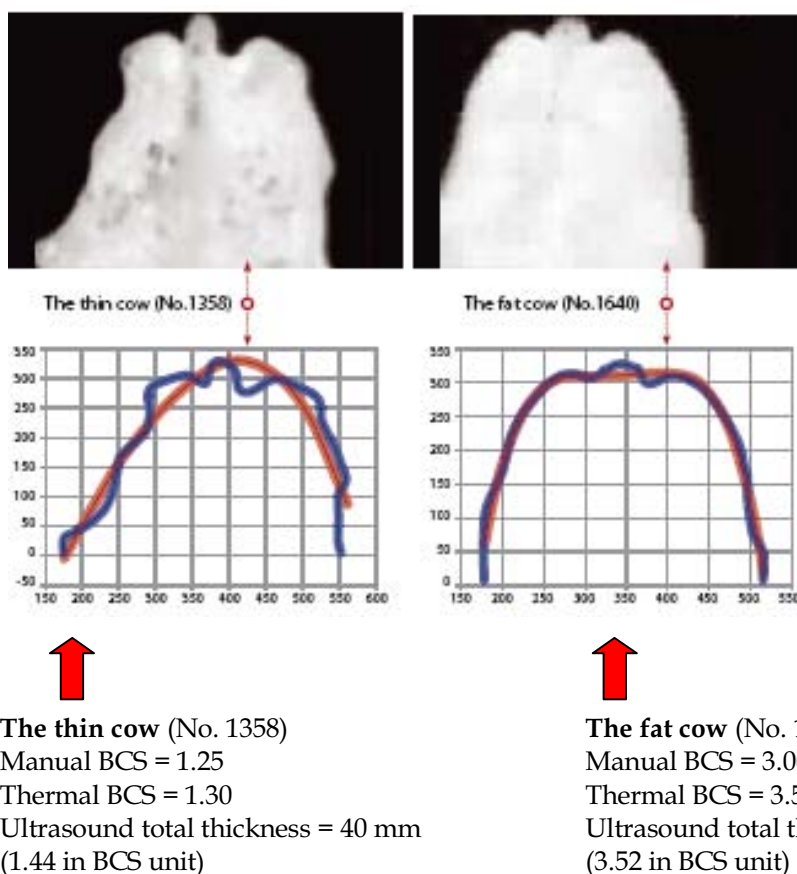


Figure 1. Model inputs: thermal images taken from bird's eye view (upper pictures). Model outputs: Cow contour vs. fitted parabola (lower pictures).

The model outputs measured by the thermal video camera (so called Thermal Body Condition Scoring, TBCS) were compared with two reference values:

1. the thicknesses of the fat and muscles layers measures by the ultrasound; and
2. the manual body conditioning scoring (so called BCS).

It can be seen that a correlation between the TBCS and the manual BCS; was 0.32 and a correlation between the TBCS and the thickness of fat and muscle layers (which was measured by the ultrasound) was 0.47. A correlation between the ultrasound and manual BCS was 0.38. All the correlation coefficients are presented together with the averages and standard deviation in table 1. The higher correlation was found between TBCS and the ultrasound (0.47).

The consistency check is presented in table 2. The daily averages are within 5% difference and the variation is within the 10% limits. The correlation between days reached 0.67.

In table 3 it can be seen the manual BCS had a constant shift of 0.25 score. Technician 2 was higher.

Results

Table 1. Model validation: comparison thermal camera, ultrasound and manual body condition scorings.

	Average	STD	Cross Correlation Coef.		
			BCS	TBCS	US
BCS	2.17	0.30	1	0.32	0.38
TBCS	2.14	0.62		1	0.47
US	2.16	0.69			1

US=Ultrasound; TBCS= Thermal camera; BCS=Manual body condition scoring

Table 2. Model validation: Consistency check; thermal camera body condition scorings (TBCS) measured in days 1, 2 and 3.

	Average	STD	Cross Correlation Coef.		
			Day 1	Day 2	Day 3
Day 1	1.99	0.62	1	0.46	0.67
Day 2	1.99	0.66		1	0.61
Day 3	1.95	0.59			1

Table 3. Consistency check of the reference numbers; manual BCS measured by technicians 1 and 2.

	Average	STD	Cross Correlation Coef.	
			Technician 1	Technician 2
Technician 1	1.99	0.41	1	0.78
Technician 2	2.22	0.33		1

Discussion

Coffey *et al.* (2003) found that the correlation between tail head curvature and condition score was 0.55 and between Pin bone and body condition score was 0.59. In our case, the correlation between the manual BCS and TBCS was 0.36 and between TBCS and ultrasound measurements was 0.48. The difference between the studies (Coffey *et al.*, 2003 and the current study) can be explained by the number of cows rejected from the database. In our experiment only 9 cows (had hooks or tailhead exceed the visual area of the camera lens) were removed from the database. Coffey *et al.* (2003) reports that out of 190 cows, only 36 cow images were suitable for data extraction. Perhaps, if more cows had been filtered out of the database our correlation might have been higher. Coffey *et al.* (2003) advised the development of body shape parameter. The correlation between both technicians (observers) was 0.78 and is in agreement with the result reported by Ferguson *et al.* (2006). Their correlation coefficients between observer 1 and observer 2 through 4 were 0.78, 0.76 and 0.79, respectively.

The thermal camera's zoom should capture most of the cow back. Those cows where the hooks were outside the visible area were most likely to be expelled from the model. This result is in agreement with Bewley (2008) who also found the hooks as the easiest to identify and that angles around the hooks and tailhead have the highest correlations with BCS. Correlation between USBCS (Edmondson *et al.*, 1989) and hook posterior angle is 0.52, between USBCS and hook angle is 0.48 and between USBCS and tailhead is 0.31. Correlations between UKBCS (Lowman *et al.*, 1976) and all three body traits are lower, but still significant. Correlation between UKBCS and hook posterior angle is 0.46, between UKBCS and hook angle is 0.33 and between USBCS and tailhead is 0.19. Higher camera installation or wider lens angle may improve the results. A 3D picture, i.e. using an additional camera, may further improve the accuracy of the device.

The main advantage of using a thermal camera over a regular digital camera is the ease of recognition of cow pattern; in our case almost all the cows' images were suitable for analysis. However, our measurements were taken in September in Scotland, at 5am to 8am. Perhaps in hot climate conditions, such as in an Israeli summer, where the ambient temperature might be similar to the temperature of the cow skin temperature, identifying the cow contour may not be so easy. In further research the influence of hot climate on the cow appearance by the thermal image should be investigated.

In further research, body shape parameters should be adjusted for other dairy breeds, beef or dual purpose breeds. It is also possible that the parabola shape might not fit other breeds, if a thin cow also exhibits a rounded shape.

In the development of a new device, accuracy may be validated against a reference number. The manual BCS is commonly used but is subjective. It depends on the technician and has a discrete-points scale i.e. 1.5, 1.75, 2, 2.5 etc. Our study proposed a continuous scale. Trying to correlate the results from continuous scale (the new device output) with a discrete-points (manual BCS, our reference number) is statistically inferior. Grouping the continuous results into discrete clusters may improve the statistics but degenerate important feature of the new device – the continuous scale. Ultrasound has a continuous scale and our initial thought was that it is objective. During the experiment in the barn and later whilst analysing the results in the lab it appeared, however, that an ultrasound operator might influence the results by (1) not returning to the exact location in every different cow and (2) by his reading of the ultrasound picture. In further research, the selection of the objective

method is crucial if higher statistically correlation is desired. Both drawbacks the discrete-points scale and the subjective issues can be overcome by examining a large number of cows using several technicians on one occasion.

Our study focused on dairy cattle, however, a low-cost, moveable device, after calibrating its parameters, may be potentially applicable to beef cattle. Applications include informing decisions on moving a group from one grazing field to another grazing field, and in determining the optimal marketing time in feedlots. The functionality of “a low cost, automatic and accurate BCS” in daily herd management is not under question. However for genetic purposes, Pryce *et al.* (2006) stated that there would be little benefit in including BCS as an independent trait in the breeding worth dairy index. BCS is already included in New Zealand as a predictor in the genetic evaluation of fertility; breeding values for BCS will be estimated routinely from the fertility model.

A thermally sensed body condition scoring model was designed and implemented on a small number of cows. Results suggest that further study with more cows may open the gate for automating the BCS monitoring. Suggestions were made for further research. The onus is now on industry to take the methodology described above through further steps into a commercial working device in every dairy farm.

The study was financed by EC Marie Curie Actions TOK-IAP project OptiScore, number MTKI-CT-2005-029863. Thanks to IceRobotics staff Robert Boyce, Antonia White Oliver Lewis, Chloe Capewell and Robin Dripps for the technical support, especially at early mornings in the farm. We appreciate the scientific advice given by the other partners of the project: Dr. Jeffrey Bewley (Kentucky Univ. USA) Dr Peter Løvendahl, and Dr. Lene Munksgaard (Aarhus University Faculty of Agricultural Sciences, Research Centre Foulum, Denmark).

Anonymous, 2005. The Image Processing Toolbox User's Guide. Matlab, Publisher: The MathWorks, Inc. 3 Apple Hill Drive, Natick, MA 01760-2098 USA.

Anonymous, 2007. <www.serif.com/MoviePlus/MoviePlus4/index.asp>

Bewley J.M., A.M. Peacock, O. Lewis, D.J. Roberts, M.P. Coffey & M.M. Schutz, 2007. Estimation of body condition score in dairy cattle using digital images. V: 58th Annual Meeting of European Association for Animal Production (EAAP), <www.eaap.org/Dublin/Sessions/Session_21.htm>

Bewley J.M., 2008. Automated body condition scoring of dairy cattle: technical and economic feasibility. PhD Thesis. Purdue University,

Bewley J.M., A.M. Peacock, O. Lewis, R.E. Boyce, D.J. Roberts, M.P. Coffey, S.J. Kenyon & M.M. Schutz, 2008. Potential for Estimation of Body Condition Scores in Dairy Cattle from Digital Images. J. Dairy Sci. 91: 3439-3453

Conclusion

Acknowledgment

List of references

Coffey, M.P., T.B. Mottram & N. McFarlane 2003. A feasibility study on the automatic recording of condition score in Dairy Cows. Proc. of annual meeting of the British Association of Animal Science. Held in York March 2003. Publisher: The British association of animal science. BSAS. PO Box 3. Penicuik. Midlothian EH26 0RZ. United Kingdom. ISBN 0906562 41 4

Dechow C.D., G.W. Rogers & J.S. Clay, 2002. Heritability and correlations among body condition score loss, body condition score, production and reproductive performance. J. Dairy Sci. 85: 3062-3070

Edmondson A.J., I.J. Lean, C.O. Weaver, T. Farver & G. Webster, 1989. A body condition scoring chart for Holstein cows. J. Dairy Sci. 72: 68-78

Ferguson J.D., G. Azzaro & G. Licitra, 2006. Body Condition Assessment Using Digital Images. J. of Dairy Sci. 89: 3833-3841

Gillund P., O. Reksen, Y.T. Grohn & K. Karlberg, 2001. Body condition related to ketosis and reproductive performance in Norwegian dairy cows. J. Dairy Sci. 84: 1390-1396.

Halachmi I, P. Polak, D. Roberts & M. Klopčič, 2008. Cow Body Shape and Automation of Condition Scoring. J. of Dairy Sci. 91: 4444-4451.

Heinrichs A.J. & V.A. Ishler, 2004. Body condition scoring as a tool for dairy herd management. Extension Circular 363, Pennstate, pp. 14.

Keren E.N. & B.E. Olson, 2007. Applying thermal imaging software to cattle grazing winter range. J. of Thermal Biology 32: 204-211.

Kriesel M.S. & G.L. McQuilkin, 2005. Apparatus and methods for the volumetric and dimensional measurement of livestock. United States Patent 20050257748 Filing Date: 05/19/2005 (Saint Paul, MN, US); Publication Date: 11/24/2005.

Laven R., 2002. Condition Score Management. NADIS, 2002, pp. 4.
<www.mdcfmp.org.uk/uploadeddocuments/Disease/Condition%20Score%20and%20Disease.pdf>.

Leroy, T., J. M. Aerts, J. Eeman, E. Maltz, G. Stojanovski, and D. Berckmans. 2005. Automatic determination of body condition score of cows based on 2D images. In: Precision Livestock Farming '05. (Ed.: Cox S.), Wageningen Academic Publishers, The Netherlands: 251-255.

Lowman B.G., N.A. Scott & S.H. Somerville, 1976. Condition scoring of cattle. Bull. No. 6, East Scotland Coll. Agric., Anita. Prod., Advisory Dev. Dep.

Mizrach A., U. Flitsanov, E. Maltz, S.L. Spahr, J.E. Novakofski & M.R. Murphy, 1999. Ultrasonic assessment of body condition changes of the dairy cow during lactation. Transactions of the ASAE, Vol. 42, No. 3, pp. 805-812.

Pompe, J. C. A. M., V. J. de Graaf, R. Semplonius, and J. Meuleman. 2005. Automatic body condition scoring of dairy cows: extracting contour lines. In: Book of Abstracts 5 ECFA-2ECPLF. JTI-/Swedish Institute of Agricultural and Environmental Engineering, Uppsala, Sweden: 243-245.

Pryce, J.E., M.P. Coffey & G. Simm, 2001. The relationship between body condition score and reproductive performance. J. of Dairy Sci. 84: 1508-1515.

Pryce J.E., B.L. Harris, D.L. Johnson & W.A. Montgomerie, 2006. Body condition score as a candidate trait in the breeding worth dairy index. Proceedings of the New Zealand Society of Animal Production 2006, Vol. 66: 103-106.

Schröder U. J. & R. Staufenbiel, 2006. Invited Review: Methods to Determine Body Fat Reserves in the Dairy Cow with Special Regard to Ultrasonographic Measurement of Backfat Thickness. J. Dairy Sci. 89(1):1-14.

Sharony D., 2003. Imaging system and method for body condition evaluation. European patent 1537531. filing date: 07/27/2003 (Israel). Publication date: 06/08/2005 .

Williams A.R., 2002. Ultrasound applications in beef cattle carcass research and management. J. Anim. Sci. 80 (E. Suppl. 2): E183 – E 188

**Special session on
"Presentation of ICAR Sub-Committees,
Working Groups and Task Forces"**

Report of the ICAR Subcommittee on Animal Identification

O.K. Hansen

*Danish Agricultural Advisory Service, Udkaersvej 15,
Aarhus, Denmark*

The Sub-Committee had the busiest years ever of testing of electronic identification devices. Manufacturers started requesting performance testing of transponders. Test protocols have been available for years but no one used them. When the requests started coming in test configurations had to be built up which occurred in the middle of the transition process from ICAR test protocol into ISO standard. Results from the first performance tests should be available shortly.

The Sub-Committee started performance tests of plastic ear tags. The first round of test has now reached the field test phase and the second test round is about to start. The test document has been reviewed and a test protocol for plastic ear tags with electronic identification has been developed.

These years in many countries the responsibility for identification and registration of animals and animal movements moves from breeders organisation to competent authorities due to the demand for traceability. For this reason the Sub-Committee is now increasingly active in offering experience and expertise to national and regional authorities.

At the ICAR session in Kuopio, Finland, 2006, Dr. Reinhard Pauw, Germany, who was then chairman, left the subcommittee. Dr. Pauw had served as chairman of the Sub-Committee for more than 10 years and had to stop due to the ICAR bylaws. Current Sub-Committee members want to thank Dr. Pauw for his leadership and for his contribution to bringing the ICAR test and approval programme to its current high level. Dr. Pauw received ICAR's Distinguished Service Award

The current Sub-Committee members are:

- Folkert Onken, Germany (since 2007).
- Henry Richardson, UK.
- Jay Mattison, USA.
- Louise Marguin, France.
- Ole Klejs Hansen, Denmark (Chairman).
- Peter Bailey, Australia.

Summary

Introduction

According to its terms of reference the Sub-Committee covers the following subjects related to identification and registration:

- Preparation of guidelines for the relevant appendices of the International Agreement on Recording Practices with regard to ID-device testing.
- Stimulation of new developments in and report on new equipment, procedures and methods dealing with:
 - Electronic identification.
 - Other identification devices.
 - Standardised layout of ear tags for individual animals
- Advising the ICAR Board on approval of:
 - Institutes serving as ICAR test-centres
 - Identification devices used in individual animal identification

ICAR's philosophy is to provide tests that can be directly accepted by most authorities and user groups worldwide. This means that the tests must be quite comprehensive covering characteristics that all users want. The adoption of one worldwide main test standard is to the benefit of users, authorities and manufacturers, even if the test might initially be more expensive than individual national tests needed to access markets in different countries. The economies follow when national authorities accept the ICAR standard as an alternative to their own.

Test of electronic identification devices

2006 and 2007 were the busiest years ever in ICAR's conformance testing of transponders and 2008 is well on its way to also become quite active. After many years of testing and mainly using electronic identification (EID) in pets we are now moving into the phase of using EID in farm animals and in official identification and traceability systems. In EU it was expected that EID of sheep and goat might be mandatory as of January 2008 and manufacturers prepared for that, which may be the reason for the high activity levels in 2006 and 2007.

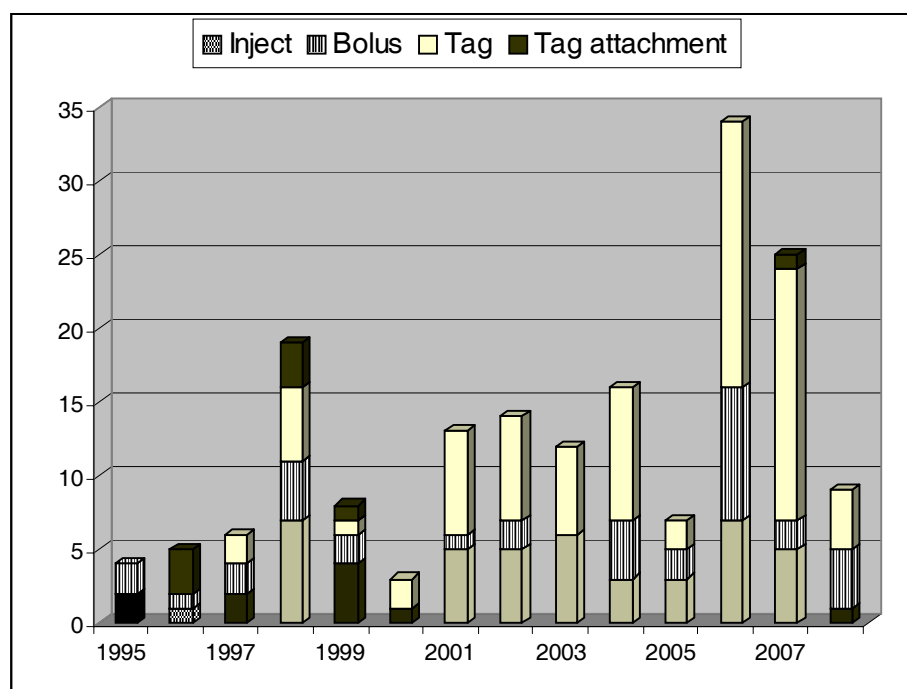


Figure 1. Transponders approved per year.

The conformance test shows whether the transponder works in conformance with ISO standards 11784 and 11785 but it does not provide information about the level of performance. ICAR has for years had protocols for performance testing, but no manufacturers asked for testing until 2007. This again may have been triggered by the expected EU requirements in which performance tests according to the ICAR test procedure are needed for all EID tags to be used in sheep and goats in EU. Here also transceivers (readers) must be conformance tested. ICAR is also active in this field.

As long as the use of EID was voluntary and only for on farm management purposes it might be left to the market to choose tags performing to the level needed. However, when EID becomes part of mandatory and official identification systems there is a need for also testing performance.

Currently ICAR has a list of transponders lining up for performance test. The test has been delayed due to the transition of the ICAR test protocols into an ISO standard, but the first transponders performance tested by ICAR should be available within weeks.

Please find further information about tested products on the ICAR website www.icar.org

ICAR is currently working on improving the website with all conformance tested transponders so that users will be able to search products based on several criteria.

In 2004 ICAR published a test protocol for conventional plastic ear tags with or without machine readable (visual) printing. This test protocol was inspired by the comprehensive test programme used in France. Also for plastic ear tags with electronic identification a protocol has been developed and published based on the protocol for conventional tags. These test protocols include:

1. Preliminary assessments.
2. Laboratory test.
3. Preliminary field test (3 months).
4. Extended field test (9 months).

Tags must pass successfully each step before being allowed to enter next step. Preliminary approval may be granted after successfully passing the preliminary field test and full approval after successfully passing the extended field test. Normally the whole test period should be about 18 months.

Test of plastic ear tags is an ICAR activity outside the agreement with ISO. However, ISO standards are used as much as possible in the protocols. This is to incorporate as much technical expertise as possible in the protocols and to support the international acceptance of the ICAR test and approval programme.

The first test round for conventional ear tags was invited in the summer of 2006. Tests started in early 2007 and the tags remaining in the test are now entering the phase of field tests. First preliminary approvals are expected by the end of 2008. Second test round will be invited this summer.

This first round demonstrated the need to define in more detail parts of the preliminary assessments and another few minor adjustments in the test protocol. These elements are included in the proposed new versions of the protocols to be approved at the general assembly this year.

Test of plastic ear tags

Test Centres

According to the ICAR-ISO agreement ICAR shall set up approval criteria for test centres for testing of EID devices. ICAR must approve all centres complying with the approval criteria and applying to become an ICAR approved test centre. In order to achieve international recognition of the test ICAR requires test centres to be ISO 17025 certified and ISO 17011 audited. This has to be done by third party since ICAR is no certification organisation or audit organisation. On top of those requirements ICAR has set up further criteria for obtaining ICAR approval.

The three current test centres will have to qualify by the same criteria. Current test centres are:

- IMAG test centre in Wageningen, The Netherlands (ICAR test centre for EID since 1995).
- JRC test centre in Ispra, Italy (IDEA project, ICAR test centre since 2002).
- CETIM, Nantes, France (official French ear tag test, ICAR test centre since 2006).

ICAR and ISO

In the 90's ICAR established a liaison to ISO as an "organization that makes an effective contribution to the work of the technical committee or subcommittee." Until 2007 ICAR had an informal agreement with ISO on testing and approval of ISO 11784/11785 conforming devices. Since 2007 ICAR has a formal agreement with ISO to be the ISO Registration Authority for the International Standards ISO 11784 and ISO 11785. Tests have to be done in approved test centres and ICAR has to set up approval criteria for such centres.

The Current ICAR test protocols for RFID devices were developed in cooperation with the ISO working group on animal identification (ISO TC23/SC19/WG3) providing technical expertise. The protocols were developed in a ten year period from early 1990's covering

1. Conformance of transponders.
2. Conformance of transceivers (readers).
3. Performance of transponders.
4. Performance of transceivers (readers).

For the last few years these protocols have been in transition to become ISO standard 24631. The transition is purely editorial and the tests will still be the same, which means that previous ICAR approvals will also be valid after the transition of document status. The ICAR test protocols will remain valid until the ISO standard has been formally accepted. The first vote on ISO 24631 closes early July 2008.

The chairman of the ICAR Sub-Committee attends the meetings of ISO's working group on animal identification (TC23/SC19/WG3) and its technical working group.

ICAR and FAO

ICAR has a liaison with FAO. In July 2007 the chairman of the ICAR Sub-Committee attended a FAO/OIE workshop in Sri Lanka for South - Eastern Asian countries on identification and traceability. In May 2008 he also attended a FAO workshop in Hungary for Central and East European countries on development of animal identification and recording systems for veterinary surveillance and livestock development.

OIE (World Organisation for Animal Health) works closely with national veterinary services, whereas ICAR traditionally works closely with breeders organisations. However, there are important fields of mutual interest, such as for instance animal identification, registration and traceability. As a result of the focus on traceability of animals and animal products these issues have in many countries moved from being driven by breeder organisations into being authority driven. It is important that standards and guidelines are in conformance, and for this reason ICAR and OIE will continue to collaborate in fields of mutual interest. ICAR is particularly interested in maintaining and developing cooperation with OIE fields of animal identification and recording and evaluation of health traits of farm animals.

ICAR and OIE

The ICAR Sub-Committee on Animal Identification also offers its experience and expertise to member organisations and to national and regional authorities. This is to benefit both breeders' organisations and authorities. Animal identification, registration and traceability are important fields of mutual interest where standards and regulations should be compliant. For these purposes the Sub-Committee chairman has attended meetings Canada, Germany, Spain and USA and also meetings with EU authorities.

Other international activities

The Sub-Committee had a meeting in Kuopio, Finland, June 2006, and two meetings 2007 in Paris, January and September. These meetings mainly were about reviewing the performance test protocol for conventional plastic ear tags and developing a new test protocol for plastic ear tags with EID. Also the transition from ICAR protocols into an ISO standard on testing EID devices and the consequences of the ICAR-ISO agreement formally making ICAR the Registration Authority of ISO for the standards 11784 and 11785 were important issues. Between meetings the Sub-Committee has been very actively and effectively communicating and working through e-mails.

Sub-Committee activities

Report of the ICAR Sub-Committee on Milk Analysis

O. Leray

Actilait-Cecalait, BP 70129, 39802 Poligny Cédex, France

The scope of the subcommittee has been broadened to include and every analytical methods, devices and systems whatever the location of analysis. Accordingly the group was renamed in Sub-Committee on Milk Analysis (MA SC).

Introduction

At the date of the present report, the Sub-Committee is composed of 10 members:

- Christian Baumgartner (Germany).
- Egil Brenne (Norway).
- Roberto Castañeda (Argentina).
- Marina Gips (Israel).
- Olivier Leray (France).
- Silvia Orlandini (Italy).
- George Psathas (Cyprus).
- John Rhoads (United States).
- Gavin Scott (New Zealand).
- Harrie Van den Bijgaart (The Netherlands).

From the last ICAR session the foreseen extension of the membership to Latin America was concretised with Roberto Castañeda (manager of INTI-Lacteos, Argentina) as a new member. Uggo Paggi retired and was replaced by Silvia Orlandini from the same organisation AIA-LSL.

Further membership extensions to other areas such as Asia and Africa are still planned to enlarge worldwide representation in MA SC.

The activities were carried out thanks to email communication and regular meetings either of the whole Sub-Committee or of part of it (project groups) as follows:

- MA SC: München (Germany) , 23 May 2007, IDF/ISO Analytical Week 2007.
- MA SC: Montreux (Switzerland), 22 May 2008, IDF/ISO Analytical Week 2008.
- MA SC: Niagara Falls (USA), 17 June 2008, 36th Biennial ICAR Session.
- PG Reference system ; PG Education & Training: Rome (IT), 18-19 October 2007.
- Working Party on On-farm Milk Analysis (1st meeting): Rome (IT), 27 November 2007.
- PG Reference system: Joint ICAR/IDF meeting: Berlin (DE), 20-21 January 2008.
- Working Party on On-farm Milk Analysis (2nd meeting): Niagara Falls (USA), 17 June 2008.

Working programme and current activities

A working programme was drawn up according to proposals and conclusions of the laboratory meetings in Kuopio (Reference Laboratory Network and MTL WG) and was approved by MA SC in early 2007. It is split into ten work items/ fields dealt with each by two to five project leaders from MA SC (see Annex). The status of current activities is reported in the minutes of MA SC meeting in Montreux (CH) on 23 May 2008 and Niagara Falls on 17 June 2008. Significant progress is noted.

Key issues

An horizontal working group called Working Party on on-farm Milk Analysis (OMA WP) was created in the end of 2007 to define guidelines suitable for milk analysers installed on-farm.

Milk analysis on-farm

OMA WP is composed of Marina Gips, Christian Baumgartner, Harrie van den Bijgaart, Olivier Leray (SC Milk Analysis), Pierre Billon (SC Recording Devices), Jean-Michel Astruc (WG Milk Recording in Sheep), Filippo Miglior (WG Lactation Calculation Methods), Reinhard Pauw (TF Milk Recording Practices), Norbert Wirtz (WG Animal Recording Data).

A draft document for guidelines was produced and circulated for comments to the members of OMA WP. The draft was discussed in Niagara Falls to prepare last amendments. Completion of work was targeted to end of 2008.

Milk analyser approval by ICAR

Launching of the process was made in July 2006 with a dispatch of information to main (known) manufacturers in July and September. Since then additional interests have been shown by manufacturers for:

- Defining a procedure to carry out milk analyser evaluation in three countries in short delays, either in parallel or in sequence, as an alternative to the step-by-step way based on three national approvals. MA SC proposal is it would be directly managed by ICAR (Service-ICAR) in contact with manufacturers and ICAR would entrust expert laboratories to carry out the evaluation work.
- Broadening of the scope of the ICAR protocol (limited today to rapid routine milk recording analysers) so as to enable evaluation/approval for manual analysers as possible master instruments.

Adaptations of procedures should be developed accordingly.

International reference systems

The ICAR analytical quality assurance system involving the ICAR Reference Laboratory Network has shown evidence for a strong potential in the harmonisation of analytical results through international reference materials. Such an approach is being thought through and developed jointly by ICAR and IDF in an IDF project on somatic cell counting. Four experts of MA SC participate tightly in the project as project leaders. The aim will be to provide reference materials for SCC internationally recognised and used for both regulatory and private purposes in a sustainable way. Service ICAR might be involved at the stage of practical implementation. The project is at a start-up stage.

It was renewed in 2007 and 2008 for cow milk with no change and renewal for 2009 was approved in Niagara Falls. The convention between Service-ICAR and the organiser (Actilait/Cecalait, France) will be updated and the new proposals for 2009 dispatched with the usual annual information/announcement letter in December. Proficiency studies in sheep and goat milk analysis are still not proposed in 2008 but the door is open in case needs are expressed by laboratories for 2009. An update of the laboratory network situation and proficiency study activities as made in Niagara Falls during the meeting of ICAR Reference Laboratory Network and are reported in relevant proceedings.

Annual international proficiency testing programme

It has been identified as a new issue of major importance in analytical harmonisation. Today it is developed mainly through communication in dedicated workshops. In this way, regular meetings of ICAR Reference Laboratory Network during biennial ICAR sessions are appropriate to provide general orientation and promote optimum methods and practices.

Education and training

A reflection is underway about ways and supports through which suitable information can be distributed to laboratories in ICAR countries. A preliminary document was produced. The principle lies in education and training actions to be made through lab network members and MA SC to promote national/local action and indicate essential points, provide standard tools.

On the latter point, the possibility to develop video clips as supports to analytical method standards is under consideration by both ICAR MASC and IDF.

Regular information is given by e-mail through the annual letter on reference laboratory network activities and the updates of the list of network members, through the website of ICAR where report, survey results, protocol, procedures, etc are posted, and thanks to open meetings of MA SC and ICAR Reference Laboratory Network held during international events such as ICAR sessions and IDF/ISO analytical weeks.

Information to ICAR and ICAR members

As an example, the last laboratory workshop held in Niagara Falls was made to get provision of information on existing reference and calibration system within ICAR and point out adequate procedures and methods. Presentations and findings will be all reported and posted on the website of ICAR.

Development of tools to improve the access to information is underway (on-line questionnaire on laboratory situation) or under consideration (ICAR laboratory data base in milk recording).

The next meetings will be organised during the next IDF and ICAR international events as follows

Next meetings

- Kislovodsk (RU), 18-22 May 2009, IDF/ISO Analytical Week 2009.
- Montreal (CA), 17-21 May 2010, the IDF/ISO Analytical Week.
- Latvia, 1-4 June 2010, 37th ICAR Session.

Four yearly programme of Sub-Committee on Milk Analysis (MA SC) 2007-2010

Work item	1	2	3	4	5	6	7	8	9	10	11
Theme	Analytical QA (toolbox)	Analytical QA (toolbox)	Analytical QA (toolbox)	Analytical QA (toolbox)	Analytical QA (toolbox)	Laboratory network & harmonisation	Laboratory network & harmonisation	Laboratory network & harmonisation	Laboratory network & harmonisation	Laboratory network & harmonisation	International co-ordination & consistence
Title	Guidelines on organising proficiency study	Guidelines on organising centralised calibration	Guidelines on on-farm analytical devices	Reference materials	ICAR approval of new milk analysers	On-line questionnaire on laboratory situation within ICAR	Website data base on laboratories of ICAR countries	International proficiency studies	Reference Laboratory Network meeting	Education & training on analytical matters	Liaison to other (international) groups of experts
Experts	<i>O Lery G Psathas S Orlandini</i>	<i>C Baumgartner O Lery S Orlandini</i>	<i>C Baumgartner H v d Bijgaart M Gips O Lery E Brenne</i>	<i>C Baumgartner O Lery S Orlandini</i>	<i>3 examiners + All</i>	<i>G Psathas G Scott + ICAR HO</i>	<i>O Lery G Psathas + ICAR HO</i>	<i>O Lery S Orlandini</i>	<i>All</i>	<i>C Baumgartner S Orlandini + ICAR HO</i>	<i>H v d Bijgaart O Lery</i>
Objectives	ICAR guidelines and IDF/ISO IS	ICAR guidelines and IDF/ISO IS	ICAR guidelines	To be considered	Eval. report examination / advising ICAR	Two-yearly information	Regular updated information	Evaluation services	Two-yearly information	Improving laboratory testing performances	Information and feed-back / Horizontal work
2007	- Introduction - Outlines	- Introduction - Outlines	- Introduction - Outlines	Consideration for interest : - Provision of information - Guidelines on RM Qualification - Qualifying RMs	On-going process			Annual Programme	Programming	Elaboration of supports for teaching/training (movies on methods)	Setting up of a horizontal ICAR working party on on-farm testing (composition, work programme, meeting) Liaison persons with IDF MCM & QASADS SC
2008	Working draft	Working draft	Working draft		On-going process	Definition of content, structure, reporting	Content & design definition	Annual Programme	Organising	On-going process Video clip project	Meeting of on-farm testing WP
2009	- Reviewed draft - MO draft	- Reviewed draft - MO draft	- Reviewed draft - MO draft		On-going process	- February: Launching the on-line survey - May : Report to ICAR Session	Developing existing RLN part	Annual Programme	Programming	On-going process Video clip project	Meeting of on-farm testing WP
2010	Final draft: - G.A. approval - Inclusion in ICAR guidelines	Final draft: - G.A. approval - Inclusion in ICAR guidelines	Final draft: - G.A. approval - Inclusion in ICAR guidelines		On-going process		Implementing country web spaces and self-maintenance facilities	Annual Programme	Organising	On-going process Video clip project	Meeting of on-farm testing WP

Report of the ICAR Task Force for Developing Countries

B. Besbes

FAO, V.le delle Terme di Caracalla, Rome, Italy

This Task Force was launched in March 2008. Its overall objective is to assist developing countries in planning and implementing sound and sustainable animal Identification and Recording (I&R) systems which will contribute to improving productivity of the livestock sector and, consequently, enhancing food security and rural development. More specifically, its aim is to draw lessons learnt from past and current experiences in implementing animal identification, traceability and recording systems and use them for developing a decision-support tool for implementing animal I&R systems for developing countries, based on existing ICAR and FAO standards and guidelines.

As this Task Force is neither species nor trait specific, it will interact with other ICAR task forces, working groups and sub-committees, as needed.

A series of e-mail exchanges were conducted from March to May 2008. After self-introduction by the members, the terms of reference of the task force were introduced and discussed. Then, a questionnaire was sent to all members to report about their national programs. The answers were compiled by Inamura Mitsuhiro (FAO) in a spreadsheet to be validated and discussed during the physical meeting which took place from 26 to 29 May 2008 at the FAO Sub-regional office in Budapest. We are grateful to Elena Couto (ICAR) for organizing the travels and to Andriy Rostanlyy (FAO-SEUR) for helping with the logistics related to our stay and meeting. The contribution of Ole Hansen, Chairman of the ICAR Subcommittee on Animal Identification, was very much appreciated.

The first day was dedicated to reviewing animal identification, traceability and performance recording systems in the TF members' countries. In order to facilitate the comparison between the different 'case studies', the members were asked to follow the sequence of the questionnaire for their presentation. An extensive discussion about the roles of the different stakeholders and the indicators of sustainability followed.

Objectives

Activities

Main outcomes of the meeting

Table 1. Members of the ICAR Task Force for Developing Countries.

Name	Organization	Country	E-mail
Badi Besbes (Chairman)	FAO	Italy	Badi.Besbes@fao.org
Alexander Toto	Ministry of Agriculture, Water and Forestry	Namibia	toto@nammic.com.na
Cuthbert Banga	Agricultural Research Council (ARC)	South Africa	cuthbert@arc.agric.za
Liliana Chazo	Holstein Association in Argentina (ACHA)	Argentina	l_chazo@yahoo.com.ar; info@acha.org.ar
Gabriel Rovere	National Institute for Dairy Herd Improvement	Uruguay	grovere@mejoramientolechero.org.uy
Kamlesh R Trivedi	National Dairy Development Board (NDDB)	India	krt@nddb.coop
Gyula Mészáros	Livestock Performance Testing Ltd.	Hungary	gymeszaros@atkft.hu
Jean Noel Bonnet	Institut de l'élevage	France	Jean-Noel.Bonnet @inst-elevage.asso.fr

The second day was dedicated to revisiting the proceedings of previous joint ICAR/FAO workshops on animal identification, traceability and recording in developing countries. Each member summarized the outcomes, lessons and recommendations of the workshop assigned to him/her prior to the meeting. The discussion which followed tried to answer the following questions: what has changed since the initiation of these workshops (in the last decade)? Can we draw a typical profile/situation by region (and by species)? How to make the best use of this information? The group was cautious that this exercise should not be a rewrite of what is already there.

The rest of the meeting was dedicated to drafting the outlines of a background paper which will be used as a road map for the TF in preparing the decision support-tool for implementing animal I&R systems in developing countries. The paper starts with a preamble explaining why this group was set up. Acknowledging that there are different definitions for certain terms like identification, recording or registration, it gives the TF's definitions for these terms. The following sections describe the global context and the driving forces for implementing I&R systems in developing countries, and review the stage of development by region (Africa, Asia, Latin America and Eastern Europe) and purpose (Ownership, Traceability, Performance recording). Then, based on the outcomes of this survey, the reasons of failures and the requirements for success are compiled and a series of recommendations is suggested. The last section of the paper presents the framework of the decision support-tool for implementing animal I&R systems in developing countries.

The outcomes of the 1st TF-DC meeting were presented at the FAO regional workshop on "Development of animal identification and recording systems for veterinary surveillance and livestock development in countries of Central and Eastern Europe" which took place at the same venue from 29 to 30 of May 2008.

Report of the ICAR Task Force on Pig Recording

M. Kovac & S. Malovrh

*University of Ljubljana, Biotechnical Faculty,
Animal Science Department, Slovenia*

Pig recording and genetic evaluation is pure responsibility of breeding programs in some extend required by state regulations (EU, for example). The exchange of testing schemes, recording systems, genetic evaluation as well as herd management is limited mainly to personal contacts between breeding programs. In cattle breeding, ICAR and Interbull set up the system the breeding organizations may use at every stage of development they are. If they just joined ICAR and Interbull, publications would be a large help to choose one of the proven procedures. On the other side, already running breeding programs can obtain many services or tools to solve their problems or serve their needs. The activity boost up software development in genetic evaluation and herd management. The exchange of experience in data management and its evaluation helps up to built efficient solutions for individual breeding programs. Competitiveness among cattle breeders was one of the reason for quick development in recording systems, genetic evaluation, and other usage of data. In addition, cattle breeding have gained much from international genetic evaluation of bulls which can be used also for decision making which bulls from foreign populations may be selected to upgrade local populations. The similar activities may be offered to pig breeding organizations.

The main objective of the paper is to give a short report about an interest in international cooperation in area of pig recording, genetic evaluation, and exchange of EBV's. The basic for the proposition was base on the survey in 2006 and personal contacts.

Questionnaire contained 22 questions about breeding organization itself, their breeding schemes, recording system, genetic evaluation and the way of publishing results. At the end, they were asked if they see any need for international cooperation under ICAR organization due to standardization of pig recording. They were also asked for comments in case of agreement as well as disagreement.

The survey was send electronically to national breeding organizations, breeding societies, breeding companies, and researchers working in pig genetic evaluation. The letter gave some basic information about ICAR and the intention. In addition, we promised, that the informations will not be used for any other purposes. The receivers was asked to forward the questionnaire if they could not fill the survey.

Introduction

Survey

The addresses were collected from various sources: participants of international meetings concerning pig breeding and internet. The questionnaires sent are stored by authors.

Response

The way the survey was distributed, it was not expected that all receivers would return it. Nevertheless, the response on the survey was low. We received 14 answers from 13 countries. Most of the answers were received from Europe. There were Sweden, Finland and Estonia from northern Europe, Germany (Bavaria) and Switzerland from the middle, Italy from south, and a group of Slavic countries: Czech Republic, Slovak Republic, Slovenia, Croatia, and Serbia (two). There were only two answers from other continents, both from North America (USA, Canada). We received letter from Australia asking for additional information, but after that, there were no response. Although most of organizations declared themselves as national organization, some of them have not covered the whole pig breeding in a particular country while part of them have already been working internationally. In some countries, the breeding is done by some national or international breeding companies and other breeding societies. One explanation for low response may be that the questionnaire did not reach the right person.

The organizations responding declared themselves as national or herd-book breeding organizations. There were no answers from breeding companies. Two responses were negative, one was "not sure", and 11 positive. The positive and negative answers were expected. The large proportion of positive responses were most probably obtained while the questionnaire was returned mainly by people, who are interested in cooperation.

Some breeding organizations are taking care only for purebred populations while others implemented the full 3- or 4-way crossbreeding schemes. This become more and more important because information from crossbred populations become important in genetic evaluation of breeding stock. The number of traits included from only one trait up to 24 traits. There is also large discrepancies what information are collected and the way the data are stored. There are breeding programs still working with flat files and ad hoc applications while other use up-to date technologies. Easy manipulation of the data is necessity for efficient data usage for genetic evaluation and herd management as well. Genetic evaluation is performed as often as every day or as seldom as every second week. Answers to specific questions are presented in appendix. They show that breeding programs in pigs differed much from each other.

Arguments for negative response

Both negative responses were supported with arguments. The remarks were written by people that knew ICAR activities. In one case, the author expressed opinion which could be heard often from pig breeders when talking about international cooperation. Therefore, we will try to summarize them.

Firstly, they claim that breeding goals in pigs are quite different in different markets. "The market is very competitive and operates with scarce profit margin." The nucleus herds needs to be small, kept in specialized herds. Hybrids are used in production level can be quickly reproduced through relatively small multiplier population. The production cycle in pigs is much shorter than in other species.

Secondly, the breeding companies are not prepared to share their know-how regarding testing procedures and genetic evaluation. The pig companies must respond quickly to a new situation. The exchange of ideas between companies already exists, but without any obligation.

There are some countries that have built up some testing procedures to give independent results about performance of different hybrids. The trials should fit to the market situations hybrids are tested for. Thus, the test should be different.

In the other negative case, they acknowledge that exchange of genetic material is increasing. The main concern was that the cost might be greater than benefit. This concern would be heard probably more often if we got more responses from breeding companies.

Among positive answers, only two contained additional comments. From Nordic countries we learned that they already cooperate. They share the nuclei and have a large exchange of boar semen. They are interested for greater exchange of genetic material.

Even more encouraged message was sent from Canada. We are including their notice as it is. They wrote, "There has been significant exchange of genetics between Canada and other countries. Pigs and semen are imported in Canada. At the same time, Canadian genetics is also exported to several other countries around the world. In view of similar situation for other countries as well, there is need for comparing the EBVs from one country to the other. We have developed conversion equation for comparing French EBVs to Canadian equivalent. Similar comparison can be done with other countries as well that would really make a strong international collaboration in genetic evaluations." They even give an idea to extend international cooperation to genetic evaluation.

The responding countries already participate in ICAR activities and are its active members. The additional comments were received especially from countries that already have some experience with over border cooperation and exchange of genetic material. Thus, it is not easy to list the expectations. We will try to identify the most important points from contacts at different occasions and informal meetings. Thus, the list may still be incomplete. The important expectations may be grouped into following categories:

- International exchange of genetic material.
- Accounting for genotype environment interaction.
- Exchange of knowledge about pig recording and genetic material.
- Quality guarantee for genetic material.
- Help for setting up and running breeding programs.

From international cooperation, they see benefit in the exchange of genetic material. They have already started cooperation in some areas (Nordic countries, Canada-France) and they would like to see an extension of international activities. The international comparison of EBVs is needed because genotype environment interaction is also present in pigs. Thus, the breeding organizations would like to select robust pigs which may easily be adopted to different environments. To test the environment sensitivity, they need to get data from different rearing conditions.

Arguments for positive response

Discussion

In some countries, they would simply like to have some standards set up which will guarantee the quality of pigs sold from various breeding programs. Many times, company leaflets promise a lot of characteristics which are very appealing. However, closer look to their certificates shows that they are not reported and not included in the total merit index. The official regulations are limited to a certain country or a group of countries and usually require that the results shown are correct and obtained by acceptable procedure. Political decisions do not always reflect current knowledge in breeding and minimum standards for breeding animal is set very low - to two generation pedigree, for example.

On the other hand, breeding practice was almost stopped after transition in the East European countries. They did not apply modern methods for genetic evaluation. Thus, they might expect some help to rebuilt their breeding programs with regards to know-how as well as easy access to the appropriate genetic material. There is a tendency to use locally adapted breeds in harsh environment from different reasons. There are different breeds under conservation scheme while others are used for intensive production, however with more emphasis on animal welfare and usage of local resources. Such production systems require more robust pigs.

The opinion, that pig breeding is so different from breeding other species, is not true. There are, of course, discrepancies based on generation interval, selection intensity, and reproduction rate. However, similar statistical methods are used to analyze the data in all species. The studies about generalization of information systems proved, that data structure in various species and in different production systems is very similar. How ICAR deals with different production systems can be seen in cattle and small ruminants.

Formation of task force

The willingness to participate actively in the working group under ICAR was shown by Canada, Slovakia, Denmark, and Slovenia. We would like to have one or two participants more. Because of their international cooperation, participation of France, Germany, Spain and/or USA will be appreciated. This group has large interest of international evaluation of breeding stock. At the same time they agree, that differences in data definition make the comparison more difficult.

In the near future, we intend to fill up the working group and set up priorities. It seems more natural to start with recording system and data definition, however, the group may be more interested also for faster results in international genetic evaluation.

Report of the ICAR Working Group on Lactation Calculation Methods

*F. Miglior¹, G. de Jong², Z. Liu³, S. Mattalia⁴,
L.R. Schaeffer⁵, A. Tondo⁶ & P. VanRaden⁷*

¹*Agriculture and Agri-Food Canada, CDN, 150 Research Lane,
Guelph, ON, N1G 4T2 Canada*

²*NRS, Postbus 454, 6800 AL Arnhem, The Netherlands*

³*VIT, Heideweg 1, D - 27283 Verden / Aller, Germany*

⁴*Institute d'Elevage, 149 Rue de Bercy, F-75595 Paris, France*

⁵*CGIL, University of Guelph, Guelph, ON, N1G 2W1 Canada*

⁶*AIA, Via G. Tomassetti n., 9 I-00161 Rome, Italy*

⁷*Animal Improvement Programs Laboratory, Agricultural
Research Service, USDA, Beltsville, MD, USA*

A summary of the last 2-year activities of the Lactation Working group is presented. Main activities include the drafting of new guidelines for 24-hour milk calculation using daily data collected with electronic milk meters. Future focus of the group includes research in order to provide guidelines for milk recording using on-farm milk analyzers.

Key words: *Electronic milk meters, On-farm milk analysis.*

The activities of the ICAR Lactation Working Group focused on the following areas:

1. Organization of Symposium at the joint annual meeting of ADSA and ASAS in 2007.
2. Interaction with Sub-Committee of Recording Devices.
3. Participation to Working Party for On-farm Milk Analysis.
4. Drafting of guidelines for milk recording with Electronic Milk Meters.
5. Analysis of methods proposed by UK for am/pm milk recording.

The symposium was organized together with Dr Marj Faust (ABS Global, USA). It was titled "New Challenges and Opportunities From Automation of Animal Data Recording" and took place during the annual meeting of the American Dairy Science Association in San Antonio, Texas, in July of 2007. Four international speakers were invited to discuss the topic from the perspective of manufacturer, DHI, genetic evaluation unit and farmer/consultant. Dr Katz (Afimilk, Israel) presented "Current

Summary

Introduction

ADSA Symposium

and near term technologies for automated recording of animal data for precision dairy farming”, showcasing the details of the new device AfiLab that analyze various milk components on-line at the farm at each milking for all cows. Mr. Petreny (CanWest DHI, Canada) presented “Thriving in a declining market – the new service paradigm for DHI’s”, illustrating the challenges but also opportunities for milk recording agencies from the installment of new on-farm technologies in dairy farms. Dr Wiggans (USDA, USA) presented “Harnessing automatic data collection to enhance genetic improvement programs”, identifying the potential enhancement of dairy cattle genetic improvement with the use of new and more accurate data collected on farms. Finally, Dr Thomson (TMC, USA) presented “Harnessing automatic data collection to enhance profitability of dairy farms”, pointing out the perspective of the dairy farmer.

Support to other ICAR technical teams

There has been several email exchanges with Uffe Lauritsen, Chair of the Sub-Committee of Recording Devices. Discussion peaked at a live meeting in East Lansing, Michigan, in October 2007. During this meeting, attended by some members of SC-RD, the Chair of Lactation WG and the ICAR President, improvements were discussed to add integrity in regard to:

1. Test day/multi-day volume measurement.
2. Sample/vial ID.
3. Cow ID policy established by member organizations.
4. Write-up of examples of good practices (in integration of recording and ID).

Also, milk meter categories were update and partly re-defined. Furthermore, a standalone approval was agreed for milk meters and respective samplers, and finally it was decided to integrate new technologies in the guidelines, particularly multi-day milk meters.

In the fall of 2007 a new technical body was created: Working Party of On-farm Milk Analysis. The focus of this working party is to provide some background policies with different aspect related to milk analysis in the farm for milk recording purposes, when new on-farm devices are used. Representatives from different technical groups of ICAR are part of this WP, including the Chair of Lactation WG. Olivier Leray is Chair of this ad-hoc WP. A live meeting in Rome, Italy, in November 2007 was attended by members, and, since then, there has been email exchange with drafting of preliminary guidelines. The Lactation WG is not yet fully involved as data are needed to perform proper research.

New guidelines for milk recording with electronic milk meters

New guidelines for 24-hour milk yield collected with electronic milk meters were drafted. The guidelines are based on research by Hand et al. (2006) presented at ICAR meeting in Kuopio, Finland. The guidelines shows how multiple day averages provided by electronic milk meters software can be used to calculate 24-hour milk yield. In fact, better accuracy of the estimation of the true performance using 3 to 7 days averages than a performance estimated on a 24h basis only. However, 24-hour fat and protein yields should be determined from the 24 hr yield on the day of sampling, and not the averaged value.

Furthermore, new guidelines for cumulative milk yield collected with electronic milk meters were drafted. These guidelines are an extension of Test Interval Method for lactation calculation, and are based on research by Wirtz *et al.* (2006) presented at ICAR meeting in Kuopio, Finland. A more accurate calculation of the lactation

performance can be carried out using an average 24 hour milk yield of each test interval calculated from automatically collected single milk weights on the farm. However, a stable and reliable on farm recording system for milk yields and milking intervals is required for using this method. This method is very flexible as it can change between standard and detailed test interval methods

Finally, the Lactation WG reviewed a study provided by NMR, UK, which evaluated various statistical models for estimating daily yield from AM/PM testing schemes. Both herds milked twice daily (2x) and three-times daily (3x) were considered in the analysis. Wiggans factors (derived from US data) resulted in reasonable predictions when applied to UK data. The study provides new weights to enable single test records to be properly included in a test day model or the current records-in-progress procedure. Differences in milking interval among individual cows within herd cannot be taken into account, but advances in electronic identification might make this possible in future. The study concluded that the inability to account for individual cow differences in milking interval is likely to limit the further improvement in accuracy of models to predict daily yield from single measured milkings.

Future focus of the Lactation WG is on performing research with on-farm milk analyzers. However, data from manufactures are needed in order to carry out research in this area. An additional focus is to survey all countries regarding the labeling of various milk recording protocols used worldwide.

Future challenges

K. J. Hand, D. Lazenby, F. Miglior, D.F. Kelton and M.A. Quist-Moyer. 2006. Use of Daily Milk Weight to Predict Lactation and 24-hour Yields. Proceedings of the 35th ICAR Meeting EAAP Publication no. 121: 37-40.

N. Wirtz, A. Bunger, K. Kuwan, F. Reinhardt, and R. Reents. 2006. Calculation of the lactation performance from daily milk recording data Proceedings of the 35th ICAR Meeting EAAP Publication no. 121:49-56.

List of references

Report of the ICAR Working Group on Milk Recording of Sheep

*J.M. Astruc¹, F. Barillet, A. Carta, M. Fioretti,
E. Gootwine, D. Kompan, F.J. Romberg & E. Ugarte*

¹Institut de l'Elevage, BP 27, 31326 Castanet-Tolosan, France

The report of the working group on milk recording in sheep presents an overlook of its activities over the last two years, in relation with the terms of reference of the group. The main activities have concerned the on-line enquiry, which has been implemented and is now available to 39 ICAR members. The report focuses on the valorization of the database, using data from 13 countries. Emphasis is given on the increasing use of simplified methods of quantitative and qualitative recording. The other important activity is the co-operation with other bodies of ICAR, especially in relation with recording and analysis devices, the purpose being to take into account the specificities of dairy sheep production and sheep milk when establishing the requirements for the guidelines.

Key words: *Enquiry, Guidelines, Qualitative recording, Breeding schemes.*

The terms of reference of the Working Group on Milk Recording in Sheep (MRS WG) may be synthesized in four main items: evolution of the guidelines, cooperation with relevant bodies of ICAR, dairy sheep enquiry, contact with non-ICAR organizations in the dairy sheep field. Several updates of the guidelines, prepared between 2000 and 2004, have been approved in Sousse in 2004. No update is planned at the moment. The main activities of the MRS WG during the last 2 years have focused, firstly on the cooperation within ICAR, especially with working groups or sub-committees involved in recording devices and analysis devices, secondly on the on-line enquiry implemented since May 2006. A first valorization of this on-line enquiry, following 7 biennial surveys "on paper" carried out between 1988 and 2004 is presented in this report, permitting to establish the state of the art on different topics related to the terms of reference of the working group. Basically, a key objective of the group is to spread simplified methods of recording, especially qualitative recording, while keeping the relevance of the measures for genetic purposes.

Summary

Introduction

Main activities of the WG in the last two years

Renewing the members of the Working Group

After some “historical” members have left the Working Group, it was important to introduce new participants in order to keep the balance between dairy sheep production regions, and also to maintain a critical mass for the efficiency of the work of the group. The current members are:

- Jean-Michel Astruc, Institut de l’Elevage, France.
- Francis Barillet, INRA, France.
- Antonello Carta, IZCS, Italy.
- Mauro Fioretti, AIA, Italy.
- Elisha Gootwine, Volcani Center, Israel.
- Drago Kompan, University of Ljubljana, Slovenia.
- Franz-Josef Romberg, Dienstleistungszentrum Ländlicher Raum Westpfalz, Germany.
- Eva Ugarte, Neiker, Spain.

Meetings involving the Working Group of Milk Recording in Sheep

- *Meetings of the Working Group* - The last meeting of the MRS WG was held in Kuopio (Finland) on 6 June 2006 with only 4 participants. The main issues of the agenda were the dairy sheep enquiry on-line, the position of the group about the requirements of recording devices in dairy sheep, the perspectives concerning the WG. The next meeting will be held in Niagara Falls on 17 June 2008. Between two biennial sessions, the exchanges are mainly done by e-mail.
- *Meeting of the ICAR Board with Chairperson in Verona on 30th May 2007* - Presentation of the work of the group, reviewing the main items of the terms of reference: guidelines, co-operation within ICAR, yearly enquiry, contact with non-ICAR organizations in the dairy sheep field.
- *Meeting with ICAR bodies* - Participation at the first meeting of the working party on On-farm Milk Analysis (WPOMA) which was held in Roma on 27 November 2008 (see below).

Updating the ICAR Guidelines of sheep milk recording

The last evolutions date back to 2005 and are reported in the guidelines published in the booklet “International Agreement of Recording Practices” (ICAR Guidelines, 2007), in the section 2.2. The emendations concerned the systematization of the classification of the methods of milk recording, the introduction of the D and E designs and the clarification of the terms for milk yield in dairy sheep. No update is planned at the moment. It is intended to develop, if necessary, a glossary of the main terms specifically related to dairy sheep.

Co-operation with the relevant SCs and WGs of ICAR

The MRS WG co-operated over the last 2 years with the following bodies of ICAR:

- Cross-participation with the WG on Milk Recording in Goats, the chairman of each group participating at the work of the other group.
- Close co-operation with the Sub-Committee on Milk Recording Devices about the requirements for sheep. The main decision was, on the one hand, that ICAR give a separate approval for the devices for sheep and goats, given the differences of fat and protein content in both species, on the other hand, that the guidelines for sheep were relevant and therefore should not be relaxed. Currently, two meters have been tested over the last years for sheep, the main difficulty to fulfill the requirements being for bias and standard deviation for fat. One meter

has up to now a provisional agreement. The chairman of the WG was invited at the meeting of the Sub-Committee in Kuopio during the last biennial session to present the position of the group.

- The MRS WG is represented in the working party on On-farm Milk Analysis, created in summer 2007, and which a first meeting was held on 27 November 2007 in Roma. This working party deals with the issue of analysis de-localized on the farm with on-farm milk analyzer (at-line or in-line milk analyzer). The aim is to propose recommendations and requirements to be fulfilled by manufacturers with regards to analytical devices, milk producers with regard to use, milk recording organizations with regard to external control of routine analysis.

As the survey on the situation of milk recording in sheep, with extension to connected issues such as breeding schemes, selection criteria, molecular information in sheep, recording devices, is one of the main terms of reference of the MRS WG, we proposed, with the help of ICAR Secretariat, to develop the possibility to fill in the questionnaire on-line. This on-line enquiry has been ready to accept submission of data since May 2006. The dairy sheep enquiry can be filled in on the ICAR website, in the space dedicated to the yearly milk enquiries.

The dairy sheep enquiry is divided in 7 tables, representing 7 different topics.

- Basic information on population, recording methods and percentages.
- Milk yield: type of lactation calculation + milk yield results.
- Optional test for milk composition.
- Recording of non-milking traits.
- Milk recording equipment used in case of machine milking.
- Breeding programs using insemination (AI).
- Molecular information.

It was too early at the Kuopio Session to present the first results of this new modality for the enquiry. Up to now (May 2008), 12 countries have answered the on-line enquiry, a 13th country sending information without using the ICAR site. We may be quite disappointed by the fact that countries with substantial population of dairy sheep did not answer the questionnaire, despite sometimes several recalls. We also would suggest that even countries with very small dairy sheep population (even if there is no recording) should at least give the information of the number of flocks and ewes of dairy sheep, as well as the breeds present in the country.

The main results of the on-line enquiry are described below. Additional tables which could not be included in this report are available on the ICAR website.

The table 1 summarizes the impact of milk recording in the countries having answered the on-line enquiry over the last 3 years.

Official milk recording is carried out in every country. If we look at the countries with the largest dairy sheep population, all situated in the Mediterranean area (Greece, Italy, Spain, France), the impact of milk recording is quite different: high in France (59% on the whole, 20% when considering only official milk recording), medium in Spain and Italy (respectively 12.8 and 7.8%), low in Greece (less than 1%). Italy, France and Spain represent 90% of all the animals in official milk recording.

Dairy sheep enquiry on-line

Dairy sheep enquiry on-line

Situation of milk recording in dairy sheep

In the other countries, with smaller population, milk recording represents few flocks and ewes, from 160 in Canada to 18 600 in Israel.

However, as shown in the table 2, the impact of official milk recording has steadily increased in most of the countries, especially when the countries have adopted simplified design of official milk recording, such as AT or AC method. Whereas in 1988, 2 countries only used simplified method (France with AC method, Spain with AT method in Latxa breed), this number reached up to 6 countries in 1998, and 7 countries in 2008. The Working Group has surely contributed to this evolution, since it has been one of its main tasks to promote simplified methods of milk recording. Indeed, fixed costs are high in sheep compared to cattle and simplified methods are

Table 1. Size of population of dairy sheep, impact of quantitative recording in ICAR member countries.

Countries	Year	Size of population	Quantitative recording (official milk recording)		Methods used Yes/Not
			Number of recorded ewes	% recorded ewes	
Belgium	2007	1 000	200	20.0	AT
Canada	2005		160	-	AT
Croatia	2006	34 270	5 361	15.6	AT
Czech Rep.	2007		443	-	AT (part), E (part)
France	2007	1 483 000	302 199 ¹	20.4	AC
Germany	2007	9 000	705	7.8	A4 (64%), AT (8%), E (28%)
Greece	2006	12 000 000	70 658	0.6	A4
Israel	2007	35 000	18 600	53.1	On-farm, daily basis
Italy	2007	6 150 000	482 698	7.8	AT, AC
Slovak Rep.	2004	216 000	12 869	6.0	AC
Slovenia	2007	4 900	3 396	69.3	AT
Spain	2006	1 739 000	222 358	12.8	AT (80%), AC (20%)
Sweden	2006	10-15 flocks		-	

In addition, 570 755 ewes are recorded with D method (non official milk recording) without qualitative recording

Table 2. Evolution of official milk recording over the last 20 years in ICAR member countries.

	1988			1998			2008		
	Recorded ewes (official)	%	method	Recorded ewes (official)	%	Method	Recorded ewes (official)	%	Method
Italy	140 000	2.8	A4	331 024	5.0	A4	482 698	7.8	AT/AC
France	202 000	16.8	AC	281 070	20.9	AC	302 199	20.4	AC
Spain	110 000	2.8	AT	141 044	6.2	AT	222 358	12.8	AT/AC
Greece	37 000	0.5	A4	26 600	0.3	A4	70 658	0.6	A4
Portugal	7 600	1.5	A4	38 571	15.2	A4/AT			
Israel				6 200	12.4	B4/AC	18 600	53.1	
Slovak R.				5 100	2.3	A4/AC/AT	12 869	6.0	AC
Slovenia				1 474	19.8	A4	3 396	69.3	AT
Germany	356	2.2	A4	836	3.3	A4/B4	705	7.8	A4/AT/E
Czech R.				177	35.0	AT	443		AT/E
Total	496 956			832 096			1 113 926		

the way to increase and develop milk recording in dairy sheep. Among the countries with large population, Greece still uses the standard A4 method and, therefore, remains with a low impact of milk recording, less than 1%.

The use of the D method, which is a non-official milk recording, is described only in France. In France, the D method is a very simplified method consisting in 2 to 4 flock-visits per year, whatever the visit intervals (monthly to bimonthly), in order to get 2 to 4 test-day per ewe. This design is applied to the flocks out of the nucleus scheme, in order to help the breeder to optimize culling and replacement. Therefore, the D method is used in addition to the official design, which is implemented only in the nucleus flocks. D method is a quantitative recording. In France, D method represents roughly two-third of the recorded ewes.

The additional tables, available on the ICAR website, show that four breeds are up to 100 000 recorded ewes: Sarda and Valle de Belice (Italy), Lacaune and Manech Red Face (France).

Conversely to dairy cattle, qualitative milk recording is optional in official milk recording in sheep, as established in the ICAR guidelines (ICAR guidelines, 2007), considering that the cost of qualitative milk recording may be crippling. Qualitative recording becomes useful and necessary when selection on milk yield is efficient. Its cost-effectiveness is based upon the implementation of a simplified design. The main features of the table 3 can be summarized as following:

- The impact of qualitative recording among the recorded population is high only in countries with a quite small population (from 37% in Croatia to 100% in Czech Republic and Germany).

Simplification of qualitative recording in dairy sheep

Table 3. Qualitative recording in ICAR member countries.

Countries	Qualitative recording				Categories of ewes (lactation)
	Yes/Not	Recorded ewes	% of the recorded ewes	Method used	
Belgium	No	-	-		
Canada	No	-	-		
Croatia	Yes	2 000	37%	AT	
Czech Republic	Yes	443	100%	AT/E	
France	Yes	84 000	28%	Part-lactation sampling (AC)	Lacaune: L1/L2 Pyrenean breeds: L1
Germany	Yes	705	100%	A4/AT/E	
Greece	Yes	?	?		
Israel	No	-	-		
Italy	Yes	24 642	5%	Part-lactation sampling (AC)	Sarda: L1
Slovak Republic	Yes	6 870	53%	AC	L1/L2/L3
Slovenia	Yes	3 396	100%	AT	
Spain	Yes	119 500	45%	AT,AC	Churra: AI ewes Manchega: all Latxa: some flocks / L1/L2
Sweden	No	-			

- In countries with a large population, the impact reaches 45% in Spain, 28% in France and 5% in Italy. Qualitative recording concerns only some breeds, some parities (lactation 1 or lactation 1 and 2). It is implemented within a simplified design of milk recording, with one sample per test-day (AC or AT method).

Definition of milk traits (see additional table on www.icar.org)

The guidelines specify the different terms of lactation calculation, in relation with the specificities of dairy sheep about the management of the lactation. In most breeding systems, the lactation is divided in a suckling period followed by a milking-only period after the weaning of the lamb(s). In this case, ICAR recommends to compute the lactation at the milking-only period (TMM = total milked milk). Nevertheless, some countries continue to implement a calculation at the whole lactation (TSMM = total suckled and milked milk). In some breeding systems (Israel or Germany), the lambs are removed from the ewe very soon after lambing, so that the whole lactation is exploited by milking. In this case the calculation is the TMY (total milk yield).

Milk recording equipment (see additional table on www.icar.org)

ICAR has recently agreed on-farm milk meters for sheep. No portable meter has been agreed until now. The enquiry does not allow to have a comprehensive overview of the impact of this new agreed meters. According to the enquiry, we observe a wide variety of devices (jars or meters, measuring volume or weights, with or without sampler), which most often are portable and used by a field technician.

Other additional tables (www.icar.org) present information about the following topics: molecular information in sheep and recording of other traits.

Breeding schemes, objective and selection criteria

Breeding programs based on progeny-test of rams by AI or by combining AI and controlled natural mating are implemented in a few breeds, in France, Italy and Spain (table 3). AI remains not very widespread, probably due to the same reason of cost as milk recording. AI is practiced in sheep mostly with fresh semen (except for half of the AI of the Churra breed in Spain) with a low dilution, with synchronization of the heat (one AI per ewe, whatever the result, the return being realized by natural mating). The diffusion rate of a ram is at least 100 to 1000 times lower than a bull. As the table 4 shows, the selection criteria are still based on milk yield on most situations, with, in addition, fat, protein, udder morphology. Only the Lacaune breed has included in its selection criteria somatic cell count (SCC) and udder morphology in addition to the production traits, giving the same weight on the one hand to production traits and on the other hand to udder functional traits (SCC and udder morphology).

Given the difficulty and cost to implement an efficient breeding program for local breeds, some breeds are currently spread in more and more countries: East Friesian in the northern and central European countries, Assaf particularly in Spain and Portugal and Lacaune everywhere. If the situation, through the ICAR enquiry is well known for the local breeds, the whole population and the recorded population remains almost unknown for this exogenous breeds out of their area of origin.

Table 4. Importance of breeding programs and selection criteria¹.

Country	Breed	AI progeny-tested rams	AI	Selection criteria ²
France	Lacaune	479	387 000	(FY+PY+1/16F%+1/8P%) + .5 SCC + .5 Udder
	Manech Red face	135	57 400	FY+PY
	Manech Black face	37	9 300	FY+PY
	Basco-Béarnaise	43	13 800	FY+PY
	Corse	29	6 700	MY
Italy	Sarda	60	13 500	MY + Udder
Spain	Latxa blond faced	38	13 300	MY
	Latxa black faced	60	16 800	MY
	Karrantzana	8	234	MY
	Manchega	130	34 000	MY
	Churra	48	15 250	MY + P%

¹MY=milk yield, FY=fat yield, PY=protein yield, F%=fat content, P%=protein content, SCC=somatic cell count, Udder=udder morphology.

²Most of the breeding schemes include selection for scrapie resistance (PrP gene).

The constitution of the MRS WG has been updated in 2008 and two new members have replaced resigned or retired members. Over the last two years, the MRS WG has mainly focused on the on-line enquiry and its valorization, and on the co-operation with other parties of ICAR, in the field of recording devices and analysis devices. The issue of on-farm devices (for recording and / or analysis), which is a current concern for cattle, must also be faced in sheep. The challenge of the group will be both to continue to promote simplified methods of recording, especially for qualitative recording, while keeping enough relevance to each individual measure. It is important that ICAR continues to take into consideration the specificity of small ruminants, particularly with regards to the high cost of milk recording, compared to cattle. The on-line enquiry is a useful tool to follow the recommendations suggested by the MRS WG, through different topics such as methods of milk recording used in ICAR member countries, devices used for recording and analysis, breeding programs. The MRS WG will encourage, with the help of ICAR secretariat, each ICAR members to fill in the enquiry regularly, as it is done for cattle.

Recording of functional traits exists in some countries (udder traits, reproduction traits). Defining these functional traits in the guidelines, given the specific dairy sheep situation, should be a task of the working group in the next years.

ICAR guidelines, 2007. International Agreement of Recording Practices. Guidelines approved by the General Assembly held in Kuopio, Finland on June 2006. Section 2.2, pp.55-65.

ICAR website. www.icar.org.

Conclusion

List of references

Report of the ICAR Working Group on Animal Fibre

M. Antonini

*ENEA CR Casaccia Dept. BAS secondment at the Industrial
Liaison Office, University of Camerino, Italy*

The ICAR Executive Board approved in 2007 the new “Animal Fibre” Task Force currently Working Group (AF-WG). Soon the AF-WG defined their terms of reference. ICAR presented the AF-WG and its terms of reference in the International Conference “The wool roads” held in Italy on 12 October 2007

The ICAR Animal Fibre Working Group, at present, is composed by the following nine members:

- Marco Antonini (Italy) ENEA / University of Camerino.
- Lou Yujie (China) Jilin Agricultural University.
- Claudio Tonin (Italy) CNR Italian National Research Council.
- Hugh Galbraith (United Kingdom) University of Aberdeen.
- Oscar Toro (Peru) Ong DESCO.
- Eduardo Frank (Argentina) Catholic University of Cordoba.
- Moises Asparin (Peru) Michell Group.
- Malcolm Fleet (Australia) SARDI Research Scientist (Wool).
- Fabrizio Castagnetti (Italy) Ermenegildo Zegna Group.

The AF-WG members represent 6 Universities/Research Centres and 3 private companies worldwide. The Peruvian member DESCO is also ICAR affiliate.

During the 36th Niagara Falls ICAR Session (June 2008), a participant at the section on Alpaca fibre production, Mr. Davis Barbosa from the Alpaca Owner and Breeders Association, expressed the interest to participate at the AF-WG as representative for the USA area.

During the reference period the ICAR AF-WG actions were conducted by email and produced the following activities:

- Participation at the ICAR Meeting held at Verona (Italy) in May 2007. During the event a proposal of the AF – WG members and the terms of reference have been illustrated to the ICAR Board, which approved the proposal giving the new WG activities the green light;

Introduction

Activities

- According to the terms of reference at the moment two of them have been agreed: the Alpaca identification methods and the guidelines of Alpaca fibre harvesting and grading.
- In order to offer an active service to the Alpaca breeders and to the Alpaca textile processors, ICAR AF-WG suggests a common approach to Alpaca breed management with particular attention at the fibre product management, in order to exploit at the best the animal selection development.
- According to the auto certification methodology still applied in other advanced fibre animal breeding systems, critical points for Alpaca fleece collection have been identified.
- For the above reasons AF-WG drafted an ICAR official document for the definition of the instruments and methods for Alpaca breeding identification (ICAR rules, standards and guidelines on methods of alpaca identification) and an other official document on the standard definition of correct methods of Alpaca fibre harvesting and grading (ICAR Guide Line for Alpaca shearing management, fibre harvesting and grading).
- ICAR final goals in the Alpaca fibre production is a correct approach to solve the fibre heterogeneity problems which affect strongly the textile factories end users.
- All the activities have been presented at the 36th Niagara Falls ICAR Session (June 2008) in a specific meeting organized by the AF-WG on Alpaca. During the meeting ICAR Guidelines for alpaca shearing management, fibre harvesting and grading have been presented;
- Genetic Improvement Programmes on Alpaca of the Caylloma Province, Promege (Peru) and ITALPACA: The first experience of Alpaca Genetic Improvement programme in Europe. The reunion has been closed with Round Tables on Recording systems method in domestic South American Camelids roundtable in which participated representatives of Breeders association from USA, South Africa, Peru and Italy.
- Finally ICAR AF-WG together with the Michell Group presented actions and services at industrial level in Peru, one of the most important Alpaca fibre, producing countries and ICAR member, in March 2008, and in Italy, one of the main Alpaca fibre textile processing countries, during a meeting held in Biella in May 2008 with Ermenegildo Zegna Group and Trivero Spinning Mill.

Working programme

The future actions of the ICAR AF-WG foresee a first period of activities addressed towards Alpaca fibre production according to the ICAR terms of reference. Firstly, the WG should define objective criteria to describe Huacaya and Suri fibre type; present action should be carried out during the period 2008/09. At the same time ICAR AF-WG will have to define the objective and criteria in Alpaca fibre selection programme worldwide. Defined the above parameters (type of fibre, objective and criteria of selection), the following step foresees the contribution to determine adequate analysis of performance quality of Alpaca fibre for recording purposes worldwide.

Subsequently, AF-WG will establish liaisons with International Organizations/bodies involved in natural fibre analysis in order to discuss and define together specific parameters of fibre certification taking into account the issues

dealt by ICAR. The final goal will be the development of a reference document and standards on methods of Alpaca fibre analysis and quality certification in laboratories, which could be applied to animal fibre recording.

At present, we are verifying possible cooperation with CCMI - Cashmere and Camel Hair Manufacturers Institute <www.cashmere.org/cm/index.php>.

Finally AF-WG will explore the opportunities to open a branch with the purpose of studying other domestic animal species and breeds for textile fibre (i.e. merinos sheep, Angora goat, cashmere goat etc.). At this moment we would like to verify together with the Australian member of the AF-WG the possibility of proposing International Guidelines for determining quality of merino sheep wool, starting from the Australian wide experience on wool production and selection.

Part of the natural textile industry is still animal based, the value of animals has become directly related to their fibre diameter and the textile factories require more quality than quantity. Therefore, the major demand is currently for fine (and preferably white) fibre. By improving alpaca fibre, generally animal fibre quality and its preparation, producers will be better able to define common objective of selection. The ICAR guidelines will have to comply to the Alpaca breeders needs in the improvement of the final quality products and in the more accurate animal fibre recording method in the perspective of the planning of genetic selection. Present guidelines represent the first step of ICAR service for alpaca breeders at the international level. ICAR aims to approach the problems of Alpaca fibre heterogeneity due to the great variability in type of fleece and type of fibre in order to supply the end users with the best raw material possible.

For these reasons during the ICAR board meeting held in Niagara fall, the AF-WG convenor suggested to involve, as ICAR members, the highest number possible of interested Textile factories, in order to create the necessary and fruitful links between breeders and end users, links that have never had an important role, especially in fine fibre production from Alpaca, Cashmere and Mohair.

Conclusion

Report of the ICAR Interbeef Working Group

B. Wickham

ICBF, Shinagh House, Bandon, Co. Cork, Ireland

To develop international genetic evaluation service for beef breeds and traits:

- To be provided through Interbull.
- Using phenotypes.
- Costs covered by users.

Objective

- Three year project from 1st June 2007
- Resources:
 - □80K/year to Interbull Centre funded by ICAR/Interbull and participating countries
 - One FTE provided by each of ICBF and INRA
 - Contributions by participating countries
- Co-ordinated by Interbeef Working Group:
 - Country Representatives:
 - France - Isabelle Boulesteix,
 - UK - Mike Coffey,
 - Ireland - Brian Wickham,
 - Nordic Countries - Anders Fogh
 - Interbull Subcommittee
 - Freddy Fikse
 - Beef Working Group
 - Clara Diaz
 - Research and Development Team
 - Eric Venot, Thierry Pabiou, Valentina Palucci, Flavio Forabosco, Eildert Groeneveld

Strategy

- Service Agreement and Fees.
- Rules for Participation - Roles and Responsibilities.
- Operating Procedures.
- Data Flows and Interfaces.
- Quality Control and Query Support.
- Methods and Models.

Key issues to be addressed

**Workshop on
"ICAR Reference Laboratory Network"**

Update on ICAR Reference Laboratory Network

O. Leray

Actilait/Cecalait, Poligny, France

A policy for quality assurance on milk recording analysis has been developed from fourteen years by ICAR according to the orientation proposed in Ottawa in 1994. So called analytical quality assurance system has been based on the adoption and use by laboratories of same technical guidelines produced by ICAR and a structuring model based on national networks for laboratory monitoring at country levels and an international network of reference laboratories as the corner stone of a system which allows to anchor countries a common international reference. Objectives, organisation and stage of implementation and development are presented.

Summary

Key words: Milk recording analysis, Quality assurance system, Reference laboratory network.

A policy for analytical quality assurance (AQA) was introduced at the 29th ICAR Session in Ottawa in 1994 that should cover every aspect of milk recording analysis and can provide confidence to stakeholders, ensure equivalence of genetic evaluation and enable analytical system recognition between countries.

History

That policy was handled by the Working Group on Milk Testing Laboratories and from 2006 continued by the new Sub-Committee on Milk Analysis.

From 1994 the working group has defined essential guidelines so as to assure a minimum precision in milk recording analysis provided the recommendations are applied and, from 1996, created a network of expert laboratories expected to become the basis of an international analytical quality assurance system for milk recording, called ICAR Reference Laboratory Network.

The international reference laboratory network has become an essential piece of the AQA system aiming at analytical harmonisation as its members are entrusted to be intermediaries between national levels and the international level where optimum methods and practices are defined (IDF/ISO guides and standards, ICAR Guidelines) to transmit adequate information to milk testing laboratories.

Structure and architecture

The international network constitutes a structure through which, thanks to interlaboratory studies, it becomes possible to provide an international anchorage to routine laboratories and estimating overall accuracy of milk recording measurement and absolute measurement uncertainty in individual laboratories.

This is realised through two levels of network implementation (possibly three), national (or regional) and international. The national reference laboratories operate as bridges for precision traceability between both national and international levels where interlaboratory studies are carried out respectively. A third layer can exist for instance in federal countries where as well regions can organise labs in network or could be developed in the future for on-farm analysis in the prospect of possible sub-network monitored by regional laboratories.

Membership

This makes that any laboratory commissioned to monitor routine testing laboratories should be invited by their national organisation to join the network. For specific situation where only few laboratories with no national co-ordination, individual routine laboratories may also join the network so as to benefit to a direct anchorage to the international level whereas, in well structured local situations, so-called reference laboratories can establish the junction between routine labs and the international level.

Competence and expertise requested as eligibility criteria to belong to the network are one or more of the followings:

1. National ring test organizer	2. Information on analytical methods
3. Reference Material supplier	4. Evaluation of analytical methods/instruments
5. Master laboratory for centralized calibration	6. Research on analytical methods
7. Teaching and training in laboratory techniques	8. National regulatory control of DHI analyses

The ideal situation being where the reference laboratory covers every competence item and therefore can ensure consistency and continuity in missions to routine laboratories.

Evolution

The numbers of laboratories qualified for various scientific/technical mission have increased gradually from 1996 to 2003, with its membership raised up to 38 members and since then it keeps stable about 38. In mid 2008 there are 38 of 32 countries involved in cow milk analysis, of which as well 16 work for goat milk and 14 for sheep milk.

Meanwhile the number of declared eligibility criteria continues to increase thus showing a qualitative development of the network towards maturity. In 2008, 75% of competence items realised by 34% of members, and 50% by 63% (Table 1).

Table 1. Numbers and proportions of eligibility criteria of network members in 2008.

Criteria number N	Proportion %	Lab number with N	Lab % with N	Lab number with at least N	Lab % with at least N
8	100	5	13	5	13
7	88	4	11	9	24
6	75	4	11	13	34
5	63	4	11	17	45
4	50	7	18	24	63
3	38	3	8	27	71
2	25	2	5	29	76
1	13	4	11	33	87
0	0	5	13	38	100

ICAR INTERNATIONAL REFERENCE LABORATORY NETWORK

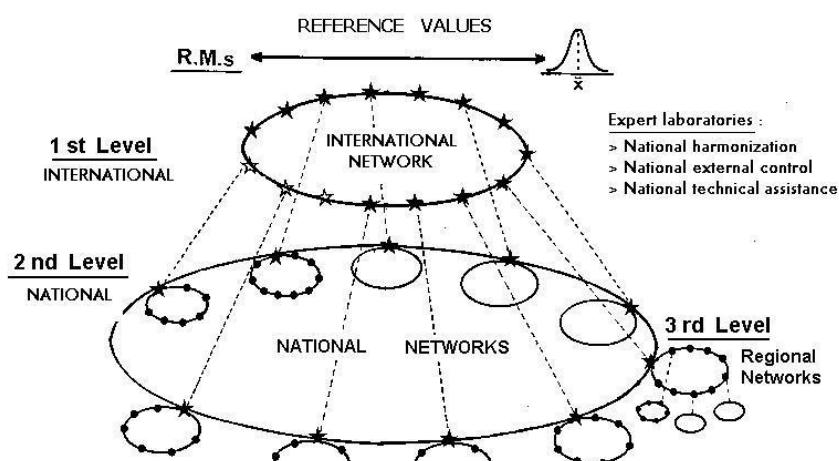


Figure 1. Architecture of ICAR Reference Laboratory Network.

Since 1996 an annual interlaboratory proficiency scheme has been regularly run twice a year for methods used as reference to calibrate routine methods for fat, protein and lactose in cow milk. It was complemented from 1999 with methods for methods for urea and somatic cell counting. In 2008 participant number is stable with about 20 for fat, 21 for protein, 1 for lactose, 15 for urea and 21 for SCC.

Significant improvement of analytical performances has been noted and today the overall precision observed within the network appears better than that of respective method standards thereby brings proofs of the efficiency of the scheme.

Interlaboratory proficiency studies

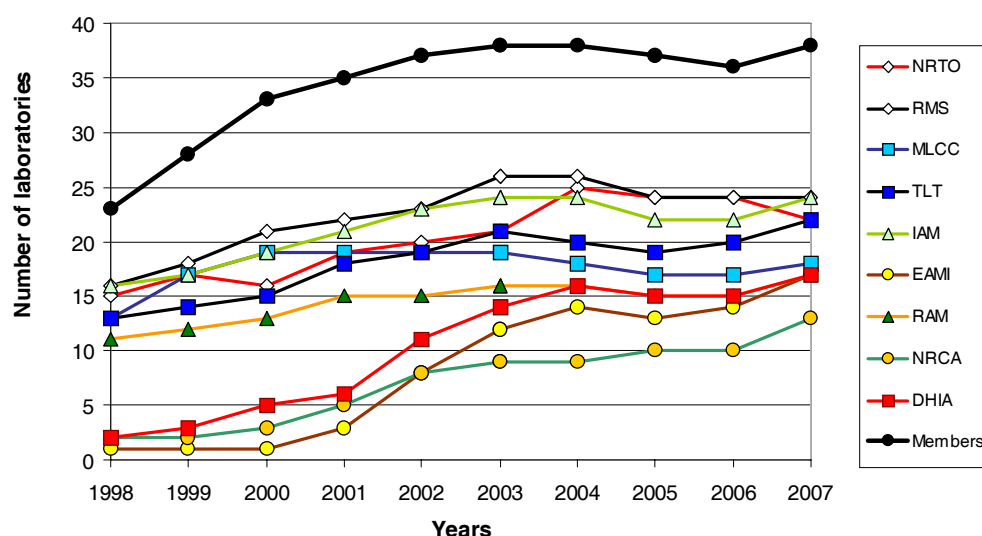


Figure 2. Evolution of ICAR Reference Laboratory Network membership from 1998.

Stage of progress in AQA implementation with the network

The end of the first phase of implementation of the network was stated in ICAR Session in Kuopio 2006 and the launching of a second phase declared. As the general frame and architecture has been drawn and established time has come to feed the system with installing sustainable operations and activities for the benefit of harmonisation in ICAR member countries.

Proper models are to be given through guidelines to organise proficiency studies at national levels adequate for calibration purposes, define methodologies to orient and implement centralised calibration, evaluate analytical precision traceability, establish the international anchoring thanks to ICAR Reference Laboratory Network.

Beside education and training for laboratory practitioners should be promoted through the network with regard to analytical methods for milk and the respective former items and implemented at national levels based on international guidelines and standards.

Conclusion

The AQA system launched by ICAR in 1996 has already shown efficiency at the network member level. The analytical quality of national level remains under the responsibility of network members to which appropriate tools and guidance should be brought and developed where missing. The work has been undertaken by the Sub-Committee on Milk Analysis since 2006.

ICAR AQA strategy – International anchorage and harmonisation

O. Leray

Actilait/Cecalait, Rue de Versailles, BP 70129,
F-39802 Poligny Cédex, France

A reference system for milk recording analysis based on national and international laboratory networks has been developed to respond to the need of analytical harmonisation between countries. Proficiency testing schemes implemented nationally by countries and at the international level in a reference laboratory network by ICAR can be used for the benefit of laboratory quality assurance, through providing international reference anchorage and traceability. An international reference laboratory network like ICAR 's one can be used to certify reference materials that can further benefit to the harmonisation and improvement of analytical performances. High performance with methods is required from reference laboratories involved and proficiency studies can be used to select or qualify suitable candidate laboratories.

Key words: Milk recording, laboratories, Harmonisation, Quality assurance, Reference, Anchorage, Network.

The policy for analytical quality assurance (AQA) implemented from 1994 has been based on the harmonisation of laboratory practices and analytical performance laboratories in ICAR member countries thanks to missions devoted to expert laboratories, so-called reference laboratories as justified by strong technical competence. Those missions refer to lab monitoring, expertise and service supply for quality assurance (QA) and quality control (QC). ICAR countries have been invited to nominate or create minimum one such a laboratory for national milk recording so that the whole of reference laboratories can become members of an active international reference laboratory network.

The international reference laboratory network has become an essential piece of the AQA system aiming at analytical harmonisation as its members are entrusted to be intermediaries between national levels and the international level where optimum methods and practices are defined (IDF/ISO guides and standards, ICAR Guidelines) to transmit adequate information to milk testing laboratories.

Summary

Introduction

International anchorage

International anchorage is made:

- First, through same/similar practices in every ICAR countries which is achieved through using same international standards and guides.
- Second, establishing concrete technical links between the high level of expertise (international reference laboratories) and routine testing laboratories in every country.

A technical linkage is to be made between the unknown truth given by the consensus of international milk recording community – represented by average results produced by the international reference laboratory network – and the final results obtained by testing laboratories.

It can be achieved through two major tools that can be implemented in parallel at both national and international levels with proper connection, correspondence and relay.

- Interlaboratory proficiency schemes: measuring lab performances. Through adequate combination, it is possible to establish and measure the chaining of errors in analytical steps that contribute to the final result (with regard to the reference methods and routine methods).
- Interlaboratory certification schemes: determination of true (or reference) values for reference materials (RMs).

Performance evaluation

A protocol was adopted by ICAR for regular ICAR proficiency studies – international level – and is to be proposed in guidelines to ICAR countries for national implementation. Trials use $q=10$ samples evenly distributed throughout the concentration range of usual milk analyser calibration and labs perform duplicate analyses ($n=2$).

Lab evaluation is made through the laboratory bias - average of differences $\bar{d}_{Lk}$ measured between lab results and the reference value $\bar{X}_S$ (grand mean of all the labs per sample) - and the standard deviation of differences as an indicator of consistence (outlier result).

Laboratory score $\bar{d}_L = \sum \bar{d}_{Lk} / q = \bar{x}_L - \bar{X}$ must lay within the limits associated to uncertainty of $\bar{d}_L$

$$U_{dL} = \pm 2 \cdot (U_{xL}^2 + U_{\bar{X}}^2)^{1/2} \text{ or } U_{dL} = \pm 2 \cdot [(\sigma_R^2 - \sigma_r^2 \cdot (1-1/nq)) \cdot (1+1/p)]^{1/2}$$

Beside punctual elements of within lab reproducibility can be estimated through

$$sR_L^2 = s_r^2 \cdot (1-1/n) + \bar{d}_L^2 + s_d^2$$

with estimate calculated by averaging precision elements of several successive trials. Within lab reproducibility standard deviation can then be used for determining uncertainty of test results.

Precision and accuracy elements produced through PT results and analyser monitoring and calibration allow to calculate the overall accuracy and uncertainty of routine testing results in a laboratory. To realise adequate estimation elements used are to be obtained from sufficient numerous data.

For the reference methods (q samples and n replicates) it is calculated according to ISO 5725-6 as

$$U_{\text{ref}} = \pm u_{0.975} \cdot [sR_{L,\text{ref}}^2 - sr_{L,\text{ref}}^2 \cdot (1-1/nq)]^{1/2} \text{ and with high } nq \text{ (calibration)}$$

$$U_{\text{ref}} \approx \pm u_{0.975} \cdot (sR_{L,\text{ref}}^2 - sr_{L,\text{ref}}^2)^{1/2}$$

For routine (alternative) methods, it is estimated according to ISO 8196 through

$$U_{\text{alt}} \approx \pm u_{0.975} \cdot (sR_{L,\text{alt}}^2 + s_{y,x}^2)^{1/2}$$

Overall uncertainty of routine testing results U is obtained by combining both types of error as

$$U \approx \pm u_{0.975} \cdot (sR_{L,\text{ref}}^2 - sr_{L,\text{ref}}^2 + sR_{L,\text{alt}}^2 + s_{y,x}^2)^{1/2}$$

The reference laboratory of every national laboratory network participates in national and international proficiency studies in parallel. Special training and procedures to ensure trueness and performance stability what is checked through international PT results (re qualification of reference laboratories).

The bridge between national and international levels is calculated through the difference D between national and international references of parallel trials (Figure 2). The latter difference is calculated through the scores obtained by the reference laboratory M (master) in one and the other trials $\Delta = \bar{d}_{MN} - \bar{d}_{MI}$ provided laboratory bias is shown constant (established by several successive international PTs).

Since then any laboratory L can estimate a virtual equivalent international score from its national score by subtracting Δ : $\bar{d}_{LI} = \bar{d}_{LN} - \Delta$

Uncertainty of the estimate must take into account several steps involved in bridging so it is larger than a direct performance evaluation.

$$U_{dLI} = \pm 2 \cdot [(\sigma_R^2 - \sigma_r^2) \cdot (1-1/nq) \cdot (3+1/p)]^{1/2}$$

- with large nq and p (labs) values: $U_{dLI} \approx \pm 2 \cdot \sqrt{3 \cdot (\sigma_R^2 - \sigma_r^2)}$
- with highly qualified master laboratories ($\sigma_{RM} \approx \sigma_{rM}$) and large nq and p values: $U_{dLI} \approx \pm 2 \cdot (\sigma_R^2 - \sigma_r^2)^{1/2}$

At a single level national or international it is easily realised through the difference

$$\bar{d}_{1,2} \text{ of scores of respective laboratories L1 and L2 (Figure 1), since } \bar{d}_{1,2} = \bar{x}_{L1} - \bar{x}_{L2} = \bar{d}_{L1} - \bar{d}_{L2}$$

It is expected to stay between

$$\pm 2 \cdot \sqrt{2} U_{dL} = \pm 2 \cdot [(\sigma_R^2 - \sigma_r^2) \cdot (1-1/nq) \cdot (2+1/p_1+1/p_2)]^{1/2} \approx \pm 2 \cdot \sqrt{2} \cdot (\sigma_R^2 - \sigma_r^2)^{1/2}$$

Result uncertainty

Traceability to an international reference

Comparison between laboratories

Between different trials, a virtual equivalent international differences can be estimated provided reference laboratories can establish correspondence to the international level (Figure 3) where the virtual difference can be calculated by

$$\Delta = \bar{d}_{LI1} - \bar{d}_{LI2} = (\bar{d}_{LN1} - \bar{d}_{LN2}) - (\Delta_1 - \Delta_2)$$

With $\Delta_1 = \bar{d}_{MN1} - \bar{d}_{MI1}$ the bias of the reference of Trial 1 to that of the international trial

$\Delta_2 = \bar{d}_{MN2} - \bar{d}_{MI2}$ the bias of the reference of Trial 2 to that of the international trial

Uncertainty of the difference must take into account the several steps involved in bridging for two national networks and is calculated from uncertainty of the uncertainty of international correspondence formerly mentioned through

$\pm 2. \sqrt{2} \cdot U_{dLI} = U_{dLI} \approx \pm 2. \sqrt{6} \cdot (\sigma_R^2 - \sigma_r^2)^{1/2}$ and with highly qualified master laboratories ($\sigma_{RM} \approx \sigma_{rM}$) $U_{dLI} \approx \pm 2. \sqrt{2} \cdot (\sigma_R^2 - \sigma_r^2)^{1/2}$

Certification of reference materials

Same type of trials as PT studies can be used to determine true value for reference materials provided the experimental design permit so.

ICAR protocol fit for purpose since proficiency testing and possible reference material are made to assess reference method and/or calibrate routine methods. For that reason it is recommended the sample number must be the same as that used for calibration. The minimum stated in ISO 8196 is 9. Guidelines are to be develop with this respect in the future.

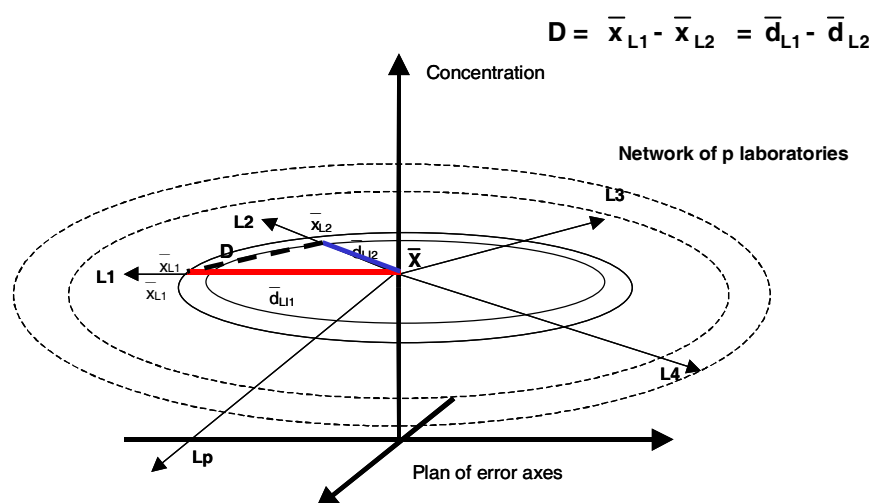


Figure 1. Between laboratory comparison through an interlaboratory study.

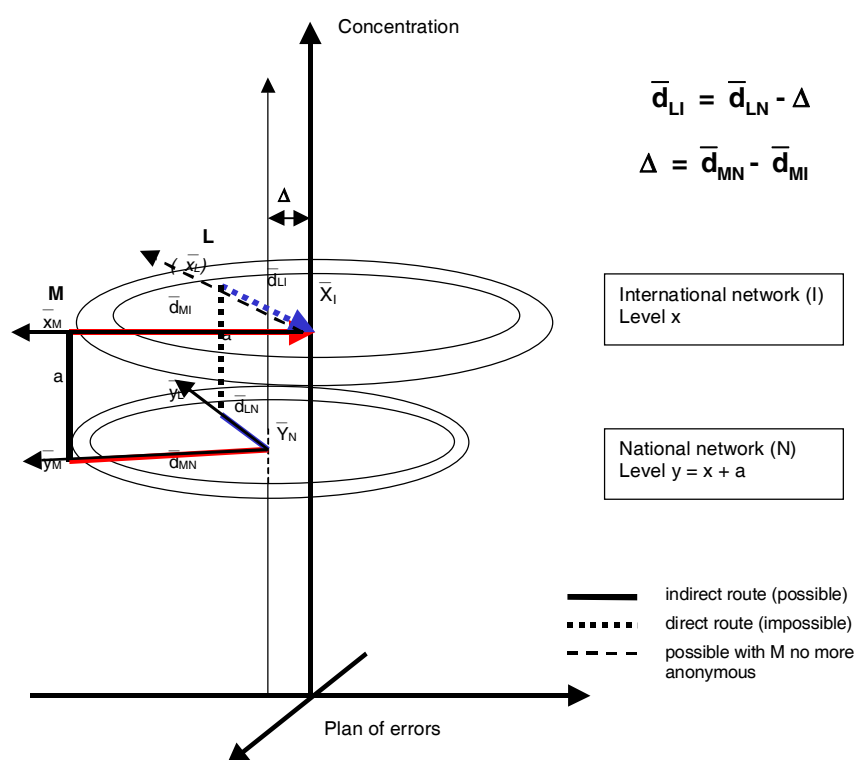


Figure 2. Assessment of the absolute performance of a laboratory versus an international reference via a master laboratory.

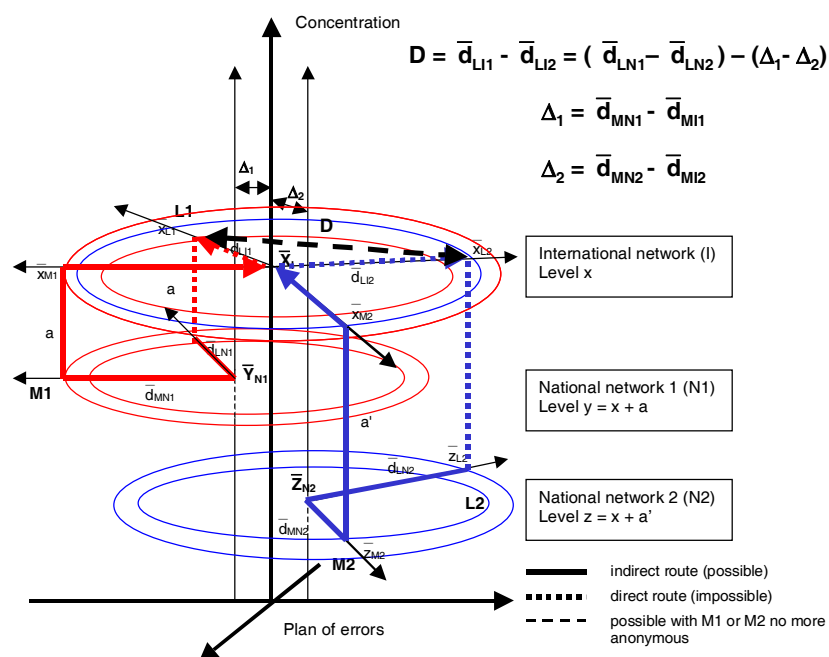


Figure 3. Absolute assessment and between laboratory performance comparison via master laboratories.

Thanks to performance evaluation through proficiency studies, it is possible to select best performing laboratories to establish true (reference) values for RMs. Otherwise the whole of participants can be used provided proper discarding of outlier results and laboratories.

ISO 5725 provides adequate recommendation for calculation of true values and the associated uncertainty valid for both lab performance evaluation studies and reference material certification studies.

Conclusion

International laboratory anchorage passes through interlaboratory studies organised for dedicated laboratory network implemented on national and international level. Connection between levels is established by expert laboratories members of networks at both levels.

Technical tools already exist to take full benefit of the system developed other are to be developed from the theory and prospects above presented.

ICAR Reference Laboratory Network is the corner of the system and must be enhance with increased worldwide representativeness and competence of members.

List of references

International Dairy Federation. 1999. Quality Assurance and Proficiency Testing. Report of Group E29. Bulletin of IDF 342/1999, 23-30.

ISO 8196-2. 2000. Milk - Definition and evaluation of the overall accuracy of indirect methods of milk analysis - Part 2: Calibration and quality control in the dairy laboratory.

ISO 5725-6. 1994. Accuracy (trueness and precision) of measurement methods and results - Part 6: Use in practice of accuracy values.

Leray O. 1995: Contrôle qualité et harmonisation des pratiques dans les laboratoires laitiers: Un enjeu pour le contrôle laitier/Quality control and harmonisation of laboratory practices in dairy laboratories: A challenge to milk recording. Proceedings of 29th Biennial Session of the International Committee for Animal Recording (ICAR). Ottawa, Canada, July 31-August 5, 1994. EAAP publication n°75, 1995, 179-182.

Interlaboratory reference systems and centralised calibration – Prerequisites and standard procedures

O. Leray

Actilait/Cecalait, Poligny, France

For the need of the international harmonisation and worldwide equivalence recognition of analytical data in milk recording, ICAR has undertaken the task to develop practical tools and methodologies in guidelines dedicated to laboratories to render calibration easier and cheaper as well as more efficient. Reference systems combining solid reference obtained through collaborative studies and centralised calibration are under focus and the underway description of adequate methods and procedures is presented.

Key words: *Reference, Calibration, Materials, Laboratories, Milk.*

Genetic evaluation on milk composition has become possible only through the generalised use of rapid automated method of milk analysis. Mid infra red spectroscopic methods and fluoro-opto-electronic methods have become predominant till being the only techniques used in large milk routine testing for milk composition and somatic cell counting.

For such methods calibration of routine methods is the key operation but also the most expensive to laboratories as it requires a lot of time and competence in sample preparation and reference analysis.

Sharing calibration cost between several laboratories thus amortising over many milk sample testing appears an economical alternative for laboratories beside the possibility to optimise both calibration sample quality and harmonise reference results through same values to all the laboratories. Indeed such calibration system can be easily associated to interlaboratory studies in order to optimise of the trueness of reference values for calibration.

Promoting the implementation of robust reference established by laboratory groups and centralised calibration in so-called reference system has become a new objectives of ICAR from 2006. Recommendations as pre-requisites and optimum procedures for implementation are needed for international harmonisation.

Summary

Introduction

Objectives and prerequisites

The objectives are to establish reference values for an appropriate material (milk) that can be valid for a community of laboratories (spread over a collect territory), transfer consensus reference values to the laboratories to calibrate routine methods and at end assess effectiveness of the system.

Prerequisites refer to the accuracy of routine methods, the harmonisation of laboratories, appropriate logistic conditions.

- Depending on the variation of milk composition in the collect areas and the sensitivity of methods to matrix effects, the accuracy value can become larger than in usual calibration. Before implementing centralised calibration it is of major importance to evaluate whether or not the extent of accuracy is acceptable for the intended purpose i.e. milk recording. With this respect it can be referred to experiment results presented in Kuopio (O. Leray, 2006).
- Methods, expression units (e.g. m/m, m/v, per 100 or per Kilo), criterion expression (e.g. True protein vs Crude protein) should be harmonised within the laboratory group so that calibration sample characteristics suit to every instrument equally.
- Sample preservation and transportation facilities should be adequate to analyse sample within short delays with no change in the physicochemical composition of calibration milk samples.

Means and tools

To achieve its goal, ICAR intends to produce suitable guidelines for laboratories on organising interlaboratory proficiency studies (PT) and centralised calibration (CC) and provide relevant services to countries.

International PT services are already supplied for the sake of the international reference harmonisation through a reference laboratory network according to a protocol approved by ICAR. This protocol should be detailed and become part of ICAR guidelines.

Developing/certifying international reference materials as gold standards is part of ICAR strategy beside promoting the use of national/local reference materials to relay international standard in countries either for checking reference methods or calibration.

Guidelines for proficiency studies

They will be in agreement with other general international standard on the subject which would be referred to but will additionally include specific requirements related to calibration and alternative methods thus establishing consistency with ISO 8196.

Particularly:

- The experimental design will be well stated with minimum numbers (e.g. 9 samples, 3 levels, 2 replicates) and concentration arrangement for optimised assessment (according to ISO 9622).
- Standard statistical analysis and presentation recommended using performance scores and target figures. Slope, linearity, interactions assessment will complete the statistical analysis for studies with routine methods. Examples were published in ICAR Session proceedings in Rotorua (1998) and the IDF Bulletin 342/1999.

Guidelines will indicate protocols to:

- Evaluate the overall accuracy in a centralised calibration system.
- Define the characteristics of calibration reference material.
- Assign reference values.
- Provide indications for line adjustment in the laboratory.

It can be performed by two ways, either once prior implementation of the system through an experiment provided natural conditions would not later, or through regular proficiency studies involving reference and routine methods.

Two protocols can be proposed depending on the situation:

1. In-lab experiment. It is carried out prior implementation with a unique instrument provided pre-required condition of harmonisation will be maintained later. A number of representative samples are collected in milk testing lab areas and analysed by the experimenting laboratory for both reference and routine methods. Operations are evenly repeated throughout a campaign of milk production and regional and seasonal effect are measured through ANOVA.
2. Interlaboratory studies. It is compared the reproducibility of routine methods to that of reference methods to decide whether or not centralised calibration provide equivalent laboratory bias distributions. In that case the information is general as the routine methods can be different with no relation to a well define analytical method. Recommendations of ISO 5725 are followed.

Adequate recommendation will be given to guarantee physicochemical quality of milk, sample preparation and batch homogeneity, preservation and shelf life, in particular with concern to the choice of the milk, milk and sample handling, chemical preservatives and sample containers.

Also indications for appropriate component arrangement and concentration range will be provided referring to optimisation of calibration and accuracy through specific designs with recombined (modified) milk samples (O. Leray, 1998, FAIR CE 1997-1999).

To limit the risk of systematic bias and get the agreement of all laboratories and parties they should not be established by a single laboratory but instead by all the laboratories of the concerned group.

The way to define reference values relates on whether or not matrix effects exist with the routine methods.

Where there is no matrix effect representativeness of calibration milk is of lower importance and focus is made only on physicochemical quality and concentration characteristics. Reference values are determined using the means of reference results of all the laboratories obtained in an interlaboratory study (Figure 1).

This is the same way also used in case of matrix effects when using milk materials well representative of the area (e.g. silo bulk milk) but choice must then be made on whether or not final calibration adjustments are locally required in laboratories with regard to laboratory biases observed. The assigned values are here used for

Guidelines for centralised calibration

Evaluation of the overall accuracy of a centralised calibration system

Characteristics of RMs for calibration

Assigning reference values

pre-calibration (assessing slope, linearity, inter-correction fittings) whereas calibration is completed using one or more bulk milks representative of the area (Figure 2).

When using recombined (so-called modified) milk samples, greatest interest must be given in maintaining the native physicochemical quality of milk hence representativeness may not be reached. Through the matrix effect so-prepared calibration sample are not on the average line of the population. The assigned values are then obtained through a correction from the bias between the routine and the reference method with one or more bulk milks representative of the area. Calibration can be completed or not for individual labs (as above mentioned) depending on the range of local biases and the need of milk testing purpose.

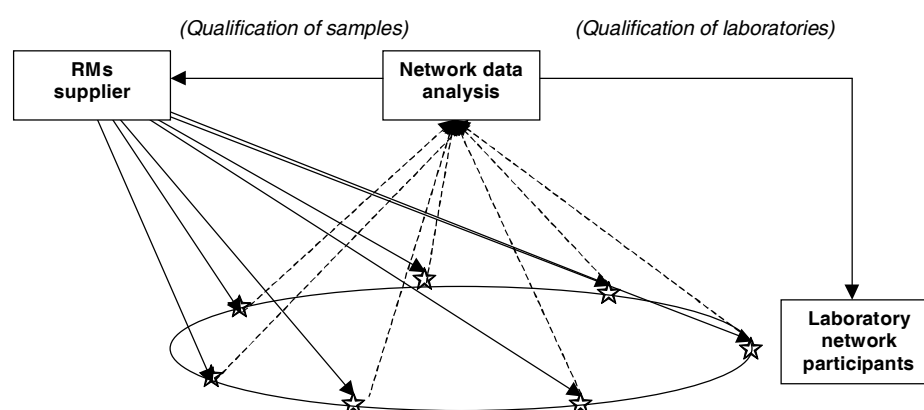


Figure 1. Scheme of assigning reference values for reference materials using interlaboratory proficiency studies.

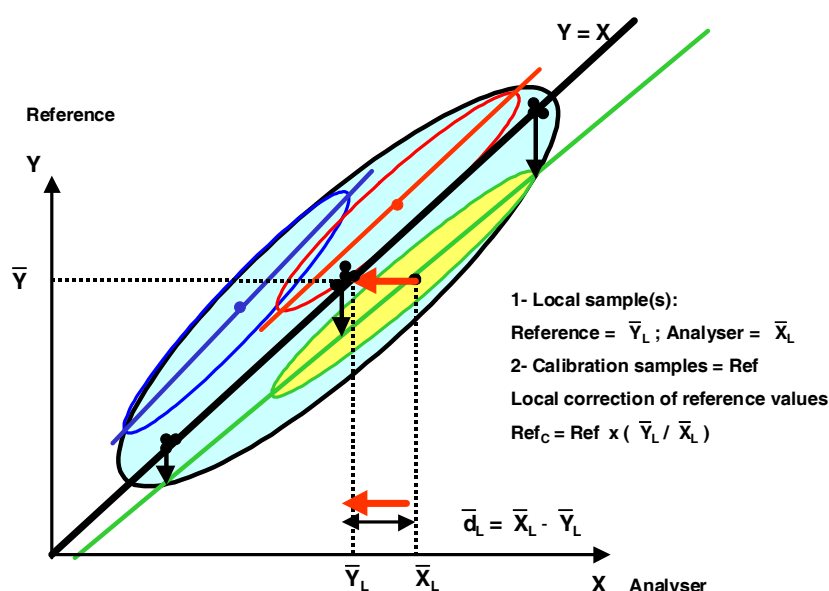


Figure 2. Correction of assigned values (Y) of calibration samples (black arrow) to reduce the laboratory bias (red arrow) analysing the yellow population.

Recommendations for calibration operations are to follow the normal procedures of manufacturers and ISO 8196 in which centralised calibration is mentioned as a possible option. This is to 1- Check and where needed optimize instrument fittings (pre-calibration), 2- Adjust calibration, 3- Assign values for control samples.

Centralised calibration associated to collective determination of reference values for calibration is considered as an optimum combination to assure harmonisation of milk recording analytical data. Methodologies and technical tools have already been defined, experimented showing large efficiency. Such a combined system should serve ICAR countries to evolve towards easier and cheaper calibration systems and respond to forthcoming analytical demands of milk recording (for instance on-farm analysis).

International Dairy Federation. 1999. Quality Assurance and Proficiency Testing. Report of Group E29. Bulletin of IDF 342/1999, 23-30.

ISO 5725. 1994. Accuracy (trueness and precision) of measurement methods and results – All parts

ISO 8196-2:2000 | IDF 128. 1999. Milk - Definition and evaluation of the overall accuracy of indirect methods of milk analysis - Part 2: Calibration and quality control in the dairy laboratory.

ISO 9622. 1999. IDF 141:2000 - Whole milk – Determination of milk fat, protein and lactose content – Guidance on the operation of mid-infrared instruments.

Leray, O. 1988. Protocole de préparation d'échantillons de lait reconstitués destinés à l'étalonnage des appareils infra-rouge. Note Technique ITEB-INRA Poligny n°1, France.

Leray, O. 1989. Ajustement/calcul des intercorrections des spectromètres utilisés pour les dosages TB-TP-TL du lait en moyen infra-rouge. Note Technique ITEB-INRA Poligny n°2, France.

Leray, O. 1990. Procédure d'étalonnage des analyseurs infra-rouge au moyen de gammes d'échantillons de lait reconstitués. Proceedings of the 27th Biennial Session of ICAR. Paris.

Leray O. 1998. Quality control of conventional mid-infra-red milk analysers using recombined milk samples. Proceedings of 31st Biennial Session of the International Committee for Animal Recording (ICAR). Performance Recording of Animals. State of the art, 1998. EAAP publication n°91, 1998, 131-138.

Calibration

Conclusion

List of references

The way to reference systems and centralised calibration for milk recording testing. Present status in Germany

C. Baumgartner

Milchpruefring Bayern e.V., Hochstatt 2, D-85283 Wolnzach, Germany

Summary

In a globalizing world analytical results play a major role in free and fair trade. Global trade needs global validity of analytical results! This means that analytical results have to be equivalent worldwide at any place, at any time and despite what method has been used.

Some sources of error are affecting this analytical equivalence: Bad performance of reference methods and/or reference labs in characterizing (secondary) reference materials, insufficient reference materials in terms of imprecise target values and/or problems with shelf life, shipment etc. and failures in calibration of routine methods as well as information gaps and misinterpretations are hindering the optimal use of capabilities.

IDF has started a discussion about how to cope with these problems. In Bulletin 427/2008 a paper outlines the way towards a reference system for somatic cell counting as an example of how to come to a solution.

In this paper the author deals with the present status of implementing such a reference system in Germany. After a short description of the dairy sector in Germany and especially Bavaria, a picture is drawn of the DHI system and the laboratory work. Different aspects of QA in laboratories and the interlaboratory reference system in Germany are highlighted and it is shown, how the German system is interlinked with the ICAR Reference Laboratory System.

The author strongly pleads for cooperation between analysts on all levels. ICAR should join the IDF activities and assist in creating an international structure for reference systems. Centralized calibration procedures could be one of the tools to step forward.

Key words: *Analytical reference systems, Centralised calibration, Equivalence of analytical results, Dairy sector in Germany, Interlaboratory reference system.*

Reference system and centralized calibration for milk recording testing in Argentina

R. Castañeda

INTI Lácteos. Buenos Aires, Argentina

Milk production in Argentina was over 10 billion liters in 2006. This figure positions the country in the 11th place in the ranking of world milk producers, and in the 2nd as regards Latin America. There are 2.5 million dairy cows, most of them pertaining to *Holando-Argentina* breed, producing approximately 4 000 liters of milk/cow/year. The Argentine dairy industry is geographically distributed all over the country. Five provinces making up the so-called Pampeana Region produce 94% of the milk in a surface area of 800 000 square kilometers. The country has 14 000 dairy farms and 1 100 dairies of different sizes where milk products are manufactured. This milk is mainly used in the production of cheese (45%); milk powder (24%); pasteurized and sterilized fluid milk (19%) and other products.

The “*Holando- Argentina*” breed was introduced into Argentina from Holland in 1880. These cows are medium sized with the height of 1.40 to 1.5 meters, having a large barrel allowing them to have a high intake of forage. In 1944, breeders create an organization to promote the breed and to provide necessary technical support named *Holando- Argentina* Breeders Association, ACHA. In 1981, the government (Department of Agriculture) delegate by law the “*official dairy herd improvement*” system in ACHA. The breeder association is a full member of ICAR in 1991 and subscribed an agreement with INTI, the National Institute of Industrial Technology in 2003, for the creation of a technical assistance and control laboratory network that began to work the follow year, committing DHI laboratories to participate in proficiency testing schemes under REDELAC, the network of INTI.

Since early in the 20th Century milk producers in the Argentine Republic started to control their cows’ production with the purpose of improving cattle quality. Nowadays we have: 2 000 dairy farms in “official milk control”, 510 000 cows under this system, 11 DHI laboratories that analyze the composition of the milk and a reference national laboratory that control the performance of DHI laboratories. Tests carried out include milk fat and protein content, and somatic cell count.

Introduction

Milk control in Argentina

Testing laboratories for milk recording

There are currently 11 laboratories conducting tests for official milk control in different provinces. Most of them are private and/or provincial laboratories, independent of producers or of the industry, supplying services to the milk chain, essentially as regards milk control, milk payment according to quality standards and other process control tests. Testing laboratories are distributed in different provinces according to the list in table 1.

On a monthly basis, results obtained at these laboratories participate in control schemes with the National Reference Laboratory namely INTI-LÁCTEOS who has, jointly with ACHA, the mission to supervise the laboratories supplying services to Official Milk Control Entities, as well as to provide technical support in equipment calibration and training the corresponding human resources.

National reference laboratory

INTI LÁCTEOS is the laboratory appointed by ACHA as the reference laboratory, with vast experience in technical assistance to milk labs; it is also the supplier of interlaboratory trials and reference materials. In turn, and complying with ICAR instructions, ACHA has requested the inclusion of INTI Lácteos as the national reference laboratory (NRL) for Argentina in ICAR laboratory network.

INTI LACTEOS is the Technological Research Center for the Milk Industry and was created in 1968. It is one of the nearly 40 INTI centers, the National Institute of Industrial Technology, a decentralized entity depending upon the Argentine Ministry of Economy. INTI, among many other responsibilities, is the National Metrology Institute in Argentina.

Seventy five professionals and technicians work at INTI LÁCTEOS, providing consultancy and technical support to all links in the milk chain, and among them, to testing laboratories. The center is headquartered in the city of San Martín, in the province of Buenos Aires and in the city of Rafaela, in the province of Santa Fe. Its scope includes training, assistance, development, innovation and testing activities. INTI LACTEOS has laboratories for milk quality, physicochemical testing, microbiology, residues and contaminants, sensory evaluation, and others.

Table 1. List of milk testing laboratories operating for milk recording in Argentina.

Name	City	Province	Belongs to
Alecol	Esperanza	Santa Fe	Milk producers
Ceret	General Pico	La Pampa	Provincial state
Funesil	Villa Maria	Cordoba	Private
Insulab	Venado Tuerto	Santa Fe	Private
Labrolac	Las Varillas	Cordoba	Milk producers
Labvima	Trenque Lauquen	Buenos Aires	Private
Labvima	Villa Maria	Cordoba	Private
Lacle	Buenos Aires	Capital Federal	Private
Lever	Paraná	Entre Rios	Provincial
Matco	Lujan	Buenos Aires	Private
Sancor	Sunchales	Santa Fe	Dairy Industry

In compliance with ICAR requirements regarding the mandatory character of maintaining certified quality systems, INTI Lácteos labs in Buenos Aires and Rafaela conduct analytical assessments, organize proficiency test programs and supply reference milk material pursuant to ISO 17025, ISO 43, ILAC G13, and ISO 34 systems, certified by the official Argentine Accreditation Body (OAA) and the National Accreditation Entity of Spain (ENAC).

Since 1991 INTI LÁCTEOS has also been the reference laboratory for REDELAC (www.redelac.gov.ar), a network of Argentine milk laboratories developed by INTI itself, whose purpose is to provide such laboratories with the tools to maintain their technical competence. Milk industry laboratories are included in this network; there are many of them with high technical competence, and some of food laboratories in general. INTI LÁCTEOS maintains a wide suitability testing program for different milk matrixes that has been accredited by ENAC since 10/15/04, through Certificate 001/PPI001. It has also developed a centralized calibration system for milk analysis instruments, called SICECAL, currently in the certification process under ISO 34 Standard.

Technical assistance and control of milk testing laboratories result from a wide experience in this field, where work has been done since 1991 in order to obtain homogeneity in results and maintain metrological traceability between the testing laboratory, the national reference laboratory and international labs.

Assistance consists in training actions, both in analytical tests subjects and in quality assurance subjects. Laboratory control is carried out through a scheme based on:

1. Centralized calibration.
2. Control of performance of laboratories.
3. An evaluation of the laboratories by an ACHA-INTI committee to ascertain its performance and to set the adequate corrective actions if required.

SICECAL is a system of preparation, analysis and delivery of reference materials in dairy matrix for calibration and control equipment. It is a widely used tool in Argentina to calibrate different types of analyzers used in milk laboratories. It consists in sending monthly standard samples for

- Calibration of infrared analyzers (fat, proteins, totals solids, lactose, ash).
- Adjustment of fluoro-opto-electronic equipment for somatic cell count.
- Calibration of milk cryoscopes.
- Others.

The use of these Reference Materials is not mandatory, and this is so since there are big laboratories that prepare their own materials.

This Reference Materials are produced in INTI Lácteos in Rafaela according the requirements of the guide ISO 35. For calibration or IR equipment, 11 and 5 samples of raw milk are sent in the first week of the month. Composition: fat: 2.50 to 5.00 g/100 ml, protein: 3.00 to 3.60 g/100 ml, lactose: 4.60 to 5.00, ash: 0.68 to 0.82 and dry matter content: 11.80 to 13.80. Milk composition is informed with the pertinent uncertainty. Participants receive a delivery schedule early each year.

Assistance and external control of milk testing laboratories

Centralized calibration system SICECAL

For adjustment of somatic cell equipments, 3 samples of raw milk are sent in the first week of the “pair” months. Composition: “low” somatic cells counting (170 000 cel/ml); “medium” (430 000 cel/ml); and “high” (700 000 cel/ml).

Samples are prepared with mixed raw milk. The reference value is obtained by IDF reference methods in quadruplicate. There are checks of the reference value (named “previous SICECAL”) where the laboratory test the value in four (4) IR-equipment or SC-equipment in other recognized laboratories. Test of homogeneity and stability are performing according to the requirements in guide ISO 35. With these samples, laboratories calibrate, re-calibrate, verify or adjust testing equipment.

Performance assessment of DHI laboratories

The control of performance of DHI laboratories is carried out through two types of actions:

- *Monthly check* of results of laboratories. Every second Tuesday of the month, (one week after centralized calibration), laboratories receive one sample to analyze fat, total proteins and somatic cells count by their routine methods. They are obliged to send results in time to INTI Lácteos.
- *An Bi-annual interlaboratory trial*. Each six month, the laboratories receive 10 samples to analyze fat, total proteins and SCC. They must submit results in time to INTI Lácteos.

In the monthly check DHI laboratories receive one blind sample for each parameter to check, to be analyzed in a period of time. The comparison of results with INTI Lácteos permit assures the suitability of the equipment to conduct milk control tests. Samples are prepared with mixed raw milk. Composition: 2.5-4 % of fat, 2.8-3.5 % total proteins, 100 000 700 000 SCC, and others. Test of homogeneity and stability are performing according ISO 13528 standard. Usually, as these laboratories also analyze samples for milk payment purpose, they also receive additional samples to check the results of other milk quality parameters (antibiotic residues, bacteria total count and freezing point). It is interesting to remark that logistics for sending these samples is not a minor topic, since samples have to arrive at laboratories in time and good state of preservation.

Results of laboratories are compared against the reference value obtained by INTI Lácteos in Buenos Aires by using IDF reference methods, and applying an ISO 17025 quality system accredited by the OAA. The reference value must be not statistically different of the robust media (26 laboratories nowadays). If yes, the NRL studied the reason and decide which reference will be use. Next, a results report is issued where it is shown whether results obtained for each test are comparable to results obtained by NRL, the performance of the latest 12 month of the laboratory and a comparison of the laboratory with the other laboratories participating in the PT scheme.

In the bi-annual interlaboratory trial, laboratories must participate in a proficiency test where 10 samples with variable percentages of fat, protein, lactose, total solids content and somatic cell count are sent. This inter-comparison scheme is improved under an ISO 43 / ILAC G13 quality system accredited by ENAC. The NRL send 10 different samples for each component. They are prepared with raw milk as IDF Standard 141:2000 by separation and recombination of components. The composition is: range of 2.5-4 % for fat; 2.5-3.5 % for total proteins; and 100 000-700 000 for SCC. Test of homogeneity and stability are performing according

ISO 13528. The reference value is obtained by consensus of all laboratories, calculating robust media. INTI Lácteos analyze also the samples by IDF reference methods, in duplicate, to assure results.

The results of these reports are analyzed by an INTI-ACHA Advisory Committee created within the framework of the technological linkage agreement subscribed by both institutions. This advisory committee hold meeting every two month and decides the actions to follow according the evaluation of each laboratory.

Evaluation of results

The reference system for milk recording testing in Argentina is based on the action of a national reference laboratory and DHI dairy laboratories, which interchange information, technical assistance and control mechanisms. The characteristics of our country and our milk permit a centralized calibration of testing equipment and a frequent control of milk recording testing laboratories. At a time, the NRL check your own performance by means of PT schemes with international institutions. These metrological scheme permit Argentina maintain a good traceability between laboratories and international institutions by means of inter-comparisons. This characteristics show a metrological system for milk measurements according the importance of the argentine dairy industry.

Conclusion

Reference system and centralised calibration for milk (payment) testing

D. Barbano

Cornell University, Department of Food Science, Ithaca, NY 14853

A modified milk calibration set has been developed for use in a network of payment testing laboratories in the US. The set of calibration samples consist of 14 samples produced with an orthogonal matrix of composition with respect to variation in fat, protein, and lactose. The range of fat content is from 0.2 to 5.8%, true protein from 2 to 4.3%, and anhydrous lactose from 3.9 to 5.2%. The modified milk calibration samples are produced 12 times per year and serve as a proficiency test for the reference chemistry methods performed in all the laboratories and a set of calibration samples for infrared milk analyzers. These samples are used to set slope and intercept of the intercorrected mid-IR signal.

The modified milk calibration samples serve three purposes. First, each month the testing of these samples provides a proficiency test of the fat by ether extraction, the true protein by Kjeldahl, the anhydrous lactose by enzymatic, and total solids by oven drying methods. The orthogonal matrix of composition of the set of samples provides some interesting diagnostic and trouble shooting opportunities that are used to improve the performance of the laboratories that run the chemistry methods. The performance of individual laboratories and the group of laboratories for the chemistry methods has been improved. Second, the all-laboratory mean with outliers removed is used to create a fat, protein, and lactose reference value for each sample. Third, the samples are used for 1 month to set the slope and intercepts for each instrument. Because of the orthogonal matrix of composition, the data can be used to evaluate the linearity and intercorrection response of each instrument. These evaluation calculations and protocols are built into a software package we have written called IR-QC. Instrument Calibration Performance has been improved by using the modified milk calibration samples and all-lab mean reference values. The standard deviation of the difference between reference chemistry and instrument values on all components is $< 0.015\%$ and often $< 0.01\%$ using a traditional filter based calibration approach. The size of the 95% confidence interval around the slope of the regression line has been reduced greatly by the use of the modified milk calibration samples, compared to the performance that is achieved by using raw milks from individual farms for calibration. This is due to the homogeneity of the matrix of the modified milks and elimination of the influence of high leverage samples from the calibration set.

The network of laboratories does monthly pre-calibration performance evaluations of instrument performance. Homogenizer performance is monitored by a central laboratory at Cornell University using laser light scattering particle size analysis. Homogenizers that have failed the homogenization performance evaluation by particle size analysis are inspected by microscopic evaluation to determine the cause of failure.

In our research we have developed an optimized set of traditional “virtual” sample and reference filter wavelengths for use in FTIR instruments and we are in the process of publication of that information. We have also made a quantitative determination of the impact of variation in fatty chain length and unsaturation on Fat B and Fat A on absorbance at sample and reference wavelengths with a model sample system. That work is complete and in the process of publication. We continue to work toward the goal of improving the accuracy of the infrared milk testing to achieve the most accurate testing results on any instrument, on any sample, at any time.

**Workshop on
"Use of genomic tools in animal breeding"**

Bull selection strategies using genomic estimated breeding values

L.R. Schaeffer

CGIL, University of Guelph, Guelph, Ontario, Canada N1G 2W1

Several strategies for selecting bulls in an artificial insemination (AI) stud under Canadian conditions using genomic estimated breeding values (GEBV) as the selection criterion were compared for genetic response in the cow population and cost of operation using stochastic simulation of AI stud operations over 55 years. A constant population size of 1 million cows and an AI stud currently testing 400 young bulls per year were assumed. Correlations between GEBV and true breeding values (TBV) were varied between 0.4 to 0.8. Different numbers of young bulls to be genotyped were varied from 500 to 4000 per year. Scheme A selected young bulls for progeny testing on the basis of GEBV. Scheme B assumed that young bulls with GEBV could be used immediately as sires of sons based on their GEBV. Other variations between Schemes A and B were also compared. Results showed that use of GEBV increased genetic gains in the population regardless of the correlation between GEBV and TBV. Using young bulls with high GEBV at one year of age to sire the next generation of young bulls gave greater genetic responses in the cow population at almost 1/4 the cost of the traditional progeny test program. Initially, AI studs will likely continue with progeny testing, but may use young bulls with high GEBV at one year of age to sire a portion of the new young bulls. Once producers are comfortable with GEBV, then the AI stud could switch entirely to Scheme B. Turnover rates of bulls in the AI stud will be more rapid when GEBV are used than in PT.

Summary

Key words: *Single nucleotide polymorphisms, Simulation model, Genome-wide selection schemes.*

Panels of thousands of single nucleotide polymorphisms (SNP) spread approximately evenly over the genome are available for genotyping of dairy cattle. Each SNP location in the genome has three possible genotypes, and attempts are made to estimate the effects of each genotype at all locations on the genome simultaneously using estimated breeding values (EBV) or de-regressed proofs of bulls as the observations. Different methodologies have been proposed and are being used for this purpose. Estimates of the SNP genotype (or haplotype) effects

Introduction

can be summed together based on the genotype of the animal to give a genomic estimated breeding value (GEBV). The GEBV can have accuracy equal to or greater than a parent average (PA) derived from EBV of parents. The primary advantage of the GEBV is that it can be obtained shortly after an animal is born (or possibly even in an early stage of embryonic development) such that selection decisions can be made early. In a progeny testing (PT) scheme, young bulls wait for their progeny-based EBV until they are six years of age.

The objective of this study was to use simulation to compare bull selection strategies for a typical AI stud under Canadian conditions that use GEBV for young males, in terms of genetic gain in the cow population and costs of operation for the AI stud. Various possible alternatives were compared.

Simulation model

Progeny testing assumptions

A population of 1 million cows serviced by a single AI stud that currently tests 400 young bulls per year was assumed. In any year, 50 proven sires were used to breed the population of cows, and the best 20 sires were used as sires of the next generation of young bulls. Dams of young bulls were randomly chosen from the top 5% of the cow population based on their EBV having an assumed reliability of 0.50.

Young bulls were assumed to have enough matings to provide 100 daughter records in their first progeny test proofs. Proven sires were differentially mated to the remaining population based on their EBV. The top 10 bulls had 20% of the matings, the next 10 had 50%; the next 10 bulls had 20%, and the last 20 bulls had only 10% of the matings. Every 12.5 matings resulted in a daughter record for proven bulls.

Bull calves were purchased at birth, test mated at one year of age, and proven at 6 years of age during the PT program. Cost of purchasing a young bull for PT was \$10 000. At proof time, all newly proven bulls plus the current group of 50 proven sires were ranked on their EBV, and the best 50 kept for the next year, with the top 20 being sires of sons for the next generation. Cost of keeping a bull in the stud for one year was \$6 000. All dollar figures were kept constant over the simulation period of 55 years.

A single trait, representing an overall index, was simulated having a heritability of 0.30. A total of 55 years of operation was simulated, with the first 20 years being the same for all schemes compared in this study. Changes in selection strategy began in year 21. Thus, comparisons were for years 21 to 55. One hundred replicates were run for each scenario.

Genome-wide selection schemes

The cost of genotyping an animal was \$300. The correlation of GEBV with TBV was assumed to be constant over time. In reality the correlation is expected to decrease, if the SNP genotype estimates are not updated. Thus, the assumption was made that research and methodology will at least keep the correlation constant over time. Another possibility would be that research could increase the correlation over time, but that would make the results better than reported here. The correlation was varied from 0.4 to 0.8.

In this scheme, a number of young bulls from top dams were genotyped and a GEBV computed with a reliability equal to the square of the correlation between GEBV and TBV. From this group the best were kept to enter the PT program. The number of bulls genotyped was varied from 500 to 4 000, and the number kept for PT was varied from 100 to 400. The purchase price was still \$10 000 per young bull.

Scheme A would be used when producers do not trust the reliability of GEBV, and still want to see daughters in lactation before they decide to use a bull. The cost of Scheme A will be at least the same as PT, but there will be the additional costs of genotyping young bulls.

Scheme B would be used if there were complete confidence in the reliability of GEBV, and animals with a GEBV were considered “proven”. The AI stud genotypes a number of young bulls at birth and calculates their GEBV. The young bulls are purchased and brought into the stud if their GEBV is greater than the minimum proof of the current “proven” sires, up to a maximum of 50 young bulls per year. The cost of buying these young bulls was assumed to be \$20 000 instead of \$10 000. If a young bull was in the top 20, then that bull was used as a sire of sons at one year of age.

Scheme B was less costly than Scheme A because fewer young bulls were purchased per year, and fewer bulls were in the stud. Scheme B should give better genetic gain than Scheme A because the genetically superior bulls are used at one year of age instead of waiting until they are 6 years old.

An AI stud has a big investment in facilities for handling a large number of young bulls per year plus the labour force to make it run. Thus, converting from PT to Scheme B in one year would be very disruptive. Also, some producers will be reluctant to use young bulls as proven sires. Thus, there could be an intermediate plan that progeny tests young bulls chosen on their GEBV, and the AI stud could use a portion of those young bulls as sires of sons. As producers accept GEBV bulls, then fewer young bulls could be progeny tested, and a greater percentage of young bulls could be used as sires of sons. Eventually, Scheme A would evolve to Scheme B. The number of young bulls chosen for PT was reduced from 400 to 200, and the number of young bulls used as sires of sons was either 5 or 10. Young bulls chosen as sires of sons were only used for one year, then returned to the PT. The bull could possibly return to the top 20 if its progeny test proof was very high. However, such an event was very unlikely. The cost of Scheme C would be intermediate to Schemes A and B, depending on the number of young bulls progeny tested per year. Genetic gain may be closer to that of Scheme B, because some young bulls are being used as sires of sons.

Usual progeny testing gave a response of 0.26 genetic standard deviations (GSD) change per year at a cost of \$18.7 M. There was a turnover of 26 bulls per year of the top 50 proven bulls or approximately one half of the top 50 bulls were replaced annually.

Results for 10 versions of Scheme A are given in Table 1. Schemes A1 to A4 used a correlation of 0.4 between GEBV and TBV while the number of young bulls that were genotyped ranged from 500 to 4 000. As more bulls were genotyped the genetic

Scheme A – GEBV to select young bulls for progeny testing

Scheme B – Using young bulls with GEBV as proven sires

Scheme C – Between Scheme A and Scheme B

Results and discussion

Scheme A

gain per year was increased, but also the cost of the operation was increased above that for usual PT. The turnover of bulls in the top 50 also increased to 33 out of 50 bulls being replaced annually.

Schemes A5 to A8 and A3 can be used to observe the trend due to an increase in the correlation between GEBV and TBV from 0.4 to 0.8. The increase in genetic gains were very small, while the costs remained constant at \$20.0 M. The turnover rate increased from 32 to 34 bulls per year.

Schemes A9 and A10 were made to see the effect of reducing the number of young bulls that were progeny tested. Costs were greatly reduced while genetic gains were not greatly affected. Turnover of the top 50 proven bulls was slightly lower than when testing 400 bulls per year (Table 1).

Spelman *et al.* (1999) conducted a similar study where all four pathways of selection were changed by using marker information. Although the population they simulated was smaller and the number of bulls in the progeny test was only 140 per year, the results were similar to those presented here.

Scheme A does not take advantage of the fact that the genetic merit of a bull is known at birth with an accuracy better than a parent average EBV. The young bull still goes through the same waiting period to receive a progeny test EBV before it is used for general breeding in the population. The gains here are due to slightly better accuracy in picking the 400 bulls for progeny testing. Thus, increasing the number of young bulls that are genotyped increases the selection intensity amongst choices of young bulls for progeny testing. The correlation between GEBV and TBV has a very small contribution to greater genetic gains.

Scheme B

Use of young bulls as sires of sons of the next generation when they are just 1 yr of age results in bigger genetic gains than PT or Scheme A because of the advantage of having a GEBV at birth. Scheme B4 gives twice as much gain than PT, and 1.47 times as much as A4 in Table 1. The effect of number of young bulls genotyped at birth also has a greater effect than in Scheme A. At the same time, because no more than 50 young bulls are purchased per year, the costs of operation are 64% smaller

Table 1. Comparison of genetic gains and costs of operation for selecting young bulls for progeny testing using GEBV.

Label	Corr.	No. Geno.	No. PT	Turnover	GSD/yr	\$\$M
PT			400	26	0.26	18.7
A1	0.4	500	400	28	0.28	19.4
A2	0.4	1000	400	30	0.31	19.6
A3	0.4	2000	400	32	0.34	20.0
A4	0.4	4000	400	33	0.36	20.6
A5	0.5	2000	400	32	0.34	20.0
A6	0.6	2000	400	33	0.34	20.0
A7	0.7	2000	400	34	0.34	20.0
A8	0.8	2000	400	34	0.35	20.0
A9	0.6	2000	200	32	0.35	10.8
A10	0.6	2000	100	28	0.34	6.1

(B4 versus PT). The effect of increasing the correlation between GEBV and TBV offers more gain than in Scheme A, but this is a small effect. Turnover of bulls is higher than for Scheme A (Table 2).

Scheme A makes minimal use of GEBV at an early age, and Scheme B uses GEBV immediately to select future sires of sons. Both gains and costs are improved greatly by using GEBV. AI studs, however, have a large investment in facilities and labour that are no longer needed with Scheme B. From a management and human relations viewpoint, switching to Scheme B in one year would not be possible. Two scenarios were examined. Both scenarios assumed a correlation of 0.6 between GEBV and TBV, genotyping of 2000 young bulls per year, and progeny testing only 200 per year instead of 400, as in Scheme A6. In addition, the best 5 or 10 young bulls were used as sires of sons along with the current proven bulls. After being used as a sire of sons the young bulls were returned to the PT program.

The genetic gains were 0.43 GSD per year for 5 young bulls as sires of sons, and 0.46 GSD per year for 10 young bulls. The cost of each scheme was \$10.1 M per year. Therefore, Scheme C would be 1.23 times better than Scheme A9, 0.83 times less than Scheme B6, and 1.65 times better than PT.

Advantages of Scheme C are that it accommodates producers that will hang on to the proven bull concept, and also the producers that want to be aggressive in their genetic improvement program. The AI stud is positioned to switch entirely to Scheme B when the time is appropriate, and the costs of operation are reduced from the current PT scheme.

As with bull selection, genetic gains are going to be greatest when genotyping females at birth and selecting them as dams of sires and dams of future cows at birth before they are old enough to be bred. The reliability of GEBV on females should be just as accurate as they are for males. Also, GEBV on females should be free of the effects of preferential treatment that commonly affect EBV of dams of sires. AI studs may have to help finance the genotyping of prospective dams of sires, and may need to have different kinds of contracts with producers to prevent costs of new young bulls getting too high.

Table 2. Comparison of genetic gains and costs of operation when young bulls are used as sires of sons at one year of age.

Label	Corr.	No.Geno.	Turnover	GSD/yr	\$\$M
B1	0.4	500	29	0.44	3.1
B2	0.4	1 000	32	0.47	4.0
B3	0.4	2 000	34	0.50	5.1
B4	0.4	4 000	37	0.53	6.7
B5	0.5	2 000	35	0.51	5.4
B6	0.6	2 000	36	0.52	5.8
B7	0.7	2 000	38	0.53	6.4
B8	0.8	2 000	40	0.55	7.3
B9	0.6	500	31	0.45	3.5
B10	0.6	1 000	34	0.49	4.5
B11	0.6	4 000	39	0.55	7.5

Scheme C

Genotyping females

Producers are concerned about AI studs having knowledge about their cows' GEBV that they may not have. Thus, Canada is planning for a public distribution of GEBV to all industry members. GEBV will be combined with EBV by Canadian Dairy Network, and the combined values will be released to the public. Exact rules and regulations around this ideal still need to be determined.

Problems will arise as SNP panels will likely change over time, and there could be several competing panels existing at one time. Associated with that will be the estimation of SNP genotype effects for each SNP panel.

Inbreeding

Rates of inbreeding were not included in this study, but the anticipation is that inbreeding rates could increase faster than with PT. The turnover rates of bulls will be greater, as in Scheme B, and this could lead to greater rates of inbreeding. However, the number of sons per sire of sons should be evenly distributed. If large numbers of young bulls are genotyped per year (2 000 - 4 000 bulls), then these could represent a larger group of dams in the population, and might help keep inbreeding rates low. Female bloodlines not commonly used in PT might be discovered.

If animals are genotyped, then a comparison of their genotypes would give an indication of their relatedness, and then the mating could take place or be avoided. Inbreeding rates could be kept low by close monitoring of matings.

Conclusions

GEBV will become the primary tool for bull and cow selection in the future. The genetic potential of an animal will be known at the animal's birth with reasonable accuracy, such that the animal will be considered "proven" without having made a record or having any progeny. Progeny testing will become obsolete as a tool for genetic improvement in dairy cattle. Nearly all animals that are born will be genotyped for a large number of SNP.

Molecular genetics will continue to make advancements, such that SNP will be replaced with the actual genes. Thus, GEBV will become more accurate over time. Genes with large effects will become known for many traits. However, there is still a lot of work to be done to make these ideas successful.

**List of
References**

Spelman, R.J., D.J. Garrick, & J.A.M. van Arendonk. 1999. Utilisation of genetic variation by marker assisted selection in commercial dairy cattle populations. *Livest. Prod. Sci.* 59, 51-60.

Genomic selection in New Zealand and the implications for national genetic evaluation

B.L. Harris, D.L. Johnson & R.J. Spelman

LIC, Private Bag 3016, Hamilton, New Zealand

The BovineSNP50 BeadChip provides genome-wide dense-marker data. LIC genotyped 4,500 sires using the BovineSNP50 BeadChip. Genomic breeding values (GBVs) were estimated for 25 traits. There were several methods used to analyse the SNP data. Increased accuracy was obtained by using MCMC Bayesian methods compared to BLUP. However, the increased accuracy was small, often in the range of a 2-3% increase in the correlation between progeny test and genomic breeding values. The training statistical analysis was undertaken within and across breeds. The SNP estimates calculated from the Holstein-Friesian (HF) training data did not produce accurate GBVs in the Jersey test data and vice-versa. However, correlations for the crossbred bulls (HF – Jersey crosses) were largest when all sires of all breeds were included in the training data subsets. GBVs for young sires without phenotype records from daughters had reliabilities of between 50-67% for the milk production traits, live weight, fertility, somatic cell and longevity. This increase in reliability compared to parent average has allowed LIC to reduce the size of the progeny test scheme, and to market teams of unproven bulls based on their GBVs. Methods to incorporate genomic information in to national and international genetic evaluation systems need to be developed. If genomic information is not integrated in to these systems, these systems will no longer be the primary source for selection information in the future.

Key words: *Genomic evaluation, Single nucleotide polymorphism, Dairy cattle, Genomics, Selection, Markers, Breeding value.*

Genome-wide dense marker-data are available for dairy cattle. Recently, Illumina, Inc. (San Diego, CA), have released the BovineSNP50 BeadChip that was developed by Van Tassell *et al.*, (2008). The BovineSNP50 BeadChip contains over 50 000 SNP uniformly distributed over the genome. Genome-wide SNP data can be used to estimate genomic breeding values (GBVs) as outlined by Meuwissen *et al.*, (2001). First, SNP effects are estimated with a training data set containing individuals with marker genotypes and trait phenotypes. Second, GBVs of any genotyped individual in the population can be calculated using the estimated marker effects. LIC genotyped 4 500 sires born in the 1980s to the present using the BovineSNP50 BeadChip. The data included approximately 2 400 Holstein Friesian, 1 500 Jersey and 650 Holstien Friesian-Jersey crossbred sires. The data was divided into training and test data sets based on birth year. Analyses were undertaken both within breed and across breed.

Summary

Introduction

The test data sets were used to assess the accuracy of the GBVs by comparing BVs calculated from phenotypic records on daughters with GBVs calculated from SNP data. This paper will outline the results from the SNP analysis, the likely changes to the LIC progeny testing program and discuss the implications for the national genetic evaluation system.

Analysis of the genomic marker data

The SNP data on the 4 500 sires was subjected to a number of data checks. Approximately 1 400 loci had a deletion or an identified third allele which resulted in lower than average call rates and these SNPs were removed. SNPs were removed for low call rates, minor allele frequencies less than 2%, non-Mendelian inheritance and failed Hardy Weinberg tests. A total of 44 146 SNPs were retained for analysis from the original 48 465. The SNP data included 0.13% missing values. The missing values were imputed using breed and sire information. Also, the statistical analysis included an option to remove SNPs in complete or near complete linkage disequilibrium with SNPs on the same chromosome.

The first data analysis undertaken was a validation analysis. Genomic breeding values (BV_s) were estimated for 25 traits; milk volume, milkfat, protein 270-day yields, live weight, fertility, somatic cell score, longevity, 12 linear conformation traits, 4 farmer scored linear traits, calving difficulty and gestation length. The input data for the analysis was de-regressed breeding values (Banos and Sigurdsson, 1996) with expected daughter equivalents (Fikse and Banos, 2001) as the associated measure of accuracy of each data point. The de-regression of breeding values avoided double accounting of genetic relationships in both the numerator relationship matrix and the SNP effects. The data were divided into two subsets, a training subset and a test subset. The training subset included all sires born prior to 2001. The test subset included all sires born between 2001 and 2003. Sires in both the training and test subsets had estimated BV_s from progeny testing. The SNP effects were estimated in the training data set and then these estimated effects were used to estimate GBVs in the test data set. The accuracy of the GBVs was estimated by the correlation between these GBVs and the BV_s based on progeny test daughters.

There were several methods of analysis used for training; BLUP, BayesA and BayesB (Meuwissen *et al.*, 2001), Bayesian regression (Xu *et al.*, 2003), Bayesian model selection (George and McCulloch, 1997), least angle regression (LARS) (Efron *et al.*, 2004) and Bayesian Inference Machine Learning (Tipping, 2001). On average the accuracy of LARS and Bayesian regression was considerably poorer than the other methods regardless of trait or breed. In a number of cases the BayesA, BayesB and Bayesian model selection methods outperformed BLUP. However, the increased accuracy obtained by these methods was small, often a 2-3% increase in the test correlations compared to BLUP.

The training statistical analysis was undertaken within and across breeds. The SNP estimates calculated from the Holstein-Friesian (HF) training data did not produce accurate GBVs in the Jersey test data and vice-versa. The test correlations ranged from -0.1 to 0.3 when the SNP effects from one breed were used to calculate GBVs in another breed. Conversely, the test correlations for the crossbred bulls (HF - Jersey crosses) were largest when all sires of all breeds were included in the training data subsets. Overall the test correlations for the crossbred bulls were 5-10% higher than for each of the two breeds.

From the validation analysis it was apparent that Genomic BVs should be calculated within breed for HF and Jersey sires and assigning equal variance to each SNP was close to optimal. To compute genomic BVs for proven and unproven sires simultaneously the genomic mixed model equations (MME) outlined by Van Raden (2007) and Habier *et al.*, (2007) was used. The input data for the models was de-regressed breeding values for proven sires. The MME uses a genomic relationship matrix rather than a numerator relationship matrix. In the MME analysis all the data is used, there is no distinction between training and test data subsets. The specification of genomic relationship matrix is flexible allowing individual SNP effect to have their own variance ratio. For this analysis the genomic relationship matrix was formed assuming equal variance for each SNP analogous to the BLUP method of (Meuwissen *et al.*, 2001). The reliabilities of GBVs were estimated by direct inversion of the mixed model equations. The GBVs for young bulls do not contain all the parent information that is contained in the national genetic evaluation. To incorporate the parent information from the national genetic evaluation a selection index approach was used. The parent information from the national genetic evaluation and the GBV are not independent sources of information. The covariance between the parent information and the GBV was approximated by the reliability of the additive parent information in the genomic MME. This was calculated substituting the genomic relationship matrix with the numerator relationship matrix based on sire-maternal-grandsire relationships in the genomic MME. Furthermore, the parent average and genomic BVs were expressed as deviations from a breed and birth year mean prior to applying the selection index to avoid over expansion of fixed breed and genetic groups effects contained with the BVs. The resulting breeding values for young sires had reliabilities of between 50-67% for the milk production traits, live weight, fertility, somatic cell and longevity compared to an average of 34% for parent average BVs. Reliability for the linear type traits were lower, ranging from 40-50%, compared to an average of 31% for parent average BVs.

Providing breeding values on young sires based solely on genomic and parent information highlights the problem of the overestimation of parent average as a predictor of breeding values based on progeny test for elite sires. The overestimation is commonly caused by (intentional or unintentional) preferential treatment and non-additive genetic effects in bull dams, such as epistasis and dominance, that are not passed on to offspring. It is important to remove the bias from the young sires breeding values.

In a conventional dairy progeny testing system, it takes 7 years to obtain a proven bull from progeny testing. Currently, LIC progeny tests 300 bulls per year. Each bull obtains a first proof based on 80 daughters. The unproven bulls are used in approximately 500 dedicated sire proving scheme herds. Genomic selection using the 50k Illumina SNP chip can generate breeding values on unproven bulls with a reliability of 50-60% compared to 35% on parent information alone. This increase in reliability allows breeding companies to reduce the size of the progeny test scheme and to market teams of unproven bulls based on their combined SNP and parent average breeding values. LIC is currently redesigning its breeding scheme to market teams of young bulls at 2 years of age. The young bulls will be used in the sire proving scheme as yearlings to generate future phenotypic records from daughters and check that the young sires do not transmit any gross genetic abnormalities to their offspring. The size of sire proving scheme will be considerably smaller than the current scheme. The acquisition of young bulls to enter the progeny testing

Genomic breeding values for unproven sires

LIC progeny testing program redesign

scheme is likely to change dramatically. In the current scheme 1500 elite females are contracted to produce 300 bull calves. In the future, it is possible that elite females and bull calves will be screened using the SNP chip technology. It is envisaged that thousands of bull calves will be screened prior to entry and the best 100-150 bull calves selected for progeny testing. The rate of genetic gain in the Breeding Worth index (a measure of net profitability) is likely to increase 50-60% to approximately 0.3 genetic standard deviation units per year.

**Impact of
genomic
selection on the
national genetic
evaluation**

The national genetic evaluation system calculates breeding values for cows and sires and is based on weighting three sources of information; parent information, own performance and progeny performance. Conceptually genomic selection provides a fourth source of information, SNP or DNA information.

Integrating genomic information in to an existing genetic evaluation system is more difficult than integrating other new information sources such as foreign daughter performance. This is because the accumulation of information does not follow the usual numerator relationship rules. For example, in conventional genetic evaluation, a sire with an increasing number of daughters lactating for the first time will see a steady increase in his reliability as the extra information accumulates. Also, diminishing returns prevail as the number of daughters increase. In a genomic setting, where the sire is genotyped, as an increasing number of his progeny are genotyped there is no extra information or increased reliability attributed to the sire. New approaches are required for combining genomic information with conventional breeding values. It may be possible to combine the numerator relationship matrix (for non-genotyped animals) and genomic relationship matrix (for genotyped animals) in a single analysis. In such an analysis it would be important to distinguish modes of SNP relatedness, identity by descent and identity in state, and that these modes are modeled appropriately.

Solving large-scale national genetic evaluation systems are currently feasible because simple rules exist to invert the numerator relationship matrix (Henderson 1976). Procedures such as iteration on data (Misztal and Gianola, 1987) are efficient for solving large-scale systems of equations in part due to the sparse nature of the inverse of the numerator relationship matrix. In the genomic MME, the genomic relationship matrix is a dense matrix. There are currently no rules to indirectly invert the matrix. As the number of genotyped animals increases with time, direct inversion of the genomic relationship matrix may become infeasible, and solving the genomic MME will become increasingly difficult.

Another challenge facing national genetic evaluation systems will be the emergence of SNP chips that contain a subset of SNPs from the BovineSNP50 BeadChip. These chips may allow large scale screening of individuals at a relatively low cost. This technology will enable breeding companies to preselect animals prior to being genotyped by the BovineSNP50 BeadChip. It is conceivable that breeding companies or individual dairy farmers would like the results from the smaller SNP panels to be incorporated in the national genetic evaluation system in the near future.

Interbull currently provides international comparisons among proven sires from a number of different countries. In New Zealand genomic evaluations are available on young sires with no progeny. Semen exporting companies will want Interbull international comparisons on young sires that include genomic information. Providing an international genetic evaluation system that combines daughter performance and genomic information from different sources will be a challenging project. The genomic information from different countries cannot be simply treated

as independent sources of information and presumably environment by genomic interactions will exist as well. Countries using different combinations of SNPs and applying different weights to individual SNPs to predict future performance could further compound the problem.

The availability of genome-wide dense marker data for dairy cattle has allowed GBVs to be estimated on young sires with no progeny information. The GBVs are of sufficient accuracy to allow LIC to redesign its breeding scheme and market teams of young sires based on their GBV evaluations. Farmers will want genomic information incorporated into the national genetic evaluation when the first progeny from the young sires are born (July 2009). It is likely that the methods for calculating GBVs from SNP data will improve and the accuracy of GBVs will increase with time. As the accuracy of GBVs increases there will be a greater usage of young sires based on their GBV evaluations increasing the pressure on national genetic evaluation procedures to incorporate genomic information. Similarly, the semen exporting companies will require international genetic evaluations to include genomic information in the near future. If genomic information is not integrated in to these systems then these systems will no longer be the primary source for selection information and their usefulness is limited.

Technology will improve, higher density SNP chips will become available and in time complete sequence data could be available on individual sires at relatively low cost. The genetic evaluation solutions will need to evolve with the advances in DNA technology.

The authors thank Drs. George Wiggans and Paul VanRaden (USDA) for stimulating discussions during the authors visit to USDA Beltsville; and funding support from Dairy New Zealand.

Banos, G. & A. Sigurdsson. 1996 Application of contemporary methods for the use of international data in national genetic evaluations. *J. Dairy Sci.* 79(6): 1117-1125.

Efron B., T. Hastie, I. Johnstone & R. Tibshirani. 2004. Least Angle Regression. *Annals of Statistics* 32: 407-499.

Fikse, W.F. & G. Banos. 2001. Weighting factors of sire daughter information in international genetic evaluations. *J. Dairy Sci.* 84:1759-1767.

George E.I. & R.E. McCulloch. 1997. Approaches for Bayesian Variable Selection. *Statistica Sinica* 7: 339-74.

Habier, D., R.L. Fernando & J.C.M. Dekkers. 2007. The Impact of Genetic Relationship Information on Genome-Assisted Breeding Values. *Genetics* 177: 2389-2397

Henderson C.R. 1977. A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. *Biometrics*, 32: 69-83.

Discussion

Acknowledgements

List of references

Meuwissen, T.H.E., B.J. Hayes & M.E. Goddard. 2001. Prediction of total genetic value using genome-wide dense marker maps. *Genetics* 157: 1819–1829.

Misztal, I. & D. Gianola. 1987. Indirect solution of mixed model equations. *J. Dairy Sci.* 70: 716–723.

Tipping, M.E. 2001. Sparse Bayesian Learning and the Relevance Vector Machine. *J. of Machine Learning Research*, 1: 211-244

VanRaden, P.M. 2007. Genomic measures of relationship and inbreeding. *Interbull Bull.* 37: 33–36.

Van Tassell C.P., T.P.L. Smith, L.K. Matukumalli, J.F. Taylor, R.D. Schnabel, C.T. Lawley, C.D. Haudenschild, S.S. Moore, W.C. Warren & T.S. Sonstegard. 2008. SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. *Nature Methods* 5: 247–252.

Xu, Shizhong. 2003. Estimating Polygenic Effects Using Markers of the Entire Genome. *Genetics* 163: 789-801

Incorporation of genotype effects into Animal Model Evaluations when only a small fraction of the population has been genotyped

E. Baruch¹ & J. I. Weller²

¹Faculty of Agriculture, Hebrew University of Jerusalem, Israel

²Institute of Animal Sciences ARO, The Volcani Center, Bet Dagan, Israel

The method of Israel and Weller (1998) to estimate QTL effects when only a small fraction of the population was genotyped was investigated by simulation. QTL effect was underestimated in all cases, but bias was greater for extreme allelic frequencies, and increased with the number of generations included in the simulations. Apparently, as the fraction of animals with inferred genotypes increases, the genotype probabilities tend to “mimic” the effect of relationships. Unbiased estimates of quantitative trait locus effects were derived by a modified “cow model” without inclusion of the relationship matrix on simulated data, even though only a small fraction of the population was genotyped. This method yielded empirically unbiased estimates for the effects of the genes *DGAT1* and *ABCG2* on milk production traits in the Israeli Holstein population. Based on these results, an efficient algorithm for marker assisted selection in dairy cattle was proposed. Quantitative trait loci effects are estimated and subtracted from the cows records. Genetic evaluations are then computed for the adjusted records. Animals are then selected based on the sum of their polygenic genetic evaluations and QTL effects. This scheme differs from a traditional dairy cattle breeding scheme in that all bull calves were considered candidates for selection. At year 10 total genetic gain was 20% greater by the proposed algorithm as compared to selection based on a standard animal model for a locus with a substitution effect of 0.5 phenotypic standard deviations. The method is flexible with respect to the model used for routine genetic evaluation. Any number of genetic markers can be easily incorporated into the algorithm, and the reduction in genetic gain due to incorrect QTL determination is minimal. It is only necessary to genotype breeding males, which are a very small fraction of the entire population.

Summary

Key words: *Marker-assisted selection, Dairy cattle, Animal model, Quantitative trait locus*

Introduction

Most modern dairy cattle breeding programs are based on the progeny test scheme, and genetic evaluations are generally derived by application of the “animal model” (AM). Estimated breeding values (EBV) are derived for each animal, based on the production records of females and the relationship matrix including both breeding males and females. Genetic gains of ~0.1 phenotypic standard deviations per year can be obtained in modern progeny test schemes for a trait with a heritability of 0.25 (Nicholas and Smith, 1983). In trait-based selection programs only additive genetic variance is utilized, and selection is based only on animals that express the economic traits or their relatives. Trait-based selection is inefficient for low heritability traits or for traits with negative genetic correlations.

Marker-assisted selection (MAS) within a breed can increase genetic progress by increasing the accuracy of genetic evaluations, increasing the selection intensity, or decreasing the generation interval. Once a segregating quantitative trait locus (QTL) has been detected via linkage to genetic markers, application is difficult, because QTL-marker phase varies among individuals; only a small fraction of the population is genotyped; and to correctly rank candidates for selection, it is necessary to correctly weigh marker, pedigree, and trait information. Fernando and Grossman (1989) proposed a “gametic” model extension to the AM that assumes that the two QTL alleles of each individual are random effects sampled from a distribution with a known variance. Breeding values are estimated for all individuals in a population, including QTL effects via linkage to genetic markers. This method is suitable for any population structure, accommodates the fact that QTL-marker phase is generally unknown, and also can incorporate non-linked polygenic effects and other “nuisance” effects, such as herd or block. The disadvantages are that the method assumes that all animals have been genotyped, and that both recombination frequency and the variance due to the QTL are known *a priori*. Two additional equations are added to the mixed model equations for each animal for each QTL included in the analysis. Each individual with unknown parents is assumed to have two unique alleles. Thus the prediction error variances of the effects for any individual are quite large. Finally, the assumption of a normal distribution of possible QTL allele effects may not be realistic. Meuwissen and Goddard (1999) proposed methods to estimate breeding values by this approach for individuals that were not genotyped, but only for specific population structures. Recombination frequency and the variance due to the QTL can be estimated by REML for multiple linked markers, but are completely confounded for a QTL linked to a single marker (van Arendonk *et al.*, 1994).

Unlike the model of Fernando and Grossman (1989), the model of Israel and Weller (1998) assumes complete linkage between the QTL and a single marker, and only two QTL alleles are segregating in the population. The model further assumes that either a daughter or granddaughter design has been applied to determine QTL genotypes of the family ancestors. The QTL effect is then included in the complete animal model analysis as a fixed effect. For individuals that are not genotyped, probabilities of receiving either allele are included as regression constants. These probabilities can be readily computed for the entire population using the segregation analysis method of Kerr and Kinghorn (1996). Israel and Weller (2002) extended this method to a situation of a QTL bracketed by two genetic markers, based on the regression analysis method of Whittaker *et al.* (1996).

The method of Israel and Weller (1998, 2002) has been tested extensively on simulated populations, and was able to yield virtually unbiased estimates of QTL effect and location, even though only 25% of the individuals were genotyped. Two and three generation populations were analyzed. However, when this model was applied to actual data from the Israeli Holstein population for the *DGAT1* locus segregating

QTL on chromosome 14 that affected milk production traits (Grisart *et al.*, 2002), the QTL effect was strongly underestimated relative to alternative estimation methods (Weller *et al.*, 2003). Reasons for this discrepancy may be due to differences between the actual and simulated data sets. The actual data set differed from the simulated data sets in three aspects. A much smaller fraction of the total population was genotyped in the actual data, <1% of the total population; frequency of one allele was very low, ~10%, in the actual data; and the actual data included ~8 generations, while the simulated data included on 2-3 generations.

The objectives of the current study were to determine the reasons for the discrepancy between the results on simulated and actual data, to modify the method of Israel and Weller (1998) so that unbiased QTL estimates are obtained, to develop a practical algorithm for MAS in which all sources of information are correctly weighted, and to test this method on simulated populations and real data.

Dairy cattle populations under selection for a single trait with heritability of ~0.375 were simulated. The founder population included 40 bulls and 2 000 cows. Inseminations and calvings occurred at the beginning of each year, and lactation records were available for analysis at the end of each year. The interval from insemination to calving and the interval between calvings were both assumed to be one year. Each cow could produce up to five lactations, with a probability of 0.6, for each additional lactation after first. For each cow, the probability of male or female offspring at each calving was 0.5. All female progeny became milking cows, and all male progeny were potential mating bulls. All animals were assumed to reach sexual maturity at the age of one year, and first calving of cows occurred at the age of two years.

Until year six, bulls to mate cows were selected at random among the founder bulls and all other bull calves produced that reached sexual maturity. At this point, the daughters of the founder bulls completed their second lactations, and AM genetic evaluations were computed for the first time. Based on these evaluations the five best bulls were mated to the 80 best cows to produce potential bull calves. The remaining cows were mated to the 20 best bulls including the five best. In both cases bulls were selected from those bulls selected previously as mating bulls and all one year old bull calves, including the sons of the non elite cows. Thus this scheme differs from a traditional progeny test scheme in which only bulls that have been progeny tested on a sample of test daughters are mated to the general cow population.

Bull calves not selected for breeding at the age of one year were culled. Genetic evaluations of the year-old calves were based on pedigree. In simulations which utilized QTL information, this data was also used to rank bull calves, as described below. Mating between bulls and cows were randomly determined within the elite and regular cow groups. Thus except for the five best bulls, all bulls selected for breeding would produce approximately the same number of offspring each year. After year six, genetic evaluations were computed yearly until the end of the simulation. Bulls selected for mating were not culled, and could potentially be used for mating as long as their evaluations remained among the top 20 for the general population or top 5 for elite cows.

Material and methods

Production records were simulated as follows:

$$Y_{ijk} = a_i + p_i + h_j + q + e_{ijk}$$

where:

Y_{ijk} = lactation record for cow i in herd-year-season j , of parity k ;

a_i = random additive genetic effect of cow i ; p_i = random permanent environmental effect of cow i ;

h_j = fixed effect of herd-year-season j ;

q = fixed regression effect of inferred QTL genotype for cow i ; and

e_{ijk} = random residual.

All effects other than q were simulated by selection from a normal distribution with a mean of zero. Variances were 0.25 for the polygenic effect, 0.125 for the permanent environmental effect, 0.25 for the herd-year-season effect and 0.5 for the residual. For the QTL we assumed that only two alleles were segregating in the population, and that the effect was codominant. Thus the variance due to the QTL = $2p(1-p)a^2$ where p = the frequency of one of the QTL alleles and $a = 0.5$ = the QTL substitution effect. Therefore for $p = 0.5$, the variance due to the QTL = 0.125; the total phenotypic variance, excluding the herd-year-season effect = 1; and heritability = 0.375. For the founders, a polygenic effect was generated by sampling from a normal distribution with a variance of 0.25. For all other animals, polygenic effects were generated as the sum of half the sire and half the dam genetic effects plus a "Mendelian sampling" effect generated by sampling from a normal distribution with a variance of 0.125. Thus the variance of the polygenic effect was 0.25 for all animals. For founders QTL genotype was determined by sampling twice (for each allele) from a uniform distribution. If a value smaller than the initial allele frequency was obtained, then the individual was assumed to receive a positive allele, and otherwise the individual received the negative allele. For all other individuals QTL genotype was determined by randomly selecting one allele from each parent with a frequency of 0.5.

The first group of simulations was continued for 25 years or ~5 generations, and the total number of animals included in each simulated population was ~200 bulls and ~18 000 cows. Selection after year six was by a standard AM. These simulations were used to compare analysis models 1 and 2 described below. For estimation of QTL effects, only genotypes of bulls and one year old bull calves were assumed known. Genotypes of cows were inferred from the genotypes of their sires, as described by Israel and Weller (1998). The initial frequency of the positive QTL allele was varied from 0.1 to 0.9, but changed during the simulation due to selection on this allele. Ten simulations were computed for each value of the initial QTL allelic frequency. The second set of simulations was continued to year 30, and included ~270 bulls and ~37 000 cows. These simulations were used to compare traditional selection and the proposed MAS algorithm. Ten populations were generated for each selection scheme.

Two models for estimation of QTL effects were compared. "Model 1" was the same as Israel and Weller (1998), except that a fixed parity effect was included even though no parity effect was simulated. This effect was included because this is generally the case for analysis of commercial populations. The assumed value for the total additive genetic variance was 0.375, and the assumed values for the other variance components were equal to the simulated values. The mixed model included the inverse of the numerator relationship matrix for the polygenic effect. All ancestors, including males without records were included in computation of the relationship matrix. The assumed value for the polygenic additive genetic variance was 0.25, because the QTL was considered a fixed effect, and the assumed values for the other variance components were equal to the simulated values.

The following “cow model” was denoted “Model 2:”

$$Y_{ijk} = c_i + h_j + m_k + q + e_{ijk}$$

where:

c_i = random effect of cow i ;

m_k = the fixed parity effect, and the other terms are as described previously.

This model differs from the model of Israel and Weller (1998) in that only cows with production records are included, and covariances among cow effects are assumed to be zero. That is the relationship matrix is not included. The assumed value for the cow variance was 0.375 (sum of additive polygenic and permanent environmental variances), because the QTL was considered a fixed effect; and the assumed values for the residual variance was 0.5, as simulated.

Although Model 2 can be used to obtain unbiased estimated of QTL effects (as will be shown), it cannot be used for routine genetic evaluation, which requires incorporation of the relationship matrix. We therefore propose the following algorithm for MAS in dairy cattle.

1. For animals with unknown genotypes for the QTL infer genotypes based on the algorithm of Kerr and Kinghorn (1996).
2. Estimate QTL effects by Model 2, as described previously.
3. Subtract the known or inferred QTL genotype effect, based on the Model 2 estimated QTL effect, from the cows' production records.
4. Compute AM breeding values for all animals from the adjusted cow records. These EBV are now based only on the polygenic effect.
5. Derive adjusted breeding values by summing the EBV with the inferred or known QTL effect of each animal.
6. Use the adjusted breeding values to rank candidates for selection.

Standard AM and “adjusted” EBV computed by the proposed algorithm were compared on the second set of simulated populations as described previously. The QTL was assumed to an initial frequency of 0.3 for the positive allele. Beginning in year 6, the simulated populations were analyzed by a standard AM and the proposed MAS algorithm was applied. In the standard breeding scheme bull calves without progeny were ranked on the mean of their sire and dam EBV. In the MAS scheme adjusted breeding values (ABV) for bull calves were computed as follows:

$$ABV = \frac{1}{2} (\text{sire PBV}) + \frac{1}{2} (\text{dam PBV}) + \text{QTL effect.}$$

Where PBV = polygenic breeding value, that is the sire and dam EBV without the QTL effects. QTL genotypes of all bull calves were assumed known. Genetic evaluations of bulls, cows, and young sires were compared to the simulated values and genetic evaluations from a standard AM. Polygenic variance was assumed to be 0.25 in the MAS breeding scheme, and additive genetic variance was assumed to be 0.375 in the standard AM breeding scheme. Overall genetic trends and genetic trends for the polygenic and QTL effects were compared for the two selection schemes.

Model 1 estimates of the QTL effects are given in Table 1. The QTL effect was underestimated in all simulations. Since there is selection for the “positive” allele, the frequencies of the two alleles in the population are closest to equality when the initial frequency of the negative allele is high. Bias is greatest when the initial frequency of the negative allele is low, because in this case the overall frequency of the negative allele is lowest, making it more difficult to accurately estimate the QTL effect. This is also reflected in the higher SD among the simulations in this

Results

case. Bias also increased with the number of generations included in the simulations (data not shown). Thus these results conform to the results of Weller *et al.* (2003) for analysis of *DGAT1*. Bias is apparently due to confounding between the inferred QTL genotype and the relationship matrix. Apparently, as the fraction of animals with inferred genotypes increases, the genotype probabilities computed for these individuals tend to “mimic” the effect of relationships. In the extreme case of no known genotypes, the genotypes of all individuals would be inferred by the same principles used to construct the relationship matrix.

Estimates of the Model 2 QTL effect were nearly unbiased for all initial QTL frequencies. As expected, the standard deviations increased with reduction of the initial frequency of the negative allele, the allele whose frequency decreases during selection.

“Adjusted” and standard EBV for cows with records and their sires are compared in Table 2. Correlations were nearly equal to unity, but regression of adjusted EBV on the standard AM EBV were greater than unity. Evaluations of both models were nearly unbiased, that is regressions of simulated genetic values on evaluations were close to unity.

Genetic trends for total genetic gain, polygenic gain, and gain in the QTL effect from year 6 to year 24, approximately five generations of selection, are presented in Figure 1. Values prior to year 6 are not presented, because there was no genetic gain until then. The curves represent the sums of all ten simulations for each selection scheme. The trends in the simulated values are given, although the EBV trends are nearly identical. For both schemes progress is zero until year six in which the first genetic

Table 1. Effect of allele frequencies on the estimate of QTL substitution effect¹.

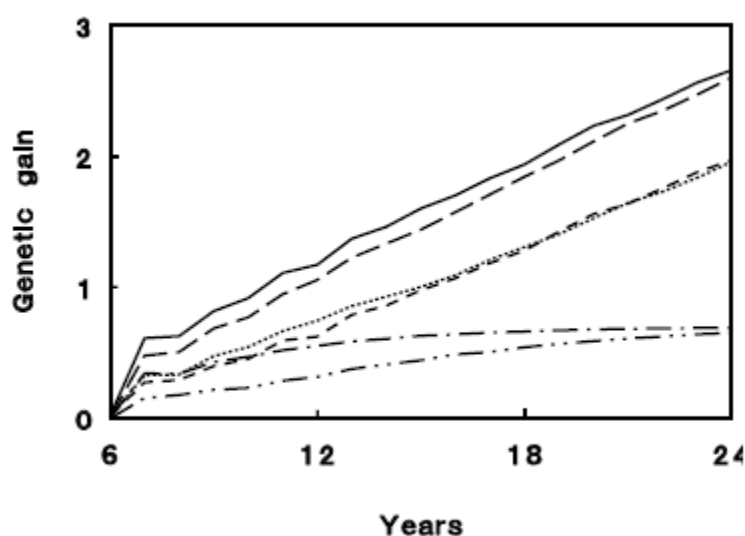
Initial frequency of negative allele	Estimated QTL effect	Standard deviation ²
0.1	0.12	0.06
0.2	0.21	0.08
0.3	0.31	0.05
0.4	0.37	0.06
0.5	0.39	0.07
0.6	0.42	0.05
0.7	0.39	0.06
0.8	0.42	0.04
0.9	0.45	0.05

¹The simulated QTL effect = 0.5.

²Empirical values based on the results of 10 simulations for each set of initial values.

evaluations are computed. The mean annual genetic gain from year 10 through 30 was ~0.1 SD for both schemes, similar to values found in previous simulations (Nicholas and Smith, 1983). As expected, slightly greater genetic progress is obtained by traditional selection for the polygenic effect until year 15, because less selection intensity is applied to the QTL effect. The QTL and the polygenic effects can be considered a two-trait breeding objective. If greater selection pressure is applied to the QTL in the MAS scheme, then selection for the polygenic effect should be slightly less. After year 20 greater genetic progress is obtained by MAS, apparently because from this point onward the assumed variance components for the standard

AM selection scheme are no longer correct. This scheme assumed an additive genetic variance of 0.375 throughout. Greater genetic progress for the QTL effect is obtained for the MAS scheme. Since the initial frequency of the positive QTL allele is 0.3, maximum obtainable progress for the QTL is 0.7, and this value is approached for the MAS scheme by year 24. Total genetic gain was greater for the MAS scheme. The difference in genetic trends increased until year 11 and then decrease. At year 10 total genetic gain was 0.15 SD greater by MAS, but only 0.05 by year 24. Even at year 30 the MAS scheme is still higher than the traditional scheme. Thus genetic gain with trait-based selection did not surpass MAS over the long-term as noted by Gibson (1994). The "Gibson effect" was also not detected by de Koning and Weller (1994) in a series of long-term MAS simulations. The gain of 0.15 by MAS at year 10 represents an increase of nearly 20% over the traditional scheme. Alternatively, we note that the SD for milk production of Israeli Holsteins is 1 400 kg. Thus advantage of the MAS scheme = 210 kg at year 10.



Total genetic gain: — —, standard AM; — —, modified AM. Polygenic genetic gain: ... , standard AM; - - -, modified AM. QTL genetic gain: — · · —, standard AM; — · · —, modified AM.

Figure 1. Total and polygenic genetic gain and genetic gain in mean QTL value as a function of year of simulation.

Table 2. Correlations between simulated genetic values and genetic evaluations, and regressions of simulated values on genetic evaluations.

	Standard AM		Adjusted model	
	Regression	Correlation	Regression	Correlation
Bulls	0.984	0.960	1.00	0.963
Cows	0.949	0.780	1.047	0.808

Conclusions

Estimates of QTL effects derived from the Model of Israel and Weller (1998) are biased due to confounding between the inferred genotypes and the relationship matrix. Unbiased estimates of QTL effects were derived by a “cow model” without relationships even though only a small fraction of the population was genotyped. An efficient algorithm for marker assisted selection in dairy cattle is presented, and tested for a QTL with a substitution effect of 0.5 phenotypic standard deviations. At year 10 total genetic gain was 20% greater by MAS as compared to standard animal model. The proposed method is easy to apply, and all required software are “on the shelf.” It is only necessary to genotype males, which are a very small fraction of the entire population. The method is flexible with respect to model for general genetic evaluation, single trait AM, multitrait AM, etc. Any number of genetic markers can be easily incorporated into the algorithm.

List of references

Cohen-Zinder, M., E. Seroussi, D.M. Larkin, J.J. Looor, A. Everts-van der Wind, J.H. Lee, J.K. Drackley, M.R. Band, A.G. Hernandez, M. Shani, H.A. Lewin, J.I. Weller and M. Ron, 2005. Identification of a missense mutation in the bovine ABCG2 gene with a major effect on the QTL on chromosome 6 affecting milk yield and composition in Holstein cattle. *Genome Research* 15, 936-944.

de Koning, G.J. and J.I. Weller, 1994. Efficiency of direct selection on quantitative trait loci for a two-trait breeding objective. *Theoretical and Applied Genetics* 88, 669-677.

Fernando, R.L. and M. Grossman, 1989. Marker assisted selection using best linear unbiased prediction. *Genetics Selection and Evolution* 21, 467-477.

Gibson, J.P., 1994. Short-term gain at the expense of long-term response with selection on identified loci. In *Proceedings of the Fifth World Congress for Genetics Applied to Livestock Production*. Vol 21 pp. 201-204. Guelph, ON, Canada.

Grisart, B., W. Coppieters, F. Farnir, L. Karim, C. Ford, P. Berzi, N. Cambisano, M. Mni, S. Reid, P., P. Simon, R. Spelman, M. Georges and R. Snell, 2002. Positional candidate cloning of a QTL in dairy cattle: Identification of a missense mutation in the bovine DGAT1 gene with major effect on milk yield and composition. *Genome Research* 12, 222-231.

Israel, C. and J.I. Weller, 1998. Estimation of candidate gene effects in dairy cattle populations. *Journal of Dairy Science* 81, 1653-1662.

Israel, C. and J.I. Weller, 2002. Estimation of quantitative trait loci effects in dairy cattle populations. *Journal of Dairy Science* 85, 1285-1297.

Kerr, R.J. and B.P. Kinghorn, 1996. An efficient algorithm for segregation analysis in large populations. *Journal of Animal Breeding and Genetics* 113, 457-469.

Meuwissen, T.H.E. and M.E. Goddard, 1999. Marker assisted estimation of breeding values when marker information is missing on many animals. *Genetics Selection and Evolution* 31, 375-394.

Nicholas, F.W. and C. Smith, 1983. Increased rates of genetic change in dairy cattle by embryo transfer and splitting. *Animal Production* 36, 341-353.

van Arendonk, J.A.M., H. Bovehuis, S. van der Beek and A.F. Groen, 1994. Detection and exploitation of markers linked to quantitative traits in farm animals.

In Proceedings of the Fifth World Congress for Genetics Applied to Livestock Production. Vol 21, pp. 193-200. Guelph, ON, Canada,

Weller, J.I., 1994. Economic Aspects of Animal Breeding. Chapman & Hall. London, UK. Weller, J.I., 2007. Marker assisted selection in dairy cattle. In: Marker-Assisted Selection, Current status and future perspectives in crops, livestock, forestry and fish. E. Guimarães, J. Ruane, B., D. Scherf, A. Sonnino and J. D. Dargie (Eds.) Food and Agriculture Organization of the United Nations. Rome, Italy, pp. 199-228.

Weller, J.I., M. Golik, E. Seroussi, E. Ezra and M. Ron, 2003. Population-wide analysis of a QTL affecting milk-fat production in the Israeli Holstein population. Journal of Dairy Science 86, 2219-2227.

Whittaker, J.C., R. Thompson and P.M. Visscher, 1996. On the mapping of QTL by regression of phenotype on marker-type. Heredity 77, 23-32.

Genomic data and cooperation result in faster progress

*P.M. VanRaden¹, C.P. Van Tassell², G.R. Wiggans¹,
T.S. Sonstegard², R.D. Schnabel³, J.F. Taylor³ & F. Schenkel⁴*

*¹Animal Improvement Programs Laboratory, Agricultural
Research Service, USDA, Beltsville, MD, USA*

*²Bovine Functional Genomics Laboratory, Agricultural Research
Service, USDA, Beltsville, MD, USA*

³University of Missouri, Columbia, MO, USA

⁴University of Guelph, Guelph, ON, Canada

Genotypes for 38 416 markers of 5 335 Holstein bulls were combined with traditional evaluations to test predictive ability. Genomic evaluations were significantly ($P < 0.0001$) more accurate than official parent averages for all 27 traits tested. Squared correlations with future daughter deviations averaged 37% for young bulls as compared with 19% for parent averages. Correlations with future evaluations also increased for older, proven bulls. Genomic gains increased strongly with numbers of bulls genotyped and moderately with numbers of markers. Further increases in reliability are easily possible, for example, by obtaining more genotypes for domestic or foreign proven bulls.

Key words: *Genomic evaluation, Parent average, Reliability.*

Genomic selection uses thousands of markers to trace the inheritance of small chromosome segments. Each small DNA segment may account for only a very small fraction of the total genetic variance. Thus, very large numbers of genotyped animals may be required to estimate the many small effects that contribute to quantitative inheritance. Genetic markers act as a third source of data to increase the response to selection as compared to using only phenotypes and pedigrees.

Summary

Introduction

Previous progress from marker assisted selection (MAS) was limited because markers or QTL with large effects explained only a small fraction of genetic variance for most traits (Schrooten *et al.*, 2004). Progress increases when more markers are genotyped (Van der Beek, 2007). Recent MAS in France resulted in squared correlations with eventual daughter evaluations 5-19% higher for genomic predictions than for parent average (Boichard *et al.*, 2006). Expected gains in reliability from simulation were slightly lower (Guillaume *et al.*, 2008).

Breeding organizations and researchers in North America joined forces to develop genotyping methods and to obtain DNA from the very large families needed to produce accurate genomic predictions. This report summarizes initial results, examines potential increases in genetic progress, and outlines directions for future cooperation in this new field of genomic selection.

Genomic data

Genotypes for 38 416 single nucleotide polymorphisms (SNP) of 6 005 Holsteins were examined. The selected SNP were from the Illumina BovineSNP50 Genotyping BeadChip (Van Tassell *et al.*, 2008) and had minor allele frequencies greater than 5% in Holsteins. Genotyping and DNA extraction were done at six locations: Bovine Functional Genomics Laboratory, University of Missouri, University of Alberta, Geneseek, GIVF, and Illumina. AI organizations in North America cooperated to contribute DNA and funding.

Genomic predictions were tested using historical data from August 2003 for 3 576 bulls born before 1999 to predict current data for 1 759 bulls born 1999-2002. Then, official April 2008 evaluations for 5 335 proven bulls and 75 cows with records were combined with genomic data to compute predictions for 623 young bulls and 29 heifers. Results were distributed to AI organizations and to animal owners in April 2008 to enable genomic selection.

Squared correlations

Advantages of genomic selection were tested using weighted regressions of current daughter deviations on traditional and genomic evaluations computed from 2003 data. For young bulls, genomic predictions had squared correlations significantly ($P < 0.0001$) higher than those from parent average, with increases ranging from 0.38 to 0.02 for the 27 traits tested. Largest increase was for fat percentage and smallest for service sire calving ease. When averaged across traits, squared correlations were nearly twice as high (0.37 *vs.* 0.19) for genomic predictions as compared with parent averages.

Squared correlations for proven bulls also increased significantly ($P < 0.001$) for 26 of 27 traits when genomic information was added. The only gain that was not significant was for service sire calving ease. Proven bulls included in these tests were those that added daughters and had at least 10% more reliability in 2008 than in 2003. Cows with records should have gains in reliability intermediate between those of young and proven bulls because traditional reliabilities for most cows are only somewhat higher than their parent average reliabilities.

Actual R^2 is lower than expected reliability for several reasons:

1. Daughter deviations contain error.
2. Parents are selected.
3. Genetic effects reside between rather than at the markers.
4. The genotypes include a few errors.

Also, gains in R^2 may have large standard errors because of the limited number of bulls predicted. A realized genomic reliability that partially accounted for these effects was obtained by dividing the R^2 values from parent average and the genomic model by average reliability of the daughter deviations, and then the difference between the published and observed reliability of parent average was added to the adjusted genomic R^2 . Expected reliabilities were obtained by inverting mixed model equations that included genomic relationships.

More predictor bulls can increase reliability by providing more data to estimate each SNP effect. Large numbers of records are required to accurately estimate the small effects of individual genes. Numbers of bulls were compared using subsets of the bull genotypes as these became available. Squared correlations for net merit of younger bulls were compared using three progressively larger subsets that included 1 402, 2 391, and 3 319 bulls. Methods were the same as for the full set of 5 335 bulls, and results are in table 1.

Gains in R^2 for net merit were nearly linear with increasing numbers of predictor bulls. Gains for most other individual traits followed this same pattern. While linear increases cannot continue indefinitely, the results suggest that the genotyping of additional predictor bulls will be profitable and that genomic selection within small populations will not achieve the large gains obtained in this North American Holstein population. Genomic predictions were expected to have 67% reliability with 3 576 older bulls included, whereas the realized reliability was 53% calculated from adjusted R^2 . This compares with 30% for published parent average of young bulls, for a reliability gain of 23% in net merit.

Numbers of genotyped animals could grow very quickly over the next few years. Computer programs were tested on a simulated data set larger than is currently available to determine what resources would be required and how reliability might further increase with population size. The largest data set used 15 197 older bulls to predict 5 987 younger bulls, for a total of 21 184. This largest test simulated not just North American bulls but instead included all bulls born in the period 1995-1997 with reliability in 2003 of >65% on U.S. scale for net merit in the INTERBULL file.

Computer times for the largest data set were reasonable for both inversion and iteration. Calculation of genomic relationships required 20 hours, followed by inversion, which required 33 hours. Traditional relationships among the 81 697 animals in the pedigree were calculated by tabular method using a series of animal subsets and required 7 Gigabytes of memory and 1.5 hours. The simulated

Population size

Table 1. Squared correlations ($\times 100$) for parent average (PA) and for genomic predictions of net merit from subsets of bulls.

Bulls		Squared correlation		
Older	Younger	PA	Genomic	Gain
1 151	251	8	12	4
2 130	261	8	17	9
2 609	510	8	21	13
3 576	1 759	11	28	17

number of markers was 40 000 and the simulated number of QTL with effects was 10 000, but the distribution was heavy-tailed so that the largest QTL explained about 3% of genetic variation.

Nonlinear genomic predictions after 200 rounds of iteration and 13 hours of computing had 0.4% higher reliability than linear predictions from the same data. The genomic predictions are limited more by processing time than by memory. Average reliabilities for the younger bulls across 5 replicates were 74.3% and 74.7% for linear and nonlinear predictions, respectively, as compared with 80.3% expected by inverting the linear model equations that included genomic relationships among 15 197 older bulls. At equal population sizes, observed R^2 and reliability tend to be higher with simulated than with actual data.

Predictive ability should continue to increase with additional genotyping because many bulls are needed to separately estimate so many small genetic effects. Data sharing is very important to the success of genomic studies (National Human Genome Research Institute, 2003). In cattle breeding, new policies are needed to allow data sharing or access to predictions while ensuring that those who genotype historical populations can profit from their investment. Animal breeders should not expect free access to expensive data but could benefit greatly from service for a fee. Faster progress should result from cooperation, negotiation, and trade than from isolated studies and total genomic secrecy.

Marker densities

Many researchers are interested to know how increasing the numbers of available SNP will affect the accuracy of genomic selection. The edited set of 38 416 SNP with > 5% minor allele frequency in Holsteins (labeled 40K) was compared with subsets of exactly half or exactly one quarter of those SNP, resulting in 19 208 (labeled 20K) or 9 604 (labeled 10K) obtained by keeping every other or every fourth SNP sequentially across each chromosome.

Results for 5 yield traits, 3 fitness traits, and net merit were obtained using the nonlinear model. Table 2 compares increases in R^2 above parent average for the three SNP densities and indicates that 20K density would provide about 90% of the gain provided by 40K density and 10K density would provide about 80% of the gain.

Table 2. Squared correlations for parent average (PA) and for predictions with differing marker densities.

Trait	PA	Marker density		
		10K	20K	40K
Net merit	11	25	26	28
Milk	28	45	47	49
Fat	15	41	43	44
Protein	27	45	46	47
Fat %	25	59	61	63
Protein %	28	48	53	58
Longevity	17	24	25	27
Somatic cell	23	34	36	38
Days open	20	27	28	29

As more bulls are genotyped, more phenotypes are available to estimate each SNP effect and more crossover events are observed between adjacent loci. This increases the value of having more SNP. Affordable SNP chips with higher density will likely become available in the future. However, exchange and combination of data are much easier if all populations choose to genotype a common set of SNP.

Genetic progress results from choosing the best males and females of one generation to be parents of males and females of the next via the four paths of traditional selection (Rendel and Robertson, 1950). With MA, breeders have the opportunity to select on genotype and phenotype, or genotype or phenotype or to not select within each of the four paths. Optimum strategies depend on the accuracies, generation intervals, and costs for each type of selection within the four paths of selection. Equations similar to Schrooten *et al.* (2005) were used to compare strategies and determine progress.

In the near future, males should all be genotyped before selection for breeding. If predictions at 1 year of age have reliability of 60% for total merit, optimum use of young bulls *vs.* progeny tested bulls could increase to 90% from the current 20%. About 1% of females might be profitably genotyped with the current chip and many more with a less expensive SNP subset. The path of females to produce sons could include 80% heifers with genotype only and 20% cows with genotype and phenotype. Females to produce daughters will still be a limiting pathway unless embryo transfer or sexed semen increase in popularity. Genetic progress should increase by about 50% when breeders are convinced that predictions are accurate.

Genomic predictions were much more accurate than PA as verified by use of historical data from 2003 to predict 2008 daughter deviations. R² improved when more bulls and more markers were used in predictions. Genomic evaluations of proven bulls were also significantly more reliable than traditional evaluations from the animal model.

Reliabilities increased further and computing times were reasonable when the same methods were applied to simulated genotypes for 21 184 bulls from all countries in the Interbull file instead of just North American bulls. Genomic selection has immediate benefits that will grow as more genotypes become available from larger populations. Rapid progress is possible with access to very large genomic data sets. More cooperation is required for genomic selection than was required for progeny testing.

This project was supported by National Research Initiative Grant nos. 2006-35205-16888 and 2006-35205-16701 from the USDA Cooperative State Research, Education, and Extension Service and by the National Association of Animal Breeders, Holstein Association USA (Brattleboro, VT) and American Jersey Cattle Association (Reynoldsburg, OH). Many of the results were computed by Mel Tooker and Leigh Walton.

Progress

Conclusions

Acknowledgements

**List of
references**

- Boichard, D., S. Fritz, M.N. Rossignol, F. Guillaume, J.J. Colleau & T. Druet.** 2006. Implementation of marker-assisted selection: practical lessons from dairy cattle. Proc. 8th World Congr. Genet. Appl. Livest. Prod., Communication 22-11.
- Guillaume, F., S. Fritz, D. Boichard & T. Druet.** 2008. Estimation by simulation of the efficiency of the French marker-assisted selection program in dairy cattle. Genet. Sel. Evol. 40: 91-102.
- National Human Genome Research Institute.** 2003. Reaffirmation and extension of NHGRI rapid data release policies: large-scale sequencing and other community resource projects, <www.genome.gov/page.cfm?pageID=10506537>.
- Rendel, J.M. & A. Robertson.** 1950. Estimation of genetic gain in a closed herd of dairy cattle. J. Genetics 50: 1.
- Schaeffer, L.R.** 2006. Strategy for applying genome-wide selection in dairy cattle. J. Anim. Breed. Genet. 123: 218-223.
- Schrooten, C., H. Bovenhuis, J.A.M. Van Arendonk & P. Bijma.** 2005. Genetic progress in multistage dairy cattle breeding schemes using genetic markers. J. Dairy Sci. 88: 1569-1581.
- Van der Beek, S.** 2007. Effect of genomic selection on national and international genetic evaluations. INTERBULL Bull. 37: 111-114.
- VanRaden, P.M.** 2007. Genomic measures of relationship and inbreeding. INTERBULL Bull. 37: 33-36.
- VanRaden, P.M.** 2008. Efficient methods to compute genomic predictions. J. Dairy Sci. 91: 4414-4423.
- Van Tassell C.P., T.P.L. Smith, L.K. Matukumalli, J.F. Taylor, R.D. Schnabel, C.T. Lawley, C.D. Haudenschild, S.S. Moore, W.C. Warren & T.S. Sonstegard.** 2008. SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. Nature Methods 5: 247-252.

Genomic evaluations in the United States and Canada: A collaboration

G.R. Wiggans¹, T.S. Sonstegard¹, P.M. VanRaden¹,
L.K. Matukumalli^{1,2}, R.D. Schnabel³, J.F. Taylor³, J.P. Chesnais⁴,
F.S. Schenkel⁵ & C.P. Van Tassell¹

¹Agricultural Research Service, USDA, Beltsville, MD, USA

²Bioinformatics and Computational Biology,
George Mason University, Manassas, VA, USA

³Division of Animal Sciences, University of Missouri, Columbia, MO, USA

⁴Semex Alliance, Guelph, ON, Canada

⁵University of Guelph, Guelph, ON, Canada

The United States and Canada have collaborated in developing genomic evaluations that utilize genotypes obtained from high-density single-nucleotide polymorphism (SNP) chips. The DNA for genotyping was obtained from semen from 7 major artificial-insemination (AI) companies in North America through the Cooperative Dairy DNA Repository (CDDR) and from other sources. In collaboration with Illumina, Inc., the BovineSNP50 BeadChip was developed to genotype >50 000 SNP in a single assay. To determine the accuracy of genomic prediction, evaluations calculated in 2003 for bulls with evaluations (born mostly before 1999) were used to predict April 2008 evaluations for bulls without evaluations in 2003 (mostly born in 2001 and 2002). The accuracy of genomic evaluations is closely tied to the number of animals in the predictor group. For Holsteins, 7 AI organizations have had several thousand young bulls genotyped for initial application of genomic evaluation. Over 12 500 Holstein, 1 250 Jersey and 350 Brown Swiss genotypes have been processed to check for conflicts between parent and progeny DNA and to impute some of the missing genotypes. The SNP effects were estimated using current evaluations for over 8 700 genotyped bulls and cows that were based on lactation records from >10 million cows.

Genomic evaluations of the nominated animals were calculated by combining SNP effects with parent averages for yield, functional, calving and type traits as well as the net merit economic index. For Holsteins, genomic information provided a substantial improvement in accuracy over parent average for all traits, and the amount of improvement increased as the number of bulls in the predictor group increased. Jersey and Brown Swiss results indicated that more predictor animals were necessary for adequate accuracy, and additional genotypes are being obtained. The first release of genomic evaluations was in April 2008 for Holsteins. Estimated SNP effects are updated 3 times each year with the national genetic evaluations. Additional updates provide evaluations for newly genotyped animals based on previously estimated SNP effects. In 2009, genomic evaluations are expected to become official in the United States and Canada and will also affect evaluations of

Summary

descendants that have not been genotyped. Genomic evaluations of bulls currently are released only to the owner and AI organization until the bulls are enrolled with the National Association of Animal Breeders or a Canadian AI organization or they reach 2 years of age. Genomic evaluations will be routinely available for cows later in 2008.

Methods to exchange genomically enhanced evaluations across countries need to be developed. Genomic evaluations, which can be obtained shortly after birth, are expected to revolutionize dairy cattle breeding programs by changing how bulls are selected for and culled from AI service and how cows are chosen to produce sons. Some bulls will be marketed at 2 years of age based solely on genomic evaluations, which creates a potential for a large increase in rate of genetic gain because of the much shorter generation interval possible.

Key words: *Genomic evaluation, Single nucleotide polymorphism, Dairy cattle, Genomics*

Introduction

In 2007, researchers in quantitative and molecular genetics in the United States and Canada began to collaborate on the development and implementation of genomic evaluations and the integration of those evaluations into national genetic evaluations for dairy cattle. This collaboration is an outgrowth of the establishment of CDDR in 1999 (Ashwell and Van Tassell, 1999), which has been collecting semen from North American AI organizations for almost 10 years. Five U.S.-based and 2 Canadian-based AI organizations currently contribute to CDDR. The repository now contains semen from >17 400 bulls and is a primary source of DNA for investigating genomic evaluation of dairy cattle.

In collaboration with Illumina, Inc. (San Diego, CA), the BovineSNP50 BeadChip was developed (Van Tassell *et al.*, 2008). That effort involved selection and discovery of high-quality SNP that were uniformly distributed over the genome and that had high minor allele frequency. Over 50 000 SNP were incorporated into the chip.

For the collaborative project, DNA was extracted from semen from the CDDR as well as from independently obtained semen. Genotyping was performed primarily by the Bovine Functional Genomics Laboratory, U.S. Department of Agriculture (USDA; Beltsville, MD), the University of Missouri (Columbia, MO) and the University of Alberta (Edmonton, AB). Some genotypes were provided by GeneSeek (Lincoln, NE), the Genetics & IVF Institute (Fairfax, VA) and Illumina, Inc. The project was funded by multiple research grants from USDA as well as contributions by U.S. AI organizations through the National Association of Animal Breeders (Columbia, MO) and the Semex Alliance (Guelph, ON) and by Holstein Association USA (Brattleboro, VT) and American Jersey Cattle Association (Reynoldsburg, OH).

Data editing included removing SNP that were monomorphic or had a minor allele frequency of <5%. For routine analysis, this limit was reduced to 2%. Additionally, each SNP was compared with all others to eliminate those that were redundant because of complete linkage disequilibrium ($r^2 = 1$). Over 38 000 SNP remained for prediction of genomic evaluations (Wiggans *et al.*, 2008). To determine the accuracy of genomic prediction, evaluations calculated in 2003 were used to predict April 2008 evaluations for bulls without evaluations in 2003. That restriction generally meant that bulls born before 1999 were used to predict bulls born in 2001 and 2002 (VanRaden *et al.*, 2008b).

Field test

The prediction accuracy reported by Van Raden *et al.* (2008b) was sufficient to proceed with a field test, which began in April 2008. The first release in April was followed by releases in July and August; >5 300 animals nominated by 7 AI organizations were included. The nominated animals were primarily bull calves, and their genomic evaluations were used to select which full brother to purchase from an embryo flush. Some bulls awaiting the results of progeny testing were genotyped to determine if they should be culled. Additionally, some bulls with current evaluations were included to improve prediction accuracy. Cows were also included to assess their suitability as bull dams.

The AI organizations mainly arranged to have blood samples collected and sent to GeneSeek, Genetics & IVF Institute, or the University of Alberta for DNA extraction and genotyping. In some cases, semen, hair or previously extracted DNA was provided. Some genotyping of nominated animals also was done at the Bovine Functional Genomics Laboratory in fulfillment of a research commitment. Holstein Association USA assisted by offering a low-cost American ID plan, which enabled the AI organizations to enroll all animals in a national ID program. The variability of ID reporting required a considerable reconciliation effort. Work continues on streamlining the processing of sample ID, which now includes bar coding of samples and standardization of ID.

Accuracy of sample ID was determined by checking genotypes for inconsistencies between parent and progeny when the parent had been genotyped. If the genotype for a SNP had been determined for both animals, the number of times that each animal was homozygous for different alleles was counted. The low rate of genotyping errors for the assay meant that usually <5 inconsistencies were found of usually >15,000 SNP where both animals were homozygous when the parent-progeny assignment was correct. However, several thousand inconsistencies usually were found when the parent-progeny assignment was incorrect, which enabled easy detection of sample ID mix-ups or pedigree inconsistencies.

The genomic relationship matrix (VanRaden, 2007) was calculated as part of the genomic evaluation. Comparison of the genomic and pedigree relationships was also used to detect pedigree errors, particularly for animals with an incorrectly identified maternal grandsire. To estimate gene frequencies in the base population, allele frequency estimates were generated for all genotyped animals and their ancestors. The oldest genotyped bull was born in 1952. When the genotype for a particular SNP of a genotyped animal was missing, the estimated frequency (VanRaden *et al.*, 2008a) was used to set the genotype to 0, 1 or 2 (number of the counted allele present) if the frequency was within 10 percentage units of 0, 50 or 100%, respectively.

Genomic evaluations were calculated with the system of VanRaden *et al.* (2008b) based on genotypes for 7,195 animals, including 1,263 cows. Twenty-seven traits were evaluated: 5 yield (milk, fat, and protein volumes and fat and protein percentages), 3 functional (somatic cell score, productive life, and daughter pregnancy rate), 2 calving (calving ease and stillbirth), 16 type (final score and 15 linear traits: stature, strength, body depth, dairy form, rump angle, rump width, rear legs-side view, rear legs-rear view, foot angle, fore udder attachment, rear udder height, udder cleft, udder depth, front teat placement and teat length), and net merit (a lifetime genetic-economic index). Estimates of SNP effects were combined with parent average or genetic evaluation to produce a genomic evaluation. That critical step required determining the contribution of genomic data beyond

traditional evaluations. The genomic contribution was calculated by comparing the results from an animal model evaluation for only genotyped animals with their genomic evaluation.

The addition of animals to the predictor group increased evaluation reliability substantially compared with earlier evaluations for the group being predicted. For genomic evaluations, mean expected reliability of 689 nominated young bulls ranged from 63 to 75% across traits (VanRaden *et al.*, 2008c). Those reliabilities are theoretical and may exceed what is actually realized. Because all genotyped animals with evaluations were used to estimate SNP effects, realized reliability could not be determined. Genomic evaluations of the nominated animals were provided to nominating organizations and owners in the United States, and the evaluations of the predictor bulls were made available on a web site as preliminary research results.

Routine genomic evaluation

Based on field trial results, USDA is implementing routine genomic evaluations. Estimates of SNP effects will be updated 3 times per year with each national evaluation. Newly genotyped animals will be evaluated once or more between those updates based on the volume of genotype data received. Over 12 500 Holstein, 1 250 Jersey and 350 Brown Swiss genotypes currently have been processed to check for conflicts between parent and progeny DNA and to impute some of the missing genotypes.

Animals to be genotyped will be assigned national ID and have their pedigree recorded before their DNA samples are processed to avoid sample ID and logistic issues. Commercial laboratories will perform the genotyping and report genotypes for a set of SNP that can be reliably scored. A system for confirming sample ID through checks for parent-progeny SNP genotype inconsistencies will be developed. The checks will be facilitated by a freely available database with genotypes for a subset of SNP for all animals that have been genotyped. Breed associations are expected to work on resolving conflicts as they do now with parentage testing.

Animal gender for each sample will also be confirmed by checks for heterozygous SNP not in the pseudoautosomal region of the X chromosome. In most cases, females have several hundred heterozygous SNP and males almost none. However, a female can have a very low number of heterozygous SNP if she inherited both X chromosomes from the same ancestor.

Under agreements between the requester and the genetic evaluation centers, the laboratories will send BovineSNP50 genotypes to the evaluation centers. The U.S. and Canadian centers will share genotypes and computer software. Requesters can be AI organizations, breed associations or individual owners. In recognition of their contribution, the AI organizations that provided semen and financial support to the project have exclusive rights to have genomic evaluations calculated for bulls until March 2013.

The U.S. and Canadian evaluation centers plan to exchange evaluations so that each country has evaluations for all genotyped animals with evaluations and their ancestors. Exchange of evaluations and generation of conversion equations before release are necessary to include the latest evaluations for foreign animals. The International Bull Evaluation Service (INTERBULL, Uppsala, Sweden) calculates evaluations only for bulls, and those evaluations are not available soon enough to provide needed information.

In 2009, USDA expects to make genomic evaluations the official evaluation for all genotyped animals and to allow those evaluations to affect evaluations of descendants that have not been genotyped (Gengler and VanRaden, 2008). As the official evaluation, genomic evaluations will appear in pedigrees from breed associations. Because AI organizations wish to protect their investment in genomic evaluations for bull calves, those evaluations are not official until the bull is enrolled with the National Association of Animal Breeders or a Canadian AI organization or reaches 2 years of age.

INTERBULL plays an important role in international semen sales by enabling comparison of evaluated bulls across countries. If the genotype is available, the national center can calculate a local genomic evaluation for a bull with no local progeny. Semen exporters will want importing countries to use genotypes of their bulls when they provide local evaluations. Availability of genomic evaluations may help to overcome the evaluation reduction that occurs for top bulls because of correlations of <1 between daughter performance in individual countries. Genomic evaluations will be most accurate if populations in the exporting and importing countries are similar genetically. If those populations are quite different, the SNP effects estimated in the importing country may be less accurate in predicting the daughter performance for foreign bulls than for domestic bulls. For countries that do not calculate genomic evaluations, INTERBULL is the only source of evaluations for bulls from other countries that are expressed on their domestic scale. To serve those countries fully, INTERBULL will need to provide evaluations for bulls that are marketed solely on their genomic evaluations, which would necessitate that INTERBULL remove the current requirement that a bull have daughters in 10 herds.

Another concern is how to exchange and combine genomically enhanced evaluations across countries (van der Beek, 2007). If only 1 country provides such an evaluation, then current procedures used by INTERBULL could provide an appropriate result if accuracy of the genomic contribution is reflected in the measure of evaluation accuracy. New procedures are required to avoid duplicate information when 2 countries or more submit genomically enhanced evaluations. Genomic information from different countries is not independent and should only be included once, not for each country that contributes such an evaluation. Enough information will need to be provided to allow INTERBULL to apply the principles already used to avoid duplicating pedigree information. Genomic information may be more complicated to accommodate than pedigree information because different SNP may be genotyped across countries.

A system to share genotypes across countries would be most efficient but will take some time to develop. Genotypes are expensive to obtain but provide a wealth of information. They may have uses not yet envisioned and may affect the competitiveness and role of various organizations. Careful consideration should be given to how to share genotypes, particularly internationally.

Implementation of genomic evaluations illustrates the synergism that can be achieved when public, private and academic institutions cooperatively pursue the same objective. One of the most important factors affecting accuracy of genomic evaluations is the number of predictor bulls used. For Holsteins, genomic information provided a substantial improvement in accuracy over parent average for all traits,

INTERBULL

Collaboration

and the amount of improvement increased as the number of bulls in the predictor group increased. Jersey and Brown Swiss results indicated that more predictor animals are necessary for adequate accuracy, and additional genotypes are being obtained. Full participation by the North American AI industry through the CDDR is providing the large families needed to study the small effects of individual genes.

A joint U.S.-Canadian project also helps with industry acceptance of results and promotes understanding of a profound change in the way that bulls will be selected and semen marketed. Keeping the characteristics of the fundamental evaluation system outside the realm of marketing will help the process remain unbiased and gain wider acceptance across the entire industry. The industry appreciates assurance that the system is appropriate by having both U.S. and Canadian research teams involved.

Impact

Genomic evaluations are expected to revolutionize dairy cattle breeding programs because they can be obtained shortly after birth. They will change selection and culling of bulls for AI service as well as choice of cows to produce sons. Some bulls will be marketed at 2 years of age based solely on genomic evaluations. The resulting shorter generation interval will create the potential for a large increase in rate of genetic gain.

Acknowledgements

The authors thank Drs. Bevin Harris, David Johnson and Anne Winkelman of Livestock Improvement Corporation (Hamilton, New Zealand) for their visit and sharing their experiences, which confirmed many results and gave ideas for improvements. This project was supported by National Research Initiative Grant Nos. 2006-35205-16888 and 2006-35205-16701 from the USDA Cooperative State Research, Education and Extension Service and by the National Association of Animal Breeders Holstein Association USA (Brattleboro, VT) and American Jersey Cattle Association (Reynoldsburg, OH).

List of references

Ashwell, M.S. & C.P. Van Tassell. 1999. The Cooperative Dairy DNA Repository—a new resource for quantitative trait loci detection and verification (abstract). J. Dairy Sci. 82(Suppl. 1): 54.

Gengler, N. & P.M. VanRaden 2008. Strategies to incorporate genomic prediction into population-wide genetic evaluations (abstract). J. Dairy Sci. 91(E-Suppl. 1): 506.

van der Beek, S. 2007. Effect of genomic selection on national and international genetic evaluations. INTERBULL Bull. 37: 115–118.

VanRaden, P.M. 2007. Genomic measures of relationship and inbreeding. INTERBULL Bull. 37: 33–36.

VanRaden, P.M., M.E. Tooker & N. Gengler. 2008a. Effects of allele frequency estimation on genomic predictions and inbreeding coefficients (abstract). J. Dairy Sci. 91(E-Suppl. 1): 506.

VanRaden, P.M., C.P. Van Tassell, G.R. Wiggans, T.S. Sonstegard, R.D. Schnabel & F. Schenkel. 2008b. Reliability of genomic predictions for North American dairy bulls (abstract). *J. Dairy Sci.* 91(E-Suppl. 1): 305.

VanRaden, P., G. Wiggans, C. Van Tassell, T. Sonstegard & L. Walton. 2008c. Genomic prediction. Changes to evaluation system (April 2008), <<http://aipl.arsusda.gov/reference/changes/eval0804.html>>.

Van Tassell C.P., T.P.L. Smith, L.K. Matukumalli, J.F. Taylor, R.D. Schnabel, C.T. Lawley, C.D. Haudenschild, S.S. Moore, W.C. Warren & T.S. Sonstegard. 2008. SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. *Nature Methods* 5:247–252.

Wiggans, G.R., T.S. Sonstegard, P.M. VanRaden, L.K. Matukumalli, R.D. Schnabel, J.F. Taylor, F.S. Schenkel and C.P. & Van Tassell. 2008. Selection of single nucleotide polymorphisms and genotype quality for genomic prediction of genetic merit in dairy cattle (abstract). *J. Dairy Sci.* 91(E-Suppl. 1): 507.

Distribution and location of genetic effects for dairy traits

J.B. Cole¹, P.M. VanRaden¹, J.R. O'Connell³, C.P. Van Tassell^{1,2},
T.S. Sonstegard², R.D. Schnabel⁴, J.F. Taylor⁴ & G.R. Wiggans¹

¹Animal Improvement Programs and ²Bovine Functional Genomics
Laboratories, USDA Agricultural Research Service,
Beltsville, MD, USA 20705-2350

³University of Maryland School of Medicine, Baltimore, MD, USA

⁴University of Missouri, Columbia, MO, USA

A nonlinear model with heavy tails allows markers with large effects to be regressed away from the mean and regresses markers with small effects towards zero, reflecting the biology of traits such as DGAT. These models provide better fits to the data than models that allow only a finite number of loci to have non-zero effects. No advantage was gained by including interactions between heavy tails and the number of non-zero marker effects. Linear model predictions were intermediate to the heavy-tailed and finite loci models.

Markers on BTA 18 centered on SNP ARS-BFGL-NGS-109285 had large effects on economic merit, longevity, calving ease, and conformation. Relationships among those traits may be attributable to a gene product or regulatory element associated with calf birth weight. The presence of significant marker effects resulted in greater-than-expected proportions of explained genetic variance.

Key words: *Genomic data, Non-linear model, Linear and non-linear predictions, X chromosome, Marker effects.*

The high-speed genotyping of large numbers of single nucleotide polymorphisms (SNP) has recently become affordable for dairy cattle, which has allowed development of genomic selection programs. A number of questions must be answered before genomic evaluation becomes routine, including the optimal choice of models of gene action, the size, location, and distribution of marker effects, and the proper treatment of X chromosome effects.

Marker locations and effects can be used to assess alternative models of gene action, and to identify chromosomal segments of interest for functional genomic study. Different prior assumptions about the distribution of marker effects correspond to varying models of gene action. Markers with large effects on traits of economic importance may be used to identify regions of the genome that merit further study.

Summary

Introduction

This paper describes the effect of different priors on the reliability of genomic predictions, reports the location and size of a marker on BTA 18 that is associated with dystocia, conformation, economic merit, and longevity, and describes how to account for effects on the X chromosome.

Genomic data

Genotypes for 39 314 SNP of 5 360 Holsteins were examined. The selected SNP were from the Illumina Bovine SNP50™ chip (Van Tassell *et al.*, 2008) and had minor allele frequencies greater than 5% in Holsteins. Genotyping and DNA extraction was done at six locations: Bovine Functional Genomics Laboratory, University of Missouri, University of Alberta, Geneseek, GIVF, and Illumina. Cooperating AI organizations in North America contributed the DNA.

Prior assumptions about the distribution of marker effects were tested using historical data from August 2003 for 3 576 bulls born before 1999 to predict current data for 1 759 bulls born 1999-2002. Advantages of various models were tested using weighted regressions of current daughter deviations on traditional and genomic evaluations computed from 2003 data.

Reported marker locations with largest effects used official April 2008 evaluations for 5 285 proven bulls and 75 cows with records.

The genomewide association method of Aulchenko *et al.* (2007) was also used to calculate marker effects for data visualization.

Linear and nonlinear predictions

Predictions were computed by linear and nonlinear genomic models (VanRaden, 2008). For linear predictions, the traditional additive genetic relationship matrix is replaced by a genomic relationship matrix and is equivalent to assigning equal genetic variance to all markers. Differing assumptions about numbers and sizes of QTL effects can result in better or poorer predictions, but may be appropriate in some cases, such as when a single gene is known to have a large effect on a trait. Three different nonlinear models were considered: an infinitesimal alleles model with a heavy-tailed prior in which smaller effects are regressed further toward 0 and markers with larger effects are regressed less to account for a non-normal prior distribution of marker effects (model A), a finite locus model with a normal distribution of marker effects (model B), and a finite locus model with heavy-tails (model AB). Infinitesimal alleles models assume that all loci have non-zero effects, and finite loci models assume that only a fixed number of alleles have effects. Models A and AB are analogous to the Bayes A and B methods of Meuwissen *et al.* (2001), respectively.

Model A had little advantage in R^2 over the linear model except for fat and protein percentages with increases of 8% and 7%, respectively (Table 1). Gains obtained in simulation averaged 3% but were mostly smaller with real data, indicating that most traits are influenced by more loci than the 100 QTL used in simulation (VanRaden, 2008).

Model B provided similar or poorer fits than Model A for all traits assuming 5 000, 10 000, or 20 000 loci with non-zero effects. Model AB produced better R^2 for the percentage traits than model B, which provided results similar to those of the linear model, but provided similar results to model A.

With the exception of fat and protein percentages, for which there are known genes of large effect (Grisart *et al.*, 2004; Zinder *et al.*, 2005), models assuming that all markers have some effect rather than that most have no effect provided better R^2 . Slight decreases in R^2 were noted for most traits in model A when the variance beyond 2 SD was increased (data not shown).

The largest marker effects were for fat percentage on BTA 14 flanking the DGAT1 gene (Grisart *et al.*, 2004), with lesser effects on both milk and fat yield. Large marker effects for protein percentage were also present on BTA 6 flanking the ABCG2 gene (Cohen-Zinder *et al.*, 2005). This demonstrates that the genomic predictions work by tracking the inheritance of causal mutations. Markers on BTA 18 centered on ARS-BFGL-NGS-109285 had the largest effects for several traits: productive life, sire calving ease, daughter calving ease, rump width, stature, strength, and body depth (Figure 1). Another marker on BTA 18 had the largest effect of any on net merit, in the region previously identified by Ashwell *et al.* (2004) as having a large effect on daughter pregnancy rate. This marker had a greater effect on economic merit than DGAT (Figure 2).

Correlations (r) among chromosome 18-specific EBV (data not shown) reveal favorable correlations among longevity and economic merit ($r = 0.88$); undesirable correlations among conformation and calving ease traits ($r = 0.78$ to 0.95); and unfavorable correlations among economic merit and longevity and conformation and calving ease ($r = -0.44$ to -0.72). Selection for extreme conformation (larger body size) has resulting in larger calves and increased rates of dystocia which are largely attributable to fetus-pelvic incompatibility (Meijering, 1984). The increase in calf size is apparently not offset by increasing internal pelvic size of cows.

The expected proportion of genetic variance for each trait accounted for by SNP on a chromosome was calculated based on chromosome lengths assuming that all markers had equal effects. Chromosome 18 was expected to account for 2.2% of genetic variance for each trait, but actually accounted for 2.9% (economic merit) to 7.6% (sire calving ease) of genetic variation.

Table 1. Squared correlations for sire predicted transmitting abilities from predictions using different numbers of QTL and prior distributions of QTL sizes.

Trait	Model ¹			
	Linear	A	B	AB
Net Merit	28.2	28.4	27.6	27.6
Milk	47.2	48.5	46.7	47.3
Fat	41.8	44.2	41.5	43.6
Protein	47.5	47.0	46.8	46.6
Fat %	55.3	63.3	57.5	63.9
Protein %	51.4	57.7	51.4	56.6
Longevity	25.6	27.4	25.4	26.4
Somatic cell	37.3	38.3	37.3	37.6
Days open	29.5	29.0	29.4	29.2

¹Linear = linear model; A = heavy tails model with a prior of 1.12; B = finite alleles model with 20 000 markers; AB = finite alleles model with 20 000 markers and a heavy tails prior of 1.08.

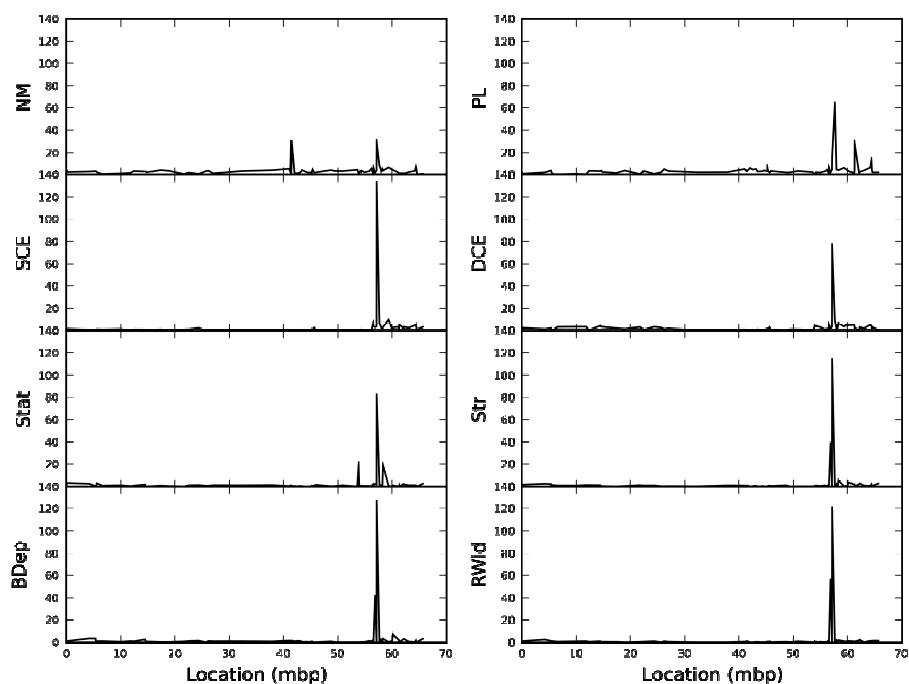


Figure 1. Size (in SD) and location of marker effects on BTA 18 affecting net merit (NM), longevity (PL), sire (SCE) and maternal calving ease (DCE), stature (Stat), strength (Str), body depth (BDep), and rump width (Rwid).

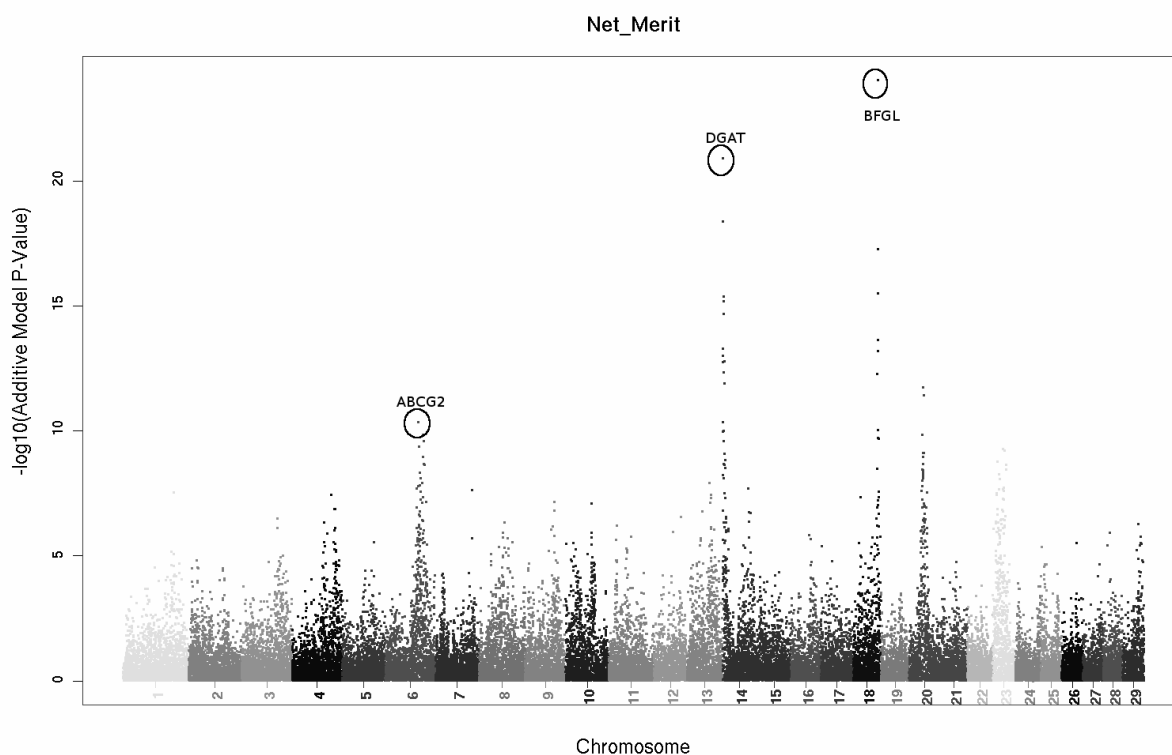


Figure 2. Genome-wide significance of marker effects associated with net merit.

Marker effects for most other traits were evenly distributed across all chromosomes, with only a few regions having larger effects. This may explain why the infinitesimal model and standard quantitative genetic theories have worked well. The distribution of marker effects indicates that favorable alleles will not become homozygous quickly, and genetic variation will remain even after intense selection. Thus, dairy cattle breeders may expect genetic progress to continue for many generations.

The X chromosome of a bull is inherited by all of his daughters but by none of his sons. Thus, two estimates of his genetic merit can be provided: EBV for his daughters is the sum of all marker effects, whereas EBV for his sons excludes effects of 487 markers on the X chromosome. Thirty five markers located on the pseudo-autosomal region were included in the autosomal sum. There are fewer identified SNP on the X chromosome, and markers are spaced more widely than on the autosomes.

Females can also have differing EBV for daughters than sons. Effects on the X are doubled for producing sons because the X transmitted to sons will be transmitted to 50% of the granddaughters instead of the 25% expected for autosomes. Differences between EBV from daughters and average of sons' EBV from 796 genotyped sires that had at least 10 evaluated sons were used to test if effects for net merit on the X chromosome were real. Effects were small but had significant ($P < 0.0001$) associations with differences between the genetic merits of a bull's sons and his daughters.

This project was supported by National Research Initiative Grant nos. 2006-35205-16888 and 2006-35205-16701 from the USDA Cooperative State Research, Education, and Extension Service and by the National Association of Animal Breeders. The computational assistance provided by M. E. Tooker is gratefully acknowledged.

Ashwell, M.S., D.W. Heyen, T.S. Sonstegard, C.P. Van Tassell, Y. Da, P.M. VanRaden, M. Ron, J.I. Weller & H.A. Lewin. 2004. Detection of quantitative trait loci affecting milk production, health, and reproductive traits in Holstein cattle. *J. Dairy Sci.* 87: 468–475.

Aulchenko, Y. S., D.-J. De Koning & C. Haley. 2007. Genomewide rapid association using mixed model and regression: a fast and simple method for genomewide pedigree-based quantitative trait loci association analysis. *Genetics* 177: 577–585.

Cohen-Zinder, M., E. Seroussi, D.M. Larkin, J.J. Looor, A. Everts-van der Wind, J.H. Lee, J.K. Drackley, M.R. Band, A.G. Hernandez, M. Shani, H.A. Lewin, J.I. Weller & M. Ron. 2005. Identification of a missense mutation in the bovine ABCG2 gene with a major effect on the QTL on chromosome 6 affecting milk yield and composition in Holstein cattle. *Genome Res.* 15: 936–944.

Grisart B., F. Farnir, L. Karim, N. Cambisano, J.J. Kim, A. Kvasz, M. Mni, P. Simon, J. M. Frere, W. Coppieters & M. Georges. 2004. Genetic and functional confirmation of the causality of the DGAT1 K232A quantitative trait nucleotide in affecting milk yield and composition. *Proc. Natl. Acad. Sci. U.S.A.* 101: 2398–403.

X chromosome

Acknowledgements

List of References

Meijering, A. 1984. Dystocia and stillbirth in cattle – a review of causes, relationships, and implications. *Livest. Prod. Sci.* 11: 143–177.

Meuwissen, T.H.E., B.J. Hayes & M.E. Goddard. 2001. Prediction of total genetic value using genome-wide dense marker maps. *Genetics* 157: 1819–1829.

VanRaden, P.M. 2007. Genomic measures of relationship and inbreeding. *Interbull Bull.* 37: 33–36.

VanRaden, P.M. 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.* 91: (Submitted).

Van Tassell C. P., T.P.L. Smith, L.K. Matukumalli, J.F. Taylor, R.D. Schnabel, C.T. Lawley, C.D. Haudenschild, S.S. Moore, W.C. Warren & T.S. Sonstegard. 2008. SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. *Nature Methods* 5: 247–252.

Single nucleotide polymorphisms for parentage testing, individual identification, and traceability¹

B.W. Woodward¹ & T. Van der Lende²

¹Merial Limited, 3239 Satellite Boulevard, Duluth, GA 30096-4640, USA

²ProPhys Animal Science Consultancy, Klaproosdreef 21,
8255 JP Swifterbant, The Netherlands

Molecular markers have become the chosen technology for parentage determination, individual identification, and traceability. Types of markers have varied over time, but the advantages of single nucleotide polymorphisms (SNPs) have led to the increasing adoption of these particular molecular markers for identification and diagnostic testing for qualitative and quantitative traits. SNP advantages include highly abundant, more accurate allele calling, high-throughput capability, low mutation rate, very abundant in the genome, amenable to multiplexing, and low per marker cost. Molecular marker panels ranging in size from hundreds to as large as 50,000+ SNPs are currently being used commercially worldwide for genetic identification and diagnostic testing.

Summary

Key words: SNP, Parentage, Identification, Traceability.

Sites in the genome with at least two different bases at the same location are referred to as single nucleotide polymorphisms (SNPs). Almost all SNPs are biallelic, i.e., two different bases can be found at the location under consideration. SNPs are highly abundant and can be found, on average, at one in 1 000 nucleotide positions throughout the genome. SNPs represent, in fact, the most abundant class of polymorphisms. The enormous interest in SNPs is due primarily to their use as markers to identify genes associated with complex genetic diseases (human and veterinary medicine) and to identify genes and quantitative trait loci underlying complex health, production, and reproduction traits (animal science). Over the last

Introduction

¹Presented at the 36th International Committee for Animal Recording Session in Niagara Falls, NY, June 18, 2008, and the 31st Conference of the International Society for Animal Genetics in Amsterdam, Netherlands, July 21, 2008.

few years, the interest in using SNPs for what may be referred to collectively as SNP-based identification has increased substantially. SNP-based genetic identification includes parentage testing (Werner *et al.*, 2004; Ayres, 2005; Rohrer *et al.*, 2007; Van Eenennaam *et al.*, 2007; Fisher *et al.*, 2008), individual identification (Kerr *et al.*, 2004; Werner *et al.*, 2004; Sobrino *et al.*, 2005; Li *et al.*, 2006; Pakstis *et al.*, 2007; Rohrer *et al.*, 2007), and traceability (Heaton *et al.*, 2005; Hurnik, 2005; Loftus, 2005; Weller *et al.*, 2006; Cunningham, 2008).

**SNP-based
genetic
identification**

Traditionally, genetic identification is based on highly polymorphic microsatellite markers (short tandem repeat markers or STRs). At present, the interest in using SNPs for genetic identification is increasing rapidly. The reasons for this increase are (see, e.g., Krawczak, 1999; Werner *et al.*, 2004; Ayres 2005; Weller *et al.*, 2006; Van Eenennaam *et al.*, 2007):

- SNPs are abundant.
- SNPs are robust in terms of laboratory handling.
- SNPs are amenable to fast semi-automatic multiplex typing (high throughput, low cost).
- SNPs have a low rate of genotyping errors.
- SNPs have a relatively stable inheritance.
- SNPs have a low mutation rate.
- SNPs are compatible with easy standardization between laboratories.
- SNPs specifically chosen for genetic identification are included as part of the 50 000+ SNP chip being used worldwide to genotype tens of thousands of influential animals in many breeds.

The informative value of a single biallelic SNP is less than that of a multiallelic STR. Therefore, genetic identification requires larger SNP panels than STR panels for similar discriminatory power (Ayres, 2005; Weller *et al.*, 2006; Van Eenennaam *et al.*, 2007). However, because of the advantages of SNPs over STRs mentioned above, it is expected that the use of SNPs for genetic identification will be broadly accepted as the preferred method for genetic identification. Commercial genetic testing laboratories currently offer genetic identification using SNPs and thus, it is only a matter of time until SNPs replace the use of STRs in many applications. Lower costs associated with genotyping animals with SNPs in contrast to STRs will be one of the primary drivers of this shift from STRs to SNPs.

**SNP selection
for genetic
identification**

SNPs included in a SNP panel for universal genetic identification (including parentage inference) should span a large portion of the genome and should have high heterozygosity in each population (or for example, breed within species) in which the SNP panel is to be used. This means that for each SNP included in the panel the fixation index (Wright's F_{st}) should be globally low, and the average minor allele frequency (MAF) should preferably approach 0.5 (see, e.g., Krawczak, 1999 and Pakstis *et al.*, 2007). Heaton *et al.* (2007) developed a panel of 121 SNPs with a MAF of 0.41 based on a group of 216 diverse sires that represent 19 beef and 4 dairy breeds. Most of these markers were included on the 50 000+ SNP chip developed by a consortium of researchers in 2007 and offered commercially by Illumina, Inc. Since then, this 121 SNP panel has been evaluated in additional cattle breeds of the world, bringing the total number involved to 44 beef and dairy cattle breeds using 24 diverse animals from each breed (Mike Heaton, personal communication).

In humans, using a panel of 31 informative SNPs (4 medium informative, 27 high informative), combined with 28 SNP loci on HLA-DRB1 and ABO genes (major histocompatibility complex and blood group genes, respectively), Li *et al.* (2006) found a matching ability of 9.02×10^{-15} and exclusion probabilities in duos (parent-offspring) and trios (both parents/offspring) of 98.94% and 99.92%, respectively. These authors concluded that these 59 SNPs yield the same power in forensic identification as the 13 CODIS (Combined DNA Index System) STRs (selected by the FBI for forensics) used at the time of their study. Pakstis *et al.* (2007) reported the selection of 40 low Fst, high heterozygosity SNPs for universal individual identification of humans. This panel had a match probability that ranged from 2.02×10^{-17} to 1.29×10^{-13} in 40 populations investigated. (These authors did not consider parentage testing.) Each of the selected SNPs had an Fst of less than 0.06 for all 40 populations. The average heterozygosity in the 40 populations was higher than 0.43 (maximum reachable is 0.50) for each of the 40 selected SNPs.

Weller *et al.* (2006) used analytical and simulation approaches to determine how many genetic markers, SNPs and STRs, might be required for individual animal identification when accounting for genotyping errors. They report STRs have an inherent genotyping error rate of approximately 1%, whereas the rate for SNPs is lower. However, more SNPs are required to attain the same exclusion probabilities. By simulating STRs with five alleles and SNPs with two, Weller *et al.* (2006) concluded exclusion probabilities were approximately the same when using 2 to 2.25 SNPs for each STR.

The successful use of SNPs for genetic identification of cattle and pigs has been reported by Heaton *et al.* (2002, 2007), Werner *et al.* (2004), and Rohrer *et al.* (2007). In cattle, Heaton *et al.* (2002) used a panel of 32 SNPs distributed among 18 autosomes and estimated that the probability that two randomly selected, unrelated individuals will possess identical genotypes for all 32 loci (probability of identity) was 2.0×10^{-13} for multi-breed composite populations and 1.9×10^{-10} for purebred Angus populations. The 121 SNP panel Heaton *et al.* (2007) developed using 23 breeds of cattle has an exclusion power of 0.99999 when no dam is available. Also in cattle, using a panel of 38 SNPs (including one gender-specific SNP), Werner *et al.* (2004) found theoretical probabilities of identity of 8.59×10^{-15} , 8.54×10^{-13} and 1.30×10^{-13} in German Holstein (GH), German Fleckvieh (GF), and German Braunvieh (GB), respectively. The MAF varied largely for these SNPs within each of the three breeds studied (GH: 0.11 to 0.48; GF: 0.05 to 0.50; GB: 0.02 to 0.50; average per breed not given). The theoretical exclusion power of the SNP panel when used for parentage testing was estimated to exceed 99.99% in all three breeds. In pigs, Rohrer *et al.* (2007) used a panel of 60 SNPs, each with a MAF greater than 0.15, and found the overall identity power across the four breeds studied (US purebred Duroc, Hampshire, Landrace, and Yorkshire) was 4.6×10^{-23} , but within-breed values ranged from 4.3×10^{-14} (Hampshire) to 2.6×10^{-23} (Yorkshire). Parentage exclusion probabilities with only one sampled parent ranged from 95.94% (Hampshire) to 99.63% (Yorkshire). Sire exclusion probabilities when the dam's genotype was known ranged from 99.87% (Hampshire) to 99.97% (Yorkshire). Rohrer *et al.* (2007) concluded that the power of exclusion with the 60 SNPs is similar to that of 10 STRs. However, the SNP panel was more sensitive for individual identification.

SNPs can also be used for whole herd parentage assignment or parentage verification (see, e.g., Anderson and Garza, 2006 and Van Eenennaam *et al.*, 2007). Anderson and Garza (2006) have shown by Monte Carlo simulation studies that 60 to 100 SNPs may allow accurate pedigree reconstruction, even in situations involving thousands of potential mothers, fathers and offspring, both in large managed and/or natural populations. Recently, Fisher *et al.* (2008) used simulation and empirical

Use of SNPs for genetic identification: State of the art

data to show that the combination of 40 SNPs (average MAF=0.35) and on-farm data (i.e., mating records, birth dates of progeny, and calving dates of dams) is extremely powerful for parentage assignment. Without the on-farm data, even a 60 SNP panel was not as powerful as the 40 SNP panel with on-farm data. Independent of on-farm data, 40 SNPs were at least comparable to, if not more powerful than, a commercial STR panel consisting of 14 STRs for dairy cattle parentage in New Zealand.

Baruch and Weller (2008) evaluated three different minimum MAFs (0.10, 0.20, and 0.30) for each of three scenarios:

1. single putative parent,
2. two putative parents, and
3. one known parent and one putative parent.

“The numbers of markers required to obtain 99% exclusion probabilities based on a single conflict for the three minimum MAFs were 54, 45, and 39 for scenario 1; 17, 16, and 15 for scenario 2; and 28, 25, and 24 for scenario 3.” If one allows at least two conflicts for exclusion, the number of markers required increased by approximately 45% for all three scenarios and all three minimum MAFs.

Successful use of SNPs for verification of sample tracking in beef processing has been described by Heaton *et al.* (2005). They used a selected panel of 20 bovine SNP markers located on 12 different chromosomes. The panel was sufficiently informative to verify the accuracy of sample tracking in slaughter plants. The average MAF of this SNP panel was 0.36 in 96 selected beef cattle and 0.33 in 168 randomly selected market cattle. Not unexpectedly, this study indicates that the reliability of tracking necessitates great accuracy in tissue sampling procedures and sample labeling. Mistakes were largely due to human errors and rarely due to genotyping errors. Weller *et al.*, 2006 point out SNPs have a lower genotyping error rate than STRs and used simulation to determine that a single STR was approximately equivalent to 2 to 2.25 SNPs for traceability. At least 8 SNPs were required to reach a 99% probability of exclusion between two individuals; 25 SNPs resulted in a <1% chance of a match between any five million individuals.

Effect of genetic identification on selection and genetic gain

Genetic markers have been used to determine that the misidentification rate contributing to pedigree recording errors in recent studies involving dairy cattle ranges from 7 to 15% (Spelman, 2002; Visscher *et al.*, 2002; Weller *et al.* 2004; Sanders *et al.* 2006). Several studies have used actual estimates of pedigree errors or simulated misidentification rates in the reported range to determine that these errors decrease genetic gain anywhere from 2.5 to 15% (Israel and Weller, 2000; Banos *et al.*, 2001; Spelman, 2002; Visscher *et al.*, 2002;). It should be noted that the magnitude of the decrease in gain is affected by the heritability of the trait, misidentification rate, and number of daughters per progeny test sire. Sanders *et al.* (2006) showed that pedigrees with wrong sire information reduced the efficiency of genetic gain from a breeding program 1.4 times more in comparison to pedigrees with missing sire information. Beef producers also have the opportunity to realize greater genetic gains at a lower cost through more accurate sire selection and/or culling by determining which bulls in multi-sire mating pastures actually sired the resulting calves. Van Eenennaam *et al.* (2007) used STRs and SNPs to assign paternity on 625 calves and found that 5 out of 27 bulls exposed to the cow herd through AI and natural service sired 50% of the calves. In contrast, 10 bulls produced no progeny. There is a clear trend for business-minded producers, companies whose business model requires accurate parentage, and breed associations needing pedigree integrity to choose

DNA marker technology for genetic identification. Those interested in increased precision, faster turnaround time, the ability to include diagnostic markers for quantitative and qualitative traits, multiplexing that can lead to lower costs, and being on the cutting edge are choosing SNPs.

Breed associations have processes in place to verify parentage on certain animals that are registered by its members. Currently, multiple breed associations conduct both SNP and STR parentage with IGENITY®². One of the primary downsides of STR marker usage for parentage is the frequent need for re-reading STR gels to see if changing one or more calls by two base pairs will allow a match between parent and progeny. This does not occur with SNPs, which is a fully automated process and thus less prone to errors (Vignal *et al.*, 2002; Weller *et al.*, 2006). For clarification, a re-check, or re-read, of the genotyping result is conducted if a sire/ dam does not qualify as a parent with one to three exclusions. The amount of time required for a data technician to prepare each re-check request averages about 11 min. This re-check time does not include the amount of time required by a lab technician to find and re-read the STR gel. Because all of the re-checking and re-reading processes are manual, there is an increased likelihood of introducing additional human errors with STRs that does not occur with SNPs. Note that when one or more sire or dam STR genotype call is changed, it will impact all other previously assigned matches between progeny and those parents. These changes can also result in a sire or dam no longer qualifying to be the progeny of their parents, resulting in a ripple effect occurring as a result of changing the STR call. Furthermore, it is not possible to re-read STR gels to revise genotype calls when outside labs have conducted the original genotyping work and transferred only the final calls to IGENITY, which obviates the benefit of having ISAG STRs to some extent.

In a large-scale project to evaluate parentage assignment in registered dairy cattle, 6 302 animals were genotyped in 1 639 herds. The IGENITY parentage and identity panel of 99 SNPs used for this project was a subset of those developed by Heaton *et al.* (2007). More than 85% of the animals had 80 or more successful genotype calls for comparison between sire and progeny; 11.8% had between 61 and 80 genotypes. The power of the SNP panel is evident in the distribution in number of exclusions: 76.2% with 0 exclusions, 5.2% with 1 exclusion, 1.1% with 2 exclusions, and 0.5% with 3. (In contrast, the percentage of samples with 1 or more exclusions genotyped with STRs is much higher.) The misidentification rate ranged from an average of 10.3% in herds with <100 cows to a high of 24.2% in herds with more than 2 000 cows; however, there were herds with a misidentification rate approaching 100%.

Anderson, E.C. & J.C. Garza. 2006. The power of single-nucleotide polymorphisms for large-scale parentage inference. *Genetics* 172, 2567-2582.

Ayres, K.L. 2005. The expected performance of single nucleotide polymorphism loci in paternity testing. *Forensic Sci. Int.* 154, 167-172.

Commercial Examples - STRs and SNPs

List of references

²IGENITY is a registered trademark of Merial in the United States of America and elsewhere.

- Banos, G., G.R. Wiggans & R.L. Powell.** 2001. Impact of paternity errors in cow identification on genetic evaluations and international comparisons. *J. Dairy Sci.* 84, 2523-2529.
- Baruch, E. & J.I. Weller.** 2008. Estimation of the number of SNP genetic markers required for parentage verification. *Anim. Gen.* (In press).
- Cunningham, P.** 2008. Using DNA traceability to track meat and ensure safety. *Gen. Engin. Biotech News* 28 (8).
- Fisher, P.J., B. Malthus, M.C. Walker, G. Corbett & R.J. Spelman.** 2008. The number of SNPs and on-farm data required for whole-herd parentage testing in dairy cattle herds. *J. Dairy Sci.* (submitted).
- Heaton, M.P., G.P. Harhay, G.L. Bennett, R.T. Stone, E. Casas, J.W. Keele, T.P. Smith, C.G. Chitko-McKown & W.W. Laegreid.** 2002. Selection and use of SNP markers for animal identification and paternity analysis in U.S. beef cattle. *Mamm. Genome* 13, 272-281.
- Heaton, M.P., J.E. Keen, M.L. Clawson, G.P. Harhay, N. Bauer, C. Shultz, B.T. Green, L. Durso, C.G. Chitko-McKown & W.W. Laegreid.** 2005. Use of bovine single nucleotide polymorphism markers to verify sample tracking in beef processing. *J. Am. Vet. Med. Assoc.* 226, 1311-1314.
- Heaton, M.P., W.M. Snelling, T.P. Smith, J.W. Keele, G.P. Harhay, R.T. Wiedmann, G.L. Bennett, B.A. Freking, C.P. Van Tassell, T.S. Sonstegard, L.C. Gasbarre, S.S. Moore, B. Murdoch, S.D. McKay, T. Kalbfleisch & W.W. Laegreid.** 2007. A marker set for parentage-based DNA traceback in beef and dairy cattle. *Plant and Animal Genome Abstract* P516.
- Hurnik, D.** 2005. Traceability options for the Canadian pork industry. London Swine Conference – Production at the Leading Edge, April 6-7.
- Israel, C. & J.I. Weller.** 2000. Effect of misidentification on genetic gain and estimation of breeding value in dairy cattle populations. *J. Dairy. Sci.* 83, 181-187.
- Kerr, R., D. Rosenfeld, M. Spencer, M. Torres, R. Roman & S. Denise.** 2004. Validation of a bovine SNP panel for parentage and identity. *Proc. 29th International Conference on Animal Genetics (ISAG2004/Tokyo)*, Abstract A 008, pp. 33.
- Krawczak, M.** 1999. Informativity assessment for biallelic single nucleotide polymorphisms. *Electrophoresis* 20, 1676-1681.
- Li, L, C.-T. Li, R.-Y. Li, Y. Liu, Y. Lin, T-Z. Que, M-Q. Sun & Y. Li.** 2006. SNP genotyping by multiplex amplification and microarrays assay for forensic application. *Forensic Sci. Int.* 162, 74-79.
- Loftus, R.** 2005. Traceability of biotech-derived animals: application of DNA technology. *Rev. Sci. Tech. Off. Int. Epiz.* 24, 231-242.
- Pakstis, A.J., W.C. Speed, J.R. Kidd & K.K. Kidd** 2007. Candidate SNPs for a universal individual identification panel. *Hum. Genet.* 121, 305-317.
- Rohrer, G.A., B.A. Freking & D. Nonneman.** 2007. Single nucleotide polymorphisms for pig identification and parentage exclusion. *Anim. Genet.* 38, 253-258.

Sanders, K, J. Bennewitz & E. Kalm. 2006. Wrong and missing sire information affects genetic gain in the Angeln dairy cattle population. *J. Dairy Sci.* 89, 315-321.

Sobrino, B., M. Bríón & A. Carracedo. 2005. SNPs in forensic genetics: a review on SNP typing methodologies. *Forensic Sci. Int.* 154, 181-194.

Spelman, R.J. 2002. Utilisation of molecular information in dairy cattle breeding. *Proc. 7th World Cong. Genet. Appl. Livest. Prod., Montpellier, France.* Communication No. 20-02.

Van Eenennaam, A.L., R.L. Weaber, D.J. Drake, M.C.T. Penedo, R.L. Quaas, D.J. Garrick & E.J. Pollak. 2007. DNA-based paternity analysis and genetic evaluation in a large, commercial cattle ranch setting. *J. Anim. Sci.* 85, 3159-3169.

Vignal, A., D. Milan, M. Sancristobal & A. Eggen. 2002. A review on SNP and other types of molecular markers and their use in animal genetics. *Genet. Sel. Evol.* 34, 275-305.

Visscher, P.M., J.A. Wooliams, D. Smith & J.L. Williams. 2002. Estimation of pedigree errors in the UK dairy population using microsatellite markers and the impact on selection. *J. Dairy Sci.* 85, 2368-2375.

Weller, J.I., E. Feldmesser, M. Golik, I. Tager-Cohen, R. Domochofsky, O. Alus, E. Ezra & M. Ron. 2004. Factors affecting incorrect paternity assignment in the Israeli Holstein population. *J. Dairy Sci.* 87, 2627-2640.

Weller, J.I., E. Seroussi & M. Ron. 2006. Estimation of the number of genetic markers required for individual animal identification accounting for genotyping errors. *Anim. Gen.* 37, 387-389.

Werner, F.A.O., G. Durstewitz, F.A. Habermann, G. Thaller, W. Krämer, S. Kollers, J. Buitkamp, M. Georges, G. Brem, J. Mosner & R. Fries. 2004. Detection and characterization of SNPs useful for identity control and parentage testing in major European dairy breeds. *Anim. Genet.* 35, 44-49.

**Workshop on
"DHI managers"**

Herd testing in the USA

S.J. Sievert

*Quality Certification Services, Inc., a subsidiary of National Dairy Herd
Information Association, Verona, Wisconsin, United States*

The United States has seen slow and steady growth in participation of herd recording programs. At the end of 2007, there were over 4.4 million dairy cows from 23 000 dairy operations participating in recording programs. The DHI industry in the United States continues to offer a wide range of programs for herds of all sizes. In addition to the 27 certified field service a provider working directly with dairy producers, the recording industry in the United States is supported by 49 certified laboratories, 45 certified meter calibration centers, and 4 dairy records processing centers. The combined efforts of these entities provide for a vibrant and growth-oriented milk recording industry that is focused on data accuracy, service to dairy producers, and flexibility to meet the needs of dairy herds of any size.

Summary

Key words: *milk recording, Quality Certification Services, meters, Calibrations, Processing data.*

The milk recording industry in the United States has experienced significant changes over the past two decades. Traditionally, milk recording organizations were organized as non-profit entities, often working with land-grant universities as part of the Cooperative Extension Service. These organizations served defined territories (usually state lines) and were supported by resources and staff as needed to serve the dairies in their trade area.

Background

At present, the milk recording industry is markedly different. While certain regions of the country are still served by traditional milk recording organizations, other geographic regions are now served by organizations that no longer resemble the former. The organizations currently providing milk recording services to dairies include sole proprietorships, privately held corporations, cooperatives and federated (either partially or fully) associations. These organizations no longer operate within a defined trade area; but rather compete in an open-market climate. In addition, the meter centers and laboratories providing services to the recording industry have seen similar changes in business structure, trade area and competition.

Overview of herd testing

Figure 1 provides a schematic for the flow of dairy within the milk recording industry in the United States. While this view is simplified for demonstration purposes, the diagram clearly demonstrates the interconnectivity of allied and industry partners.

All data generated from the various components of the recording entity are processed at one of four dairy records processing centers prior to submission to the Genetic Evaluation Program (GEP). Like the field service, meter center and laboratory entities, these processing centers have diverse business structures and compete in an open-market environment.

One of the challenges in this open-market climate is to maintain standards among competing organizations. The dairy industry in the United States has long realized the need for a quality certification program to ensure that the minimum standards of services are maintained and to assure the accuracy of data flowing between milk recording industry entities and flowing to the Animal Improvement Programs Laboratory (AIPL) and Interbull.

Figure 2 illustrates the areas reviewed for compliance by Quality Certification Services. The multi-level quality certification programs provides numerous checkpoints to assure data accuracy prior to reaching one of the dairy records processing centers, and then a final checkpoint of accuracy of processed data leaving each processing center. One important point is that Quality Certification Services does not determine if an entity should exist, only if each entity is operating with compliance to mutually agreed upon guidelines for the recording industry. In addition to providing a review of compliance at all levels, Quality Certification Services Inc. and its auditors serve in an educational and resource role to aid all herd testing program participants.

Field collection of data and milk samples

At the present time, there are 27 certified field service providers working directly with dairy producers participating in herd recording programs in the United States. Each of these field services is unique in their business structure and services offered to dairy producers, but all operate under uniform operating procedures and abide by a code of ethics. Combined these 27 field service organizations have 3 018 well-trained field technicians that work directly with over 4.4 million dairy

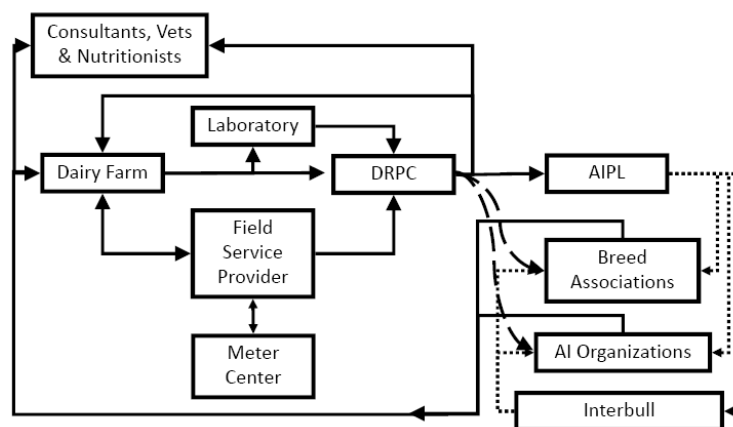


Figure 1. Overview of herd testing in the United States.

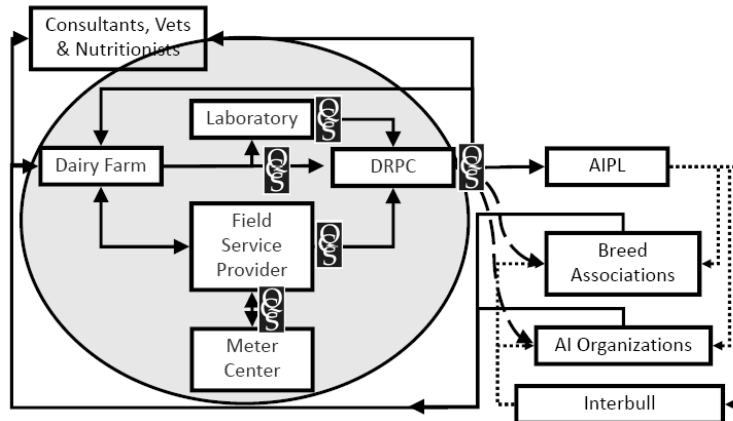


Figure 2. The Role of Quality Certification Programs in the United States.



Figure 3. Certified Providers of Field Services in the United States.

cows on a regular basis. As expected, these field service affiliates are located near areas of concentrated dairy cattle populations (Figure 3), but the entire United States and Puerto Rico are served by at least one field service provider.

Participation in milk recording programs has seen a steady growth over the last five years in the United States (Figure 4). At the end of 2007, there was approximately 47% of the United States dairy cow population participating in DHI (herd recording) programs. Contributing to the growth in dairy cows on recording programs is the fact that each of the individual field service affiliates working with dairies in their respective trade area continue to develop, build value, and market recording services to herds that aid not only provide data to the nationwide genetic evaluation program, but provide timely and useful data to individual dairy producers to aid in the daily management of their respective operations. As detailed in Figure 5, there is a relatively flat distribution of dairy herd size when looking at participation in herd recording programs. While it is probable that the herds of the smallest and largest size (dairy cow numbers) are not on an identical recording program, each of these herds is enrolled in an approved test plan with a certified provider. As a result, dairy cattle

Cows on DHI Programs

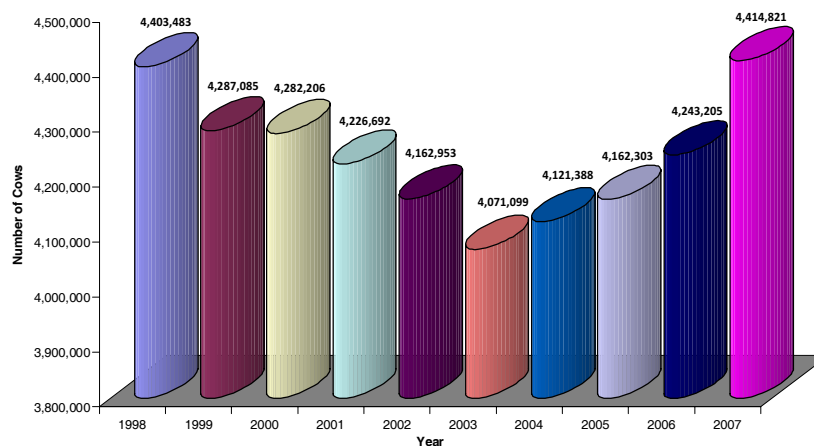


Figure 4. Participation in milk recording programs in the United States (1998-2007).

DHI Cows by Herd Size

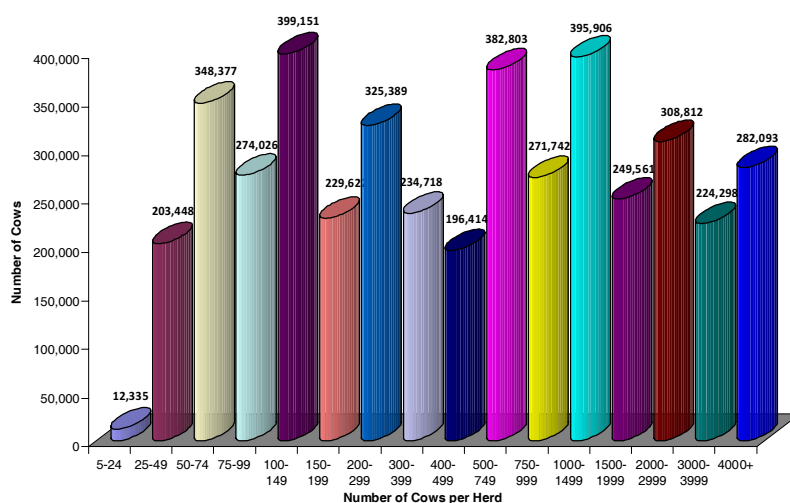


Figure 5. Distribution of herd size for cows enrolled in milk recording programs in the United States, 2007.

from herds of all sizes, geographic locations, and varying management programs are included in the genetic evaluations generated from the United States dairy cattle population.

As required by the quality certification program in the United States, all recording devices used in herd recording programs must be approved by ICAR and National DHIA. Serving the DHI industry in the United States are 45 certified meter calibration and repair centers, once again located near concentrations of dairy cattle populations. Each meter center is inspected and audited on-site biennially. Further, all meter technicians performing calibration and repair services are also audited biennially as well as attend periodic training schools or seminars.

All portable (monthly) meters are required to be calibrated at least once every 12 months in the United States. During 2007, the 45 certified meter centers calibrated 108 139 portable meters. In addition, over 66 000 electronic (daily) meters were evaluated for performance on their respective dairies. Calibration data from both daily and monthly meters are reported to Quality Certification Services each year for review as part of the certification audit for each of the aforementioned 27 field service providers.

Use and calibration of recording devices in herd recording

The DHI laboratories providing services to the recording industry have seen similar changes in business structure, trade area and competition. At the end of 2007, the milk recording industry in the United States was served by 49 certified laboratories (Figure 6). Based on reported statistics, the cumulative total of samples analyzed by all laboratories is approximately 4.7 million samples monthly, with a range of 8 000 samples monthly at the smallest laboratory to 410 000 samples at the largest. These samples were analyzed on 204 unique instruments from three different manufacturers. As part of a comprehensive quality certification program, each laboratory is inspected and audited biennially on-site. In addition, each laboratory participates in a monthly unknown samples program to monitor and assess performance and accuracy.

DHI laboratories in the United States

Each of these laboratories competes in an open marketplace, offering a range of services to dairies participating in recording programs. All laboratories provide milk component and somatic cell count analysis of samples. Other services provided to dairy farmer include analysis of milk urea nitrogen (MUN), ELISA analysis of milk samples for Johne's and/or leukosis, and microbiology analysis. Figure 1 highlights the locations of the certified DHI laboratories operating withing



Figure 6. Certified DHI Laboratories in the United States.

the United States. These labs are located near dairy cow populations (Figure 6) and provide for rapid analysis of milk samples. The average turn-around time from milk sample collection at the dairy farm to lab analysis is 1.45 days across all nationwide DHI laboratories.

**Processing data
from
participating
herds**

Handling the data on over 4.4 million cows the 23 005 enrolled in herd testing programs in the United States are four distinct dairy records processing centers (DRPC). Each of these DRPC are voluntary participants in the quality certification program as well – audited both monthly and annually for accuracy of data calculations and data transfer. As with DHI field service providers and DHI laboratories, these processing centers compete in an open-marketplace environment for business. In addition to providing data to the Animal Improvement Programs Laboratory (AIPL), they each provide reports and tools direct to dairy producers to aid in the daily management of individual dairy operations.

Conclusion

The United States milk recording industry is served by a dynamic herd testing system that efficiently and cost effectively meets the needs of dairy producers of any herd size in all geographic locations. Participation in herd recording programs continues to grow, and the United States DHI system is flexible to adapt to the needs of our nation's diverse dairy operations. Each organization, though distinct in business structure and size, participates in a common certification program. The quality certification program in the United States is neutral on many fronts – business structure, size, geography or other external factors – and provides a basis for compliance by all entities within the recording industry without providing a barrier to entry. As a result, users from within the system along with industry partners such as dairy studs, breed associations, and other interested parties can be assured of the accuracy of data generated from the United States dairy cow population.

Overview of DHI laboratory services in the USA

S.J. Sievert

Quality Certification Services, Inc., a subsidiary of National Dairy Herd Information Association, Verona, Wisconsin, USA

The milk recording industry in the United States is served by a variety of certified laboratories – each unique in business structure, services and analyses offered, and marketing programs. DHI laboratories in the United States compete in an open marketplace and analyze approximately 4.7 million individual DHI milk samples monthly. While significant differences exist in each of the laboratories, all DHI laboratories participate in a voluntary quality certification program administered by Quality Certification Services, a subsidiary of National DHIA. This program, operating on approved guidelines, monitors each participating laboratory on a monthly basis for compliance and performance. The end result is a certification program that is size-neutral, provides for a level field of competition in an open marketplace, and assures accurate and timely milk component data from cows participating in recording programs.

Key words: *Quality certification, Milk recording industry, Laboratory Advisory Committee, Routine analysis.*

At the end of 2007, there were 4 414 821 dairy cows in the United States participating in milk recording programs. While the number of cows on programs fluctuates, the United States has seen a small, but steady growth in the participation in milk recording programs by dairy operations over the last five years. All data and milk samples are collected at the dairy level by field technicians working with a certified milk recording organization (27 certified field service affiliates/milk recording organizations in the United States). Each of the aforementioned field technicians are required to complete training with respect to field services programs, including but not limited to data handling and proper milk sampling and collection procedure.

Traditionally, milk recording organizations served defined territories (usually state lines) and were supported by resources and staff as needed to serve the dairies in their trade area. At present, the milk recording industry is markedly different. While

Summary

Background

certain regions of the country are still served by traditional milk recording organizations, other geographic regions are now served by organizations that no longer resemble the former. The organizations currently providing milk recording services to dairies include sole proprietorships, privately held corporations, cooperatives and federated (either partially or fully) associations. These organizations no longer operate within a defined trade area; but rather compete in an open-market climate.

DHI laboratories in the United States

The DHI laboratories providing services to the recording industry have seen similar changes in business structure, trade area and competition. At the end of 2007, the milk recording industry in the United States was served by 49 certified laboratories. Based on reported statistics, the cumulative total of samples analyzed by all laboratories is approximately 4.7 million samples monthly, with a range of 8 000 samples monthly at the smallest laboratory to 410 000 samples at the largest. These samples were analyzed on 204 unique instruments from three different manufacturers.

Each of these laboratories competes in an open marketplace, offering a range of services to dairies participating in recording programs. All laboratories provide milk component and somatic cell count analysis of samples. Other services provided to dairy farmer include analysis of milk urea nitrogen (MUN), ELISA analysis of milk samples for Johne's and/or luekosis, and microbiology analysis. Figure 1 highlights the locations of the certified DHI laboratories operating withing the United States. These labs are located near dairy cow populations and provide for rapid analysis of milk samples. The average turn-around time from milk sample collection at the dairy farm to lab analysis is 1.45 days across all nationwide DHI laboratories.



Figure 1. Certified DHI Laboratories in the United States (Puerto Rico not shown).

DHI laboratories in the United States' milk recording industry are audited by Quality Certification Services, Inc. (QCS). Each participating laboratory is evaluated on a routine basis to assure compliance with all aspects of the current auditing guidelines as approved by the dairy industry. It is important to note that these guidelines are business-structure neutral and do not exist to determine if an entity should be in business – rather to certify that the entity is operating within compliance. In addition, DHI laboratory managers have a mechanism of input on the certification guidelines. A Laboratory Advisory Committee (LAC) meets annually, and suggestions, clarifications, or revisions to the guidelines are proposed and reviewed. The end result is a dynamic system that ensures auditing guidelines for DHI laboratories are current, relevant, and serve the best interest of the milk recording industry.

To receive or retain certification, each DHI laboratory must be within compliance with both components of certification. These components are:

1. A monthly analysis of Samples Unknown (test samples with actual component analysis unknown to the laboratory). Specific tolerances for lab accuracy and deviation have been established as part of the auditing guidelines, and each DHI laboratory must demonstrate on a monthly basis that all instruments are operating in compliance.
2. A biennial on-site audit of all laboratory procedures, instruments, and documentation conducted by QCS. This comprehensive review ensures the processes and systems are in place to ensure accurate sample analysis and data integrity. In addition, the auditor may serve as an educational resource to assist DHI laboratories in the improvement of procedures or processes.

The United States milk recording industry is served by a wide variety of laboratories that routinely analyze milk samples. These laboratories operate in an open marketplace setting that encourages competition, excellent service, timely analysis, and accuracy. While the DHI laboratories serving milk recording industry in the United States range in size and scope, a common certification program exists to assure the accuracy of the data flowing from the system. The quality certification program in the United States is neutral on many fronts – business structure, size, geography or other external factors – and provides a basis for compliance by all entities within the recording industry without providing a barrier to entry. As a result, over 4.7 million samples are accurately analyzed each month in the United States milk recording industry, providing useful information to the dairy industry on both the management and genetic levels.

Quality certification of DHI laboratories

Conclusion

Serving the diverse production information needs of agriculture

J. Zimmerman

Dairy One Cooperative, Inc., Ithaca, New York, USA

Dairy One Cooperative, Inc. is a diverse farm information services business with origins very similar that of many other agricultural service businesses. The predecessor organizations to Dairy One go back to the first half of the 20th century. Fostered through local county Cooperative Extension, the Dairy Herd Improvement system began with farmers recognizing their need for production information on their cattle, then building the platform for recording and delivering the information.

In 1949 the New York Dairy Herd Improvement Cooperative was formed as a federation of county DHIA's, again fostered through Cooperative Extension. This federation lasted into the 1970s. During the 1970s many of the local county organizations were consolidated into multicounty groups or at the state level within New York. Eventually all of the counties in New York were consolidated into a single state organization of NY DHIC. During this period there was much involvement in the DHIA system by the Land Grant universities in program development, support, and management.

During the 1980s a majority of the northeastern U.S. state DHIA's consolidated in a single, centrally operated organization that became to be known as Northeast DHIA. In the mid 1990s DairyOne Cooperative, a milk marketing cooperative based in Syracuse New York, was moving down a path of developing and providing an array farm management services for its members. DairyOne had a desire to get more involved in herd management services and was contemplating some type of DHIA service. At the same time Northeast DHIA was considering opportunities to partner with others in the dairy industry as it looked to the future. Since there were many leaders in common between Northeast DHIA and DairyOne, it was natural for discussions to begin. After investigation of business synergies and opportunities Northeast DHIA and DairyOne formed Dairy One on January 1, 1997. There was immediate consolidation of a number of business activities including administration, laboratories, and milk sample transportation.

In 2000 the former Mid East DHIA region consolidated into Dairy One and in 2003 Pennsylvania DHIA merged with Dairy One. Both were driven by opportunities to contain costs and maintain or improve services to farmers.

Today Dairy One is a farmer owned cooperative structured as a 501(c) 5 educational not-for-profit, governed by a 19 member farmer board of directors. Dairy One has a unique relationship with DairyOne – similar to a parent organization – that provides

tremendous opportunities to Dairy One. Dairy One has two member organizations, DairyOne and Dairy Farmers of America. Dairy One employs close to 300 people and has gross sales of \$18 million.

Dairy One's strategic focus is to provide production information from all production sectors of a dairy farm while helping farmers and advisors manage the information and implement management strategies through the use of technology.

The mission of Dairy One is carried out through the delivery of products and services proved through four primary business units, DHIA services, analytical services, software sales and support, and Farmland Environmental.

Through Dairy One's DHIA services 5 200 farms with over 600 000 cows in a 13 state region are served. This is Dairy One's largest business segment, but today I will focus on the non- DHIA activities in which Dairy One is involved.

Dairy One operates four milk analysis laboratories providing DHIA testing and producer payment analysis. Through partnerships with Cornell University and the Pennsylvania Diagnostic Laboratory, Dairy One has developed a milk culturing service that helps dairy farmers manage cow udder health. As a way to move cow information and culture results from the farm to the lab, to the advising veterinarian, and back to the farm, Dairy One developed the Culture Tracker software that simplifies data input and management.

The Dairy One forage laboratory is one of the largest laboratories in the U.S. with customers in all 50 U.S. states and 30 foreign countries. Its primary customers are feed companies and feed advisors working in the livestock industries. Additional customer bases are seed companies and zoos. The laboratory provides a full complement of NIR and wet chemistry analyses and is a leader in analysis development. The Dairy One forage laboratory has begun the process of developing affiliated laboratories outside of its traditional territory in the U.S. and around the world. An important arm of the forage lab is Equi-Analytical, a division of the lab focused on serving the equine market.

As part of Dairy One's strategic focus it established soil analysis services in 2006. This is helping Dairy One to move into the area of agronomy information and leverage its resources.

The Dairy Management Resources (DMR) division of Dairy One is comprised of a group of 12 people who are responsible for selling and servicing herd management software systems to farmers. Additionally, the group supports the Dairy One field force in its use of software related to DHIA activities. The strength of the DMR group is that they understand dairy cattle management, and have expertise in software and computers. Support for complex cattle management schemes at the farm has become increasingly important to the industry. DMR has become increasingly involved with the installation and support of computer networks at the farm level, connecting data systems and multiple facilities.

Recently, Dairy One initiated a new business division named Farmland Environmental. The purpose of Farmland Environmental is to help farmers and their advisors organize, optimize, and control issues associated with crop production and environmental management. The initial focus of Farmland Environmental is to provide geo-referenced field maps, Comprehensive Nutrient Management Plans (CNMPs), and a software suite for managing crop production and environmental compliance.

Moving into a new sector of agriculture, Dairy One will begin providing juice and wine analysis services to wineries in the Finger Lakes region of New York State beginning in fall 2008. The wine industry is growing significantly in the region and is in need of the same types of information and analytical services as other sectors of agriculture.

As agriculture continues to grow and change, Dairy One will be focused on how it can continue to service its information and management needs.

In the right hands, PocketMeter is indispensable

B.L. Winters¹ & J.S. Clay²

¹DHI Cooperative, Inc., Columbus, Ohio, USA

²Dairy Records Management Systems, Raleigh, North Carolina, USA

DHI service providers must utilize modern technology whenever it enables them to deliver improved dairy management information and systems. Although handheld computers have been part of everyday experiences for many in modern societies for years, it is only in the past five or six years that the hardware capabilities and cost have enabled DHI to embrace it in the milking parlor or stanchion barn. Technician software for rapid and efficient collection of data from the milking process has enhanced the performance and image of DHI. Additionally, it has improved the quality of the work life for the technician workforce as it has improved the quality of data collected.

Key words: *Handheld, Technology, DHI, Management.*

Recording on-farm data on test day is one of the core functions of DHI businesses. During milkings, the technician must quickly and efficiently record cow identities, milk weights and other data in the parlor with minimal disruption of the dairy's employees. Additionally, workers must focus on data integrity to ensure positive cow identity and accurate milk weights. PocketMeter, the software for handheld computers from Dairy Records Management Systems (DRMS), empowers the technician to perform his/her test day responsibilities in a manner that enables the DHIA system to deliver the highest quality management reports and data to clients.

PocketMeter operates on handheld computers with either Palm, Inc. or Microsoft's PocketPC operating systems. Although some DHIA's are tempted to deploy ruggedized handheld computers, most PocketMeter users purchase consumer grade computers from local electronic supply stores. The two advantages of ruggedized hardware are longer battery life and built-in protection of sensitive electronics. However, a cost ratio of 1:2 or better and the ready availability of computers are obvious reasons for most DHIA's to use consumer grade hardware.

Summary

Introduction

Equipment can be consumer grade or ruggedized

Consumer grade computers become more ruggedized when they are protected from drops on hard surfaces and water sprays by the use of sealed plastic cases such as the OtterBox® from Online Fitness. These relatively cheap protectors increase the expected lifetime of handheld computers. Modest priced commercially available extended life batteries allow consumer grade computers to function during milking shifts that last as long as 10 hours. When both of these features are added to consumer grade computers, the package can favorably compete in cost, battery life and durability with ruggedized units.

PocketDairy operating features

1. Herd Setup
 - a. Herd number and date of test
 - b. Barn type
 1. Stanchion
 - a. Enter all data for each cow before entering data for the next cow
 - b. Enter cow ID, milk weight, batch number and Condition Affecting Record (CAR)
 2. Parlor
 - a. Enter cow ID as cows enter the parlor
 - b. Enter milk weights, batch number and CAR as cows finish milking
 - c. Number of cows per side (one side for rotary parlors)
 - c. Confirm milk weights upon entry (Yes/No)
 - d. Minimum and maximum acceptable milk weight
 - e. Backup
 1. Length of interval can be chosen by user (default = 3 minutes)
 2. To memory card
 - f. Radio Frequency Identification Device (RFID) for certain cow ID
 - g. Size of number pad: small, medium or large
 - h. Split Entry for basement parlors with two handhelds
 - i. Optionally interface with desktop software PCDART from DRMS, SuperV from DHI-Provo and Dairy Comp from Valley Agricultural Services
2. Data entry
 - a. Cow ID can be either cow number or barn name
 - b. Conditions Affecting Record
 1. Customized for desktop software (see item 1.i above)
 2. Example from PCDART: A=abnormal, H=heat on test day, E=milk weight missed, I=injected on test day and F=sample missed
 - c. Sample numbers
 1. None
 2. Entered manually by technician
 3. Automatically incremented as cow IDs are entered
 4. Automatically incremented as milk weights are entered
 - d. Batch/Pen/Temporary String numbers
 1. None
 2. Identify location or pen number
 3. Change with each pen change
 4. Used to quickly confirm cow location on test day
 - e. RFID
 1. "Wand" cows as they enter the parlor
 2. Faster and easier than tapping cow IDs
 - f. Split Entry for basement parlors with two handhelds
 1. Enter cow ID upstairs in one handheld

2. Enter milk weights, sample number, batch number and CAR downstairs in another handheld
 3. At the conclusion of the milking shift
 - a. Sync the first handheld with cow IDs
 - b. Sync the second handheld with milk weights, sample numbers, batch and CAR
 - c. Data files will be merged
 - g. Allow entry of multiple cows at the end of a parlor “side”
 - h. Notes for tasks to complete can be entered at any time during the milking shift
3. Error checking options
 - a. Duplicate cow IDs
 1. Resolve immediately: technician must enter non-duplicated ID before proceeding
 2. Resolve later: technician must enter non-duplicated ID before syncing to PCDART
 - b. Warn if user unintentionally taps a replacement ID or milk weight
 - c. Verified cow ID for users linked to PocketDairy
 4. Closeout at the end of milking
 - a. Resolve duplicate cow IDs
 - b. Sync with PocketMeter Link
 1. Make data corrections
 2. Create file to import into desktop software
 5. Lookup, lists and reports
 - a. Find cows by cow ID, milk weight or sample number
 - b. Lists can be sorted by cow ID, milk weight or sample number
 - c. Print to infrared printer
 6. Use PocketDairy for greater access to cow’s data
 - a. Quick lookup of cow’s status, history and/or recent changes
 - b. Input of status changes for cows calving, dry or left herd

The portability of a handheld computer and PocketMeter enables the technician to tap cow IDs or milk weights into the software at cowside. This flexibility eliminates the need to write data on notepads for keying later. Probably just as importantly, the cow IDs are checked to be certain that the cow exists and milk weights are checked for validity and the proper range.

Cowside entry not only improves efficiency by reducing the number of steps in the parlor but the computer works well in cramped parlors where often there is insufficient space for a notebook computer. Technicians are free to move throughout the parlor and are not tied to a single location where their notebook computer is stationed.

Because the PocketMeter data is edited when entered, the close-out process at the end of milking is quick. Technicians devote less time to tasks such as identifying cow IDs missing milk weights, cow IDs with milk weights but not in the herd and cow IDs with multiple weights. Therefore, personal time for the technician can increase because the workday shrinks.

Advantages of PocketMeter for the technician

**Advantages of
PocketMeter for
the producer**

Producers benefit because PocketMeter eliminates errors resulting during transcribing milk weights, reduces parlor disruptions and enables a quicker test day. But, PocketMeter's cowside checks for valid and duplicate cow IDs during milking are probably its most important features for producers because they help ensure that milk weights will be credited to the correct cow.

A shorter test day results in the management reports and data being delivered sooner. Often finishing the test day duties just a few hours sooner can make the difference between a herd's samples being processed by the laboratory on test day or the next day. As a producer with 240 cows and whose daughters milk all cows stated "My daughters were very happy with our first test on PocketMeter. There were no errors or duplicate cows and the tester left an hour sooner than before."

**Advantages of
PocketMeter for
the DHIA
management**

Although there might be hesitance to invest in additional hardware, DHIA managers have embraced PocketMeter because:

1. PocketMeter eliminates more expensive and fragile notebook computers from barns and parlors. With PocketMeter in use, the notebook computer becomes a command center relegated to the dairy office for access to telecommunications at the end of the milking shift. Ruggedized and water proofed handheld computers are more durable and easier to protect than notebook computers.
2. In most cases, PocketMeter reduces the number of technicians in large parlors. For example, prior to PocketMeter, a 3 200 cow dairy needed three technicians plus a data entry person for each of the two milking shifts (eight people total). With PocketMeter, two technicians worked each milking shift – a reduction of four people. This PocketMeter solution reduced both fatigue for the technicians and cost for the producer.
3. The milking process is not slowed down as much by DHI technicians using PocketMeter so the producer is more satisfied with the service.
4. Technicians realize that they portray a more modern image than when they were using paper and pencil, and, many of them enjoy using the technology. "Cool hardware" becomes a central component of their work day.
5. Training is relatively easy for technicians of all ages and there is little or no follow-up training.

Conclusions

PocketMeter and similar handheld software for DHI technicians have changed the DHIA service such that technicians are more satisfied with their jobs, producers receive better management information, and DHIA management can minimize costs and employ a workforce that delivers a higher quality service.

Using PocketDairy with RFID for herd management

P.A. Dukas

Dairy Records Management Systems, Raleigh, North Carolina, USA

Herd management software for use on mobile devices continues to grow in popularity and in the number of features. The addition of RFID as the identification driver significantly reduces the labor involved in data collection, and increases accuracy of the on-farm database.

Key words: *Mobile devices, Handheld computers, Dairy herd improvement, RFID, PDA.*

Since the early 1970s, one of the most popular reports provided by Dairy Records Processing Centers has been the pocket-sized herd management report. The obvious disadvantage was that the data were only refreshed following the monthly Dairy Herd Improvement (DHI) test. The freshness of data took a step forward with the advent on on-farm management software, but as herds grew in size, even these locally-printed pocket reports became unwieldy. Harnessing the first widely successful mobile platform (Palm), PocketDairy was released in 2000 as the first comprehensive program for dairy management data input and access. The mobile device is synchronized with a desktop herd management system (PCDART) to extend the farm database to cowside and field locations. With the release of ISO-compliant radio-frequency identification (RFID), all lookup and input functions in PocketDairy were enabled for this form of identification.

Numerous attempts to require RFID in animal agriculture at the federal level have not been successful. At the current time, numerous states have implemented phased regulatory approaches to RFID adoption, but the DHI organizations cannot rely on mandatory RFID adoption on which to build an RFID services market. This has forced RFID solution providers to develop strategies based on sound economic return at the farm level. Milking systems manufacturers have recently been investing

Summary

Introduction

RFID environment in the USA

in solutions based on passive RFID, but adoption is only at the earliest stages. However, farms employing this solution provide an excellent opportunity for early adoption of RFID-based mobile devices.

**General benefits
of mobile
devices**

Virtually all management action data are available in PocketDairy for all cows, heifers and bulls at all times. This reduces the delay in performing ad hoc cow management tasks that rely on the availability of current data.

**"One-time" data
entry**

The most apparent benefit of mobile data entry is the elimination of the labor needed to transfer data from the pocket notepad or clipboard to the desktop system. However, the greater impact on farm operations is likely due to the savings generated by the reduction in errors. Anecdotal reports indicate that numerous errors are trapped at the mobile entry point due to real-time error checking in the mobile device and the presence of the cow handler at the time of data entry to correct the flagged entries.

Real-time data entry

On most large farms, manual data recording is performed by the field staff, and input into the onfarm system is accomplished by an office staff working in batch entry mode. Therefore, recent inputs are not available to other cow handlers until hours or days following input. Using PocketDairy, mobile input data can be synced numerous times per day, making up-to-date information available to all handlers.

The managers at two early PocketDairy installations (using five to eleven devices) have reported a significant change in the daily decision-making process. Rather than rely on office staff to input the previous day's events, all cow handlers sync their devices throughout the day. At the end of the day, the farm management staff reviews reports based on the day's activities, and is prepared to adjust the tasks scheduled for the next shift of workers. This eliminates one-half to a full day from the decision-action loop.

Consultant data entry

Informal use of PocketDairy by consultants, veterinarians, and genetic industry field staff has been reported throughout the PocketDairy market. This usage reduces data entry and data transfer delays.

**Primary
management
uses for
PocketDairy**

Numerous forms of identification are stored in PocketDairy, but a very significant linkage is made between the RFID number and the index number. This linkage can be made on the desktop, but is usually accomplished in the barn upon the first encounter with the new animal. The linkage screen is accessed during a dedicated registration task or whenever an animal is encountered that does not have a registered RFID tag. Once the linkage is made, the user is not exposed to the RFID number again.

The most frequently accessed screen is the Cow Page, providing basic status and production data. Additional user-defined fields are available for download of custom items.

Cow page lookup

The types of data entered using the mobile device are targeted to cowside entry activities, but are generally similar to data entered at the desktop computer, such as calving, breeding, pregnancy, treatments, disposal, and new animal entry. Even without RFID, data entry is surprisingly efficient due to the use of droplists preloaded with frequently used selections.

Data input

Using RFID, various PocketDairy functions are enhanced significantly, including:

RFID enhancements

- **Cow Page with Audio Playback** – Users can link an audio file to cow records that satisfy a particular query. The user then rapidly walks through the barn while scanning cows in a hands-free mode until a cow of interest triggers the audio file. In this manner, cows of interest can be quickly located for treatment, group changes, etc.
- **Lost Animal Feature** – In large dairy operations, cows are frequently placed in an incorrect group. By wandling and comparing against the correct group number in the mobile database, the “lost cow feature” alerts the user to the presence of cows in the incorrect group.
- **Treatments, Chores and Protocols** – PCDART provides a system for active management of tasks scheduled for individual cows or groups of cows. Various settings are available in PocketDairy to permit scripted data input and to allow data to be applied to an entire group of cows.

Numerous mobile devices (up to 99) can be synced with PCDART by direct connection or wirelessly. During the sync, mobile inputs are edited for accuracy and applied to the PCDART database and processed. All updated records are returned to the mobile device within the same sync session.

Interfacing with PCDART

The farm manager can set administrative options to restrict users to various read/write options and subsets of the entire farm database. One commonly requested feature at large farms using multiple devices is the ability to review the quality of the input received from the mobile devices.

The evolution of the PocketDairy system began solely on the Palm operating system. During the period from 2000-2003, the Windows CE and successive operating systems were extremely unstable. Once the Windows OS stabilized in 2004, PocketDairy was ported to that platform. However, the significant installed base of Palm users were resistant to the higher cost and complexity of the Windows OS. In addition, the upgrades of the Windows Mobile OS are often more intrusive and more complex than Palm OS upgrades. In 2008, PocketDairy continues to be available on both platforms, with no plans to deprecate either platform.

Supported operating systems

The changing mobile devices market

Market conditions in the mobile device hardware market can significantly influence the success of the mobile systems deployment. As various vendors enter and leave the market, the mobile customer base alternates between enthusiasm (over new product releases) and apprehension (over the obsolescence of recently-purchased hardware).

The release of new Palm devices is slowing significantly as Palm, Inc. focuses exclusively on smartphones. The sales of consumer-level Windows devices are also fairly stagnant following the departure of Dell from the mobile device market. Fortunately, devices for vertical field management applications, such as produced by Socket, are filling the void. Pricing is attractive for use by DHIA field management and on large dairy farms, but may be too high for widespread adoption by moderate-sized herds. The only mobile platforms experiencing growth at this time are Blackberry and Apple, in form factors that appear inappropriate for on-farm use.

Processing of data discrepancies for U.S. dairy cattle and effect on genetic evaluations

G.R. Wiggans & L.L.M. Thornton

*Animal Improvement Programs Laboratory, Agricultural Research Service,
USDA, Beltsville, MD, USA*

Genetic evaluations depend on accurate data for

1. Accuracy of the recorded trait.
2. Information on how much emphasis the trait should receive and how it should be adjusted.
3. Which other animals the trait should influence.

Errors in any of those areas reduce accuracy of all evaluations. When problems are detected, data are rejected or modified to remove the inconsistency. Annotated records that indicate rejection or change are returned to processing centers for review by their personnel to assist in data correction and to explain actions taken. With increasing computing power, reducing the number of data errors and discrepancies should be possible, and error reports and correction should be simpler.

Key words: *Milk recording, Data conflicts, Dairy herd improvement.*

Data integrity and verification are important parts of data utilization (Decker and Martinenghi, 2006). Particularly with multiple contributors, care must be taken to ensure that data are accurate and remain intact when updates are made (Karpovsky *et al.*, 2003; Smith *et al.*, 2005).

The Animal Improvement Programs Laboratory (AIPL) calculates genetic evaluations of U.S. dairy cattle for yield traits, longevity (productive life), mastitis resistance (somatic cell score), fertility and calving traits of dairy cattle as well as conformation (type) traits for some breeds. Those evaluations depend on accurate data from several sources. Five dairy records processing centers provide milk recording data. Breed registry societies provide pedigree and type data. Data on calving traits and bull status for artificial-insemination service are provided by the National Association of Animal Breeders (NAAB). Extensive data checking is done to enforce consistency. For example, errors and changes in animal identification (ID) can cause data from 2 animals to be assigned to the same animal or data from the same animal to be treated as 2 animals. Formatting or entry errors can result in reporting of impossible values; however, unusual values that are correct must be allowed.

Summary

Introduction

Genetic evaluations depend on accurate data for:

1. Accuracy of the recorded trait (e.g., milk weight).
2. Information on how much emphasis the trait should receive and how it should be adjusted (e.g., milking frequency, number of milkings weighed).
3. Which other animals the trait should influence (e.g., parents, progeny and contemporaries) (Wiggans *et al.*, 2007).

Errors in any of those areas reduce accuracy of all evaluations. Banos *et al.* (2001) documented the effect of misidentification on accuracy of genetic evaluations. As genomic information becomes more prevalent and is used in genetic evaluations, data integrity becomes more important, and additional checking must be added to verify accuracy of both traditional phenotypic data and genomic information (Kemmeren *et al.*, 2002).

Data flow

For national genetic evaluations of the U.S. dairy population, pedigree and yield records are processed by the main editing program, which checks pedigree and yield fields before records are added to the AIPL master database. For new animals, their ID is checked to see if it is valid. A valid ID includes a valid breed, country code and ID number. Canadian animal ID is validated against a list of ID supplied by the Canadian Dairy Network (Guelph, ON). For 9-digit American ID, the last digit is a check digit that can detect some invalid ID. An animal's birth date then is checked against its parents' birth dates to see if the sire or dam was either too young or too old to be a parent. If a dam has lactation records, her progeny's birth date is matched with her calving dates. Differences of <1 month are allowed. If an animal is from embryo transfer, comparison with dam calving date is omitted. Parents without information in the database are added with an estimated birth date that is assigned to be 3 years before the reported animal's birth date. Estimated dates are revised if information from older siblings is received.

Detection of additional ID (aliases) for an animal is complex. Animals that have the same birth data and are full siblings but not twins are investigated. The within-herd ID (control number) is valuable in determining whether the ID is for a new animal or an alias. Bulls registered in >1 country have been a common cause of an animal's being treated as >1 animal. That problem has subsided as countries have accommodated foreign ID and have stopped re-registering bulls. Identification numbers that differ by only 1 digit (either different or missing) are investigated as possibly invalid ID for the same animal. For cows with lactation data, yield data must not conflict for data from 2 ID to be combined as data for the same cow.

Yield data are edited based on 2 ranges. Values outside the widest range are rejected as invalid. Values outside a more narrow range determined for each cow's lactation are stored; however, when they are used, they are changed to a floor or ceiling derived from other test-day data. Careful consideration is given to determining which herd a cow was in when she produced a test-day record. A herd test-date record identifies valid herd test dates. Otherwise, cows with a test day in a previous herd would have those data assigned to the current herd. Checking also is done to assign events to the correct calving date, which most often is an issue with breeding information. A missing calving date causes such events to be associated with the previous calving.

Error reports

When an error or conflict is detected, a record that has been annotated to indicate an editing action of reject, notify, or change is returned to the processing center to assist in data correction and to explain what action was taken. Typically, those records are stored to assist in answering queries and, in some cases, forwarded to the supervisor or producer for action. Records that are rejected also are available by query on the AIPL website (<http://aipl.arsusda.gov>) to assist in answering questions and correcting problems. Table 1 shows common errors and their frequencies for 1 day's edits of pedigree records from 1 breed registry society and lactation records from 1 dairy records processing center.

Table 1. Frequency of common errors in pedigree and lactation records submitted on 1 day from 1 breed registry society and 1 dairy records processing center for addition to the U.S. database of records for calculation of genetic evaluations for dairy cattle.

Record type	Error code	Definition	Disposition	Frequency (no.)
Pedigree (n = 12 000)	1Nd	Merging input to animal in master	Notify	207
	1Oh	Update input to twin	Change	138
	3Ib	Dam identification (ID) differs from master, source not verified	Notify	107
	1Od	Sibling updated to twin	Notify	106
	2Be	Sire ID not preferred	Change	82
	3Be	Dam ID not preferred	Change	75
	5Fc	Birth date and dam calving date not the same	Notify	69
	2Jc	Sire ID differs from service sire ID	Notify	64
	2Ib	Sire ID differs from master, source not verified	Notify	60
	4Jc	Master same as cross-reference	Change	52
Lactation (n = 93 000)	2De	Grade sire misidentified	Reject/change	2 738
	1Be	ID not preferred ID	Change	2 611
	6Td	Parity and age mismatched	Change	2 334
	0Jd	Multiple birth code ignored	Change	2 235
	7Ic	Abnormal recorded milk yield	Change	1 967
	2Gd	Sire ID differs from master	Change	1 902
	7Ob	Quality control code incorrect	Notify	1 899
	5Bd	Birth date differs from master	Reject	1 801
	3Gd	Dam ID differs from master	Change	1 707
	7Mb	Milkings weighed not the same as for herd	Change	1 472

Editing principles

When errors are encountered, data are either rejected or modified. Data rejection causes loss of possibly valuable information and often results in no genetic evaluation for animals of interest. Therefore, the system is designed to retain data whenever possible. However, data elimination is preferred to retention of conflicting data. For example, if an animal's birth date conflicts with its dam's calving date and both animals already have data in the system, the dam ID is removed to resolve the conflict and to allow records for both animals to remain in the database.

Importance of types of data

Milking times

To save labor costs, most U.S. herds are enrolled in an a.m. - p.m. test plan in which not all milkings are supervised and daily yield is estimated from the recorded milking. That estimation is based on the interval since the previous milking. Although the start time for each milking is critical, milkings vary in length (e.g., supervised milkings generally are longer). A more accurate estimate of the interval between milkings can be derived from the midpoints of consecutive milkings instead of starting times, which is why an end time also is required for each milking.

Alternation of supervised milking

The purpose of milk recording is to estimate yield accurately for a dairy. Because each dairy is unique, a.m.-p.m. estimation formulas derived for the national population are not an exact fit for individual dairies. If supervised milkings alternate over time between morning and evening, systematic errors should average out, and lactation records would be unbiased. Such alternation of supervised milkings sometimes is difficult to achieve with large herds.

Herdmate ID

Genetic evaluations rely heavily on pedigree data, particularly so that bulls of superior genetic merit can be identified. Therefore, data from cows with unknown sires are not included in evaluations. Only evaluated cows can serve as herdmates of other cows; thus, even large herds may have small contemporary groups if most cows are not sire identified.

Breed reporting for crossbreds

All breeds are included in the U.S. across-breed genetic evaluation (VanRaden *et al.*, 2007), and the breed percentages for an animal are derived from its pedigree. The breed determines the breed base on which a cow's evaluation is reported unless the breed is coded as XX (crossbred). Sire breed determines the breed base for evaluations of crossbred cows. Generally, an animal's breed should reflect the breed with the highest percentage from within the animal's pedigree. For crossbred herds, genetic evaluations are likely to be reported on different breed bases. For animals with equal breed percentages (e.g., 50% Holstein, 50% Brown Swiss), using the predominant breed for the herd is beneficial.

Data collection rating

The data collection rating (DCR) measures how much data from a particular test plan are expected to vary from a standard. The less information that is collected, the lower the DCR. However, DCR does not measure bias directly. For example, if the same milking is sampled every month in a herd enrolled in a.m.-p.m. testing with component sampling, the estimates of component yields will be biased by the degree that national estimation formulas do not fit the herd. However, the amount of

information collected is not different; thus, the variance of the error is not increased, and the DCR is the same. The DCR for unsupervised milkings is arbitrarily set to 75% of that for a supervised milking. A similarly discounted DCR could be used for herds enrolled in a.m.-p.m. testing when the sampled milking is not alternated if that information were reported to AIPL.

Automatic milk recording (AMR) equipment provides an opportunity for increased recording accuracy. However, AMR systems must monitor their own accuracy and detect when a unit needs maintenance. Because they depend on accurate cow ID, they can be subject to misread ID and scrambling of cow order while filling stalls. Typically 5- to 10-day averages are reported, which limits the effect of assigning an individual milking to the wrong cow. The AMR system should detect atypical cow yields and exclude them. The editing system for the AIPL database cannot detect common AMR problems; thus, accurate meter calibration is important.

The AIPL system used for checking data used in national U.S. genetic evaluations of dairy cattle is highly complex. Records from various sources are combined, and conflicting data are harmonized based on which data are expected to be most accurate. Conflicting data are deleted when necessary. Data for pedigree, yield and animal status all affect genetic evaluations, which can only be as accurate as the contributing data. Invalid records can diminish the accuracy of evaluations for other animals. Accurate data are most likely to be generated if those collecting it understand how the information is used and how accurate information benefits the entire data scheme.

The authors acknowledge the contributions of John Clay at Dairy Records Management Systems (Raleigh, NC), Dan Webb at the University of Florida (Gainesville, FL) and Lillian Bacheller at AIPL (Beltsville, MD).

Banos, G., G.R. Wiggans & R.L. Powell, 2001. Impact of paternity errors in cow identification on genetic evaluations and international comparisons. *J. Dairy Sci.* 84: 2523–2529.

Decker, H. & D. Martinenghi, 2006. Avenues to flexible data integrity checking. 17th Inter. Conf. on Database and Expert Systems Applications (DEXA'06), pp. 425–429.

Karpovsky, M.G., L.B. Levitin & A. Trachtenberg, 2003. Data verification and reconciliation with generalized error-control codes. *IEEE Transactions on Information Theory* 49: 1788–1793.

Kemmeren, P., N.L. van Berkum, J. Vilo, T. Bijma, R. Donders, A. Brazma & F.C.P. Holstege, 2002. Protein interaction verification and functional annotation by integrated analysis of genome-scale data. *Molecular Cell* 9: 1133–1143.

Automatic milk recording

Conclusions

Acknowledgements

List of references

Smith, A., D. Greenbaum, S.M. Douglas, M. Long & M. Gerstein, 2005. Comment: Network security and data integrity in academia: an assessment and a proposal for large-scale archiving. *Genome Bio.* 6: 119.

VanRaden, P.M., M.E. Tooker, J.B. Cole, G.R. Wiggans & J.H. Megonigal, Jr., 2007. Genetic evaluations for mixed-breed populations. *J. Dairy Sci.* 90: 2434–2441.

Wiggans, G.R., M.A. Faust and F. Miglior, 2007. Harnessing automatic data collection to enhance genetic improvement programs (abstract). *J. Dairy Sci.* 90 (Suppl. 1): 377.

Managing DHI employees in a large-herd environment

W.R. Skip Pringle

San Joaquin DHIA, USA

As herds increase in size, with the ever changing design of milking parlors, more employees were needed at each facility to test a herd. We have always maintained 10 Milk Test Supervisors. We expected them to test 9 000 cows per month. Our commission plan, insurance base and bonuses, were all based on 9 000 cows per tester, per month. We now have grown to over 100 000 cows, and are able to still maintain only 10 Milk Tester Supervisors.

Because of the strict labor laws in California, and the different milking times of each dairy, it was important to develop a schedule that would:

1. Meet all labor rules.
2. Minimize the amount of overtime we had to pay.
3. Assure that adequate rest is received between herds.

California's labor-day can be set by a twenty four hour clock. You determine what time your day starts and ends. At San Joaquin our day starts a 12:00 am. To help you understand this better, if a tester starts a herd at 4:00 pm and finishes that herd at 4:00 am, and starts another herd at 8:00 pm, he has work 12 hours straight, but because the hours fall into different work days, he has worked two eight hour days. You are only required to pay the worker at a straight time rate that meets or exceeds the states minimum wage rate (\$7.50 per hour). Scheduling is important to avoid time and one half for overtime.

Herds by size

Herds	Herd Size
9	12 – 200
17	201 – 299
15	300 – 499
22	500 – 699
18	700 – 899
14	900 – 1199
17	1200 – 1499
20	1500 – 4000

I would like to say that handling the increase was a magic formula that I developed. But credit must be given, were credit is due. San Joaquin has three brothers that started the labor shift that we still use today:

1. One helps the other and they share the commission, or
2. Barter the hours (you help me x hours and I will work x hours for you).

Table 1. Assisted testers, herds, number of cows and herds.

	No. herds	Cows tested	Herds assisted	Total herds
<i>Full time testers</i>				
John Silva	18	22 500	4	22
Joe Borba	25	21 500	3	28
Dennis Smith	17	11 500	2	19
J Dias	17	11 000	4	21
R Zamora	21	9 000	4	25
N Silva	6	9 000	2	8
E Padilla	18	9 000	2	20
<i>Retired</i>				
M Silva	3	3 000	2	5
Joe Silva	5	6 000	3	8
Ray Silva	2	3 000	1	3
10	132	105 500	27	

Table 2. Information on specific parlors and design.

	Cows milked	Testers required	Milking time	Travel time
Largest parlors				
Double 34	3 902	4	10 hrs	4.0 hrs
Double 32	3 500	4	11 hrs	0.5 hrs
2Double 24	3 745	2	10 hrs	0.5 hrs
Double 30	2 750	3	10 hrs	0.5 hrs
3 barns	2 350	3	10 hrs	0.5 hrs
Double 30	2 333	2	10 hrs	0.5 hrs
26 Cal Walk Tru	2 193	3	11 hrs	0.5 hrs
Double 24	1 913	2	8 hrs	0.5 hrs
3 barns	1 875	3	8 hrs	0.5 hrs
40 Round barn	1 870	3	16 hrs	0.5 hrs
Double 25	1 750	2	10 hrs	1.5 hrs
Double 16 (2x)	1 640	2	20 hrs	1.5 hrs
Double 20 (basmt)	1 588	2	10 hrs	0.5 hrs
Double 20 (basmt)	1 582	2	9 hrs	0.5 hrs
2 pits 19 each (3x)	1 510	2	16 hrs	1.0 hrs
Double 10 (2x)	1 045	2	18 hrs	1.0 hrs
2 pits 16 each (2x)	958	2	16 hrs	1.5 hrs

As herds increased in size, they began to help each other, by trading hours. The lead tester scheduled his helpers, which allowed us to test more cows, with fewer employees. Today we have seven full time testers, 3 semi- retired and 1 tester assistant.

Testers, herds, number of cows and herds that he assists are reported in table 1

Commission Pay Rate:

Am Pm milking	0.33 cents per cow with a \$10.00 Stop charge.
2 milk weight per day	0.45 cents per cow with a \$10.00 Stop charge.
3x am pm	0.45 cents per cow with a \$10.00 Stop charge.
3x (all milkings tested)	0.60 cents per cow with a \$13.00 Stop charge.

To explain how this all works we need to talk about specific parlors and design (Table 2).

We have found doing more than 20 cows per side is difficult for one tester, to keep up with the milker's. Every effort is made to maintain the normal milking times.

From the information that I have given, you can do the math. Yes, depending on how much help they need, and what herds they share, we do have Milk Test Supervisors making 60, 70 and 80 thousand dollars per year.

**So how does it
work?**

Data collection ratings and best prediction of lactation yields

J.B. Cole

*Animal Improvement Programs Laboratory, Agricultural
Research Service, United States Department of
Agriculture, Beltsville, MD, USA*

Best prediction (BP) has been used in the US to calculate lactation yields of milk, fat, protein, and somatic cell score (SCS) from test day data since 1998, when it replaced the test interval method (TIM) used since 1969. It is more complex than TIM but also more accurate, particularly when testing is less frequent. The BP software was recently modified to use breed-, parity, and trait-specific lactation curves, accommodate lactations longer than 305-d, and provide additional output, such as daily yields. Data collection ratings (DCR), which describe the accuracy of lactation records from a variety of test plans, are calculated as a function of each trait's reliability. Predictions of daily yield were validated using daily milk weights from university research herds. Data collection ratings for fat and protein increased when multiple trait BP was used. Many cows can produce profitably for >305 DIM, and the revised BP program provides a flexible tool to model records of any reasonable length and testing pattern.

Summary

Key words: *Best prediction, Daily yield, Data collection rating, Lactation yield.*

Best prediction (VanRaden, 1997; Cole and VanRaden, 2006) is a computational method derived from selection index that allows test day data to be condensed into total lactation yields and persistencies. Lactation yields have been calculated using BP since February 1998, and the International Committee for Animal Recording (ICAR, 2006) approved BP for lactation record calculation in 2002. Best prediction requires only phenotypic covariances, and assumes that herd means and variances are known. It is simpler to compute than a test-day model but still provides accurate lactation records for a variety of test plans. Reverse prediction may be used to obtain daily yields from lactation yields and persistencies. Both single- and multiple-trait prediction are supported. However, the original BP programs could not accommodate lactations longer than 305-d, did not provide daily yields, and modelled covariances among test days using functions that did not have simple biological interpretations.

Introduction

Materials and methods

Test-day data for six dairy breeds were extracted from the national dairy database (NDDB), and lactation lengths were required to be ≥ 500 -d (≥ 800 -d for SCS). Average yield and SD at any day in milk (DIM) were estimated by fitting 3-parameter Wood's curves to milk, fat, protein data and 4-parameter exponential functions to SCS data for means and SD of 15- (≥ 300 DIM) and 30-d (>300 DIM) intervals. The resulting breed-, parity-, and trait-specific curves defined a set of standard curves to which individual cow data were compared.

Best prediction requires correlations among individual DIM within and between traits. Those correlations were estimated using an autoregressive matrix to account for biological changes over the course of a lactation and an identity matrix to model daily measurement error. Autoregressive parameters were estimated separately for first and later parities. Correlations between traits were modified so that correlations between SCS and other traits may be non-zero.

The new lactation curves and correlation functions were validated by extracting test day data from the NDDB, estimating 305-d yields using the original and new programs, and correlating those results. Daily BP of yield were validated using daily milk weights from on-farm meters in university research herds.

The accuracy of lactation records from a wide variety of test plans can be compared using a data collection rating (DCR). Data collection ratings are computed from test-day data using best prediction (VanRaden, 1997) as the squared correlation of estimated and true yields multiplied by a factor of 104 to give monthly testing a rating of 100 and daily testing a rating of 104. Separate DCR are calculated for milk yield, components yield, and somatic cell score. Herd DCR are calculated as the DCR for a cow tested in a given herd and whose lactation reached 305 days in milk on the herd's most recent test day. The ratio of the error variance from daily testing to the error variance from less complete testing is also computed from the DCR and used to weight lactation records in the animal model; it differs from the squared correlation and DCR because genetic and permanent environmental effects are excluded from the variance ratio.

Results and discussion

The lactation curves used for BP need to accommodate cows with long lactations in a reasonable manner, but it is more important that the first 365-d of lactation be modelled with great precision than, say, days 600 to 700. The use of 500-d lactations represents a reasonable compromise between cows milking only to 305-d and those milking longer, and across breeds only about 5% of cows have lactations longer than 500 DIM. Records up to 999-d in length were analyzed to demonstrate that the new curves and correlation functions can accommodate lactations of any reasonable length.

Lactation curves for milk, fat, and protein yield were similar. First parity cows in all breeds have lower peak yields and flatter lactation curves on average than later-parity cows, i.e., are more persistent. Later-parity cows consistently outperform first parity cows for daily milk, fat, and protein until late in lactation.

First parity cows had consistently lower SCS than older cows for all breeds but Milking Shorthorn, where the shape of the mature cow curve was clearly affected by a few extreme observations. The curves for Holstein cows were similar to those published by Schutz *et al.* (1995), although our curves for first parity cows did not cross the mature cow curves near 305-d as did theirs. Reents *et al.* (1995) found large differences between first and later parity lactation curves for Canadian Holsteins,

as was the case with US Holsteins in this study, but they found that the older cows had lower SCS than first parity cows until about 100 DIM. These differences underscore the challenge of correctly modelling SCS curves.

Autoregressive parameters (r) were estimated separately for first- ($r=0.998$) and later-parities ($r=0.995$). These parameters were slightly larger than previous estimates due to the inclusion of the identity matrix.

Correlations within breeds and parities ranged from 0.900 to 0.988 for 305-d milk yield. The highest correlation among actual and predicted daily yields was 0.988, and the lowest was 0.015 on day 1 of lactation, which may be due to calving-related disorders that are not accounted for by BP. As expected, correlations were lowest early in lactation and highest later in lactation.

Data collection ratings for a number of testing plans are presented in table 1. Variation is affected by the test plan. Measurement errors are decreased if several daily yields are averaged as in labor efficient records. Errors are increased in AM-PM testing because only a fraction ($2/3$, $1/2$, or $1/3$) of the cow's daily yield is

Table 1. Data collection ratings (DCR), squared correlations of true with estimated milk yields, and lactation weights for various 305-day records.

Test plan	Test days (no.)	Lactation weight (%)	Squared correlation (%)	DCR
<i>Daily</i>	305	100	100	104
<i>Labor efficient record</i>				
10-d mean	100 ¹	99	100	104
5-d mean	50 ²	98	99	103
<i>Monthly supervised</i>				
All milkings ³	10	95	96	100
2 of 3 milkings	10	92	93	97
1 of 2 milkings	10	89	91	95
1 of 3 milkings	10	83	87	90
<i>Monthly owner-sampler³</i>				
All milkings ⁴	10	66	72	75
2 of 3 milkings	10	64	70	73
1 of 2 milkings	10	63	69	72
1 of 3 milkings	10	60	66	69
<i>Bimonthly supervised</i>				
All milkings ⁴	5	90	91	95
2 of 3 milkings	5	84	87	90
1 of 2 milkings	5	79	83	86
1 of 3 milkings	5	71	75	78
<i>Bimonthly owner-sampler</i>				
All milkings ⁴	5	63	69	72
2 of 3 milkings	5	61	66	69
1 of 2 milkings	5	58	64	67
1 of 3 milkings	5	53	60	62

¹A 10-day average reported in each of 10 mo.

²A 5-day average reported in each of 10 mo.

³Owner-sampler records are assigned a maximum possible DCR of 75.

⁴Milk weights were obtained from all milkings on each test day.

weighed or sampled. Measurements reported by the cow's owner instead of a supervisor also are assumed to be more prone to bias than supervised tests because supervisors are trained to provide accurate data. Finally, variation of lactation yield is affected by the number and pattern of tests within the lactation.

Lactation yields for cows calving on or after January 1, 1997 were computed using the revised programs and multiple-trait BP. The data were extracted from the database and genetic evaluations were re-calculated for Holstein bulls that received genetic evaluations in April 2008. Average reliabilities of milk and protein yield increased by about 0.5% and 1.25%, respectively, suggesting that estimates of genetic merit can be improved by using information from correlated traits.

Conclusions

Best prediction is a flexible tool for accurately modelling milk, fat, and protein yields and SCS in lactations of any length. Data collection ratings allow US dairy producers more choices of sampling programs than those in many other countries, and almost all data from the field can be used for genetic evaluation. The program provides lactation-to-date, 305-d, 365-d, and projected yields, as well as BP of daily yields. The software is in the public domain and may be downloaded from the AIPL website at: <www.aipl.arsusda.gov/software/bestpred>

List of references

Cole, J.B. and VanRaden, P.M. 2007. A Manual for Use of BESTPRED: A Program for Estimation of Lactation Yield and Persistency Using Best Prediction. Available: <www.aipl.arsusda.gov/software/bestpred> Accessed May 14, 2008.

Cole, J.B. and VanRaden, P.M. 2006. Genetic evaluation and best prediction of lactation persistency. J. Dairy Sci. 89: 2722–2728.

ICAR. 2006. International Agreement of Recording Practices. International Committee for Animal Recording, Rome, Italy.

Reents, R., Jamrozik, J., Schaeffer, L.R. and Dekkers, J.C.M. 1995. Estimation of genetic parameters for test day records of somatic cell score. Dairy Sci. 78: 2847-2857.

Schutz, M.M., VanRaden, P.M., Wiggans, G.R. and Norman, H.D. 1995. Standardization of lactation means of somatic cell scores for calculation of genetic evaluations. J. Dairy Sci. 78: 1843–1854.

VanRaden, P.M. 1997. Lactation yields and accuracies computed from test day yields and (co)variances by best prediction. J. Dairy Sci. 80: 3015–3022.

**Workshop on
"Manufacturers' showcase"**

Management of individual cows in large herds – a challenge to modern dairy farming

N. Pinsky U. Golan, A. Arazi & G. Katz

SAE Afimilk, Kibbutz Afikim, 15148, Israel

A modern dairy farm management system through individual cow management by exceptions is presented. A multi-sensors management system consisting of on-line milk analysis, activity meter, behavioural meter and more, all integrated with a reliable electronic ID, facilitates individual cow management in the modern large herds dairy farm.

The presented system supplies reliable high resolution data which avails maximizing farm performance through individual feeding, health treatment, reproduction and welfare. New sensors emerging from technological breakthroughs and their integration in the management system are demonstrated.

Key words: *On-line milk analysis, Milk meter, Activity meter, Behaviour meter, Automated data collection system, Multi-sensor integration.*

The dominating trend in the dairy industry today is herds getting bigger as small family herds evolve into large dairies with thousands of animals. Traditional 10 to 50 cows family farms built in populated areas disappear and large dairies with hundreds and thousands of milking cows are built in agriculture areas. Intimate familiarity with each individual animal by the owner is no longer an option. Owner operated farms are evolving into big organizations.

Traditional dairying techniques in which the owner is a single man task force that milks, breeds treats and manages the cows changes into teams of professional milkers, health, fertility and feeding people that works different aspects of the farm. The owner becomes a manager of a business.

These new trends requires new management skills and techniques. It is argued that these changes no longer allow caring for individual animals nor do we need to. This article wishes to rebut that argument. The basic production unit in the dairy farm is the individual cow. Herds of 10 cows comprises of the same individual animals as a herd of 10 000 cows. Each one of these cows contributes to the performance of the entire herd. By overlooking individual cows we concede any option of improving performances of these cows. Furthermore, this approach leads to leaving only the survivors in our herd. These survivors are not necessary the best cows economically. The key to success in herds of any size is taking good care of each individual animal.

Summary

Introduction

This comprehension though, is somewhat problematic. How can one manage individual cows in a large scale dairy without getting bankrupt? The answer is individual management through exceptions.

The industry of today demands advanced management tools. Developing and supplying these tools has become one of the traits of the dairy industry. The future of dairy farming seeks ways to improve the farm performance under the constraints of unfamiliarity with a collection of heterogeneous production units (the Cows).

Management systems for managing individual cows in large herds

Managing individual animals requires good familiarity with these individual's performance, analysis of this data and taking necessary actions. The data required for such management include performance data and general information. Maintaining such database in large herds is an expensive task. The only practical way to build a comprehensive database is by collecting data automatically.

This phrase "Management by exceptions" in relation to managing large herds was coined many years ago. This phrase embraces a way of thinking; it is a tool for large dairies.

Management by exceptions means that the farm manager does not have to look at each animal in the herd every day. It brings up only the animals that need attention and by doing this, it enables managing individual cows in large herds. These features can only be enabled by a comprehensive database

The primary demand of a management system is Data accuracy and cow ID accuracy. Assigning wrong data to cows may result many costly wrong decisions.

Considering all of the above, A management system is comprised of a reliable ID system, set of sensors automatically collecting relevant data and the farming know-how to perform analysis of the data to enable productive decision making.

Products and benefits

The value approach for a system is to supply the farmer with benefits and not products.

Hence, the managing system should comprise a set of solutions which are derived as applications from the different sensors.

- Heat detection and improved fertility are derived from activity measurement.
- Production monitoring, health improvement and precision milking is extracted from a Milk Meter and milk electric conductivity measurement.
- Precise individual nutrition, health improvement, diagnosis of energy balance disorders, selection, follow up of payment from the dairies are availed from milk analysis and body weight.
- Milk separation according to its quality can be performed via real time milk analysis.
- Cow welfare, cow health and calving predictions are performed by a behavior meter.

All these are integrated by management software as a daily operation tool. Performance analysis that point out exceptions allow decision making that promote evolution towards excellence rather than evolution towards mediocrity as is dictated by the non individual management approach.

The future lies in a multifactorial approach able to analyze synchronized data from all sensors.

Heat detection system continuously monitors changes in cow activity which provides an excellent detection of the animal's biological condition. The detection is based on the data collected from a pedometer which measures cow's activity.

Lehrer *et al.*, 1992, Pennington (1986) reported efficiency of visual observation at 45% and for pedometers at 78% to 96%. Other studies conducted in the USA compared various breeding methods showing that use of the pedometers resulted in lower cost per pregnancy compared with Presync, Ovsync and visual detection.

An additional new feature is a behavior meter which measures cows lying time and lying bout and can also indicate its restlessness. This new data will enhance performance of heat detection and has the potential of introducing new features to the system.

Heat detection

Milk meters and milk analyser monitor the production of the individual cow to project out any abnormal behavior, furthermore by comparing any individual's performance to any other segment of cows or to its own past performance abnormalities are highlighted. When several indicators are combined, one can get better certitude of his cows diagnostic.

Monitoring production

Milk composition changes during lactation. However, the magnitude of the change is less known. A few field tests were made on this subject and the magnitude of the variance was quite surprising. Figure 1. Displays Fat and Protein concentration of an individual cow during twenty consecutive noon milking sessions. That cow was part of large experiment that took place at Tzipori Farm in Israel (Uner, Katz and Maltz, 2003, unpublished data). In this experiment 61 cows was sampled daily during 20 days. The mean standard deviation for fat of all 61 cows was 0.475%

In another research the real time milk analyser was employed to evaluate milk components in comparison to day field test for a period of thirty consecutive milking sessions in ten consecutive days (A.R.O farm Israel 2006, 88 Holstein cows).

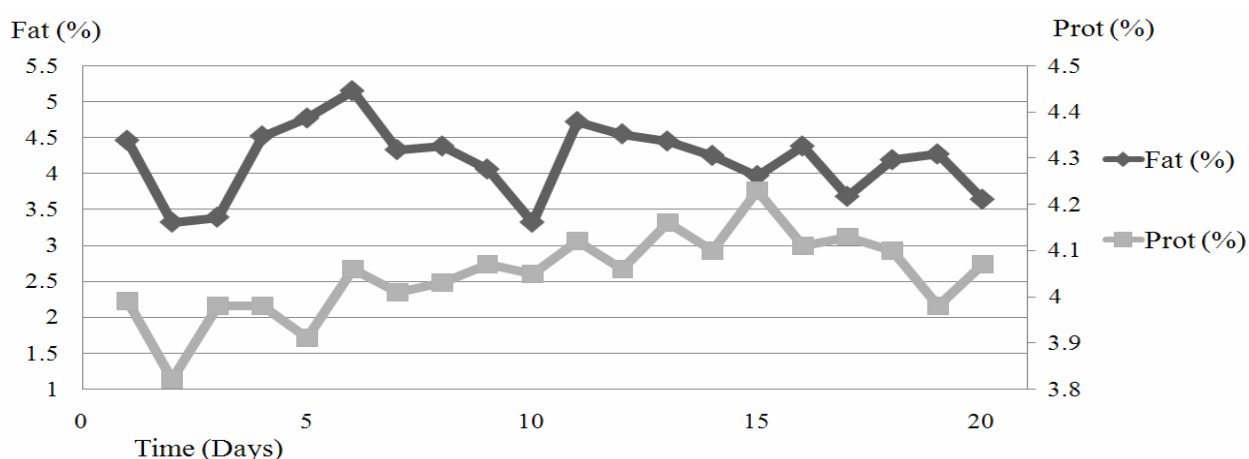


Figure 1. Fat and protein concentrations of cow #609 in Zipory farm for 20 consecutive noon milking sessions.

Figure 2 demonstrates the big fluctuation in fat concentrations during this period of time in the milk of one specific cow.

The mean standard deviation of all 88 cows was 0.57% and mean peak-to-peak of 2.16 % for fat.

These fluctuations hint that there is a great potential for production control in daily analysis of milk components and the necessity of the daily milk components measurement for advanced and modern management.

Individual nutrition

Accurate feeding management can be performed using equations which employ body weight, milk yield and milk components (like the NRC2001 formula).

An example for individual feeding is displayed Figure 3.

The data is part of a feeding research conducted by E. Maltz at A.R.O using the NRC2001 formula employing a walk through body weight, on line milk analyser and a milk meter. Data of two cows from participating in the research is displayed, Cow #302(595kg) and cow #464(713). The left panel shows the allocations and the Net energy from lactation of these cows. The right panel shows their synchronized in time milk fat and milk yield (Maltz, 2007, personal communication).

As it can be seen performance of one individual went up with allocation while the performance of the second cow was inverse to its allocation.

In the quest for maximizing performance and in the world of rising food prices individual feeding is a major incentive for individual management by exceptions.

Cow health

Early diagnosis of sub acute ruminal acidosis (SARA) and ketosis using fat, protein and body weight change in single-cow /group/herd will enable monitoring nutrition and husbandry management to shorten response for prevention.

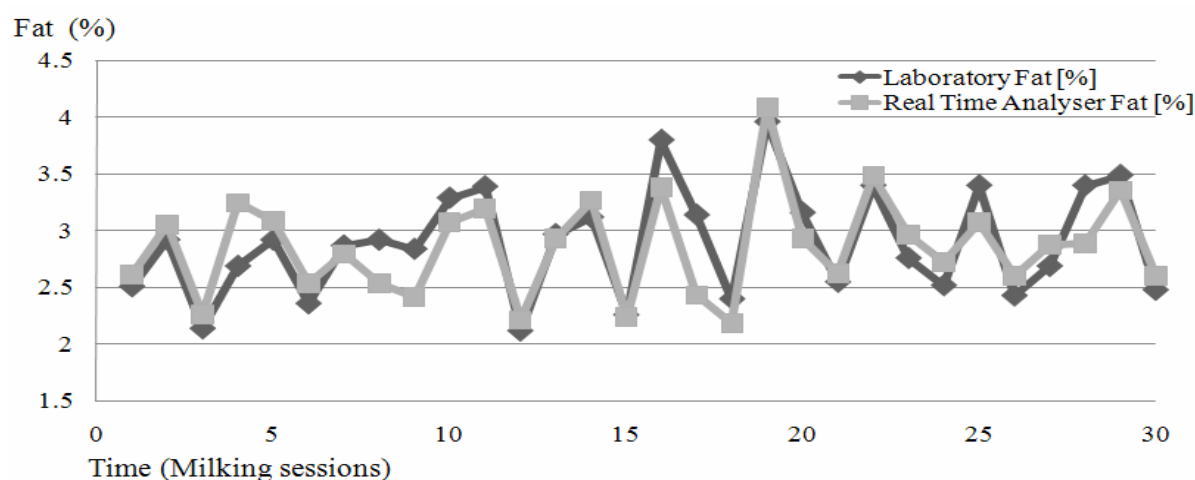


Figure 2. Fat concentrations measured over thirty consecutive milking session (ten days) cow # 2091 at A.R.O. farm a comparison between test day lab results and real time analyser.

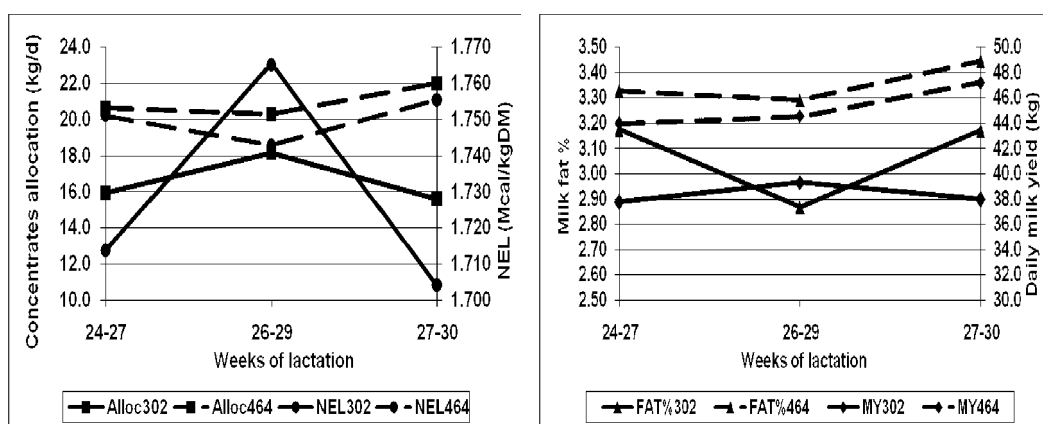


Figure 3. Left – Allocation given (square) and NEL (circle) for cow #464 (dashed) and cow #302 (line). Right – milk yield (diamond) and fat (triangle) for #464 (dashed) and cow #302 (line).

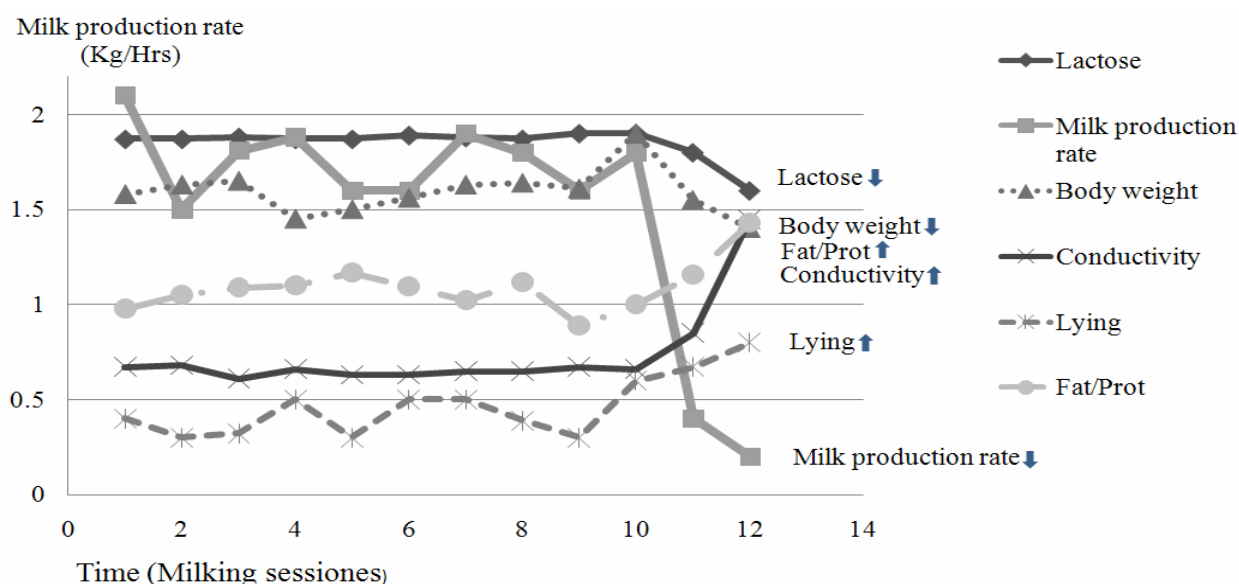


Figure 4. Multifactorial mastitis detection (cow#873 Landau farm). Milk production rate(square), lactose(diamond), body weight (triangle), fat/protein ratio, milk electric conductivity and lying time as a function of milking sessions.

Mastitis is the most costly disease affecting dairy cattle. Losses occur from decreased milk production, treatment and labor costs, non deliverable milk, veterinary fees, reduced milk quality, reduced milk price, increased risk of subsequent mastitis, culling and death of the cows. Such loss may be caused by sub clinical mastitis, which has no visible apparent symptoms. There is reliable straight forward diagnosis for sub-clinical mastitis, however using a multifactorial approach employing data flow from several sources might in the future avail early detection of mastitis.

This concept is displayed in Figure 4. Showing a case study of the evolution of mastitis following a collection of measurements from different sensors. This case of mastitis is a result of un detected E. Coli case. As it can be seen there is a drop in production rate, body weight and lactose while conductivity, lying time and fat/protein ratio rise.

Discussion

The global changes that the dairy industry is going through demands adaptation of the traditional farm management techniques to accommodate the challenges of the modern dairy business.

There are two dominating concepts for the required direction these adaptation should be taken.

The philosophy of the first claims simplification of management by synchronizing large groups towards heterogeneity of the individuals that constitute the herd. The assumption is that this will minimize production cost. However, this attempt, will resolve in evolution towards mediocrity of the individuals assembling these groups.

Such a trend will in time cause for a drop in all production parameters which will not be followed by a drop in production cost.

The second approach, supported by this paper, argues that individual management by exception will not only maximize production but will also lower down cost.

The key for success of the that approach lies in the following terms:

1. Data which is accurate consistent accessible objective and effortless. This dictates automated data collection systems, sensors and reliable ID.
2. Success in attempt to develop multifactorial data exploitation and new approaches to data analysis.

In all aspects of dairy farming displayed above (Milk production, fertility and reproduction, feeding, cow health and welfare) the impact of selections made regarding exceptions would be big on the total performance of the group.

The impact of exceptions on all group is always more than its actual weight. Therefore, by management through exceptions the selection rules for excellence of the total group are dictated.

List of references

Nordlund, K.V. 2001. Diagnosis and management of subacute ruminal acidosis in dairy herds. Pages 46-53 in Proc. 1995 Annu. Mtg. Ontario Vet. Med. Assoc., Toronto, Canada.

Maltz, E. 2007. Private communication.

Uner, E., Maltz, E. 2003 Unpublished.

Lehrer, A.R., Lewis, G.S. and Aizinbud, E. 1992. Oestrus detection in cattle: recent developments. In: Clinical Trends and Basic Research in Animal Reproduction. Dielman, S.J., Colenbrander, B., Booman, P. and Van der Lende, T. (Eds), pp. 355-361. Elsevier, Amsterdam, the Netherlands. (Reprinted from Animal Reproduction Science, Vol. 28, Nos. 1-4, 1992.

Saumande, J. 1986. Livestock Production Science, Volume 77, Issue 3, page 265.

PathoProof™ mastitis PCR assay

M.T. Koskinen

Finnzymes Oy, Keilaranta 16 A, 02150 Espoo, Finland

Finnzymes' PathoProof™ Mastitis PCR Assay is a revolutionary novel real-time PCR based method for bovine mastitis testing. The assay can identify and quantify 11 major mastitis-causing species or groups and the beta-lactamase penicillin resistance gene in just 3 hours. The assay has been optimized for use with even the most challenging milk samples from cows having clinical mastitis. The PathoProof Mastitis PCR Assay can also be used with bronopol-preserved samples, making it applicable for milk testing and dairy herd improvement schemes where mastitis testing has not been previously possible.

The PathoProof Mastitis PCR Assay identifies the following 12 bacterial targets:

1. *Staphylococcus aureus*
2. Coagulase negative *staphylococci* (all major mastitis species)
3. *Streptococcus agalactiae*
4. *Streptococcus dysgalactiae*
5. *Streptococcus uberis*
6. *Escherichia coli*
7. *Enterococcus faecalis* and *Enterococcus faecium*
8. *Klebsiella oxytoca* and *Klebsiella pneumoniae*
9. *Serratia marcescens*
10. *Corynebacterium bovis*
11. *Arcanobacter pyogenes* and *Peptoniphilus (Peptostreptococcus) indolicus*
12. Staphylococcal β -lactamase gene (penicillin resistance gene)

**Bacterial targets
identified by the
assay**

Prevalence of the species identified by the PathoProof Mastitis PCR Assay is known to vary between countries. Large-scale data sets indicate that the assay covers over 99% of pathogens responsible for clinical mastitis (e.g. Makovec and Ruegg, 2003; Pitkälä *et al.*, 2004).

The analytical specificity of the assay has been validated using an extensive culture collection of the target organisms, as well as non-target species having close phylogenetic relationships with the assay's targets. These data demonstrate excellent specificity (100%) for all mastitis pathogens identified by the test (Koskinen *et al.*, 2009).

**Bacterial
identification
and
quantification in
three hours**

The PathoProof Mastitis PCR Assay identifies all of its targets simultaneously in a total of only three hours (Figure 1). This throughput time is in many cases short enough for the veterinary practitioners to apply the test results for selecting the initial treatment for the animal. Importantly, this allows knowledge-based initial therapeutic decision, decreasing unnecessary use of antimicrobials. Furthermore, the rapid throughput time of the test may decrease the total duration of treatment, which has been suggested to improve therapeutic outcome (Barkema *et al.*, 2006), and to shorten the time required for returning to normal milk (Milner *et al.*, 1997).

The PathoProof Mastitis PCR Assay provides semi-quantitative (+, ++ or +++) results for all of its 12 bacterial targets. This is useful for example for detecting quantities of the different pathogens in multi-bacterial infections, for monitoring changes during an infection, or for accurately controlling the response of a pathogen to antimicrobial treatment.

**High sensitivity
even with
difficult-to-grow
samples**

The PathoProof Mastitis PCR Assay identifies the DNA of the bacterial targets. Hence, it does not rely on the ability of the bacteria to grow in a laboratory environment and has high sensitivity for viable but growth-inhibited, as well as dead bacteria.

This is a major advancement in mastitis testing, because in approximately 25-30% of the bovine milk samples taken from animals with clinical mastitis, no bacterial growth can be detected in conventional culturing. It has been suggested that inflammation of the mammary gland, inhibitory metabolic products of bacteria and unfavorable conditions during sample transportation may decrease the viability of bacteria to grow in culture (Todhunter *et al.*, 1985).

High sensitivity with growth-inhibited bacteria is also beneficial when testing milk from animals treated with antimicrobials: conventional culturing cannot be reliably used with such samples, but the PathoProof Mastitis PCR Assay enables repeated sampling and reliable testing of mastitis pathogens in cases where the selected treatment fails to improve the symptoms of an animal. The procedure (shown in figure 1) is hereby described with the correspondent steps, as numbered in figure 1.

1. Bacterial DNA is extracted from milk samples. Bronopol-preserved milk is also suitable.
2. Extracted bacterial DNA and the PathoProof PCR solutions are used to set up real-time PCR reactions. Four real-time PCR reactions are performed for each milk sample. Each reaction identifies three bacterial targets and also contains an internal amplification control for verification of acceptable reaction conditions.
3. The PathoProof Mastitis PCR Assay identifies 11 major mastitis bacterial species/groups and the β -lactamase penicillin resistance gene in staphylococci. While one milk sample is typically positive for only one primary pathogen, the kit can identify all 12 targets simultaneously. The test result is a cycle threshold value (Ct), i.e. the number of PCR cycles required to reach a certain species-specific fluorescence level in the reaction tube. The fewer cycles it takes to obtain the fluorescence level, the greater the amount of bacterial DNA for the given target in the reaction. The blue curves present in the reactions represent the internal amplification controls. An automated software can be used for scoring the results for every sample and bacterial target and for preparing a results report according to the needs of the user.

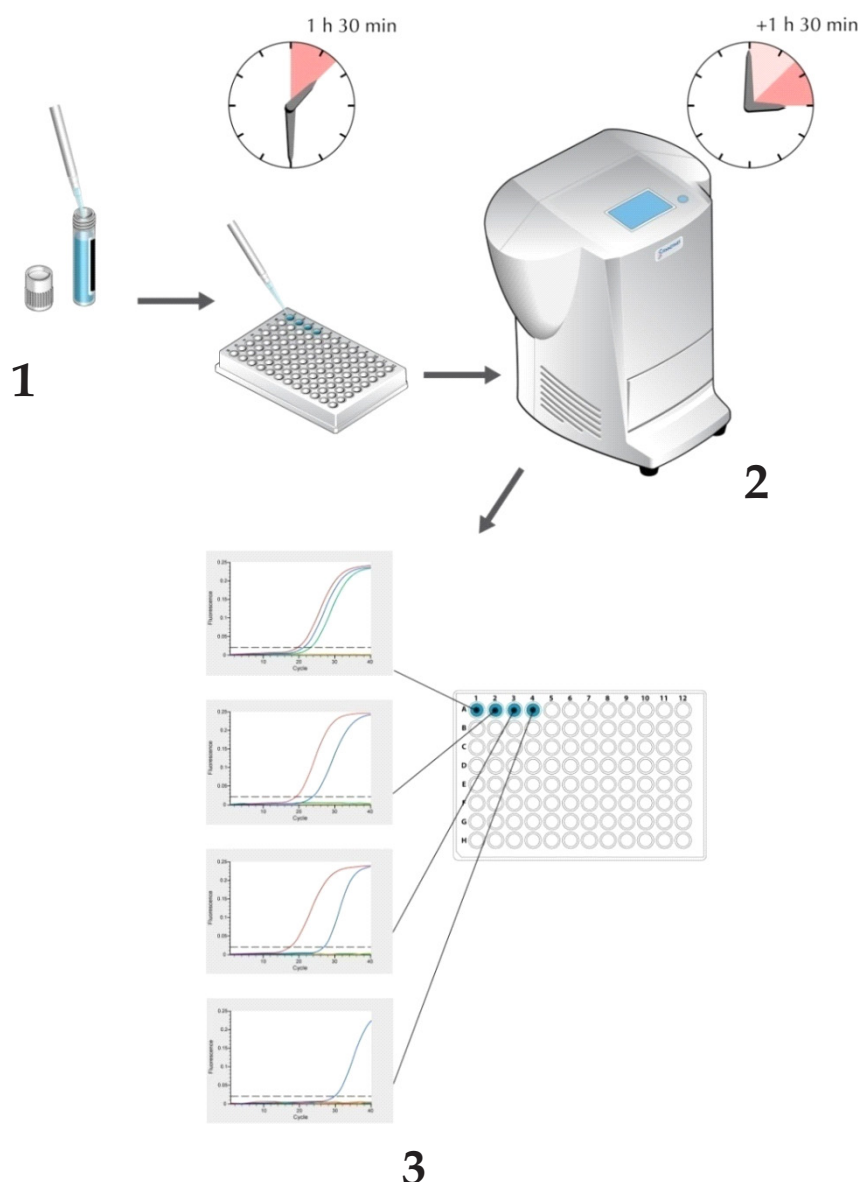


Figure 1. Laboratory workflow of the PathoProof Mastitis PCR Assay.

The PathoProof Mastitis PCR Assay has been validated for use with raw or bronopol-preserved milk samples. When preserving the milk samples when they are taken, the results obtained using the test reflect the true status of an animal at the time of sampling without any risk for bacterial growth during sample transportation.

Using the PathoProof Mastitis PCR Assay and bronopol-preserved milk is a convenient and full-proof solution to problems caused by uncontrolled microbial growth or death during transportation in ambient temperatures. In conventional testing schemes, this source of error is predicted to be common if milk samples arrive to the test laboratories without any cooling efforts (Dinsmore *et al.*, 1990).

**PathoProof
Mastitis PCR
Assay can be
used with
preserved milk
samples**

Importantly, the PathoProof Mastitis PCR Assay can also be integrated to routine milk monitoring and dairy herd improvement schemes utilizing preserved milk. Mastitis pathogen identification in connection to, for example, somatic cell count measurements from preserved samples has not been previously possible. As high somatic cell count is often due to mastitis, the PathoProof Mastitis PCR Assay can provide tremendous benefits for the dairy produce, if the assay is used for offering mastitis pathogen testing services in connection to somatic cell count measurements.

**Further
information**

diagnostics@finnzymes.fi
Tel. +358 9 5841 2299
Fax. +358 9 5841 2200

**List of
references**

Barkema H.W., Schukken Y.H. and Zadoks R.N. 2006. The role of cow, pathogen, and treatment regimen in the therapeutic success of bovine *Staphylococcus aureus* mastitis. *J. Dairy Sci.* 89: 1877-95.

Dinsmore R.P., English P.B., Matthews J.C. and Sears P.M. 1990. Effect of milk sample delivery methods and arrival conditions on bacterial contamination rates. *Cornell Vet.* 80: 243-50.

Koskinen M.T., Holopainen J., Pyörälä S., Bredbacka P., Pitkälä A., Barkema H.W., Bexiga R., Roberson J., Solverod L., Piccinini R., Kelton D., Lehmusto H., Niskala S. and Salmikivi L. 2009. Analytical specificity and sensitivity of a real-time PCR assay for identification of bovine mastitis pathogens. *J. Dairy Sci.* (In press).

Makovec J.A. and Ruegg P.L. 2003. Antimicrobial resistance of bacteria isolated from dairy cow milk samples submitted for bacterial culture: 8,905 samples (1994-2001). *J. Am. Vet. Med. Assoc.* 222: 1582-9.

Milner P., Page K.L. and Hillerton J.E. 1997. The effects of early antibiotic treatment following diagnosis of mastitis detected by a change in the electrical conductivity of milk. *J. Dairy Sci.* 80: 859-63.

Pitkälä A., Haveri M., Pyörälä S., Myllys V. and Honkanen-Buzalski T. 2004. Bovine mastitis in Finland 2001 – prevalence, distribution of bacteria, and antimicrobial resistance. *J. Dairy Sci.* 87: 2433-41.

Todhunter D.A., Smith K.L. and Schoenberger P.S. 1985. *In vitro* growth of mastitis-associated streptococci in bovine mammary secretions. *J. Dairy Sci.* 68: 2337-46

**ICAR survey on the situation of cow milk recording
in member countries**

Results for the years 2006 and 2007

Table 1. Annual milk production

ICAR survey on milk recording in member countries



Year	Country	Total number of dairy cows	Total number of dairy herds	Average of cows per herd	Average milk production per cow per year (kg)	Percent of fat production per cow per year (%)	Percent of protein production per cow per year (%)
July 2005 - June 2006	Australia	1 985 000	8 844	224	5 210	4.05	3.31
2007	Australia	1 810 000	8 055	225	5 343	4.05	3.30
2006	Austria	527 421	45 847	11.5	5 903	4.12	3.35
2007	Austria	524 500					
2006	Belgium (Wallonia Region)	223 538 (15/05/2006)	5 794 (15/05/2006)	38.6 (15/05/2006)	5 678	4.00	3.31
2006	Canada	1 048 600	15 522	67.6	8 375	3.80	3.22
2007	Canada	988 500	14 660	67.4	8 490	3.80	3.23
2006	Croatia	241 084	34 588	7.0	3 411	4.02	3.31
2007	Croatia	234 671	30 319	7.7	3 555	4.03	3.30
2006	Cyprus	23 940	247	96.9	5 853	3.66	3.37
2007	Cyprus	23 701	245	96.7	6 302	3.66	3.34
2006	Czech Republic	422 949			6 541	3.80	3.38
2007	Czech Republic	409 802			6 725	3.88	3.37
2006	Denmark	556 000	5 200	105	8 000	4.31	3.43
2007	Denmark	553 000	4 900	112	8 000	4.24	3.43
2006	Estonia	112 800	8 771	12.9	6 225	4.10	3.30
2007	Estonia	108 400	6 779	16.0	6 368	4.00	3.30
2006	Finland	308 200	14 680	21.0	7 993	4.16	3.42
2007	Finland	293 300	13 270	22.1	8 198	4.19	3.45
2006	France	3 896 000	103 000	37.8	6 084	4.17	3.49
2007	France	3 799 000	94 432	40.2	6 067	4.16	3.50
2006	Germany	4 054 400	102 200	39.7	6 849	4.16	3.42
2007	Germany	4 087 300	99 000	41.3	7 000	4.16	3.43
2006	Hungary	272 000					
2007	Hungary	265 000					
2006	Ireland	1 090 000	22 386	48.6	4 713	3.78	3.31
2007	Ireland	1 038 520	22 042	47.1	4 722	3.78	3.31
2006	Israel ¹	93 720	724	129.4	11 281	3.58	3.17
2007	Israel ¹	98 548	699	141	11 291	3.62	3.20
2006	Italy	1 814 000	46 872	38.70			
2007	Italy	1 838 000	44 373	41.42			

¹ cows in herdbook



Year	Country	Total number of dairy cows	Total number of dairy herds	Average of cows per herd	Average milk production per cow per year (kg)	Percent of fat production per cow per year (%)	Percent of protein production per cow per year (%)
2006	Japan ¹	1 011 000	24 600	41.1	7 864	3.97	
2006	Latvia	202 718	51 909	3.9	4 492		
2007	Latvia	184 928	46 306	4.0	4 636		
2006	Lithuania	427 895	146 096	2.9			
2007	Lithuania	395 921	120 982	3.3			
2006	New Zealand	3 916 812	11 630	337	3 974	4.67	3.64
2006	Norway	265 380	14 700	18	6 586	4.16	3.35
2007	Norway	261 800	13 253	19	6 757	4.21	3.38
2006	Poland	2 635 621			4 324	3.92	3.01
2007	Poland	2 677 270			4 426	3.98	3.22
2006	Slovak Republic	185 741			5 670		
2007	Slovak Republic	180 888			5 951	3.73	3.28
2006	Slovenia	106 039	9 064	11.7	4 829	4.09	3.33
2007	Slovenia	105 543	8 668	12.2	4 985	4.11	3.34
2006	South Africa	520 000	4 039	129	4 850	4.12	3.38
2006	South Africa	520 000	4 039	129	4 850	4.12	3.38
2007	South Africa	515 000	3 727	138	4 590	4.21	3.32
2006	Spain	1 067 610	29 251	36.4	5 729	3.76	3.15
2007	Spain	1 003 298	27 324	36.7	5 747	3.76	3.15
2006	Sweden	387 500	8 098	48.0	8 240	4.22	3.38
2007	Sweden	367 200	7 174	51.2	8 265	4.23	3.40
2006	Switzerland	705 400	41 200	17.1	5 690	3.99	3.32
2007	Switzerland	692 000	40 000	17.3	5 770	4.00	3.30
2006	The Netherlands ²	1 419 738	22 302	64	7 790	4.39	3.50
2007	The Netherlands ²	1 413 166	21 313	66	7 876	4.38	3.51
2006	Tunisia	215 000					
2007	Tunisia	223 000					
2006	Turkey	4 187 931	207 443	2.02	2 595		
2006	UK - (England & Wales)	784 149	5791	135	8 090	3.99	3.27
2007	UK - (England & Wales)	784 619	5423	144	8 070	3.99	3.33

¹ Total number of cows and herds, on the 1st Feb 2007

² Provisional figures



Year	Country	Total number of dairy cows	Total number of dairy herds	Average of cows per herd	Average milk production per cow per year (kg)	Percent of fat production per cow per year (%)	Percent of protein production per cow per year (%)
2006	UK - England	140 828	949	148	7 838	4.09	3.29
2007	UK - England	154 940	984	157	7 807	4.09	3.32
2006	UK - Northern Ireland	94 918	799	118	6 838	3.98	3.23
2007	UK - Northern Ireland	97 670	788	123	6 803	3.99	3.28
2006	UK - Scotland	102 344	662	154	7 499	3.97	3.28
2007	UK - Scotland	102 984	619	166	7 600	3.97	3.31
2006	UK - Wales	17 253	143	120	7 204	4.22	3.31
2007	UK - Wales	18 386	147	125	7 217	4.23	3.36
July 2005 - June 2006	Uruguay ¹	280 000	4 500	62	liters 5 786	3.56	3.09
2006	USA						
Average during 2007	USA ²	9158 000	59 135 licensed dairies		Kg 9 193	3.68	

¹ Source of submitted data: www.mgap.gub.uy/diea

² USDA-NASS

**Table 2. Position of milk recording**

Year	Country	Number of recorded cows	Percent of recorded cows	Number of recorded herds	Percent of recorded herds	Average number of cows per recorded herd	Percent of recorded herds per method A3	Percent of recorded herds per method A4	Percent of recorded herds per method A6	Percent of recorded herds per method AT	Percent of recorded herds per method B	Notes
July 2005 - June 2006	Australia	910 388	46	4 746	54.0	192						
2007	Australia	877 804	48	4 462	55.0	197						
2006	Austria	379 400	71.9	25 264	55.1	15.0				100		
2007	Austria	378 038	72.1	24 523		15.4				100		
2006	Belgium (Wallonia Region)	71 969	32.2	1 396	24.1	51.6	0	86.2	13.8	0	0	
2007	Belgium (Wallonia Region)	74 354	33.9	1 305	23.5	57.0	0	74.0	24.3	0	0.84 (B4)	0.38 (R4)
2006	Canada	697 838	66.5	10 581	68.2	66.0						
2007	Canada	718 018	72.6	10 375	70.1	69.2						
2006	Croatia	101 124	41.9	8 923	26.0	8.8				63.9		BT 36.09
2007	Croatia	111 075	47.33	9 041	29.8	8.1				62.6	37.38	
2006	Cyprus	2 569	10.7	21	9.1	122.3		100				
2006	Czech Republic	407 348	96.3	2 642		154		99.1		0.9		
2007	Czech Republic	398 431	97.2	2 417		165		99.3		0.7		
2006	Denmark	506 084	93	4 708	90.0	108		10			90	
2007	Denmark	496 770	93	4 300	91.0	119	0	10	0	0	90	
2006	Estonia	101 285	89.8	2 036	23.2	49.7					100	
2007	Estonia	99 596	91.9	1 475	21.8	67.5					100	
2006	Finland	237 779	77.2	10 159	69.2	23.4	-	0.0	-	-	97.2	C4 - 2.7
2007	Finland	229 671	78.3	9 346	70.4	24.6	-	0.0	-	-	97.3	C4 - 2.7
2006	France	2595 569	67	62 469	61.0	41.5		49.5	7.0	AT4 = 9.8 AT5 = 4.4 AT6 = 1.4	1.8	A5=21.6 A7=3.4 AR4-5-6-7=0.3 CZ4-5-6=0.7
2007	France	2 509 615	66	60 422	64.0	41.5		47.3	6.6	AT4 = 10.3 AT5 = 4.8 AT6 = 1.6	B4-5-6-7 = 2.3 BR4-5-6-7=0.5 BZ4-5-6 = 0.1	A5=21 A7=3.5 AR4-5-6-7=0.5 CZ4-5-6=1.5



Year	Country	Number of recorded cows	Percent of recorded cows	Number of recorded herds	Percent of recorded herds	Average number of cows per recorded herd	Percent of recorded herds per method A3	Percent of recorded herds per method A4	Percent of recorded herds per method A6	Percent of recorded herds per method AT	Percent of recorded herds per method B	Notes
2006	Germany	3 412 796	83.8	68 864	66.5	49.6		46.1		20.4	32.2	1.3
2007	Germany	3 475 735	85.1	66 320	67.1	52.4		45.0		20.6	33.1	1.3
2006	Hungary*	197 423	72.6	602	-	328	-	100	-	-	-	*December 2006
2007	Hungary*	195 022	73.6	584	-	334	-	100	-	-	-	*December 2007
2006	Ireland	410 407	37.7	6 224	28.2	65.9	0	32	44		24 EDIY	
2007	Ireland	436 842	42.1	6 245	28.3	69.9	0	20	52		28 EDIY	
2006	Italy	1 340 569	72.8	22 011	47.0	60.9		55.4	6.8	37.6		All cows recorded in the period October 1st. 2005 to 30 Sept. 2006
2007	Italy	1 336 689	72.7	21 483	48.4	62.2						All cows recorded in the period October 1st. 2006 to 30 Sept. 2007
2006	Japan	561 892	55.6	10 680	43.4	52.6		71.8		27.2	1.0	B=B4
2006	Latvia	117 929	58.2	10 671	20.6	11.1						
2007	Latvia	121 352	65.6	9 979	21.6	12.2						
2006	Lithuania	215 082	49.8	18 672	12.8	11.5		14		86		
2007	Lithuania	193 865	47.6	11 172	9.2	17.4		11		89		
2006	Luxembourg	33 339	85.5	768	83.5	43.4		21		28.3	47.6	3.1
2007	Luxembourg	32 445	85.5	725	81.5	44.7		18.9		26.4	52	2.7



Year	Country	Number of recorded cows	Percent of recorded cows	Number of recorded herds	Percent of recorded herds	Average number of cows per recorded herd	Percent of recorded herds per method A3	Percent of recorded herds per method A4	Percent of recorded herds per method A6	Percent of recorded herds per method AT	Percent of recorded herds per method B	Notes
2006	México ¹	41 476	5	104	n.a	423.2	0	95	4	0	1	
2007	México ²	35 874	4	92	n.a.	403.1	0	95	4	0	1	
2006	New Zealand	2790 533	71.2	8 682	74.7	321	null	null	null	22.3	77.2	22.82
2006	Norway	240 559	96	13 604	96.0						100	
2007	Norway	238 745	96	12 740	96.0	19					100	
2006	Poland ³	520 666	19.5	18 046		28.8		21.5		51.0		
2007	Poland ⁴	526 889	20.2	18 437		28.6		20.1		58.0		
2006	Slovak Republic	157 462	70.6	741		212.5		4.6		95.4		
2007	Slovak Republic	153 407		770		199		4.3		95.7		
2006	Slovenia	81 513	76.9	5 143	56.7	15.8				100		AT4 method
2007	Slovenia	82 344	78	4 998	57.7	16.5				100		AT4 method
2006	South Africa	126 924	24	723	18.0	175					100	
2007	South Africa	124 478	24	696	19.0	179					100	
2006	Spain	514 246		9 129		56.3	75			25		
2007	Spain	513 605	51.1	8 878	32.4	57.8		69		31		
2006	Sweden	331 069	85	6 212	79.0	51.3					B4: 100	
2007	Sweden	315 225	86	5 465	78.0	54.6					B4:100	
2006	Switzerland	435 474	100	26 453	100	16.6	0	57.6	0	42.4	0	
2007	Switzerland	435 799	100	25 729	100	16.9	0	53.2	0	46.8	0	
2006	The Netherlands	1 208 518	85.1	17 806	79.8	67.9	2.2	63.2	34.6			
2007	The Netherlands	1 225 726	85.5	17 300	81.1	70.9	2,0	56.6	35.5			
2006	Tunisia	32 728	15.2	1 889		17.3			23.8	11.3	32.9 (B6)	32.0 (B4)
2007	Tunisia	29 937	13.4	2 042		14.7			21.8	11.3	34.2 (B6)	32.6 (B4)

¹ All components are recorded on an AT basis

² Components are recorded all on an AT basis. 2007 figures aprox.

³ Percent of recorded herds per method A8=27.4. Percent of recorded cow per method: A4 - 34. AT4 - 48. A8 - 17

⁴ Percent of recorded herds per method A8=21.8. Percent of recorded cow per method: A4 = 33.1. AT4 = 53.26 A8 = 13.64



Year	Country	Number of recorded cows	Percent of recorded cows	Number of recorded herds	Percent of recorded herds	Average number of cows per recorded herd	Percent of recorded herds per method A3	Percent of recorded herds per method A4	Percent of recorded herds per method A6	Percent of recorded herds per method AT	Percent of recorded herds per method B	Notes
2006	Turkey	692 323	16.5	65 474	3.16	10.6	0	0	0	0	100	
2007	Turkey	750 118	17.9	68 183	3.29	11.0	0	0	0	0	100	
2006	UK - England	140 828		949		148		38	18.9		42	1.1
2007	UK - England	154 940		984		157		29	13	17	40	1
2006	UK - England & Wales	524 529	33.7	5 715	41.5	125	0.04	78.3	2.5		13.7	5.5
2007	UK - England & Wales	495 594	32.5	5 386		135	0.03	77.32	2.5		14.5	5.6
2006	UK - Northern Ireland	94 918		799		118		76.6	4.6		11.3	7.5
2007	UK - Northern Ireland	97 670		788		123		53	6.3	17.1	12.9	10.7
2006	UK - Scotland	102 344		662		154		73	10.4		12.7	3.9
2007	UK - Scotland	102 984		619		166		70	9	6	13	2
2006	UK - Wales	17 253		143		120		35	11.2		53.8	
2007	UK - Wales	18 386		147		125		26	5	14	55	
2006	Uruguay ¹	77 585	28	473	10.5							
2006	USA ²	4 162 303		24 297		181						
2007	USA ²	4 243 205		23 611		180						

¹ Source of data submitted: National Genetic Evaluation Report 2007

² DHI Participation

**Table 3. Costs and financing**

Year	Country	Cost price of milk recording per cow and per year - A4	Cost price of milk recording per cow and per year - A6	Cost price of milk recording per cow and per year - AT	Cost price of milk recording per cow and per year - B	Part of the cost price paid by the producer % - A4	Part of the cost price paid by the producer % - A6	Part of the cost price paid by the producer % - AT	Part of the cost price paid by the producer % - B	Others
2006	Argentina					100	100			C: 100
2007	Argentina					100	100			C: 100
2006	Austria			50.4				53.6		
2004 on	Belgium (Wallonia Region)	All methods depends on: many factors: time on farm tru-tests or not number of samples etc... If interested please contact jf.duckerts@mrw.wallonie.be								
2006	Croatia			25	20			50	50	
2007	Croatia			25	20			50	50	
2006	Cyprus	5.4				20.0				
2006	Czech Republic	45.5		35.0		85		100		
2007	Czech Republic	45.2		39.4		85		100		
2006	Denmark	73			45	100			100	
2007	Denmark	55			45	100			100	
2006	Estonia				31.0				62.0	
2007	Estonia				27.6				63.0	
2006	France	37 •		33 •	26 •	100		100	100	
2007	France	37.6 •		33.5 •	26.4 •	100		100	100	
2006	Germany	28-45•		21-40•	17-35•	55-98		57-97	46-97	
2006	Hungary	43.1	-	-	-	100	-	-	-	-
2007	Hungary	42.5	-	-	-	100	-	-	-	-
2006	Ireland	16.5•	14•		• 7.50 EDIY 4 visits	100	100		100	
2007	Ireland	16.5•	14•		• 8.50 EDIY 4 visits	100	100		100	
2006	Italy	96.82	77.46	72.62		30	30	30		
2007	Italy	not available	not available	not available	not available	not available	not available	not available	not available	
2006	Latvia	6.00			6.00	0			0	
2007	Latvia	6.48	-	-	6.48	0	-	-	0	
2008	Latvia	6.36	-	-	6.36	0	-	-	0	
2006	Lithuania	22.2		21.8		47.4		46.6		
2007	Lithuania	28.3		27.9		35.2		34.2		



Year	Country	Cost price of milk recording per cow and per year - A4	Cost price of milk recording per cow and per year - A6	Cost price of milk recording per cow and per year - AT	Cost price of milk recording per cow and per year - B	Part of the cost price paid by the producer % - A4	Part of the cost price paid by the producer % - A6	Part of the cost price paid by the producer % - AT	Part of the cost price paid by the producer % - B	Others
2006	México	66	60	not available	not available	100	100	not available	not available	Cost in milk liters per year
2007	México	60	55	not available	4	100	100	not available	100	Cost in milk liters per year
2006	Norway				71				100	
2007	Norway				68				100	
2006	Slovak Republic	47.61		33.61		78		78		
2007	Slovak Republic	52.00		42.00		72		72		
2007	Slovenia			120				15 - 20		Costs for AT4 method are mention in kg of milk (average milk price)
2006	Spain	116.31 (milk kg)		116.31 (milk kg)		70		70		
2007	Spain	116.31 (milk kg)		116.31 (milk kg)		70		70		
2006	Sweden				B4: 60 kg of milk				100	
2007	Sweden				B4: 45 kg of milk				100	
2006	Switzerland	65.3		64.7		32.7		19.3		
2007	Switzerland	77.65		67.74		31.45		21.10		
2006	Turkey	0	0	0	10.4•	0	0	0	100	
2007	Turkey	0	0	0	11.7•	0	0	0	100	



Year	Country	Cost price of milk recording per cow and per year - A4	Cost price of milk recording per cow and per year - A6	Cost price of milk recording per cow and per year - AT	Cost price of milk recording per cow and per year - B	Part of the cost price paid by the producer % - A4	Part of the cost price paid by the producer % - A6	Part of the cost price paid by the producer % - AT	Part of the cost price paid by the producer % - B	Others
2006	UK - England									
2006	UK - England & Wales					100	100	100	100	
2006	UK - Scotland					100	100	100	100	
2006	UK - Slovenia			160				15 - 20		
2007	UK (England & Wales)					100	100	100	100	
2006	Uruguay					100	100	100	100	
2007	Uruguay					100	100	100	100	
2006	Wales									

Table 4.1. Results of milk recording: All breeds together - All recorded cows

Year	Country	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent fat content (%)	Percent protein content (%)	Calving interval (days)
July 2005 - June 2006	Australia	701 852	316	6 626	6 626	4.00	3.3	
2007	Australia	655 212	312	6 678	6 678	4.00	3.3	
2006	Austria	318 113	299		6 627	4.17	3.40	
2007	Austria	317 570	299		6 789	4.14	3.37	
2006	Belgium (Wallonia Region)	48 361	349	8 111	7 664	4.06	3.34	417
2007	Belgium (Wallonia Region)	53 092	351	8 120	7 406	3.99	3.35	419
2006	Canada	285 418	305		9 481	3.75	3.21	430
2007	Canada	289 072	305		9 538	3.77	3.22	430
2006	Croatia	52 561			5 018	4.02	3.31	420
2007	Croatia	62 101			5 073	4.03	3.30	422
2006	Cyprus		290		7 756	3.40	3.4	
2006	Czech Republic	334 928	296	7 155	7 318	3.94	3.36	410
2007	Czech Republic	323 020	297	7 365	7 513	3.90	3.33	409
2006	Denmark ¹	506 084	365	8 778		4.31	3.43	
2007	Denmark ¹	496 770	365	8 919		4.24	3.43	
2006	England	150 163	336	9 116	8 000	4.10	3.26	428
2007	England	163 327	339	9 246	8 067	3.99	3.2	430
2006	Estonia	98 947	340	6 862	6 882	4.15	3.31	421
2007	Estonia	95 398	337	7 052	7 103	4.10	3.30	421
2006	Finland	237 779	305	8 639		4.17	3.44	405
2007	Finland	229 671	305	8 795	8 823	4.20	3.47	406
2006	France	2 595 569	326	7 814	6 960	4.02	3.38	408
2007	France	2 509 615	337	8 085	7 135	3.99	3.38	409
2006	Germany	3418 867	318	7 747	7 673	4.15	3.42	404
2007	Germany	3422 769	320	7 867	7 803	4.13	3.42	405
2006	Hungary	151 978	298	8 122		3.52	3.17	435
2007	Hungary	149 177	298	8 362		3.51	3.16	438
2006	Ireland	410 407	297	6 723		3.77	3.36	382
2007	Ireland	428 179	298	6 639		3.80	3.39	381
2006	Israel	62 109	353	12 471	11 150	3.58	3.16	417
2007	Israel	65 504	357	12 546	11 118	3.62	3.20	419
2006	Italy	841 190	305	8 356	8 356	3.69	3.29	
2007	Italy	829 975	305	8 484	8 484	3.68	3.30	

¹ 365 d. rolling average



Year	Country	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent fat content (%)	Percent protein content (%)	Calving interval (days)
2006	Japan	380 375	360	10 031	9 162	4.01	3.32	431
2006	Latvia	88 750	356	5 296	5 223	4.37	3.27	
2007	Latvia	92 946	360	5 478	5 420	4.34	3.27	
2006	Lithuania	169 725	305	5 592	5 427	4.36	3.38	406
2007	Lithuania	154 560	305	5 863	5 693	4.28	3.36	407
2006	Luxembourg	33 339		7 473		4.22	3.43	416
2007	Luxembourg	32 445		7 505		4.17	3.42	419
2006	New Zealand	2 058 206	222 weighted average	3 974 weighted average	5 018	4.67	3.64	368
2006	Norway	161 543	298	6 586	6 339	4.18	3.33	383
2007	Norway	160 369	299	6 757	6 429	4.15	3.35	382
2006	Poland	520 666	305	6 664	6 664	4.18	3.32	420
2007	Poland	526 889	305	6 688	6 688	4.22	3.33	426
2006	Slovak Republic	117 778	295	6 267	6 426	3.97	3.25	426
2007	Slovak Republic	113 175	296	6 517	6 665	4.02	3.22	424
2006	Slovenia	79 376	358	6 505	5 803	4.09	3.26	414
2007	Slovenia	79 682	360	6 778	6 016	4.06	3.25	415
2006	South Africa	123 946	319	6 186	6 135	4.15	3.44	425
2007	South Africa	124 478	316	6 948	6 948	4.11	3.38	425
2006	Spain	324 102	352	10 116	8 945	3.69	3.16	405
2007	Spain	329 448	362	10 394	9 028	3.65	3.12	405
2006	Sweden ¹	331 069	365	9 108		4.15	3.41	404
2007	Sweden ¹	315 225	365	9 217		4.15	3.44	404
2006	Switzerland	335 258	316	7 252	7 060	3.99	3.32	399
2007	Switzerland	334 318	316	7 284	7 091	4.00	3.30	399
2006	The Netherlands	846 802	350	9 109	8 429	4.34	3.46	415
2007	The Netherlands	826 346	352	9 278	8 538	4.33	3.46	417
2006	Tunisia	9 483	350	6 012	5 949	3.59	3.16	448
2007	Tunisia	18 335	346	5 451	5 950	3.60	3.17	438

¹ 365 days rolling average



Year	Country	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent fat content (%)	Percent protein content (%)	Calving interval (days)
2006	UK - England & Wales	532 479	355	9 010	8 090	3.99	3.27	418
2007	UK - England & Wales	502 914	358	9 040	8 070	3.99	3.33	420
2006	UK - Northern Ireland	88 398	318	7 922	7 142	3.94	3.22	411
2007	UK - Northern Ireland	92 620	318	8 012	7 176	3.93	3.19	413
2006	UK - Scotland	109 353	334	8 614	7 632	3.95	3.25	423
2007	UK - Scotland	109 349	333	8 740	7 710	3.88	3.20	426
2006	UK - Wales	17 570	339	8814	7755	4.18	3.28	430
2007	UK - Wales	18 225	337	8578	7507	4.14	3.22	432
Average during 2006	USA	4 292 565	305	10007	10007	3.70	3.08	
Average during 2007	USA	4 338 693	305	10049	10049	3.69	3.09	

Table 4.2. Results of milk recording: All breeds together - Cows in herdbook

ICAR survey on milk recording in member countries



Year	Country	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent fat content (%)	Percent protein content (%)	Calving interval (days)
July 2005 - June 2006	Australia	99 114	337	7 436	7436	3.99	3.31	
2007	Australia	94 921	332	7 478	7478	3.99	3.35	
2006	Austria	308 484	299		6639	4.17	3.40	
2007	Austria	309 395	299		6804	4.14	3.37	
each year	Belgium (Wallonia Region) ¹							
2006	Czech Republic	303 253	297	7 270	7 416	3.95	3.36	410
2007	Czech Republic	299 087	297	7 467	7 617	3.90	3.34	409
2006	Denmark ²	506 084	365	8 778		4.31	3.43	
2007	Denmark ²	496 770	365	8 919		4.24	3.43	
2006	Estonia	82 998	341	7 063	7062	4.14	3.31	422
2007	Estonia	80 384	341	7 245	7288	4.09	3.31	423
2006	Finland	36 718	305		9693	4.04	3.39	
2007	Finland	36 076	305		9817	4.06	3.42	
2006	France	2 595 569	326	7 814	6 960	4.02	3.38	408
2007	France	2 509 615	337	8 085	7 135	3.99	3.38	409
2006	Germany	2 440 410	319	8 033	7938	4.13	3.43	404
2007	Germany	2 469 293	321	8 138	8053	4.12	3.44	406
2006	Hungary	145 133	298	8 161		3.52	3.16	435
2007	Hungary	141 991	299	8 406		3.51	3.16	439
2006	Italy	841 190	305	8 356	8356	3.69	3.29	
2007	Italy	829 975	305	8 484	8484	3.68	3.30	
2006	Japan	317 320	359	10 073	9220	4.01	3.32	430
2006	Latvia	5 319	339		6435	4.52	3.33	
2007	Latvia	10 454	351		6565	4.46	3.29	
2006	Poland	402 938	305	6 625	6625	4.14	3.27	
2007	Poland	403 000	305	6 789	6789	4.14	3.26	
2006	Slovak Rep	35 865	296	6 417	6 563	3.97	3.29	
2007	Slovak Rep	31 939	296	6 590	6 740	4.03	3.25	424
2006	Slovenia	79 376	358	6 505	5803	4.09	3.26	414
2007	Slovenia	79 682	360	6 778	6016	4.06	3.25	415
2006	South Africa	72 580	321	7 012	7 012	4.17	3.45	423
2007	South Africa	72 097	323	7 358	7 358	4.12	3.38	425

¹ all cows in milk recording = all cows in herdbook

² 365 d. rolling average



Year	Country	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent fat content (%)	Percent protein content (%)	Calving interval (days)
2006	Spain	324 102	352	10 116	8 945	3.69	3.16	405
2007	Spain	329 448	3619	10 394	9 028	3.65	3.12	405
2006	Switzerland	335 258	316	7 252	7 060	3.99	3.32	399
2007	Switzerland	334 318	316	7 284	7 091	4.00	3.30	399
2006	The Netherlands	753 207	351	9 237		4.40	3.51	
2007	The Netherlands	736 570	353	9 395		4.37	3.50	
2006	Tunisia	9 483	350	6 012	5 949	3.59	3.16	438
2007	Tunisia	18 335	346	5 451	5 950	3.6	3.17	438
2006	Turkey	129 344	336	6 438	5 739			410
2006	UK - England	126 170	338	9 297	8145	4.11	3.25	428
2007	UK - England	136 580	342	9 434	8217	3.99	3.19	431
2006	UK - Northern Ireland	44 290	327	8 599	7676	3.96	3.21	419
2007	UK - Northern Ireland	48 282	331	8 735	7738	3.93	3.18	421
2006	UK - Scotland	64 552	339	9 102	8010	4.00	3.27	429
2007	UK - Scotland	64 840	341	9 295	8140	3.92	3.22	432
2006	Wales	15 721	341	8 913	7 828	4.19	3.27	431
2007	Wales	16 043	342	8 771	7 654	4.17	3.21	435

**Table 4.3. Results of milk recording: Main breeds - All recorded cows**

Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
July 2005 - June 2006	Australia	Australian Reds	6 361	307	5 852	5 852	4.11	3.45	
2007	Australia	Australian Reds	6 403	302	5 863	5 863	4.11	3.49	
July 2005 - June 2006	Australia	Ayrshire	3 532	307	5 445	5 445	4.13	3.33	
2007	Australia	Ayrshire	3 432	295	5 445	5 445	4.09	3.37	
July 2005 - June 2006	Australia	Brown Swiss	3 643	325	6 091	6 091	4.12	3.46	
2007	Australia	Brown Swiss	3 725	321	6 063	6 063	4.16	3.52	
July 2005 - June 2006	Australia	Guernsey	2 028	323	5 374	5 374	4.33	3.47	
2007	Australia	Guernsey	1 773	317	5 426	5 426	4.33	3.47	
July 2005 - June 2006	Australia	Holstein	474 728	320	7 701	7 701	3.85	3.24	
2007	Australia	Holstein	444 431	315	7 123	7 123	3.85	3.28	
2007	Australia	Illawarra	6 120	307	5 879	5 879	4.07	3.45	
July 2005 - June 2006	Australia	Illawarra	6 515	313	5 910	5 910	4.08	3.43	
July 2005 - June 2006	Australia	Jersey	79 096	305	5 026	5 026	4.83	3.71	
2007	Australia	Jersey	4 925	300	5 097	5 097	4.83	3.74	
2006	Austria	Braunvieh	50 472	301		6 740	4.15	3.41	
2007	Austria	Braunvieh	49 070	301		6 846	4.13	3.39	
2006	Austria	Fleckvieh	224 158	298		6 464	4.18	3.43	
2007	Austria	Fleckvieh	224 298	298		6 648	4.16	3.40	
2006	Austria	Grauvieh	2 878	295		4 751	4.01	3.29	
2007	Austria	Grauvieh	2 927	295		4 806	3.97	3.27	
2006	Austria	Holstein	32 735	301		8 036	4.13	3.25	
2007	Austria	Holstein	33 425	301		8 158	4.12	3.23	
2006	Austria	Pinzgauer	7 082	298		5 400	3.90	3.27	
2007	Austria	Pinzgauer	6 994	298		5 440	3.90	3.26	
2006	Belgium (Wallonia Region)	Blanc-Bleu Belge	2 860	274	3 819	4 404	3.53	3.23	398
2007	Belgium (Wallonia Region)	Blanc-Bleu Belge	3 084	272	3 807	4 004	3.48	3.26	389
2006	Belgium (Wallonia Region)	Holstein	37 532	356	8 618	7 925	4.05	3.33	420
2007	Belgium (Wallonia Region)	Holstein	41 699	359	8 628	7 794	3.98	3.34	423
2006	Belgium (Wallonia Region)	Montbéliarde	640	326	6 903	6 810	3.97	3.43	398
2007	Belgium (Wallonia Region)	Montbéliarde	733	324	6 818	6 524	3.92	3.44	399
2006	Belgium (Wallonia Region)	Normande	360	333	6 203	5 979	4.16	3.50	408
2007	Belgium (Wallonia Region)	Normande	417	339	6 244	5 876	4.12	3.52	410



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	Belgium (Wallonia Region)	Red Holstein	6 969	343	7 349	7 000	4.21	3.40	410
2007	Belgium (Wallonia Region)	Red Holstein	7159	343	7 265	6 798	4.15	3.40	411
2006	Canada	Ayrshire	9 323	305		7 423	3.96	3.32	
2007	Canada	Ayrshire	9 244	305		7 422	3.97	3.34	
2006	Canada	Brown Swiss	1 528	305		8 064	4.06	3.46	
2007	Canada	Brown Swiss	1 545	305		8 159	4.06	3.48	
2006	Canada	Canadienne	203	305		5 412	4.24	3.60	
2007	Canada	Canadienne	180	305		5 353	4.25	3.61	
2006	Canada	Guernsey	422	305		6 540	4.55	3.43	
2007	Canada	Guernsey	401	305		6 673	4.51	3.46	
2006	Canada	Holstein	264 903	305		9 677	3.71	3.18	
2007	Canada	Holstein	268 463	305		9 733	3.72	3.19	
2006	Canada	Jersey	8 809	305		6 331	4.83	3.77	
2007	Canada	Jersey	8 967	305		6 412	4.82	3.78	
2006	Canada	Milking Shorthorn	230	305		6 552	3.65	3.29	
2007	Canada	Milking Shorthorn	272	305		6 558	3.65	3.31	
2006	Croatia	Brown	959			5 052	4.03	3.43	423
2007	Croatia	Brown	1 329			5 264	3.93	3.37	435
2006	Croatia	Holstein	16 930			6 161	3.94	3.25	452
2007	Croatia	Holstein	19 421			6 339	3.98	3.25	453
2006	Croatia	Simmental	34 672			4 459	4.07	3.35	405
2007	Croatia	Simmental	41 351			4 473	4.07	3.34	406
2006	Czech Republic	F Fleckvieh	152 811	294	6 175	6 347	4.08	3.46	400
2007	Czech Republic	F Fleckvieh	144 570	295	6 352	6 513	4.05	3.43	400
2006	Czech Republic	Holstein	105 115	299	8 336	8 461	3.81	3.26	425
2007	Czech Republic	Holstein	106 654	300	8 527	8 634	3.77	3.24	423
2006	Czech Republic	Montbéliarde	1 401	296	7 892	8 071	3.87	3.41	402
2007	Czech Republic	Montbéliarde	1 354	295	7 719	7 914	3.81	3.38	404



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	Denmark ¹	Danish Holstein	366 084	365	9 232		4.12	3.35	
2007	Denmark ¹	Danish Holstein	361 517	365	9 372		4.05	3.35	
2006	Denmark ¹	Jersey	59 948	365	6 436		5.92	4.06	
2007	Denmark ¹	Jersey	58 448	365	6 555		5.89	4.06	
2006	Denmark ¹	Red Danish	41 923	365	8 560		4.25	3.50	
2007	Denmark ¹	Red Danish	40 333	365	8 663		4.18	3.50	
2006	Denmark ¹	Red Holstein	5 164	365	8 296		4.36	3.45	
2007	Denmark ¹	Red Holstein	5 059	365	8 419		4.28	3.44	
2006	Estonia	Estonian Holstein	72 894	344	7 069	7 114	4.10	3.28	426
2007	Estonia	Estonian Holstein	70 816	340	7 273	7 331	4.06	3.28	426
2006	Estonia	Estonian Red	25 348	330	6 338	6 303	4.29	3.40	407
2007	Estonia	Estonian Red	23 842	329	6 476	6 515	4.24	3.40	410
2006	Finland	Finnish Ayrshire	164 516	305	8 472	8 504	4.29	3.46	406
2007	Finland	Finnish Ayrshire	156 230	305	8 616	8 642	4.32	3.50	408
2006	Finland	Finnish Cattle	2 641	305	6 218	6 412	4.33	3.48	394
2007	Finland	Finnish Cattle	2 529	305	6 250	6 462	4.37	3.51	399
2006	Finland	Holstein Friesian	70 514	305	9 122	9 160	3.93	3.39	402
2007	Finland	Holstein Friesian	70 804	305	9 283	9 303	3.96	3.42	403
2006	Finland	Jersey	5	305	7 651	7 120	5.10	3.99	
2007	Finland	Jersey	12	305	7 766	7 597	5.21	3.96	392
2006	France	Abondance	21 267	288	5 155	4 919	3.72	3.48	395
2007	France	Abondance	21 073	292	5 254	5 010	3.69	3.48	394
2006	France	Brune	16 664	323	6 784	6 069	4.19	3.56	412
2007	France	Brune	16 813	333	6 958	6 163	4.16	3.56	412
2006	France	Montbéliarde	386 933	296	6 451	6 061	3.92	3.43	389
2007	France	Montbéliarde	382 965	305	6 671	6 238	3.89	3.42	389
2006	France	Normande	263 095	308	5 901	5 443	4.31	3.62	392
2007	France	Normande	251 739	319	6 128	5 612	4.27	3.62	393

¹ 365 d. rolling average



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	France	Pie Rouge des Plaines	9 681	310	6 993	6 487	4.25	3.42	396
2007	France	Pie Rouge des Plaines	9 330	321	7 298	6 714	4.23	3.43	394
2006	France	Prim'Holstein	1 823 725	337	8 508	7 470	4.01	3.35	415
2007	France	Prim'Holstein	1 746 688	349	8 823	7 662	3.98	3.35	416
2006	France	Simmental Française	14 042	292	5 702	5 405	4.01	3.49	386
2007	France	Simmental Française	14 104	300	5 875	5 545	4.00	3.49	386
2006	Germany	Braunvieh	181 363	322	6 774	6 749	4.23	3.58	411
2007	Germany	Braunvieh	178 266	324	6 845	6 839	4.18	3.60	416
2006	Germany	Fleckvieh	877 859	315	6 628	6 473	4.15	3.47	393
2007	Germany	Fleckvieh	872 880	320	6 822	6 653	4.13	3.49	394
2006	Germany	Gelbvieh	4 753	314	5 671	5 630	4.20	3.51	402
2007	Germany	Gelbvieh	4 241	315	5 656	5 668	4.20	3.53	402
2006	Germany	Holstein B&W	1 964 899	320	8 421	8 392	4.12	3.38	409
2006	Germany	Holstein R&W	253 284	318	7 489	7 469	4.26	3.39	400
2007	Germany	Holsten B&W	1 976 702	322	8 511	8 501	4.12	3.39	410
2007	Germany	Holsten R&W	249 284	320	7 582	7 581	4.23	3.40	403
2006	Hungary	Hungarian Holstein Friesian	141 282	298	8 243		3.51	3.16	436
2007	Hungary	Hungarian Holstein Friesian	138 355	299	8 486		3.5	3.16	440
2006	Hungary	Hungarian Red Spotted	3 852	293	5 166		3.8	3.32	412
2007	Hungary	Hungarian Red Spotted	3 637	293	5 343		3.8	3.32	406
2006	Italy	Castana	4 477	305	2 837	2 837	3.46	3.37	
2007	Italy	Castana	4 313	305	2 844	2 844	3.48	3.39	



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	Italy	Grey of Alps (Grigio Alpina, Grauvieh)	6 205	305	305	4 975	3.74	3.37	
2007	Italy	Grey of Alps (Grigio Alpina, Grauvieh)	6 161	305	5 029	5 029	3.71	3.36	
2006	Italy	Italian Brown (Bruna Italiana)	72 955	305	6 734	6 734	3.97	3.47	
2007	Italy	Italian Brown (Bruna Italiana)	69 656	305	6 841	6 841	3.96	3.48	
2006	Italy	Italian Friesian (Frisona Italiana)	683 760	305	8 895	8 895	3.66	3.27	
2007	Italy	Italian Friesian (Frisona Italiana)	673 980	305	9 032	9 032	3.65	3.27	
2006	Italy	Italian Red Spotted (Pezzata Rossa Italiana)	31 692	305	6 389	6 389	3.92	3.41	
2007	Italy	Italian Red Spotted (Pezzata Rossa Italiana)	32 463	305	6 513	6 513	3.90	3.41	
2006	Italy	Jersey	4 241	305	5 700	5 700	5.29	3.98	
2007	Italy	Jersey	4 433	305	5 876	5 876	5.19	3.97	
2006	Italy	Valdostana Red Spotted (Valdostana Pezzata Rossa)	11 020	305	3 825	3 825	3.50	3.25	
2007	Italy	Valdostana Red Spotted (Valdostana Pezzata Rossa)	10 510	305	3 833	3 833	3.53	3.27	
2006	Japan	Holstein	377 522	360	10 058	9 180	4.01	3.32	432
2006	Japan	Jersey	2 568	340	6 330	6 002	4.93	3.89	411



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	Latvia	Holstein Black and White	30 622	360		5 854	4.24	3.20	
2007	Latvia	Holstein Black and White	30 753	368		6 061	4.21	3.19	
2006	Latvia	Latvian Blue	264	330		4 412	4.38	3.34	
2007	Latvia	Latvian Blue	352	329		4 325	4.39	3.35	
2006	Latvia	Latvian Brown	65 656	346		4 926	4.45	3.33	
2007	Latvia	Latvian Brown	62 043	347		5 035	4.45	3.32	
2006	Lithuania	Angler	287	305	6 085	5 680	4.76	3.64	416
2007	Lithuania	Angler	299	305	6 179	6 130	4.73	3.60	433
2006	Lithuania	Ayrshire	455	305	6 470	5 998	4.66	3.44	417
2007	Lithuania	Ayrshire	696	305	6 688	6 401	4.35	3.47	413
2006	Lithuania	Danish Black & Whites	192	305	6 824	6 838	4.37	3.46	461
2007	Lithuania	Danish Black & Whites	239	305	7 276	7 209	4.48	3.38	437
2006	Lithuania	Danish Reds	274	305	6 092	6 007	4.74	3.56	422
2007	Lithuania	Danish Reds	349	305	6 482	6 215	4.49	3.55	425
2007	Lithuania	Dutch Black & Whites	164	305	6 635	6 451	4.28	3.54	437
2006	Lithuania	German Black & Whites	1 078	305	6 054	6 061	4.44	3.33	429
2007	Lithuania	German Black & Whites	1 016	305	6 301	6 306	4.34	3.32	432
2006	Lithuania	German Red & Whites	308	305	6 451	6 119	4.35	3.34	412
2007	Lithuania	German Red & Whites	310	305	6 243	6 420	4.43	3.35	419
2006	Lithuania	Holstein	1 507	305	6 926	6 404	4.025	3.36	439
2007	Lithuania	Holstein	2 868	305	6 669	6 569	4.23	3.40	431
2006	Lithuania	Lithuanian Black & Whites	126 589	305	5 612	5 453	4.31	3.35	405
2007	Lithuania	Lithuanian Black & Whites	113 766	305	5 867	5 685	4.25	3.33	406



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	Lithuania	Lithuanian Reds	37 262	305	5 365	5 223	4.51	3.49	406
2007	Lithuania	Lithuanian Reds	32 818	305	5 677	5 535	4.39	3.47	405
2006	Lithuania	Native Ash - grey	409	305	5 232	5 051	4.24	3.35	399
2007	Lithuania	Native Ash - grey	339	305	5 402	5 200	4.17	3.29	411
2006	Lithuania	Native White - Backed	356	305	5 198	5 117	4.26	3.34	395
2007	Lithuania	Native White - Backed	311	305	5 506	5 396	4.21	3.32	403
2006	Lithuania	Swedish Black & Whites	121	305	8 301	8 021	4.59	3.41	483
2007	Lithuania	Swedish Black & Whites	149	305	7 430	8 440	4.32	3.45	474
2006	Lithuania	Swedish Red & Whites	443	305	7 195	7 140	4.37	3.54	410
2007	Lithuania	Swedish Red & Whites	481	305	6 927	7 102	4.41	3.50	424
2007	Luxembourg	Holstein-RBT	6 484		6 752		4.32	3.47	413
2006	Luxembourg	Holstein-SBT	24 766		7 766		4.18	3.41	419
2006	Luxembourg	Holstein -RBT	7 358		6 728		4.35	3.46	409
2007	Luxembourg	Holstein-SBT	24 806		7 769		4.13	3.41	421
2006	México ¹	Holstein	44 158	365	8 542	8 778	3.40	3.17	444
2007	México ²	Holstein	41 452	365	8 433	9 374	3.41	3.21	445
2006	New Zealand	Ayrshire	21 587	226	3 829	4 757	4.26	3.49	
2006	New Zealand	Friesian	942 121	220	4 352	5 509	4.24	3.64	
2006	New Zealand	Friesian/Jersey Cross	749 713	223	3 910	4 902	4.83	3.71	
2006	New Zealand	Jersey	344 785	223	3 086	3 870	5.58	4.00	
2007	Norway	Jersey	1 005	293		4 887	5.97	3.87	382
2006	Norway	Norwegian Red	154 221	299		6 374	4.16	3.27	383
2007	Norway	Norwegian Red	152 634	300		6 458	4.14	3.35	382

¹ Only cows with more than 305 dim are considered for 365 d production



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	Poland	Jersey	1 068	305	5 070	5 070	5.41	3.92	401
2007	Poland	Jersey	1 061	305	4 977	4 977	5.40	3.88	411
2006	Poland	Polish Holstein-Friesian (HO)	492 119	305	6 715	6 715	4.18	3.32	421
2007	Poland	Polish Holstein-Friesian (HO)	493 019	305	6 760	6 760	4.22	3.32	427
2006	Poland	Polish Holstein-Friesian (RW)	15 034	305	6 305	6 305	4.21	3.32	410
2007	Poland	Polish Holstein-Friesian (RW)	15 793	305	6 178	6 178	4.25	3.33	416
2006	Poland	Polish Red	1 492	305	4 028	4 028	4.28	3.34	395
2007	Poland	Polish Red	1 720	305	4 016	4 016	4.26	3.31	400
2006	Poland	Polish Red-White	1 556	305	5 687	5 687	4.13	3.28	
2007	Poland	Polish Red-White	2 159	305	5 193	5 193	4.11	3.27	407
2006	Poland	Simmental	4 602	305	4 785	4 785	4.01	3.36	394
2007	Poland	Simmental	5 967	305	4 943	4 943	4.06	3.36	400
2006	Slovak Republic	Cross Breeds	80 422	294	6 098	6 268	3.99	3.24	424
2007	Slovak Republic	Cross Breeds	73 479	295	6 304	6 464	4.03	3.21	422
2006	Slovak Republic	Holstein	22 776	298	7 691	7 826	3.84	3.2	440
2007	Slovak Republic	Holstein	25 640	298	7 884	8 023	3.90	3.17	436
2006	Slovak Republic	Slovak Pinzgauer	1 108	290	4 195	4 536	4.02	3.36	415
2007	Slovak Republic	Slovak Pinzgauer	1 072	290	4 323	4 489	4.03	3.34	406
2006	Slovak Republic	Slovak Simmental	13 472	294	5 035	5 175	4.1	3.36	414
2007	Slovak Republic	Slovak Simmental	12 984	294	5 204	5 349	4.19	3.32	411
2007	Slovenia	Black & White	29 439	375	8 318	7 204	3.98	3.20	426
2006	Slovenia	Brown	13 900	359	6 065	5 380	4.11	3.33	420
2007	Slovenia	Brown	13 612	361	6 294	5 553	4.08	3.32	420
2006	Slovenia	Holstein	28 734	372	8 006	6 978	4.02	3.20	425
2006	Slovenia	Simmental	34 698	346	5 537	5 023	4.17	3.29	410
2007	Slovenia	Simmental	34 458	347	5 757	5 213	4.13	3.28	407
2006	South Africa	Ayrshire	6 658	308	5 919	5 694	3.99	3.36	445
2007	South Africa	Ayrshire	5 969	318	6 549	6 549	3.98	3.30	423



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	South Africa	Guernsey	1 147	323	6 132	6 132	4.28	3.48	418
2007	South Africa	Guernsey	1 112	319	5 924	5 924	4.28	3.43	412
2006	South Africa	Holstein	66 116	336	8 238	8 238	3.77	3.23	429
2007	South Africa	Holstein	60 047	341	8 463	8 463	3.81	3.20	441
2006	South Africa	Jersey	49 282	320	5 428	5 428	4.63	3.75	410
2007	South Africa	Jersey	50 686	321	5 458	5 458	4.66	3.72	423
2006	Spain	Frisona	322 839	353	10 129	8 954	3.68	3.15	
2007	Spain	Frisona	328 456	363	10 404	9 036	3.66	3.15	402
2007	Spain	Parla Alpina	992	300	7 046	6 433	3.79	3.5	402
2006	Sweden	Swedish Holstein	163 626	365	9 645		4.00	3.34	413
2007	Sweden	Swedish Holstein	157 299	365	9 741		4.00	3.37	413
2006	Sweden	Swedish Jersey	2 078	365	6 445		5.71	3.94	401
2007	Sweden	Swedish Jersey	2 100	365	6 544		5.75	3.99	401
2006	Sweden	Swedish Polled	1 607	365	5 510		4.48	3.57	404
2007	Sweden	Swedish Polled	1 422	365	5 547		4.50	3.6	410
2006	Sweden	Swedish Red	146 884	365	8 633		4.32	3.73	398
2007	Sweden	Swedish Red	137 916	365	8 754		4.30	3.53	398
2006	Switzerland	Braunvieh	138 936	300	6 730	6 814	3.99	3.35	409
2007	Switzerland	Braunvieh	136 303	300	6 745	6 829	3.99	3.35	404
2006	Switzerland	Eringer	762	305	3 246	3 246	3.60	3.43	
2007	Switzerland	Eringer	724	264	3 288	3 174	3.65	3.38	
2006	Switzerland	Fleckvieh	157 531	332	7 561	7 078	3.99	3.30	390
2007	Switzerland	Fleckvieh	156 937	334	7 618	7 115	4.00	3.26	391
2006	Switzerland	Grauvieh	117	295	3 879	3 977	3.71	3.22	399
2007	Switzerland	Grauvieh	143	296	3 920	4 009	3.72	3.28	399
2006	Switzerland	Hinterwälder	93	297	3 971	4 051	4.03	3.48	387
2007	Switzerland	Hinterwälder	88	296	3 870	3 958	4.00	3.42	387
2006	Switzerland	Holstein	36 547	305	8 081	8 081	3.96	3.24	
2007	Switzerland	Holstein	38 587	301	8 010	8 084	3.98	3.23	408
2006	Switzerland	Jersey	1 272	299	5 145	5 222	5.47	3.88	404
2007	Switzerland	Jersey	1 536	299	5 187	5 265	5.39	3.87	404
2006	The Netherlands	B&W	600 908	354	9 500	8 618	4.36	3.49	
2007	The Netherlands	B&W	588 973	356	9 651	8 720	4.34	3.48	



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2007	The Netherlands	R&W	139 774	341	8 464	7 891	4.55	3.57	
2007	UK - Scotland	Ayrshire	9 480	418	7 429	6 809	4.08	3.32	418
2006	UK - Scotland	Ayrshire	9 962	317	7 207	6 612	4.11	3.36	413
2006	UK - Scotland	British Friesian	1 081	310	6 693	6 225	4.08	3.40	397
2007	UK - Scotland	British Friesian	1 198	309	6 668	6 140	4.04	3.34	402
2006	UK - Scotland	Brown Swiss	241	348	7 727	6 759	4.13	3.53	427
2007	UK - Scotland	Brown Swiss	192	339	7 558	6 685	4.17	3.46	440
2006	UK - Scotland	Guernsey	31	283	5 950	5 462	4.82	3.65	406
2006	UK - Scotland	Holstein	96 198	336	8 835	7 801	3.91	3.22	424
2007	UK - Scotland	Holstein	96 301	335	8 958	7 873	3.84	3.19	427
2006	UK - Scotland	Jersey	1 401	325	5 915	5 230	5.75	4.06	418
2007	UK - Scotland	Jersey	1 634	333	5 853	5 172	5.53	3.98	420
2007	UK - Scotland	Shorthorn	177	274	5 067	4 818	3.67	3.38	394
2007	UK - England	Ayrshire	1 216	306	6 972	6 413	4.05	3.29	431
2006	UK - England	Ayrshire	1 145	309	6 721	6 153	3.98	3.34	425
2006	UK - England	British Friesian	1 622	327	6 775	6 224	4.25	3.36	412
2007	UK - England	British Friesian	1 833	324	6 721	6 178	4.11	3.33	415
2006	UK - England	Brown Swiss	375	330	7 170	6 336	4.41	3.46	429
2007	UK - England	Brown Swiss	380	332	7 307	6 482	4.26	3.49	423
2006	UK - England	Guernsey	444	315	5 565	5 004	4.91	3.64	421
2007	UK - England	Guernsey	618	301	5 114	4 473	4.81	3.58	448
2006	UK - England	Holstein	140 729	338	9 323	8 167	4.05	3.23	429
2007	UK - England	Holstein	152 522	342	9 477	8 252	3.95	3.19	432
2007	UK - England	Jersey	5 617	308	5 484	5 023	5.47	3.82	405
2006	UK - England	Jersey	4 858	304	5 519	5 037	5.61	3.85	403
2006	UK - England	Shorthorn	500	298	6 422	5 983	3.84	3.31	399
2007	UK - England	Shorthorn	531	299	6 398	5 911	3.7	3.27	405
2007	UK - Northern Ireland	Ayrshire	1 751	298	6 128	5 751	4.02	3.29	406
2006	UK - Northern Ireland	Ayrshire	1 564	290	5 993	5 658	4.08	3.31	409
2006	UK - Northern Ireland	British Friesian	422	300	6 505	6 109	4.18	3.31	398
2007	UK - Northern Ireland	British Friesian	447	314	6 799	6 325	4.14	3.3	391
2006	UK - Northern Ireland	Holstein	84 441	319	8 009	7 211	3.93	3.21	411
2007	UK - Northern Ireland	Holstein	87 883	319	8 116	7 258	3.91	3.18	414



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2007	UK - Northern Ireland	Jersey	1 132	285	5 053	4 614	5.11	3.77	394
2006	UK - Northern Ireland	Jerseys	778	307	5 208	4 767	5.19	3.83	387
2006	UK - Northern Ireland	Shorthorn	613	305	7 026	6 585	3.93	3.26	397
2007	UK - Northern Ireland	Shorthorn	674	304	7 207	6 601	3.88	3.24	404
2007	UK - Wales	Ayrshire	228	299	5 966	5 549	4.58	3.35	412
2006	UK - Wales	British Friesian	187	324	6 574	6 048	4.11	3.32	389
2007	UK - Wales	British Friesian	190	327	6 758	6 239	4.06	3.35	405
2006	UK - Wales	Holstein	16 733	340	8 938	7 853	4.14	3.26	432
2007	UK - Wales	Holstein	17 254	339	8 714	7 612	4.13	3.21	434
2006	UK - Wales	Jersey	355	312	5 821	5 317	5.67	3.87	411
2007	UK - Wales	Jersey	386	314	5 817	5 304	5.43	3.85	410
Average during 2006	USA ¹	Ayrshire	5 796	305	7 037	7 037	3.91	3.16	
Average during 2007	USA ¹	Ayrshire	5 756	305	7 076	7 076	3.91	3.17	
Average during 2006	USA ¹	Brown Swiss	15 007	305	8 234	8 234	4.06	3.37	
Average during 2007	USA ¹	Brown Swiss	14 798	305	8 198	8 198	4.06	3.39	
Average during 2006	USA ¹	Guernsey	7 862	305	6 986	6 986	4.52	3.35	
Average during 2007	USA ¹	Guernsey	7 652	305	7 019	7 019	4.5	3.36	
Average during 2006	USA ¹	Holstein	3906 258	305	10 237	10 237	3.66	3.06	
Average during 2007	USA ¹	Holstein	3 923 973	305	10 290	10 290	3.65	3.07	
Average during 2006	USA ¹	Jersey	186 581	305	7 315	7 315	4.61	3.59	
Average during 2007	USA ¹	Jersey	193 745	305	7 334	7 334	4.6	3.59	
Average during 2006	USA ¹	Milking Shorthorn	2 641	305	6 657	6 657	3.73	3.10	
Average during 2007	USA	Milking Shorthorn	2 055	305	6 339	6 339	3.54	3.10	

¹ DHI Herd averages

**Table 4.4. Results of milk recording: Main breeds - Cows in herdbook**

Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
July 2005 - June 2006	Australia	Ayrshire	552	328	6 078	6 078	4.15	3.34	
July 2005 - June 2006	Australia	Brown Swiss	600	344	6 751	6 751	4.19	3.57	
July 2005 - June 2006	Australia	Guernsey	375	336	5 798	5 798	4.32	3.42	
July 2005 - June 2006	Australia	Holstein	75 867	342	7 979	7 979	3.77	3.20	
July 2005 - June 2006	Australia	Illawarra	1 716	317	6 546	6 546	4.02	3.39	
July 2005 - June 2006	Australia	Jersey	17 378	318	5 460	5 460			
2006	Austria	Braunvieh	49 565	301		6 755	4.15	3.41	
2007	Austria	Braunvieh	48 292	301		6 860	4.13	3.40	
2006	Austria	Fleckvieh	219 320	298		6 483	4.18	3.43	
2007	Austria	Fleckvieh	219 995	299		6 666	4.16	3.40	
2006	Austria	Grauvieh	2 818	295		4 764	4.01	3.29	
2007	Austria	Grauvieh	2 869	295		4 815	3.98	3.27	
2006	Austria	Holstein	29 151	301		8 134	4.13	3.25	
2007	Austria	Holstein	30 601	301		8 243	4.12	3.23	
2006	Austria	Pinzgauer	6 917	298		5 398	3.90	3.27	
2007	Austria	Pinzgauer	6 863	298		5 438	3.90	3.26	
2006	Belgium (Wallonia Region)	All	All cows in milk recording = All cows in herdbook						
2006	Czech Republic	F Fleckvieh	141 963	294	6 162	6 334	4.08	3.46	399
2007	Czech Republic	F Fleckvieh	136 988	295	6 329	6 489	4.04	3.43	398
2006	Czech Republic	Holstein	161 290	299	8 246	8 370	3.83	3.28	420
2007	Czech Republic	Holstein	162 099	299	8 428	8 555	3.79	3.26	419



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	Denmark ¹	Ayrshire	194	365	8 180		4.13	3.44	
2006	Denmark ¹	Danish Holstein	366 084	365	9 232		4.12	3.35	
2007	Denmark ¹	Danish Holstein	361 517	365	9 372		4.05	3.35	
2006	Denmark ¹	Jersey	59 948	365	6 436		5.92	4.06	
2007	Denmark ¹	Jersey	58 448	365	6 555		5.89	4.06	
2006	Denmark ¹	Red Danish	41 923	365	8 560		4.25	3.50	
2007	Denmark ¹	Red Danish	40 333	365	8 663		4.18	3.50	
2006	Denmark ¹	Red Holstein	5 164	365	8 296		4.36	3.45	
2007	Denmark ¹	Red Holstein	5 059	365	8 419		4.28	3.44	
2006	Estonia	Estonian Holstein	61 002	345	7 273	7 309	4.09	3.28	428
2007	Estonia	Estonian Holstein	59 410	345	7 477	7 533	4.04	3.28	428
2006	Estonia	Estonian Red	21 575	330	6 520	6 449	4.28	3.41	407
2007	Estonia	Estonian Red	20 583	331	6 630	6 658	4.24	3.40	409
2006	Finland	Finnish Ayrshire	24 139			9 477	4.16	3.41	
2007	Finland	Finnish Ayrshire	22 900			9 615	4.18	3.45	
2006	Finland	Finnish Cattle	908			6 507	4.27	3.48	
2007	Finland	Finnish Cattle	1 046			6 524	4.36	3.50	
2006	Finland	Holstein Friesian	11 666			10 389	3.80	3.34	
2007	Finland	Holstein Friesian	12 123			10 484	3.84	3.37	
2007	Finland	Jersey	6			7 509	5.45	4.06	
2006	Finland	The National Organisation cannot get data before year 2003 (due to an old database)							
2006	France	Abondance	21 267	288	5 155	4 919	3.72	3.48	395
2007	France	Abondance	21 073	292	5 254	5 010	3.69	3.48	394
2006	France	Brune	16 664	323	6 784	6 069	4.19	3.56	412
2007	France	Brune	16 813	333	6 958	6 163	4.16	3.56	412
2006	France	Montbéliarde	386 933	296	6 451	6 061	3.92	3.43	389
2007	France	Montbéliarde	382 965	305	6 671	6 238	3.89	3.42	389
2006	France	Normande	263 095	308	5 901	5 443	4.31	3.62	392
2007	France	Normande	251 739	319	6 128	5 612	4.27	3.62	393
2006	France	Pie Rouge des Plaines	9 681	310	6 993	6 487	4.25	3.42	396
2007	France	Pie Rouge des Plaines	9 330	321	7 298	6 714	4.23	3.43	394
2006	France	Prim'Holstein	1 823 725	337	8 508	7 470	4.01	3.35	415
2007	France	Prim'Holstein	1 746 688	349	8 823	7 662	3.98	3.35	416
2006	France	Simmental Française	14 042	292	5 702	5 405	4.01	3.49	386
2007	France	Simmental Française	14 104	300	5 875	5 545	4.00	3.49	386

¹ 365 d. rolling average



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	Germany	Braunvieh	144 453	319	6 974	6 923	4.23	3.59	410
2007	Germany	Braunvieh	143 261	319	7 040	7 012	4.18	3.61	414
2006	Germany	Fleckvieh	628 732	315	6 854	6 675	4.14	3.48	391
2007	Germany	Fleckvieh	633 426	317	7 040	6 847	4.12	3.50	392
2006	Germany	Gelbvieh	4 383	314	5 721	5 668	4.20	3.51	401
2007	Germany	Gelbvieh	3 965	315	5 711	5 704	4.20	3.53	401
2006	Germany	Holstein B&W	1 484 291	321	8 672	8 613	4.11	3.39	410
2007	Germany	Holstein B&W	1 504 888	323	8 747	8 722	4.10	3.39	411
2006	Germany	Holstein R&W	144 866	320	7 964	7 887	4.23	3.40	402
2007	Germany	Holstein R&W	146 340	322	8 030	7 973	4.21	3.41	411
2006	Hungary	Hungarian Holstein Friesian	141 281	298	8 243		3.51	3.16	436
2007	Hungary	Hungarian Holstein Friesian	138 354	299	8 486		3.5	3.16	440
2006	Hungary	Hungarian Red Spotted	3 852	293	5 166		3.8	3.32	412
2007	Hungary	Hungarian Red Spotted	3 637	293	5 343		3.8	3.32	406
2006	Italy	Castana	4 477	305	2 837	2 837	3.46	3.37	
2007	Italy	Castana	4 313	305	2 844	2 844	3.48	3.39	
2006	Italy	Grey of Alps (Grigio Alpina)	6 205	305	4 975	4 975	3.74	3.37	
2007	Italy	Grey of Alps (Grigio Alpina, Grauvieh)	6 161	305	5 029	5 029	3.71	3.36	
2006	Italy	Italian Brown (Bruna Italiana)	72 955	305	6 734	6 734	3.97	3.47	
2007	Italy	Italian Brown (Bruna Italiana)	69 656	305	6 841	6 841	3.96	3.48	
2006	Italy	Italian Friesian (Frisona Italiana)	683 760	305	8 895	8 895	3.66	3.27	
2007	Italy	Italian Friesian (Frisona Italiana)	673 980	305	9 032	9 032	3.65	3.27	
2006	Italy	Italian Red Spotted (Pezzata Rossa Italiana)	31 692	305	6 389	6 389	3.92	3.41	
2007	Italy	Italian Red Spotted (Pezzata Rossa Italiana)	32 463	305	6 513	6 513	3.90	3.41	
2006	Italy	Jersey	4 241	305	5 700	5 700	5.29	3.98	
2007	Italy	Jersey	4 433	305	5 876	5 876	5.19	3.97	
2006	Italy	Valdostana Red Spotted (Valdostana Pezzata Rossa)	11 020	305	3 825	3 825	3.50	3.25	
2007	Italy	Valdostana Red Spotted (Valdostana Pezzata Rossa)	10 510	305	3 833	3 833	3.53	3.27	



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	Japan	Holstein	315 364	359	10 096	9 235	4.01	3.32	430
2006	Japan	Jersey	1 853	337	6 354	6 099	4.91	3.88	408
2006	Latvia	Holstein B&W	806	358		7 573	4.25	3.21	
2007	Latvia	Holstein B&W	3 040	371		7 502	4.23	3.18	
2006	Latvia	Latvian Brown	4 271	336		6 195	4.57	3.35	
2007	Latvia	Latvian Brown	6 950	342		6 139	4.56	3.34	
2006	México ¹	Holstein	44 158	365	8 542	8 778	3.40	3.17	444
2007	México ¹	Holstein	41 452	365	8 433	9 374	3.41	3.21	445
2006	Poland	Polish Holstein-Friesian (HO)	381 954	305	6 676	6 676	4.14	3.26	
2007	Poland	Polish Holstein-Friesian (HO)	378 466	305	6 864	6 864	4.14	3.26	
2006	Poland	Polish Holstein-Friesian (Rw)	11 738	305	6 343	6 343	4.19	3.29	
2007	Poland	Polish Holstein-Friesian (RW)	11 916	305	6 301	6 301	4.18	3.29	
2006	Poland	Polish Red	1 252	305	3 929	3 929	4.25	3.33	
2007	Poland	Polish Red	1 362	305	3 984	3 984	4.25	3.30	
2006	Poland	Simmental	3 447	305	4 590	4 590	4.00	3.33	
2007	Poland	Simmental	4 381	305	4 704	4 704	4.00	3.34	
2006	Slovak Republic	Holstein	8 499	299	8 136	8 258	3.79	3.22	440
2007	Slovak Republic	Holstein	7 870	299	8 307	8 342	3.86	3.17	436
2006	Slovak Republic	Slovak Pinzgauer	1 582	288	4 298	4 486	3.99	3.35	415
2007	Slovak Republic	Slovak Pinzgauer	1 385	290	4 489	4 662	3.95	3.33	406
2006	Slovak Republic	Slovak Simmental	3 099	295	5 557	5 698	4.18	3.34	414
2007	Slovak Republic	Slovak Simmental	2 927	296	5 775	5 906	4.2	3.32	411
2007	Slovenia	Black & White	29 439	375	8 318	7 204	3.98	3.20	426
2006	Slovenia	Brown	13 900	359	6 065	5 380	4.11	3.33	420
2007	Slovenia	Brown	13 612	361	6 294	5 553	4.08	3.32	420
2006	Slovenia	Holstein	28 734	372	8 006	6 978	4.02	3.20	425
2006	Slovenia	Simmental	34 698	346	5 537	5 023	4.17	3.29	410
2007	Slovenia	Simmental	34 458	347	5 757	5 213	4.13	3.28	407
2006	South Africa	Ayrshire	5 824	308	6 275	6 275	4.00	3.35	419
2007	South Africa	Ayrshire	5 801	315	6 387	6 387	3.93	3.28	423
2006	South Africa	Guernsey	487	316	6 682	6 682	4.27	3.46	427
2007	South Africa	Guernsey	476	319	6 253	6 253	4.26	3.41	414
2006	South Africa	Holstein	32 748	336	9 285	9 285	3.76	3.23	434
2007	South Africa	Holstein	30 734	334	9 308	9 308	3.78	3.18	441

¹ Only cows with more than 305 dim are considered for 365 d production



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	South Africa	Jersey	33 521	322	5 806	5 806	4.65	3.75	410
2007	South Africa	Jersey	34 193	320	5 836	5 836	4.67	3.70	423
2006	Spain	Frisona	322 839	353	10 129	8 954	3.68	3.15	383
2007	Spain	Frisona	328 456	363	10 404	9 036	3.66	3.15	383
2006	Spain	Parda	1 263	301	6 818	6 724	3.80	3.47	403
2007	Spain	Parda Alpina	992	300	7 046	6 433	3.79	3.50	402
2006	Switzerland	Braunvieh	138 936	300	6 730	6 814	3.99	3.35	409
2007	Switzerland	Braunvieh	136 303	300	6 745	6 829	3.99	3.35	404
2006	Switzerland	Eringer	762	305	3 246	3 246	3.60	3.43	
2007	Switzerland	Eringer	724	264	3 288	3 174	3.65	3.38	
2006	Switzerland	Fleckvieh	157 531	332	7 561	7 078	3.99	3.30	390
2007	Switzerland	Fleckvieh	156 937	334	7 618	7 115	4.00	3.26	391
2006	Switzerland	Grauvieh	117	295	3 879	3 977	3.71	3.22	399
2007	Switzerland	Grauvieh	143	296	3 920	4 009	3.72	3.28	399
2006	Switzerland	Hinterwälder	93	297	3 971	4 051	4.03	3.48	387
2007	Switzerland	Hinterwälder	88	296	3 870	3 958	4.00	3.42	387
2006	Switzerland	Holstein	36 547	305	8 081	8 081	3.96	3.24	
2007	Switzerland	Holstein	38 587	301	8 010	8 084	3.98	3.23	408
2006	Switzerland	Jersey	1 272	299	5 145	5 222	5.47	3.88	404
2007	Switzerland	Jersey	1 536	299	5 187	5 265	5.39	3.87	404
2006	The Netherlands	R&W	151 238	339	8 205	7 692	4.51	3.54	
2006	Turkey	Brown Swiss	4 909	329	5 154	4 660			408
2006	Turkey	Holstein Friesian (Black and White)	121 227	336	6 521	5 808			410
2006	Turkey	Holstein Friesian (Red and White)	323	340	6 524	5 787			405
2006	Turkey	Simmental	2 885	329	5 151	4 663			410
2006	UK - England	Ayrshires	882	322	7 121	6 495	4.01	3.29	426
2007	UK - England	Ayrshires	963	309	7 135	6 568	4.00	3.27	438
2006	UK - England	British Friesian	1 569	328	6 819	6 263	4.25	3.36	410
2007	UK - England	British Friesian	1 618	327	6 796	6 262	4.12	3.32	410
2006	UK - England	Brown Swiss	118	375	7 963	6 748	4.42	3.47	434
2006	UK - England	Guernsey	397	321	5 650	5 071	4.98	3.65	422
2007	UK - England	Guernsey	301	448	5 106	4 493	4.81	3.58	249
2006	UK - England	Holstein	118 605	340	9 506	8 314	4.05	3.22	430
2007	UK - England	Holstein	128 067	343	9 666	8 402	3.95	3.18	433



Year	Country	Breed	Number of lactations	Length of the lactations (days)	Milk yield per recorded cow (kg)	Milk per cow in 305 days (kg)	Percent of fat content (%)	Percent of protein content (%)	Calving interval (days)
2006	UK - England	Jersey	4 567	305	5 520	5 030	5.62	3.85	402
2007	UK - England	Jersey	5 187	310	5 523	5 053	5.5	3.82	407
2007	UK - Northern Ireland	Ayrshire	1 274	300	6 210	5 833	4.05	3.29	406
2006	UK - Northern Ireland	Ayrshires	1 198	292	6 068	5 734	4.11	3.32	411
2006	UK - Northern Ireland	British Friesian	331	296	6 203	5 888	4.26	3.34	397
2007	UK - Northern Ireland	British Friesian	397	314	6 690	6 244	4.18	3.33	389
2006	UK - Northern Ireland	Holstein	42 288	328	8 725	7 776	3.94	3.20	420
2007	UK - Northern Ireland	Holstein	45 976	332	8 872	7 845	3.91	3.16	422
2007	UK - Northern Ireland	Jersey	612	297	5 245	4 702	5.15	3.81	399
2007	UK - Scotland	Ayrshire	6 484	321	7 626	7 001	4.10	3.33	419
2006	UK - Scotland	Ayrshires	6 964	317	7 375	6 776	4.13	3.36	415
2007	UK - Scotland	British Friesian	752	311	6 969	6 431	4.12	3.41	408
2007	UK - Scotland	Brown Swiss	83	361	8 249	7 160	4.11	3.48	451
2006	UK - Scotland	Friesian	787	314	7 148	6 662	4.10	3.41	405
2006	UK - Scotland	Holstein	55 476	342	9 422	8 250	3.94	3.24	432
2007	UK - Scotland	Holstein	56 095	343	9 604	8 368	3.87	3.19	434
2006	UK - Scotland	Jersey	1 226	325	5 881	5 198	5.80	4.08	420
2007	UK - Scotland	Jersey	1 317	336	5 880	5 187	5.61	4.01	422
2007	UK - Wales	Ayrshire	121	323	6 944	6 484	4.92	3.32	412
2006	UK - Wales	British Friesian	186	325	6 586	6 057	4.11	3.32	389
2007	UK - Wales	British Friesian	190	327	6 758	6 239	4.06	3.35	405
2006	UK - Wales	Holstein	15 055	342	9 033	7 921	4.15	3.25	433
2007	UK - Wales	Holstein	15 319	343	8 883	7 739	4.13	3.20	436
2006	UK - Wales	Jersey	331	312	5 870	5 373	5.69	3.88	413
2007	UK - Wales	Jersey	360	319	5 898	5 380	5.46	3.85	412

Participants to the 36th ICAR Session

Argentina

Roberto Castaneda - INTI Lacteos
 Patricia Labaca - National Institute of Industrial
 Maximo Russ - Asociacion Criadores de Holando

Australia

Daniel Abernethy - Australian Dairy Herd
 Improvement
 Peter Bailey - Dept of Primary Industries, Victoria
 Kon Konstantinov - Australian Dairy Herd
 Improvement

Austria

Franz Schallerl - ZAR

Belgium

Catherine Bastin - Gembloux Agricultural University
 Nicolas Gengler - FNRS / Gembloux Agricultural
 University
 Mathieu Meers - World Holstein Federation
 Helene Soyeurt - Gembloux Agricultural University

Brazil

Jose Alonso Kafer - Saint-Gobain Ceramic & Plastics
 Joao Durr - Universidade de Passo Fundo
 Luis Henrique Amadeu - Saint-Gobain

Canada

Jarmila Bohmanova - University of Guelph
 Edward Burnside - Geno Global, SA
 Richard Cantin - CanWest DHI
 Nicolas Caron - Semex Alliance
 Jacques Chesnais - Semex Alliance
 Brian Corrigan - Valacta
 Kevin Dalrymple - Ketchum Manufacturing Inc.
 Travis Freeman - CanWest DHI
 Gladys Huapaya - Canadian Dairy Network
 Janusz Jamrozik - University of Guelph
 Matthew Kelly - University of Guelph
 Gerrit Kistemaker - Canadian Dairy Network
 John Komarnicki - CanWest DHI
 Rachid Kouaouci - Valacta
 Tom Kroetsch - The Semex Alliance
 Sylvia Lafontaine - Valacta
 Pierre Laliberte - Semex Alliance
 Paul Laronde - Destron Fearing
 Sarah Loker - University of Guelph

Lyle Martin - CanWest DHI
 Filippo Miglior - Agriculture & Agri-Food Canada
 Stephen Miller - University of Guelph
 Robert Moore - Valacta
 Blair Murray - OMAFRA
 Timothee Neuenschwander - University of Guelph
 Neil Petreny - ICAR
 Ward Robinson - Agriculture and Agri-Food Canada
 Ian Rumbles - CanWest DHI
 Larry Schaeffer - University of Guelph
 Jay Shannon - Holstein Canada
 Nicolaas Smit, PhD - Safeguard BioSystems
 Brad Speiss - MFC Testing & Research Inc.
 Peter Sullivan - Canadian Dairy Network
 Deb van de Water - CanWest DHI
 Brian Van Doormaal - Canadian Dairy Network
 Cindy Whytock - CanWest DHI

Colombia

Jose Zuluaga - Cooperative Colanta LTDA

Croatia

Zdravko Barac - Croatian Livestock Center
 Maja Drazic - Croatian Livestock Center

Cyprus

George Psathas - Cyprus Milk Industry Organization

Czech Republic

Pavel Bucek - Czech Moravian Breeders' Association
 Antonin Macek - Research Institute for Cattle Breeding
 Jan Riha - Research Institute for Cattle Breeding
 Martin Verner - Czech Moravian Breeders' Association

Denmark

Gert Aamand - Nordic Cattle Genetic Evalaution
 Tove Asmussen - Lattec
 Soren Borchersen - VikingGenetics
 Mads Damgaard - Tru-Test Scandinavia
 Anders Fogh - Danish Cattle
 Ole Hansen - Danish Cattle Federation / RYK
 Steen Kold-Christensen - FOSS
 Uffe Lauritsen - Danish Cattle Federation
 Jens Ulrik Nielsen - Danish Cattle
 Nicole Uvenbeck - FOSS

Egypt

Samy Mohamed - Cattle Information
Systems/Egypt (CISE)

Estonia

Kaivo Ilves - Estonian Animal Recording Centre
Mart Kuresoo - Estonian Animal Recording Centre
Kalle Pedastsaar - Estonian Animal Recording Centre
Aire Pentjarv - Estonian Animal Recording Centre
Mart Uba - Estonian Animal Recording Centre
Kaija Uuskam - Veterinary and Food Board

Finland

Mikko Koskinen - Finnzymes Oy
Juho Kyntaja - ProAgria
Esa Mantysaari - MTT Agrifood Research
Sinikka Tommila - Agricultural Data Processing Centre
Anna-Maria Tyriseva - MTT Agrifood Research Finland

France

Jean Michel Astruc - Institut de l'Elevage
Francis Barillet - INRA
Marc Belvalette - France Contrôle Laitier
Pierre Billon - Institut de l'Elevage
Jean Noel Bonnet - Institut de l'Elevage
Isabelle Boulesteix - Institut de l'Elevage
Mickael Brochard - Institut de l'Elevage
Vincent Corbet - Institut de l'Elevage
Vincent Ducrocq - INRA
Sebastien Duroy - Institut de l'Elevage
Marie Noelle Fouilloux - Institut de l'Elevage
Alain Gastebled - Institut de l'Elevage
Pierre Louis Gastinel - Institut de l'Elevage
Philippe Grosperren - France Contrôle Laitier
Laurent Journaux - UNCEIA
Christophe Lecomte - France Bovins Croissance
Olivier Leray - CECALAIT (Actilait)
Bruno LO-RE - MAINtag
Alain Malafosse - UNCEIA
Christine Marlin - Assemblée Permanente des
Chambres d'Agriculture (APCA)
Sophie Mattalia - Institut de l'Elevage
Stephanie Minery - Institut de l'Elevage
Michel Pivard - FIEA
Erik Rehben - Institut de l'Elevage
Rene Rognant - FIEA
Michel Sady - France Contrôle Laitier
Georges Salomon - FIEA
David Saunier - France Contrôle Laitier
Jean-Marc Vacelet - French Montbeliarde Breed
Association
Eric Venot - INRA

Germany

Johann Bartels - AG Deutscher Rinderzuechter
Christian Baumgartner - Milchpruefring Bayern e.V.
Ernst Bohlsen - LKV Weser-Ems
Joerg Dodenhoff - Bavarian State Research Center for
Agriculture
Lothar Doering - Landeskontrollverband
Sachsen-Anhalt
Hans Epp - Milchpruefring Bayern e.V.
Egbert Feddersen - German Holstein Association
Heinz Francke - WestfaliaSurge GmbH
Hubert Goeft - FOSS
Eildert Groeneveld - FLI
Manfred Hammel - LKV Brandenburg e.V.
Stephan Hartwig - Landeskontrollverband
Mecklenburg-Vorpommern e.V.
Ulrich Janowitz - AG Deutscher Rinderzuechter
Sven Koenig - Institute of Animal Breeding
Manfred Kohler - Landeskontrollverband
Mecklenburg-Vorpommern e.V.
Friedhelm Lemmer - Lemmer-Fullwood GmbH
Zengting Liu - vit w.V.
Reinhard Nehls - Caisley International GmbH
Bernd Neutsch - Hauptner-Herberholz
Folkert Onken - AG Deutscher Rinderzuechter
Claus Pohl - GEPE
Reinhard Reents - vit w. v.
Stephan Rensing - vit w.V.
Hans-Joerg Roesler - Landeskontrollverband
Sachsen-Anhalt
Carl Stephan Schaefer - AG Deutscher Rinderzuechter
Christoph Schildmann - Caisley International GmbH
Fred Schulze - LKV Brandenburg e.V.
Hermann Swalve - Martin-Luther-University Halle
Helge Taeubert - vit w.V.
Henrik Winkeler - Caisley International GmbH
Norbert Wirtz - Vereinigte Informationssysteme
Tierhaltung w.V.

Greece

Georgios Banos - Aristotle University of Thessaloniki
Andreas Georgoudis - Greek Holstein Association

Hungary

Pal Gombacsi - Central Agricultural Office
Peter Wellisch - National Institute for Agricultural
Quality Control

Ireland

Donagh Berry - Teagasc
Martin Burke - Irish Cattle Breeding Federation
John Carty - Department of Agriculture, Fisheries and
Food
John Comer - Irish Cattle Breeding Federation
Tom Corcoran - National Cattle Breeding Centre

Andrew Cromie - Irish Cattle Breeding Federation
 Bernard Eivers - National Cattle Breeding Centre
 Ross Evans - Irish Cattle Breeding Federation
 Pat Mulvehill - Munster Cattle Breeding Group
 John O'Sullivan - Irish Cattle Breeding Federation
 Thierry Pabiau - Irish Cattle Breeding Federation
 Brian Wickham - Irish Cattle Breeding Federation

Israel

Alon Arazi - SAE Afikim
 Alexander Kapitulskiy - SAE Afikim
 Gil Katz - SAE Afikim
 Niv Pinsky - SAE Afikim
 Yoel Zeron - SION

Italy

Marco Antonini - Università di Camerino
 Omar Bonetti - Italian Brown Cattle Breeders' Association
 Fabiola Canavesi - ANAFI
 Antonello Carta - AGRIS
 Elena Couto - ICAR Secretariat
 Andie Dimitriadou - ICAR Secretariat
 Raffaella Finocchiaro - ANAFI
 Mauro Fioretti - Associazione Italiana Allevatori
 Juhani Maki-Hokkonen - ICAR
 Cesare Mosconi - ICAR
 Silvia Orlandini - AIA, Laboratorio Standard Latte
 Roberto Proietti - Associazione Italiana Allevatori
 Matteo Ratti - Milkline
 Andrea Rosati - ICAR Secretariat
 Attilio Rossoni - Italian Brown Cattle Breeders' Association
 Enrico Santus - Italian Brown Cattle Breeders' Association
 Alessia Tondo - Associazione Italiana Allevatori
 Milan Zjalic - ICAR Secretariat

Japan

Koichi Hagiya - National Livestock Breeding Centre
 Kan Itabashi - Livestock Improvement Association of Japan Inc.
 Junichi Saburi - National Livestock Breeding Center

Korea

Joo Hyeon Cho - Dairy Cattle Improvement Center of National Agricultural Cooperative Federation
 Youlim Choi - National Institute of Animal Science
 Cho Kwanghyeon - National Institute of Animal Science
 Seung-Soo Lee - Korean National Institute of Animal Science
 Byoung-ho Park - National Institute of Animal Science

Latvia

Erna Galvanovska - State Agency Agriculture Data Centre
 Dainis Rungulis - Ministry of Agriculture
 Evija Skujina - State Agency Agriculture data centre
 Inguna Slice - State Agency Agriculture data centre
 Ivans Vorslovs - State Agency Agriculture data centre
 Rita Zutere - State Agency Agriculture data centre

Lithuania

Vytenis Cukauskas - Agri-information and Rural Business Center
 Jonas Kareckas - SE
 Jurij Lavrinovi - Agri-Information and Rural Business
 Irena Tabakajeviene - SE

Mexico

Ariadna Reyes - Holstein de Mexico A.C.
 Felipe Ruiz - CNOG Mexico

Netherlands

Harrie Bijgaart - Qlip NV
 Gerben De Jong - CRV
 Kees de Koning - Animal Sciences Group WUR
 Gerrit Keizer - Prionics Lelystad BV
 Dick Koorn - CRV Holding BV
 Rene Van der Linde - CRV BV
 Mathijs Van Pelt - CRV
 Kees Van t Klooster - WG3 Animal Identification
 Jan Venneman - CRV Holding BV
 Hans Wilmink - CRV Holding BV

New Zealand

Stuart Bay - LIC
 Ted Coats - LIC
 Mark Dewdney - LIC
 Brett Ellis - Tru-Test
 Mike Gardner - ZEE TAGS
 Bevin Harris - Livestock Improvement
 Nick Howarth - Tru-Test Ltd
 Bill Montgomerie - New Zealand Animal Evaluation Ltd.
 Geoff Nathan - Tru-Test Ltd
 Des Scott - SAILL Dairy Laboratory

Norway

Bjorg Heringstad - Geno
 Tone Roalkvam - TINE BA

Peru

Carlos Pacheco - Study Centre and Promoting

Poland

Leszek Hadzlik - Polish Federation of Cattle Breeders and Dairy Farmers
Joanna Jaroszewska - National Animal Breeding Centre
Marta Kierblewska - Stacja Hodowli i Unasienniania Zwierzt Sp. z o.o.
Danuta Radzio - Polish Federation of Cattle Breeders and Dairy Farmers
Andrzej Sciubisz - Bentley Polska Sp. z o.o.
Anna Siekierska - Polish Federation of Cattle Breeders and Dairy Farmers
Tomasz Strabel - University of Life Sciences in Poznan
Joanna Studziska - Stacja Hodowli i Unasienniania Zwierzt Sp. z o.o.
Zbigniew Urny - Polish Federation of Cattle Breeders and Dairy Farmers

Romania

Ionel Scurtu - Grassland Research Institute

Slovakia

Marta Dianova - Plemenarske sluzby SR, s.p.
Stefan Ryba - Plemenarske sluzby SR, s.p.
Vladimir Tancin - SCPV Nitra

Slovenia

Janez Jenko - Agricultural Institute of Slovenia
Marija Klopčič - University of Ljubljana, Biotechnical Faculty, Zootechnical Department
Drago Kompan - University of Ljubljana, Biotechnical Faculty, Zootechnical Department
Milena Kovac - University of Ljubljana, Biotechnical Faculty, Zootechnical Department
Jurij Krsnik - University of Ljubljana, Biotechnical Faculty, Zootechnical Department
Betka Logar - Agricultural Institute of Slovenia
Klemen Potonik - University of Ljubljana, Biotechnical Faculty, Zootechnical Department

South Africa

Bernice Mostert - Agricultural Research Council
Helena Theron - Agricultural Research Council
Jacob Van der Westhuizen - ARC
Pierre van Rooyen - SA Stud Book & Anim. Impr. Assoc.

Spain

Alfredo Martin - Ministry of Agriculture, Fisheries and Food
Juan Pena - CONAFE

Sweden

Jan-Ake Eriksson - Swedish Dairy Association
Freddy Fikse - Interbull Centre
Flavio Forabosco - Interbull
Eva Hjerpe - Interbull Centre, Sweden
Jette Jakobsen - Interbull Centre
Kjell Johansson - Swedish Dairy Association
Hossein Jorjani - Interbull Centre
Nils-Erik Larsson - Swedish Dairy Association
Fernando Mazeris - DeLaval International AB
Valentina Palucci - Interbull Centre
Jan Philipsson - Interbull Center
Hans Stalhammar - VikingGenetics
Eva Stormwall - Swedish Dairy Association
Erling Strandberg - Dept Animal Breeding & Genetics, SLU
Anne Torsell - Interbull Centre

Switzerland

Joseph Crettenand - Swiss Red and White Cattle Breeders'
Tilman Hoefelmayr - WMB AG
Jürg Moll - Swiss Brown Cattle Breeders' Federation
Axel Prediger - WMB AG
Urs Schnyder - Schweizerischer
Ulrich Witschi - Swissgenetics

Tanzania

Sachindra Das - Ministry of Livestock Development and Fisheries
Hassan Mruttu - Ministry of Livestock Development and Fisheries

Ukraine

Iryna Baranenko - Art-master Ltd.
Maksym Bykhovtsov - JSC
Kravchenko Nataliya - JSC
Sergey Volkov - State Enterprise Agency for Animal Identification and Registration

United Kingdom

Lucy Andrews - HOLSTEIN UK
Frank Armitage - ICAR
Mike Coffey - SAC
Susan Cope - Cattle Information Service
Tony Craven - National Milk Records plc
Suzanne Harding - Holstein UK
Bill Luff - World Guernsey Cattle Federation
Raphael Mrode - Scottish Agricultural College
Henry Richardson - Centre for Dairy Information (UK)
Greg Ward - HOLSTEIN UK
Marco Winters - DairyCo breeding+

United States

Mark Adam - NorthStar Cooperative
 Robert Albrecht - ISDA
 Katie Allen - Dairy One Cooperative
 Joel Amdall - AgSource/CRI
 Jeannine Anderson - Gaze Acres Alpacas
 Patrick Baier - AgSource/CRI
 Phil Bailey - Central Counties DHIA
 David Barboza - Alpaca Owner & Breeders Assn.
 Darin Barnes - Central Life Sciences
 Josh Bartels - Bartels Music
 Rick Bealer - Southern Counties DHIA
 Brian Bolton - Allflex USA
 Pierre Broutin - Bentley Instruments Inc.
 Tyler Brown - Global Animal Management
 Dixie Burris - Dairy One, Inc
 Todd Byrem - Antel BioSystems Inc.
 Steve Chamberlain - Dairy One Cooperative
 David Chedotal - Capitol Plastics
 John Clay - Dairy Records Management Systems
 John Cole - USDA Animal Improvement Programs Laboratory
 Joan Cooper - University of Tennessee
 Peter Costas - Delta Instruments
 Ken Crandall - DHI Computing Service, Inc
 Sheila Cranker - Capitol Plastics
 George Cudoc - Dairy One Cooperative
 Carol Decker - Fox Valley DHI Lab
 Cathy Dei - DHI Computing Service
 Tom DeMuth - AgSource/CRI
 Gordon Doak - National Association of Animal Breeders (NAAB)
 Bruce Dokkebakken - Minnesota DHIA
 Philip Dukas - Dairy Records Management Systems
 Alfred Duran - California DHIA
 Andy Flis - ITW Reyflex North American
 Mary Fogal - Universal Lab Services
 Colin Foster - Y-Tex Corporation
 Steve Frank - United DHIA
 Tim Gallagher - ThermoFisher Scientific
 Michael Gallenberger - Gallenberger Dairy Records
 Jim Garrity - Dairy One Cooperative
 Peter Giacomini - AgSource/CRI
 Peter Groeneveld - Delta Instruments
 Christine Hackler - Central Counties DHIA
 David Harrison - ReQuest
 Joel Hastings - DairyBusiness Communications
 Dave Heald - Dairy One Cooperative
 Steve Hershey - National DHIA & Lancaster DHIA
 Jere High - Lancaster DHIA
 Paul Jandrin - AgSource/CRI
 John Johnson - Capitol Plastics
 Robert Kleemeier - I.D.ology
 David Knupp - Global Animal Management
 Roman Kwasiborski - FOSS
 Richard La Croix - AgSource/CRI
 Thomas Lawlor - Holstein USA
 Susan Lee - Idaho DHIA & National DHIA Board of Directors
 Lee Maassen - National Dairy Herd Information Association
 Stu Marsh - Central Life Sciences
 Thomas Matthews - Lely USA, Inc.
 Jay Mattison - National Dairy Herd Information
 Ignacy Misztal - University of Georgia
 Kerry Moncur - Central Life Sciences
 Bob Nedley - Destron Fearing
 Steven Nelson - Ram Mechanical, Inc.
 Muril Niebuhr - MNDHIA Zumbrota Laboratory
 Kathleen Noble - Dairy One Cooperative
 H. Norman - Animal Improvement Programs Lab, ARS, USDA
 Tony Nunes - Tulare DHIA
 Erin Ogden - Murphy Desmond S.C.
 Julee O'Reilly - DHI Cooperative, Inc.
 Anthony Pappas - Delta Instruments
 Jim Parker - WestfaliaSurge
 Randy Perkins - Dairy One Cooperative
 Skip Pringle - San Joaquin D.H.I.A.
 John Rhoads - Eastern Lab Services
 Gary Rogers - University of Tennessee
 David Rothfuss - Dairy One Cooperative
 Charles Sattler - National Dairy Herd Information
 Tod Schilling - Bentley Instruments Inc.
 Mark Schweisthal - USDA
 Stacie Shafer - Dairy One Cooperative
 Dan Sheldon - National Dairy Herd Information
 Steve Sievert - NDHIA
 Vincent Silverman - Avid Identification Systems
 Darwin Stoner - Lancaster DHIA
 David Sukup - Heart of America DHIA
 Christian Svensgaard - FOSS
 Scott Taylor - California DHIA
 Huub te Plate - Cooperative Resources International
 Susan Tellez - Suri Network
 Leslie Thoman - NDHIA
 Chris Thompson - Bentley Instruments Inc
 Dani Thon - Dairy One Cooperative
 Scott Unruh - Ram Mechanical, Inc.
 Jack Van Almelo - Dairy One Cooperative
 Simon Vander Woude - High Desert Dairy Lab, Inc
 Paul VanRaden - USDA-AIPL
 Jay Waldvogel - LIC
 Donna Walker - Dairy One Cooperative
 Daniel Webb - University of Florida
 Kent Weigel - Nat'l Association Animal Breeders (NAAB)
 Ray West - Southeast DHIA, Inc
 Steve White - Astoria-Pacific
 Greg Wickham - DairyLea / DFA
 George Wiggans - AIPL-ARS-USDA
 Brian Winters - DHI Cooperative Inc.
 Cari Wolfe - American Jersey Cattle Association
 Brent Woodward - Merial Limited
 Jamie Zimmerman - Dairy One Cooperative
 Paul Zubrod - FOSS

Uruguay

Federico Guerra - Instituto Nacional Mejoramiento
Lechero

Gonzalo Matho - Instituto Nacional Mejoramiento
Lechero

Gabriel Rovere - Instituto Nacional Mejoramiento
Lechero

This book contains the Proceedings of the 36th ICAR Session that was held, for the first time in the history of ICAR, in the USA. Niagara Falls hosted the event that was held from 16 to 20 June 2008.

Around 400 participants took part in the meeting which focused on the last developments of animal recording (technologies and scientific principles), animal evaluation (traits and production) and technology developments (tools and knowledge).

This publication presents the various aspects of domestic animal recording, aimed at improving the management of herds and increasing their productivity. New strategies for identification and recording are pointed out and the most updated technologies are shown, presenting as well the possible national practices where such technologies have been implemented.

The 36th Session also hosted interesting satellite meetings, whose papers are also presented in this publication, like some manuscripts presented during the workshop "DHI managers" and the workshop "Manufacturers' showcase".

Considering the new scenarios enabled by technology and the continuous changes provided and requested by technicians, the meeting offered the possibility of presenting and debating the new genomic tools in animal breeding in a specific satellite workshop, whose papers are also listed in this book. Experiences in various countries were presented and examples of potential uses of polymorphisms for parentage testing, individual identification, and traceability were discussed. Future challenges and opportunities in this field and the definition of the future developments in the sector were also debated.

Another section of the publication deals with the "ICAR Reference Laboratory Network", where the reference systems, the principles and the practices for calibration systems for routine milk testing are presented.

The last section of this publication shows the national statistics of the "Yearly enquiry on the situation of cow milk recording in member countries" for the years 2006 and 2007. A total of 31 pages describes the methodologies used at national level for milk recording, the national data for milk production, the costs of recording and the productivity and numbers of recorded cattle at national level (divided by species and by herdbook).