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THE GLOBAL STANDARD FOR LIVESTOCK DATA

Network. Guidelines. Certification.

ICAR Technical Series no. 24

NEW TRAITS AND ADDING VALUE TO THE RECORDING AND ID SERVICES IN THE ANIMAL PRODUCTION

Proceedings of the ICAR Conference held in Prague, CZ, 17-21 June 2019

Editors: J. Kucera, P. Bucek, D. Lipovsky, X. Bourrigan and M. Burke

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December 2019

Preface

In June 2019, the ICAR conference was held for the first time in the Czech Republic. Taking place in the capital city Prague, the event was hosted by the Czech Moravian Breeders' Corporation, Inc. and supported by the congress agency GUARANT International and the ICAR Secretariat. Like previous editions, this year's event was organised in conjunction with ISO/IDF Analytical Week, bringing together experts from across organisations to foster interdisciplinary collaboration.

Both events saw more than 430 delegates from 58 countries attending. The organisers were particularly pleased to have the opportunity to promote the rich agricultural heritage of the country. Attendees had the opportunity to visit a selection of the country's leading cattle farms, including the UNESCO world heritage site, the Kladruby nad Labem stud farm, home to the oldest indigenous Czech horse breed, the Kladruber.

Prague is one of the most beautiful historic cities in Europe. Known as the city of a hundred spires, Prague is home to hundreds of historical sights and buildings. It was among the most important cities in Europe during the Medieval, Renaissance and Baroque eras, with much of the impressive architecture from these periods still visible throughout the city. Prague Castle is the largest ancient castle in the world and served as the seat of Czech rule going back more than 1000 years. Other historic places of note include the Lesser Town, the Old Town and the Jewish Quarter. Prague was added to the UNESCO World Heritage List in 1992. The city is famed for Charles University founded in 1348 and, also, the Czech University of Life Sciences, one of many agricultural universities in the Czech Republic.

The ICAR programme comprised meetings by various working groups and subcommittees, supplemented by two milk recording workshops and an Interbeef meeting. This year's event was created to reflect the wide interests of all ICAR members, with topics covering all species. The manufacturers showcase provided an opportunity for those working in the industry to exhibit their products and exchange information, while an expert panel convened to discuss the future of cattle milk recording. In total, there were more than 140 technical and scientific presentations. Participants were introduced to animal breeding in the Czech Republic through various field trips.

The organisers wish to thank all speakers for their insightful contributions and also acknowledge the professional work of the volunteer members serving on ICAR's working groups and subcommittees, who together form the cornerstone of the organisation's continued success. Recognition must also be given to the tireless organising team, comprising the Czech Moravian Breeders' Corporation and GUARANT International.

Huge thanks also goes to the Czech Ministry of Agriculture for their financial support, the ICAR Secretariat, the members of the Programme and Scientific Committee, and to all our sponsors, without whom this event would not have been possible.

Josef Kucera
CEO Czech Moravian Breeders Corporation

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The dairy cattle industry in the Czech Republic

J. Kucera and P. Bucek

Czech Moravian Breeders´ Corporation, Inc., Hradistko, Czech Republic

Cattle breeding and organised milk recording have enjoyed a long tradition in the territory of present-day Czech Republic. The first official milk recording system was implemented in 1905. The first breeding organisations in the Czech Republic were established following the founding of various agricultural societies in 1769. In 1890, an associated cattle cooperative began to keep herd books. Gregor Johann Mendel, the founder of modern genetics (born in 1822) established many of the rules of heredity, which are now used as the laws of Mendelian inheritance and represent the building blocks of ICAR's and Interbull's work. In 1990, a breeders' association was re-established as the main driver of genetic improvement in the Czech Republic.

In 1996, this became the Czech Moravian Breeders' Corporation (CMBC), created for the purpose of serving farmer needs. As of early 2019, the Czech Republic had a total of 1,415,770 cattle, including 364,263 dairy cows and 226,255 beef cows. The number of beef cows has increased over the last couple of years, with the majority of dairy cows comprising Holstein (60%) and Fleckvieh (37%) and other breeds making up the remaining 3%. There has been a notable increase in milk production over the last twenty years. In 2018, milk yields from Holstein cattle reached 10,059 kg/milk and in the case of Fleckvieh, 7,591 kg/milk.

The proportion of recorded cows in the CR is one of the highest among ICAR countries, with 347,950 cows recorded in September 2018, representing 96.4% of the total number of cows recorded. The country also boasts the highest average herd and company sizes among ICAR members. The Czech Republic uses the AZ4, A4 and AT4 milk recording methods as specified in the ICAR Guidelines. The milk sector has a central position within the food supply chain, generating a source of regular income. For the year 2018, raw milk production totalled 3,078,390 tonnes and 2,978,411 tonnes in sales. The Czech Republic is also an active exporter, engaging in the international trade of milk, yogurts, whey and live animals.

As a premium breeder, the Czech industry also exports animals and genetic material to many countries. The CMBC provides a wide range of services for domestic and international breeders. As an umbrella organisation, it oversees animal identification and registration as well as its ISO-accredited milk analysis and DNA laboratories. Its DNA laboratory is accredited by ICAR for parentage verification and genotyping of the most common animal species. Other services include genetic evaluation, linear classification of dairy cattle, technical herdbook maintenance, and data processing with regard to all aspects of cattle breeding. The CMBC complies with regular ICAR audits under the ICAR Certificate of Quality programme for dairy and beef cattle. The company is a founding member of Interbeef and has been a member of ICAR since 1991 and Interbull since 1994.

Internet of cows – Opportunities and challenges for improving health, welfare and efficiency in dairying

C. Egger-Danner[1], B. Fuerst-Waltl[2], P. Klimek[3], O. Saukh[4], T. Wittek[5] and D4Dairy-Consortium[6]

[1]ZuchtData EDV-Dienstleistungen GmbH, Dresdner Str. 89, 1200 Vienna, Austria
[1]Corresponding author: egger-danner@zuchtdata.at
[2]Department of Sustainable Agricultural Systems, Division of Livestock Sciences, University of Natural Resources and Life Sciences (BOKU), Gregor-Mendel-Str. 33, 1180 Vienna, Austria
[3]Medical University Vienna / Complexity Science Hub Vienna, Josefstaedter Strasse 39, 1080 Vienna, Austria
[4]Graz University of Technology / Institute of Technical Informatics, Inffeldgasse 16/I, 8010 Graz / Complexity Science Hub Vienna, Josefstaedter Strasse 39, 1080 Vienna, Austria
[5]Clinic of Ruminants, University of Veterinary Medicine, Veterinaerplatz 1, 1210 Vienna, Austria
[6]D4Dairy Consortium / www.d4dairy.com

Abstract

With the growing world population, climate changes and the simultaneous increase in the demand for animal products challenges such as production efficiency, animal health, resilience and environmental impact are becoming increasingly important. Social sensitivity for animal welfare, appropriate feeding and housing and food safety is of increasing concern as well. Those changes in the production circumstances as well as the need for economical sustainability are reflected in broadening breeding goals. At the same time, new technologies are revolutionising the dairy industry. In addition to achievements in omics technologies (e.g. genomics, metabolomics), information and communication technologies (e.g. Internet of Things, sensor technology) are also finding their way into modern dairy herds. Instead of punctual measurements, sensors record animal behavioural patterns that allow drawing conclusions on animal health, animal wellbeing and welfare. The large amount of data generated by monitoring and the integration of various already existing data sources thus promise completely new insights into animal health and welfare. Optimised processes e.g. feeding improve efficient use of resources and reduce the daily workload of farmers. Better trait defintions are expected to result in higher heritabilities and higher genetic gain. Traditional data pipelines with information from performance recording in combination with indicators for metabolic disturbances, such as veterinary diagnoses, feeding information, test of ketone bodies, body condition score, and mid-infra-red spectra have existed for some time. With regard to metabolic disorders, they already provide more precise possibilities to predict health status than some traditional traits such as fat-protein-ratio. For claw health, information from claw trimming, veterinary diagnoses and lameness scoring has only been partly made available. Sensor technology provides alarms based on irregularities of normal behaviour for early detection of disordes. Advanced methodology offers the possibility to combine various environmental information and genomic background to gain new insights into the occurance of or susceptibility to disorders. To explore these opportunities, the big challenge is the integration of different data sources. In practice, data are often generated by different hardware and software products, which makes data integration more difficult due to different data exchange

formats of the communication partners involved. Traits are defined differently by different products. Volume, velocity, variety and veracity of data are topics to consider. It is therefore necessary to create structures to bring these data sources together in order to provide farmers with maximum support for herd management. Another challenge of data integration from different sources is compliance with legal data protection regulations, since this is often associated with lack of clarity in practice. Cooperation between different partners and integrating different data is the precondition for successfully applying advanced data technologies based on complex trait definitions. Based on the COMET-project D4Dairy steps to overcome these challenges are presented.

Keywords: data integration, health, welfare, advanced data technologies.

Introduction

Growing world population with currently 7.5 billion, and 9.7 billion to be expected by 2050 (UNO, 2015)), demands for higher efficiency and sustainability. Climate change needs to be approached by reducing emissions but also by developing strategies that improve resilience on the levels of individual animals, farms, and the entire sector. Increased consumer concerns for food safety, animal health and animal welfare add to the urgency of these issues. Economic constraints result in growing farm sizes with pressure for optimization and sustainability and increased workload on farmers. Enormous technological progress and a rapidly increasing number of farms with various types of automation (automatic milking systems, animal sensors and feeding systems, ...) are observed worldwide. A recent survey amongst Austrian farms in the project D4Dairy showed that more than 30% of the farms with more than 50 cows are equipped with a milking robot and animal sensors with further expected increase. These advances offer many new possibilities and have the potential to change traditional structures within short time. A recent example is genomics where with decreasing prices for genotyping animal breeding has changed substantially in no more than ten years (VanRaden, 2019). Progeny testing has been widely replaced by genotyping and selecting calves for providing the next generation. Herd genotyping projects with more and more females being genotyped offer huge additional potential for the future. Advances in OMICS technologies with different technical tool boxes will give more insight in the origin of diseases (Wagner, 2018). A large variety of miniaturized low-power smart sensors in combination with low-power wireless communication and embedded data analytics is the base for implementation of highly integrated „real-time" alarm and decision support tools.

Many new phenotypes are being generated more or less automatically by different sensors and robotic systems. Artificial intelligence algorithms are deriving a wide range of predictors. Presently many systems are still stand-alone solutions with no or a low level of integration or communication between different data sources (Rutten *et al.* 2013). A survey conducted in Austria by farmers and veterinarians (Perner *et al.* 2016; Weissensteiner *et al.* 2018) revealed the importance of linkage of data. Farmers do not want to record the same information more than once nor do they want to have many systems for displaying the information. They expect the best service out of their data. The challenge is to link different data sources and knowledge across disciplines. Novel statistical approaches and machine learning techniques are needed to harmonize, integrate, and make sense out of such heterogeneous data. Multi-actor approaches are required to exploit these new possibilities towards the common aim of improving animal health, welfare and sustainability.

Current situation

Animal breeding has a long tradition of recording data and organising herd- and animal specific data in big central databases worldwide. The level of data integration differs across countries and organisations. Data from animal registration, performance recording and specific data related to breeding (conformation, marketing, ...) are routinely gathered; health data are becoming more and more integral part for breeding and herd management. Genome data and predictors based on advanced technologies like mid-infra-red spectra are increasingly available. Data from claw trimmers, labs, bulk milk from dairies, data from slaughterhouses and animal health organisations are partly centrally available. Presently, there is little communication between the new systems provided by the technology providers.

However, these data reside often in isolated silos along the value chain from production to the consumer with no or little communication across the chain. As of now, the potential of these systems in regard to efficiency or optimised tools has therefore been barely exploited. It follows that there is an urgent need for data linkage.

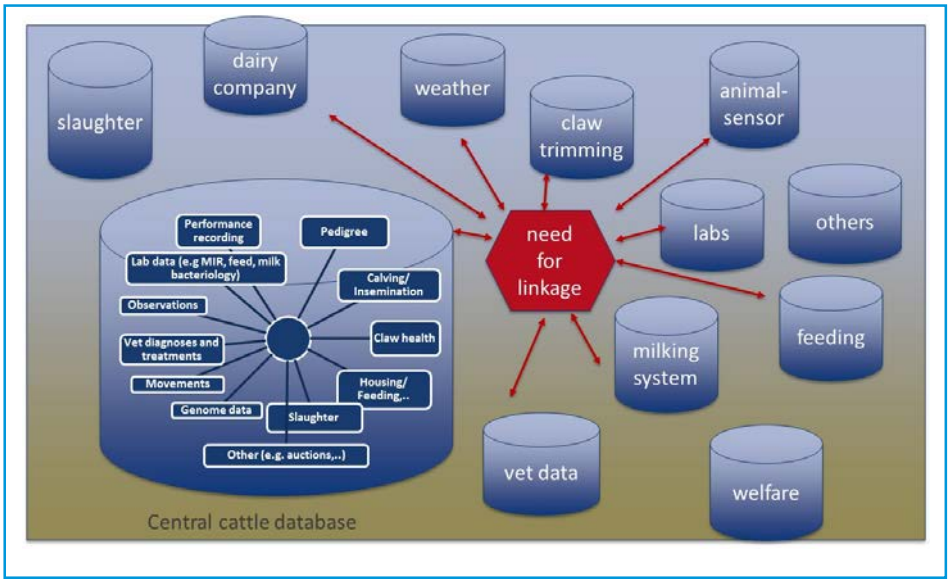

Figure 1. Overview over data sources within dairy cattle husbandry.

Opportunities

Due to recent technological advances, many novel phenotypes are coming up. Sensors measure activity in terms of lying or eating times, rumination and ph-values in the rumen, etc. Stangaferro *et al.* 2016 showed that based on reduction of rumination time ketosis can be predicted already 5 days in advance. The detection rate in this study was 91%.

A high level of data integration offers new possibilities of advanced methods of analysing data. Rutten *et al.* 2013 pointed out that so far little communication is between existing data streams and sensor systems. The potential of integrating various data sources (herd information, environment, economic aspects, etc.) to generate advice based on decision support tools is highlighted. If various data streams (ranging from the level of animals over herds to the environment, ...) are integrated, advanced statistical approaches are often required to make datasets captured across multiple scales of space and time “talk to each other” (Kivelä *et al.*, 2014). Approaches that computationally derive multi-layer networks from separate datasets can indeed

disentangle causative relationships for diseases (Klimek *et al*., 2015). These networks serve as highly context-dependent book-keeping systems on what gene, metabolic pathway, or toxicogenomic substance interacts with which other for how long, how strong, and under which conditions in order to learn more about disease-causing relationships, going beyond mere correlations (Zanin *et al*., 2017). Beside more insight in risk factors and reasons for diseases, the new information is also expected to be more effective in genetic improvement of low heritable traits like health traits. The new information available almost in real time offers also now possibilities for decision support and monitoring of animal health and animal welfare.

There is the need to collect data, to integrate it and generate information, to analyse and generate knowledge and finally to provide support for decisions to farmers and other stakeholders that their action will result in better animal health, welfare and more sustainability (Figure 2). Process optimisation becomes possible when systems are communicating and exchanging information. For instance, optimised feeding will result in cost saving as well as more efficiency and sustainability in production. Beside better tools, a key factor is the reduction of work load for the farmer.

Figure 2. From data collection to decision support to improve animal health, welfare and sustainability.

Challenges

Interoperability of systems

Many different hardware and software systems underlying different standards and parameter definitions, leveraging different technologies and proprietary data analysis methods are available worldwide. The challenge is that this information has to be recoded in the right time in the right place. Moreover, it needs to be available without violating data privacy, transparency and data protection concerns of farmers, technology providers and data users. The key approach to overcome these challenges is by means of data sharing platforms. Examples of the state-of-the-art data exchange platforms are Nordic Cattle Data Exchange, JoinData or 365 Farmnet and others (Papst *et al*. 2019). To use these systems and truly benefit from the functionalities they offer the data providers and farmers need to develop trust in these technologies.

Data integration and data communication

The challenge with regard to data integration and data communication is beside the technical network also the harmonisation of data to address the issues of different data formats ("36 C" vs. "100100 Celsius"), data meaning and interpretation ("36 C" vs. "96.8 F"), and data quality ("36 C" vs "36.7 C"). The main challenge is to get access to the data. The question of data protection plays an important role, but also serves business and privacy interests (Römer, 2018). Standardization initiatives by ICAR are crucially important to address these challenges above and to reduce the redundant work of all involved partners. It is particularly important that the developed standards are used in practice!

Comparability of results / Standardisation

To meaningfully combine the data from different sources the key question is whether e.g., the results from different labs are comparable, and the results from different sensors are comparable. The study on harmonisation of bacteriological findings (Obritzhauser *et al.* 2019) revealed the importance of harmonisation of various steps in the lab processes to ensure comparability of the results. Harmonised coding is one issue but the source of the trait definition needs to be taken into account as well.

Data privacy protection

Another challenge of data integration from different sources is compliance with legal data protection regulations, since this is often associated with a lack of clarity in practice. Cooperation between different partners and integrating different data is the precondition for successfully applying advanced data technologies based on complex trait definitions.

Within the COMET-project D4Dairy the mentioned challenges and possibilities are approached and solutions for various examples are being developed.

Project D4Dairy

D4Dairy's overall goal is to provide digital support to dairy management via a data-driven, networked information system, exploiting the potential of advanced technologies and advanced data analysis (mid-infra-red spectra, genome information, etc.) to further improve animal health, nutrition, animal welfare and product quality. Based on the COMET-project ADDA the existing network along the milk value chain was extended by technology providers and science partners with the focus on new technologies to the D4Dairy consortium. In D4Dairy, 13 scientific partners and more than 30 industrial partners are working together towards common goals. The project duration is 4 years ending in 30.9.2022 with a budget of 5,5 million Euro.

The 4D Concept

Digitalisation: Optimisation of dairy industry production processes along the value chain with the exploitation of new digital possibilities.

Data Integration: Integration of farm data (central cattle database system, sensors, automated feeding systems, housing climate) and further integration of external data (e.g. slaughter data) with the aim of developing meaningful herd management tools for prevention and production control, quality assurance and workload reduction.

Detection: The application of new methods (big data analyses, results from MIR milk spectral data, antimicrobial resistance analyses) enables risk factors and informative parameters to be investigated and derived for early detection of diseases and/or treatment efficacy.

Decision support: Data-based decision support tools are developed, e.g. whether or not an animal should be dried off with antibiotics. Data on the pathogen status at the farm, disease history of the animal, environmental factors, ... are processed electronically and a proposal, e.g. for vets, is prepared.

The project is organized in 2 areas and 9 subprojects where research is based mainly on a common dataset based on 100 farms with a high level of automation. Precondition for sharing data for the respective research question is trust of the farmers and involved data providers. Transparent legal arrangements and the accompanied technical solutions are the base for data driven research in the project. An overview of the research topics is given in Figure 3. More detailed information can be assessed under *www.d4dairy.com.*

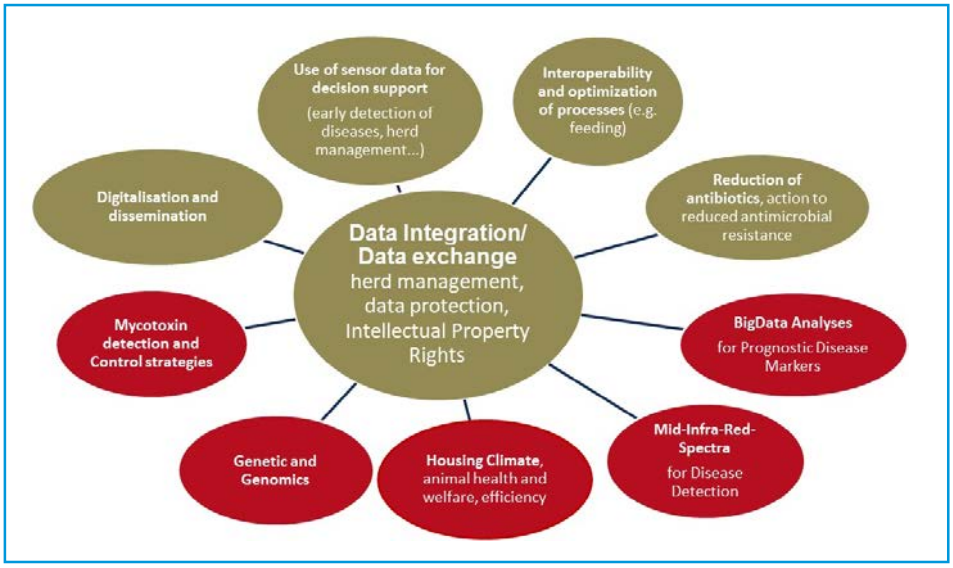

Figure 3. Overview of the main research topics within the D4Dairy project.

Conclusions

There are many new opportunities due to technological advances with the expectation to get better and more efficient tools for prevention, early detection as well as improving animal health, welfare and efficiency in general. Communication between systems can improve the benefit of these technologies for the farmer. Farmers do expect communication between systems while taking privacy and data protection seriously. The technical challenges due to interoperability of the systems, data exchange, and data harmonisation in the context of business interests of the involved parties and data protection regulations need to be solved to exploit the opportunities and benefits of Big Data analysis.

Multi-actor approaches are important. The key to success is a win-win cooperation with shared benefit. The overall aim is that „Internet of Cows" will benefit the farmer and the community by improving health, welfare and sustainability in dairying.

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Breeding for improved feed efficiency and reduced enteric methane of dairy cattle

Y. de Haas and R.F. Veerkamp

Animal Breeding and Genomics of Wageningen University and Research, P.O. Box 338, 6700 AH Wageningen, the Netherlands
Corresponding Author: Yvette.deHaas@wur.nl

With the successful incorporation of genomic information into breeding schemes the reliance on very large populations of phenotyped animals is relaxed. This has opened up opportunities to breed for novel traits, like feed efficiency and enteric methane emissions of dairy cattle, even though a reference population of several thousand animals is still required to estimate the contribution of each genomic region to expression of the phenotype under investigation.

In the Netherlands a breeding value for dry matter intake (DMI) is published since April 2016. A breeding value for feed intake in isolation has its limitations. All it says is something about the amount of feed consumed by a cow, irrespective of what that feed is actually used for. Therefore, a breeding value for feed efficiency is published since December 2017. This breeding value for feed efficiency is defined as 'saved feed costs for maintenance' in order to save on feed not used for milk production, but on maintenance and activity. These breeding values are estimated with a reference population of 5600 dairy cows, of which 2300 are genotyped. The breeding values are based on a combination of direct feed intake records, predictor traits (e.g., milk yield and live weight) and genomic predictions. Current reliabilities of the breeding values for sires are ~60%. The current aims are:

1. to improve the accuracy of genomic prediction, and
2. to record feed intake on more daughters, so that the predictor traits become less important.

By combining data of multiple countries we demonstrated that using dairy cattle DMI phenotypes and genotypes from multiple populations increased the accuracy of the genomic prediction, but to enlarge this joint dataset further, it is needed to extend it beyond research collaborations. A business model and clear agreements are required for this. The business model is under discussion with the ICAR Feed&Gas Working Group, amongst others, and encompass aspects of amount of data to be shared, and efforts in collecting new feed intake records.

In order to be able to estimate breeding values for enteric methane emissions of dairy cattle in the near future, we are currently recording individual methane emissions on 15 commercial farms in the Netherlands, of which all cows are genotyped. Next steps are:

1. to compare methane emissions of these different farms and identify factors causing these differences, and
2. to estimate genetic parameters for enteric methane; heritability and genetic correlations with production, health, fertility and longevity.

With the experiences in METHAGENE we will then also be able to combine this database with other international databases in order to improve the power of the analyses and increase the accuracy of the genomic predictions. Most likely the first breeding value will also be based on a combination of direct records, predictor traits and genomic predictions.

Impact of genomic selection on organisational structures in milk recording and breeding

R. Reents and S. Rensing

IT Solutions for Animal Production, vit, Verden Germany
Corresponding Authors: Reinhard.reents@vit.de, stefan.rensing@vit.de

Summary

In the last decade genomic selection has become a standard tool in Holstein breeding in major dairy countries. Within this time period genomic breeding values (GEBV) based on bull reference populations have become the dominant base for selection within the breeding programs. Use of GEBV enables effective selection of young animals and thus generation interval in sire to son path has been significantly reduced from 6 to 2 years and the dam to son frm 4 to 2 years, respectively. Because of the genetic superiority of young AI bulls their market share in most countries is more than 50% some reaching 98%. In most European countries number of new AI bulls introduced to the market dropped by 50% or more compared to number of bulls in the former progeny-test program. These new opportunities have led to fewer Holstein breeding programs through mergers or acquisitions of organisations.

So far milk performance testing organizations have been less affected by genomic selection. This may change with the current development of moving from the bull to cow or mixed reference populations mainly for the purpose of establishing genomic selection for new traits. On average, 3-8 reference cows (genotyped cow with phenotypic information) are as informative as one genotyped reference bull with phenotypic data of 100 (not genotyped) daughters included in traditional genetic evaluation. For an informative cow reference population, therefore, only a small proportion of all cows under milk recording would be needed. In parallel genotyping has become cheaper and a whole-herd genotyping as base for genomic herd management has become a new tool for commercial dairy herds. In future, the breeding programs may rely increasingly more on data from herds in the whole-herd genotyping program than the complete national milk recording program. Especially for new traits of economic importance these herds with genotyped cows will contribute the data on the new traits. Overall, these developments detangle the traditional strong link and synergy effects of breeding and nation wide milk recording.

The very dynamic developments in on-farm data recording by sensors have the potential for further breaking down the traditional relationship between dairy farmers, DHI and breeding organizations. Data are collected on farm continuously by sensors and information for daily herd management is provided by apps from the sensor providers. For breeding or genomic herd management the dairy farmer is interested in GEBV of his animals. At the same time the breeding program and genomic evaluation system, could be interested in the sensor data for extending the reference population. Therefore, it is crucial for the future of DHI organizations to find its role in providing management services for farmers but at the same time be part of the collection of new phenotypes for selection. These developments may also change the traditional nation-wide genetic evaluation i.e. breeding structures. Relatively few well equipped (big) farms could provide sufficient reference cows for effective genomic evaluation. This could enable main players in the dairy breeding market establish an own genomic evaluation system apart from the national genomic evaluation.

Innovative tools for phenotypic characterization and genetic improvement of meat quality in the Piemontese breed

S. Savoia[1,2,3], G. Bittante[2] and A. Albera[3]

[1]Interbull Centre, Department of Animal Breeding and Genetic, SLU, Uppsala, Swede
Corresponding author: simone.savoia@slu.se
[2]Department of Agronomy, food, natural resourses, animals and environment (DAFNAE), University of Padova, Legnaro (PD), Italy
[3]Associazione Nazionale Allevatori dei Bovini di Razza Piemontese (Anaborapi), Carrù (CN), Italy

Abstract

The aims of this study were: to predict meat quality traits (pH, color, purge and cooking losses, shear force) of Piemontese young bulls comparing two portable spectrometers (Micro-NIRS and Vis-NIRS); to estimate genetic parameters for measured meat quality traits and their predictions; to assess the possibility of the improvement of meat quality traits by genomics.

The study was carried out sampling 1,327 Piemontese young bulls, all registered in the Italian Piemontese Herdbook. Twenty-four hours after slaughter, absorbance spectra were collected directly at the abattoir with two very different portable spectrometers after the division of carcasses in two quarters on the exposed *Longissimus thoracis* muscle. Then, individual samples of the *Longissimus thoracis* muscle were collected between the fifth and sixth thoracic vertebrae and transferred to the laboratory. After 8 d of ageing physical attributes of meat samples were assessed by measurement of lightness, redness, yellowness, pH, purge losses, cooking losses and Warner Bratzler shear force. All young bulls were genotyped with the “GeneSeek Genomic Profiler Bovine LD” array containing 30,111 SNPs.

Micro-NIRS and Vis-NIRS predicted colour traits and purge losses satisfactorily, whereas pH, cooking losses and shear force predictabilities were rather poor, as a consequence of the large slaughter batch and residual variances affecting reference analyses. All the predicted traits, except shear force, showed moderate heritabilities and were highly genetically correlated with measured traits, allowing their use for selection purposes. The very simple, small, and cheap spectrometer (Micro-NIRS) yielded results not much inferior to the reference one (Vis-NIRS).

The accuracy of prediction of genomic breeding values was large enough, ranging from 0.216 (pH) to 0.380 (shear force), to consider genomic selection as a valid tool to improve meat quality traits in the Piemontese breed.

The general results indicate that the genetic improvement of meat quality traits which are difficult to select with traditional methodologies could take advantage from the application of new phenotyping technologies, such as Vis-NIR sprectroscopy, and by genomics.

Key words: Portable Near-infrared spectrometers, Genomics, Meat quality, Piedmontese.

Introduction

A selection programme for meat quality traits could be better established if easy routine phenotypes recording, directly at the slaughterhouse and without samples collection, is possible.

Portable Visible and Near infrared (Vis-NIR) spectrometers, allowing rapid and frequent measurements, fast and simple or no sample preparation, suitable for on-line use and simultaneous determination of different attributes (Prevolnik *et al.*, 2004), offer a number of important advantages over conventional laboratory instrumental analysis for phenotypes collection of meat quality traits. From a genetic point of view, beside calibration parameters, heritabilities of predicted traits and their genetic correlations with reference analyses must be investigated to determining the effectiveness of their use as indicator traits for selective breeding.

As alternative to large scale phenotypes collection and traditional breeding values estimation, genomic selection (Meuwissen *et al.*, 2001) can be considered an innovative tool for the genetic improvement of meat quality.

The main aim of this study was then to perform a comprehensive investigation of the possibility for the improvement of meat quality traits in the Piemontese breed, focusing on the application of innovative tools as portable Vis-NIR spectrometers and genomics.

Material and methods

Data collection

The study was carried out on 1,327 Piemontese young bulls. Animals were fattened in 135 farms and slaughtered at the same commercial abattoir (Operti, Centallo [CN], Italy) from April 2015 to February 2017. The young bulls selected were sired by 204 artificial insemination purebred sires on 1,286 dams, all registered in the Italian Piemontese Herd Book. The beef farming systems, feeding regimes, fattening conditions and slaughter performances of the young bulls are described in detail in Savoia *et al.* (2019a). Twenty-four hours after slaughter, Vis-NIRS spectra were collected directly at the abattoir with two different portable spectrometers (Vis-NIRS: wavelength: 350 to 1,830 nm measured every 1 nm 1,481 data points per sample, weight 5,600g; Micro-NIRS: 905 to 1,649 nm measured every 6 nm 125 data points per sample, weight 60g), after the division of carcasses in two quarters on the exposed *Longissimus thoracis* muscle. Then, individual samples of the *Longissimus thoracis* muscle were collected between the fifth and sixth thoracic vertebrae and transferred to the laboratory. The collection, ageing and laboratory analyses of beef samples are described in detail in a previously published work (Savoia *et al.*, 2019a). Briefly, after 8 d of ageing physical attributes of meat samples were assessed by measurement of lightness (L*), redness (a*), yellowness (b*), pH, purge losses (PL), cooking losses (CL) and Warner Bratzler shear force (WBSF, N).

The 1,327 Piemontese young bulls were genotyped by using the array “GeneSeek Genomic Profiler Bovine LD” (GGP Bovine LD) containing 30,111 SNP. Quality control was performed both on SNP markers and animals.

Statistical analyses

A Bayesian model (Bayes B) implemented in the BGLR library of the R software (Pèrez and De Los Campos, 2014) was used to develop calibration equations for each beef quality trait as described by Ferragina *et al.* (2015). As Savoia *et al.* (2019a) reported that the most important source of variation of meat quality traits was the sample batch (animals slaughtered on the same date, the meats aged together and analyzed on the

same day), external validation was carried out. This was done by predicting the observations for all the animals slaughtered on a given batch from the regression equations developed using the data from all the other batches, and repeating this procedure for every slaughter batch. Determination coefficients, calculated as the square of the correlation between the observed and predicted values in the calibration set (R^2_{CAL}) and in the external-validation set (R^2_{EXT}), were used to evaluate the accuracy of the predictions. For each of the meat quality traits, estimation of (co)variance components was performed using the VCE software (version 6.0, Groeneveld *et al.*, 2010) through separate bivariate analyses including the measured trait and its prediction obtained by Vis-NIR or Micro-NIR spectrometers, respectively. In matrix notation, the 2-traits statistical model utilized can be written as:

$$y = X\beta + W1c + W2q + Zu + e$$

where y contains observations for measure trait and NIRS pred ictions, β is the vector of non-genetic fixed effects, c is the vector of random herd effects (98 levels), q is the vector of random effect of slaughter batch (106 levels), u is the vector of animal additive genetic effects, e is the vector of random residual effects, and X, W1, W2 and Z are incidence matrices of proper dimensions. Except for shear force, for all meat quality traits the model included the effect of carcass weight. For pH and for L* the model included also parity of dam effect and age at slaughter effects. To facilitate comparisons with literature estimates, we estimated intraherd heritability defined as:

$$h^2 = \sigma^2_a/(\sigma^2_a + \sigma^2_e)$$

where σ^2_a is the additive genetic variance and σ^2_e is the residual variance.

Meat quality phenotypes were pre-corrected for all the non-genetic effects and used as dependent variables in a SNP-BLUP model (GS3 software by Legarra *et al.*, 2016). For each trait, the entire data-set was randomly splitted into training population (80% of animals) and validation population (20% of animals), for 15 times. Using the estimated SNP effects, direct genomic breeding values (DGV) were calculated for the young bulls in the validation populations. To evaluate the prediction ability of DGV, the mean of the correlation coefficient between pre-corrected phenotypes and DGV of validation populations, divided by the square root of the heritability (h) of the trait (Pryce *et al.*, 2012), was used.

Results and discussion

The prediction abilities obtained for color traits with Vis-NIRS (R^2_{CAL} 0.62 to 0.88) and Micro-NIRS (R^2_{CAL} 0.51 to 0.81) were similar to those obtained by Cecchinato *et al.* (2011) in a previous study on Piemontese young bulls. For pH, the R^2_{CAL} (0.57 with Vis-NIRS and 0.30 with Micro-NIRS) was lower than most of the literature reports (Prieto *et al.*, 2008; De Marchi *et al.*, 2013) while the low R^2_{CAL} values for purge and cooking losses found in our study were in the range of the published literature (Andres *et al.*, 2008; Leroy *et al.*, 2003) and slightly higher than the findings of Cecchinato *et al.* (2011). The accuracy of NIRS prediction of meat shear force was also very limited (R^2_{CAL} 0.34 for the Vis-NIRS, and 0.16 for the Micro-NIRS). As expected, the R^2_{EXT} obtained were always smaller than R^2_{CAL}, and ranged from 0.52 to 0.80 for colour traits while were lower than 0.32 for the other meat quality traits. The results reveal that the ability of portable or hand-held spectrometers to predict meat quality traits in the abattoir is comparable to that of bench-top instruments in laboratory conditions, and the two portable spectrometers compared in this study, although very different in their suitability for practical use in the abattoir, produced similar results in terms of prediction accuracy in the external validation.

Table 1. Descriptive statistics of reference Piemontese beef quality traits and performance of their prediction by Vis-NIRS and Micro-NIRS instruments.

Item	Color traits:			Meat pH	Meat losses (%):		Shear force
	L*	a*	b*		Purge	Cooking	(N/cm^2)
Carcasses, N	1147	1148	1150	1144	1146	1157	1147
Descriptive statistics							
Mean	39.89	28.59	9.66	5.55	4.51	16.75	27.16
SD	3.49	1.74	1.66	0.05	1.19	3.43	9.61
Vis-NIRS							
R^2_{CAL}	0.88	0.62	0.70	0.57	0.29	0.26	0.34
R^2_{EXT}	0.78	0.55	0.63	0.30	0.31	0.16	0.16
RMSE-$_{EXT}$	1.43	1.22	1.06	0.05	1.05	3.36	10.69
Micro-NIRS							
R^2_{CAL}	0.81	0.51	0.63	0.30	0.20	0.10	0.16
R^2_{EXT}	0.80	0.52	0.61	0.22	0.27	0.19	0.19
RMSE-$_{EXT}$	1.67	1.23	1.04	0.05	1.07	3.20	10.69

Table 2. Variance components and intraherd heritability of colour traits measured with laboratory analyses and their predictions by Vis-NIRS and Micro-NIRS instruments.

	Traits								
	L*			a*			b*		
	Meas.	Vis NIRS	MicroN IRS	Meas.	Vis NIRS	MicroN IRS	Meas.	Vis NIRS	Micro NIRS
Phenotypic variance	11.64	9.96	9,74	3.12	1.83	1.52	2.79	1.88	1.67
Variance components[1]									
Additive genetic	0.23	0.32	0.28	0.09	0.04	0.04	0.10	0.02	0.04
Day of slaughter	0.18	0.15	0.15	0.25	0.31	0.22	0.23	0.26	0.16
Herd	0.06	0.06	0.05	0.11	0.11	0.10	0.08	0.08	0.07
Residual	0.54	0.46	0.52	0.55	0.53	0.64	0.59	0.64	0.73
Intraherd h^2	0.30	0.41	0.35	0.14	0.08	0.07	0.14	0.04	0.05
SE intraherd h^2	0.095	0.104	0.107	0.070	0.066	0.050	0.070	0.044	0.060

[1]ratio to phenotypic variance

Heritability of measured meat quality traits (from 0.13 for purge losses to 0.31 for shear force) was in the range of most literature reports (Johnston *et al.*, 2003; Riley *et al.*, 2003). As shown in Tables 2 and 3, the predictions of meat quality traits by Vis-NIRS and Micro-NIRS displayed heritability values lower than the corresponding traits measured in the laboratory on aged meat samples, with the exception of L* and purge losses. However, heritabilities of meat quality predictions in most of the cases were large enough to be exploited for selection.

The genetic correlations of the measured colour traits and purge losses with both Vis-NIRS and Micro-NIRS predictions were extremely high, and consistent with those reported by Cecchinato *et al.* (2011). However, a superiority of the Vis-NIRS over the Micro-NIRS was observed in the other meat quality traits (pH 0.70 vs 0.45, cooking losses 0.70 vs 0.25 and shear force 0.81 vs 0.42).

Table 3. Variance components and intraherd heritability of meat quality traits measured with laboratory analyses and their predictions by Vis-NIRS and Micro-NIRS instruments.

	Traits											
	pH			Purge Losses, %			Cooking Losses, %			Shear Force, N		
	Meas.	Vis NIRS	Micro NIRS	Meas.	Vis NIRS	Micro NIRS	Meas.	Vis NIRS	Micro NIRS	Meas.	Vis NIRS	Micro NIRS
Phenotypic variance	0.30[3]	0.13[3]	0.06[3]	1.39	0.36	0.28	11.78	2.07	0.57	113.14	23.33	15.41
Variance components[1]												
Additive genetic	0.08	0.08	0.06	0.10	0.17	0.10	0.10	0.03	0.01	0.16	0.00	0.05
Slaughter day	0.61	0.48	0.49	0.14	0.21	0.16	0.42	0.54	0.13	0.42	0.53	0.40
Herd	0.06	0.07	0.05	0.05	0.04	0.15	0.04	0.04	0.03	0.06	0.07	0.07
Residual	0.25	0.37	0.40	0.71	0.58	0.69	0.44	0.40	0.83	0.37	0.41	0.48
Intraherd h^2	0.25	0.18	0.13	0.13	0.22	0.13	0.19	0.07	0.01	0.31	0.00	0.10
SE intraherd h^2	0.087	0.077	0.087	0.072	0.103	0.070	0.085	0.057	0.043	0.097	0.036	0.074

[1] ratio to phenotypic variance
3×10^{-2}

Table 4. Additive genetic correlations of colour and meat quality traits measured with laboratory analyses with their predictions (SE in parentheses) obtained with Vis-NIR and Micro-NIR spectrometers.

Traits	Vis-NIRS	Micro-NIRS
L*	1.000 (0.001)	1.000 (0.001)
a*	0.958 (0.173)	0.783 (0.225)
b*	1.000 (0.001)	0.930 (0.189)
pH	0.701 (0.164)	0.448 (0.256)
Purge Losses, %	0.979 (0.085)	0.879 (0.162)
Cooking Losses, %	0.703 (0.168)	0.248 (0.271)
Shear Force, N	0.805 (0.187)	0.418 (0.316)

Table 5. Accuracies of genomic predictions measured by Pearson's correlation between pre-corrected phenotypes and direct genomic breeding values (r(y,DGV)) divided by the square root of the heritability (h) of the trait and regression coefficient of the pre-corrected phenotypes on direct genomic breeding values (b(y,DGV)) for meat quality traits of Piemontese young bulls based on SNP-BLUP methods.

Trait	n. training	n. validation	r/h	b
L*	910	246	0.324	1.00
a*	910	246	0.290	1.34
b*	909	250	0.357	1.73
pH	915	242	0.231	1.25
Purge Losses, %	905	249	0.305	1.48
Cooking Losses, %	919	247	0.216	1.54
Shear Force, N	897	249	0.380	1.65

The accuracy of genomic predictions was 0.23 for pH, 0.31 for purge losses and 0.22 for cooking losses. Colour traits showed similar accuracies. The highest accuracy was reported for shear force with a value of 0.38. Considering all traits together, the gain of raw accuracy, calculated as the correlation between direct genomic breeding values and pre-correct phenotypes, was associated with an increase of the heritability of the trait as supported by the findings of Bolormaa *et al.*(2013). Except for Lightness, direct genomic breeding values underestimated the pre-corrected phenotypes of animals in validation populations.

Conclusions

Portable and hand-held spectrometers have been tested at the abattoir level on a large number of carcasses. Good results have been obtained for the prediction of colour traits and purge loss, but with less reliable results for meat pH, cooking loss and shear force. The estimated genetic parameters showed that NIRS predictions of colour traits, pH and purge losses can be used as indicator traits of the corresponding

measurements for selection purposes. For cooking losses results were more controversial, while estimates for shear predictions were not reliable. The accuracies reached by genomic breeding values in all the investigated traits suggested that young candidates for selection could be evaluated for meat quality traits using genotype information.

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Nordic breeding values for beef breed sires used for crossbreeding with dairy dams

E. Carlén[1], W.F. Fikse[1], R.B. Davis[2], J. Pösö[3] and G.P. Aamand[4]

[1]Växa Sverige, Box 288, 75105 Uppsala, Sweden
Corresponding Author: Emma.Carlen@vxa.se
[2]SEGES Cattle, Agro Food Park 15, 8200 Aarhus N, Denmark
[3]Faba co-op, P.O. BOX 40, FIN-01301 Vantaa, Finland
[4]Nordic Cattle Genetic Evaluation; Agro Food Park 15, 8200 Aarhus N, Denmark

Abstract

The use of beef semen in dairy herds has increased considerably during the past years in Denmark, Finland and Sweden. This has created a need for the dairy farmers to be able to, in the best possible way, select the beef breed sires best suited for crossbreeding with dairy cattle. Nordic Cattle Genetic Evaluation has developed joint Nordic breeding values that will aid farmers in their choice of the right beef sires to use on their dairy cows. An important feature of the breeding values is that they are comparable across sire breed and country of origin. Breeding values are currently estimated for seven traits belonging to one of two trait groups: calving and carcass traits. This paper describes the new beef × dairy evaluation that gives the Nordic dairy farmers a better possibility for a profitable production of beef × dairy crossbred animals.

Keywords: crossbreeding, genetic evaluation, calving traits, carcass traits.

Introduction

In the last decade there has been a large increase in the use of beef semen in dairy cattle herds in both Denmark, Finland and Sweden. The strategy of inseminating dairy cows not needed to produce replacement heifers with beef semen has several advantages for the profitability of the dairy farms. Combining this strategy with other modern breeding tools at herd level such as the use of sexed semen and genomic breeding values has been proven efficient (Ettema *et al.*, 2007) and is expected to increase even further in the future.

Nordic Cattle Genetic Evaluation (NAV) has for more than 10 years run a joint genetic evaluation and breeding goal for the dairy breeds Red dairy cattle (RDC), Holstein and Jersey in Denmark, Finland and Sweden (http://www.nordicebv.info/about-nav). More recently the cooperation has been extended to also develop joint evaluations for beef breeds; both for beef breed sires used on dairy cattle and for pure breeding. Due to the rapidly increased use of beef semen in dairy herds, it was of high priority to develop breeding values for beef breed AI-bulls based on their beef × dairy crossbred offspring (in this paper referred to as beef × dairy evaluation). The new breeding values make it possible for the Nordic dairy farmers to select the beef breed sires that produce the economically best crossbred calves, that is calves that are easily born and with a high growth capacity and carcass quality. An important feature of the evaluation is that all beef bulls are comparable across sire breed, dam breed and country.

The aim of this paper is to describe the newly developed joint Nordic beef × dairy evaluation, including available data and its structure, trait definitions, evaluation model and results. Further, a brief status of future developments for the beef × dairy evaluation is given.

Material and methods

The national cattle data bases in Denmark, Finland and Sweden contain most important information on both purebred and crossbred animals such as pedigree, production results and inseminations. In the beef × dairy evaluation, we include all crossbred calves born in the three countries from 2000 and onwards if they are:

1. After a purebred dairy dam of the breed RDC, Holstein or Jersey.
2. After a purebred beef breed AI-sire of one of the major beef breeds in our countries and
3. Born on a milk producing herd. Beef sire breeds considered were Belgian Blue (BBL), Blonde d'Aquitaine (BAQ), Aberdeen Angus (AAN), Limousin (LIM), Charolais (CHA), beef Simmental (BSM) and Hereford (HER).

There has been an increase in the use of beef semen in dairy herds in both Denmark, Finland and Sweden (Figure 1). However, the number of beef × dairy crossbred calves as well as the trend over years differs between countries. By tradition, Finland has used more beef semen in dairy herds than the other countries. The most rapid increase in the last decade has however been observed in Denmark. In the August 2019 evaluation, calving records from 714 380 beef × dairy crossbred calves were included. The corresponding number for the carcass traits was 273 417.

Data structure

The distribution of sire breeds has varied much over time. Figure 2 displays the proportion of the crossbred calves, across all countries, after the major beef sire breeds. Considering crossbred calves born in 2018, the majority have either a BBL (41%) or BAQ (28%) sire. The remaining calves are more evenly distributed on the other sire breeds, and none of them exceeding 10%.

The use of sire breeds however differs across countries. Again, considering crossbred calves in 2018, BBL was the dominating breed used in Danish dairy herds (accounts for over 80% of Danish crossbred calves). BAQ sires are especially used in Finnish dairy herds and this breed has increased in popularity over recent years (currently it accounts for around 50% of Finnish crossbred calves). In Sweden, on the other hand, there is a more equal use of the remaining sire breeds (BSM, HER, CHA, LIM and AAN each accounting for about 30 to 15% of the Swedish crossbred calves). Another difference between countries in the use of beef semen in dairy herds is that Sweden to a larger extend uses beef semen on heifers. However, the great majority of inseminations of beef on dairy cows are on cows in all three countries.

The connection between sire breeds is good since many of the dairy herds use several beef sires per year and also beef sires of different breeds. Furthermore, all beef breeds are used on all dam breeds. This enables a fair comparison of beef bulls across breed. Table 1 illustrates that connectedness between beef sire breeds by listing the number of common herd-years by sire breed for multiparous cows. An exception from the use of several beef breeds per year occurs in some Danish herds where only BBL sires have been used.

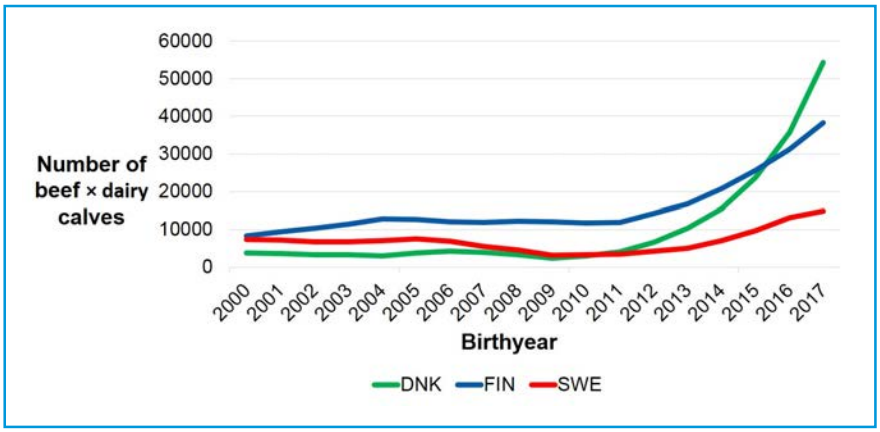

Figure 1. Number of beef × dairy crossbred calves born in Denmark, Finland and Sweden from year 2000 and onwards.

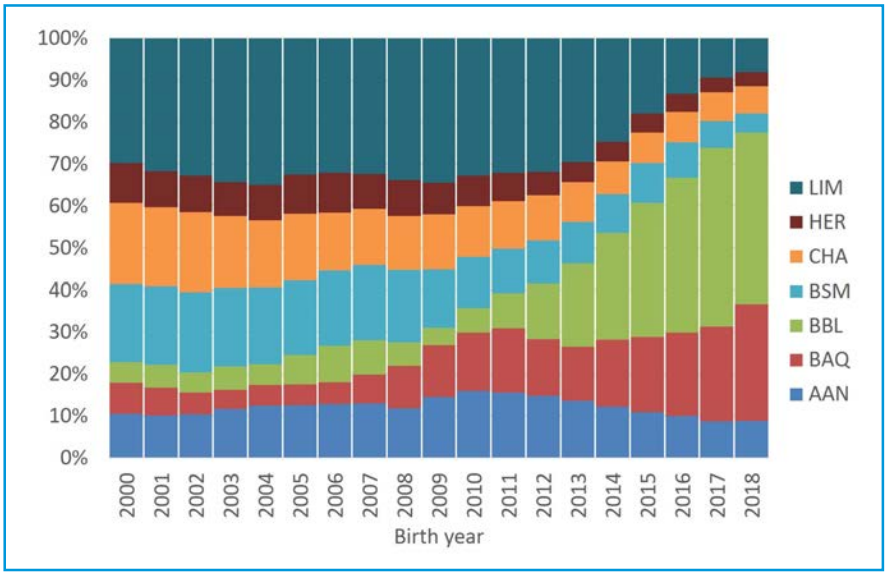

Figure 2. The distribution of sire breeds for beef × dairy crossbreeds born between 2000 and 2018. Aberdeen Angus (AAN), Blonde d'Aquitaine (BAQ), Belgian Blue (BBL), beef Simmental (BSM), Charolais (CHA), Hereford (HER) and Limousin (LIM).

Another difference between the countries is related to the rearing system of animals for slaughter, which affects the average age at slaughter for both males and females (Figure 3). In Denmark, all crossbred calves are reared more intensively with an average age at slaughter below 550 days (18 months) for both males and females. In Finland and Sweden, on the other hand, the rearing period is longer and more extensive with an average age at slaughter above 550 days. In Finland, females are slaughtered at an earlier age, whereas in Sweden the opposite is true. In Denmark there is no clear sex difference for age at slaughter. The differences in rearing systems, explained by differences in pricing systems between countries, are important to consider and they have affected the trait definitions in the beef × dairy evaluation.

Table 1. Cross table of common herd-years by sire breed for multiparous cows.

Sire breed	BAQ*	BBL	BSM	CHA	HER	LIM
AAN	4673	162	3393	2967	2583	8446
BAQ		387	3589	3602	1423	8996
BBL			623	444	55	1302
BSM				5028	2679	7936
CHA					2643	7414
HER						3852

*AAN: Aberdeen Angus; BAQ: Blonde d'Aquitaine; BBL: Belgian Blue; BSM: beef Simmental; CHA: Charolais; HER: Hereford; LIM = Limousin.

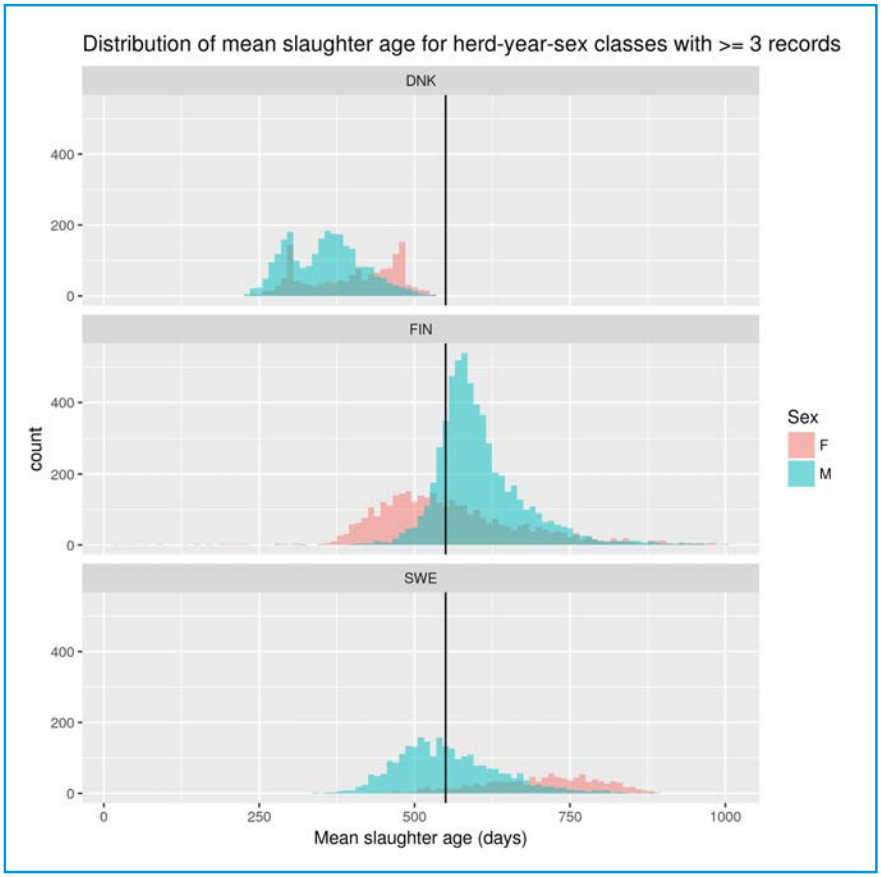

Figure 3. Distribution of mean slaughter age (days), by country and sex.

Trait definitions

In the Nordic beef × dairy evaluation, there are in total seven breeding values published from two trait groups.

The calving evaluation has a core of four traits recorded in all three countries: calf survival and calving ease based on cows in 1st and later lactations, respectively. Calf survival is defined as calves born alive and still alive 24 hours after birth. Calving ease is also scored according to international standards on a scale 1(easiest) to 4 (most difficult). The reason for treating records from first and later lactation as genetically different traits is that the genetic correlation is generally different from one (e.g. Eriksson

et al., 2004). Information of calf size is used as an indicator trait in the evaluation (data only available from Denmark). Calf size is a subjective assessment made by the farmer and is scored in four categories from small to big.

The carcass evaluation is based on slaughterhouse records, comprised of cold carcass weight and EUROP scores for carcass conformation and carcass fat (both scored in 15 categories) for slaughtered animals. Age at slaughter is calculated as the difference between date of slaughter and date of birth. The trait carcass daily gain (kg/day) is calculated as the difference between cold carcass weight and half the birth weight, divided by age at slaughter (in days). Individual birth weight records are not available, and tabulated breed averages are used.

About 60% of the slaughter records are for male beef × dairy crossbreds, and the other 40% pertain to females. Growth and carcass traits in males and females are treated as genetically different but correlated traits. This is done to account for differences between males and females in phenotypic variances of growth and carcass traits, and because the genetic background of these traits is slightly different between sexes.

Rearing practices and targets for slaughter weight differ substantially between the three countries, resulting in rather different average slaughter ages. As the growth typically follows a sigmoid curve, the trait carcass daily gain was split into two traits, carcass daily gain for short and long rearing period, to ease modeling of the trait.

Genetic evaluation model

Two multiple-trait linear sire models, one for calving traits and one for carcass traits, are used in the Nordic beef × dairy evaluation.

Fixed effects

- Sire beef breed.
- Herd-year of calving/slaughter .
- Country-year-month of calving.
- Age of dam at calving/age of crossbred animal at slaughter.
- Dam breed-year.

Random effects

- Genetic effect of sire.

Comments to the models

The effect of sire beef breed is to adjust for systematic sire breed differences. The breed effect is added back to the individual sire solutions to get the final breeding value of a bull. The dam breed-year effect is included to account for the fact that we have three different dam breeds with different genetic levels (and trends) over the years.

Beef sires are only evaluated for the direct genetic effect. The maternal genetic effects that are usually included in the analyses of calving traits are not included here as it is assumed that crossbred animals are only produced for slaughter and not to be used as suckler cows. Maternal effects expressed by dairy dams are modelled through the dam breed effect.

Variance components were estimated from the complete dataset. Variance components and breeding values were estimated using the DMU software package (Madsen and Jensen, 2008).

Publication of breeding values

Four breeding values are published for calving traits: calf survival in first and later lactations and calving ease in first and later lactations. These breeding values are published if the bull has a minimum reliability of 50 for breeding value for calf survival or stillbirth in later lactations.

For carcass traits, three combined breeding values are published: daily carcass gain, carcass conformation score and carcass fat score. Carcass gain is based on combining breeding values for bulls and heifers with short (<550 days) and long fattening periods, respectively, with equal weights. Conformation and fat score are based on combing breeding values for bulls and heifers with equal weights. All three breeding values are published if the bull has a minimum reliability of 50 for breeding value for carcass conformation score.

Breeding values are expressed such that: 1) a recent cohort of beef × dairy crossbreds (born 2-5 years prior to the publication date) have an average sire breeding value equal to 100, and 2) the genetic variance on the published scale is equal to 10. This expression of breeding values follows that for breeding values of dairy bulls; we chose this practice as the target users of the Beef × Dairy breeding values, the dairy producers, are familiar with it.

Results and discussion

Genetic parameters

Estimated heritabilities for calving traits were generally low, ranging from 0.01 for calf survival, multiparous cows to 0.11 for calving ease, primiparous cows (Table 2). Calf size had moderately high heritabilities. Estimated genetic correlations among the same trait recorded in primi- versus multiparous cows were around 0.9. The genetic correlations between calf survival and calving ease were moderately high, around 0.6-0.7. By and large, these parameters are similar to the genetic parameters used by NAV in the calving traits evaluation of dairy breeds (NAV, 2019).

Carcass traits were moderately high heritable, with values ranging from 0.2 to 0.4 (Table 3). Genetically, growth for the short and long rearing period appears to be the same, as indicated by a genetic correlation larger than 0.95. The genetic correlation between traits recorded in male and female was high, around 0.8-0.9.

Distribution of breeding values

There is a negative genetic correlation between the calving and carcass traits. Comparing breeds, a similar pattern is observable where breeds good for carcass traits generally are not as good for calving traits. It is apparent that lighter breeds, such as AAN, have higher average breeding values, compared to the heavier breeds,

Table 2. Genetic parameters for calving traits; estimated heritabilities on the diagonal and estimated genetic correlations on the off-diagonals.

	CSu1*	CSu2+	CE1	CE2+	CSi1	CSi2+
CS1	**0.049**	0.88	0.70	0.67	0.80	0.58
CS2+		**0.013**	0.61	0.62	0.53	0.43
CE1			**0.114**	0.97	0.89	0.93
CE2+				**0.049**	0.80	0.84
CS1					**0.171**	0.83
CS2+						**0.091**

* CSu1, CSu2+ : calf survival in first respectively later parities; CE1, CE2+ : calving easy in first respectively later parities; CSi1, CSi2+: calf size in first respectively later parities.

Table 3. Genetic parameters for carcass traits; estimated heritabilities on the diagonal and estimated genetic correlations on the off-diagonals.

	dgs, ♂[1]	dgl ♂	bcs, ♂	fats, ♂	dgs, ♀	dgl, ♀	bcs, ♀	fats, ♀
dgs, ♂	**0.19**	0.97	0.30	-0.21	0.83	0.86	0.22	-0.27
dgl, ♂		**0.21**	0.34	-0.10	0.85	0.86	0.25	-0.21
bcs, ♂			**0.32**	-0.17	0.31	0.24	0.92	-0.12
fats, ♂				**0.23**	-0.20	-0.13	-0.19	0.88
dgs, ♀					**0.33**	0.97	0.35	-0.30
dgl, ♀						**0.33**	0.25	-0.22
bcs, ♀							**0.36**	-0.18
fats, ♀								**0.25**

[1] Dgs: carcass daily gain, short fattening period; dgl carcass daily gain, long rearing period; bcs: carcass conformation score; fats: carcass fat score; ♂ and ♀ specifies whether it is a trait male respectively female trait.

such as BBL (Figure 4). There is also a large variation within breed for the calving traits. In Figure 5, the distribution of breeding values for carcass daily gain is shown. Here the opposite of the calving traits is apparent, where heavier breeds, such as CHA and BBL, on average have higher breeding values compared to lighter breeds. However, there is large variation within all sire breeds. It is therefore very important that the dairy farmers should look at the breeding values of individual beef sires regardless of breed since there is large variation not only across but also within breed.

The performance of the beef × dairy crossbreds is affected by heterosis. However, a heterosis effect is not included in the model as the data structure (only F1) does not enable separating additive effects from heterosis effects. Thus, the breeding values do include (part of) the heterosis effects. The primary purpose of the beef × dairy evaluation is to chose beef sires such to get the best possible beef × dairy crossbred offspring, meaning that heterosis will be expressed in the future offspring as well. Hence, not accounting for heterosis has no effect when selection beef bull for producing cross breed offspring.

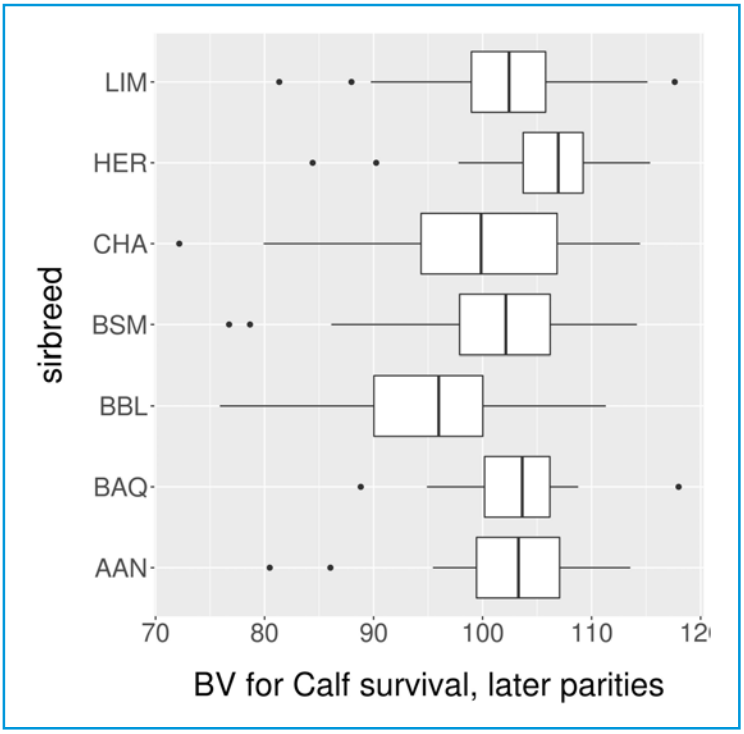

Figure 4. The distribution of breeding values for calf survival in later parities by sire breed: Aberdeen Angus (AAN), Blonde d'Aquitaine (BAQ), Belgian Blue (BBL), beef Simmental (BSM), Charolais (CHA), Hereford (HER) and Limousin (LIM).

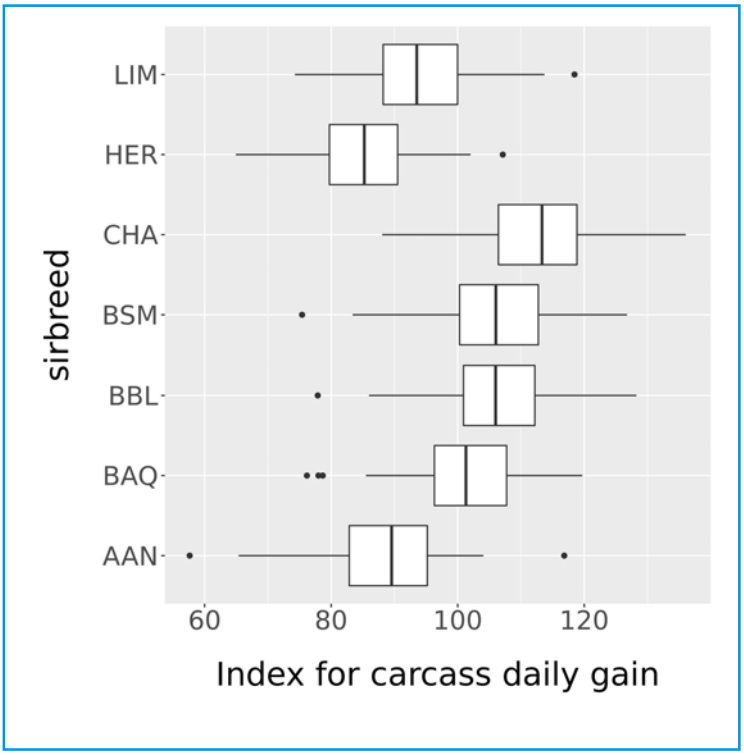

Figure 5. The distribution of the index for carcass daily gain by sire breed: Aberdeen Angus (AAN), Blonde d'Aquitaine (BAQ), Belgian Blue (BBL), beef Simmental (BSM), Charolais (CHA), Hereford (HER) and Limousin (LIM).

Future perspectives

Communication and improved advisory service related to the new beef × dairy breeding values are ongoing activities. To make a more efficient selection tool available for the dairy farmers, development on combining the calving and carcass traits in a total merit index for beef × dairy has been nearly completed. The Nordic beef × dairy index (NBDI) will be implemented in the end of 2019. NBDI will be available for both short and long rearing period since the length of the rearing period has a large impact on the economic weight for growth and carcass traits. In the future, the NBDI can be further improved by including other traits of relevance to the production of crossbred beef × dairy animals.

Furthermore, new traits are currently planned to be developed. The first trait that will be investigated is young stock survival. Breeding values for young stock survival on beef × dairy crossbred calves are already published in Denmark (Davis *et al.*, 2019).

Conclusions

The new breeding values for beef breed sires based on their crossbred beef × dairy offspring was first published by NAV in December 2018. Breeding values are routinely published four times a year. They offer the opportunity for Nordic dairy farmers to select the best beef breed sires across breed to be used for insemination on the dairy cows in their herd. For a profitable production of crossbred animals, it is important to consider both calving and carcass traits. An important message is that the dairy farmer should look at the breeding values of individual beef sires regardless of breed since there is large variation not only across but also within breed.

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A single-step, multiple-trait genomic evaluation model increase the accuracy for suckling performance in beef cows

A. Michenet[1,2], D Boichon[3], R Saintilan[2,4], F Phocas[5] and E Venot[5]

[1]Interbull, Uppsala, Sweden
Corresponding Author : alexis.michenet@slu.se
[2]ALLICE, 149 rue de Bercy, 75012 Paris, France
[3]AURIVA, Les Nauzes, 81580 Soual, France
[4]GenEval, 78350 Jouy en Josas, France
[5]GABI, INRA, AgroParisTech, Université Paris-Saclay, 78350 Jouy en Josas, France

Abstract

Suckling performance of beef cows is of major importance for the income of livestock farmers. This trait is estimated with commercial farm data recording by the maternal genetic effect on weaning weight which is lowly heritable (0.09). In the Blonde d'Aquitaine breed, the breeding program includes a progeny testing station where eight sires are tested each year. Milk yield is recorded by the weigh-suckle-weigh technique on daughters and constitute a heritable (0.40) early selection criterion for bulls intended for artificial insemination. A dataset with 2403 milk yield records collected in station and 137,943 weaning weights from field records was used to genetic parameters in relation with suckling performance. A strong genetic correlation (0.75) was obtained and allowed performing a multiple-trait evaluation model. BLUP animal model and single-step genomic BLUP models were tested and theoretical average accuracies on a population of 813 candidates for selection were compared.

The reference population was made of 1 039 animals phenotyped and genotyped or imputed in 50K SNP density. Best correlations (0.20 to 0.30) were obtained with candidates that were moderately or strongly related to the station reference population. For other cases, accuracies were below 0.15.

The combination of farm and station performance is a good way to increase accuracy of candidate for selection, in particular for animal related to the reference population. The single-step GBLUP including performance from many non-genotyped animals leads to a more efficient use of maternal EBV in beef cattle breeding programs. In the near future, this method associated with an increase of genotyped animals will help to improve breeding choice accuracy and genetic progress.

Introduction

Considering maternal traits in beef cattle selection programs is of major importance because these traits directly impacts the income of the breeders (Roughsedge *et al.*, 2008). It concerns in particular the suckling performance of the cow-calf pair which influences the calf growth and weaning weight (Phocas *et al.*, 1998). The performance record is difficult to establish at farm level and there is a lack of efficient selection tools to improve such traits.

In Blonde d'Aquitaine breed, the French artificial insemination bulls selection program relies on progeny testing in station to evaluate the primiparous daughters' performance, since the mid-eighties. The weigh-suckle-weigh technique applied to the daughters' calves of 8 AI candidates for selection are evaluated for milk yield (MY) each year. Recording phenotypes on testing station following a strict protocol (homogeneous farming conditions, limited number of technicians that record the phenotypes) leads to high heritability estimates (0.35), (Michenet *et al.*, 2016). Moreover, the French official farm indexation allowed evaluating hundreds of natural service bulls for their maternal genetic effects on weaning weight (WW), since the mid-nineties. The heritability of this trait is lower (0.10) because it is a more complex trait accounting for milk quality, maternal and calf behaviours, and impacted a lot by the environmental conditions.

Based on a reference population of 2327 genotyped animals in Blonde d'Aquitaine breed (Venot *et al.*, 2016), the new statistical methodologies provides now solutions to develop efficient genomic selection for these complex traits.

This study was focused on two objectives: the first was to estimate the genetic correlation between maternal weaning weight recorded on farm and milk yield recorded in station, and then the second objective was to assess the interest of a single-step and multiple-trait genomic model for suckling performance to estimate the breeding values for maternal traits the most accurately possible.

Materials and methods

Phenotypes

The weigh-suckle-weigh technique was used to assess the milk yield in progeny testing station (Pabiou, 2005). A total of 2403 females were recorded from 1996 to 2014. Measurements were performed in the morning and evening on the 60th and 120th days after calving. MY was estimated from the weighted average of the 60-day measurement and 120-day measurement, with respective weightings of one-third and two-thirds. The average MY was 5.66 kg, with a standard deviation of 1.46 kg.

These data overlapped farm data since some primiparous daughters recorded in station for MY were recorded on farm for their own weaning weight (WW) and WW of their descendants. The field data considered in this study was collected from the 484 largest herds (contemporary group sizes above 10) out of the 1122 herds of birth for the 2403 females recorded in station. A total of 137,943 WW records were retained for the analysis. The average WW (standardized at 210 days) was 285.4 kg, with a standard deviation of 45.1 kg.

Genotypes

The station reference population was made up of 1155 females recorded for MY from 2005 to 2014. They were genotyped either with the Bovine SNP50 BeadChip® medium-density chip with 54,000 single nucleotide polymorphisms (SNP) (223 females) or the EuroG10K BeadChip® low-density chip with 10,000 SNP (933 females). Among the farm reference population, 1039 animals with weaning weight data collected in the 484 herds of the current study were genotyped as followed: 62 AI sires with the Bovine HD BeadChip®, 650 bulls with the Bovine SNP50 BeadChip® and 327 animals with the EuroG10K BeadChip®. In addition, a population of 813 young candidates for selection were genotyped with the Bovine SNP50 BeadChip®. After quality controls that included a call rate higher than 90% and a Hardy-Weinberg equilibrium test (P-value > 10-4), 43,801 SNP from the medium-density chip were retained, and 7,660

SNP for the low-density chip. A total of 2690 medium-density genotypes were used for the imputation of the female genotypes from low to medium density with BEAGLE 3.3.0 software (Browning and Browning, 2007). Allelic imputation error rates were estimated at 1.3% (Saintilan *et al.*, 2014).

The population of the 813 young bulls candidates for selection only have their own WW recorded on-farm. The birth years of the candidates and the degree of their relationship with the station reference population is described in Figure 1. A kinship analysis was performed to split the candidate population into three categories: 463 male progeny of sires tested on the station which are strongly related to the reference population, 189 candidates having one grandsire tested on the station which are moderately related to the reference population, and the remaining 161 which have a low relationship to the reference population.

Models

As a reference for accuracies of MY and WW, a pedigree BLUP-animal models was performed with univariate analysis. The model for MY only considered the animal breeding values as a random effect. The model for WW performance (y) involved the calf's direct genetic effect, the maternal genetic effect and the permanent environment effect of its dam as follows: $y = X\beta + Z_1u + Z_2m + Z_3p + e$ where **y**, ², **u**, **m**, **p** and ***e*** are the vectors of performance, fixed effect, direct genetic effect, maternal genetic effect, permanent environmental random effect and the residuals of the model. **X**, $\mathbf{Z}_1$, $\mathbf{Z}_2$ and $\mathbf{Z}_3$ are the incidence matrices for ², **u**, **m** and **p** respectively. Hereafter, the direct genetic effect on WW is named WWd and the maternal genetic effect WWm.

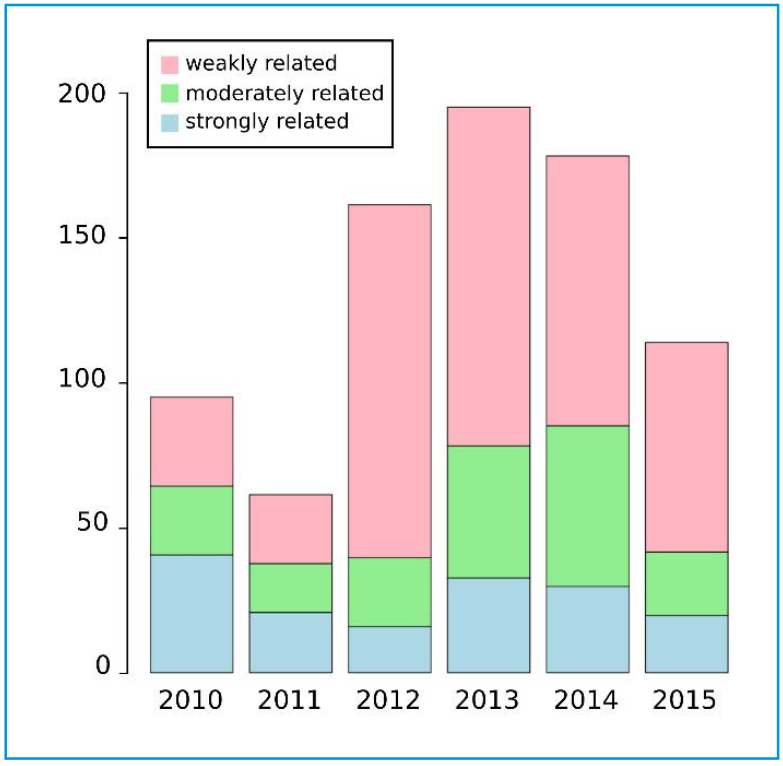

Figure 1. Distribution of the population of candidates for selection according to their birth year and their degree of relationship with the station reference population.

The fixed effects were the contemporary group, whether the calving was assisted (hard pull or caesarian) or not, and the age of the heifer at calving as a covariable for MY. The calf contemporary group (combination of birth year, herd and calf sex), the calf birth season and its dam parity were considered for WW.

The two traits were combined in a multiple-trait pedigree BLUP with maternal effects. A single-step genomic BLUP (ssGBLUP) was used to combine pedigree information for all phenotyped animals and genomic information for the subset of animals with genotypes (Aguilar *et al.* 2010).

A population of 813 young bulls candidate to selection was used to estimate the potential advantage of combining two kinds of phenotypic information for increasing EBV accuracies for suckling performance. Results from the univariate pedigree BLUP were compared to the multiple-trait model pedigree BLUP and ssGBLUP. The BLUPF90 software package (Misztal *et al.*, 2002) was used to estimate genetic parameters by AIREML and to solve pedigree BLUP and ssGBLUP.

Results and discussion

Genetic parameters

With more data and considering an animal model, the heritability estimate of MY was higher (0.41) than the earlier estimate (0.30) from data collected in the same station (Phocas and Sapa, 2004). The study of MacNeil and Mott (2006) also provided a lower heritability of 0.25 for MY recorded in station for 403 Hereford cows. For WWd and Wwm, the heritabilities are in accordance with the estimates obtained in the same breed (Phocas and Laloë, 2004) and also in Hereford (Torres-Vázquez and Spangler, 2016).

A negative genetic correlation (-0.39) was estimated between direct and maternal effects on WW. However, the genetic correlation between WWd and MY was estimated to be null. A strong (0.75) genetic correlation was computed between MY and Wwm, in agreement with the MacNeil and Mott (2006) study. Even if MY is a good estimator of suckling performance, it does not take into account the quality of the milk that could impact WWm. Meyer *et al.* (1994) also showed that MY was the main factor affecting WWm and was not correlated with WWd. Negative genetic correlations between direct and maternal effects on WW are frequently seen in literature (Vargas *et al.*, 2014). These negative estimates are more likely to be statistical artefact rather than a biological antagonism due to the difficulty of estimating covariances without bias in maternal effect models (Robinson *et al.*, 1996, Dodenhoff *et al.*, 1999, Clément *et al.*, 2001).

The study of Michenet *et al.* (2016) highlighted several common quantitative trait loci detected for MY and WWm. These results are in accordance with the strong genetic correlation estimated between the two traits.

Table 1. Heritabilities and genetic correlations of milk yield (MY), direct (WWd) and maternal (WWm) genetic effects on weaning weight.

	MY	WWd	WWm
MY	**0.41** (0.07)[1]	0.01 (0.12)	0.75 (0.10)
WWd		**0.30** (0.02)	-0.39 (0.04)
WWm			**0.09** (0.01)

[1]Heritabilities in bold on the diagonal, genetic correlations above the diagonal (standard errors in brackets)

Accuracy of multiple-trait EBV

A multiple-trait model combining correlated traits is supposed to increase accurracy. On the figure 2, the mean accuracy of the EBV of candidates for selection were plotted for MY and WWm comparing multi-trait model and single trait models.

The accuracy of EBV for MY in the single-trait BLUP varied greatly depending on the degree of relationship of the candidates to the reference population, from 0.02 for weak relationships to 0.18 for strong relationships with the reference population. The average gain in EBV accuracy for MY in a multiple-trait BLUP was +0.05 across the three categories of candidates. The accuracy of the BLUP-EBV for WWm (0.16) was on average higher than for BLUP-MY (0.09). This difference is due to th fact that WW records were available for at least one parent of the candidates whatever its category. In consequence, the increase in the accuracy of the BLUP-EBV for WWm when considering a multiple-trait model was low. The candidates strongly related to the reference population had the highest gain (+0.03).

According to the reference population size, the heritability of the trait, and the effective population size, genomic information is theoretically expected to increase the accuracy of EBV in comparison to the pedigree BLUP (Goddard and Hayes, 2009). The gain in accuracy was of the same order when integrating genomic infornation into the single-trait ssGBLUP across the three categories of candidates (+0.07 for MY, +0.02 for Wwm). These gains were comparable to those obtained in Angus breed (Lourenco *et al.*, 2015) with a reference population that includes 1628 bulls.

The multiple-trait ssGBLUP model gace the best results in term of accuracy. The gain in EBV accuracy compared to the multiple-trait BLUP was on average +0.07 for MY and +0.05 for WWm across the categories of candidates. Moreover, the average accuracy gain was +0.05 for MY compared to the single-trait ssGBLUP EBV. Concerning WWm, the gain was +0.06 for candidates which were strongly related to the station reference population while it was only +0.03 for the two other categories of candidates.

Conclusion

Increase in accuracy of EBV for suckling performance is possible pooling correlated traits with differents heeritabilities (a low heritable trait (WWm) and a higher heritable trait (MY)) from different origins (recorded on farm and on progeny testing station).

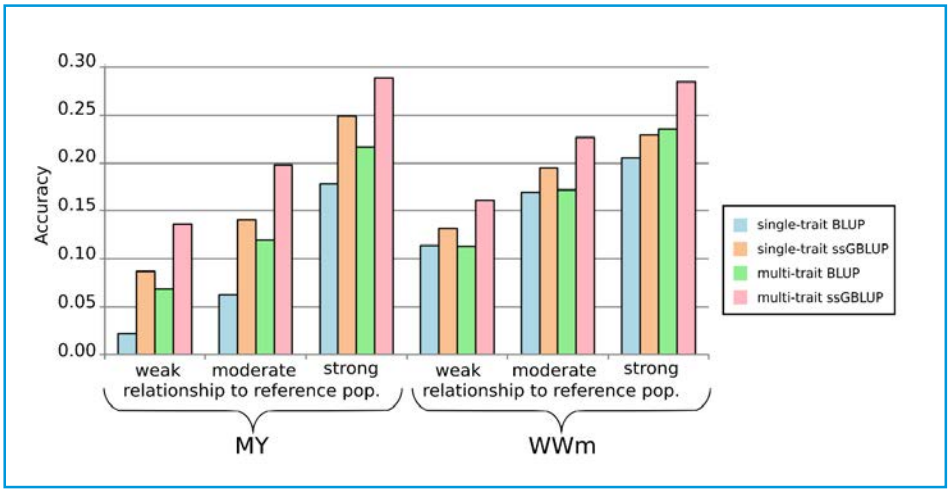

Figure 2. Mean accuracy of EBV for MY and WWm for the candidates according to their degree of relationship to the station reference population and the genetic evaluation model: single-trait pedigree BLUP or ssGBLUP and multi-trait pedigree BLUP or ssGBLUP models.

These results are confirmed by other studies with pedigree-BLUP models (Jia *et al.*, 2012 and Ismael *et al.*, 2017) for other performance traits.

The single-step and multi-trait genomic BLUP model is the one leading to the highest EBV accuracies for maternal traits. However, for animals that are only weakly related to the station reference population, accuracy of maternal EBV remained very low (below 0.15). The multi-trait ssGBLUP provided EBV accuracies for MY and WWm in average between 0.20 and 0.30 for the populations of candidates for selection which are moderately or strongly related to the station reference population. These categories of young bulls represent half of the candidate population in the breeding programmes now. These results paved the way for an efficient use of the maternal EBV in beef cattle breeding programmes using multi-trait ssGBLUP.

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Developments in multi-source genetic evaluations for beef cattle: A BREEDPLAN perspective

B.J. Crook, S.J. Skinner and H.P. Nivison

Agricultural Business Research Institute, University of New England, 2351, Armidale, Australia

Abstract

ABRI provides the BREEDPLAN® genetic evaluation service to both Australian and international clients, and so represents the most widely used genetic evaluation service for beef cattle internationally. Approximately 63 separate BREEDPLAN evaluations have been developed, representing over 40 million animals, almost 40 beef cattle breeds and at least 100 breed associations distributed across 14 countries. This paper provides an overview of current initiatives and developments being undertaken by ABRI regarding multi-country and multi-breed BREEDPLAN evaluations.

Keywords: BREEDPLAN, beef cattle, genetic evaluation, multi-country, multi-breed.

Introduction

The provision of commercial services for the genetic evaluation of beef cattle represents a rapidly changing context. With advancements in computational speed and analytical approaches as well as the increasing needs of beef seed-stock breeders for gains in production efficiency and sustainability, we are seeing the development of more complex, more frequent and globally-focused initiatives as service providers. Where national breed-specific evaluations were once common place, there is now a growing interest and opportunity for countries to combine their pedigree and performance data into larger-scale multi-country genetic evaluations. This allows individual animals to be compared directly on EBV across countries, allowing breeders to take a more informed approach to the selection of possible genetics from “beyond the borders”. This also means that superior local genetics can be more accurately identified when benchmarked within the wider international gene pool.

The Agricultural Business Research Institute (ABRI) is a commercial company founded in 1970 at the University of New England, Armidale Australia. The primary business of ABRI is to provide both domestic and international livestock industries with a wide range of multi-species agribusiness information services, including: integrated pedigree and performance database systems (ILR2), genetic analyses, breed registry services and extension services.

One of ABRI’s flagship products is BREEDPLAN®, a comprehensive suite of multi-trait genetic evaluation technologies developed by the Animal Genetics and Breeding Unit (AGBU)[1] for the beef cattle industry. As a member of ICAR, ABRI currently facilitates the inclusion of Australian data on behalf of the Charolais and Limousin breeds participating in the respective INTERBEEF evaluations.

[1] AGBU is a joint venture of the University of New England (UNE) and NSW Department of Primary Industries (NSW DPI), with support from Meat and Livestock Australia (MLA).

ABRI provides the BREEDPLAN service to both Australian and international clients under a commercialisation licence from the owners of the **BREEDPLAN technology**.[2] At present, approximately 63 separate BREEDPLAN genetic evaluations have been developed, with most conducted either monthly or fortnightly. This represents over 40 million animals, almost 40 beef cattle breeds and at least 100 breed associations distributed across 14 countries, with most BREEDPLAN clients accessing 12-24 genetic evaluations per year, subject to the needs of their members. This makes BREEDPLAN the most widely used genetic evaluation service for beef cattle internationally.

A detailed description of the traits and models associated with BREEDPLAN is provided by Graser *et al* (2005). For the purposes of the present paper, it is worth emphasising that all subsequent developments of the commercial BREEDPLAN service, including the transition towards multi-source evaluations and the incorporation of genomics, have sought to uphold the integrity of a multi-trait model combining birth, growth, fertility, ultra-sound and carcase traits and the potential opportunities afforded to participants where complete recording of all such traits is either financially prohibitive or impractical. Likewise, the BREEDPLAN analytical software makes provision for database-specific trait definitions and pre-adjustment of phenotypes, heterogeneity of variances, sire by herd interactions and a comprehensive approach to genetic groupings, all of which can assist in accommodating some of the considerations required when combining datasets from different sources, whether countries or breeds.

ABRI has facilitated multi-source BREEDPLAN evaluations for over 20 years (e.g. Australia with New Zealand; South Africa with Namibia) and a number of larger scale evaluations for the last 10 years (e.g. Pan American Hereford evaluation: joint analysis of the USA, Canada, Uruguay and Argentina). However, the changing commercial

Table 1. Example of beef breeds available for International BREEDPLAN evaluation.

Breed	Countries[1]	Evaluations[2]	Total animals	Total WW
Hereford	7	3	4,003,689	2,280,596
Angus	5	3	2,974,496	1,817,725
Brahman	4	2	1,038,349	385,023
South Devon	4	3	396,786	197,138

[1] Separate databases
[2] Separate BREEDPLAN genetic evaluations, with each evaluation conducted monthly or fortnightly

context of beef cattle genetic evaluation means we have now moved towards significantly larger and more complex evaluations that combine multiple sources of pedigree, phenotypic and genomic information.

At present, there are two primary initiatives being undertaken by ABRI. The first involves progression towards International evaluations, working with client countries of ABRI where performance (and genomic) data is recorded on the same breed and for which there is some degree of genetic linkage between the respective populations. A summary of breeds for which developments in multi-country evaluations can be considered is given in table 1. This paper will focus on the Hereford and Brahman breeds only. The second initiative involves multi-breed evaluations, using intentionally-designed multi-breed populations that allow the wider population of component breeds to be combined for genetic evaluation within the one analysis. The focus here will be a domestic one,

[1] The owners of the BREEDPLAN technology are: MLA, UNE and NSW DPI.

featuring advances made in the genetic evaluation of tropically adapted breeds in Northern Australia. This paper provides an overview of these initiatives and developments to date.

Multi-country BREEDPLAN evaluations

As the international trade in beef cattle genetics increases, so too does the exchange of information that allows for developments in the provision of commercial services for multi-country and international beef genetic evaluations. One topic of primary focus at the 14th World Hereford Conference (2004) was how to provide Hereford breeders around the world with access to genetics best suited to their respective breeding objective, regardless of where those genetics originated. Interest in a global evaluation of the Hereford breed fostered a genetic linkage project (Donoghue, 2004), development of a web-based global cross-reference table (Johnston, 2004), plus a range of analytical approaches (Graser, 2004) and customised software (Donoghue *et al*, 2007). However, progression towards a commercial outcome and a strategy for ongoing maintenance of the global cross-reference table did not proceed.

An alternative strategy is now being evaluated by ABRI, in collaboration with 7 Hereford breed associations. This initiative is facilitated via the ABRI ILR2 database system, used by the Hereford associations in Australia, New Zealand, Canada, the UK and Namibia. For the associations in Uruguay and Argentina, where domestic registry systems are used, data extracts are supplied to ABRI and loaded to ILR2 systems configured for each country. A parallel strategy is also being progressed for the Brahman breed, based on previous research and development undertaken by ABRI for clients in Australia, South Africa, Namibia and the USA. This initiative represents an international first, in that a *Bos indicus* breed is now being represented in what has long been the domain of *Bos taurus* developments.

The ABRI ILR2 system provides a global language by which data can be extracted automatically in a standardised format for BREEDPLAN genetic analysis, and also provides cross-referencing capability. This means new imported genetics can be recorded using conventional country-specific identifiers, while also providing storage of the animal's identification as recorded in the country of export. ABRI software then extracts and collates this information across ILR2 systems to create global cross-reference files as required for various combinations of data. This removes any additional demand on breed association staff to create data extracts or engage directly in the cross-referencing process. Furthermore, access to the ILR2 DNA table allows genomic data (if collected) to be integrated with the pedigree and performance data residing on the breed association's ILR2 system – and provides ready access to SNP data extracts for use in Single-Step BREEDPLAN evaluations (Johnston *et al*, 2018). This provides a standardised approach for the inclusion of genomic information in International BREEDPLAN evaluations.

Table 2 summarises the traits currently considered in developing an International BREEDPLAN evaluation for the Hereford and Brahman breeds, as well as the total number of phenotypes included across all countries within breed. Importantly, while certain traits are recorded in all countries (e.g. weaning and yearling weights), the remaining traits are more variable, with either low levels of recording relative to weaning weights in some countries, or no recording of the trait at all. It is also worth noting that countries differ in their approach to whole-herd recording and completeness of recording, such that one country might represent a higher percentage of records for a particular trait, even though they account for a smaller percentage of animals in the total analysis. In this way, the combining of data across countries can afford opportunities to all participants.

Table 2. Performance records in multi-country BREEDPLAN evaluations: Hereford and Brahman.

Trait	Hereford	Brahman
Birth weight	1,749,276	795,466
Weaning weight	2,229,446	540,945
Yearling weight	1,374,949	260,690
Final weight	769,455	234,152
Mature cow weight	128,461	60,079
Scrotal circumference	243,519	52,922
Eye muscle area (EMA) - scan	469,172	45,814
Rib fat (RIB) - scan	471,333	43,474
Intramuscular fat% (IMF) - scan	270,090	-
Total records	7,705,701	2,033,542
Number of countries	7	4

The approach taken by ABRI in developing an international evaluation for any given breed is summarised as follows:

A. *For each country*:

- Use ILR2 software to create BREEDPLAN-ready data extracts à conversion to metric units;
- Use ILR2 software to extract cross-referencing information;
- Estimate adjustment factors (per trait) relating to significant non-genetic sources of variation (e.g. age of animal at measurement; age of dam; sex-specific);
- Estimate variance components (per trait): including maternal genetic and dam permanent environment effects (birth weight; weaning weight) and sire by herd interactions (SxH);

B. *For multi-country analysis*:

- Estimate across-country correlations (per trait), for those countries where sufficient records are available;
- Create multi-country covariance matrix using pooled variance components (per trait, including SxH) and off-diagonals based on country representing the most comprehensively recorded multi-trait data source;
- Configure genetic groupings parameter file to allow for country, year and “other breed” representations among base animal population;
- Create global cross-reference file and create multi-country (merged) BREEDPLAN extracts;
- Conduct International analysis using current BREEDPLAN software;

C. *Assessment of outcomes*:

- Conduct single-country analyses:
  - model 1: using current “national” (co)variance matrix;
  - model 2: using country-specific variances and multi-country off-diagonals;

  - model 3: using multi-country (co)variance matrix;
  - comparison of EBVs from models 1-3 à evaluation of assumptions regarding multi-country (co)variance matrix;
- Single vs multi-country:
  - comparison of multi-country EBVs with single-country (model 3) EBVs;
  - cross-validation studies using LR method (Legarra and Reverter, 2018) to demonstrate prediction of future phenotypes, per country: using both single-country (model 3) and multi-country models;

D. *Web-based search engine*:

- collation of within-country listing of published sires;
- display of multi-country results on ABRI's web-based search engine;

Run time for these international evaluations is relatively quick, at 9 hours for Hereford and 3 hours for Brahman, making them an extremely attractive option for a regular, commercial service. These processing speeds are achieved by ABRI's ongoing investment in computer processing capacity combined with more recent enhancements made by AGBU to the solver algorithm used in BREEDPLAN evaluations. This enhanced solver algorithm has the capacity to solve more than 450 million equations in less than 24 hours, thus facilitating the implementation of single-step GBPLUP procedures into routine BREEDPLAN evaluations (Johnston *et al*, 2018).

The main BREEDPLAN multi-trait model can readily accommodate a wider range of traits, including: gestation length; days-to-calving; carcase traits; eating quality traits; net feed intake; % normal sperm. Furthermore, there are additional BREEDPLAN models for analysis of calving ease scores, docility scores and structural trait scores. Phenotypic data is available for most of these traits in both the Hereford and Brahman breeds, and preliminary multi-country evaluations including these traits have been completed to determine the impact on convergence and run times. Similarly, genomic data has been incorporated using single-step GBPLUP procedures, to determine impact on convergence and run time. Initial indications suggest that completion of complex multi-trait International BREEDPLAN evaluations, including those with genomic information, could be achieved in less than 24 hours.

To date, ABRI has completed the single-country and multi-country analyses required for developing an International BREEDPLAN evaluation for the Hereford and Brahman breeds. Assessments of outcomes and the undertaking of validation studies have been scheduled for later in the current year.

Multi-breed BREEDPLAN evaluations

In contrast to ABRI's development of multi-country BREEDPLAN evaluations, where the priority has been set by our international (breed-specific) clients, our development of multi-breed BREEDPLAN evaluations has been driven by the research, development and extension priorities as set by the Australian beef industry (MLA, 2016). Primary focus has been given to multi-breed evaluations involving the tropically-adapted breeds of northern Australia, such as the Brahman, Santa Gertrudis and Droughtmaster breeds, which account for 22% of Australian seedstock registrations but have overall lower levels of performance recording (especially fertility traits) relative to breeds in southern Australia.

It is beyond the scope of this paper to outline the research and development undertaken to improve the levels of performance recording, especially of fertility-based traits, in these northern breeds. However, Johnston *et al.* (2017) provides a concise description of a large-scale phenotyping and genotyping project using designed multi-breed matings. Pedigree and performance information has been loaded to an ILR2 database, complete with cross-reference details that facilitate linkage to individual breed ILR2 system. This Northern Multi-breed (NMB) ILR2 database has provided one of the critical components necessary in developing a range of multi-breed BREEDPLAN evaluations for northern Australia. To date, collaboration between ABRI and AGBU has enabled the NMB data to be included in the monthly BREEDPLAN evaluations of the Australian Brahman and Santa Gertrudis breeds, with the Brahman analysis using single-step GBLUP procedures. Work is currently underway to combine the NMB data with that of the Droughtmaster and Belmont Red breeds, as well as a database representing Tropical Composites.

While these developments may fall in the "multi-breed" category, they are in fact single-breed evaluations that make use of a multi-breed data set to improve the accuracy of prediction of traits relevant to the main breed. As a consequence, how the NMB data is used in a BREEDPLAN analysis depends on the model and (co)variance matrix specific to the main breed for which the analysis is being conducted. Furthermore, EBVs are only reported for animals relevant to the main breed. Currently there is no provision to report on how one breed compares to another, or to rank sires on genetic merit across breeds. ABRI has therefore undertaken development of a more practical and dynamic pathway for combining data from each of the four main tropical breeds, along with the NMB data, to create a "Northern Tropical" BREEDPLAN extract. Running this extract through a test analysis configured as per the current Brahman Single-Step BREEDPLAN analysis - including Brahman-specific parameter files, complete multi-trait (birth, growth, fertility, scan, carcase, eating quality traits) and a G-matrix comprising Brahman genotypes only – convergence was reached in just 2 hours. Admittedly, this represents a very basic first step only. Further work is needed to determine an appropriate (co)variance matrix, or whether multiple (breed-specific) matrices might be required, as well as enhancing the single-step GBLUP procedures to accommodate genotypes from multiple breed sources.

Conclusion

Every multi-source evaluation to be developed requires a range of assumptions and validations to be made and agreed upon by the participating parties and the commercial service provider, if such an evaluation is to move beyond the "research project" into commercial production. The development pathway used by ABRI for multi-country BREEDPLAN evaluations is no different. We assume that a multi-trait model holds more appeal to our clients and we assume that across-country correlations are sufficiently high to negate the need for modelling country-specific genetic expressions of a trait. Our research to date for the Hereford and Brahman breeds gives some validity to these assumptions. We also assume that this will be assisted by accommodating sire by herd interactions, heterogeneity of variances and comprehensive genetic groupings in the model. We also assume that our clients will require an assessment of outcomes, including validation studies to demonstrate the accuracy of prediction of future phenotypes based on multi-country EBVs. We see this as a logical extension of our commercial service, because the outcome would be an international evaluation using ILR2 systems and BREEDPLAN software.

In terms of multi-breed initiatives, ABRI continues to explore the opportunities available to our clients in combining breed-specific databases where linkage exists via shared information: whether by linkage to other multi-breed research databases or via registers

of cross-bred animals recorded on a breed association's ILR2 system. Our expertise in agribusiness information services allows ABRI to provide critical input in the development of multi-breed BREEDPLAN evaluations.

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Interbeef international genetic evaluation for calving traits

Z. Vesela[1], M. Brzakova[1], A. Svitakova[1], L. Vostry[1] and P. Bucek[2]

[1]Institute of Animal Science, Pratelstvi 815, 10400, Prague Uhrineves, Czech Republic
[2]Czech Moravian Breeders' Corporation, Benesovska 123, 25209, Hradistko, Czech Republic

Abstract

Since 2007, Interbull Centre, with the help of ICBF (Ireland) and INRA (France), has developed the different tools to run Interbeef joint genetic evaluation of beef cattle. The first official run was performed in 2014 on Charolais (CHA) and Limousine (LIM) weaning weight. The second group of traits of interest was calving traits (calving ease - CAE and birth weight - BWT). The Czech Republic (Institute of Animal Science) is responsible for the estimation of genetic correlations between countries and for the development of international genetic evaluation for these traits. The first official routine run for calving traits was performed in 2018 for CHA, LIM, and Beef Simmental (BSM). The model chosen for international genetic evaluation is an animal multiple trait model based on raw performance data and considering each country as a separated trait. The both calving traits (CAE and BWT) are evaluated jointly as correlated traits in multiple trait model as well. Nine countries are currently involved in international genetic evaluation for calving traits:

1. for all breeds Czech Republic, Denmark, Finland, Ireland, Sweden.
2. for LIM and CHA France.
3. for CHA South African Republic.
4. for LIM United Kingdom and
5. for BSM Germany.

Across-country genetic correlations were estimated by two series of pairwise country analysis successively:

1. Animal model with direct genetic effect (DIR) and maternal permanent environmental effect (MPE) and
2. Animal model for DIR and maternal genetic effect with MPE effect.

The resulting matrices were bended to make them positive definite. Average direct genetic correlations for BWT across countries were 0.7 (CHA), 0.79 (LIM), 0.84 (BSM) and for CAE 0.67 (CHA), 0.70 (LIM), 0.45 (BSM). Average maternal genetic correlations for BWT between countries were 0.47 (CHA), 0.45 (LIM), 0.49 (BSM) and for CAE 0.58 (CHA), 0.53 (LIM), 0.79 (BSM).

Keywords: beef cattle, Interbeef, calving traits, genetic correlation, international genetic evaluation

Introduction

Efforts to create an international genetic evaluation for beef cattle started in 2001 with the EUropean BEeaf EVALuation project (EUBEEVAL). Phocas et al. (2005) suggested that the optimal model for beef cattle is an across-country animal model with maternal effect applied to raw phenotypes. Venot et al. (2006) performed the first pilot study and estimated across country genetic correlations for weaning weights between France (FRA), Ireland (IRL), and the United Kingdom (GBR) for Charolais (CHA) and Limousine (LIM) breeds. Three years later, genetic correlations were estimated for FRA, IRL, GBR, Sweden (SWE), and Denmark (DNK) (Venot et al., 2009). In 2008 Interbeef working group was established in ICAR, and the IDEA database at the Interbull center started to be used for pedigree and data exchange for beef cattle. Pabiou et al. (2014) estimated genetic correlations for weaning weight between eight member countries of Interbeef for CHA and LIM. These genetic correlations were provided to Interbeef for tests and routine runs. Since then, Interbeef extended his service for more countries and breeds. Now provides services for five breeds (CHA, LIM, Beef Simmental (BSM), Aberdeen Angus (AAN), and Hereford (HER)) and nine countries. The development of methods for international genetic evaluation for new traits, breeds, and countries is carried out in cooperation with research partners. The Czech Republic is responsible for the development of evaluation for calving traits (calving ease – CAE, birth weight – BWT). This paper summarizes the results of our work.

Material and methods

Data. Phenotypic and pedigree data were extracted from the IDEA database in autumn 2017 (CHA, LIM) and spring 2018 (BSM). Seven populations were participating in calving traits project – Czech Republic (CZE), Germany (DEU), Denmark + Finland + Sweden sending data as one joint population (DFS), France (FRA), United Kingdom (GBR), Ireland (IRL) and South African Republic (ZAF). However, not all populations were participating in all breed/trait combinations (Table 1). The definition of birth weight performance was the same in all countries. The definition of calving ease was different and based on national evaluation practices:

1. four points scale in CZE, IRL, and ZAF.
2. five points scale in DEU, DFS, FRA, and GBR.

Data edits. Each country had uploaded phenotypic performances edited according to their national evaluation standard. For the genetic parameter estimation, we further edited files. Main edits on performances were the exclusion of duplicate records (one animal sent from more countries), embryo transfer calves, calves without known sire and maternal grandsire (MGS), herds without variation, small-sized contemporary groups (CG), and CGs with only one sire. After that, performance data files were

Table 1. Number of records in pedigree and performance files extracted from the IDEA database.

	CHA		LIM		BSM	
	BWT	CAE	BWT	CAE	BWT	CAE
Pedigree	10,220,079	10,419,521	5,754,435	6,048,151	218,045	504,665
Performances						
CZE	62,898	62,898	17,184	17,184	26,394	26,394
DEU	np	np	np	np	np	197,232
DFS	271,760	298,493	207,446	273,543	137,994	178,941
FRA	8,740,872	8,728,358	4,859,658	4,830,350	np	np
GBR	np	np	201,865	181,711	np	np
IRL	38,318	222,070	18,440	208,399	5,970	55,789
ZAF	49,153	np	np	np	np	np

np – country not participating for the specified breed/trait combination

prepared for pairwise country genetic parameter estimation according to the genetic connection between countries. Large performance data files were reduced to maintain optimum connection with other countries.

Model. Each country described its preferred genetic evaluation model and defined its own environmental effects according to their national genetic evaluation system. (Co)variance components were estimated by a two-trait (CAE and BWT) animal model using AIREMLF90 (Misztal et al., 2002) for pairwise combination of countries. Estimations were performed in two steps: 1. Animal model with direct genetic effect and maternal permanent environmental effect (AM-DE-MPE) and 2. Animal model for direct and maternal genetic effect with maternal permanent environmental effect (AM-DE-ME-MPE), in which were across-country co-variances between direct and maternal genetic effect fixed to zero. For most countries, the AM-DE-ME-MPE model was preferred. For IRL and DEU, the AM-DE-MPE (without the maternal genetic effect) model was chosen. Pedigree file was built for each pairwise combination and contained five generations with a phantom parent group constructed according to country of origin of animal with unknown parent.

After that, the full direct and maternal correlation matrix was constructed. Non-converged direct correlations from the AM-DE-ME-MPE model between countries were set to values obtained from the AM-DE-MPE model, or average value with standard error 0.4 if no result was estimated from both models. Non-converged maternal correlations were set to average value with standard error 0.4. Matrices of direct and maternal correlations were bended with standard errors used as weights (Jorjani et al., 2003). And finally, the full Interbeef multicountry two-trait correlation matrix was bended to become positive definitive using Jorjani et al. (2003) weighted bending procedure where the weighting factors were equal to the reciprocal of the number of common sires multiplied by 10 for direct correlations and by 5 for maternal correlations.

Results and discussion

The largest population of Limousine and Charolais was from France and represented more than 90% of the performance dataset (Table 1). In Beef Simmental, the size of populations was more balanced with DFS and DEU representing the two largest populations in the dataset (Table 1).

In tables 2, 3, and 4 are estimated genetic correlations for CHA, LIM, and BSM. For all three breeds, average direct genetic correlations for BWT were higher than for CAE, which is probably caused by higher heritabilities of BWT and differences of definition of CAE scoring between countries. Average direct genetic correlations for BWT were 0.70 for CHA, 0.79 for LIM and 0.84 for BSM and for CAE 0.67 (CHA), 0.70 (LIM) and 0.45 (BSM). These correlations are slightly lower than average Interbeef genetic correlations estimated for weaning weight by Pabiou et al. (2014). We observed slightly higher correlations for LIM than CHA for weaning weight. Pabiou et al. (2014) came to the same result for weaning weight and explained it by the absence of GBR data in the CHA run and therefore missing linkage through GBR sires. The strongest direct genetic correlations in CHA were observed between FRA-DFS (0.86), FRA-IRL (0.83), DFS-IRL (0.83) for BWT and between IRL-CZE (0.72), DFS-CZE (0.70) and FRA-IRL (0.70) for CAE. In LIM, the strongest direct genetic correlations were observed between DFS-CZE (0.87), FRA-CZE (0.87) and DFS-IRL (0.83) for BWT and GBR-IRL (0.85) and FRA-IRL (0.84) for CAE. In BSM, all three direct correlations for BWT (DFS-CZE, IRL-CZE, DFS-IRL) were higher than 0.8. The situation in CAE was much more complicated. Low genetic correlations between DEU and other countries is caused by differences in methods of national genetic evaluation. This problem should be solved in the future by the harmonization of methods in cooperation with DEU.

Table 2. Heritabilities (diagonal) and across-country genetic correlations (below diagonal) for Charolais.

			Direct effect									Maternal effect						
			Birth weight					Calving ease				Birth weight				Calving ease		
			CZE	DFS	FRA	IRL	ZAF	CZE	DFS	FRA	IRL	CZE	DFS	FRA	ZAF	CZE	DFS	FRA
Direct effect	CAE	CZE	0.21															
		DFS	0.64	0.38														
		FRA	0.60	0.86	0.41													
		IRL	0.66	0.83	0.83	0.40												
		ZAF	0.81	0.55	0.64	0.63	0.31											
	BWT	CZE	0.25	0.05	0.31	0.12	0.11	0.17										
		DFS	0.08	0.00	0.21	0.00	-0.07	0.70	0.16									
		FRA	0.29	0.51	0.83	0.54	0.30	0.66	0.59	0.10								
		IRL	0.10	0.05	0.36	0.37	-0.03	0.72	0.68	0.70	0.05							
Maternal effect	CAE	CZE	-0.48	-0.12	-0.04	-0.09	-0.13	-0.01	0.10	0.12	0.10	0.05						
		DFS	-0.12	-0.15	-0.08	0.00	0.06	0.10	0.00	-0.01	0.01	0.61	0.09					
		FRA	-0.03	-0.22	-0.48	-0.11	-0.12	0.04	0.01	-0.47	-0.02	0.31	0.44	0.10				
		ZAF	-0.07	0.04	-0.05	0.03	-0.03	0.07	-0.01	-0.02	-0.01	0.47	0.47	0.52	0.10			
	BWT	CZE	0.04	0.12	0.04	0.11	0.14	-0.47	-0.09	-0.13	-0.12	0.42	0.08	0.12	0.03	0.03		
		DFS	0.09	0.00	-0.01	-0.01	-0.02	-0.08	-0.20	-0.04	0.03	0.09	0.00	0.05	-0.03	0.58	0.08	
		FRA	0.15	-0.04	-0.30	0.01	-0.03	-0.14	-0.02	-0.40	0.00	0.12	0.03	0.69	0.06	0.58	0.59	0.06

Table 3. Heritabilities (diagonal) and across-country genetic correlations (below diagonal) for Limousine.

			Direct effect										Maternal effect							
			Birth weight					Calving ease					Birth weight				Calving easeCAE			
			CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	IRL	CZE	DFS	FRA	GBR	CZE	DFS	FRA	GBR
Direct effect	BWT	CZE	0.21																	
		DFS	0.87	0.38																
		FRA	0.87	0.80	0.43															
		GBR	0.78	0.81	0.73	0.30														
		IRL	0.72	0.83	0.68	0.79	0.40													
	CAE	CZE	0.25	0.08	0.27	0.25	0.10	0.17												
		DFS	0.11	0.00	0.26	0.12	-0.07	0.62	0.16											
		FRA	0.41	0.28	0.68	0.38	0.35	0.60	0.73	0.05										
		GBR	0.21	0.13	0.33	0.53	0.27	0.71	0.66	0.71	0.11									
		IRL	0.17	0.06	0.38	0.33	0.37	0.63	0.63	0.84	0.85	0.05								
Maternal effect	BWT	CZE	-0.48	-0.17	-0.28	-0.15	-0.10	-0.01	0.09	0.02	0.11	0.12	0.05							
		DFS	-0.10	-0.15	-0.19	-0.04	0.00	0.06	0.00	0.04	0.02	0.03	0.42	0.09						
		FRA	-0.43	-0.32	-0.61	-0.22	-0.08	0.06	0.05	-0.20	0.09	0.06	0.43	0.69	0.09					
		GBR	-0.12	-0.03	-0.13	-0.37	0.00	0.08	0.02	0.05	-0.15	0.02	0.42	0.37	0.38	0.06				
	CAE	CZE	0.04	0.16	0.04	0.13	0.13	-0.47	-0.04	-0.11	-0.12	-0.06	0.42	0.08	-0.01	0.06	0.03			
		DFS	0.09	0.00	-0.03	0.03	0.01	-0.04	-0.20	-0.10	-0.02	0.05	0.05	0.00	-0.01	0.01	0.50	0.08		
		FRA	-0.11	-0.10	-0.45	-0.05	-0.06	-0.14	-0.17	-0.56	-0.14	-0.23	0.09	-0.04	0.28	-0.05	0.52	0.52	0.02	
		GBR	0.10	0.03	-0.06	-0.15	0.05	-0.08	0.00	-0.16	-0.35	-0.10	0.02	0.00	-0.02	0.01	0.50	0.51	0.63	0.06

Table 4. Heritabilities (diagonal) and across-country genetic correlations (below diagonal) for Beef Simmental.

			Direct effect							Maternal effect			
			Birth weight			Calving ease				Birth weight		Calving ease	
			CZE	DFS	IRL	CZE	DFS	IRL	DEU	CZE	DFS	CZE	DFS
DIR	BWT	CZE	0.21										
		DFS	0.85	0.38									
		IRL	0.83	0.84	0.40								
	CAE	CZE	0.25	0.09	0.43	0.17							
		DFS	0.08	0.00	0.51	0.60	0.16						
		IRL	0.47	0.41	0.83	0.68	0.89	0.05					
		DEU	0.01	-0.05	-0.01	0.27	0.17	0.08	0.05				
MAT	BWT	CZE	-0.48	-0.15	-0.12	-0.01	0.10	0.04	0.02	0.05			
		DFS	-0.10	-0.15	-0.06	0.07	0.00	0.00	-0.01	0.49	0.09		
	CAE	CZE	0.04	0.14	0.08	-0.47	-0.11	-0.06	-0.03	0.42	0.08	0.03	
		DFS	0.14	0.00	-0.01	-0.14	-0.20	-0.10	0.01	0.14	0.00	0.79	0.08

Conclusion

This study has provided Interbeef with a set of genetic correlations across participating countries and allows Interbeef to proceed to an official run of international genetic evaluation for calving traits. The first run was held in 2018, and resulting international breeding values were distributed to member countries. By now Interbeef provides international breeding values for weaning weight for five beef breeds (CHA, LIM, BSM, AAN, and HER) and calving traits (BWT and CAE) for three beef breeds (CHA, LIM, and BSM). Further research is focused on the development of international genetic evaluation for new traits (female fertility and carcass traits), calving traits for ANN and HER and estimation of genetic correlations for new member countries.

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Optimizing mate selection: a genetic algorithm approach

D. de Carvalho Neves da Fontoura[1,2], S. da Silva Camargo[1], R. Augusto de Almeida Torres Junior[3], H. Gomes de Carvalho[4] and F. Flores Cardoso[1,4]

[1]Graduate Program on Applied Computing - Federal University of Pampa and Embrapa South Livestock, Bagé, RS, Brazil
Corresponding Author: fernando.cardoso@embrapa.br
[2]Federal Institute of Education, Science and Technology, Bagé, RS, Brazil
[3]Embrapa Beef Cattle, Brazilian Agricultural Research Corporation, Campo Grande, MS, Brazil
[4]Embrapa South Livestock - Brazilian Agricultural Research Corporation, Bagé, RS, Brazil

Abstract

Background: Genetic Improvement Programs (GIP) aim to enhance production efficiency of beef cattle. The main way to guide this enhancement is by choosing the best mates among sires and cows, in order to maximize the offspring Genetic Qualification Index (QGI), which is measured by an index defined by the GIP and computed for each animal of the herd. This paper describes a genetic algorithm, which can recommend an optimal set of matings among sires and cows, in order to maximize the QGI of the herd. Breeders can define constraints regarding level of problems, which must be avoided, and they also can alter the traits relative importance considered in QGI, according their particular interests. This algorithm was applied to a herd of a Brazilian breeder, which participates of a GIP, and it found optimal matings in order to increase QGI value. We have simulated different scenarios considering variations on fitness functions, which combine QGI and level of problems, in order to find the optimal matings. Proposed approach was successfully used to recommend optimal mating decisions by Brazilian Hereford and Braford cattle breeders Association leading to an improvement of offspring QGI.

Keywords: Genetic Improvement, Beef Cattle, Artificial Intelligence, Evolutionary Computing.

Background

In recent decades, genetic improvement has been used as an approach for enhancing production efficiency of beef cattle. In order to measure and guide this enhancement, recording and evaluation programs have been collecting phenotypic, genetic and pedigree relationship data about the animals (Miller, 2010). Data typically involves values of economic importance traits, which should be optimized. The main way to guide this optimization provided by a genetic improvement program is by choosing the best mates among sires and cows.

Some examples can be found in literature regarding mate selection for genetic improvement using artificial intelligence techniques, like evolutionary computing or genetic algorithms (GA). Carvalheiro; Queiroz and Kinghorn (2010) developed a solution, based on the Differential Evolution (DE) technique, which searches for the

optimal genetic contribution during the selection of reproduction candidates. The fitness function used Expected Progeny Difference (EPD) data and penalty restriction for inbred matings. The results show the program was computationally efficient and feasible to be applied in practical situations. Expected consequences of its application, when compared to empirical inbreeding control procedures and/or selection based only on the expected genetic value, would be the improvement of future genetic response and more effective limitation of inbreeding rate. Authors concluded that it is possible to use differential evolution as an optimization method to make the optimal selection of genetic contribution. Kinghorn (2011) described a mating selection algorithm, which has an extension allowing the application of restrictions in certain matings, according the groups to which sires and cows belong. As a result, this algorithm is faster than the DE from its previous publication and it can penalize constraint-breaking solutions. This way, the performance of this new algorithm extended the use of partner selection and allowed implementation in relatively large genetic improvement programs. Barreto Neto (2014) has applied the genetic contribution theory to optimize the next generation genetic value of 12 selective matings nuclei, which contained 500 Santa Inês ewes. The author used GA to find the optimal genetic contribution to the next generation of these animals, which have a structured pedigree and EPDs of economic importance traits estimated through Best Linear Unbiased Predictors (BLUP). The results showed the effectiveness of the use of animal selection using BLUP-EPD, as well as the efficiency of the GA in the process. Results also shown the increasing exchange of genetic material between nuclei is highly recommended to increase genetic gain and Artificial Intelligence may be a method to achieve this goal, if an inbreeding control measure is also being used.

In this context, this paper aims to describe development and testing of an evolutionary computing tool to optimize mating decisions by beef cattle breeders. This solution was successfully implemented in a Genetic Improvement Program. Among specific objectives, can be cited:

1. Use a customizable index for herd specific breeding objectives;
2. Use a penalty for offspring inbreeding;
3. Use a definable minimum and maximum number of offspring per parent; and
4. Use a penalty for low performance on independent culling traits.

The remainder of this paper was divided into three sections. In Material and Methods, we present requirements and decisions taken during the process of solution implementation, the Results and Discussion section approaches the experiments done and a critical analysis of results obtained, and, finally, in Conclusions we summarize some findings and limitations of the solution.

Material and methods

Approval of Animal care and use committee was not needed due to the usage of existing datasets historically collected by the animal breeding program. Experiments were done using R version 3.5.2 (R Core Team, 2018), GA package version 3.2 (Scrucca, 2017), and Rcpp package version 1.0.2 (*https://cran.r-project.org/web/packages/Rcpp/index.html*).

Data source

Data source was provided by the PampaPlus Hereford and Braford GIP conducted by the Brazilian Hereford and Braford Association and Embrapa Pecuária Sul, both institutions located in Bagé, Rio Grande do Sul, Brazil (-31.33; -54.10) (Cardoso *et al.*,

2016). PampaPlus controls performance of herds located in several states of Brazil, and in Uruguay and Paraguay. Sires and cows data, including their EPD traits data, were selected directly from the database of PampaPlus GIP. Main parameters for the optimization include maximum and minimum utilization for each sire and maximum inbreeding value for the calves. Fourteen EPDs were available in our dataset: Birth Weight (BW), Weaning Weight (WW), WW Maternal - Milk (WWm), Total Maternal (TM), Yearling Weight (YW), Post Weaning Gain (PWG), Mature Cow Weight (MCW), Scrotal Circumference (SC), Muscling Score (MSC), Height Scores (HSC), Body Capacity Score (BCS), Cow Body Score (CBC), Navel Size Score (NSC), and Eye Pigmentation (EP).

Proposed solution

Developed genetic algorithm followed the canonical model presented by Goldberg (1989). Each chromosome represents a possible solution for the matings, defining a set of mates among sires and cows. Chromosomes are composed by genes, which amount is equals to the number of cows in a simulation. The content of each gene is the identifier of a sire, which will mate with the cow. The fitness function, which evaluates the quality of each calf generated by the mating, can be computed through any combination of trait values. In our simulations, we have used the traits their respective weights as defined in the PampaPlus GIP Index

(QGI = 30%TM + 15%PWG + 15%YW + 12.5%MSC + 12.5%HSC + 15%SC)

However, each breeder in each simulation can alternatively set traits and weights according to a specific breeding objective. The quality of each solution, or chromosome, is computed by the averages of each fitness values of each gene. As result, the approach will search for the best solutions, or chromosomes, which maximize the fitness function.

Among the fourteen EPD traits measured in the PampaPlus GIP, three of them that are included in the Index should be minimized, namely BW, MCW and NSC. That is, the lower the value is, the better is the calf. This way, the weight of these EPD are negative in fitness function that is, the decreasing of them leads to a increasing of the fitness value.

Generation of new chromosomes must satisfy some constraints, which leads to a penalization of non-valid chromosomes. These restrictions are:

1. User can set minimum and maximum amount of matings to each bull.
2. The maximum calf inbreeding for each mating must be respected.

The first step in a GA execution involves generating an initial set of random chromosomes, which size must be defined. We have used the chromosome population size as twice the amount of cows in the simulation (Carvalheiro; Queiroz and Kinghorn, 2010; Kinghorn, 2011). Random chromosomes which does not obey the constraints are penalized in 50% of their fitness.

We have search for ways to speedup the finding of the best chromosomes. At first, we have used the addicted roulette selection, which gives to individuals with higher fitness value greater odds to be selected for the crossover. Because invalid chromosomes are penalized by the fitness function, valid chromosomes are more likely to be selected. During the tests, convergence was slow. Afterwards, we have combined addicted roulette and tournament. These hybrid technique led to a most efficient selection of valid chromosomes for reproduction. This way, the final implementation of the selection works as follows: 2 chromosomes are chosen through the addicted roulette and a

tournament is held between these two chosen chromosomes, selecting the one with highest fitness value. The process is repeated to select the second parent (chromosome).

After parent selection to the reproduction process, selected parents are combined through the crossover process. Crossover is performed based on a random choice of a position of the chromosomes. Two new chromosomes are generated, combining the old ones. Another concept used was the mutation rate, which is an adjustable probability from 0 to 100%. In order to mutate a gene, a randomly chosen sire replaces the original sire previously defined to mate a cow on that gene.

The stopping condition must be defined to a GA. In our experiments, depending on the parameters, we have verified a convergence between 400 and 800 generations, which is the name given to each cycle where crossover occurs in all chromosomes. This way, we have defined 1000 generations as stopping criteria. When reaching the stopping criteria, the best valid chromosome is indicated as the optimal mating combination.

Results and discussion

We have done four simulations, testing different values for Genetic Algorithm parameters in order to evaluate and optimize the results obtained by our approach. We also have used an actual database, provided by Brazilian Hereford and Braford Cattle Breeders Association. We have selected a single breeder, which represents a typical case in terms of amount of animals owned. In the experiments, we had used 568 cows and 37 sires. Table 1 represents the summary of the results obtained in these four simulations.

The first simulation reported here aims to verify if the GA can find a solution by selecting the best subset of available sires. We have defined 3% as the constraint for maximum inbreeding and 30 as the maximum utilization of each sire. No constraint for minimum utilization was defined. The evaluation fitness of calves generated by each mating was computed by using the PampaPlus QGI index. Thus, sires with higher QGIs were supposed to be chosen and matched with cows in order to maximize the value of the mating fitness. However, Table 1 shows that 48% of proposed matings (275 out of 568) have some level of problem regarding poor performance for undesirable traits, namely in this experiment BW, NSC, and EP. For these traits, a value of one standard deviation below average of the active animals of the PampaPlus GIP was considered the level of problem (LP) for the future progeny performance. The training process for the GA in this simulation is presented in Figure 1. The convergence happened around generation 500. The initial population average fitness was around 50 and in the final generation an average fitness above 250 was reached. The best valid solution, the best solution (which can violate some restriction), and the average of all solutions, or chromosomes, were presented in Figure 1.

While in the simulation 1, the fitness function for genetic algorithm considered only the QGI, in simulation 2 the metric was composed by a combination of 90% QGI and 10% LP. This experiment aimed to evaluate how the impact of LP could be reduced without compromising the QGI. As a result, the final QGI from matings recomended by our solution decreased around 1%, while reduction of LP was near 45%. Consequently, results shows that including LP in fitness function can generate a representative impact in reducing the level of problems, producing a small effect on herd average QGI. The training process for the GA in this simulation is presented in Figure 2. The convergence also happened around generation 500. The initial population average fitness was around

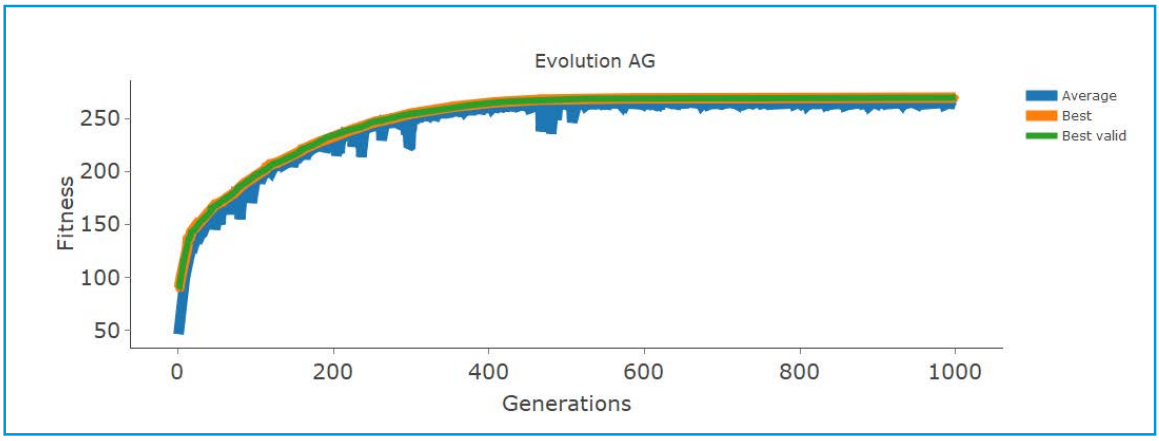

Figure 1. Evolution of fitness values using 100% QGI.

Table 1. Simulation parameters.

Parameter	Value
Amount of Sires	37
Amount of Cows	568
Population size	1136
Inbreeding	<= 3%
Mutation	10%
Stopping generation	1000
Sire maximum utilization	30
Comment	Any sire can mate with any cow up to the its maximum limit of each sire, with no minimum defined

45 and in the final generation an average fitness around 240 was reached. The best valid solution, the best solution (which can violate some restriction), and the average of all solutions, or chromosomes, were presented.

Due to positive results obtained in simulation 2, it was done a new experiment where the weight of LP was incremented to 20% and the weight of QGI was reduced to 80% in the fitness function. In this third simulation, results show a QGI decrease around 4% and 60% in LP. This training process is presented in Figure 3. The convergence happened around generation 700. The initial population average fitness was around 40 and increased to near 200.

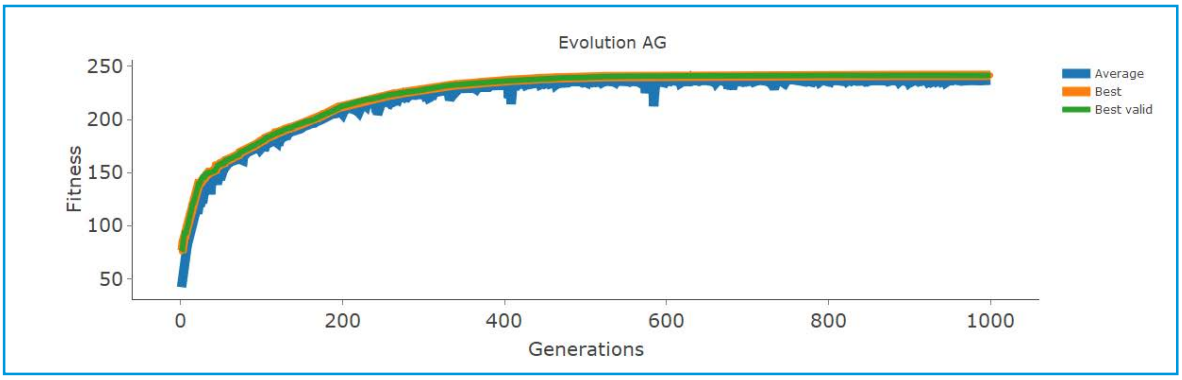

Figure 2. Evolution of fitness values using 90% QGI and 10% LP.

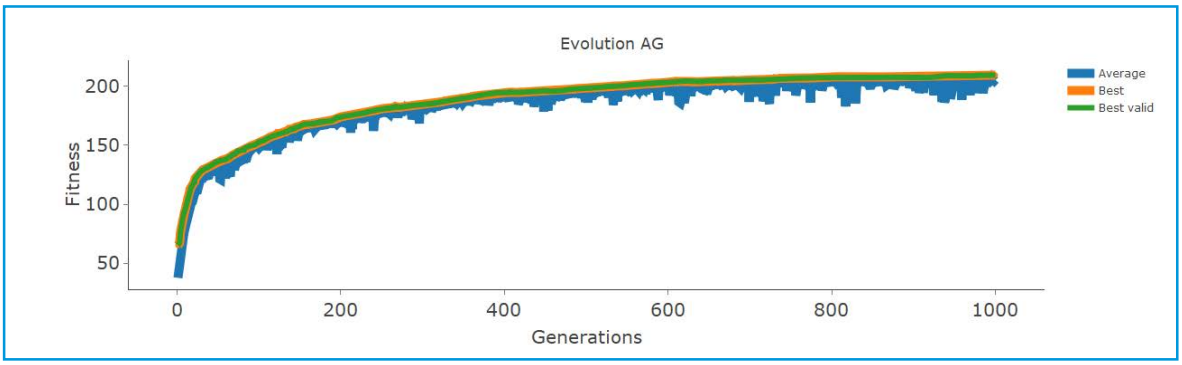

Figure 3. Evolution of fitness values using 80% QGI and 20% LP.

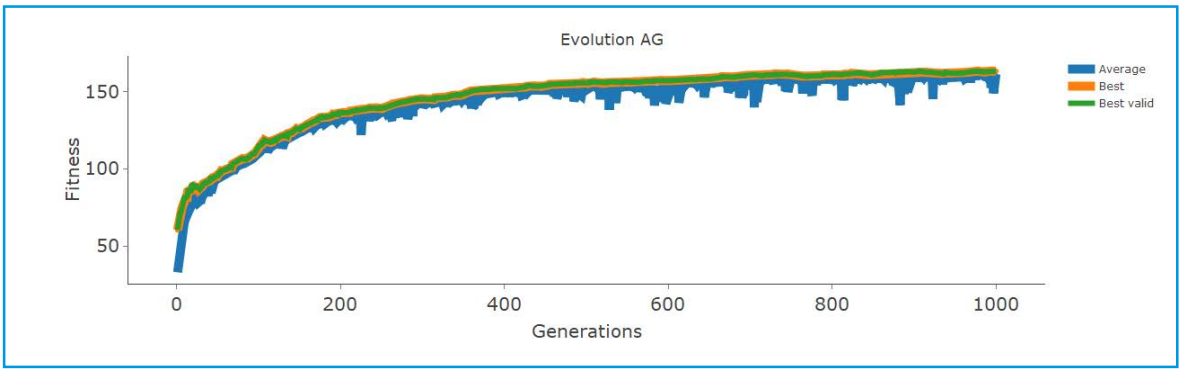

Figure 4. Evolution of fitness values using 70% QGI and 30% LP.

In simulation 4, the QGI represents 70% of the fitness function value while the LP represents 30%. As result, the mating QGI decreased around 14%. Moreover, the LP reduction was near to 87%. Figure 4 presents the evolution of GA of this simulation. The convergence happened around generation 800 and the initial population average fitness was around 35 and increased to near 150.

Table 2 summarizes the results of our simulations combining different weights for QGI and LP in the fitness function. Values of QGI and LP for the best solution are presented, and the amount of undesirable matings (p) as well.

Figure 5 presents the results of our four simulations with different combinations weights for QGI and LP in the fitness function. Considering 568 matings in our simulations, the amount of undesirable matings was divided by 568, in order to be transformed to a proportion. As can be seen in simulations, there is a slight reduction of the QGI index as the weight of QGI in fitness function also decreases. On the other hand, the decreasing of matings with some problem is more significant when the weight of LP increases on the fitness function. In this sense, when LP represents 30% of the fitness function, the amount of undesirable matings was reduced to around 5%.

Conclusions

In this paper we have presented a Genetic Algorithm based approach for optimizing mate selection in Genetic Improvement Programs of beef cattle. The approach uses Expected Progeny Difference and pedigree relationship data in order to evaluate the matings recomended by the algorithm. Different scenarios were tested, combining QGI and LP weights in fitness function. Results showed a slight reduction of QGI of the herd while reaching a significant reduction of the level of problem of calves as the weight of LP is increased in the fitness function. In this sense, our experiments shows

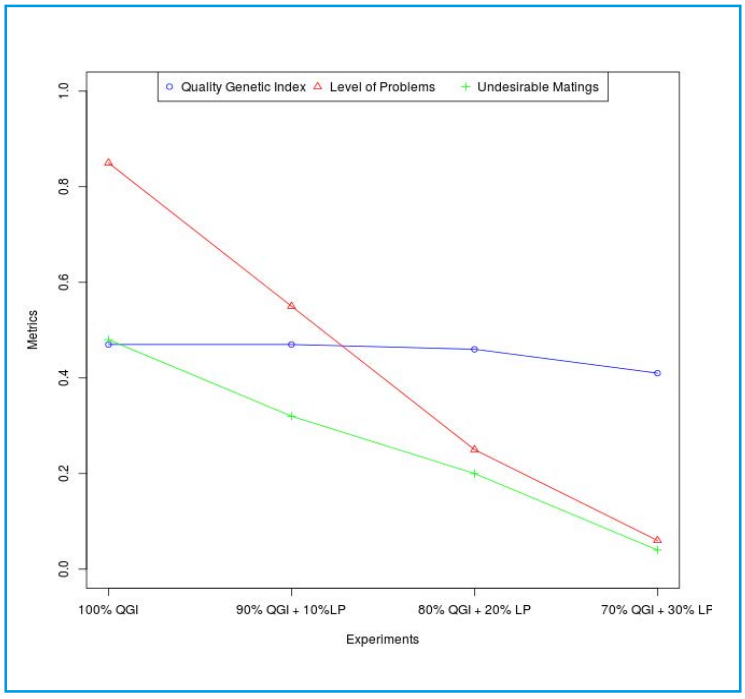

Figure 5. Results of QGI, Level of Problems and Undesirable matings in tested simulations

Table 2. Average genetic qualification index (QGI), level of problems (LP) and proportion (p) of undesirable matings according to different combinations of QGI and LP i the fitness function.

Simulation	Fitness Function	Best Solution		
		QGI	LP	p
1	100% QGI	0,474815	0,845915	275
2	90% QGI + 10% LP	0,472351	0,545775	179
3	80% QGI + 20% LP	0,459677	0,248239	112
4	70% QGI + 30% LP	0,409432	0,063380	24

evolutionary computing was successfully used to optimize mating decisions by Brazilian Hereford and Braford cattle breeders, combining index, independent level culling traits, inbreeding and offspring size.

As future works, this approach will be integrated in the Pampaplus mating tool to guide matings and increase genetic gain. Moreover, relative importance of QGI index and level of problems, in the fitness function, need to be tested in a broader range of scenarios.

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Sensor validation from a manufacturer point of view

C. Bagenvik

DeLaval International AB, P.O. Box 39, 147 21 Tumba, Sweden

Abstract

The general trend over the world is that dairy farms are getting larger and that it is difficult to find skilled labour. Farmers are more and more starting to utilize automation and technology to increase their efficiency. Effective milk production, doing more with less, with healthier animals that live longer also reduces the environmental footprint on farm and increases the profitability for the farmer.

One section of the automation process that is taking place is the development of sensors to monitor different conditions in the animals or at the farm. There are many different sensors available in the market, some used for farm management and some more for genetic evaluation and research. At DeLaval, we see a strong need in standardizing the validation of sensors to make it easier for our customers to compare and select the sensors best suited for their needs and operations.

Keywords: Cecilia Bagenvik, DeLaval, Sensors, Validation.

Introduction

At DeLaval we have the vision to make sustainable food production possible; helping our customers to do more with less. Sustainability for us is represented by four areas:

- Environment
- Social responsibility
- Animal welfare
- Farm profitability

Sensors in milk production can help in all four of these areas if they are used correctly. If we, as technology providers, can help in keeping the animals comfortable, stress free, and healthy we can help our farmers in becoming more efficient and extending the life time of their animals.

Sensor validation

Sensors and data in dairy production

There are many different parameters a sensor can measure on a dairy cow. For some of these areas there are commercial sensors available, but not for all.

The question is what is worth the most to measure. Which areas contributes the most to the environment, social responsibility, animal welfare and farm profitability. When working with innovation and product development at DeLaval, those are the four questions that we ask ourselves.

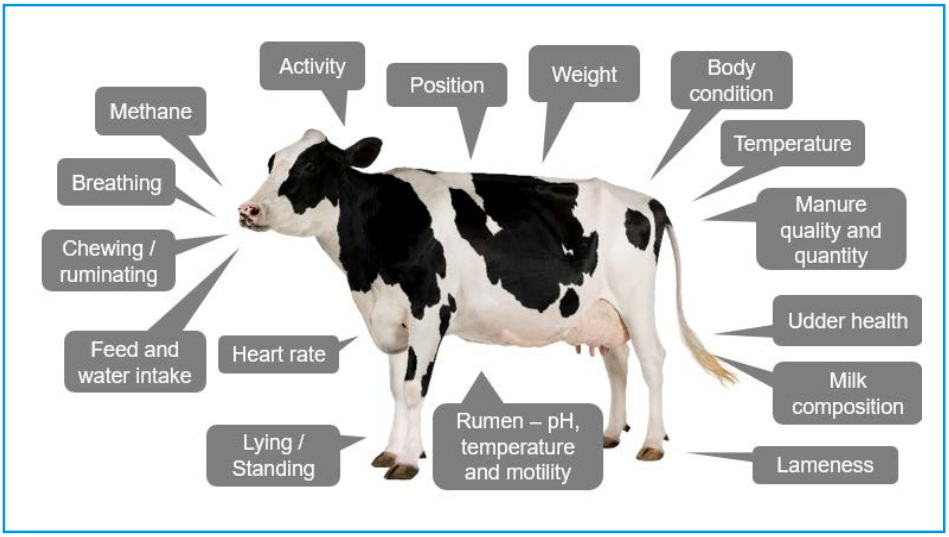

Figure 1. Parameters that potentially can be measured on a dairy cow.

There are many contributors to data on a dairy farm. Not only the sensor data but the animals themselves and other equipment used on the farm contributes tremendously with data, for example sort gates, milking systems or feed stations. All this data can then be further processed in traditional models or machine learning algorithms to tell us a lot of different things about the individual cow or a group of cows.

For the farmer, all that data in itself doesn't provide much value. It is what we can tell or predict from the data that results in an action that is valuable. The farmer needs to be alerted on the animals in the herd that need attention, animals that need a specific treatment or action. Then less attention can be given to the group of cows that are productive and healthy.

Sensor validation – to be able to compare

One area that is quite mature in the sensor segment is heat detection. Many different technologies are available. For the farmer, there are many aspects to consider when selecting sensor technology. For example the method. Heat detection can be provided in many different ways, for example by measuring activity and other behaviors with a tag in the ear, on the neck or attached to the leg. It could also be to measure hormone level in milk, or animals standing to be mounted.

In the search for the right technology, there are many definitions and difficult words used, and it cannot be easy as a farmer to understand what to select. Some manufacturer statements are based on serious research, some are based on more limited tests and sometimes the marketing statement more describes a vision in the future, not what the sensor can do here and now. To standardize the sensor validation would make the different heat detection sensor options more comparable to each other. Then the customers can make conscious decisions about which sensor that is best suited for them. A sensor that has proven quality and is based on evidence.

Sensor data – for different purposes

When working with sensor development in DeLaval our main focus is to help our farmers in achieving their specific goals at the farm, for example to improve reproduction, health or productivity. This means that our focus is on farm management. In the ICAR Sensor Device Task Force, we are also working with the areas of sensor data for genetic evaluation and research. If we take the BCS camera as an example, a 3D camera that automatically measure the body condition score of an animal, it has been developed as a farm management tool, but of course the data can be used also for other purposes.

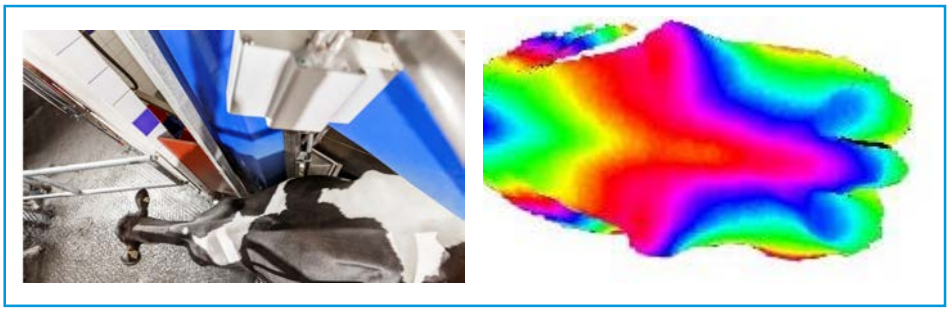

Figure 2. DeLaval Body Condition Scoring BCS

In the farm management application, the camera is replacing the traditional manual body scoring. We are going from a score a few times per lactation or monthly to scoring several times per day. The data is further processed in the biomodels of DeLaval DelPro and consumed by the farmer through reports, graphs or standard operating procedures, SOPs. The farmer is interested in different parameters during different parts of the lactation. Here the relative value and trends in the data is most important. In this application the absolute value of BCS is not as important.

If the BCS data on the other hand should be used for genetic evaluation the absolute value is the important data point. This puts other requirements on the sensor and the algorithms. Many different breeds, ages of animals, stages of lactation etc. must be included. The relative values and the trends are not as important in this application.

Another example of where a discussion and method for sensor validation is really needed is for Somatic Cell Count, SCC. When we want to validate a sensor that measures SCC from the farm management perspective, one value that we can provide is a sensor that detects clinical and subclinical mastitis cases without giving too many false alarms. That can be validated for example in sensitivity and specificity of detecting mastitis. This can be achieved by measuring SCC but also by a combination of other data sources such as cow specific information, electrical conductivity, milk yield and flow, LDH, or activity of the cow. The accuracy of the SCC sensor is only one part of the puzzle, it is the complete system to detect mastitis that is important to validate.

The same SCC sensor can also be used for measuring milk quality and securing that bulk tank SCC is on a good level. For this application, the validation process needs to target the ability of the sensor to measure SCC accurately. When using SCC in genetic evaluation or research it is also the accuracy of the measured SCC that is important, not the mastitis detection in itself.

Sensor validation against golden standard

Another aspect of sensor validation is when the golden standard available is lacking or weak. If we take BCS as example, the golden standard is manual observations. Manual scorers varies between each other but also the same scorer varies. It is difficult to be consistent. Even if scorers are trained in the same method it is quite common that the score varies ± 0.25 score. Looking at the graph in the picture below we can see the green line in the middle is the scoring of 1000 cows by the 3D camera. The blue and red lines represents ± 0.25 score. And the blue small dots in the back represents the manual scoring for the same animals. The sensor that we want validated, the camera, is much more consistent and repeatable than the golden standard, the manual scoring.

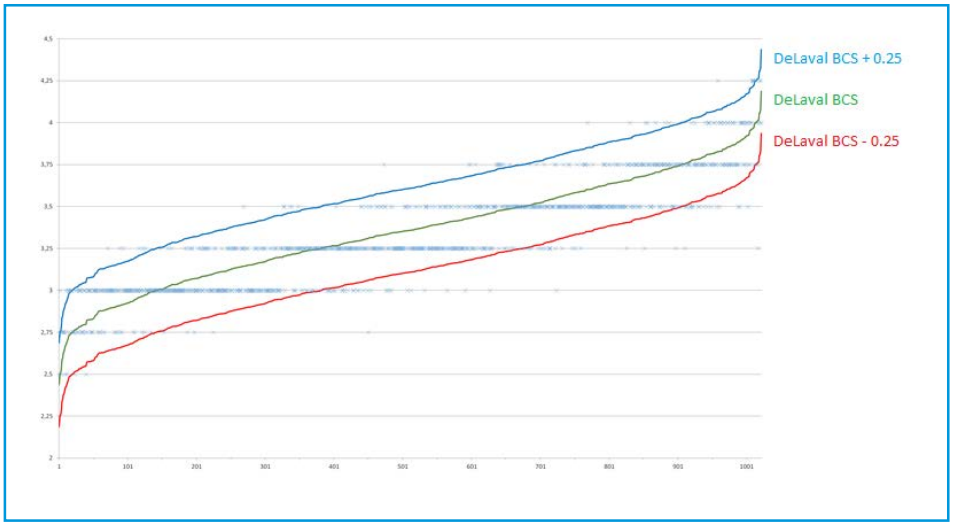

Figure 3. BCS data from individual animals.

The need of sensor validation

We at DeLaval chose to be part of the ICAR Sensor Validation Task Force because we see all these challenges that I have shown a few examples of. Both for us as manufacturers but mostly for the community of farmers. We also think that precision dairy farming is and will be an important area in the near and coming future. Many of our customers are investing and we want them to make decision based on facts and figures.

We see it as a benefit to have the possibility to get a quality stamp from an independent organization such as ICAR and that we can show that we have good accuracy and good quality in our products measured in a comparable way with other manufacturers. We also see it as a good opportunity to get guidance in our work with product development, verification and validation to ensure that we provide our customers with sensors that will help them in the right way. Making sustainable food production possible.

Genetic identification of beef and dairy cattle breeds in five regions of Russia

A.E. Kalashnikov[1], Y. Kabitskaya[2], L.A. Kalashnikova[1], E. Boyko[2], V.P. Prozerin[3], V.L. Yaluga[3], N. Furaeva[4], E. Zvereva[5] and A.A. Novikov[1]

[1]All Russian Research Institute of Animal Breeding, Ministry of Agriculture RF, Moscow, Russia
[2]Tyumen State Agrarian University of Nothern Ural, Tyumen, Russia
[3]Arkhangesk Scientific Research Institute of Agriculture RAS, Arkhangelsk, Russia
[4]Yaroslavl State Agricultural academy, Yaroslavl, Russia
[5]Yarosavl tribal association, Yaroslavl, Russia

Introduction

The primary documentation in breeding farms is kept electronically in the form of Selex databases (Plinor Ltd). When filling out the database with primary cattle accounting data, errors inevitably occur, the magnitude of which is not always known. In order to identify these errors, the relationship between cattle is determined mainly using immunogenetic and DNA analysis (microsatellite loci). As part of the research process for determining the relationship is carried out by STR and SNP genotyping. The commercial assays of companies of the Institute L.K. Ernst (VIZ, Ministry of Education), Gordiz (Skolkovo), VNIIPLEM (Ministry of Agriculture), Termo Fisher were used for genotyping. There are a number of regional laboratories that use the methodology of Gordiz Ltd. and VNIIPLEM. Only the last three tests are designed according to ISAG rules. VIZ uses its own genetic testing algorithm. Therefore, the harmonization of the method of determining the relationship and bringing the methods of data acquisition, storage and processing, determining the relationship of animals are the main tasks before determining the breeding value (EBV) (from 2018).

Materials and methods

According to national rules for parentage testing, genetic identification is used to genotype 10% of the total breeding stock by analyzing of 11-15 microsatellite loci (BM1818, BM1824, BM2113, CSRM60, CSSM66, ETH10, ETH225, ETH3, ILSTS006, INRA023, SPS115, TGL0 , TGLA122, TGLA126, TGLA227) (ISAG). The genetic identification of cattle was carried out on a total of 8483 animals in the Moscow, Arkhangelsk (N = 150), Tyumen (N = 2091), Novosibirsk (N = 6179) and Yaroslavl (N = 63) regions. The Yaroslavl, Kholmogorsky, Holstein, Black and White, Salers, Aubrac, Aberdeen-Angus, Hereford breeds participated in the parentage testing. The panel of microsatellite loci was developed and jointly tested by Grodno state University and CMSCH, which was already certified according to the ISAG standard for cattle genotyping.

Results and discussions

The causes of errors in the primary registration of cattle are unintentional errors in the recording of the birth or purchase of an animal, and deliberate distortions. In the latter case, an error occurs when the data provided in the report is distorted. In this case, the breeding farm examines the livestock to determine kinship in a larger quantity of individuals (triples), and provides data that are correct in a predetermined amount. In this case, we cannot estimate the magnitude of the errors encountered, but we assume them based on our practice.

In breeding farms, the conditional range of errors of primary accounting of relationships is 5-30%, and in ordinary farms it can reach up to 45%. During genetic testing, in view of the intentional error described above, in the breeding farms revealed an overly low value error in determining the relationship from 0 (0-3) to 11% for the Holstein and up to 7% for the Black-and-White breeds. For other milk cattle breeds the error was 15-45%. When determining the relationship between meat cattle the error was 30-45% and higher.

The genotyping errors to ISAG values of Ngr, Ger, Aga, and Rga was 168-341, 0-172, 0.63-0.99, respectively. The high variance of the obtained error data is due to the application of tests from different manufacturers on the same breed at the same time.

Currently, only the commercial private company Gordiz Ltd has received the certificate of conformity ISAG and ISO in Russia. In Russia there are no laws requiring the conduct of quality control analyzes and cross-checks. The most accurate analysis is provided by laboratories that use @Gordiz, @VNIIplem and @Termo reagents.

The only thing that can be done to improve this situation is to create a network of independent and non-profit laboratories that are independent and loyal to the Ministry of Agriculture. These laboratories must adhere to ISAG / ICAR / ISO standards and pass international and national quality system audits.

Unfortunately, according to the law, immunogenetic parentage testing of livestock is still the predominant testing method. At this time, the genotyping databases for microsatellite loci and SNP chips are in the hands of commercial companies (Ministry of Education and Science and Skoltechh) and are a trade secret.

Conclusion

Currently in Russia in the field of animal genetic identification, ICAR / ISAG / ISO standards are being introduced. It is planned to implement these standards to breeding work with breeding cattle and when selling animals. Implementation of open databases on animal genotyping is needed.

During testing, an artificially low level of identification error was revealed. It is necessary to work on the elimination of errors with the use of international quality standards and regulations.

The National Research Center for Breeding (VNIIplem) receives and collects data on genotyping of livestock and organizes the receipt of these data in accordance with the part international standard ISAG / ICAR since 2018. The experts of VNIIPLEM starts to follow ICAR guidelines when developing methods for collecting productivity data and assessing breeding value.

Acknowledgements

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Analysis of the accuracy of C method for estimating 24-hour (yields) with alternated protocols

X. Bourrigan[1], H. Leclerc[1] and G. Augier[2]

[1]Institut de l'Elevage, 149, rue de Bercy, 75595 Paris, France
Corresponding Author: xavier.bourrigan@idele.fr
[2]France Conseil Elevage, 42, rue de Châteaudun, 75009P aris, France

Summary

In France, the number of farms using alternated protocols has increased in the last ten years and the percentage has reached 25% in 2018. Milk Recording Organisations (MRO) want to adapt and simplify protocols to the realities encountered in the field by using ICAR methods to estimate 24-hour yields in alternated one-milking recording (T), one-milking sampling with milk weights from more than one milking (Z). Another way consists by using constant one-milking recording (C).

The aim of this study is to analyse the accuracy of the C method on test-day record and on lactation (milk yields, fat yields, protein yields, fat percent and protein percent). Performances adjusted based on method derived from "Liu method" from constant one-milking recording and alternated one-milking recording were compared with the reference on a 24-hour yields and 305-days lactation basis on a large dataset.

A validation of the model was done on an independent data set: 138 222 test-day - 12 666 lactations for training data *vs* 69 982 test-day - 6 381 lactations for validation study.

The model adjustment was estimated through Determination Coefficient (R^2), Mean bias and Standard Deviation of bias. The results show that on test-day record the R^2 is lower in pm milking compared with am milking. R^2 is higher than 0.939 for milk, protein yields and protein percent. Fat yields and fat percent show a higher residual variability, with R^2 between 0.871 and 0.881 for fat yields and 0.776 and 0.834 for fat percent, in favour of morning milking. On lactation, the loss of accuracy ($1-R^2$) in comparison with the reference 305-days is lower than 1.2% for T method and 6.0% for C method for all traits except for fat percent which the loss of accuracy reaches 3.9% and 14.8% respectively. For all traits, the results of accuracy are lower with C method compared with T method. Estimated bias is on average very low. The results obtained with C method in this study are similar to a study carried out by Berry *et al.* (2005) on alternative milk recording protocols.

Keywords: milk recording, alternated protocols, adjustment, 24-hour yields, 305-days lactation.

Introduction

In France, the percentage of dairy farms which use alternated one-milking recording (T), one-milking sampling with milk weights from more than one milking (Z) has increased by more than 10% between 2005 and 2018. Since 2011 and after a collaboration with the VIT (Germany), the French Guidelines allows to estimate 24-hour yields for T and Z protocols by using Liu's method approved by ICAR (Bourrigan, 2011; ICAR Guidelines, 2017; FGE Guidelines, 2018).

This method proposed by Milk Recording Organisations (MRO) to the breeders is able to simplify and to reduce the cost of milk recording with the condition to respect alternation milking between test-day records.

The aim of this work is to study the possibility of using constant one-milking recording (C method, ICAR Guidelines, 2017) to answer the expectations of the MRO's, the breeders, the required quality for cow management and genetic evaluation, with using of Liu's method.

On the published literature, a study has been made about the accuracy of predicting milk yields from alternative milk recording schemes and particularly on C method (Berry et al., 2005).

The current study was conducted in 2018 about C method and consisted:

- to test the method for estimating 24-hour for milk yields, fat percent, fat yields, protein percent, protein yields;
- to evaluate the accuracy of the method on test-day record and on lactation;
- to propose changes of the France Genetics Breeding (FGE) dairy cattle milk recording Guidelines, according to the results achieved.

Material and methods

Presentation of the "Liu's method" model used in the study

This method is based on a multiple regression model for estimating daily yields and component percent from pm or am milking (Table 1).

The French "Liu's method" model considers separate regressions (Table 2) for 120 combinations

- 5 milking interval classes;
- 2 parity classes;
- 12 lactation stage classes.

The regression coefficients of the "Liu's method" have been defined from a reference data set of 208 204 test-day records, 146 herds, 14 396 cows mainly Holstein breed (Table 3). A validation study of the model was done on an independent data set: 138 222 test-day records for training data (2/3) *vs* 69 982 test-day records for validation study (1/3).

Table 1. Presentation of the "Liu's method".

yA4 [ijk] = b0 [ijk] + b1 [ijk] yAT [ijk]
yA4 = estimated 24-hour
b0 = intercept
b1 = regression coefficient
yAT = pm or am milking test-day results
[ijk] = effect of parity, milking interval, lactation stage

Table 2. Definition of effect classes considered in the French "Liu's method" model.

Milking interval classes	5 classes	pm milking: <10h; 10h-10.5h; 10.5h-11h; 11h-11.5h; >11.5h am milking: <12.5h; 12.5h-13h; 13h-13.5h; 13.5h-14h; >14h
Parity classes	2 classes	1st lactation, 2nd and later lactations
Lactation stage classes	12 classes	30 days per class

Description of both datasets used in the study

Data were collected by Milk Recording Organisations from herds in A4 scheme with use of Electronic Milk Meter Lactocorder and recording of one milk weight, one sample at each milking (pm and am). Data were selected in order to constitute two relevant datasets for the different steps of the study.

Five criteria has been used to exclude raw data : too large difference in milk weight between milking, permitted range of the daily recorded values (defined in ICAR Guidelines, 2017), records with missing information, days in milk between 5 and 360 days, number of lactation grower than 9 (Table 3).

In a first step, the reference 24-hour has been calculated from 208 204 test-day records for milk yields, fat percent and fat yields, protein percent and protein yields. In a second step, the regression coefficients of the "Liu's method" was applied to the 208 204 test-day records respectively from pm and am milking to calculate 24-hour yields for C method and T method (both adjusted).

The statistical analysis was carried out by comparing the reference 24-hour yields on pm and am milking (for all traits) with C method adjusted and T method adjusted.

The results of the accuracy (R^2, Mean bias, Standard Deviation of bias) published on test-day record come from the 69 982 test-day records used to validate the "Liu's method" regression coefficients.

Table 3. Description of the dataset for analysis on test-day record.

Criteria	Dataset
# Test-day records	208 204
# Cows (93% Holstein breed)	14 396
# Herds	146
Average milk weight pm - am milking - kg	12.9 - 15.9
Average fat pm - am milking - %	4.23 - 3.74
Average protein pm - am milking - %	3.26 - 3.20
Average interval pm - am milking - h:decimal	10.7 - 13.3

For the analysis of lactation results, the Fleischman calculation method's was used to define a reference 305-days lactation. A total of 19 047 lactations fulfilled the conditions (Table 4).

The statistical analysis was carried out by comparing the reference 305-days lactation (for all traits) respectively with C method adjusted (all pm and all am) and T method adjusted (pm/am and am/pm).

The results of the accuracy (R^2, Mean bias, Standard Deviation of bias) published on lactation come from 6 381 lactations for validation study.

Table 4. Description of the dataset for analysis on lactation.

Criteria	Dataset
# Lactations 305 days	19 047
Average milk yields - kg	9 172
Average fat - %	3.85
Average fat yields - kg	351
Average protein - %	3.12
Average protein yields - kg	285

Results - Analysis of the accuracy

Results on test-day record

The level of accuracy on test-day record (Table 5) is the same between C method adjusted and T method adjusted on pm and am milking for all traits.

The results show that on test-day record the R^2 is lower in pm milking compared with am milking.

R^2 is higher than 0.939 for milk yields, protein yields and protein percent. Fat yields and percent show a higher residual variability, with R^2 between 0.871 and 0.881 for fat yields and 0.776 and 0.834 for fat percent, in favour of morning milking. For all traits, the results of Standard Deviation of bias are higher in pm milking compared with am milking.

Table 5. Mean bias, Standard Deviation of bias and Correlations (R^2) between reference 24-hour yields and C method adjusted, T method adjusted (N= 69 982)

	Mean bias		SD of bias		Correlations (R^2)	
Traits - Milking	C method adjusted	T method adjusted	C method adjusted	T method adjusted	C method adjusted	T method adjusted
Milk yields kg - pm	-0.02	-0.02	1.97	1.97	0.940	0.940
Milk yields kg - am	0.07	0.07	1.64	1.64	0.959	0.959
Fat% - pm	0.00	0.00	0.32	0.32	0.776	0.776
Fat% - am	0.00	0.00	0.28	0.28	0.834	0.834
Fat yields kg - pm	0.00	0.00	0.11	0.11	0.871	0.871
Fat yields kg - am	0.00	0.00	0.10	0.10	0.881	0.881
Protein% - pm	0.00	0.00	0.07	0.07	0.956	0.956
Protein% - am	0.00	0.00	0.06	0.06	0.971	0.971
Protein yields kg - pm	0.00	0.00	0.06	0.06	0.965	0.965
Protein yields kg - am	0.00	0.00	0.05	0.05	0.975	0.975

Results on lactation

The results show that on lactation (Table 6) the loss of accuracy (1-R^2) in comparison with the reference 305-days lactation is:

- lower than 6.0% for C method adjusted for all traits (milk yields, fat yields, protein percent and protein yields) on all pm, all am milking except for fat percent which the loss of accuracy is equal to 14.8% on all pm milking,
- lower than 1.2% for T method adjusted for all traits (milk yields, fat yields, protein percent and protein yields) on pm/am, am/pm milking except for fat percent which the loss of accuracy is equal to 3.9% on am/pm milking.

For all traits, the results of accuracy are lower on C method compared with T method, while mean bias is on average very low on C method and T method for all traits.

The level of Standard Deviation of bias is higher for C method than T method with large difference for some traits (milk yields, fat yields).

Table 6. Mean bias, Standard Deviation of bias and Correlations (R^2) between reference 305-days lactation and C method adjusted, T method adjusted (N= 6 381).

Traits 305 days - Milking	Mean bias	SD of bias	Correlations (R^2)
C method adjusted			
Milk yields kg - all pm	0.5	352.5	0.966
Milk yields kg - all am	21.3	262.7	0.978
T method adjusted			
Milk yields kg - pm/am	11.1	154.8	0.997
Milk yields kg - am/pm	10.7	152.2	0.997
C method adjusted			
Fat% - all pm	0.004	0.18	0.852
Fat% - all am	0.018	0.18	0.856
T method adjusted			
Fat% - pm/am	0.009	0.10	0.964
Fat% - am/pm	0.009	0.10	0.961
C method adjusted			
Fat yields kg - all pm	0.6	18.4	0.940
Fat yields kg - all am	1.1	18.4	0.940
T method adjusted			
Fat yields kg - pm/am	0.9	12.0	0.989
Fat yields kg - am/pm	0.8	12.2	0.988
C method adjusted			
Protein% - all pm	0.000	0.48	0.955
Protein% - all am	-0.001	0.34	0.973
T method adjusted			
Protein% - pm/am	-0.001	0.22	0.996
Protein% - am/pm	-0.001	0.21	0.997
C method adjusted			
Protein yields kg - all pm	0.3	9.6	0.971
Protein yields kg - all am	0.5	7.5	0.981
T method adjusted			
Protein yields kg - pm/am	0.4	4.3	0.997
Protein yields kg - am/pm	0.4	4.3	0.997

Discussion and conclusion

This French study about the analysis of the accuracy of C method for estimating 24-hour yields was carried out on test-day record, on lactation from two relevant datasets. The study also allowed to update the accuracy results of T method carried out by FGE in 2011.

Milk weights and analysis results have been estimated by an ICAR approved method, the Liu's method in this current case. The regression formula has been defined from a first relevant dataset and validated from a second independent dataset.

On test-day record, the accuracy of C method adjusted (equal to T method adjusted) is better on am milking compared with pm milking for all traits analysed (milk, fat, protein). The lowest level of R^2 concerns fat percent with respectively 0.776 and 0.834 in pm milking and am milking.

On lactation, the loss of accuracy of C method is equal to 14.8% and 14.4% for fat percent (respectively on all pm and all am milking), equal to 6% for fat yields on both milking.

The loss of accuracy of T method is equal to 3.9% and 3.6% for fat percent (respectively on pm/am and am/pm milking), equal to 1.2% and 1.1% for fat yields (respectively on am/pm and pm/am milking). For all statistical criteria and all traits analysed, the level of accuracy is lower on C method compared with T method.

The results of C method accuracy's obtained in this French study have been compared with those obtained by the Berry and al., 2005 study's on 305-days lactation for milk yields, fat yields and protein yields. The comparison between both studies showed that:

- the level of R^2 is better from 2% to 3% in the French study;
- overall the level of Mean bias and Standard Deviation of bias is the same;
- the level of performance 305-days lactation is different (performance level of 6 000 kg in Berry and al., study against more than 9 000 kg in the French study).

After analyzing the results of this French study, the FGE board has proposed a program of implementation of C method in the dairy cattle milk recording Guidelines by the end of 2019 with conditions:

- to use the Liu's method for estimating 24-hour yields;
- to describe a Standard Operating Procedure (SOP);
- to define ponderations (for milk yields, fat percent, fat yields, protein percent, protein yields) among the level of individual lactation qualification model use by FGE and applied for genetic evaluation.

The latest ICAR survey about global 24-hour calculation trends in classical milk recording systems (ICAR Conference 2019 - Prague) showed that 5 ICAR organisations in the world use constant one-milking recording (C) scheme.

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Assessing the usefulness of fat content and milk yield data gained during ICAR farm tests of milk recording and sampling devices to estimate carry-over in milking systems

C. Ammon

Leibniz-Institute for Agricultural Engineering and Bioeconomy (ATB), Max-Eyth-Allee 100, 14469 Potsdam, Germany

Abstract

Carry-over between milkings can affect sampling results that are used for herd management, breeding or diagnostic purposes in dairy cows. Giving an estimate of a milking system's carry-over therefore would be a useful additional part of the ICAR certification of a recording and sampling device.

Current methods of estimating or calculating carry-over between subsequent milkings require additional expenses for e.g. tracer chemicals or constituents of milk that can be used as a tracer and their analysis, respectively. Another factor required for these methods is time, which also translates into additional expenses. However, during an ICAR farm test of a recording and sampling device all relevant data required for an estimation of carry-over can potentially be recorded. This aim of this article is to evaluate the usefulness of these data (milk yields, fat contents, milking sequences) for estimating a given milking system's carry-over.

Data gained during ICAR farm tests are used in different statistical models (regression analysis, linear mixed model analysis with repeated measures) to estimate the carry-over of the combination of milk recording device and sampling device under test. This includes at least four different manufacturers and different milking systems (three automatic milking systems, one conventional milking system).

Data from experimental farms are used as a base to create "virtual" herds of dairy cows. These herds are used to simulate different setups of an ICAR farm test: conventional milking systems and automatic milking systems with short and long sequences of subsequent milkings per day and milking time, as well as different levels of carry-over. Carry-over is then estimated in simulations using the above-mentioned statistical methods. The simulations indicate the level of carry-over that could be detected in ICAR farm tests as well as the inherent test power for the different setups.

The results of the simulations are compared to the ICAR farm tests with a similar setup, and as a conclusion possible options for future farm tests are derived.

Introduction

Milk samples are used for several types of laboratory diagnostics, spanning from e.g. fat and protein content to somatic cell count and pregnancy or disease detection. For some of these lab diagnostics it is important to have an idea about the carry-over of the milking system the samples were gained from, since the robustness of the diagnostic

methods against carry-over may not always been given, and hence carry-over can affect the results. If the expected amount of carry-over is known, this knowledge can be used to assess the usefulness of a given sample. Lab methods can be adjusted to provide reliable results, or the sampling procedure in a given milking system can be adjusted to take samples in a way that reduces or avoids carry-over, if samples are taken for a specific purpose. Simply put, knowing a milking system's carry-over can be very useful.

Established methods for determining carry-over in milking systems require conducting "milkings" in a milking system with known concentrations of a tracer substance of some kind, e.g. color tracers or mixtures of artificial milk with known constituent concentrations. These methods require special equipment, possibly larger amounts of milk, and certainly also additional labor and time. Calculation of carry-over is finally done using the values for amounts of milk from subsequent milkings and values for e.g. fat content – values that are available from ICAR farm tests for certification of milk meters and samplers anyway. Therefore the aim of this study was to assess the usefulness of ICAR farm test data to estimate carry-over in milking systems.

Methods

An easy way to calculate carry-over is using a linear regression model. The most basic approach uses the observation of the fat content of the current milking and tries to explain this using the fat content of the previous milking and the current milking's milk yield as regression factors:

$$f_t = \mu + a \cdot f_{t-1} + b \cdot m_t + \varepsilon \qquad (1)$$

with f_t as the observed fat content f in milking t, μ as the intercept, a as the regression coefficient for f_{t-1}, f_{t-1} as the fat content f in milking t-1, b as the regression coefficient for m_t, m_t as the milk yield in milking t, and å as the random residual. The regression coefficient a is the estimate of carry-over, and the regression coefficient b provides the information whether carry-over depends on milk yield or not.

However, there is more information available in an ICAR farm test that may be put to use in estimating carry-over. There can be farm effects, milk meter effects, sampler effects, or cow effects that come to mind. When tests on a farm are done with the same devices on more than one day, there also might be a day effect to consider. For use with the data available for this study, model (1) therefore was adjusted as follows:

$$f_{dt} = \mu + a \cdot f_{dt-1} + b \cdot m_{dt} + dev_{ik} + c_{jk} + \varepsilon \qquad (2)$$

with, in addition to model (1), d denoting the milking time, dev_{ik} as the effect of device i on farm k, and c_{jk} as the random effect of cow j on farm k.

The data available for analysis included data from three AMS farm tests and one conventional milking system farm test. An overview about the available data is shown in table 1.

Using this statistical model will result in some carry-over estimates, but that does not give enough information yet. It is also important to know how reliable these results are. In this case this means that it is necessary to know if a farm test setup is able to detect a carry-over if it actually exists. In statistics this can be addressed by calculating the power of a statistical model. For more complex models like the one above it is necessary to run some simulations to estimate the test power. A test power to aim for

Table 1. Overview of structure of available data from ICAR farm tests.

Device	Farms	Meters/ samplers	Milking sequences	Cows	Milkings
AMS 1	2	4	8	180	256
AMS 2	1	2	2	63	74
AMS 3	1	1	2	77	120
CON 1	1	6	2	190	240

is at least 80 % usually. A value of 50 % means that flipping a coin will lead to a result comparable with the test setup, and conducting a test in that case must be considered a waste of resources.

In the second part of this study data from an experimental farm was used to set up simulated farm tests. The original data set consisted of 16 years of data from official milk recording from a research farm, a total of 29,533 data sets from 1,108 individual cows. These data were classified per cow by lactation levels (1, 2, 3-5 and 6+) and days-in-milk levels (d” 95 d, d” 185 d, d” 305 d, and > 305 d). For each combination the mean milk yield and fat content per cow was calculated. These values were considered a pool of “cows” to select from when setting up a simulated herd, with about 7,500 individual records. This is sufficient for setting up a test with individual milking times, where every cow can only be milked once per sequence. For an AMS test setup it needs to be considered that the same cow can be milked again after a certain time. To take this into account, every milking requires having an associated milking duration, so that it can be simulated when a cow is back in the pool of cows to choose from when setting up a milking sequence for an AMS system simulation. This can be done by also giving each “cow” an average milk flow rate.

Based on this data set, the simulation process can be started. The simulation consisted of several steps, as follows:

1. Choose type of device: AMS or conventional milking system. This predefines the number of devices and samplers per farm, the number of total milkings and the number of milkings per milking sequence. In an AMS system it is common to test two samplers on two farms with one AMS box each, with at least 50 valid milkings per combination. A test in a conventional milking system usually consists of testing four devices and samplers per farm, with at least 40 valid milkings per device.
2. Choose number of cows per farm or group. This determines how many milking sequences are necessary to get the required number of valid milkings.
3. Create the test herds: select the desired amount of “cows” from the aforementioned pool. Then randomly select “cows” from that herd to create a milking sequence for every milking time. In a conventional system every “cow” may only turn up once per milking time. In an AMS simulation “cows” can return to the pool after they have been selected and then waited for a minimum amount of time. In this study a minimum waiting time of 6 h was used.
4. Create the carry-over: Schedule a “true” carry-over for the system under test, and apply some variation for each individual milking. This can be done by using standard error estimates from the real data, for example. Then use milk yields and fat contents to calculate the “true” fat content for every milking. Based on the true fat content and the true carry-over the resulting fat content in the samples can be calculated.

5. Run the statistical linear model for carry-over estimation with the simulated data set. Check if the carry-over estimate is significantly different from zero, and check the deviation of the estimated value from the true value.
6. Repeat steps 2 to 5 to get a good estimate for the test power, i.e. the percentage of simulation that found a significant result for the carry-over estimate. For this study 100 repetitions were made. The simulation then can be repeated for different "true" carry-over values to get a better idea about the boundary conditions for detecting carry-over with sufficient test power.

Results and discussion

The results from the mixed linear model (2) can be found in table 2. None of the carry-over estimates was significant. This may be true for AMS 1, for the other AMS systems some carry-over could be expected. Standard errors are high for the AMS systems, which indicate that it will be more difficult to detect a true carry-over. The conventional system actually has some carry-over, so the result from the linear model is likely false in this case.

Figure 1 shows the estimated carry-over values from 100 simulations for ten different "true" carry-over values ranging evenly from 2 % to 20 %, based on an ICAR test setup for an AMS. It can be seen that variation between the simulations within each carry-over value is high, likely resulting from both high initial carry-over variation as well as variation from "herd composition", selected "cows" and "milking sequences".

In figures 2 and 3 the test power estimates for various carry-over levels are shown. Low carry-over values are rarely detected properly in these test setups – the paradoxically increased number of detected carry-over-levels for the conventional milking system actually stems from negative carry-over estimates that are different from zero. All in all, a somewhat sufficient detection of existing carry-over can only be found for higher values of 16 % or higher.

In figure 4 the variation of carry-over estimates between conventional milking system setups and AMS setups can be compared. The values are slightly higher for the AMS simulation, which might be due to the lower number of devices in the AMS test setup compared to the conventional milking system. The longer milking sequences in the AMS test setup and the potential repeated measurements on the same cow being milked twice in an AMS sequence probably cannot make up for the larger number of devices in the conventional system with regard to variation between simulations.

Table 2. Results for carry-over estimates for different milking systems from ICAR farm tests. SE denotes the standard error of the carry-over estimate.

Device	Carry-over estimate	P-value (t-test)	SE
AMS 1	0.03	0.5557	0.05
AMS 2	0.15	0.0628	0.08
AMS 3	-0.01	0.8326	0.05
CON 1	0.00	0.9615	0.01

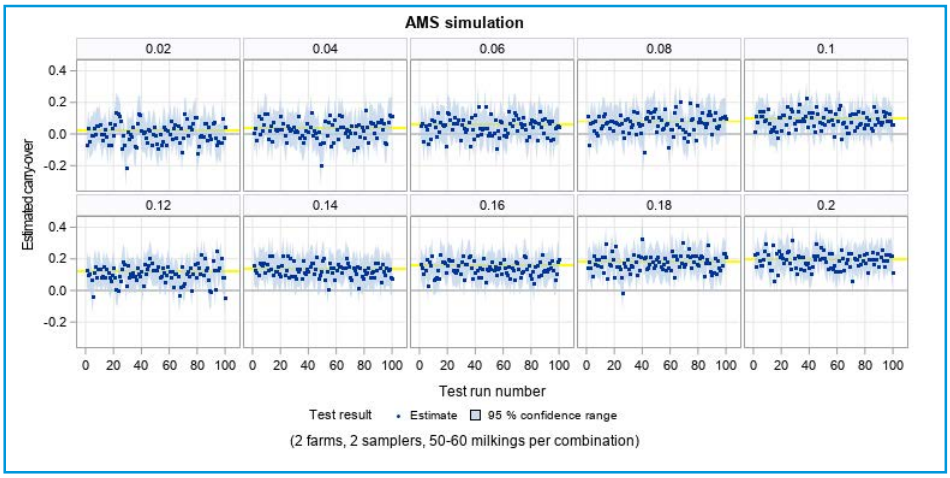

Figure 1. Results from several carry-over estimations for an AMS system ICAR test setup.

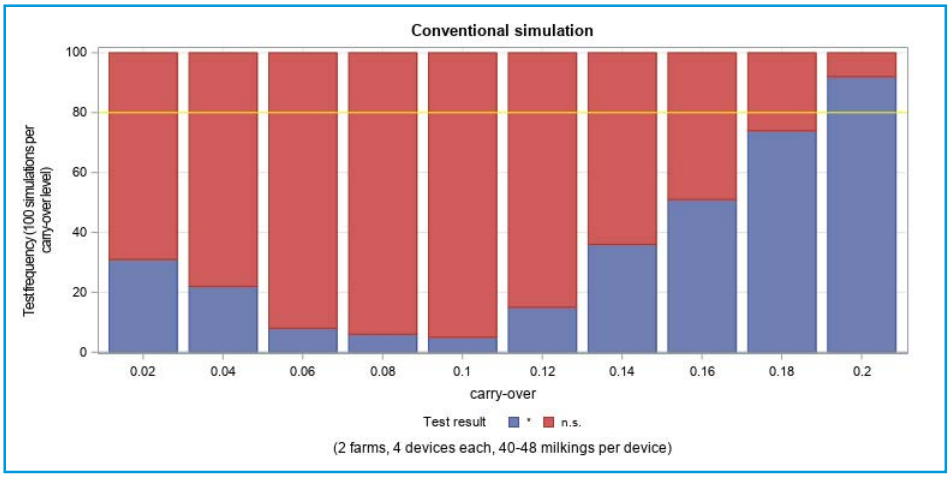

Figure 2. Test power estimates for ten different carry over levels, for a conventional milking system ICAR test setup.

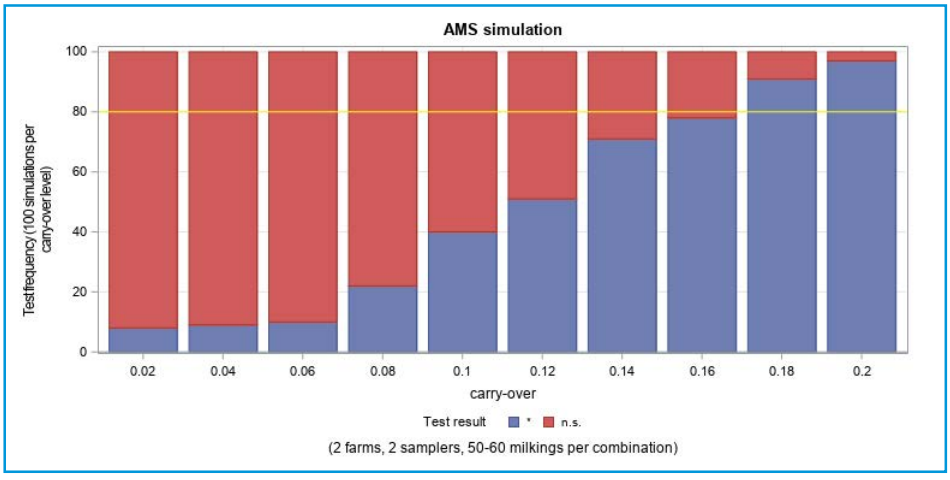

Figure 3. Test power estimates for ten different carry-over levels, for an AMS system ICAR test setup.

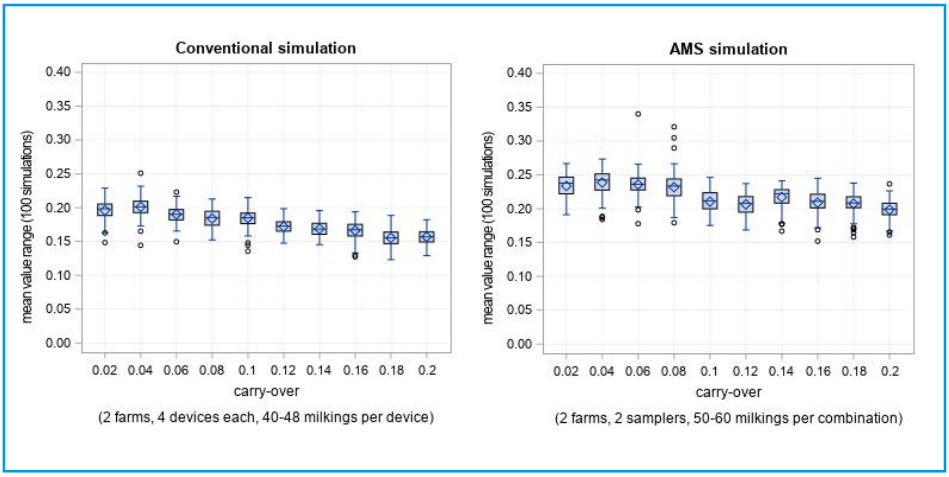

Figure 4. Estimated carry-over value ranges, for a conventional milking system ICAR test setup (left) and an AMS system ICAR test setup (right).

It must be considered that the data from the original ICAR farm tests can be improved. For three of the four milking systems only half the amounts of data were useful, since there were no cow IDs for the other test farms available. This can lead to smaller standard errors and in consequence also to less variation in the simulations.

Conclusion

Based on the simulation results it is difficult to justify using data from ICAR farm tests for carry-over estimation without further adjustments. For better results more information input is necessary, especially knowing some more true carry-over levels (and their variation!) of given milking systems as reference values will be helpful. Adding data from more previous ICAR tests with potentially more than the minimum measurement requirements due to repeating tests in case the device did not pass in the first time might also be useful to get a better grasp of the ability to detect carry-over. Lastly, improving the statistical model is also necessary to avoid paradoxes like negative carry-over estimates, or to take a closer look at the dependency between carry-over and milk yield.

Overall, the critical carry-over levels to detect are in the range from 2 % to 8 % for most lab methods. At the moment this seems to be a challenge. It could be helpful to look at other traits like protein and lactose content in addition to fat content to improve estimation, or put some thought into alternative ways of estimating or measuring carry-over.

Relationships between conformation traits and milk yield, lifetime production and number of lactations in Czech Holstein cows

A. Noskova[1], J. Pribyl[1] and L. Vostry[2]

[1]Genetics and Breeding of Farm Animals, Institute of Animal Science, Praha - Uhrineves, Czech Republic
Corresponding Author: noskovaadela@seznam.cz
[2]Department of Genetics and Breeding, Czech University of Life Sciences, Prague, Czech Republic

Abstract

The phenotypic relationships between type traits and functional traits were analysed in Czech Holstein dairy cows born between years 2002 and 2015, with minimum proportion of Holstein genes 88%. Two slightly different models were used to evaluate the effects of 1 measured trait (in cm), 20 linear type traits (9 classes each), 4 composite traits, and final score (both with scales 0 – 100 points) on milk production traits and longevity. Sample for analysis of effect on milk yield included observations from 247 790 cows within one to four lactations (570 671 rows in total), second sample for longevity study included data from 228 161 cows with sums of one to maximum six lactations. Cows were required to obtain type classification scores between 30th and 210th day of the first lactation in age between 650 and 1206 days. Milk yield (in kg) records below 5079 kg and above 16 622 kg were set to absent.

Longevity traits were defined as lifetime performance, i.e. total milk yield in kg for whole productive life, and as total number of lactations. Lifetime production was between 1004 kg and 95 480 kg. Maximum number of lactations was 6, cows with higher count or cows, which were not culled before the possibility of survival of 6 lactations, were not included. Analysis were performed for linear type traits altogether as well as separately for each of 20 type traits.

Squared scores of type traits were included to derive polynomial regression and best fitting curve. They were added into the Linear models, which included fixed effects of herd-year-season of birth and classifier-herd-year-season of scoring, age at first calving and age at scoring in days, day of lactation at scoring, effect of classifier and (not for longevity model) number of lactation, service period and parturition interval. Different shapes of regression lines were obtained. Some traits showed linear relationship, straight line with both negative or positive slope (with higher contribution for 1 point or for 9 points), some were curved with best values either for middle values (4 – 6 points) or marginal values (1 and 9 points).

Also, composite traits did not show a clear linear relationship, as would be expected. The highest impacts on milk yield were from type traits (in decreasing order) body condition score, udder width, udder depth, rear udder height and angularity. The strongest influence on lifetime production was found for body condition score, udder depth, body depth, rump angle and rear legs side view. Importance of udder width, body condition score, udder depth, bone quality and rear legs side view for number of lactations was confirmed.

Some traits, such as stature, angularity, rump angle and width and body condition score, showed a clearly intermediate optimum for longevity traits, while greatest milk yield was expected for one of the extreme scores.

Keywords: linear type traits, conformation, milk yield, lifetime performance, number of lactations.

Introduction

In many studies, relationships between conformation traits and variety of production and non-production traits were investigated. Both phenotypic and genetic correlations were reported and used as a basis for selection of cows while accounting for the fact that cattle conformation is associated with production efficiency (Sawa *et al.*, 2013). Therefore, often linear scoring of type traits is carried out routinely for the total population of cows or at least for daughter groups of test bulls (Zavadilová 2011).

Linear type traits are recorded with a use of lineare score on different scales, most frequent is a use of nine-point scale. That allows the type trait to vary from one extreme to another. While correlations between the production or non-production traits and the type traits give a basic information about relationship (whether it is negative or positive, strong or weak), true association can vary throughout the whole scale. In reality it can mean (an often means), that a peak value of the production traits is situated around a middle score of the type traits, i.e. the relationship between conformation and production or non-production traits can vary in shape from linear to curved (hyperbolic or parabolic). This prove multiple research results, as reported by Cruickhank *et al.* (2002), Sewalem *et al.* (2004), Zavadilová *et al.* (2011) and Khan *et al.* (2016).

Longevity can be defined in different ways, as length of productive life expressed in days (Ducrocq *et al.*, 1988), as total number of lactations, lifetime performance (LP) or production per lactation (Morek-Kopec, Zarnecki, 2011). Observed length of productive life is called true longevity and after adjustment for production it is termed functional longevity (Ducrocq *et al.*, 1988). Functional longevity represents a cow's ability to avoid involuntary culling, therefore it depends mainly on a decision of the farmer regarding culling.

Because longevity is highly positively correlated with profitability (Weigel *et al.*, 1995; Norman *et al.*, 1996), reducing involuntary culling leads to improved herd profitability, e.g. reduced cost of replacement, higher intensity of dam selection, and an increased proportion of mature cows with higher production (Morek-Kopec, Zarnecki, 2011). The assessment of exact length of life or connected performance would require waiting, which for the purposes of breeding is not acceptable. Therefore, earlier estimations are being used, which involve different methods. The official genetic evaluation for longevity in the Czech Republic is carried out using survival analysis, as reported by Ducrocq and Sölkner (1998). To increase the accuracy of genetic evaluation it is possible via including correlated traits, that can be assessed during the first lactation (Weigel *et al.*, 1998). Type traits have been investigated for their suitability, regarding routine recording in most breeding programs and international conversion of sire-predicted transmitting abilities for some type traits (Brotherstone *et al.* 1997; Berry *et al.* 2004).

The objective of this study was to evaluate the relationships between conformation traits and milk yield and longevity traits in Czech Holstein cows in the level of measured (phenotypic) levels.

Material and methods

Data

Two datasets and two model equations were created in order to assess the relationships, first for milk yield and second for longevity traits. Data were obtained from the Holstein Cattle Breeders Association of the Czech Republic.

The two slightly different models were used to evaluate the effects of 1 measured trait (height at sacrum in cm (HS)), 20 linear type traits (9 classes each), 4 composite traits, and final score (FS) (both evaluated in interval 50 – 100 points) on milk yield (MY) and longevity. MY was provided in kg of milk per normalized (305-day) lactation. Longevity traits were defined as lifetime performance (LP), i.e. total milk yield in kg for the whole productive life (maximum 6 lactations), and as total number of lactations (NL).

The linear type traits were: stature (ST), chest width (CW), body depth (BD), angularity (AN), rump angle (RA), rump width (RW), rear leg set – rear view (RLR), rear leg set – side view (RLS), foot angle (FA), fore udder attachment (FUA), front teat placement (FRP), teat length (TL), udder depth (UD), rear udder attachment (RUA), medial suspensory ligament (MSL), rear teat placement (RTP), rear udder width (RUW), bone quality (BQ), locomotion (LOC), body condition score (BCS). Following composite traits, computed as a function of scores of the appropriate sets of linear type traits, were: dairy strength (DS) (from the year 2004 as a combination of dairy form and body capacity), body composition (BC), udder (U) and feet and legs (FL). Final score was computed from other composite traits. All the traits were recorded on all cows in datasets, that is for 247 790 records in first dataset and 570 671 in the second. The distributions of linear traits were not transformed, because the scores showed normal or near-normal distribution, which enabled statistical analyses. The basic description statistics of scores of analysed traits as well as production traits are presented in Table 1.

Table 1. Means, standard deviations and minimum and maximum values of height at the sacrum, linear type traits, composite traits, milk yield and longevity traits.

	Dataset 1[1]					Dataset 2[2]				
Trait	n	Mean	SD	Min	Max	n	Mean	SD	Min	Max
HS*	570,671	145.32	3.47	110	168	228,161	145.17	3.53	110	168
ST	570,671	5.68	1.20	1	9	228,161	5.70	1.22	1	9
CW	570,671	5.60	1.17	1	9	228,161	5.60	1.21	1	9
BD	570,671	5.58	1.24	1	9	228,161	5.59	1.27	1	9
AN	570,671	5.45	1.11	1	9	228,161	5.45	1.13	1	9
RA	570,671	4.74	1.09	1	9	228,161	4.75	1.11	1	9
RW	570,671	5.58	1.23	1	9	228,161	5.61	1.24	1	9
RLR	570,671	5.46	1.39	1	9	228,161	5.41	1.42	1	9
RLS	570,671	4.80	1.11	1	9	228,161	4.85	1.15	1	9
FA	570,671	5.07	1.04	1	9	228,161	5.06	1.05	1	9
FUA	570,671	5.20	1.36	1	9	228,161	5.15	1.40	1	9
FRP	570,671	5.03	1.11	1	9	228,161	5.04	1.14	1	9
TL	570,671	4.63	1.10	1	9	228,161	4.63	1.12	1	9
UD	570,671	5.83	1.28	1	9	228,161	5.79	1.34	1	9
RUA	570,671	5.52	1.25	1	9	228,161	5.48	1.29	1	9
MSL	570,671	5.69	1.37	1	9	228,161	5.64	1.42	1	9
RTP	570,671	5.80	1.28	1	9	228,161	5.78	1.32	1	9
RUW	565,193	5.54	1.32	1	9	225,446	5.48	1.37	1	9
BQ	570,671	5.78	1.31	1	9	228,161	5.76	1.34	1	9
LOC	546,362	5.10	1.48	1	9	216,463	5.10	1.51	1	9
BCS	534,687	4.93	1.02	1	9	209,233	4.90	1.06	1	9

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Trait	Dataset 1[1] n	Mean	SD	Min	Max	Dataset 2[2] n	Mean	SD	Min	Max
DS	426,167	80.57	2.39	63	90	155,957	80.52	2.44	64	90
BC	570,671	80.99	3.07	66	91	228,161	80.94	3.17	66	91
FL	570,671	80.78	3.04	66	91	228,161	80.60	3.18	66	91
U	570,671	79.62	3.60	65	90	228,161	79.37	3.73	66	90
FS	570,671	80.27	2.32	68	88	228,161	80.10	2.43	68	88
MY	570,671	9,749	2,044	5,079	16,622					
LP						228,161	22,174	14,265	1,004	95,480
NL						228,161	2.5	1.3	1.0	6.0

[1] Dataset for analyses of milk yield
[2] Dataset for analyses of longevity traits (lifetime production in thousands kg of milk, number of lactations)
[*] Height at sacrum in cm (HS), stature (ST), chest width (CW), body depth (BD), angularity (AN), rump angle (RA), rump width (RW), rear leg set – rear view (RLR), rear leg set – side view (RLS), foot angle (FA), fore udder attachment (FUA), front teat placement (FRP), teat length (TL), udder depth (UD), rear udder attachment (RUA), medial suspensory ligament (MSL), rear teat placement (RTP), rear udder width (RUW), bone quality (BQ), locomotion (LOC), body condition score (BCS), dairy strength (DS), body composition (BC), feet and legs (FL), udder (U), final score (FS).

The records consisted of Czech Holstein cows born between years 2002 and 2015, with minimum proportion of Holstein genes 88%. Animals were required to obtain type classification scores between 30th and 210th day of the first lactation in total age between 650 and 1206 days. Maximum number of lactations used for the milk yield analyses was 4. Milk yield (MY) records below 5079 kg and above 16 622 kg were set to absent. Lifetime production was between 1004 kg and 95 480 kg. Maximum number of lactations in the second dataset was 6, cows with higher count or cows, which were not culled before the possibility of survival of 6 lactations, were not included.

Model

For studying the influence of linear type traits, a single-trait model incorporating only fixed effects was used:

$$y_{ij} = \sum x_i + e_{ij}$$

Where y_{ij} is a vector containing phenotypic observations; x_i is a vector of i[th] fixed effect and e_{ij} is the random error. There were two slightly different models used for different trait analyses. In both models the linear type traits were used as fixed effects in both linear and quadratic form (landq); other effects were: combined class effect of the herd, year and season (HYS) at calving; number of days at calving (landq); combined class effect of the HYS at classifying; class effect of a classifier; age in days at classifying (landq) and number of days from calving to classifying (landq). In the first model for MY, three additional effects were used: service period (landq); calving interval (landq) and class effect of number of lactations.

The residuals were used in calculating quadratic phenotypic regressions of MY, LP and NL on each type trait individually as well as altogether. To generate the regression coefficients and subsequently the predictions, the BLUPf90 program of Misztal *et al.* (2002) was used. The estimated predictions were calculated with a use of the quadratic equation and subtracted from population mean, i.e. the mean of the dataset used (separated means for first and second dataset).

Additionally, the CORR procedure of SAS (2013) was used to estimate Pearson's simple phenotypic correlations between individual conformation traits and the production and longevity traits.

Results and discussion

The relationship between milk production and longevity traits was analysed three times: as simple phenotypic correlations, in interaction with other type traits and without interactions.

Correlations obtained between the type traits and MY, LP and NL are shown in Table 2. The strongest correlation between RUW and MY was as the strongest similarly observed by Khan *et al* (2016) – 0,5, Misztal *et al.* (1992) – 0,22, Cruickshank *et al.* (2002) – 0,44, Wasana *et al.* (2015) – 0,39 and Zink *et al.* (2014) – 0,32.

The results for correlations between type traits themselves were comparable to the ones obtained in aforementioned studies Cruickhank *et al.* (2002), Sewalem *et al.* (2004), Zavadilová *et al.* (2011) and Khan *et al.* (2016). Some differences were observed in comparison with Tapki *et al.* (2013), where the correlations were varying in both negative and positive direction, e.g. the difference for CW - AN was in the present study -0.44; FUA – UD was in the present study 0.36 against -0.41 from the Tapki *et al.* (2013). Regarding the correlations between composite traits and the production traits the study agreed with analyses from Sewalem *et al.* (2004), however in comparison with Zavadilová *et al.* (2012) the estimation effect of DS is lower.

Second type of analyses was made with the use of the model, where all the type traits were used altogether and their effect on the analysed production trait or longevity trait was derived after consideration the interactions between the type traits respectively. Results are shown in Table 3. The coefficients of reliability (R^2), i.e. the proportion of explained variability by models with the use of all effects and linear type traits altogether were 60% for MY and 36% for both LP and NL. Major part was explained by effect HYS at classifying; linear type traits explained 2.3% in decreasing order: RUW, AN, BCS, UD and BD. Type traits with the lowest R^2 were (in ascending order): RTP, FUA, RA, FRP and TL. This order of linear type traits is reflected also in the absolute value of estimated predictions of deviations for each production trait (Table 3.). According to the score, i.e. class of the cow in each linear type trait, the estimated values of kg milk or expected length of life (the expected deviation of the cow from population mean) were calculated.

In the last approach, effect of type traits on the milk yield and longevity traits was analyzed without interactions with other type traits. That means, model equations included all the fixed effects as second approach, except for other type traits. All the linear type traits, composite traits and final score were used with linear and quadratic form, separately from others. Different shapes of regression lines were obtained. Some traits showed linear relationship, straight line with both negative or positive slope (with higher contribution for 1 point or for 9 points), some were curved with best values either for middle values (4 – 6 points) or marginal values (1 and 9 points). Also, composite traits did not show a clear linear relationship, as would be expected (see Figure 1).

Table 2. Estimate of phenotypic correlations (r) among milk yield in kg (MY), lifetime production in kg of milk (LP), lifespan in number of lactations (NL), conformation traits and other conformation traits. Maximum and minimum correlations for each column are in bold.

Shortage	Trait	MY	LP	NL
	Linear type traits			
HS	Height at sacrum in cm	0.087	-0.015	**-0.056**
ST	Stature	0.071	0.029	0.001
CW	Chest width	0.042	0.032	0.017
BD	Body depth	0.089	0.046	0.009
AN	Angularity	0.087	0.023	-0.014
RA	Rump angle	-0.014	0.007	0.015
RW	Rump width	0.051	0.008	-0.012
RLR	Rear leg set - rear view	0.106	0.057	0.013
RLS	Rear leg set - side view	-0.040	-0.023	-0.004
FA	Foot angle	0.045	0.025	0.004
FUA	Fore udder attachment	0.017	0.053	0.044
FRP	Front teat placement	0.003	-0.004	-0.006
TL	Teat length	0.038	0.037	0.022
UD	Udder depth	**-0.049**	0.014	0.032
RUA	Rear udder attachment	0.093	0.083	0.045
MSL	Medial suspensory ligament	0.052	0.087	0.066
RTP	Rear teat placement	-0.009	**-0.027**	-0.023
RUW	Rear udder width	**0.189**	0.099	0.021
BQ	Bone quality	0.057	0.022	-0.005
LOC	Locomotion	0.036	0.056	0.042
BCS	Body condition score	-0.042	0.029	0.048
	Composition traits			
DS	Dairy strength	0.133	0.052	-0.006
BC	Body composition	0.077	0.031	0.000
FL	Feet and legs	0.105	0.062	0.016
U	Udder	0.089	0.110	**0.071**
FS	Final Score	0.141	**0.113**	0.053
	Mean	0.060	0.038	0.013

Table 3. Estimate of predictions of the effect of the linear type traits on milk yield (MY), lifetime production in 1,000 kg (LP) and number of lactations (NL) as deviations from the population mean. Maximum values for each trait in bold.

Type trait		Linear score (in points)								
		1	2	3	4	5	6	7	8	9
ST*	MY	6.93	16.48	28.64	43.43	60.83	80.85	103.49	128.75	**156.63**
	LP	481.69	851.32	1108.88	1254.37	**1287.80**	1209.16	1018.45	715.68	300.84
	NL	0.04	0.06	0.07	**0.08**	0.06	0.04	0.01	-0.04	-0.10
CW	MY	**-20.64**	-38.03	-52.18	-63.09	-70.76	-75.18	-76.36	-74.31	-69.01
	LP	342.84	621.06	834.65	983.62	1067.97	**1087.69**	1042.78	933.26	759.10
	NL	0.04	0.08	0.10	0.12	0.14	**0.14**	0.14	0.13	0.12
BD	MY	96.62	180.71	252.27	311.31	357.82	391.80	413.26	422.18	**418.59**
	LP	1145.16	2025.25	2640.29	2990.27	**3075.19**	2895.05	2449.86	1739.60	764.29
	NL	0.08	0.15	0.19	**0.20**	0.20	0.17	0.12	0.05	-0.05
AN	MY	43.56	86.66	129.31	171.49	213.22	254.49	295.30	335.65	**375.55**
	LP	425.32	749.38	972.16	1093.67	**1113.92**	1032.89	850.60	567.04	182.20
	NL	0.02	0.03	**0.04**	0.04	0.03	0.01	-0.02	-0.05	-0.10
RA	MY	-12.70	-23.83	-33.39	-41.38	-47.79	-52.63	-55.90	-57.60	-57.72
	LP	895.60	1630.24	2203.93	2616.66	2868.42	**2959.23**	2889.08	2657.98	2265.91
	NL	0.10	0.18	0.24	0.29	0.31	**0.32**	0.32	0.29	0.25
RW	MY	62.17	117.26	165.27	206.21	240.07	266.85	286.55	299.18	**304.73**
	LP	209.81	352.47	427.98	**436.35**	377.56	251.63	58.55	-201.68	-529.06
	NL	**0.00**	0.00	0.00	-0.01	-0.02	-0.04	-0.06	-0.09	-0.12
RLR	MY	76.48	141.45	194.92	236.88	267.34	286.30	**293.75**	289.70	274.15
	LP	192.02	352.98	482.88	581.72	649.51	686.23	**691.90**	666.50	610.05
	NL	0.01	0.02	0.03	0.03	**0.03**	0.03	0.03	0.03	0.02
RLS	MY	**-0.51**	-8.06	-22.66	-44.30	-72.98	-108.71	-151.48	-201.30	-258.16
	LP	657.50	1122.47	1394.92	**1474.85**	1362.24	1057.12	559.46	-130.72	-1013.42
	NL	0.07	0.12	0.15	**0.17**	0.16	0.14	0.10	0.04	-0.03
FA	MY	102.39	186.58	252.58	300.37	329.96	**341.36**	334.55	309.55	266.34
	LP	406.33	735.67	988.00	1163.33	1261.66	**1282.98**	1227.31	1094.63	884.95
	NL	0.02	0.04	0.05	0.06	**0.06**	0.06	0.05	0.04	0.03
FUA	MY	**-40.24**	-74.56	-102.95	-125.42	-141.97	-152.60	-157.30	-156.08	-148.94
	LP	344.90	639.58	884.03	1078.26	1222.27	1316.05	**1359.61**	1352.95	1296.06
	NL	0.04	0.08	0.11	0.13	0.15	0.16	**0.16**	0.15	0.14
FRP	MY	102.69	184.96	246.80	288.22	309.21	**309.78**	289.92	249.64	188.93
	LP	373.96	646.48	817.55	**887.18**	855.35	722.08	487.36	151.20	-286.41
	NL	0.01	0.02	**0.03**	0.02	0.01	0.00	-0.02	-0.05	-0.08
TL	MY	84.11	152.94	206.51	244.81	267.84	**275.61**	268.10	245.33	207.29
	LP	950.51	1695.83	2235.96	2570.90	**2700.66**	2625.22	2344.60	1858.79	1167.79
	NL	0.07	0.13	0.17	0.19	**0.20**	0.19	0.17	0.13	0.08
UD	MY	**-2.77**	-30.35	-82.72	-159.90	-261.88	-388.66	-540.25	-716.63	-917.82
	LP	1502.36	2700.76	3595.22	4185.71	**4472.26**	4454.85	4133.49	3508.17	2578.90
	NL	0.15	0.27	0.37	0.44	0.49	0.52	**0.52**	0.49	0.45

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Type trait		Linear score (in points)								
		1	2	3	4	5	6	7	8	9
RUA	MY	99.70	191.09	274.15	348.89	415.31	473.41	523.18	564.64	**597.78**
	LP	382.80	730.92	1044.36	1323.11	1567.18	1776.57	1951.27	2091.29	**2196.63**
	NL	0.02	0.04	0.05	0.06	0.07	0.07	**0.08**	0.07	0.07
MSL	MY	11.57	23.95	37.14	51.14	65.95	81.57	98.00	115.24	**133.29**
	LP	638.00	1201.74	1691.23	2106.47	2447.45	2714.18	2906.65	3024.87	**3068.84**
	NL	0.06	0.10	0.15	0.18	0.21	0.23	0.24	**0.24**	0.24
RTP	MY	25.68	43.82	54.41	**57.47**	52.99	40.97	21.41	-5.69	-40.32
	LP	341.61	577.35	707.23	**731.24**	649.39	461.68	168.10	-231.34	-736.65
	NL	0.03	0.05	0.07	**0.07**	0.07	0.05	0.03	0.00	-0.04
RUW	MY	13.27	52.44	117.51	208.47	325.34	468.09	636.75	831.30	**1051.75**
	LP	684.40	1325.70	1923.92	2479.05	2991.08	3460.03	3885.88	4268.65	**4608.33**
	NL	0.04	0.07	0.09	0.11	0.12	0.13	**0.14**	0.13	0.12
BQ	MY	63.46	113.48	150.06	173.21	**182.91**	179.17	162.00	131.38	87.33
	LP	1129.04	2074.74	2837.09	3416.09	3811.75	4024.07	**4053.03**	3898.66	3560.93
	NL	0.09	0.17	0.24	0.29	0.32	0.34	**0.35**	0.34	0.32
LOC	MY	28.70	51.37	68.02	78.63	**83.22**	81.78	74.31	60.81	41.29
	LP	349.83	644.34	883.50	1067.34	1195.84	1269.01	**1286.85**	1249.35	1156.52
	NL	0.03	0.05	0.07	0.09	0.10	0.11	**0.11**	0.11	0.11
BCS	MY	122.64	189.20	**199.68**	154.08	52.39	-105.38	-319.23	-589.16	-915.18
	LP	1330.63	2422.08	3274.33	3887.40	4261.27	**4395.95**	4291.45	3947.75	3364.86
	NL	0.09	0.17	0.24	0.31	0.37	0.43	0.48	0.52	**0.56**

* Stature (ST), chest width (CW), body depth (BD), angularity (AN), rump angle (RA), rump width (RW), rear leg set – rear view (RLR), rear leg set – side view (RLS), foot angle (FA), fore udder attachment (FUA), front teat placement (FRP), teat length (TL), udder depth (UD), rear udder attachment (RUA), medial suspensory ligament (MSL), rear teat placement (RTP), rear udder width (RUW), bone quality (BQ), locomotion (LOC), body condition score (BCS).

The highest impacts on milk yield were from type traits (in decreasing order) body condition score, udder width, udder depth, rear udder height and angularity. The strongest influence on lifetime production was found for body condition score, udder depth, body depth, rump angle and rear legs side view. Importance of udder width, body condition score, udder depth, bone quality and rear legs side view for number of lactations was confirmed. Some traits, such as stature, angularity, rump angle and width and body condition score, showed a clearly intermediate optimum for longevity traits, while greatest milk yield was expected for one of the extreme scores. Those results were generally consistent with those from Zavadilová *et al.* (2011). Only effect of bone quality on milk yield and especially lifetime production was concluded as more important opposite to aforementioned study, however agreed with results from Sewalem *et al.* (2004).

Most of the results from third approach corresponded to the second approach, although there were some differences. For example, effect of chest width considered in interaction with other type traits clearly shows maximum prediction of milk yield for the score 1 and lowest for 7 points. In contrast, the curve regardless interactions (third approach)

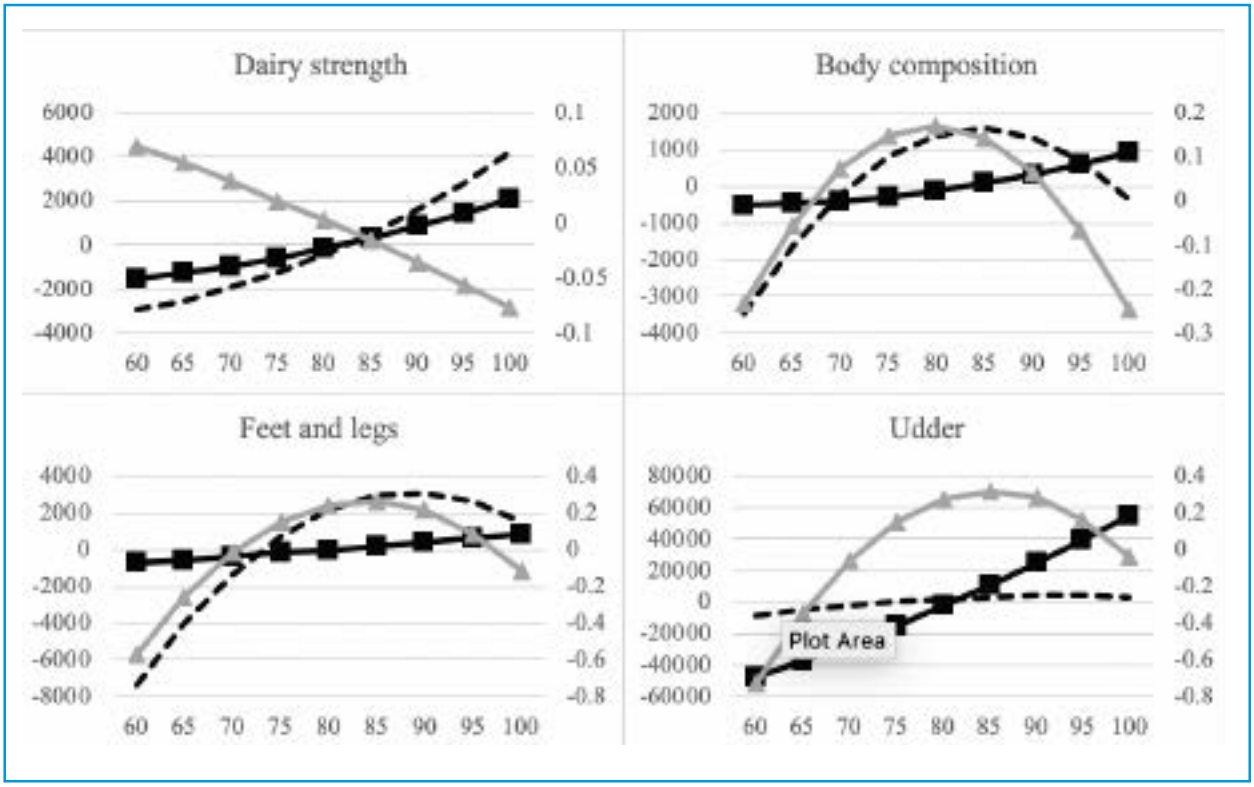

Figure 1. Quadratic relationships between composition traits and milk yield (■), lifetime production (. △) and number of lactations (second y-axis).

shows the peak of maximum values around 7 and 8 points, i.e. complete opposite trend. That can be explained also with the statement in paper from Kern *et al.* (2014), where is presented high degree of interrelations and collinearity between the type traits, especially between udder and conformation traits.

Conclusions

Different models were used to describe relationships between type traits and milk yield, lifetime production and number of lactations in Czech Holstein population. Results were generally consistent with those from studies of other Holstein populations in other countries. Important influences of body condition score, udder traits and angularity on milk yield were confirmed. The strongest influence on lifetime production was found for body condition score, udder depth, body depth, rump angle and rear legs side view.

However significant effects of the type traits were concluded, reliability of prediction of milk yield based only on phenotypic measurements was 2.3%. Another conclusion stated the importance of interactions between linear type traits itself, as demonstrated on the effect of chest width on milk yield.

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Opportunities and challenges of new technologies for performance recording with focus on claw health and metabolism

F. Grandl[1], J. Kofler[2], M. Suntinger[3], P. Majcen[4], M. Mayerhofer[3], F. Papst[5], O. Saukh[5], M. Fallast[6], A. Turkaspa[7], F. Steininger[3], K. Linke[3], J. Duda[1], T. Wittek[2], B. Fuerst-Waltl[8], F.J. Auer[9] and C. Egger-Danner[3]

[1]LKV Bayern, Landsberger Straße 282, 80687 Munich, Germany
Corresponding Author: Florian.Grandl@lkv.bayern.de
[2]Clinic for Ruminants, University of Veterinary Medicine,
Veterinaerplatz 1, 1210 Vienna, Austria
[3]ZuchtData EDV-Dienstleistungen GmbH, Dresdner Str. 89, 1200 Vienna, Austria
[4]LK Österreich, Schauflergasse 6, 1010 Vienna, Austria
[5]TU Graz, Institute of Technical Informatics, Inffeldgasse 16/I, 8010 Graz, Austria
Complexity Science Hub Vienna, Josefstädter Straße 39, 1080 Wien, Austria
[6]smaXtec, Belgiergasse 3, 8020 Graz, Austria
[7]SCR by Allflex, Hamelacha St. 18, Netanya, Israel
[8]Department of Sustainable Agricultural Systems, Division of Livestock Sciences,
University of Natural Resources and Life Sciences,
Gregor-Mendel-Str. 33, 1180 Vienna, Austria
[9]LKV Austria, Dresdner Straße 89, 1200, Vienna

Abstract

Breeding goals are broadening with more and more emphasis on health and efficiency related traits. New technologies are revolutionising the dairy industry. In addition to achievements in omics technologies, information and communication technologies (e.g., sensor technologies, Internet of Things, embedded machine learning) are also finding their way into modern dairy herds. Instead of punctual measurements, embedded sensors continuously record animal behavioural patterns that can imply on the animal well being and welfare. Large amounts of data generated by deployed sensor systems along with the integration of related data sources promise ultimately new insights into animal health.

Traditional data pipelines with information about animal performance recordings in combination with indicators for metabolic disturbances, such as veterinary diagnoses, feeding information, test of ketone bodies, body condition score, and mid-infrared spectra have been around for some time already. They provide more precise possibilities to predict diseases, such as ketosis, compared to the methods using fat-protein-ratio. In the context of the claw health, the information about the regular claw trimming visit, veterinary diagnoses and regular lameness scoring has been made available only partly so far. Sensor technology provides alarms and early warnings based on irregularities of normal behaviour for early detection of disorders. Advanced methods and technologies offer the possibility to combine various environmental information and genomic background to get new insights into the occurrence of or susceptibility to disorders. To explore these opportunities the biggest challenge is the integration of different data sources. In practice, monitoring data is often provided by different hardware and software products. This makes data integration more difficult due to the differences in the data exchange format of the partners involved. Moreover, the same traits may be defined differently by different products. It is therefore necessary

to create structures to bring these data sources together in order to provide farmers with maximum support for herd management. Another challenge of data integration from different sources is compliance with legal data protection regulations, since this is often associated with lack of clarity in practice. Cooperation between different partners and integration of different data is a precondition for successfully applying advanced data technologies based on complex trait definitions. We summarize the steps to overcome these challenges based on our research within the project D4Dairy.

Keywords: performance recording, data integration, claw health, metabolism, advanced data technologies.

Introduction

In the recent years, dairy production has seen a lot of technological advances in different areas. On the farms, technologies for automation of work processes are increasingly implemented, particularly automatic milking and feeding systems. Furthermore, livestock sensors for the acquisition of behaviour and health data as well as environmental parameters (e.g., barn climate) become widely available. These systems are able to deliver large amounts of data from which conclusions on the animal wellbeing and welfare can be drawn.

There has also been an impressive development of lab technologies in various fields that can now be exploited for dairy farming. New laboratory diagnostic methods and analyses as well as a bunch of omics technologies can nowadays be used at high-throughput and are thus available for samples from many animals. This additional information can also provide new insights into the state of the animals, be it once (e.g., when genotyping animals) or repeatedly (e.g., when analysing milk samples from performance recording).

Digitalisation adds another dimension to the use of new technologies. Networking and integration of different data sources provide the basis for enhanced data science approaches such as Big Data analyses, image and pattern recognition. The challenge of the current situation is the existence of disconnected data silos, and a heterogeneous landscape of application programming interfaces (Egger-Danner *et al.*, 2019; Papst *et al.*, 2019). Privacy concerns is one of the main reasons for the reluctance in data sharing. Farm and animal data can be considered as a farmers' trade secret. Manufacturers of automation solutions and sensor systems, which also process (and sometimes host) their customers' farm data, generate additional insights from these data by applying proprietary algorithms. Thus, part of the data of interest is coupled with the intellectual property of companies.

Use of new technologies for performance recording

The challenge for performance recording organisations and data processing centres is to integrate the variety of new data sources in the traditional data processing used to generate information and decision support for the farmers and broaden the data basis for breeding value estimation. This is particularly relevant in the field of novel phenotypes, where traditional data recording schemes are limited. In this paper, we discuss such approaches for the trait complexes metabolic status and claw health in dairy cows.

Metabolic status

So far, milk constituents (fat and protein content, fat-to-protein ratio, milk urea) have been the main information source from routine milk recording for the metabolic status of dairy cows. Additionally, some recording schemes for diagnoses exist, but these catch primarily only severe clinical cases. However, metabolic disorders often occur subclinically. Due to the economic impact, the earliest possible detection of subclinical signs is of great importance (Egger-Danner *et al.*, 2015). A promising approach to get insights into complex traits is the use of milk mid-infrared spectra, which are readily available from the analysis of routine milk recording samples (Gengler *et al.*, 2016). There are several authors who have shown the potential usefulness of spectral information for the assessment of the metabolic status of dairy cows (e.g., Grelet *et al.*, 2016, Luke *et al.*, 2019), and there already exist live applications of early warning services for farmers. Other diagnostic methods (e.g., ketone tests for use in milk or urine) that could be used in a routine monitoring program have also some potential for a large-scale recording of the metabolic state. However, their drawback is the labour intensiveness and the need to record the result before it can be further (electronically) processed. Sensor units that continuously collect potentially auxiliary trait data for the trait complex of metabolic disorders are also available. Most frequently, the deployed systems record eating and rumination behaviour, but also automatic body condition scoring and automatic weighing systems are commercially available. However, all these sensor systems provide rather unspecific health alerts and leave the necessary situation analysis to farmers and veterinarians. To further automate the performance analysis and bring precision diagnostic to the next level, e.g., to differentiate the metabolic status more precisely, integration of different information sources is of ultimate importance.

Claw health

For claw health, no traditional information pipeline exists in performance recording apart from the information from linear scoring of conformation traits and the reasons for culling. Similar to metabolic disorders, veterinary diagnoses mostly exist for very severe cases only. Additional information on claw health could greatly improve breeding for claw health (Linde *et al.*, 2010) and would be beneficial in advisory tools to improve housing conditions and prevention of claw disorders. Thus, the electronic documentation of claw health at the time of trimming is a very powerful approach to collect valuable data, if the data is integrated in the routine performance recording system (Kofler, 2013). Data integration with computerised documentation and analysis programs could also be beneficial for the claw trimmers through work reduction (e.g., automatically updated animal lists). Information from lameness scoring is a valuable auxiliary trait for improvement of claw health by management and genetics (Heringstad and Egger-Danner *et al.*, 2018; Koeck *et al.*, 2019). The detection of claw health problems through lameness or locomotion scoring is especially interesting, if the detection can be automated. Using modern data analytic tools, the lameness detection from camera image data seems to be possible (Abdul Jabber *et al.*, 2017). Other sensor technologies (e.g., accelerometers) also show great potential to serve as auxiliary information for claw health (Alsaood *et al.*, 2019).

Additional aspects for the use of novel data sources for metabolic status and claw health

When introducing novel data sources to the new trait complexes discussed above, a few aspects should be considered. With regards to the health status, it becomes more and more relevant to also record the application of preventive measures (e.g., administration of propylene glycol), since such measures can greatly influence the result when algorithms are built on routine data. As mentioned above, sensor-based

management systems often provide unspecific alarms. It has to be verified that combining such information sources indeed increases the predictive ability of the trait of interest or show a significant correlation to the target trait. Some of the novel data sources require additional sampling, thus routine farm visit schemes and milk tests might need to be redesigned. For the development of algorithms that combine novel data sources, comprehensive research data sets are needed in order to ensure high quality of predictions. Both for development and for routine use, the optimisation of data availability is crucial. Active involvement and cooperation of partner organisations around the dairy industry is essential. Projects that put emphasis on the improved interoperability and data exchange between systems, such as the COMET-project D4Dairy (www.d4dairy.com) help to provide access to various commercial and open data in a privacy-preserving way and to generate additional value for the farmers through integration and joint analysis of this data (Egger-Danner *et al.*, 2019).

What does this mean for performance recording in 2030?

The challenge for performance recording organisations in the future will be to adapt the way what and how to record data on dairy farms. There will be a need to record a wide variety of (auxiliary) traits using new recording technologies. Existing data and technologies permanently installed at the farms will need to be integrated into performance recording. Performance recording schemes will have to be aligned with the different abilities of data provision of farms and farmers. Depending on the breeding programs, data provisioning could emerge as a new business model for the farms, where precise phenotyping is needed.

We can also expect an increasing demand of new services for the performance recording organisations. Performance recording schemes need to be adapted to variable intervals and to daily/hourly/every second data flows. Decision (support) systems for farm management based on different sources of data will play a greater role as a service to the farmers. Performance recording results will have to be made available for further automation of farm work processes (e.g., milk lab results for the calibration of inline measurement systems). With regards to the still existing privacy concerns, it will be crucial that the performance recording organisations make the routine data exchange and data use along the dairy supply chain transparent and are trusted in the context of data sharing between the parties involved.

Acknowledgement

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Testing the cows' ration with a new data mining software based on NOA data base

Y. Lavon[1], A. Benzvi[1], Y. Shani[2], G. Adin[2], S. Rosen[2], Y. Bear[1] and B. Domján[1]

[1]Herd Book, Israel Cattle Breeders Association, Caesarea, Israel
[2]Dairy Cattle Department, Extension Service, Ministry of Agriculture and Rural Development, Bet Dagan, Israel

Abstract

Today, ration programing for dairy cows is usually done by the liner programing in the herd management program (NOA) or another program. This method takes into consideration just the price of the feeds and the physiological borders given to each food by the nutritionist. The liner program will find the cheapest ratio without looking at other parameters. Today, by looking on the big data base that is available in the dairy farms we can find thousands of rules that describe the connection between different feeds and ratio giving to the cows and cows' production in terms of milk (kg), fat percentage and protein percentage. To each rule we can define level of significance and from that to understand how it can affect specific physiological parameters and farm production. The purpose of this study is to look on the dairy farm historical data and according to former results plan the ratio that gave the best result. This will be led to higher efficiency and higher financial profit for the dairy farm. The first stage includes establishment of an easy way for receive the exact data on nutrition, milk level and DHI data from the NOA system. The second part was to test in 15 big dairy farms the historical data and to see if the data is fit for good analysis. From those 15 farms we found 3 that had good historical data that can be used for further analysis. Data analysis of the data from those 3 dairy farms revealed different effects of different foods on production performance and how a change in a food within the physiological range will affect production performance and profit per cow. Using this method can improve the professional and economic performance of the dairy.

Introduction

The large amounts of information available today in the Israeli dairy farms in particular and in the world in general poses many challenges in data analysis. The global and local dairy barn has undergone major changes. The number of cowshed violations has increased significantly, and detection systems have been installed with controllers to help manage the cowshed. farm management is undergoing a revolution to "smart or accurate farming" (Sundmaeker *et al.*, 2016). Analyzing a large and diverse amount of information is called Big Data. Big Data represents very large amounts of information that need advanced methods as well as advanced technology to make available and usable information for decision making (De Mauro *et al.*, 2016). Large-scale data analysis, big data, and accurate agriculture are fairly new issues in cattle and therefore lack information on practices. Recently, a conference on this topic was organized by ADSA - American Dairy Science Association Conference on improving profitability while analyzing existing data in the cowshed and changes based on the findings.

In all the major industries that use more and more powerful computers and powerful technologies that allow for new analytics options like Big Data. This term can vary between topics but in general the intention is to use large databases to make complex decisions where traditional data usage may be lacking. The key components of this method are gathering information, analyzing information, storing it and finding future solutions through it. It is also possible to analyze existing data in new and advanced ways. Recently, there has been a significant trend to examine the application of Big Data techniques and methods to the use of agriculture as a key opportunity for realizing additional value in the agricultural sector (Noyes, 2014; Sun *et al.*, 2013; Yang, 2014). Using these methods can significantly improve the efficiency of various factors in the barn which will lead to improved profitability (Esmeijer *et al.*, 2015; Gilpin, 2015). Using these methods can predict various factors related to cow's effectiveness such as milk production and food consumption. Business owners are looking for ways to improve profitability and efficiency on the one hand by lowering production costs and on the other by getting a better price for the product they market. For this, good decisions must be made that will lead to improved cow behavior and better interface decisions. In the past as well as in the present all the consulting services of experts in various fields was and still is based on knowledge coming from different studies, there is a need for data and knowledge based on the local dairy farm performance with all the conditions that affect it and may differ between farms. Using technology based on local farms data (Big Data) can help achieve these goals better (Poppe *et al.*, 2015; Sonka, 2015). For example, in the dairy industry (our industry) use of this method involves combining and analyzing many types of data such as: milk and solids production, onset of estrus, dairy expenses, health and fertility data, genetic data, feed and food consumption as well as weather data, Body condition score, body weight and more. Incorporating information with sophisticated tools for analysis will help improve decision making, operational efficiency and risk management.

The dairy industry is very suitable for this method for several reasons:

1. Characterized by the existence of a reasonable price, there is biological variability as well as weather variability as well as uncertainty.
2. There are advanced technologies that provide continuous information on the cow's milk yield and medical and physiological problems that occur to her.
3. Using this Big Data method is a breakthrough in analyzing data and in the ability to use this data for future decisions.

Currently the food ratio design in the herd management software is carried out as follows: a feeding expert sets constraint of ingredients and foods according to his experience and education. The software will choose the low-cost ratio that will fill the expert's requirements. The software does not attempt to set a maximum profit per dairy farm. The idea in this research project is to use a planning method that will maximize the profit for the farm and not look just for the ratio with the minimal price. This can be done by learning the specific farm situation (from cow and cow data) and finding the optimal ratio for each farm. In addition, this method can also be examined for additional data besides feed and try to explain the relationship between cause and effect in general parameters in the farm. Like the optimal time for inseminate the cows.

Previous work that was done in one dairy farm in Israel, test this method. The cows were divided to two groups based on their milk levels, fat and protein levels, days in milk and lactation number. The food ratio for each group was done by the two different methods:

1. By using the traditional method.
2. By using the e-learning software.

The result shows difference of 1 kg/day for the group that used the e-learning software for ratio planning compare to the traditional method. The benefit has been translated into a profit of about NIS 40,000 per year in a 4-million-liter dairy farm.

The purpose of the current study was to examine the use of the mew method (Big Data) compared to the linear program that is used today in the Israeli dairy farms.

Materials and methods

Two groups of dairy cows (n=60 in each group) were separated according to milk level, number of lactation days in milk and health status.

Ratio planning for the control group was based on the current method and done by an expert nutritionist. Ratio planning for the treatment group was done by the new method based on 8 years of historical data from the specific dairy farm.

The total mixed ratio (TMR) for control and treatment group is presented in table 1. The main difference is higher amount of Whet silage group and lower amount of Sorghum silage in the treatment compare to the control group.

The Chemical composition of the diets is presented in table 2. There is no difference between the groups. Protein % and net energy are similar and those are typical levels for high producing dairy cows in Israel.

Table 1. Ingredients of the diets (20 kg/dry mater).

Item	Control	Treatment
Ground corn grain	5.2	6.6
Premix*	2.4	2.1
DDGS	1.8	0.4
Dry gluten feed	3.0	1.6
Canola meal	2.2	3.7
Sunflower meal	0.8	1.0
Wheat silage	7.3	10.8
Sorghum silage	7.0	4.0
Wheat hay	1.6	1.5
Total	31.3	31.7

*Same premix for both experimental groups.

Table 2. Chemical composition of the diets.

Item	Control	Treatment
Protein (%)	16.6	16.5
Net energy (kg of DM)	1.77	1.75
Forge NDF	18.5	18.5
Total NDF	32.6	32.5
NSC	37.9	40.5
Ether extract	4.9	4.2

Result and discussion

TMR planning with the new method showed higher ECM production throw all the study: 36.1 vs. 35.1kg/day (figure 1). Fat percentage were also higher throw all the study: 3.74 vs. 3.65%. However, Protein level did not differ between groups. Dry matter in take was around 23.5kg dry mater/day and did not differ between groups.

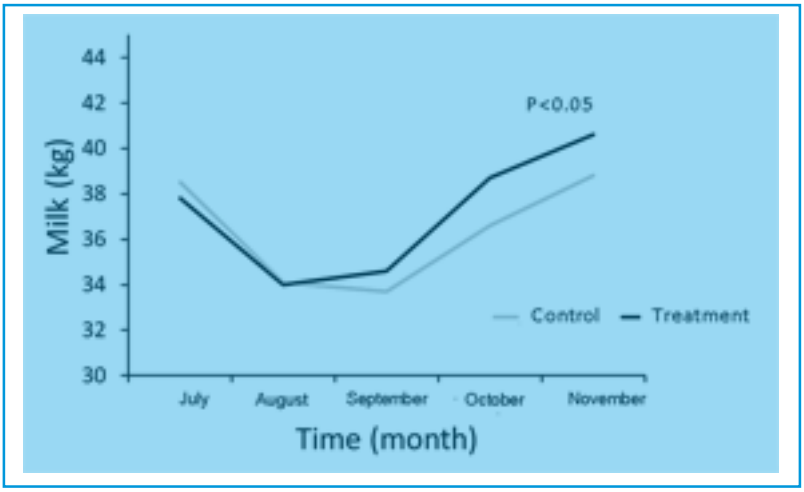

Figure 1. ECM throughout the experiment.

Data analysis shows the different effects of different foods on production level, the effect of changes in the amount of specific food in the physiological range on milk production, fat %, protein % food efficiency and profit. Using the new method require good quality database including historical data for at least 5 years. In addition, planning ratio for dairy cows using this new method can find the most profit ratio based on the historical data from a specific dairy farm and achieve higher profit for the all farm.

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GenoCells: individual somatic cell count of dairy cows by genotyping tank milk

P. Lenormand[1], F. Perrin[2], M. Calmels[1], V. Charrier[1], M. Foucher[2] and J.B. Davière[1]

[1]SEENOVIA, Research and Development Department, 141 Bd des Loges, 53942 Saint Berthevin cedex
Corresponding Author: jeanbernard.daviere@seenovia.fr
[2]AGRANIS Laboratory, Genomic Department 141 Bd des Loges, 53942 Saint Berthevin cedex

Abstract

The somatic cell count (SCC) monitoring is essential to monitor health of cows in production and to optimize milk price. GenoCells® is a revolutionary technology to determine with a high accuracy the SCC of each cow directly from the DNA analysis of a sample of tank milk. This technology is based on the correspondence between animal genotypes (= genetic identity) and presence of their DNA via their somatic cells in the mixing milk sample. Therefore, the tank milk genotype allows obtaining the SCC for each cow.

The SCC results from this disruptive genomic method are as accurate as traditional flux cytometry method.

GenoCells® is more practical than a classic milk control operation because only one tank milk sample is necessary. This method can be performed several once in a year and in less expensive by 20% compared to the classic method. The farmer can also get access to the genomic indexes to make selection schemes.

With this method, a quick decision regarding SCC can be performed and lead to a better economic impact. GenoCells® represents also a disruptive method to manage the SCC of the herd worldwide.

Keywords: cells, dna, milk tank, individual SCC.

Introduction

Monitor cells in farm is a big challenge for farmers both to optimize milk price and to have healthy cows. The current monitoring schema of cells by milk recording organization (MRO) presents some limits: low frequency and few flexibility notably in milking automation system where milk sampling is very restrictive. Blard *et al.* (2012) proposed a method to identify cows with subclinical mastitis by the analysis of tank milk. This method uses a linear model to determine the contribution of each cows to the DNA found in tank milk and only needs that all the cows are genotyped beforehand and that the milk yield of each cow contributing to tank be known. Few tests had been done in real conditions, so in 2017, Seenovia (formerly Clasel) initiated tests on four farms of different sizes and with different density chips to validate this approach in commercial farms. Following the first tests that were conclusive, the service GenoCells®

has been launch the 1rst of January, 2018. The main results of the tests done in farm are presented in a first part and the service as it was deployed on the Seenovia area is described in a second part.

Validation in farms

Material and methods

Before proposing this new service to breeders, a trial was conducted in four dairy farms to validate the method in real conditions. The smallest herd had 47 cows in lactation and the biggest 127. In total, 48 bulk samples were taken on the 4 farms between December 2015 and June 2017. The sampling was done on one or two milkings with usual operators. For each cow, SCC was determined by both the traditional method (analysis of individual sample by Fossomatic FC 6000 or FT+ and the new method GenoCells®.

Results

For all the farms, the determination of the cell counts is sufficiently accurate to be used in routine. Figure 1 presents the results of a farm of 53 dairy cows. The coefficient of determination was of 0.99 between Foss SCC and GenoCells SCC. By zooming on the 0-400 000 cells area, the coefficient of determination was of 0.97 (Figure 2).

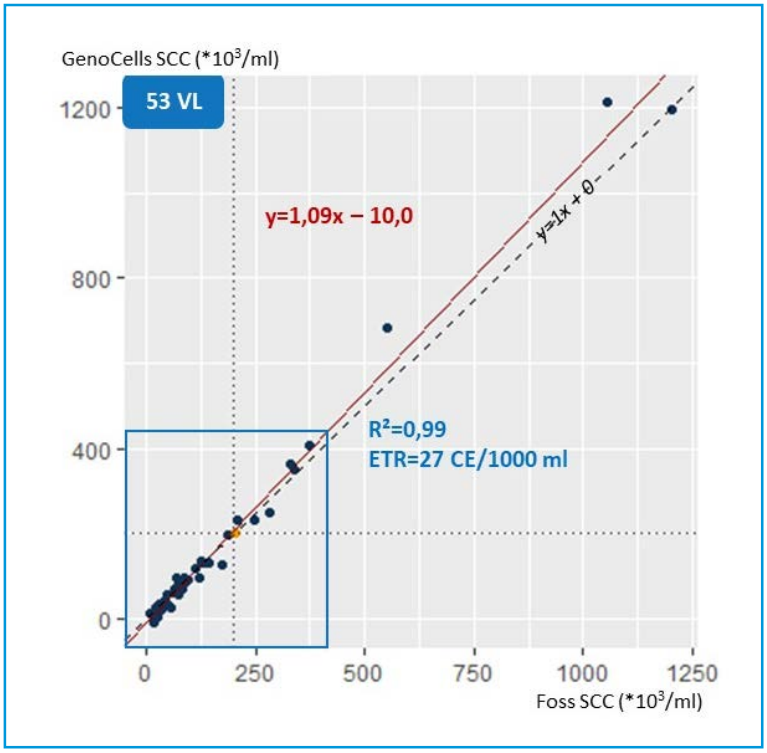

Figure 1. Results obtained with 53 dairy cows.

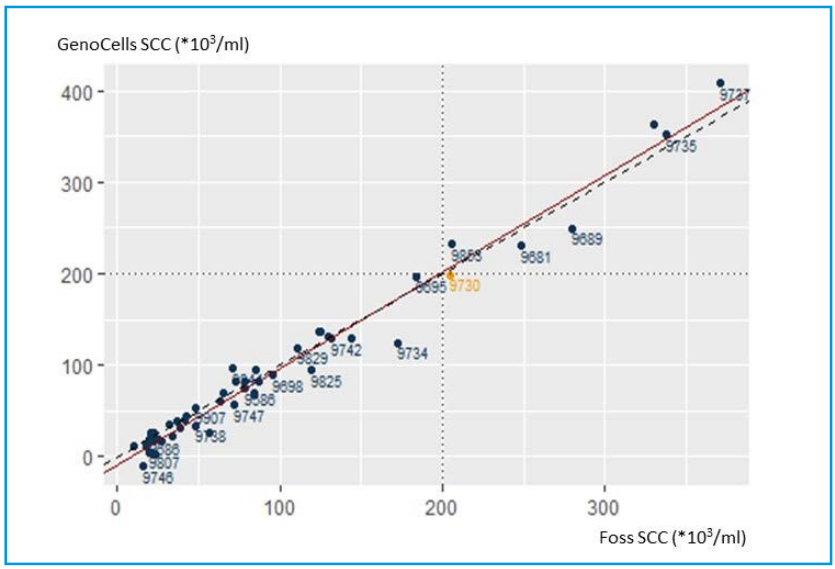

Figure 2. Zoom on the figure 1.

Deployment of the service

The results obtained during the testing phase lead to deploy GenoCells® from the 1rst of January 2018. In practice, four steps can be distinguish: sampling in farm (cows and bulk milk), laboratory analysis, calculation and result restitution (SCC and index).

Sampling in farm

The use of GenoCells® requires that all cows of the farm be genotyped. If the cow has never been genotyped, a cartilage sample is taken otherwise the genotype is retrieved from the breeding company.

To obtain individual SCC a milk sample is directly taken into the tank and the farmer has to indicate via a web interface what volume of milk has been brought to the tank by each cows. To simplify the declaration, milk yields are automatically recovered for connected milking parlors (automatic milking system, electronic milk meter). For conventional milking parlors, a first estimate of the milk yield of each cow is made from the data indicated by the farmer (bulk volume, number of milking, number of cows) and curve lactation models. The farmer can then individually correct the values if he finds significant differences. In addition to the milk yield declaration the farmer indicates via the web interface that a sample has been done and the sample is collected under 12H by a firm specialized in the logistic of fresh products. Let's keep in mind that the analisis could be done directly ont the milk payment sample.

Laboratory analysis

Genotyping process is performed using the Infinium Beadchip HTS Bovine from Illumina (USA). The first day of genotyping corresponds to the DNA amplification step. The second day corresponds to the DNA fragmentation and hybridization steps. The third day corresponds to the scanning and analysis steps.

The first day of genotyping, bulk milk samples are analysed by Fossomatic FC or FT+ to determine the total cells of bulk sampling.

Calculation and results

Once the genotype of tank milk is known, statistical analysis allows determining the cellular responsibility of each cow in the tank. This result is used to calculate individual cell counters by using the following formula: (% DNA of each cow / % milk of each cow in the bulk)*Bulk cell count

To sum up

Each week, around 800 samples are genotyped. The average interval between bulk sampling and restitution of the results is of 4 to 6 days according to the day of milk sampling.

In addition of SCC results, the farmers have access to genomic indexation results.

Conclusion and perspectives

With GenoCells, it is possible to monitor the cells:

- At herd level via the cellular responsibility
- At individual level by SCC.

The first approach is very interesting in the case of big herds (>200-300 dairy cows) by underlying only cows with high cellular responsibility. The second one interests farmers with few dairy cows.

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Comparison of milk analysis performance between NIR laboratory analyser and miniaturised NIR MEMS sensors

S. Uusitalo[1], B. Aernouts[2], J. Sumen[1], E. Hietala[1], M. Utriainen[3], L. Frondelius[4], S. Kajava[4], and M. Pastell[5]

[1]VTT Technical Research Centre of Finland, Optical Measurements, Kaitoväylä 1, 90570 Oulu, Finland
Corresponding Author: sanna.uusitalo@vtt.fi
[2] KU Leuven, Bioengineering Technology TC, Kleinhoefstraat 4. 2440 Geel, Belgium
[3] VTT Technical Research Centre of Finland, MEMS, Microkatu 1, 70210 Kuopio, Finland
[4] Natural Resources Institute of Finland Luke, Holalantie 31A, FI-71750 Maaninka, Finland
[5] Natural Resources Institute Finland Luke, Agriculture, Maarintie 6 2, 02150 Espoo, Finland

Abstract

The dairy farms have a need for on-site milk analysis to determine the fat and protein content of the milk in real-time manner during milking. Near infrared (NIR) spectroscopy has shown promise as an on-farm tool for fat and protein content determination of raw milk. However, for a successful implementation, on-site analysis requires affordable and small NIR sensors for the milk analysis. This study demonstrates the potential of using Micro-Electro-Mechanical-System (MEMS) based NIR sensors for on-farm and at-line measuring the milk fat and protein content and compares the results to golden standard analysis and commercial cooled Photo Diode Array (PDA) NIR sensor.

Keywords: MEMS, NIR, milk analysis, fat, protein

Introduction

The capacity of milk production of dairy farms is not only dependent on farm animal counts, but is also affected by the ability of single milking cows to convert the energy uptake into milk secretion. Over the past 50 years, genetic selection and improved feed and management practices have resulted in an increased milk production per cow lactation. As these modern cows are prone to production-related disorders, they need to be monitored closely to guarantee animal health and welfare. On the other hand, the ability of a farmer to predict the effect of farm animal diet to the milking capacity would benefit from near instant feedback of the milk composition in regards to the fed diet. For example, fat supplements are commonly used in order to increase dietary energy density and improve milk fat output. However, the effect of this diet may depend on factors such as the form of fat being fed and the effect of the overall diet (Lock *et al.*, 2013). Thus, monitoring the effect of diet could be advantageous economically. Additionally, due to the increasing size of dairy farms, farmers have less time available for each individual animal to monitor the animal health and the effect of nutrition. New NIR spectroscopy tools could offer useful information on individual cows and help the dairy farmer to optimize the animal management while reducing the workload.

Milk contains valuable information on the metabolic and nutritional status of dairy cows (Friggens *et al.*, 2007). Therefore, regular analysis of the produced milk is an efficient way to monitor cow health and welfare. Nowadays, farms participating in the Dairy Herd Improvement program collect information on the basic milk components of individual cows on a regular basis. However, as samples are analysed in central laboratories off-site, this procedure requires well-organized sample logistics and involves significant analysis costs. Due to the costs and the complexity of the procedure, the collection of samples occurs ones every 4 to 6 weeks, which is an insufficient basis for accurate and up-to-date analysis of individual animal health, secretion cycle and milk quality. This complicates the management of individual cow diets and delays information, which could offer indication on animal health deterioration.

Frequent milk analysis is only feasible, if it is performed on the farm with a minimal investment of labour and resources. Different studies, both in the lab and on the farm, indicate that near infrared (NIR) spectroscopy holds the potential for rapid, non-destructive and on-line analysis of the raw milk composition (Aernouts *et al.*, 2011). Nevertheless, commercial NIR detectors are typically costly and relatively large, not allowing for easy implementation in existing milking systems. In this study, we evaluated the ability of affordable MEMS-based NIR sensors to analyse the NIR transmittance and reflectance of raw milk collected from farm and predict the fat and protein concentrations from these spectra.

Methods and materials

The aim of his study was to evaluate the ability of affordable MEMS sensors on the analysis of milk ingredients. The spectral information content of milk was recorded using automated sampling device with integrated NIR MEMS sensors. The performance of the sensors was evaluated in predicting the milk fat, protein content and lactose level of individual raw milk samples. The samples were collected from the dairy research farm of the Natural Resources Institute of Finland (Luke) in Maaninka. The herd consisted of 100 cows, both primi- and multiparous, in different stages of lactation. The cows were housed in a free stall with slatted floor and cubicles and fed a total mixed ration based on grass silage supplemented with variable amounts of barley grain, oats, molassed sugar beet pulp, rapeseed meal and mineral premix. The cows were milked 2 times a day (6 AM – 8 AM and 3 PM – 5 PM) in a 2-times-8 herringbone milking parlour (SAC, Denmark). In this trial, milk samples were collected during two morning and one evening milking sessions of two successive days. One litre of milk representative for the whole milking was collected for each cow according to the ICAR standards (ICAR, 2017a). Right after collection, the milk was stirred gently and two representative samples of 50 ml were taken. 1 ml preservative (bronopol) was added to the samples to ensure conservation. The preservative does not interfere with NIR analysis results although the same calibration cannot be utilised with pure milk and preservative infused milk. Samples were stored at 4°C and analysed 3-4 days after sample collection. First sample set was analysed at Valio central laboratory at Seinäjoki for fat and crude protein content according to ISO 9622 (ISO, 2013). The second sample set was analysed with the milk analyser prototype at VTT Research facilities at Oulu. Before this analysis, the samples were heated from 4°C to 39°C with heated bath and stirred gently during the heating to ensure homogeneity. In total, 252 different raw milk samples were analysed. The milk analyser prototype developed by VTT contained four MEMS sensors of three different wavelength ranges from Spectral Engines Oy (Finland): NIRONE 1.4 with 1.1 – 1.4 µm, NIRONE 2.0 with 1.7 – 2.0 µm and NIRONE 2.5 with 2.2 – 2.5 µm wavelength range in transmission, and NIRONE 2.0 with 1.7 – 2.0 µm in reflection mode. The NIR MEMS sensors use Fabry-Perot Interferometers for wavelength scanning, which enables compact sensor packaging and fast signal collection (Rissanen *et al.*, 2017). However, the sensors are prone to

drift as they do not have cooled detectors. The system used a custom built powerful light source and hybrid metal glass cuvettes to achieve sufficient signal to noise ratio. The spectral information of milk was recorded with MEMS sensors integrated into a prototype device with milk sample handling and temperature control shown in Figure 1.

The recorded spectral data with normalised background is presented in Figure 2 for the four MEMS NIR sensors: NIRONE 1.4, 2.0 and 2.5 in transmission geometry and NIRONE 2.0 in reflection mode. The best signal to noise ratio was achieved with NIRONE 2.0 sensors. The NIRONE 2.5 showed high signal to noise ratio, which could be improved with shorter transmission path length if lower SNR would be preferred. In this study, the optical path length in milk sample was 1 mm. This can be achieved with the custom hybrid-glass cuvette. Shorter optical path would require a new type of cuvette solution and might have challenges with bubble free detection.

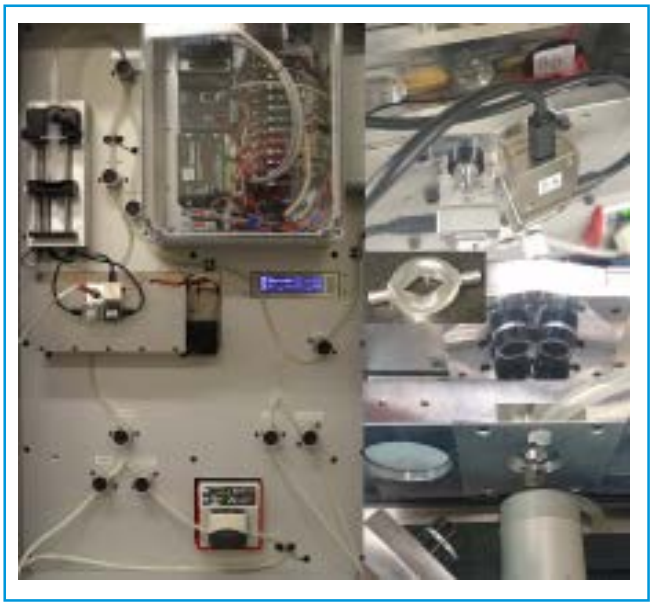

Figure 1. Sample handling with temperature control, integrated MEMS sensor modules (NIRONE, Spectral Engines), custom light source and cuvette and two optical geometries for transmission and reflectance measurements.

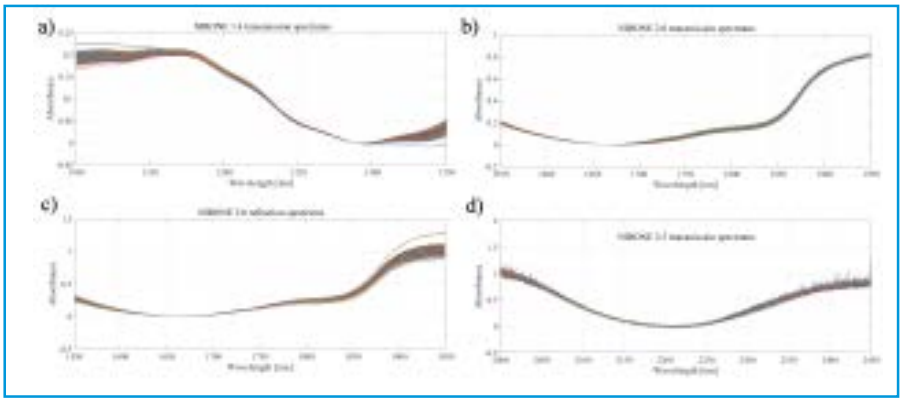

Figure 2. Absorbance spectra recorded from raw milk samples of 84 cows from 3 milking sessions: two morning milking and one evening milking.

The absorbance spectra were analysed with PLS calibration as shown in Figure 3 for fat, protein and lactose levels. The validation of the calibration gave most promising results for NIRONE 2.0 in transmission and reflectance geometry.

The NIR MEMS sensor results were compared to Tec5 spectrometer (InGaAs-PDA, drift ~2%) data using Valio laboratory NIR analysis as reference for fat, protein and lactose level. Prediction error data of sensors was compared to ICAR recommendations for on-farm analysers as shown in Table 1.

Tec5 InGaAs sensor reached best prediction results for fat, protein and lactose. Protein and lactose prediction errors were near or reached the ICAR limit. Although fat reached

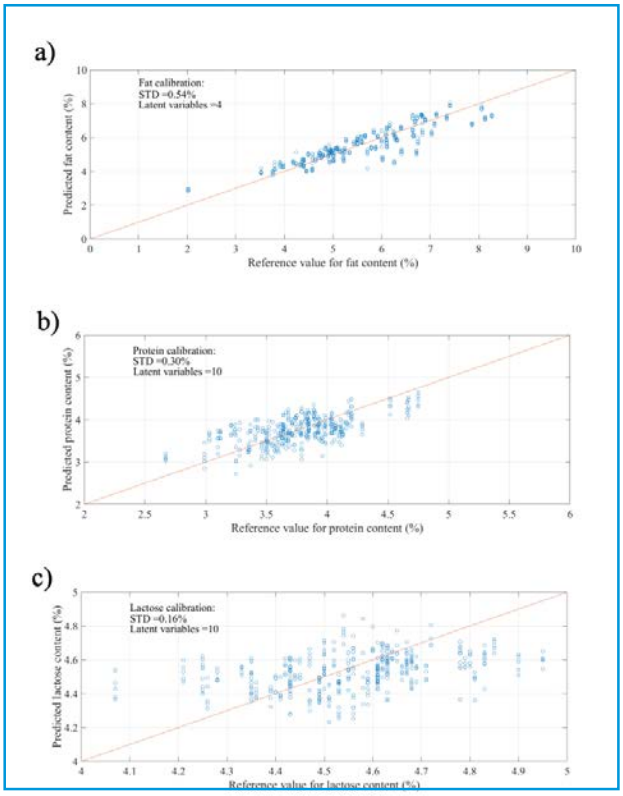

Figure 3. PLS models for raw milk absorbance spectra showing calibration curve and validation samples for a) NIRONE 2.0 transmission mode, b) NIRONE 2.0 reflectance mode and c) NIRONE 2.0 transmission mode.

Table 1. Comparison of prediction errors of MEMS sensors, Tec5 cooled spectrometer, AFI Milk and ICAR standards. The prediction error and calibration curves shown in Figure 3 are marked with bold font.

Sensor/Standard	Fat [w/w %]	Protein [w/w %]	Lactose [w/w %]
NIRONE 1.4 Transmission	0.58	0.34	0.17
NIRONE 2.0 Transmission	**0.54**	0.34	**0.16**
NIRONE 2.5 Transmission	0.54	0.35	0.17
NIRONE 2.0 Reflectance	0.56	**0.30**	0.19
Tec5 cooled InGaAs	0.51	0.13	0.07
AFI Milk on-line analyser [1]	0.62	0.24	0.28
ICAR on-farm analyser standard [2]	0.25	0.25	0.25
ICAR laboratory analyser standard	0.10	0.10	0.10

a lower prediction error than achieved with AFI Milk analyser study, the comparison of lactose, protein and fat prediction indicates that fat prediction could have reached a lower level than it did. Thus, there is a suspicion that a sampling error might have affected the fat levels between reference and measurement samples. Similarly, MEMS sensor results show quite high fat prediction. The prediction result is similar to AFI Milk analyser result. Although, the protein prediction showed higher values than AFI Milk, the lactose prediction was quite similar. As a summary we can state that the performance of the MEMS NIR sensors did not reach the level that could be achieved with cooled InGaAs sensors without future instrument development. The performance of the MEMS NIR sensors should be further optimised by adjusting the light source alignment, sensor ambient temperature and by adding more averaging into the measurement routine. The development of affordable milk sensors utilising MEMS sensors could be the route to affordable on-farm analyser, as the price range of Tec5 is ~ 10 times higher than the price for MEMS NIR sensors.

Conclusions

MEMS sensors are small and cost-effective option for on-farm and on-line monitoring of the milk quality. However, the drift of the sensors limits their performance. Although the studied NIRONE sensors can reach similar level as the AFI Milk analyser in short raw milk trial, the long-term function and stability of the sensors requires further studies. In future more advanced sensor implementation should enable more accurate analysis with lower prediction errors. The implementation of affordable MEMS sensors into milking equipment could allow for high-frequent and rapid analysis of the milk quality on farm. This would enable converting the obtained time-series of milk quality parameters into valuable information for on-farm monitoring the health of individual cows.

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Integrating bacteriological milk examination into decision support for reduced use of antimicrobials

W. Obritzhauser[1], M. Mayerhofer[1], M. Suntinger[3], Clair L. Firth[1], K. Fuchs[2], A. Käsbohrer[1], T. Wittek[1], B. Fuerst-Waltl[4] and C. Egger-Danner[3]

[1]Unit of Veterinary Public Health and Epidemiology, University of Veterinary Medicine, Veterinaerplatz 1, 1210 Vienna, Austria
Corresponding author: w.obritzhauser@dairyvet.at
[2]Data, Statistics and Risk Assessment, Austrian Agency for Health and Food Safety (AGES), Zinzendorfgasse 27/1, 8010 Graz, Austria
[3]ZuchtData EDV-Dienstleistungen GmbH, Dresdner Str. 89, 1200 Vienna, Austria
[4]Department of Sustainable Agricultural Systems, Division of Livestock Sciences, University of Natural Resources and Life Sciences, Gregor-Mendel-Str. 33, 1180 Vienna, Austria

Abstract

With respect to the increasing emergence of antimicrobial resistance, the use of antibiotics in livestock production is an issue of growing concern. In an observational study in 249 dairy herds (6475 cow-years) in Austria, antimicrobial treatments, pathogen information and various risk factors were analysed. Standardised treatment data that were provided by 17 different veterinary practices showed very diverse patterns of antimicrobials used for treatment of mastitis and for drying-off. The pathogen information was harmonised across the six laboratories. Additionally different environmental- and management information related to udder health management was collected. Management tools incorporating pathogen information additionally to routine milk recording information and veterinarian diagnoses were elaborated. Technical interfaces to the central cattle database as well as the required data protection measures were developed and are presently implemented to routine.

This study showed that the pathogens isolated from mastitis milk were predominantly contagious on some farms and mainly environmental on others. These results support the need to develop tools which lead to a more evidence-based prudent use of antimicrobials when treating mastitis and drying off dairy cattle. Analyses across routinely-recorded production data, health data and antimicrobial use provide valuable information on disease-risks as well as the cow groups at risk. Failures in management and causes of diseases can be identified more easily and eliminated at an earlier stage. Assessing the infection status of the udder, by means of milk culture results, can assist the decision-making processes regarding more precise control and prevention measures to improve udder health. The more information is available, the more targeted a treatment can be. Standardisation and integration of data, therefore, play a crucial role in the prudent use of antimicrobials on dairy farms.

Introduction

Animal health, animal welfare and food safety are of increasing concern to consumers. An important measure in the dairy industry is the improvement of udder health, which is influenced by different factors such as environmental factors and herd management,

genetics as well as targeted treatment of udder infections. In view of the rising occurrence of antibiotic resistance, prudent use of antimicrobials and pathogen-specific treatments are of high importance and can only be possible if various data sources are available and linked: farm specific environmental factors, animal specific information such as auxiliary traits including somatic cell count, and, most importantly, information on diagnoses with laboratory tests on pathogens as well as animal-specific treatment information with results from sensitivity tests of antimicrobials. In order to ensure efficient management and provide effective advice to dairy herd managers, it is important to combine this variety of different data sources and prepare simple but meaningful decision support tools for farmers and veterinarians. In the Central Cattle Database (German: *Rinderdatenverbund*, RDV) in Austria different datastreams such as farm specific information, bulk milk information, milk performance records, breeding records, genome data, as well as veterinary diagnoses, results of bacteriological milk cultures, and data on the administration and dispensing of veterinary drugs are recorded and can be accessed by the farmer and herd veterinarian online via computer or mobile phone. The precondition of integrating many different data sources into comprehensive databases and common tools is data standardisation. Within the ADDA (Advancement of Dairying in Austria) project, standardised protocols for bacteriological milk analyses and harmonised documentation of findings were developed with the respective laboratories. Within the "Electronic Herdbook" project, use of antimicrobial treatments with respect to animal and diagnoses was standardised within Austria based on the legal background in conjunction with the regulation on monitoring antimicrobial use in livestock. To develop a targeted dry off-strategy, the impact of farm-specific management and environmental factors was assessed. This paper describes the work done in regard to standardisation of pathogen information and antimicrobial treatments and gives an overview of further ongoing steps within the D4Dairy project to develop a decision support tool for a targeted dry off-strategy using existing health and production data to reduce the overall use of antibiotics.

Material and methods

In an observational study *(*Firth *et al., 2017)* over a trial period of one year from October 2015 to September 2016, data on antimicrobial use on 249 dairy farms were collected as part of the ADDA (Advancement of Dairying in Austria) research project. The dataset comprised data from 7867 antimicrobial treatments, 6700 cows and standardised treatment data provided by 17 different veterinary practices. The antimicrobial treatments were analysed and information on various risk factors was recorded.

Standardisation of bacteriological investigations

The aim was the harmonisation of bacteriological culture results and pathogen information across laboratories. A working group of researchers and representatives of the labs was formed. After analysing the current situation, harmonisation of the analyses in the labs from sample preparation, methods of testing and interpretation of results including quality assurance with continuous ring tests of participating labs was carried out. Another topic was standardisation of findings across laboratories. To enable the amalgamation of various data, technical and legal aspects of data communication between labs and the central database had to be developed as well.

Standardisation of antimicrobial treatment

Austria has a nationwide "Health Monitoring in Cattle" programme (Egger-Danner *et al.,* 2012). Veterinarian diagnoses have been recorded centrally in the Central Cattle Database since 2006. This database was recently extended to include the harmonised

electronic documentation of animal- and diagnosis-specific use of antimicrobials. The data on antimicrobial use were standardised according to EMA and ESVAC guidelines. To allow for comparison between farms, TD365 metrics based on antimicrobial consumption treatment days over 365 production days were calculated per farm (Figure 1), according to the European Medicines Agency units of Defined Daily Doses (DDDvet) and Defined Course Doses (DCDvet, for dry-off preparations) (EMA, 2015; EMA, 2016)

These metrics provide added value to the milk performance and herd health dataset and make individual herd-specific data comparable to metrics from other herds (benchmarking).

The set-up of the standardisation and integration of the data has taken the legal regulations into account. In this way it was possible to develop a mobile application for farmers where the legal documentation requirements can be complied with electronically.

Integrated tools for herd management were developed and integrated to the Central Cattle Database, where various relevant information is combined for to assist with decision making.

Calculation of the number of treatment days over 365 production days per farm (*#TD365*):

$$\#TD365 = \sum_{i=1}^{n} \frac{amount\ AS_i\ in\ period\ P\ (mg)}{DDDvet_i\ (mg/kg/day)\ x\ \#\ production\ days\ in\ period\ P\ (days) \times standardised\ weight\ (kg)}\ x\ 365$$

# TD365	= number of treatment days per year that an animal is present on the farm
amount AS_i	= amount (in mg) of active substance i used in period P; i = 1, 2, …, n
$DDDvet_i$	= Defined Daily Dose of active substance i (in mg/kg/day); i = 1, 2, …, n (EMA 2016)
# production days in period P	= number of animals present daily during period P (in days)
standardised weight	= standard animal weight at treatment (in kg)

Correction #TD365 for dry cow treatment:

*#TD365 dry cow treatment corrected = #TD365 dry cow treatment * (CI/365 * (100/100–PR))*

CI	= calving interval of the herd (days)
PR	= percentage of cows replaced

Figure 1. Calculation of antimicrobial use.

Evaluation of risk factors

Based on different surveys conducted among veterinarians, farmers and consultants, herd specific management and risk factors for udder health have been identified for each farm (Firth *et al.,* 2019). Advanced statistical analyses will be applied to further in-depth studies of risk factors (Klimek *et al.,* 2018) within D4Dairy.

Targeted dry-off strategy

Within the D4Dairy project, hypotheses based on targeted dry-off strategies are tested on pilot farms and data streams including risk factors will be combined to enable the development of targeted decision support tools.

Results and discussion

Based on the data from the ADDA observational study, standardised procedures for bacteriological analyses were developed and harmonised processes, applicable to both Germany and Austria, were defined (LKV Nordrhein-Westfahlen, 2016; Codeset 8262 Befundschluessel). The standardised procedure is described in Baumgartner *et al.,* 2018.

To legally permit the amalgamation of various data technical, certain legal aspects of data communication between labs and the central database had to be clarified; which have since been implemented into routine applications within the Central Cattle Database (RDV).

Pathogens present and antimicrobials used across farms and veterinary practices showed very diverse patterns on the farms included in the ADDA project (Firth *et al.,* 2017, Schabauer *et al.,* 2018).

Integrated tools for herd management based on the Central Cattle Database have been developed and are now available for farms and veterinarians (Suntinger *et al.,* 2018; Suntinger *et al.,* 2019). Figure 2 shows an example of such a tool based on pathogen information. Figure 3 shows the benchmarking metrics provided for farmers to compare themselves to the other farms in terms of treatment days per year in total, with respect to udder health alone, treatments used for drying off, and for each disease complex, as well as the percentage of antimicrobial substances used which are considered the Highest Priority Critically Important Antimicrobials (HPCIA) for human medicine. Figure 4 displays the potential of the mobile application for practical use for the farmers. One example is that the medicinal withdrawal period for each individual cow is always available online.

Conclusion and outlook

To enable a more prudent use of antimicrobials with targeted treatment and dry-off strategies, it is essential that all relevant data can be linked and more in depth knowledge is available with respect to risk of infection, the causative pathogens and possible antimicrobial resistance. Drying-off is one of the major reasons for use of antimicrobials in dairycows, therefore measures to reduce the use of antimicrobials while ensuring udder health are vital. Within the D4Dairy project, research is being done on further data communication and data integration, analyses of risk factors for occurrence of mastitis. For developing a decision support tool for animal-based dry-off strategies, beside the existing standardised information, testing of hypothesis for dry-off strategies

Figure 2. Example for displaying information on pathogen information from bacteriological milk sample implemented within the Central Cattle Database (RDV).

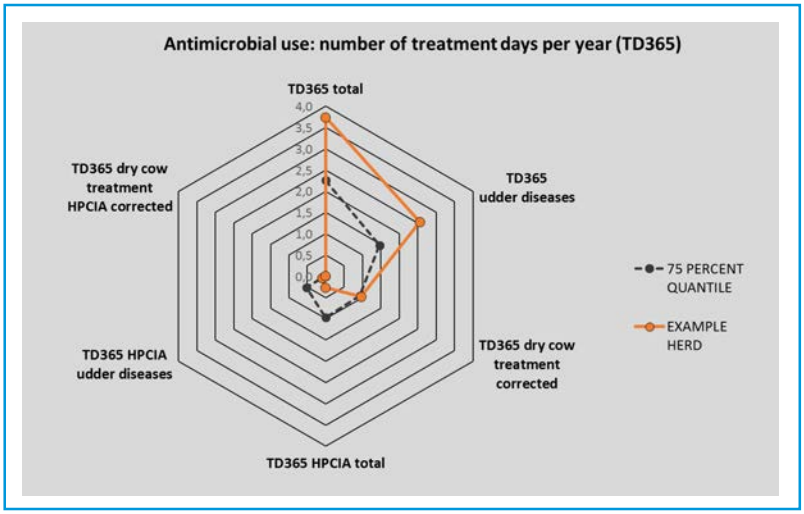

Figure 3. Herd-specific antimicrobial use in comparison with other farms milk sample implemented within the Central Cattle Database (RDV)

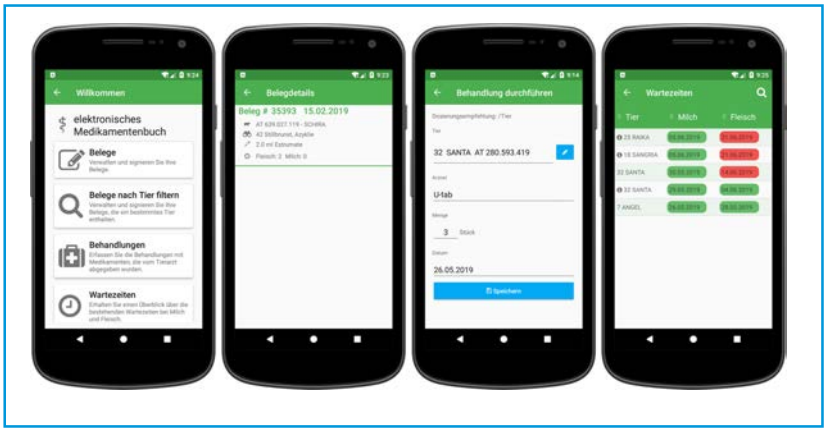

Figure 4. Mobile documentation of antimicrobial use.

and the harmonisation of antimicrobial resistance testing is a research focus within D4Dairy. Standardisation and integration of data continue to play a crucial role in supporting the prudent use of antimicrobials on dairy farms and is also essential to enable monitoring and comparisons.

Acknowledgements

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Routine infrared phosphorus determination in ex-farm milk providing better insight in the phosphorus cycle on dairy farms

M. Bastian and H. van den Bijgaart

Qlip B.V., P.O. Box 119, 7200 AC Zutphen, The Netherlands
Corresponding Authors: bastian.mikael@gmail.com; bijgaart@qlip.nl

Abstract

EU limitations incited the Dutch government in 2017 to implement a national regulation to reduce phosphorus losses from dairy husbandry. The demand for a better insight in the phosphorus cycle on Dutch dairy farms led Qlip to develop a FTIR calibration model for phosphorus measurements in raw milk.

The calibration model was developed with a training set of 210 milk samples and tested on 80 milk samples. The model allows for a precise estimation of P content (RMSEP = 2-3 mg/100 g milk). Model performance is stable across the year, similar between herd bulk milk and individual cows' milk, and robust to specific breeds, e.g. Jersey cows.

The application was successfully implemented in routine Dutch herd bulk milk testing in early 2019. With this tool, farmers can now monitor the phosphorus balance in their dairy cattle and better fine-tune the supply of phosphorus through the ration. Furthermore, these detailed milk data can serve as a basis for farm-specific reporting of phosphorus output through ex-farm milk supplies.

If wished for, the application can be extended with models on a number of other minerals.

Keywords: Phosphorus excretion, milk, infra red spectrometry.

Introduction

Phosphorus (P) is an important mineral in milk and for the dairy sector. P deficiency in cows may cause health disorders such as demineralization of the skeleton, growth problems, lameness, infertility and a decrease in milk yield (Brooks, Cook, Mansell, and Walker, 1984; Gerloff and Swensen, 1996). To avoid these negative effects, farmers have long preferred *over*feeding cows with P (Klop *et al.*, 2013). However, this costly strategy also has environmental side effects: while intake of P (P_{intake}) above the physiological needs does not further increase milk yield nor P concentration in milk (P_{milk}, Wang *et al.*, 2014), it does increase the P concentration in manure (P_{manure}) in the form of phosphates (PO_4^{3-}, P_4O_{10}). Phosphates in manure contribute to the eutrophication of soils and waters.

To face environmental challenges, the EU published her Nitrates Directive in 1991. It aimed to protect water quality across Europe by preventing nitrates from agricultural sources leaching into ground and surface waters and by promoting the use of good farming practices. In 2006, Dutch farmers with their highly productive grassland were granted a derogation (as were Germany, Denmark, UK, Ireland, Flanders and areas in Italy). Farms with at least 80% grassland were allowed to spread up to 230 to 250 kg N (instead of 170 kg N) with manure from grazing animals per hectare per year. As a consequence, national quotas on production of nitrates, but also on phosphates, were imposed.

In 2016, after the lifting of the EU milk quota system, it became apparent that the Dutch farmers did increase the number of cattle and milk production more rapidly than anticipated, and that they would exceed the phosphate quota. This led the Dutch government to regulate phosphate production via a phosphate reduction plan in 2017. This included subsidies for farmers to quit farming, reduction of the phosphate content in concentrates and a generic reduction in number of cattle. Phosphate production rights that had been awarded based on the number of cattle in 2015 underwent an overall deduction of about 8%. As a consequence, a better insight and an understanding of the phosphorus cycle on dairy farms became of economic importance in the Dutch dairy sector from 2017 on.

The phosphorus balance in dairy cows can be expressed with the following formula:

$$P_{manure} = P_{intake} - P_{milk}$$

In the calculations for regulatory purposes P_{milk} was taken as a constant of 97 mg / 100 g (of milk). Yet, other constants had been proposed before: 90 mg / 100 g (NRC, 2000; Valk, Sebek, and Beynen, 2002), and 100 mg / 100 g (Commissie Onderzoek Minerale Voeding, 2005). This degree of discrepancy for P_{milk} undermines the calculus for P_{manure}. Scientific research over the last decade (Alvarez-Fuentes *et al.*, 2016; Klop *et al.*, 2014; Soyeurt *et al.*, 2009) has shown that P_{milk} varies between cows from 56 to 149 mg / 100 g, with an average of 103 mg / 100 g and a standard deviation of 11 mg / 100 g (Alvarez-Fuentes *et al.*, 2016). This meant that P content in milk varies as much as protein content and more than lactose contents (Qlip internal data). Since the variation of fat, protein and lactose contents is routinely monitored at both individual cows and dairy farm levels, a method that can routinely measure P_{milk} was deemed to be useful to provide farmers a better insight in the phosphorus cycle on their farms and better means tofine-tune the supply through the ration.

A clear example of inter-cow and inter-herd differences are herds that are partly or totally constituted of Jersey cows. Compared to Holstein-Friesian cows, which constitute more than 90% of the Dutch dairy cattle, Jersey cows produce milk that is richer in both fat (5.0% vs. 3.6%) and protein contents (3.6% vs. 3.0%, Reinart and Nesbitt, 1956 ; Qlip data for Jersey cows in The Netherlands over the year 2018: fat: 6.0% vs. 4.4%, protein: 4.2% vs. 3.6%). Since P content is correlated with both fat and protein content, it would thus be expected that P content is higher in Jersey milk than in Holstein-Friesian milk.

The current reference method to measure P_{milk} is ICP-MS. ICP-MS requires complex laboratory procedures to measure the mineral content of a milk sample. In comparison, Fourier Transformed Infra-Red (FTIR) spectroscopy is part of the routine analysis of raw milk. Amongst other, FTIR is applied in routine to determine fat, protein, lactose and urea contents at both individual cow and herd levels. A model to predict P_{milk} based on the FTIR spectrum would allow a cost-effective estimation of P content of raw milk samples. Where FTIR spectra have been stored, the estimation can also be made for past raw milk samples.

Qlip wished to develop a FTIR-based model to predict P content in raw milk based on the work of Soyeurt *et al.*, 2009. The present paper summarises the development and validation of the final calibration model. Subsequently, the implementation in routine and large scale prediction of P content are discussed.

Development and validation of the calibration model

In-house development of a FTIR calibration model

In total, the P content of 290 raw milk samples was measured with the reference method ICP-MS (ISO 21424|IDF 243). Milk samples were collected covering the whole range of compositional variation, on multiple instruments and across various periods in the year 2018. The model was a PLS regression based on the FTIR spectra (925.92 to 5011.54 cm^{-1}) of 210 training samples (P reference: mean = 105, SD = 15, range = 64 to 179 mg / 100 g): 105 herd bulk milk samples measured with four Foss MilkoScan™ FT+ instruments and 105 individual cow milk samples measured with ten Foss MilkoScan™ FT6000 instruments (N = 100) and one Foss MilkoScan™ 7 RM instrument (N = 5), thereby having applied beforehand spectrum standardization with all instruments in accordance with manufacturer's instructions.

One way of selecting samples was by chance (e.g.: taking samples out of routine processing). These were 10 herd bulk tank milk samples and 10 individual cow milk samples in February, then in April, June, Augustus and October 2018 (total random samples: 50 herd bulk tank milk and 50 individual cow milk). In each set of 10 samples, 6 were randomly set apart for external validation, constituting a first external validation set (N = 60 samples = 6 x 2 milk types x 5 periods). The remaining 4 samples of each set of 10 samples were used in the calibration set. A second external validation set was composed of 8 Jersey herd bulk milk samples and 8 individual Jersey cow milk samples. All were collected in April 2018, regardless of milk composition (i.e. close to a selection "by chance").

Another way of selecting samples was based on milk composition or milk origin. 174 non-random samples were selected during 2018: N = 70 in January, N = 37 in February, N = 11 "extreme" samples and N = 16 Jersey milk samples (4 of which outliers) in April, N = 40 in Augustus). "Extreme" samples were selected on expected extreme P content based on the FTIR spectrum. Jersey milk samples were selected based on knowing that some dairy farms only housed Jersey cows. The rest of the non-random samples were selected on variations of fat, protein, lactose, urea and/or expected P content. These comprised a total of 85 herd bulk milk samples and 89 individual cow milk samples.

The final "whole year" calibration model was trained on 210 samples:

- 170 non-randomly selected samples (174 samples above, minus the 4 outliers).
- 40 randomly selected samples (4 remaining of each set of 10 random samples).

For simplification, the results on external validation with the two external sets (random routine N = 60 and Jersey milk N = 16 + 4 outliers eliminated from the training) were first pooled in a total set of 80 samples. Note that the "training outlier" samples were known to have had mild to severe fat distribution problems (due to the high fat content of Jersey milk) and / or high acidity. For these reasons these were not included in the training set, but they were still included in the validation set to provide an estimate of the robustness of the predictions. However, of the 80 samples two Jersey milk samples did present really abnormal values (pH = 4.8 and 6.0, urea = 62 and 46 mg/100 g, protein = 7.4% and 6.8%) and were thus excluded from the validation set.

Reference values for P content ranged from 64 to 192 mg / 100 g: 192 mg / 100 g was for one of the two samples excluded. P content thus ranged from 64 to 179 mg / 100 g in the training set (N = 210, mean = 105, SD = 15) and from 78 to 135 mg / 100 g in the validation set (N = 78).

Validation of the calibration model at Qlip

The overall performance of the calibration model on the 78 samples (60 random, 18 Jersey) in external validation was: MAE (Mean Absolute Error) = 2.1 mg / 100 g, RMSE (Root Mean Squared Error) = 2.6 mg / 100 g and R^2 = .94. In comparison, using the same training set and the same validation set but using protein content as predictor (with or without lactose, fat, or urea as co-predictors) led to a performance of MAE = 4.5, RMSE = 5.9, R^2 = .70 at best. The added value of using the spectrum was therefore that the prediction error could be reduced by a factor two as compared to predicting P content from protein content with or without co-predictors.

Figure 1 shows the external validation plot for herd bulk milk (left panel) and for individual cow milk (right panel) separately, and allows the identification of Jersey samples (triangles). There was no significant difference in performance as measured by RMSE between individual cow milk versus herd bulk milk. Similarly, although the set of Jersey samples was small, no significant / obvious degradation of performance could be found when comparing the random set (N = 60, RMSE = 2.2 and 2.9 mg / 100 g respectively for herd bulk milk individual cow milk) to the Jersey set (N = 18, RMSE = 2.7 and 2.8 mg / 100 g).In general, absolute errors were randomly distributed when the two outliers were excluded: no obvious linear or quadratic pattern involving predicted P content, reference P content, fat, protein, lactose or urea contents or pH could be found. This is important since this indicates that the model appears to be robust within the range covered in this validation set (reference P content: 78 – 134 mg / 100 g, predicted P content: 81 – 130 mg / 100 g, fat: 2.4 – 7.0%, protein: 2.6 – 4.7%, lactose: 4.1 – 5.2%, urea: 9 – 37 mg / 100 g, pH: 6.4 – 6.9). Yet, if anything, absolute errors might have been slightly larger with extreme protein values, hence providing an explanation as to why the absolute error with individual cow milk might be slightly larger than the absolute error with herd bulk milk – the range is larger. This is a possible explanation that is to

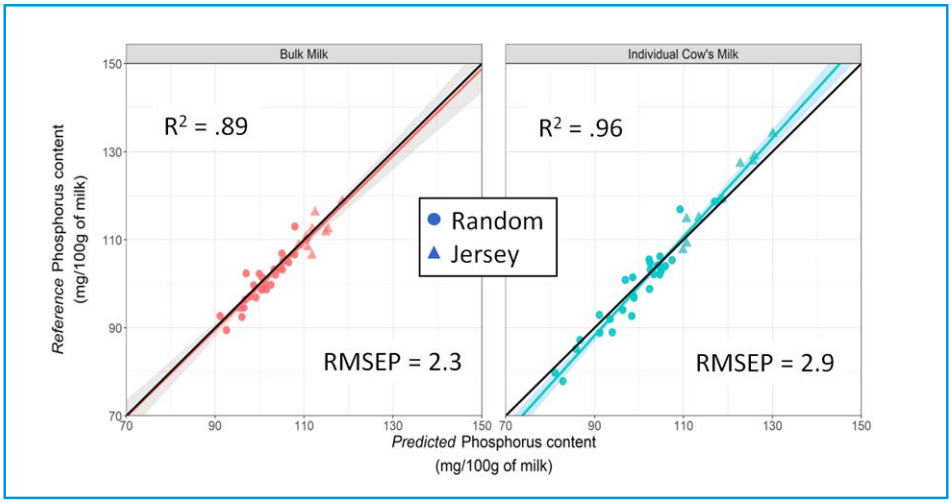

Figure 1. External validation plots for herd bulk milk and individual cow milk. RMSEP in mg / 100 g.

be confirmed with more data. Finally, no significant sinusoidal pattern could be found in the distribution of absolute error during the course of a year, suggesting no obvious effect of season on model performance, and hence a robustness to various seasons.

Validation of the calibration model by another laboratory

In the context of a collaboration with another laboratory that also measures P content in milk, 95 herd bulk milk samples with vast variation in P content (predicted P content from 80 to 122, mean 102, SD = 11) were selected in February 2019 and sent for reference analysis at this laboratory. This occurred about four months after the last results had been included in the calibration set. After correction for a known and understood bias (removing the same bias value to all samples), the agreement between Qlip's FTIR model and the extern laboratory reference method ICP-MS was MAE (Mean Absolute Error) = 2.3 mg / 100 g, RMSE (Root Mean Squared Error) = 3.0 mg / 100 g and R^2 = .96.

Comparison to previous research

In sum, the FTIR model for P content developed at Qlip has a precision between 2.5 and 3 mg / 100 g. The authors are not aware of previous research reporting P content models for bulk milk, but pioneering models for predicting P content in individual cow milk have been published (e.g. Soyeurt *et al.*, 2009) with a RMSE in cross-validation around 5.0 mg/100 g. The differences between previous research and the current work are numerous, and include:

- differences regarding the reference method (ICP-MS following an ISO norm here vs. ICP-AES on frozen-defrosted milk samples by Soyeurt *et al.* 2009);
- the use of multiple infra-red instruments and a very standardized execution of infra-red measurements in a routine laboratory (vs. 1 unique MilkoScan™ FT 6000);
- differences in sample selection and nature of the samples: our final model used herd bulk milk samples as well as individual cow milk samples. This comprised about 210 samples in the training set with a sample selection protocol focused on variability of the chemical composition of milk and of its P content (vs. focused on spectral variability and Ca content by Soyeurt *et al.* 2009).

Some statistics for herd bulk milk 2017-2018

Using the data stored at Qlip, we could derive P content predictions at a large scale, predictions that covered about 4 million herd bulk milk samples.

Overall distribution of milk samples

Herd bulk milk samples from routine were distributed around 102 mg / 100 g, ranging from 90 to 115 mg / 100 g. There was a clear effect of breed, since samples coming from dairy farms raising Jersey cows only had a distribution with higher levels of P content ranging from 100 to 130 mg / 100 g with a median of 115 mg / 100 g.

Seasonal effect

P content presented a seasonal variation that mirrored closely that of fat and protein content: in both 2017 and 2018 maximum values attained 104 mg / 100 g on average in November and December and minimum values attained were 98 mg / 100 g in June, July and Augustus. No significant / obvious difference was found between the years 2017 and 2018.

Relation to protein

P in milk is for the larger part present as phosphate (Walstra and Jenness, 1984). 10% of these phosphate groups are soluble esters and part of phospholipids that are elementary constituents of the fat globule membrane. About 20% of the phosphate groups are also organic but esterified to the protein molecules, notably the various forms of caseins. For those 20% there is therefore a direct relationship between protein and P content: more protein means more P content. The remaining part of P in milk is inorganic and bound to other minerals such as calcium – as calcium phosphate. However, these inorganic phosphate groups are for a considerable part contained in the casein micelles. The relation is here indirect, in that more protein comes with more phosphate. In sum, the majority of P content is directly or indirectly related to protein content. Yet, predicting P content from ex-farm milk at a large scale, we found that this correlation tends to vary during the course of the year, the correlation between P content and protein content being stronger in the winter (at the level of dairy farms in one given day), than in the summer (R^2 = .62 vs. R^2 = .41). The reasons for this difference are still to be explored. We speculate that dairy farm management has a stronger impact in the winter, when all cows are inside, than in the summer, when most cows are grazing. Another reason may be breed since the variability between cows is larger in winter than in summer.

The ability to predict P content at a large scale opens up possibilities to further research this question and other observations at minimal costs.

Take home message

From a trigger, available knowledge and decisive acting, Qlip was able to rapidly implement a new application in her routine FTIR testing portfolio at the beginning of 2019. The Dutch situation regarding phosphate regulation for dairy farms created the need for a better understanding of their phosphorus cycle. Reducing uncertainty about the amount of P in milk was considered helpful in 1) promoting awareness and bringing insight in the P cycle on dairy farms, 2) providing means to improve P utilization on dairy farms and 3) exploring the underpinning farm-specific registration of phosphate production.

Careful sample selection and execution of both the infra-red and the reference method allowed to develop a precise FTIR calibration model with robust performance (RMSE = 2.5 – 3 mg P / 100 g milk). Combining that with milk spectral data stored at Qlip provided insight about the past situation of phosphorus content in milk, and may well help identifying trends regarding the phosphorus cycle of dairy farms. Research institutes that would like to better understand differences in P content between farms, the effect of feed (grass, P supplementation) on P-content of milk, or even the nutritional/ technological / functional properties of P rich milk for human consumption have now, thanks to a routine implementation of the calibration model, a tool to quickly identify farms with interesting milk composition regarding P content, and this independently from protein or fat content.

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"MastiMIR" - A mastitis early warning system based on MIR spectra

L.M. Dale, A. Werner and F. Gollé-Leidreiter

Regional association for performance testing in livestock breeding of Baden-Wuerttemberg (LKV - Baden-Wuerttemberg), Stuttgart, Germany
Corresponding Author: ldale@lkvbw.de

Abstract

At farm level the mastitis disease appearance had decreased the milk production, produced veterinary costs, welfare issues, increased culling rate or caused lower milk payment. Because mastitis is associated with a wide range of characteristics that can be measured in milk and with recent advances in estimation of milk components using mid-infrared spectrometry, it is now possible to have the composition of several additional milk components such as fatty acids, lactoferrin, minerals, negative energy balance, non-esterified fatty acids and b-hydroxybutyrate or citrate, etc. The objective of this study was to build a spectrometric tool, such as MastiMIR for the determination in the milk quality of the animal health status, with the aim to evaluate the diagnosis usability and MIR indicators for the improvement of early mastitis prediction at LKV Baden-Württemberg. All data editing, modelling and calculations were done using the R statistical language and environment. The calibration data set contains around 9082 spectral data from around 1000 GMON herds. The validation approach was first cross validation 10 fold and a lot of 8 farms for an external validation. The 8 farms, chosen for the external validation, were the farms with the highest diagnosis registration and had to cover the important breeds e.g. 3 Holstein farms, 1 Red Holstein farm, 2 Brawn Swiss farms, 2 Simmental farms that are at LKV- Baden-Württemberg registered. To identify animal variables that were positively or negatively associated with mastitis determination, the spectral data set was first pre-processed by Savitzky-Golay first derivative to remove the offset differences between samples for baseline correction, before performimg Legendre polynomial modelling. Then the data was submitted to the combination of lasso regression using the "glmnet" R package. For the non-healthy group the spectral data with mastitis diagnosis for a given cow within 7 days before the new mastitis observation and the editing chosen was just test-day that had more than 400,000 somatic cell count (SCC). What come after the mastitis diagnostic was not taken into account for modelling. For the healthy group only spectra which had no diagnosis associated within ±60 days were used. For “glmnet” model were considered as fix effects the sampling moment, lactation stage and important LKV- Baden-Wtuerttemberg breeds and together with the Legendre polynomial data based on days in milk correction for the 212 OptiMIR selected wavenumbers of spectral data were input variables for MastiMIR model. Our MastiMIR calibration model showed a good accuracy (0.89) and medium prediction accuracy (0.83) we have to underline that was not finding until now any information in the literature of direct use of spectral data to predict the mastitis treat. The model provides four classes of Mastitis warning such as not, moderately, significantly and severely endangered. The moderately endangered class is a signal for the farmer. In that case the farmer would contact the veterinary and a control would be made in order to prevent the mastitis diseases. The MastiMIR model is a complementary tool for the SCC model.

Keywords: mastitis, spectrometry, MIR milk spectral data, dairy cow, cow health

Introduction

The mastitis definition is well known; mastitis is an inflammation of the mammary glands and can be caused by more than 50 different organisms. Usually, mastitis is diagnosed by cell number (SCC) and laboratory diagnostic methods. At farm level the mastitis disease appearance decreases the milk production, produces veterinary costs, welfare issues, and increases culling rate or causes lower milk payment. Mastitis is associated with a wide range of characteristics that can be measured in milk with recent advances in the estimation of milk components using mid-infrared (MIR) spectrometry. Also if a cow has mastitis, the composition of the milk will be affected and with it the MIR-milk-spectrum. The important message from the OptiMIR project was that not only the main components can be analysed with the MIR spectrometer, but also fatty acids (Grelet et al., 2014), minerals, lactoferrin (Soyeurt et al., 2011), BHB, acetate and citrates (Grelet et al., 2015), etc. complex features could also be identified, for example models for ketosis (Grelet etal., 2016), energy deficit (McParland etal., 2011, Smith et al., 2018) and methane emissions (Dehareng et al., 2012) were developed. Nowadays researches such as pregnancy detection (Laine et al., 2017) and mastitis detection tools could help farmers for better the herd management and better production. The objective of this study was to build a spectrometric tool, such as MastiMIR, for the determination of the animal health status from the milk quality, with the aim to evaluate the usability of Mastitis diagnosis in combination with MIR indicators in order to improve early mastitis risk prediction at the milk recording organisation LKV Baden-Württemberg.

Material and methods

Due to the health monitoring Baden-Württemberg (GMON cattle BW) which started in the beginning of 2010 diagnoses of approx. 1200 farms can be used for research and MastiMIR model. The diagnoses were documented by the veterinarian with the help of 86-part diagnostic keys. The gold standards to create the MastiMIR model were the mastitis diagnoses together with the spectral data. The diagnoses used for the model were: chronic, acute and subclinical mastitis, as well as coli mastitis. The model is based purely on standardized spectral data since all spectra registered at the MRO LKV- Baden-Württemberg level have been standardised starting from January 2012, due to the OptiMIR project participation. All data editing, modelling and calculations were done using the R statistical language and environment.

To identify animal variables that were positively or negatively associated with mastitis determination, the spectral data set was first pre-processed by Savitzky-Golay first derivative in order to remove the offset differences between samples for baseline correction, before performing Legendre polynomial transformation based on days in milk. Then the data was submitted to logistic regression in combination with LASSO variable selection and regularization and 10 fold cross validation using the "glmnet" R package. For the non-healthy group the spectral data with mastitis diagnosis for a given cow within 7 days before the new mastitis observation and the editing chosen was just test-day that had more than 400,000 somatic cell count (SCC). What comes after the mastitis diagnostic was not taken into account for modelling. For the healthy group only spectra which had no diagnosis associated within ±60 days were used. For “glmnet” model were considered as fix effects the sampling moment (with three variants: standard, morning and evening), lactation stage (if lactation number was greater than 5 it was taken as 5) and important LKV- Baden-Wtuerttemberg breeds (Holstein, Brown-Swiss and Simmental) and together with the Legendre polynomial data based on days in milk correction for the 212 OptiMIR selected wavenumbers of pre-processed

spectral data were input variables for MastiMIR model. The calibration data set contained around 9,082 spectral data from around 1200 GMON herds. The first validation approach was based on a random split of data, 70% of data was used for calibration model and 30% for validation model. The second validation model was based on a lot of 8 farms for an external validation in order to exclude animal and farm effects. These 8 farms were the farms with the highest diagnosis registration rate and had to cover the important breeds e.g. 3 Holstein farms, 1 Red Holstein farm, 2 Brown Swiss farms and 2 Simmental farms from LKV-Baden-Württemberg were registered. For this two validation models the same data cleaning approach as for calibration model was used. Due to the external validation with the extreme values diagnosis cases, a third validation model is proposed with production data from a whole production year. Data from 1st October 2017 till end of September 2018 in combination with diagnosis data was aimed to verify if the proposal model could be afterwards used or not in production. From a research and statistical point of view, production data approach could show what in the reality exists and if the model will be working in reality. Statistical methods such as cox event time analysis were performed in order to define the mastitis risk/danger. The class limits were determined by using statistical methods such as cumulative probability and, the class size was negatively correlated with the mastitis class.

Results and discussions

Mastitis can only be predicted to a limited extent via the number of cells. Therefore a model based on spectral data, animal parameters, and mastitis diagnoses such as MastiMIR has been developed. After modelling with GLMNET in R, a sensitivity (the percentage of sick cows that were correctly identified as having the condition) of more than 85% in calibration and 75% for the validation and external validation model could be obtained. The specificity (the percentage of healthy cows that were correctly identified as not having the condition) is more than 90% for calibration model and 1st validation model and 83% for the external validation model, 2nd validation model.

The MastiMIR calibration model showed a good accuracy (0.89) and medium prediction accuracy (0.83). It can be underlined that until now no information of direct use of spectral data to predict the mastitis treat has been found in the literature. Regarding the 3rd validation model with production data, it can be seen that the sensitivity is just 63% while the specificity is 70%. This can be explained by the probable presence of untreated Mastitis cases, subclinical mastitis and missing registration of diagnosis events in the production data. The idea was to cover this group of data by means of a mastitis risk probability provided by a presumed logistic-linear relationship (S-curve) between MastiMIR probability and the mastitis danger. This model allowed by using different thresholds to distinguish four different risk/danger classes. The class limits were negatively correlated with the mastitis class and were statistical supported by cox event time analysis.

Table 1. MastiMIR calibration and validation statistics

MastiMIR Model	Sensitivity	Specificity
Calibration	85.6%	90.3%
1st Validation	74.9%	90.4%
2nd Validation	75.6%	83.3%
3rd Validation	63.9%	70.7%

It can be seen in the distributions of the MastiMIR and the SCC classes over the lactation week, that the mastitis class distribution has the shape of the lactation curve on both models. The MastiMIR class distribution on whole population from GMON cattle BW for the year 2017 is more pronounced than SCC class. Regarding the animals with MastiMIR danger or risk it can be pointed out that mastitis can occur also when the cows have less SCC. Animals with higher SCC may still have other diseases. There is also a difference between the healthy classes and moderately endangered and also significantly endangered. The size of the group decreases as with the SCC classes with the danger. The Cox event time analysis improved the classification. If an animal has mastitis risk/danger diagnostic, it can be seen earlier with the MastiMIR model than with the SCC class model. The transition from significantly endangered to severely endangered was better separated (differentiated). The transition from healthy to moderately endangered class was displayed earlier. If a cow has health problems due to mastitis, not only does it have a lower amount of milk or higher SCC but it also reacts with a change of the main milk components: the lactose content is negatively correlated with mastitis and the protein content and the fat-lactose ratio are positively correlated. A positive correlation also applies to the milk fine components sodium, Lactoferrin and BHB, as the literature has already confirmed.

Conclusions

Until now was not publish in the literature the development of a model based on the spectral data and veterinary diagnosis. The MastiMIR model is going from the fact that the animal is already diagnose by veterinary doctor and it is trying to find in the spectral data the finger print for mastitis warning. MastiMIR could help furthers the farmer to identify the early mastitis in order to have a better herd management. The MastiMIR model provides four classes of mastitis warning such as not, moderately, significantly and severely endangered. MastiMIR can be a good warning tool to prevent mastitis. The moderately endangered class is a signal for the farmer. In that case the farmer would contact the veterinary and a control would be made in order to prevent the mastitis diseases. Compared to the SCC model, the MastiMIR model shows an earlier occurrence of the 'slightly at risk' classification. The MastiMIR model is a complementary tool for the SCC model, MastiMIR can supplement the SCC classes. An evaluation in the field within the framework of the ELENA project is currently being prepared.

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Prediction of evaluated energy balance (NEL and ME) in dairy cows by milk mid-infrared (MIR) spectra

L.M. Dale[1], A. Werner[1], H. Spiekers[2], P. Hertel-Böhnke[2], E. Stamer[3], F. Gollé-Leidreiter[1], M. Au[4] and F. Onken[4]

[1]Regional association for performance testing in livestock breeding of Baden-Wuerttemberg (LKV - Baden-Wuerttemberg), Stuttgart, Germany
Corresponding Author: ldale@lkvbw.de
[2]Institute for Animal Nutrition and Feed Management, Bavarian State Research Centre for Agriculture (LfL), Grub, Germany
[3]TiDa - Animal and Data GmbH, Westensee, Germany
[4]German Association for Quality and Performance Testing e.V., Bonn, Germany

Abstract

With the help of milk mid-infrared spectra (MIR) a wealth of information can be obtained by establishing relationships with so-called reference methods. Well-known and established is the determination of the milk ingredients fat, protein, lactose and urea. Additional to being used in herd management, fat and protein content are also used to determine the "milk price". The current research focus is the detection of indirect quantities, such as: pregnancy, mastitis, ruminal acidosis, lameness, energy balance, ketosis or methane emissions. The objective of this study was to build global spectrometric equations for energy balance calculated by the two evaluation systems net energy lactation (NEL) and metabolisable energy (ME), in order to determine the cow energy status. The application may be used in the field of herd management and also as a possible factor in breeding selection.

The present work is part of the collaborative project optiKuh, funded by the German Federal Ministry of Food and Agriculture. 12 research farms from different German states such as Baden Württemberg, Nordrhein-Westfalen, Bayern, Schleswig-Holstein, Rheinland-Pfalz, Niedersachsen and Mecklenburg-Vorpommern provided NEL and ME in between 2014 and 2017. The German Association for Quality and Performance Testing e.V. (DLQ), in which the regional MROs are united, provided approx. 40,000 milk samples available with energy balance information for the calibration equation establishment for the two energy balances. The energy balance models are built on standardised and unstandardized spectral data. To detect the outliers a difference between fat determined by the FOSS or Bentley spectrometers and the RobustMilk equation was calculated and no more than 2% difference was accepted. Out of the complete data set, 30% were considered outliers. To identify animal variables that were positively or negatively associated with cow energy status, the spectral data set was first pre-processed by Savitzky-Golay first derivative to remove the offset differences between samples for baseline correction, before Legendre polynomial modelling. Then the data was submitted to ridge regression using the "glmnet" package in R. For “glmnet” model, the sampling moment, lactation stage and important breeds such as Holstein (HOL), Red Holstein (HOL), Brown Swiss (BSW) and Simmental (SIM) and together with the Legendre polynomial data based on days in milk correction for the 212 OptiMIR selected wavenumbers of spectral data were input variables for modelling.

There were three models performed. The 1st model was based on spectral data random selection, the 2nd on random selection of animals and the 3rd, a global model with a cross-validation trial. The global energy balances, NEL and ME calibration models showed high coefficients of determination (R^2 = 0.75, respectively R^2 = 0.85%) and very poor RPD 2.00, respectively a poor RPD 2.50. The RPD is the ratio of standard deviation to standard error of cross validation. It has been underlined that a very poor model means that it allows to compare groups of cows, or to distinguish high or low values while the poor model allows rough screening. Standardised spectra showed a better robustness compared to unstandardized spectra (RPD: NEL 2.50 vs. 2.00, ME 3.04 vs. 2.47).

Keywords: energy balance, NEL, ME, MIR milk spectral data, dairy cow, cow health.

Introduction

Mid infrared spectroscopy (MIR) is using the infrared light from the electromagnetic spectrum which shows specific absorption patterns when sent through a milk sample caused by frequency dependent interactions with the chemical bonds of the chemical milk components. With the help of milk MIR spectra a wealth of information can be obtained by establishing relationships with reference methods. This technique is routinely used by milk laboratories and recording organisation (MRO) to determine the concentration of the main milk components fat, protein, lactose and urea. In the last years MIR became an increasingly applied technique that provides different molecular signatures in the dairy cattle industry. Since 2006, Soyeurt *et al.* performed different calibrations models for bovine milk fatty acids (FAs) and their milk MIR spectral predictions are used currently to generate multivariate prediction equations for over 30 FAs, these equations are routinely updated, with accuracies ranging from 68% to 100% (Grelet *et al.* 2014). The current research focus is the detection of indirect quantities, such as: methane emissions (Dehareng *et al.*, 2012), ketone bodies (Grelet *et al.*, 2016), milk protein composition (Rutten *et al.*, 2011), assessing the effect of pregnancy stage (Laine *et al.*, 2017), mastitis status (Dale *et al.*, 2019), lameness detection (Mineur *et al.*, 2017), body energy traits (McParland *et al.*, 2011), etc. The balance between energy intake and sum of energy for maintenance and production in dairy cows could be an important target for cow selection in modern breeding goals and herd management. There are few studies that are using dairy cow energy balance (NEL and ME) traits and MIR spectral data with the aim to calibrate and to generate prediction tools for use in commercial dairy herds. Since 2011, in UK prediction equations for energy balance and intake are applied to the largest spectral datasets (McParland *et al.*, 2011, Smith *et al.*, 2018) and MIR-based energy trait predictions from routinely collected national data has been used in genetic improvement of livestock to obtain sustainable energy profiles. The objective of this study was to build global spectrometric equations for energy balance calculated by the two evaluation systems net energy lactation (NEL) and metabolisable energy (ME), in order to determine the cow energy status. The application may be used in the field of herd management and also as a possible factor in breeding selection.

Material and methods

The present work is part of the collaborative project optiKuh, funded by the German Federal Ministry of Food and Agriculture, where 12 research farms from different German states such as Baden Württemberg, North Rhine-Westphalia, Bavaria, Schleswig-Holstein, Rhineland-Palatinate, Lower Saxony and Mecklenburg-Western Pomerania provided all information for the calculation of both energy balances (NEL,

ME) in between 2014 and 2017. The energy balances based on NEL were calculated in accordance with GfE (2001), and for the energy balances based on ME, the calculation was based on Susenbeth (2018). The 12 research farms collected approximately 40,000 milk samples from important breeds such as Holstein (HOL), Red Holstein (HOL), Brown Swiss (BSW) and Simmental (SIM) linked to weekly averages of individually recorded energy balance information. Local MROs and associated milk laboratories, organized in the "German Association for Quality and Performance Testing e.V." (DLQ), provided milk recording results and standardised as well as non-standardised MIR spectral data from FOSS and Bentley FTIR analysers for the calibration equation establishment of the two energy balances.

The spectral data are weekly registered at MROs and combined with energy balance data. The spectral absorbance data set was first pre-processed by Savitzky-Golay first derivative to remove the offset differences between samples for baseline correction, before Legendre polynomial transformation based on DIM was applied. To detect the outliers, the difference between the official fat content provided by the laboratories and the fat content derived from the RobustMilk MIR equation was calculated and no more than 4% for standardised spectra and 1% for non-standardised spectra of relative difference was accepted. Out of the complete data set, approximately 30% of spectral data were considered outliers. Then the data was submitted to ridge regression using the “glmnet” package in R.

The input matrix consisted of sampling moment (mixed, morning, evening), lactation stage and breeds serving as fixed effects and the 212 OptiMIR selected wavenumbers, subset of the pre-processed spectral data, were input variables for “glmnet” model. From the statistical point of view it was necessary to perform different validations models to understand better if the calibration model could be applied to different animals or just for the target animals included in calibration. Therefore there were three models performed. The 1st model was based on spectral data, a random selection of 70% of the data in the calibration model and 30% of the data in the validation model, the 2nd model was based on a random selection of animals, 25% of animals from each research farm are part of calibration model and the 3rd model, a global model with a cross-validation trial (Table 1.).

Results and discussions

Nearly 26,000 energy balances - on NEL basis and nearly 29,000 energy balances on ME basis of the 12 experimental farms have been used for the new equations. The different calibration models that are presented in Table 1, it shows the composition of the models. The 1st model was based on spectral data random selection and around 1,468 animals were part of the calibration model while around 1,145 were in the validation model. For the 2nd model, based on random selection of animals, 25% of

Table 1. Energy balance (NEL, ME) calibration and validation records.

Models		Calibration-Set Records		Validation-Set Records	
		NEL	ME	NEL	ME
Model 1	Spectra	24,159	21,705	8,040	7,221
	Animals	1,468	1,411	1,243	1,145
Model 2	Spectra	22,380	19,839	9,819	9,087
	Animals	1,110	1,085	396	365
Model 3		Cross-Validation - NEL		Cross-Validation - ME	
	Spectra	26,138		28,926	
	Animals	1,511		1,450	

Table 2. Energy balance (NEL, ME) – Model 3 calibration and validation statistics.

Model	Unit	#LV	Mean	SD	SEC	R²c	SECV	R²cv	RPDcv
EB - NEL	[MJ/d]	12	2.47	17.29	8.27	0.75	8.27	0.75	2.001
Standardised							7.53	0.84	2.502
NonStandardised							8.08	0.76	2.007
EB - ME	[MJ/d]	12	0.08	23.54	8.99	0.85	8.94	0.85	2.580
Standardised							8.41	0.89	3.049
NonStandardised							9.06	0.84	2.475

#LV = number of terms (latent variable)
SEC = standard error of calibration
R²c = calibration coefficient of determination
SECV = standard error of cross-validation
R²cv = cross-validation coefficient of determination
RPD = ratio of SD to SECV. See RPD class

animals from each research farm, it can be pointed out that 1,110 animals were used for calibration and around 396 for validation. Regarding the 3rd model, a global model with a cross-validation trial, all research farms animals (1,511) were used for final model.

It can be emphasized that there is a difference of 0.5 in RPD between standardized and non-standardized devices. But for a better variability and a better robustness of the models, was combined the standardized and non-standardized spectra and this model will be used for validation in commercial farms. It has to be pointed out that for the non-standardized spectral data only a maximum of 1% relative deviation between the official fat content provided by the laboratories and the fat content derived from the RobustMilk MIR equation was accepted. Therefore the equation quality is better and the RPD is higher as 2.

Conclusions

The global energy balances, calculated by the two evaluation systems NEL and ME calibration models showed high coefficients of determination (R^2 = 0.75, respectively R^2 = 0.85) and very poor RPD 2.00, respectively a poor RPD 2.50. The RPD is the ratio of standard deviation to standard error of cross validation. It has been underlined before that a very poor model means that it allows to compare groups of cows, or to distinguish high or low values while the poor model allows rough screening. Standardised spectra showed a better robustness compared to unstandardized spectra (RPD: NEL 2.50 vs. 2.00, ME 3.04 vs. 2.47).

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The use of fatty acid profiles from milk recording samples to predict body weight change of dairy cows in early lactation in commercial dairy farms

F. Dettmann[1,2], D. Warner[1], A.J. Buitenhuis[3], M. Kargo[3,4], A.M. Hostrup Kjeldsen[4], N.H. Nielsen[5], D.M. Lefebvre[1] and D.E. Santschi[1]

[1]Lactanet, Sainte-Anne-de-Bellevue, QC, H9X3R4, Canada
Corresponding Author: dsantschi@lactanet.ca
[2]LKV Niedersachsen e.V., 26789 Leer, Germany
[3]Aarhus University, Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, 8830 Tjele, Denmark
[4]SEGES, 8200 Aarhus N, Denmark
[5]RYK, 8200 Aarhus N, Denmark

Abstract

Most cows face energy deficits in early lactation during peak milk production, which is reflected in the milk fatty acid (FA) profile. These cows typically mobilize body reserves to maintain milk fat production, and synthetize less FA *de novo* in the mammary gland. Milk FA can be predicted routinely by Fourier-transform infrared (FT-IR) spectroscopy. This rapid milk analysis offers therefore an opportunity to develop an early indicator for body weight change (BWC) based on the milk FA profile. The objective of this study was to validate if the milk FA profile can be used to predict BWC in early lactating cows in commercial dairy farms. Data originated from 17,067 Danish Holstein cows at 7-35 days in milk across 166 herds in Denmark between March 2015 and March 2017 with body weight (BW) records from floor scales in Lely automatic milking systems at each milking. Milk FA in test-day milk samples were predicted by FT-IR on FOSS instruments providing four individual FA and seven groups of FA according to chain length and saturation. Data for BWC predictions included parity, stage of lactation, and test day data for milk production and components (fat, protein, somatic cell count, and FA concentrations). Daily BWC (median $\pm$ standard deviation) was -0.32 $\pm$ 2.66 g/kg of BW (first parity), -0.46 $\pm$ 2.82 g/kg of BW (second parity) and -0.60 $\pm$ 5.53 g/kg of BW (third parity). Predictions of BWC were based on a random forest model, an ensemble of multiple decision trees that can account for the nonlinear and high dimensional interactions among predictors and, to a certain extent, for a potential collinearity among single FA. The model was validated with ten-fold repeated cross-validation for which 20% of the herds were randomly withhold for validation such that data of a specific herd are used exclusively either to train or to cross-validate the model. The overall root mean square error of prediction after cross-validation was 1.66 g/kg of BW with the model explaining 89.6% of the variance. The five most important variables to develop the model were the short-chain FA group (C4:0–C10:0), oleic acid (C18:1), the medium-chain FA group (C12:0–C16:1), the saturated FA group, and palmitic acid (C16:0). The short-chain and some medium-chain FA are synthesized *de novo* in the mammary gland, oleic acid originates from body reserves (e.g., during energy deficits), and palmitic and palmitoleic acid (C16:1) originate either from the *de novo* FA pool or from body reserves and from feed. These results suggest that the FT-IR milk FA profile may be used as an early indicator of BWC in early lactation cows. Nonetheless, before this model can be used in commercial farms, the model needs to be validated for different herd management and feeding strategies, breeds

and country- or region-specific conditions. Further work is needed to assess the impact of the level of BWC on milk production, reproductive performance and health. Future models may gain from the inclusion of other milk components such as beta-hydroxybutyrate known to be linked to BW loss in early lactation. An early warning system may be implemented for cows with a large BW loss in early lactation based on the FT-IR milk FA profile.

Keywords: dairy herd improvement, fatty acid profile, FT-IR, body weight loss, machine learning.

Introduction

In early lactation, most dairy cows face energy deficits due to a mismatch of milk production and feed intake. Negative energy balance (NEB) varies between cows in extend and duration (Jorritsma *et al.*, 2003). These cows typically mobilize body reserves (Andrew *et al.*, 1994; Grummer and Rastani, 2003) to maintain milk fat production (Bar-Peled *et al.*, 1992). This is reflected in the milk fatty acid (FA) profile. In early lactation, *de novo* FA are synthetized less in the mammary gland and preformed FA are on a higher concentration (Palmquist *et al.*, 1993; Garnsworthy *et al.*, 2006). Furthermore the mobilization of body fat induce a reduction in BW (Grummer and Rastani, 2003). In most commercial dairy farms, BW is not routinely recorded.

In modern milk laboratories, Fourier-transform infrared (FT-IR) spectroscopy is routinely used to determine milk composition and, accordingly, to predicted the milk FA profile.

This rapid milk analysis offers therefore an opportunity to develop an early indicator for body weight change (BWC) based on the milk FA profile. Our objective was to assess whether milk FA by FT-IR analysis can be used to predict BWC in early lactating cows in commercial dairy farms.

Materials and methods

Data source, fatty acid analysis, and body weight

Cow information, test day production data, test day milk FA concentrations analyzed by Fourier-transform infrared were obtained by the Danish Cattle database (SEGES, Skejby, Denmark). Milk samples were analyzed as regular DHI milk samples for fat, protein, lactose, MUN, SCC, BHB, and acetone in addition to FA concentrations. Analyses were performed using a Foss MilkoScanFT+/FT 6000 (Foss Electric A/S, Hillerød, Denmark) for infrared evaluation of milk component, equipped with special software (Foss Application Note 0064 / Rev.5; Foss, Hillerød, Denmark) for predicting 11 FA. These FA are 4 individual FA, namely C14:0, C16:0, C18:0 and C18:1, and 7 FA fractions according to their degree of saturation, namely saturated (SFA), monounsaturated (MUFA), polyunsaturated (PUFA), and *trans*-unsaturated (TFA) FA, and their chain length, namely short-chain (SCFA), medium-chain (MCFA), and long-chain (LCFA) FA.

Cow information and BW data recorded by floor scales in Lely automatic milking systems at each milking were obtained by the Danish Cattle database (SEGES, Skejby, Denmark).

The data set of the Danish Cattle database contained:

- The actual weight measured in robot (body weight start [BWs]).
- The BWs corrected for differences between robots in one herd if differences were present (body weight corr [BWc]).
- A smoothed body weight based on locally weighted smoothing (body weight end [BWe]) of BWc.

The initial data set of FA included 232,575 test day records between days in milk (DIM) 5 to 305 of 39,209 Danish Holstein cows from 170 herds in Denmark, collected from March 2015 to March 2017, with records from parity 1 throughout 6. The initial data set of BW included 28,581,762 BW records between DIM 5 to 305 of 35,787 Danish Holstein cows from 168 herds in Denmark, collected from January 2015 to September 2017, with records from parity 1 throughout 3. The number of robots per herd spanned from 1 to 11, whereby 36.3% of the farms held two robots, 23.2% three robots, and 14.3% four robots.

The data sets were edited with numerous consecutive procedures to ensure a high quality of observations and to eliminate abnormal records. According to Hein *et al.* (2018) observations in the FA data set were removed if any of the following conditions was met:

- one or more of the 11 FA fractions was missing from an observation;
- the PUFA concentration was greater or equal to the MUFA concentration;
- the ratio of the sum of the SFA, MUFA, and PUFA contents to the total fat content was less than 0.825 or greater than 1.075 (values chosen such that 5% of remaining observations were removed);
- the ratio of the sum of the SCFA, MCFA, and LCFA contents to the sum of the SFA, MUFA, and PUFA contents was less than 0.84 or greater than 1.04 (values chosen such that 1% of remaining observations were removed).

Based on present parities of 1 to 3 in the data set of BW, we removed parities equal to or greater than 4 in the data set of FA. Therefore, the edited data set of FA included 197,058 test day records of 34,917 Danish Holstein cows from 168 herds.

Observations of BWs in the data set of BW were removed if:

- The weight were less than 300 kg or greater than 1100 kg, and if
- BWs were more than 3 times the standard error away from the smoothed weight of BWs of each cow and each robot.

For further calculations BWe was used since these values were corrected for differences in robots in each herd and were already smoothed for daily differences in body weight. To estimated BWC, we calculated a relative daily BWC for each single DIM as follows:

$$\frac{BW_{DIMx} - BW_{DIMx^{-1}}}{BW_{DIMx^{-1}}} * 100 = dailyBWC_{DIMx}\% \quad (1)$$

To combine daily BWC to a test day, we calculated an average of the last three daily BWC before test day whereby the test day was included (Figure 1). DIM 5 and 6 were removed as a calculation of an average of the last three daily BCW was not achievable. Furthermore early lactation period were defined from DIM 7 to 35. So the final data set included 19,371 test day records with the BWC of 17,067 Danish Holstein cows from 166 herds with an average milk yield of 35.87 kg (SD=10.90, range from 2.10 kg to 76.80 kg). The relative BWC is shown in g/kg of BW. All editing procedures of the initial data sets are listed in Figure 2.

The descriptive statistics of characteristics of milk components and FA of early lactation cows are presented in Table 1.

Statistical analysis

A random forest algorithm (Breiman, 2001) was used to predict BWC based FA and milk components. A random forest is an ensemble of multiple decision trees and can be understood as the sum of piecewise linear functions. The dataset is divided into smaller regions that become more manageable. As such a random forest model can deal with a multitude of linear and nonlinear relationships among predictors, and the complexity inherent to high-dimensional dataset. The model was prepared using 10-fold cross-validation with three iterations. For each iteration, a model was trained on nine splits of the data set and cross-validated on the remaining part of the data set (i.e., one split), for which 20% of the herds were randomly withhold for validation such that data of a specific herd are used exclusively either to train or to cross-validate the model. Model accuracy was estimated based on the average of the 10-fold repeated cross validation. The optimal parameter configuration for each model was evaluated for each model based on the repeated cross-validation and was set at 500 trees. The models were implemented in R (version 3.5.0; R Foundation for Statistical Computing, Vienna, Austria) using the caret modelling package workflow (Kuhn, 2008).

Results and discussion

Milk fatty acid profile

The milk FA profile is a result of complex interactions among dry matter intake, diet composition, rumen fermentation, body reserve mobilization, liver metabolism, and mammary absorption and *de novo* synthesis of FA (Garnsworthy *et al.*, 2006). The onset of lactation is a delicate period for the metabolism of the cow. Body fat mobilization (Andrew *et al.*, 1994; Grummer and Rastani, 2003) to maintain milk fat production (Bar-Peled *et al.*, 1992) lead to a change in milk FA profile and BW loss in early lactation.

In Figure 3, the distribution of the FA groups SCFA, MCFA and LCFA in g/day by lactation 1, 2, and 3 plus higher Lactations of Danish Holstein cows are shown. In early lactation (DIM 7 to 35), the concentrations of SCFA and MCFA were increased by DIM. Concentrations of LCFA are decreased rapidly by DIM. Differences in concentrations of milk FA across parity are also apparent. With increasing lactation, the concentration of FA increased due to a higher production of milk fat and a stronger mobilization of body fat due to a stronger NEB.

SCFA are synthetized *de novo* and the synthesis of these FA in the mammary gland is less in early lactation (Palmquist *et al.*, 1993; Garnsworthy *et al.*, 2006). According to Garnsworthy *et al.* (2006), the molar proportions of the FA C10:0 to C14:0 were significantly lower in early lactation than in mid lactation. Palmquist *et al.* (1993) reported in early lactation lower concentrations of FA C6:0 to C14:0 and concluded that *de novo* synthesis of FA was inhibited by LCFA from body fat.

Table 1. Characteristics of milk components and milk fatty acids (g/100g milk) in early lactation (DIM 7-35) Danish Holstein cows by parity.

	Parity 1 (n = 8,323 animals)					Parity 2 (n = 6,716 animals)					Parity 3 (n = 4,332 animals)				
Trait[1]	Mean	SD	p1	Median	p99	Mean	SD	p1	Median	p99	Mean	SD	p1	Median	p99
Fat (%)	4.50	0.97	2.56	4.38	7.44	4.25	0.91	2.43	4.16	6.86	4.33	0.98	2.41	4.25	7.25
Protein (%)	3.41	0.31	2.78	3.39	4.22	3.37	0.33	2.72	3.37	4.28	3.34	0.34	2.71	3.30	4.26
Fat:Protein	1.32	0.28	0.77	1.29	2.19	1.26	0.27	0.73	1.23	2.10	1.30	0.29	0.75	1.27	2.28
SFA	2.68	0.58	1.48	2.62	4.39	2.57	0.57	1.33	2.53	4.03	2.60	0.60	1.40	2.55	4.32
MUFA	1.33	0.41	0.66	1.27	2.67	1.23	0.37	0.62	1.17	2.42	1.28	0.42	0.62	1.21	2.65
PUFA	0.17	0.05	0.08	0.17	0.31	0.16	0.04	0.01	0.16	0.28	0.16	0.04	0.07	0.16	0.30
SCFA	0.43	0.11	0.23	0.43	0.74	0.43	0.10	0.22	0.43	0.69	0.44	0.10	0.23	0.43	0.72
MCFA	1.59	0.37	0.84	1.55	2.68	1.52	0.38	0.75	1.49	2.51	1.52	0.39	0.76	1.48	2.64
LCFA	1.90	0.59	0.85	1.81	3.74	1.76	0.54	0.78	1.69	3.42	1.83	0.60	0.79	1.75	3.77
C 14:0	0.37	0.09	0.20	0.36	0.63	0.36	0.09	0.19	0.35	0.59	0.36	0.09	0.18	0.35	0.61
C 16:0	1.11	0.25	0.62	1.09	1.87	1.05	0.25	0.56	1.03	1.74	1.05	0.26	0.56	1.03	1.81
C 18:0	0.59	0.17	0.29	0.57	1.09	0.54	0.15	0.25	0.52	0.98	0.56	0.17	0.26	0.54	1.08
C 18:1	1.20	0.40	0.54	1.14	2.46	1.11	0.35	0.51	1.05	2.22	1.15	0.40	0.51	1.09	2.48

[1]Trait: SFA = saturated fatty acids; MUFA = mono unsaturated fatty acids; PUFA = poly unsaturated fatty acids; SCFA = short-chain fatty acid; MCFA = medium-chain fatty acid; LCFA = long-chain fatty acid.

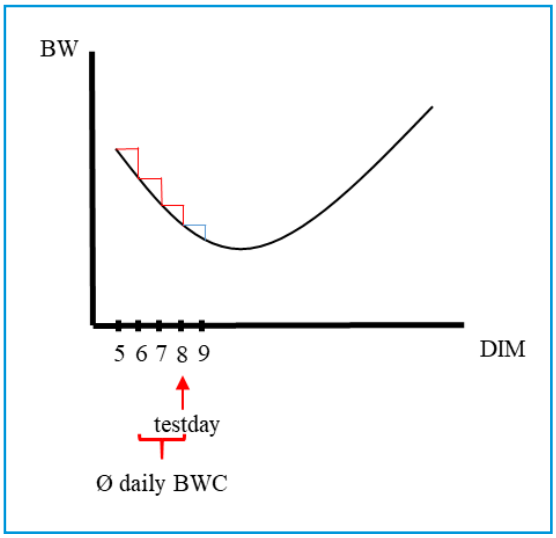

Figure 1. Calculation of BWC on test day.

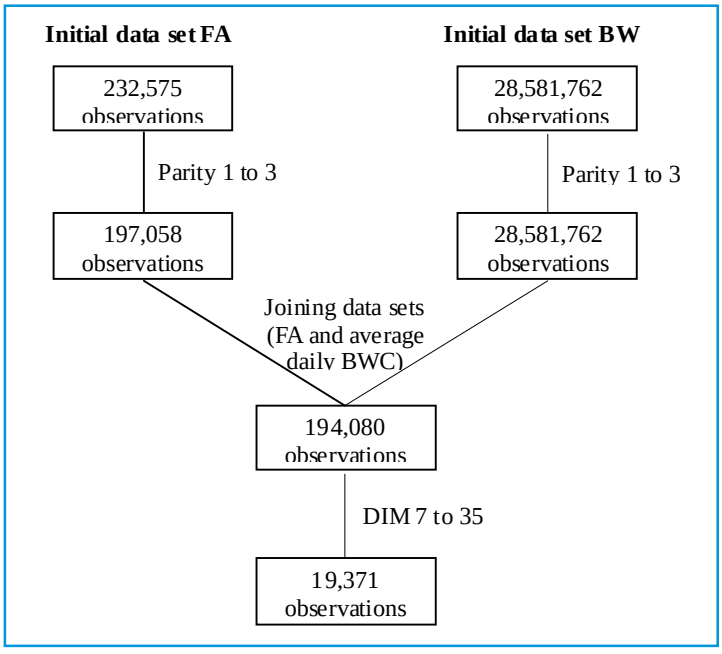

Figure 2. Editing procedures of initial data sets.

MCFA originate either from the *de novo* FA pool or from body reserves and from feed. Generally, 60% of C16:0 originate from *de novo* synthesis (Moore and Christie, 1981). In the study of Garnsworthy *et al.* (2006) the yield of C16:0 was 11% higher in early lactation than mid lactation. This is contrary to our results as seen in Figure 3. According to the Foss Application Note 0064 / Rev. 5 (Foss, Hillerød, Denmark), the prediction model estimated for MCFA the total group of C12, C14 and C16 FA. This could explain the lower concentrations of MCFA in early lactation compared to later stages in lactation.

LCFA are preformed FA and originate from body fat and from feed. In early lactation these FA are on a higher concentration than in mid lactation due to increased mobilization of body fat in early lactation (Palmquist *et al.*, 1993; Garnsworthy *et al.*, 2006). In adipose tissue, C18:1c9, C16:0 and C18:0 account for nearly 90% of the FA and are contained in approximately equal molar proportions (Christie, 1981). The mobilization of body reserves, especially body fat, would be expected to increase incorporation of these FA into milk fat. Garnsworthy *et al.* (2006) reported an 80% higher yield of C18:1c9 for early lactation cows than for mid lactation cows. 50% higher concentrations for C18:1 and C18:0 in milk fat in week 1 than week 16 was reported by Palmquist *et al.* (1993).

Relative BWC and BWC curves

BW characteristics in early lactation Danish Holstein cows by parity are shown in Figure 4. Distribution of initial BW at DIM 7 showed a normal distribution and differed across parity (570, 641, and 681 kg for first, second, and third parity, respectively).

Time from calving to nadir BW differed across parity (26, 37, and 39 DIM for first, second, and third parity, respectively). Other studies showed similar results. Maltz (1997) showed in a visual analysis of 40 primiparous and 64 multiparous Israeli Holsteins cows a BW trough by days 25-30. The BW weight data were collected after each milking (thrice daily at 8-h intervals) by a walk-through scale and averaged daily. Van Straten *et al.* (2008) reported a similar mean DIM from calving to nadir BW with 29, 34, and 38 for first, second, and third and above parity, for high-producing cows. In their study 250,920 daily BW measurements were included to constructed standard relative BW curves, which were corrected for the random effect of farm and the correlation between repeated measurements in the same cow (van Straten *et al.*,

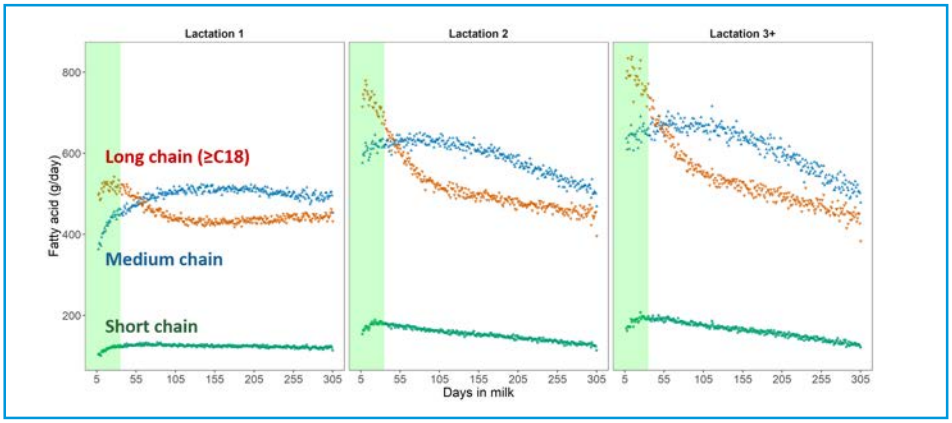

Figure 3. Distribution of the FA groups SCFA, MCFA, and LCFA in g/day for days in milk of Danish Holstein cows. The green range represent the early lactation from DIM 1 to 35.

2008). The distribution of DIM from calving to nadir BW increased with parity. These results suggest that the duration of NEB increased with an increase in parity, whereby the NEB was lower for first parity as compared to older cows (van Straten *et al.*, 2008).

The relative daily BWC differed across parity and lactation stage (Figure 5). The relative daily BWC was (median ± standard deviation) -0.32 ± 2.66 g/kg of BW, -0.46 ± 2.82 g/kg of BW, and -0.60 ± 5.53 g/kg of BW for first, second, and third parity. In the study of Maltz (1997), 77% of the multiparous cows lost 5-15% of their post-calving weight in the period of minimal BW between days 25-40. From calving to nadir BW, the standard first-parity cow lost 6.5% of its initial BW, for standard second- and greater-parity cows, relative BW loss was 8.5 and 8.4% (van Straten, 2008). Zachut and Moallem (2017) found an average BW loss from week 1 to 5 of 5.87 and 7.27 % for first-parity cows, 4.83 and 6.49 % for second-parity cows, and 5.45 and 7.80 % for third-parity cows. In the study of Zachut and Moallem (2017), BW was measured 3 times a day from calving and they distinguished between 2 groups of different BW loss: low weight loss and high weight loss. Difference in relative mean daily BWC across parity and lactation stage are shown in Figure 5. The initial rate of BWC seemed similar in the 3 parity groups. First-parity cows reached a positive daily BWC at an earlier DIM and gained BW at a greater rate than second- and third- and greater-parity cows, respectively. Second- and third- and greater-parity cows showed similar attainment of a positive daily BWC but second-parity cows gained BW at a greater rate than third- and greater-parity cows. Similar findings were reported by van Straten *et al.* (2008). By 120 DIM, first-parity cows reached 98.8% of their original BW. Second- and greater-parity cows reached 93.9 and 92.8% of their original BW (van Straten, 2008).

Maltz *et al.* (1997) described BWC as a result of two factors:

1. Changes in body reserves (mobilization in early lactation, and deposition and late lactation), and
2. Changes in gastrointestinal (GI) size and content (increased in early lactation, decreased in late lactation) as well as other metabolism-supporting organs (liver, kidney etc.).

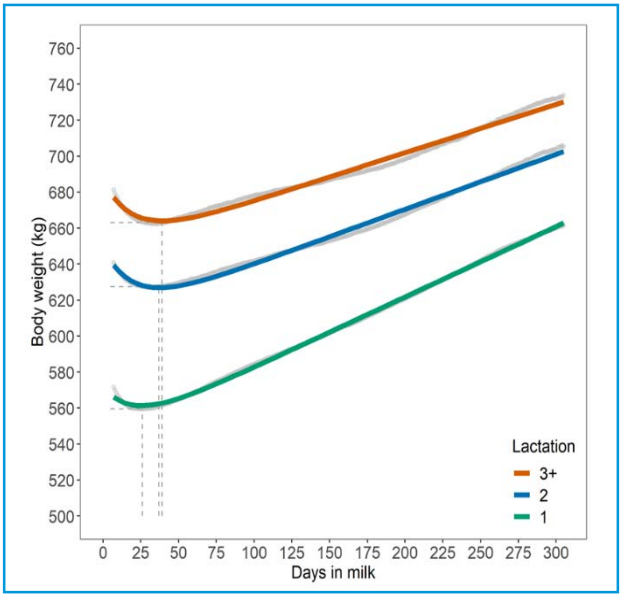

Figure 4. Daily body weight of dairy cows across 168 Danish Holstein herds with nadir body weight obtained at 26 days (1st parity), 37 days (2nd parity) and 39 days of lactation (3rd parity).

Both factors may have a contradictory effect on BW, the first one as energy-balance related factors, and the second as metabolism-related factors. In this study, changes in GI size and content as GI fill were not included because GI fill varies with intake and physiological stage (Andrew *et al.*, 1994) and BWC reflects both changes in BW as mobilisation and deposition and changes in GI fill (Grummer and Rastani, 2003).

Prediction model for BWC

To predict BWC of early lactation (7 to 35 DIM) Danish Holstein cows based on FA profile we used a random forest regression model. The random forest regression model included all FA groups and FA, milk yield, fat percentage, protein percentage, a ratio of C18:1 to SCFA, a ratio of fat percentage to protein percentage, DIM, parity, SCC, year and month, and predicted BWC at an accuracy after cross-validation of R^2_{CV} = 0.896, MAE_{CV} = 0.761, and $RMSE_{CV}$ = 1.66 g/kg of BW (Figure 6).

The random forest regression model are shown that SCFA had the highest influence, followed by C18:1, MCFA, SFA, and C16:0 (Figure 7). The effects of fat percentage and protein percentage were low as well as year and month although a seasonality of FA concentration in milk is known.

The results have shown that the prediction of the BWC in early lactation would make it possible for the herd manager to continuously know the current metabolism status of the animals in this lactation period, in the context of the monthly milk recording. The use of FA in milk samples is an economically feasible approach without the need of using technical equipment such as floor scales or 3-dimensional vision systems. BW measurements on floor scales showed daily fluctuations (Maltz *et al.*, 1997) due to milk yield, feed intake, water intake and milking times compared to weight times. Therefore, the first step in data analysis has to overcome this obstacle in order to differentiate changes of physiological significance from normal daily fluctuations (Maltz and Metz, 1994).

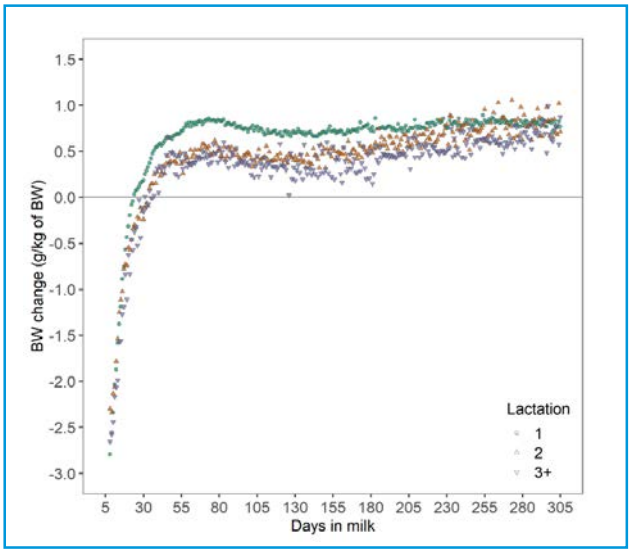

Figure 5. Relative mean daily body weight change of dairy cows across 168 Danish Holstein herds.

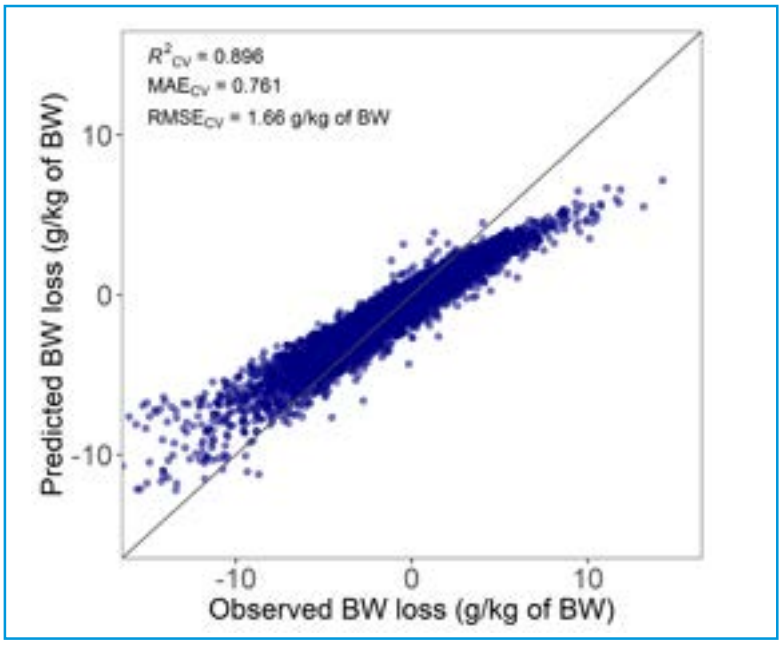

Figure 6. Random forest regression model for prediction of body weight changes based on milk fatty acid profiles.

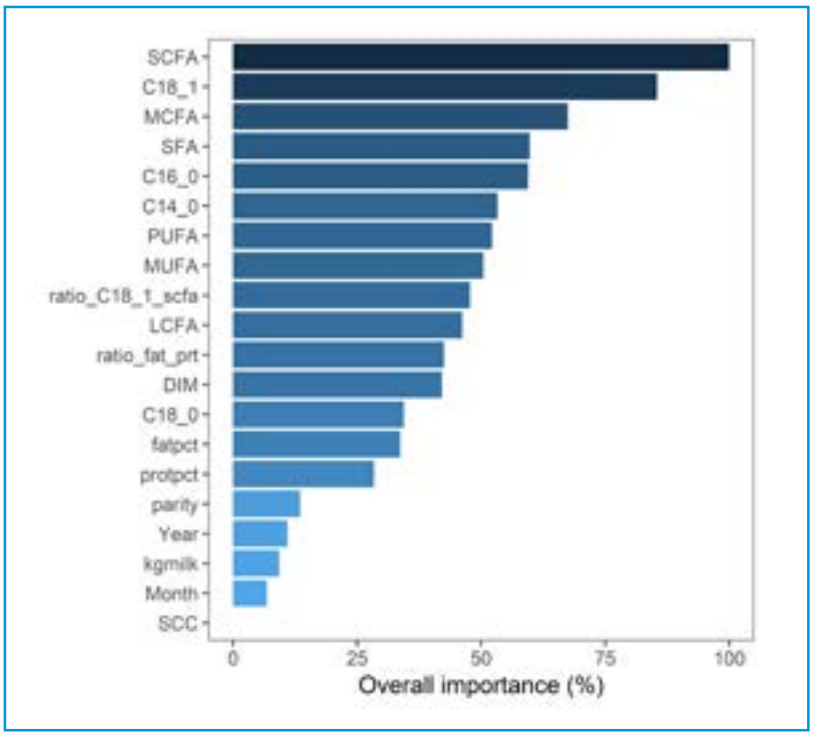

Figure 7. Relative importance of selected variables in random forest prediction model.

Conclusions

The results suggest that BWC can be estimated by FT-IR milk FA profiles in DHI samples. Nonetheless, before this model can be used in commercial farms, the model needs to be validated for different herd management and feeding strategies, breeds and country- or region-specific conditions. Further work is needed to assess the impact of the level of BWC on milk production, reproductive performance and health. Future models may gain from the inclusion of other milk components such as beta-hydroxybutyrate known to be linked to BW loss in early lactation. A prediction of BWC for a real-time decision support tool may not be feasible as any suggested modification in management strategies will likely not improve reproductive performance in the current lactation anymore. However, our prediction model might be useful to identify herd-level deficiencies and improve overall herd management to improve herd performance in future lactations.

Acknowledgments

Lely Nordic A/S (Fredericia, Denmark) for body weight data and H. Martinussen (SEGES, Denmark), I.B. Skaarup Hansen (RYK, Denmark), L. Fadul-Pacheco and R. Lacroix (Lactanet, QC, Canada) for support with data analysis.

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Quality of colostrum as estimated by different methods

L. Curda, V. Zherepa, I. Klojdova

University of Chemistry and Technology Prague, Department of Dairy, Fat and Cosmetics, Technická 5, 166 28 Prague, Czech Republic
Corresponding Author: curdal@vscht.cz

Abstract

The main quality marker of colostrum is concentration of immunoglobulins, in the broad sense content of proteins. The standard method for estimation of immunoglobulin IgG1 is radial immunodiffusion (RID), but this method is lengthy and expensive. Thirty samples of spray dried or lyophilized cow colostrum were analysed by several methods, both rapid screening methods and methods that are more precise. Three chromatographic methods were tested: size exclusion chromatography (SEC) and two variants of affinity chromatography (AC) using column with Protein A and Protein G. Good results were obtained from SEC (R2=0.95), but column is very expensive and it has short lifetime. Similar results gave affinity chromatography on Protein G column, its advantage is short analysis time (10 min). Spectrophotometric methods (Bradford and UV spectroscopy) are not demanding for instrumentation, but the sample preparation is quite complex.

Keywords: colostrum, immunoglobulin, radial immunodiffusion, affinity chromatography, size exclusion chromatography, Bradford method.

Introduction

Colostrum is initial secretion produced in mammary glands of mammals following parturition. It is rich in immunoglobulins, lactoferrin, growth factors and many other biologically active substances. Quality of colostrum is important for newborns, which have immature immune system, moreover colostrum is also widely used as food supplement (Godhia and Patel, 2013). The main quality marker of colostrum is concentration of immunoglobulins, in the broad sense content of proteins. Gapper *et al.* (2007) did an overview of methods used for colostrum analysis. The standard method for estimation of immunoglobulin IgG1 is radial immunodiffusion (RID) and many authors used it for comparison with other methods, but this method is lengthy and expensive (Quigley *et al.*, 2013; Stojic *et al.*, 2017). The aim of this work was to prove some alternative methods suitable for estimation of quality of dried colostrum from point of view of IgG content.

Material and methods

Dried colostrum (spray dried or lyophilized) was provided by Ingredia Ltd. (Frydek – Mistek, Czech Republic). IgG from bovine serum (Sigma-Aldrich) was used as standard. Samples for analysis were prepared by dissolving of 1 % (w/v) of colostrum in phosphate buffer pH 8.0. Casein was removed by precipitation at pH 4.6. Immunoglobulins were precipitated by sodium sulphate (Skalka *et al.*, 2017). Radial immunodiffusion (RID)

was used as reference method (Bovine IgG-NL RID Kit RN200.3, Rockland Immunochemicals Inc., USA). Affinity chromatography (AC) was performed as described by Copestake *et al.* (2006) and Abernethy and Otter (2010) using columns HiTrap Protein G HP 1 ml (GE Healthcare, Sweden) and BabyBio (Protein A) 1 ml (Bio-Works, Sweden). Size exclusion chromatography (SEC) was performed on column Superdex Increase 10/300 GL (GE Healthcare, Sweden) using phosphate buffer 0.05 M containing 0.15 M NaCl (pH 7.2). AC and SEC columns were attached to Agilent 1260 Infinity Bio-inert system with DAD (280 nm). Proteins were also estimated according to Bradford method (Bradford, 1976) at 595 nm. Samples after AC were precipitated by acetone and separated on 12.5 % acrylamide gel by SDS-PAGE (Laemmli, 1970). Content of IgG in standard solution was estimated by UV measurement at 280 nm using extinction coefficient ($\varepsilon_{280\ 1\ cm;\ 1\ mg/mL}$) 1.4 (Copestake *et al.*, 2006).

Results and discussion

Immunoglobulins are main part of proteins in acid whey from colostrum (AWC), therefore correlation between RID and Bradford method was examined (Figure 1) and coefficient of determination R^2 was 0,72. AWC was also analysed by size exclusion chromatography (SEC). Proteins were well separated, high R^2 was obtained (0.95), but analysis takes 40 min and high backpressure of column is limiting factor (Figure 2).

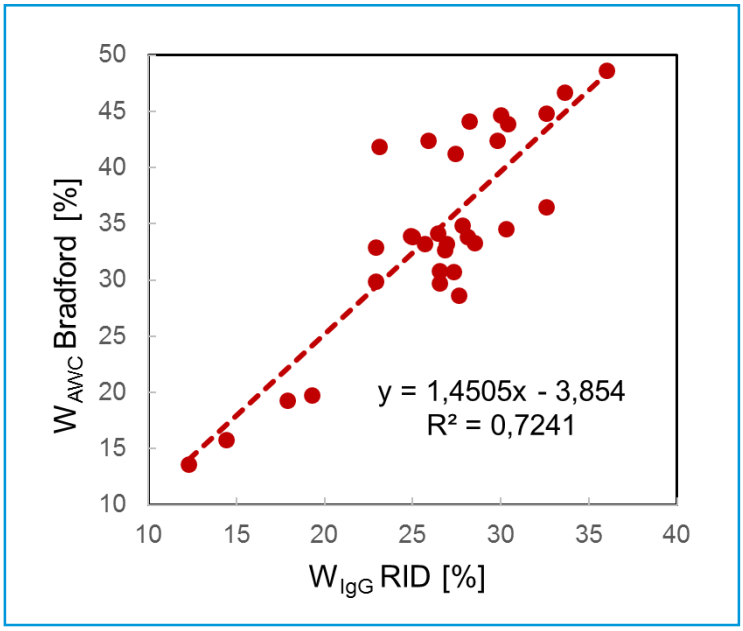

Figure 1. Correlation between RID and spectrophotometric estimation of proteins in acid whey from colostrum.

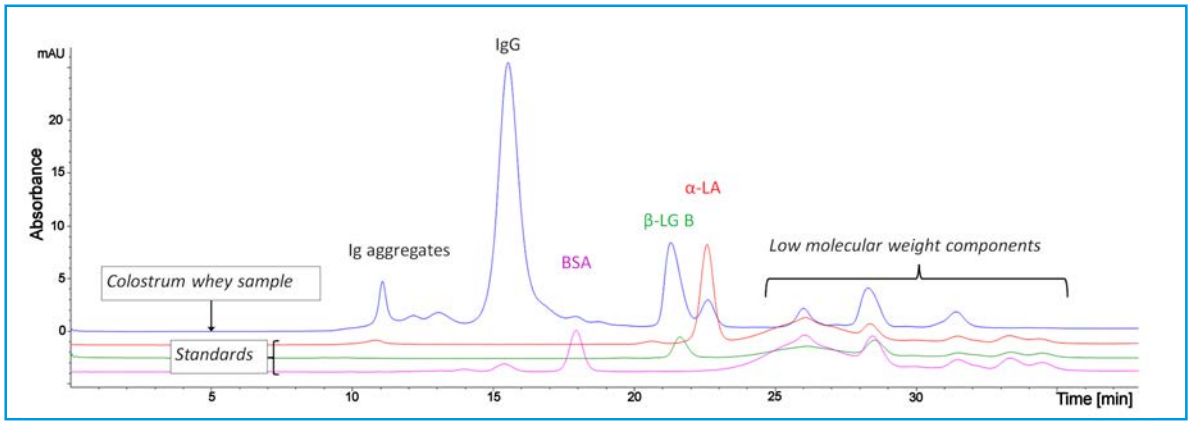

Figure. 2. Separation of acid whey from colostrum and selected standards of whey proteins by SEC chromatography.

Affinity chromatography (AC)

Columns with Protein A and Protein G were examined for AC method. Better response was obtained from Protein G column (Figure 3). Colostrum, acid whey and IgG fraction obtained by precipitation can be analysed by AC in 10 min. Collected peaks were further assessed by SDS-PAGE (Figure 4). IgG isolated by precipitation contained some other whey proteins, particularly β-LG. Peak from colostrum sample is slightly contaminated by casein and results of IgG are distorted. Coefficient of determination between results from analysis of acid whey by AC and RID was 0.88 (Figure 5).

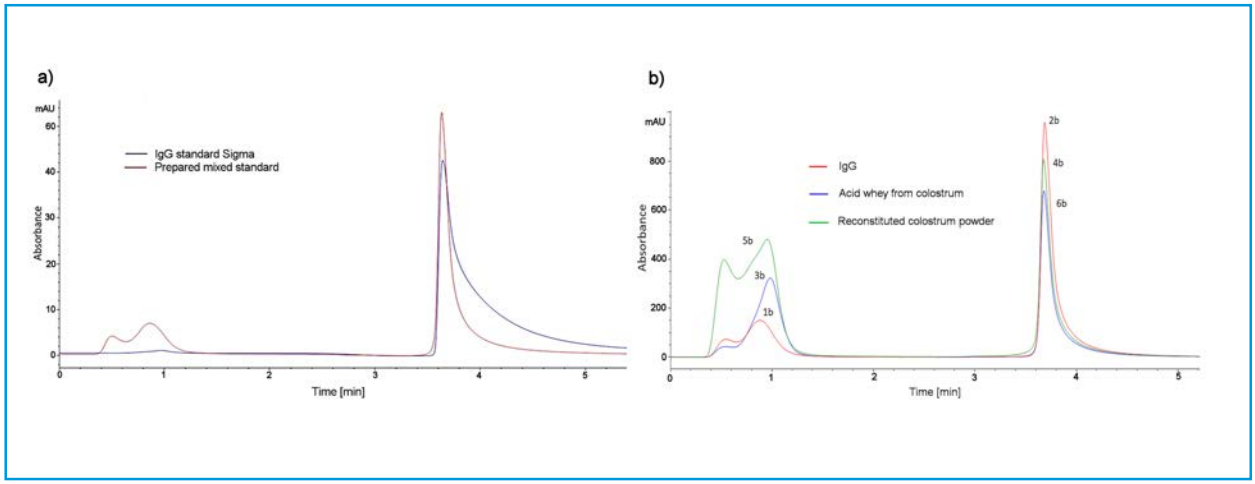

Figure 3. Affinity chromatography on Protein G column: a) chromatograms of standards (sigma and mixed standard obtained by sodium sulphate precipitation from mixture of colostrum samples); b) chromatograms of precipitated IgG (peaks 1 and 2), acid whey from colostrum (peaks 3 and 4) and colostrum sample (peaks 1 and 2).

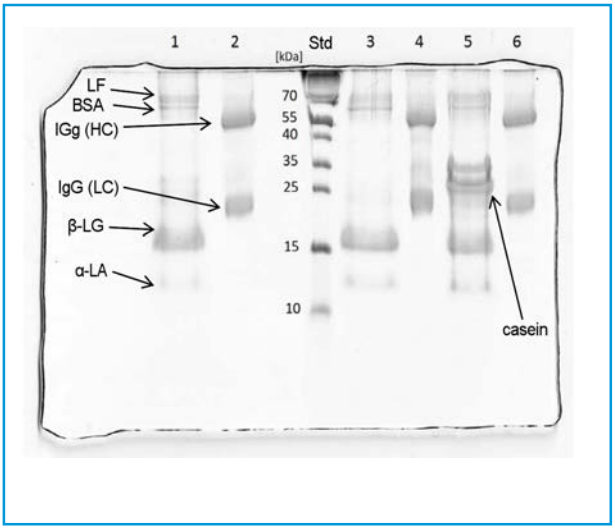

Figure 4. SDS-PAGE of samples from peaks collected from AC Protein G column.

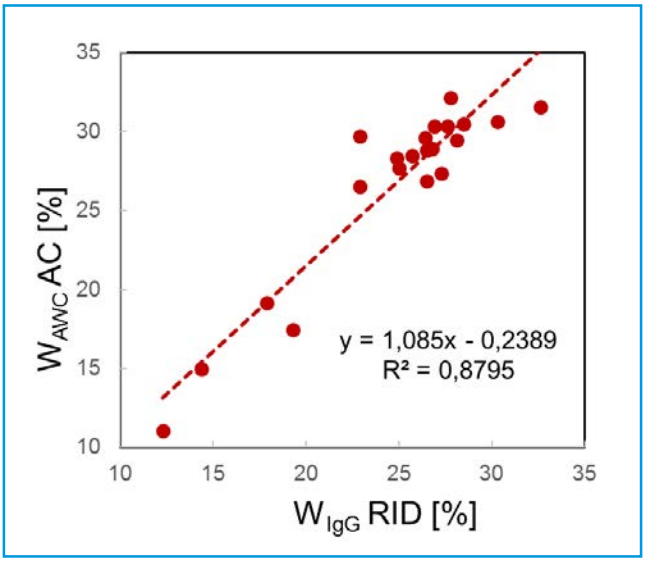

Figure 5. Correlation between RID and affinity chromatography of acid whey from colostrum (column HiTrap Protein G).

Conclusions

Estimation of proteins in acid whey from colostrum by Bradford method is simple and rapid technique for evaluation of colostrum quality. Size exclusion chromatography gave precise results, but the method is lengthy and expensive. Affinity chromatography of acid whey is a rapid method that correlates well to RID.

Acknowledgement

Financial support from the Ministry of Education, Youth and Sport of the Czech Republic (MSMT No. 20-SVV/2018) and from the National Agency of Agricultural Research (research project QJ 1210376) is acknowledged.

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Dairy sheep udder measurements and assessments in the Czech Republic

M. Milerski[1], M. Cerná[1] and J. Schmidová[1]

[1]Institute of Animal Science, Prátelství 815, 10400 Prague 10, Uhríneves, Czech Republic
Corresponding Author: milerski.michal@vuzv.cz

Abstract

The introduction of machine milking to dairy sheep industry evokes the requirement to pay more attention on morphological and functional characteristics of udders. For this reason the methodology of udder measurements and assessment were proposed for dairy sheep breeding scheme in the Czech Republic. Udder depth (UD), udder width (UW) and teat length (TL) are measured by ruler. Teat placement (TP), udder cleft (UC), rear udder attachment (RA) and fore udder attachment (FA) are subjectively assessed by linear scoring using 5-points scale. In 2018 the udder assessment methodology was implemented in recorded Lacaune population in the Czech Republic. According to preliminary results the correlation between udder width and breeding values for milk production during milking period was r=0.443. Genetic evaluation based on measured and subjectively assessed udder traits could become an effective tool in selection programs aimed at improvement of udder morphology in dairy ewes in the future.

Keywords: sheep, dairy, udder morphology, linear score.

Introduction

Functional and well-formed udder of ewe is a prerequisite for good lamb rearing and milk production. The udder shape is related to its suitability for machine milking, milk production and composition, resistance to mastitis, milking ability or lamb's ability to find and grab the teat. The ideal udder from the point of view of machine milking should be symmetrical semi-hemispherical in shape with a rigid ligament and mid-sized teats at the bottom. One of the characteristics of udder morphology is the size of the milk cisterns (*Sinus lactiferus* pars *glandularis*), since cisternal milk is achievable for release before oxytocin reflex is started. Animals with high volume of cisterns are generally better milk producers and can tolerate longer milking intervals. Specialized dairy cattle store less than 30% of the total milk yield in cisternal area, whilst in sheep, the share of cisternal milk ranges from 25-75% and in dairy breeds generally exceeds 50%. From the point of view of use the morphological characteristics of the udders in the breeding programmes, the knowledge of their heritability is important. Legarra and Ugarte (2005) found moderate coefficients of heritability for teat position $h^2 = 0.24$ in the Churra and $h^2 = 0.38$ -0.42 in the Latxa breed. Monitoring of the shape of the udders in dairy sheep is important because of the unfavourable genetic correlations between milk production and some of the shape characteristics of the udders, especially the teats position. One-sided selection for milk production can then be associated

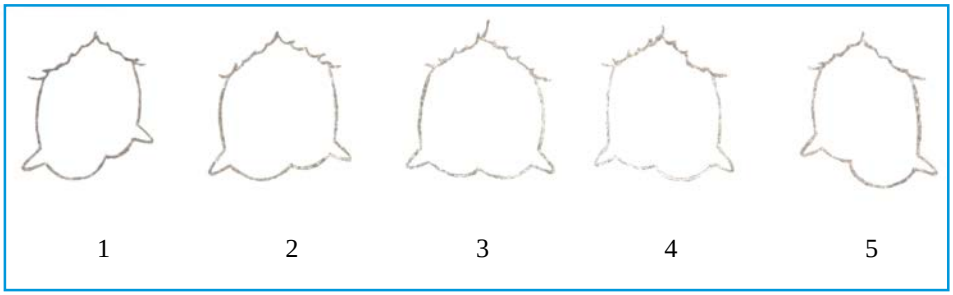
with deterioration of the udder shape (MaCuhová et al., 2008). Methodology of udder measurements and assessment were proposed on the basis of previous works (Makovický et al., 2015; Margetín et al., 2011, 2013; Milerski et al. 2006).

Methods – system of measurements and linear scoring of sheep udders in the Czech Republic

The measurements and linear scoring of udders are performed before milking (about 12 hours after the previous milking) and between 20 and 100 days of lactation. It is advisable to perform a linear description of udders on 2nd or 3rd control day of performance recording scheme.

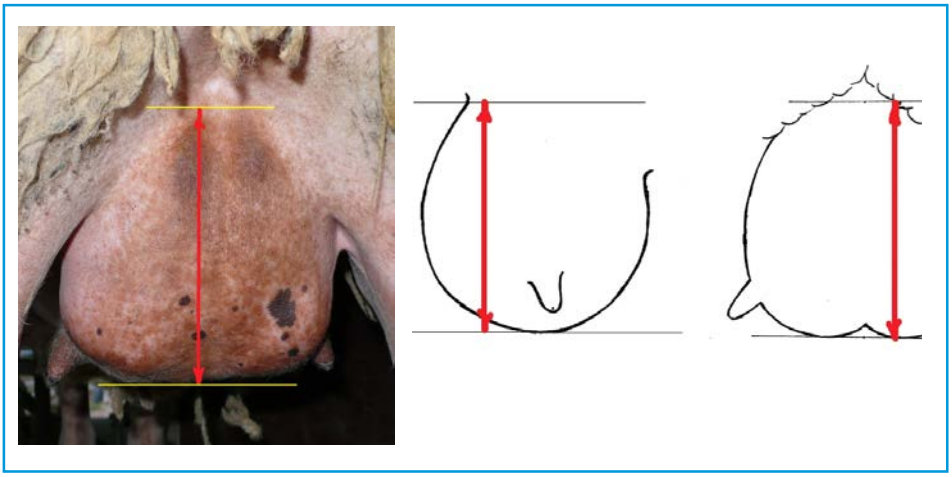
Udder symmetry

Udder symmetry is evaluated subjectively as the first of udder shape characteristics. The symmetrical udder is marked with the number 3. The udder with a significantly larger (more than three times the estimated volume) left half is marked with the number 1 and udder with a much larger right half with the number 5.



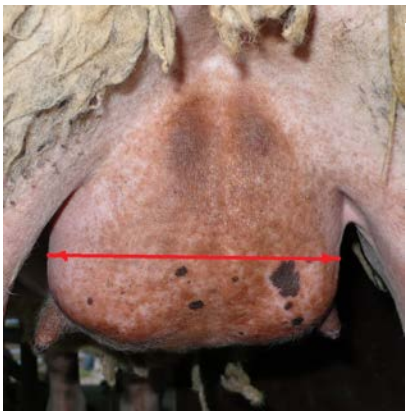
Udder depth

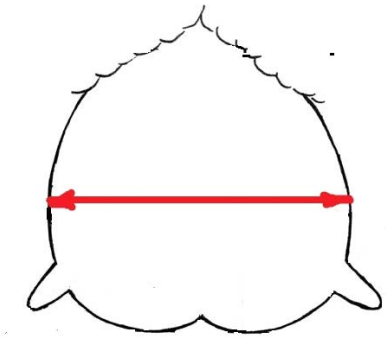
The udder depth is measured from behind from the top of the mammary gland to the lowest point of udder (not the teats).



Udder width

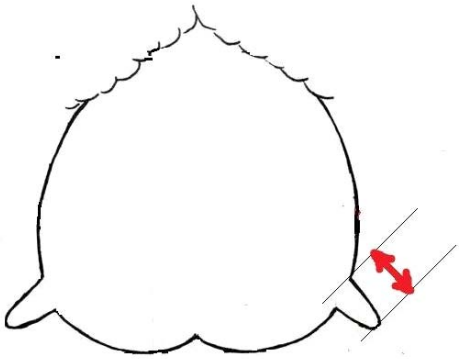
The udder width is measured from behind with the full cm accuracy at the widest part of udder. Teats are not taken into account.





Teat length

The length of the longer teat is measured from its base to the tip with 0.5 cm accuracy. If the length of both teats is visually the same, the right teat is measured.



Teats position

It is judged from the back. The location of the teats on the udder and the largely associated characteristics, such as the teats angle or the proportion of the udder below the teat level, are evaluated.

1 – nearly vertically situated teats

2 - teats slightly facing to the side, placed at the bottom of the udder

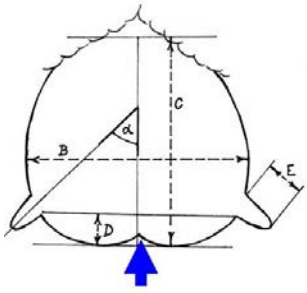
3 – teats angle cca 45?

4 -teats situated on the sides of the udder, more horizontal position

5 –horizontal teats, situated high on sides of the udder

Udder cleft

It is judged from the back. Evaluated is the degree of split udder to two halves given the depth of the medial furrow as an indicator of the strength of the udder's central suspension ligament.



1 – very distinct central suspension ligament, expressly split udder

2 – distinct central suspension ligament

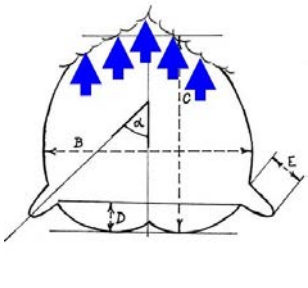
3 – less pronounced but noticeable udder cleft

4 – imperceptible cleft

5 – very weak and relaxed central suspension ligament

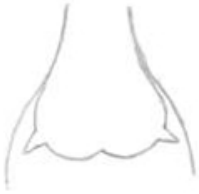
Rear udder attachment

It is judged from the back. The width of the rear udder attachment and the degree to which the udder fills the space between the hind legs are evaluated.

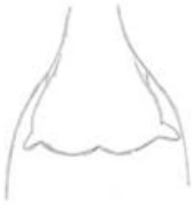


1 - very wide udder clamping, space between legs completely filled

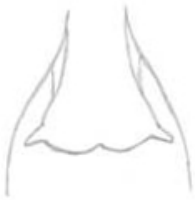
2 - wide udder clamp, space between legs almost filled



3 - medium clamping, enough space for udder



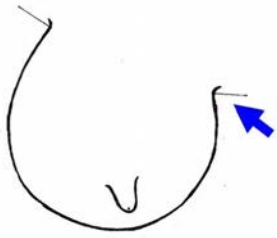
4 - weaker clamping, dropping udder

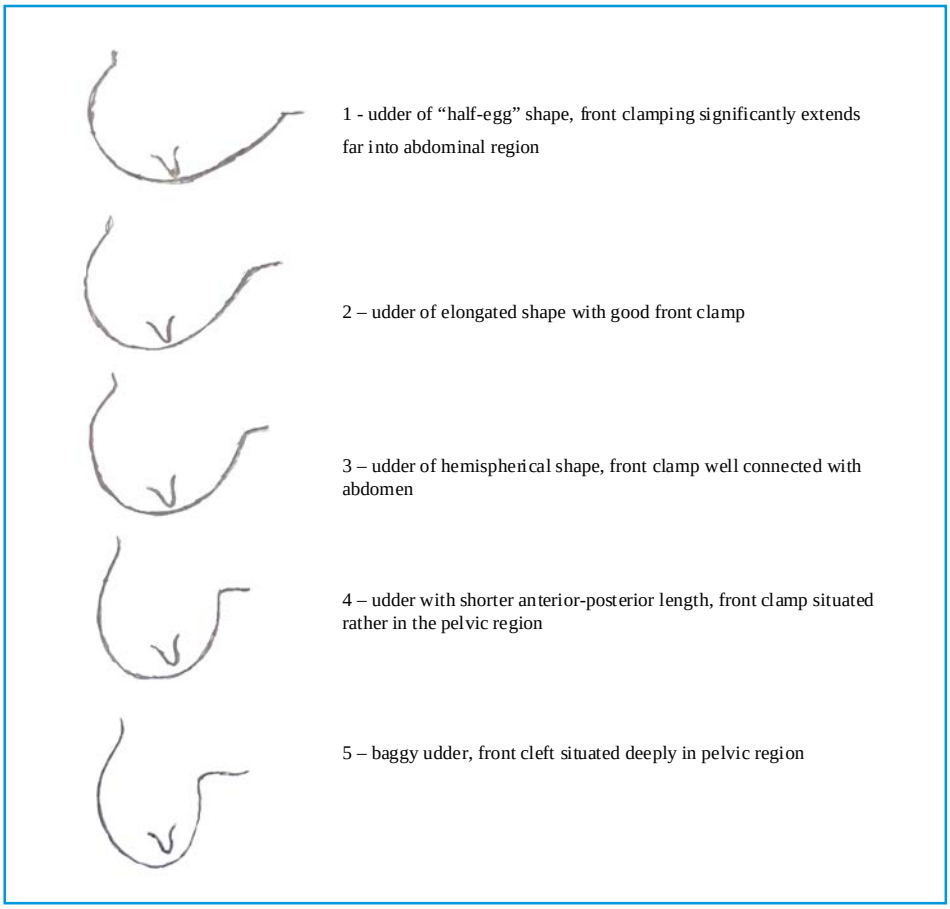


5 - very weak clamp, baggy udder, distinctive skin folds on the sides of udder

Front udder attachment

It is judged best when viewed from the side or from below using palpation. The anterior-posterior udder length and its attachment to the abdominal area of the ewe body are evaluated.





Preliminary results

In 2018 the udder assessment methodology was implemented in recorded Lacaune population in the Czech Republic. Totally 329 ewes were assessed. Averages and standard deviations for udder measurements and assessment are shown in Table 1.

According to preliminary results the correlation between udder width and breeding values for milk production during milking period was r=0.443.

Table 1. Averages and standard deviations for udder measurements and assessment.

Trait	Unit	Mean	Std. dev.
Udder symmetry	points	3.10	0.32
Udder depth	cm	18.76	2.55
Udder width	cm	18.17	1.54
Teat length	cm	2.57	0.64
Teats position	points	2.76	0.54
Udder cleft	points	2.66	0.67
Rear udder attachment	points	2.64	0.64
Front udder attachment	points	2.81	0.43

Conclusion

Genetic evaluation based on measured and subjectively assessed udder traits could become an effective tool in selection programs aimed at improvement of udder morphology in dairy ewes in the future.

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SMARTER – A European project on selection of efficiency and resilience in small ruminants with strong ICAR commitment and implication

J.M. Astruc[1], J.J. Arranz[2], J. Conington[3], R. Rupp[4], B. Servin[4], R. Pong-Wong[5], D. Berry[6], V. Thénard[4], A. Rosati[7], C. Mosconi[8], A. Meynadier[4] and C. Moreno-Romieux[4]

[1] *Institut de l'Elevage, 31321, Castanet-Tolosan, France*
Jean-Michel.Astruc@idele.fr (Corresponding Author)
[2] *University of Leon, Leon 24004, Spain*
[3] *SRUC, Edinburgh EH9 3JG, UK*
[4] *INRA, 31326, Castanet-Tolosan, France*
[5] *The Roslin Institute; University of Edinburgh, Edinburgh EH25 9RG, UK*
[6] *Teagasc, Fermoy, Co. Cork P61 C997, Ireland*
[7] *EAAP, Roma 00161, Italy*
[8] *ICAR, Roma 00198, Italy*

Abstract

SMARTER (SMAll RuminanT breeding for Efficiency and Resilience) is an H2020 EU multi-actor project (number 772787) with a large consortium of 26 academic and non-academic partners from 10 European countries that dominate small ruminant breeding as well as 3 non-European countries. SMARTER is coordinated by Carole Moreno-Romieux from INRA GenPhySE in Toulouse (France). Through its 9 work packages, SMARTER will develop and deploy innovative strategies to improve resilience and efficiency (R&E) related traits in sheep and goats. The outcome of SMARTER will be accurate genomic predictions for R&E traits in different environments for different breeds and populations. SMARTER will also create a new cooperative European and international initiative that will use genomic selection across countries. This initiative will make the selection for R&E traits faster and more efficient. SMARTER will also characterise the phenotype and genome of traditional and under-utilised breeds. Finally, SMARTER will propose new breeding strategies that utilise R&E traits and trade-offs and in doing so address economic, social and environmental challenges.

With regards to ICAR, SMARTER will help produce recommendations on the phenotyping strategies for R&E related traits, which will enrich the ICAR guidelines on small ruminants. SMARTER will also build 3 prototypes (meat and dairy sheep, dairy goat) across-country genetic evaluations. This undertaking might result in future routine international evaluations with business model options also developed in the project. Through its phenotyping and evaluation oriented purpose, SMARTER will also help lay the foundations for a European reference center for small ruminants, as mentioned in the European breeding regulation, for which ICAR could be a relevant candidate. Finally, ICAR, along with EAAP, is in charge of the dissemination and exploitation of the result of SMARTER through its vertical network of farm service providers and breeding organisations.

Keywords: small ruminants, sheep, goat, efficiency, resilience, novel phenotypes, international evaluation, genomics.

What is SMARTER project?

SMARTER stands for "SMAll RuminanTs breeding for Efficiency and Resilience ". It is an H2020 project spanning from November 2018 to October 2022 and coordinated by Carole Moreno-Romieux from INRA in Toulouse (France). This is a multi-actor project with 27 full partners (Figure 1) from 13 countries, of which 10 are European (i.e., UK, France, Italy, Spain, Greece, Ireland, Norway, Switzerland, Rumania, Hungary) all of which dominate the small ruminant breeding sector in the old continent. Half the partners are non-academic. Various stakeholders are also participating in the project.

The core objective of SMARTER is to develop and deploy innovative strategies to improve Resilience and Efficiency (R&E) related traits in sheep and goats. SMARTER will deliver on these objectives by

1. generating and validating novel R&E related traits at a phenotypic and genetic level,
2. improving and developing new genome-based solutions and tools relevant to the data structure and size of small ruminant populations,
3. establishing new breeding and selection strategies for various breeds and environments that consider R&E traits.

Figure 1. Full partners participating to SMARTER.

Which resilience and efficiency traits are studied in SMARTER

SMARTER is based on the following definitions and approaches of resilience and efficiency:

Resilience is defined as the ability of an animal and/or a system to maintain or revert quickly to high production and health status, after a challenge. Nutritional and health challenges will be carried out in SMARTER.

Efficiency in SMARTER is considered as the efficiency of feed resource use by animals. It includes feed efficiency as well as the dynamics of body tissue mobilisation. Focus will be made on the agro-ecological issues and the impact on the environment: competition with human nutrition, water consumption, greenhouse gases emission.

More specifically, the different traits that will be studied are the following:

- **for resilience**: the disease resistance, with particular emphasis on resistance to parasites, foot rot, mastitis; the functional longevity and the lamb survival and embryo mortality. The trade-off between these traits and production traits or feed efficiency and resource allocation will be quantified following a disease or nutritional challenge.
- **for efficiency**: the efficiency and resource allocation with concentrate, but also with hay and grazing. The aim is to detect usable proxies that can be deployed on-farm. Microbiota will be studied to predict digestive efficiency, in particular greenhouse gases emissions. New tools will be tested to measure gaseous emissions.

SMARTER will estimate the underlying genetic and genomic variability governing these R&E related traits. This variability will be related to performance in different environments including genotype-by-environment interactions (conventional, agro-ecological and organic systems). The outcome will be accurate genomic predictions for R&E traits in different environments across different breeds and populations. SMARTER will also create a new cooperative European and international initiative that will use genomic selection across countries. This initiative will make selection for R&E traits faster and more efficient. SMARTER will also characterise the phenotype and genome of traditional and underutilised breeds. Finally, SMARTER will propose new breeding strategies that utilise R&E traits and trade-offs as well as address economic, social and environmental challenges. The overall impact of the multi-actor SMARTER project will be ready-to-use effective and efficient tools to make small ruminant production resilient through improved profitability and efficiency.

The impact of SMARTER

SMARTER is intended to have a substantial impact on the population of small ruminants in Europe and beyond.

Through the involvement of the different countries, SMARTER will directly target 5,000 farmers and 1.5 million ewes or goats and indirectly most of the European sheep and goat industry. High-throughput phenotyping (500,000 animals) and genotyping (70,000 animals) will be used, including existing and newly generated data. Use of genomics is a key point of SMARTER.

Forty-six breeds (19 meat sheep, 13 dairy and 14 goat breeds) from 40 breeding organisations are directly concerned representing 20% of the small ruminant populations of EU. When including all the breeds present in the partners' countries, the impact increases to 70%.

The organization of SMARTER

SMARTER has 10 work packages (Figure 2), 7 research work packages (WP1-WP7), one on dissemination (WP8), one for coordination and management (WP9) and one for ethics requirements (WP10).

WP1 (novel traits to improve resource use efficiency) aims at identifying novel phenotypes related to resource use efficiency, including feed efficiency, the dynamics of body tissue mobilization and methane emissions. Novel phenotypes will be identified by combining existing datasets with new experiments in SMARTER. Experimental

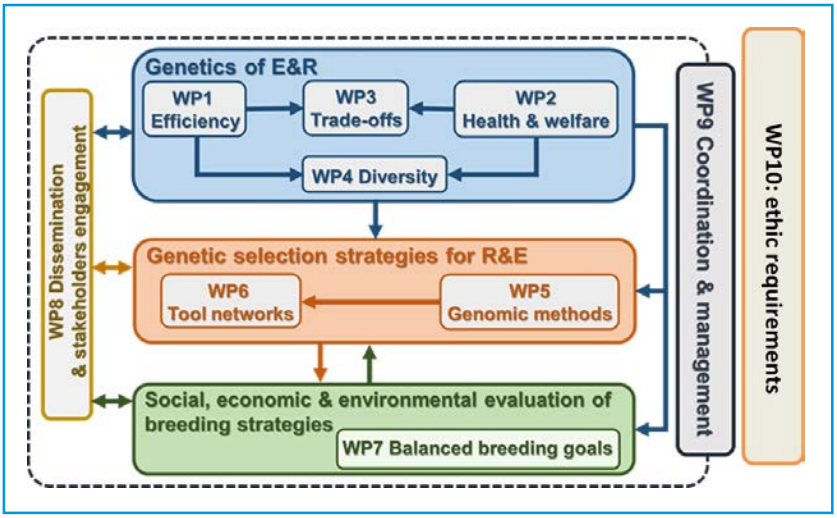

Figure 2: Organization of SMARTER project.

populations will be used to measure associated digestive, metabolic and genetic markers. The novel traits selected to be good predictors of efficiency will be measured on commercial farms to estimate genetic variability and quantify possible environments and systems interactions. The results will be applied in trade-off and diversity studies and genomic prediction models in small ruminant populations.

WP2 (novel resilience traits to improve health and welfare) aims at identifying new immunological and phenotypic indicators of resilience/resistance to parasite infections, mastitis and foot rot. These indicators will be quantified in different environments and systems. Measurements will be in tandem with performance indicators measured in the same or related livestock populations including locally-adapted and traditional breeds and crosses of sheep and goats. Lamb survival linked to neonatal lamb vigor scores, and both maternal and lamb behaviors important for maternal-offspring bonding, stress responses, passive immune transfer and new traits for ewe fertility and longevity will be recorded alongside new or existing selection programs.

In both WP1 and WP2, genetic parameters (variance components and correlations will be estimated, as well as the assessment of proxies to be used in on-farm phenotyping. Results from both work packages will be combined to provide evidence for trade-offs. They will also provide data for international collaboration and breeding program development.

WP3 (genetics of trade-offs and synergies between R&E related traits) aims to quantify the trade-offs and synergies between R&E and other production related traits under genetic control. It also aims at identifying the underlying biological mechanisms for R&E and develop prediction models to manage such trade-offs and optimise R&E in challenging conditions. Trade-offs will be identified through i) estimation of genetic correlations and identification of pleiotropic effects in existing datasets and data generated in WP1 and WP2, ii) production and analysis of experimental trade-off data in genetically selected sheep and goats undergoing nutritional and health challenges, iii) modelling trade-offs at the animal and farm levels, and iv) assessment of the effects of host genetics and management on these on resulting R&E related traits.

WP4 (genomic characterisation of hardy or under-utilized breeds' environmental adaptation) aims at quantifying the genetic diversity in hardy and under-utilised breeds and identifying signatures of selection related to the breed adaptation to specific geo-

climatic environments. New and available data on R&E phenotypic and genotypic information on different breeds from partners, from previous projects and other WPs will be used and strategies to combine such heterogeneous data will be developed.

WP5 (genomic/genetic modelling and methods of selection for R&E related traits) aims to characterise novel phenotypes defined in WP1, 2 and 3 using new and historical records from classical longitudinal traits (e.g. milk, growth) and developping genomic methods for specific features of R&E related traits. The benefit of genomic predictions in small ruminants will be enhanced by improving the properties of validation methods and by optimising methods to perform multi-population predictions (across countries or breeds). Novel strategies to manage genetic diversity within schemes using genomic information will be developed.

WP6 (practical selection tools to benefit from international harmonization and cooperation) copes with genetic selection strategies through harmonization and sharing of phenotypes and genotypes to set up an across-countries evaluation. ICAR is committed in this work package which will be described below.

WP7 (balanced breeding goals for agro-ecological resilience) aims to develop balanced breeding goals to help European sheep and goat breeders and farmers transition towards resilient breeding. These balanced breeding goals will come from i) estimating the economic, environmental and social/labor value of resilience and production traits on farms, ii) interviewing farmers and breeders about the type of animals they want and other important issues and; iii) estimating the non-economic value of R&E related traits using choice modelling. WP7 will pull together results from WP1-6 to provide practical breeding solutions (including crossbreeding) for European sheep and goat farmers and breeders (including Uruguayan and Canadian populations).

WP8 (dissemination, training and stakeholder engagement) aims at organising the dissemination and the stakeholders' network. ICAR is committed in this work package which will be described below.

ICAR commitment in SMARTER

ICAR is a full partner of SMARTER and has a strong commitment in the project, especially in the key work packages WP6 (harmonization of phenotypes and across countries evaluation) and WP8 (dissemination and exploitation of the results).

Harmonization of phenotypes and across-countries evaluation

WP6 aims at contributing to faster genetic gain for RandE through improved international cooperation by

1. Formalizing the harmonized recording of phenotypes and genotypes and an international pedigree file.
2. Generating international genetic and genomic evaluations for a selection of RandE related traits.
3. Establishing the necessary structures and procedures to facilitate cooperation in international evaluations.
4. Analyzing the cost-benefit of international genetic/genomic evaluations and cooperation including sensitivity analyses.

5. Using low density chips for genomic selection. This WP6 highlights the international cooperation and its benefice while setting up practical tools for selection. ICAR is fully concerned with all the tasks of this WP.

***Harmonizing the phenotypes**, genotypes and pedigree*. The ICAR Working Group on Sheep, Goats and Small Camelids has in charge the ICAR guidelines dedicated to these species. To-date, the existing sections of the guidelines are section 16 (milk recording in dairy sheep and goats), section 14 (fiber recording traits in alpaca and goat). A section on recording meat and reproduction in small ruminants is under construction. The ambition of SMARTER is to add a brick to these sections by producing recommendations on recording efficiency and resilience in sheep and goats. Such a harmonization is a prerequisite to facilitate future common evaluation

International evaluation. WP6 will assess the feasibility and the benefice of sharing phenotypes, pedigree, and if possible genotypes from different countries to produce an international evaluation. During the project, three pilot studies will be achieved: one in dairy sheep, one in dairy goats and 1 in meat sheep. This task is an exciting challenge because the level of exchanges and connectedness is currently low, the reference population are small, mainly due to higher cost of genotyping in small ruminants relative to value of the animals, and the phenotypes are less precise than in cattle (few if not lack of progeny testing). ICAR will be especially involved in a task that will consist in throwing the basis of future possible routine evaluation. A business plan will be conceived, according to the learning from the pilot studies, but also from surveys targeting farmers and breeding organizations on their willingness to share data for a common benefit. In this respect, Interbull and/or interbeef will be scrutinized with interest to construct such a plan.

Reference center. ICAR is also connected with the reference center topic. SMARTER has the ambition to propose, define and conceive what could be a zootechnical reference center in small ruminants, aligned with the EU regulation on Animal Breeding. In cattle such a EURC has existed since November 2018: it is Interbull who is EURC for performance testing and genetic evaluation in bovine. In small ruminants, ICAR could be this EURC.

The role of ICAR in the dissemination and the exploitation of the results of SMARTER

WP8 aims at optimising and strengthening the impact of innovation on R&E in small ruminants on targeted stakeholders by i) ensuring stakeholder commitment, and encouraging interactions and feedback among partners and other stakeholders ii) maintaining the dissemination plan iii) disseminating the project results to the scientific community and to target stakeholders; iv) training and capacity building for academics and industry and v) enhancing tools to facilitate and deepen the dissemination of the output. This WP will rely on Operational Groups, thematic networks, EAAP and ICAR partners with complementary networks of members and stakeholders. The inclusion of 13 industry partners from the different countries will be an asset to effectively disseminate regionally.

ICAR is co-leader, along with EAAP, of this action on dissemination and stakeholder engagement. ICAR leads 2 tasks. One task consists of organising the network of stakeholders through a stakeholder's platform. The purpose is to chair the dialogue between SMARTER partners and other stakeholders. The ICAR family is part of these stakeholders. ICAR also leads the task on dissemination and training for stakeholders. In this respect, ICAR will organise 2 SMARTER-oriented technical sessions in the 2020 and 2022 ICAR annual meeting. Moreover, 10 out of the 13 SMARTER countries will organise round table sessions in their local language dedicated to national stakeholders interested in the exploitation of the results.

Conclusion

International cooperation is a key factor for a successful selection of small ruminants. Small ruminants are mostly reared in harsh environments where rearing cattle is difficult if not impossible. Despite some breeds that have become international, a large variety of local breeds are still valorized because they display zootechnical adaptation to their specific environment and thus exhibit economic and social benefits. In this context, innovative methods must be developed to maintain or improve the resilience ability of small ruminants, while improving their efficiency. New technologies (genomics, cutting-edge phenotyping methods) and cooperative approaches must help to reach this overall objective.

The role of ICAR is fundamental to succeed in helping achieve this objective:

- by producing recommendations on phenotyping and proposing tools for international evaluation;
- by promoting, disseminating and exploiting these methods and tools through its network of stakeholders producing services to farmers, and by hosting an EU Reference Center on performance testing and genetic evaluation in sheep and goats.

For more information, the website of SMARTER is *www.smarterproject.eu*

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MULTIPASS: managing the consents of access to farm data in a chain of trust to make new services emerge for farmers

B. Lauga[1], B. Balvay[2], L. Topart[3], J. Leclaire[4], A. Clenet[5], F. Brun[6], F. Pinet[7], C. Roussey[7] and M. Sine[1]

[1]ARVALIS, Institut du Végétal, Agricultural Technical Institute for Arable Crops, France
[2]IDELE, The French Livestock Institute, France
[3]ORANGE, Telecommunication Company, France
[4]FIEA, France Informatique Elevage et Agriculture, France
[5]SMAG, Farm Software Provider, France
[6]ACTA, Agricultural Technical Coordination Association, France
[7]Université Clermont Auvergne, IRSTEA, UR TSCF, Clermont-Ferrand, France

Abstract

With the emergence of digital technologies, farms become a relevant source of data to meet the challenges of multi-performance agriculture. Beyond the services provided, access to farmers' data depends on a clear understanding of their use, which must be done in a transparent way. Several codes of conduct at a national or international level push for a voluntary commitment to respect some good practices in the use of agricultural data. To provide a tool and answer farmer's questions on the control of their data and the transparency of the data processing, the partners of the MULTIPASS project, have imagined an interoperable ecosystem of farmer consents management, protecting farmers from no consented uses of their data.

Farmers' expectations of such an ecosystem have been expressed during workshops. They want to better identify existing data flows, including actors, data processes, and data clusters. Based on the farmers' expectations, the MULTIPASS project stakeholders have proposed the architecture of an ecosystem integrating two consent management tools as "pilots". This ecosystem should take in charge the interoperability between each consent management tools or with future tools.

This solution is based on a shared typology of data and data processes as well as on the specifications of the consent message content. All these elements should be easily accessible to meet the interoperability need of the ecosystem. It is also based on a router, which provides unified access to consent management tools (using API). In particular, it provides the farmer (beneficiary) with an exhaustive view of his/her consents (which can be distributed on several consent management systems), meeting farmers' expectations for transparency. It is also the point where a data provider can check whether the consent required to provide data exists, without needing to know which consent management system is concerned.

In this project, the stakeholders want to demonstrate to agricultural professional organizations the benefits and feasibility of a consent management ecosystem. By strengthening the confidence of farmers to share data, the project will allow the emergence of new knowledge and new services.

Keywords: farm data, data management, consent, transparency, chain of trust.

Introduction

Farmers are engaged in a progress for sustainable and productive agriculture. With the emergence of digital technologies, farms become a relevant source of data to meet the challenges of multi-performance agriculture. These data are the basis of the decision-making process. There is a data-driven agriculture based on the data transfer within the farm. These data also make it possible to create new knowledge or tools that improve the precision and relevance of agricultural operations in order to increase yields without negative impact on the environment.

Beyond the services provided, access to farmers' data depends on a clear understanding of their use, which must be done in a transparent way (Brun et al., 2016). This is a real concern for both farmers, who cannot control the uses of their data, and also data providers who have difficulties in determining the access and reuse permissions they can provide on the farmers' data they host. Access rights must be properly managed, as well as the farmer's consent for the uses of her/his data. The conditions related to this consent must be easily accessible and modifiable by the farmer. It is this chain of trust that the MULTIPASS project wants to implement.

Through the MULTIPASS project, the partners want to make available to farmers and data producers an interoperable farmers' consent management ecosystem, protecting data exchanges improving confidence to share their data with other organizations.

Challenges for a consent management ecosystem

Towards a widespread use of consents

Consents are the adherence of one party to the request made by another. In the case of personal data, consent is one of the 6 legal bases provided by the EU General Data Protection Regulation (GDPR, 2016) which authorizes the implementation of data processing. The law does not require the systematic collection of consents before processing personal data, because other legal bases can be invoked to process these data such as a mission of general interest or a contractual commitment (CNIL, 2018). Nevertheless, consents will enable the management of agricultural data exchanges not specified in the contracts.

To authorize an agricultural data processing and to reinforce the transparency of these uses, the farmer must be able to express her/his consent as shown in Figure 1.

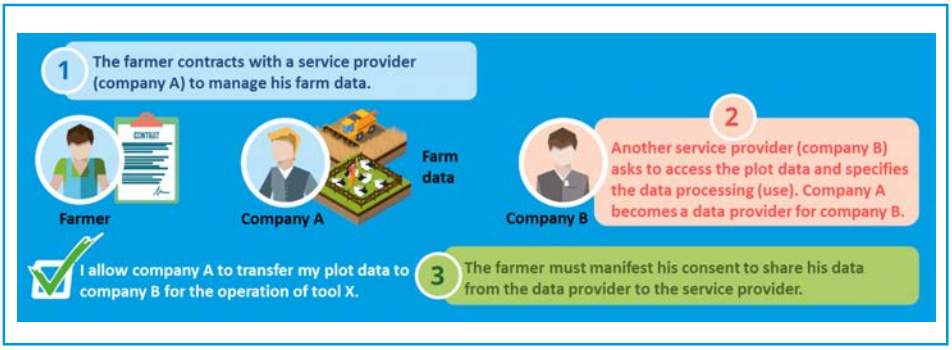

Figure 1. Example of a consent use for data exchanges.

Build a chain of trust

Our goal was to build an ecosystem of stakeholders to manage consents and to create the engagement rules of these actors. We defined the typology of stakeholders presented in Table 1 involved in any farm data exchanges and consents management.

In this chain of trust, each actor has a responsibility and must satisfy good practices related to the use of agricultural data and consents.

Table 1. Typology of actors in a consent management ecosystem.

Term	Definition
Right holder	The person who has the rights on the data. The consent of this person is needed to exchange data. In the MULTIPASS project, she/he is a farmer or breeder.
Delegatee	The right holder has delegated to a person or an organization (i.e., a delegatee) the right to give consents on her/his behalf.
Consent manager	The manager in charge of a consent management system.
Service provider	The organization that sells service to farmers and that needs an access to data. It is the beneficiary of the consent.
Data provider	The manager of the service (database) in charge of providing the data to the service provider.
Consent recorder	The organization that registers consents in the consent management system.

Respecting good practices

Jurists seem to think that, in the absence of a specific legal regulation, the control of agricultural data is ensured only by contracts with the farmer (Douville, 2019). The control will not come from the law but from a voluntary commitment made by the parties to respect some good practices in data uses. The French DataAgri code of conduct (FNSEA, 2018) leaded by the "Fédération Nationale des Syndicats d'Exploitants Agricoles" (FNSEA) and the "Jeunes Agriculteurs" (JA), and the European CODE OF CONDUCT (EU code of conduct, 2018) clearly goes in this direction.

In this context, farmers' expectations of such an ecosystem have been expressed in various workshops. Farmers regret that so far they had not been consulted much when the service providers processed their data. They expressed a need for transparency and want to better identify existing flows, including stakeholders, data uses and associated data categories. Based on farmers' expectations, the MULTIPASS project stakeholders have proposed one architecture of an ecosystem integrating two consent management tools as "pilots" and the conditions for their interoperability with each other or with future tools.

Implementation of the multipass ecosystem

Proposed architecture

There are already existing consent management solutions dedicated to agriculture. These systems are often designed for particular needs. These different consent management systems can be freely chosen by the ecosystem stakeholders. Consents are stored in the consent management systems with the only constraint to register the information expected in the MULTIPASS ecosystem interfaces.

The main tool defined in the MULTIPASS ecosystem is a router that guarantees the interoperability of the different consent management systems. It allows a unified access to consents to provide a list of them (by right holders, service providers, etc.) or to

verify the existence of consents before data exchanges. For this, it knows and can query the various consent management systems which will have interfaces (APIs) similar to those of the MULTIPASS router.

In particular, it provides the right holder with an exhaustive view of her/his consents (which can be distributed across several consent management systems), meeting farmers' transparency needs. The router also allows a data provider to check if the consent required for a data exchange exists, without needing to know in which consent management system it is managed. There is also a traceability of these controls. The use case diagram presented in Figure 2 shows the expected roles of each of the actors as well as the functional scope of the MULTIPASS router.

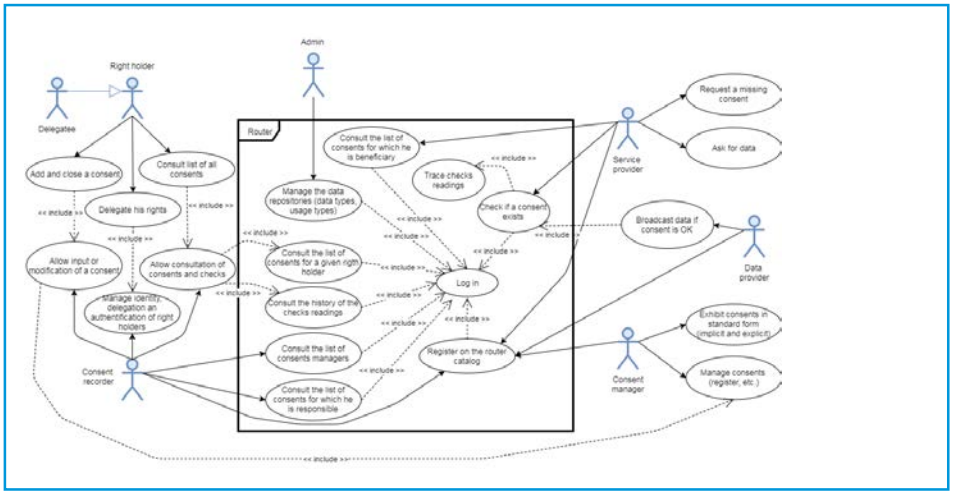

Figure 2. Use case diagram of MULTIPASS router.

All actors other than right holders must register on the router before they can use it. Their registration is validated by a router's administrator. A right holder (or her/his delegate) does not interact with the router. It is the role of the consent recorder to allow the input or the modification of consents. Only the right holder can see her/his consents once she/he is authenticated. The consent recorder cannot see them. This security is especially needed when the consent recorder is also a service provider (it must not see if the farmer works with its competitors). For this, either it will have made a contractual commitment in its contract with the farmer, or it will be committed by adhering to a charter or it will be obliged by GDPR in the case of personal data.

The management of the data repositories is the responsibility of a router's administrator.

Technical architecture

The router has a Java REST API that exposes business and administrative services. As consents are by nature sensitive data that must be secured, HTTPS is used for the exchanges. The OAuth protocol is used for authentication. A signature mechanism guarantees the API that the token issued during authentication process has been generated by the system. The passwords of the different users are stored in a SSHA

hashed form in an LDAP server. A Java human-machine interface allows system administrators to manage the different users and data repositories (data categories and uses) of the router.

A reverse proxy "HA Proxy" is used to secure the application upstream. This system will also be used for load balancing between different downstream application servers. The PostgreSQL database that registers actors, data repositories and logs could eventually be transferred into an elastic stack.

The router is an important part of the ecosystem interoperability. It is based on the main concept of consent. Consents are not managed in the database of the router, but only in the interfaces. The identification of the companies (farm, data or service provider) is done by the French SIRET identifier but the system allows the use of another identifier.

Table 2. Description of the concept of consent.

SIRET number of the farm exploitation (data producer)	**WHO: actors of the data exchange**
SIRET number of the service provider (beneficiary)	
SIRET number of the data provider	
SIRET number of the consent recorder	
Data categories	**WHAT: What is the data exchange about**
Use case (codes)	
Use case description (free wording)	
Consent beginning	**Scope of consent**
Consent end	
Restrictions on consent (and data): (optional free wording)	
Anonymisation	**Constraints**
Contract (explicit, implicit ...) : If yes, contract reference or terms of use	
Reversibility of the consent (not possible if based on a contract)	

Ontologies are one of the possible solutions for solving data interoperability issues. The word ontology covers a large number of different data sources ranging from thesauri to schemas shared on the Web through semantic Web technologies (Roussey *et al.*, 2011). In the MULTIPASS project, we studied different agricultural data exchange schemes, and in particular GIEA ("Gestion des Informations de l'Exploitation Agricole" - a model for Farm Information Management), a model created in France for data sharing (Pinet *et al.*, 2009). These schemes propose a vocabulary dedicated to agriculture, but too complex and not suitable for the uses in the context of consent management. The definition of consents will be associated with a typology of data and a typology of uses that remains to be defined. We recommend that these lists will be organized (hierarchies of category) and shared on the Web to meet the interoperability need of the ecosystem.

Discussion

A Blockchain could constitute the ecosystem on its own, but the challenge at this stage is to explore its promises in terms of trust decentralization. For this, in the second phase of the project, two consent management tools will be compared within use cases. The first one is based on a trusted third party (France Génétique Elevage, 2016) and the second one will be based on Blockchain technology.

MULTIPASS does not have the ability to interfere with consent management systems. They have to verify that the person who registers a consent is the one for whom the consent is given. It is therefore recommended to clearly identify the users with the creation of identity providers for agriculture, as there are elsewhere (French administration, Google or Facebook). Finally, it is the responsibility of the consent manager to ensure the legal value of the consents collected. The participants of the MULTIPASS workshop held on Sept 27th, 2018 (bringing together socio-economic partners of the farmer) highlighted the overlap in the regulatory bases of contracts and consents. There may be a risk of contradiction between a consent and a pre-existing contract.

Conclusions

The project aims to demonstrate to agricultural professional organizations the benefits and feasibility of a consent management ecosystem through limited but concrete use cases in France. The Blockchain technology will be evaluated to explore its promises in terms of trust decentralization. The router designed by the partners will implement a proof of concept for interoperability between existing and future consent management systems. It provides a solution ("data passport") to farmers for the control on their data and on the transparency of the data uses.

By strengthening the confidence of farmers to share their data, the project will bring new knowledge and new services. It promotes open innovation, i.e. the emergence of agricultural applications coupled with farmers' data from any data source or connected object. In this context, the goals are (1) to avoid the risk of concentration of innovation, and (2) the creation of knowledge by the analysis of massive farm data, in a chain of trust.

Acknowledgments

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Applications for comprehensive support of improving health and welfare in dairy cattle

K.F. Stock, K. May, J. Heise, F. Reinhardt and R. Reents

IT Solutions for Animal Production (vit), Heinrich-Schroeder-Weg 1, 27283 Verden (Aller), Germany
Corresponding Author: friederike.katharina.stock@vit.de

Abstract

Documentation and control of health and welfare in dairy herds have worldwide increased in importance. Given the great demand, several tools for farmers are today allowing the recording of veterinary diagnoses, findings from claw trimming and other health-related observations, so on-farm data collection on dairy health has technically become much easier than several years before. Furthermore, the ICAR Central health key, appendix of the guidelines for direct health traits, and the ICAR Claw health key and atlas are providing the basis for standardized data collection which is crucial for implementing monitoring concepts and improvement programs across farms. Among the animal-based welfare indicators, health aspects are playing a key role, implying further motivation to extend and strengthen the data basis on animal health and develop applications supporting health management and improvement. However, the often limited amount of historical data and difficulties of ensuring completeness and high quality of data across farms and over time are major challenges. Additional consideration of data which is broadly available through long-established recording routines, such as specific disposal reasons of cows, can therefore be valuable for both management and breeding. Comparative statistical analyses were performed to highlight similarities and peculiarities of distribution patterns of data which were from different sources of information and related to animal health and welfare. The study was based on data from the national genetic evaluation in German Holstein dairy cattle and included more than 1.7 millions of lactation records from almost 2.700 farms for direct health traits. Milk performance records and information on disposal of cows were used as complementary data sets. For refined analyses of data structure, a subset of data was used which included records from eight German federal states, with information on health events and health-related disposals. Similarities of distribution patterns of certain health events and respective disposals of cows support the approach of integrated data usage.

Keywords: heath data recording, disposal reasons of dairy cows, gain in reliability, improved decision support.

Introduction

In the dairy sector, the awareness of the importance of health and welfare of the cows and of their proper management has increased worldwide over the years (Egger-Danner *et al.*, 2015). Sustainability and efficiency of milk production are relying on the ability of dairy farmers to balance and maintain high milk yields with long-term stability of metabolism and health. This requires continuous, thorough monitoring of the dairy herd in order to react as early as possible to abnormalities which may indicate the

need for management measures or the treatment of individual cows. Accordingly, the proportion of farms in which systematic health data recording has become part of the on-farm documentation routines is today considerably higher than just a few years before. Furthermore, the availability of an internationally approved recording standard for health data in dairy cattle, the ICAR Central Health Key (ICAR, 2019), which was first published in 2012, has facilitated extending the range of applications around the recording and use of health data.

In Germany, the uniform reference is used in different herd management software and also in, for example, special software for veterinarians and hoof trimmers. Health reports with vertical statistics (developments within-herd over time) as well as horizontal statistics (comparison across herds) are regularly compiled and made available in different formats for several years now. However, further development, especially in the field of breeding applications, was complicated by the overall still limited access to information on direct health traits: There are relatively few historical data which are also unevenly distributed across regions;, the coverage of the population regarding the collection of health data is, also in the most recent data, much lower than of standard traits like milk yield, calving ease or reason for disposal from milk recording. Therefore, the power and reach of tools for herd health management depends on the strength of concepts to optimize the use of health-related information

The aim of this study was to illustrate how applications for direct health traits - resembling typical examples of challenging traits for which information is valuable and scarce - can benefit from data integration and combined usage with indicator traits, especially when reference is possible to the huge amount of information available through long-established routine data collection related to milk recording. In addition, we wanted to show the practical importance of providing a strong portfolio of applications relating to direct health traits by quantifying the potential gain in farm efficiency through targeted improvement of health in German Holstein dairy cattle.

Material and methods

Data bases

Data from the routine genetic evaluation for dairy cattle in Germany was used for this study. Considering health events recorded until February 2019, there were in total more than 1.7 million lactation records from almost 2,700 farms which were informative for direct health traits. The recording included veterinary diagnoses, records from hoof trimming and observation of farmers, and was comprehensive with regard to the types of health events. To reduce the overall heterogeneity of the analyzed data, a study sample was defined by region and time period: Considering data from eight German federal states from 2010 to 2018, the sample included 1.1 million lactations of 497,982 cows from 590 dairy farms. Definition of health traits was based on 1.5 million recorded health events in that time period.

Milk performance records and information on disposal of cows were used as complementary data sets. The specific and health-related disposal reasons of dairy cows were identified as potential indicator traits to be used in joint analyses with direct health information. Standardized documentation of disposal reasons is part of the data collection in all cows under milk recording since decades, and includes - besides others - the following four health-related disposal reasons: mastitis, claw disorder, metabolic disorder, reproduction disorder. A total of 169,924 health-related disposals matched to the sample data set. For the analyses on the relationship between herd health and performance, no restrictions regarding the documented disposal reasons of dairy cows were applied, and 280,000 lifetime yields of disposed cows from the 590 farms with available direct health data from 2010 to 2018 were considered.

Statistical analyses

Statistical analyses were performed for the health complexes for which information was available from health data recording and from routine documentation of disposal reasons: udder health, claw health, metabolic stability, and reproduction. Characteristic distribution patterns of health-related phenotypes, derived from the each of the two data sources, were determined and compared.

The relationships between herd health and performance were investigated by analyses of variance in general linear models using the procedure GLM of SAS software version 9.2 (SAS Institute Inc., Cary, NC, USA). For this purpose, dairy farms were grouped according to their annual disease incidence levels, distinguishing between the 25 percent of farms with the highest disease frequencies within year and region (D1) and the reminder of the farms (D0). This grouping of farms was performed separately for each of the four health complexes, and group was then considered as fixed effect in the model. Time effects were accounted for by modelling the year of recording. The following traits were considered as dependent variables: proportion of disposals related to the corresponding disposal reason, time of disposal relative to calving, life yield of milk, and daily life yield of milk.

$$y_{ijk} = \mu + GROUP_i + YEAR_j + e_{ijk}$$

with y_{ijk} = dependent variable resembling the ijk-th expression of the trait (disposal-related and efficiency-related parameters), μ = model constant, $GROUP_i$ = fixed effect of the i-th farm group (i = 1 - 2; D0, D1), $YEAR_j$ = fixed effect of the j-th year of recording (j = 1 - 9; individual years from 2010 to 2018), e_{ijk} = random residual.

Results

For all four health complexes, characteristic distribution patterns of diagnoses on the one hand and of health-related disposal reasons on the other hand were found. Regardless of the data source, there was some variation between parities. High numbers of both health events and health-related disposals in early lactation were recorded for udder health, claw health and metabolic stability, and respective distributions showed reasonable similarities across data sources (Fig. 1 - 3). For reproduction, the majority of health events was recorded up to day 150, whereas most disposals due to reproduction disorders occurred after day 200 (Fig. 4).

In the analyses of variance, significant differences between the farm groups were found in disposal- and efficiency-related parameters (Tab. 1). The higher relative importance of specific disposal reasons and earlier disposal (udder health, claw health, metabolic stability) or later disposal (reproduction) after calving was in accordance to the increased disease frequencies in the D1 farms. Results for the efficiency-related parameters indicated significant negative impact of unfavorable udder health status and claw health status of the herd, whereas high frequencies of metabolic disorders showed significant relationship with higher milk yields.

Discussion and conclusions

The different quality of available health-related information (direct versus indirect) must be considered when analyzing the data and presenting results. In previous studies, the relationships between certain diseases and reproduction traits on the one hand and disposals of cows have been addressed, and analyses revealed significant effects of parity and lactation stage (Beaudeau *et al.*, 1994; Gröhn *et al.*, 1998; Rajala-Schultz and Gröhn, 1999a,b). Our results were in agreement with what has been described as

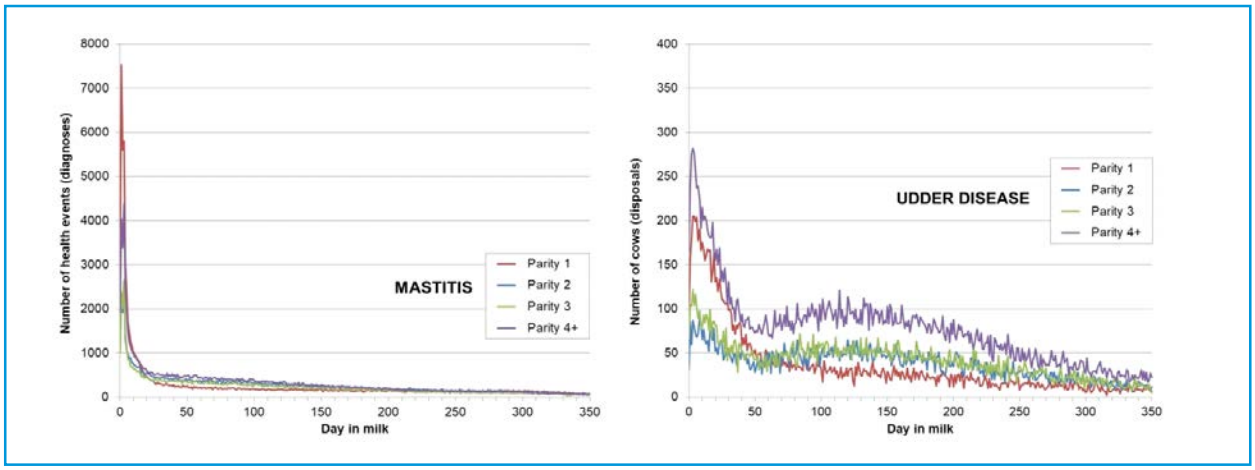

Figure 1. Distribution of recorded health events (diagnoses; on the left) and health-related disposals relative to calving (on the right) for the complex udder health.

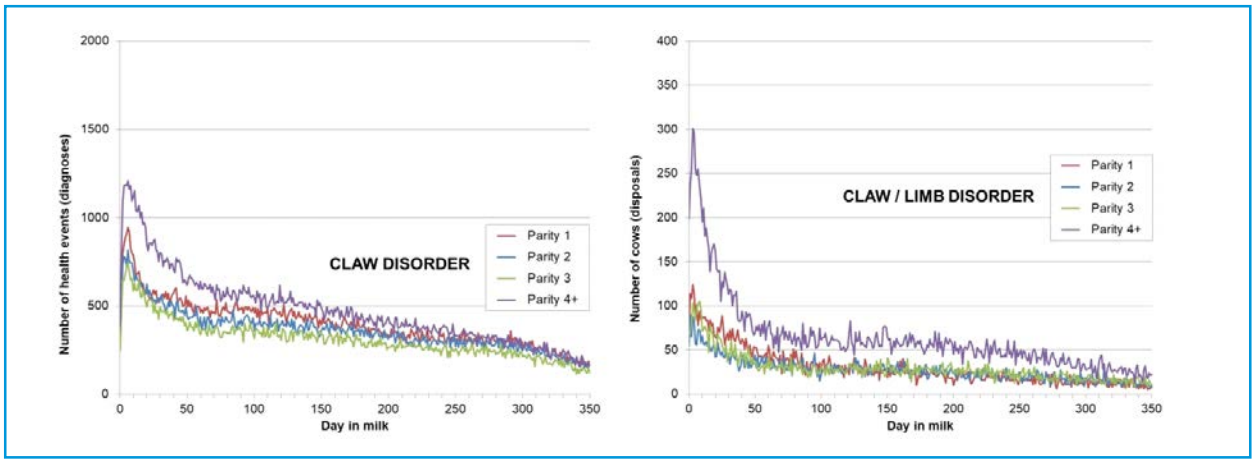

Figure 2. Distribution of recorded health events (diagnoses; on the left) and health-related disposals relative to calving (on the right) for the complex claw health.

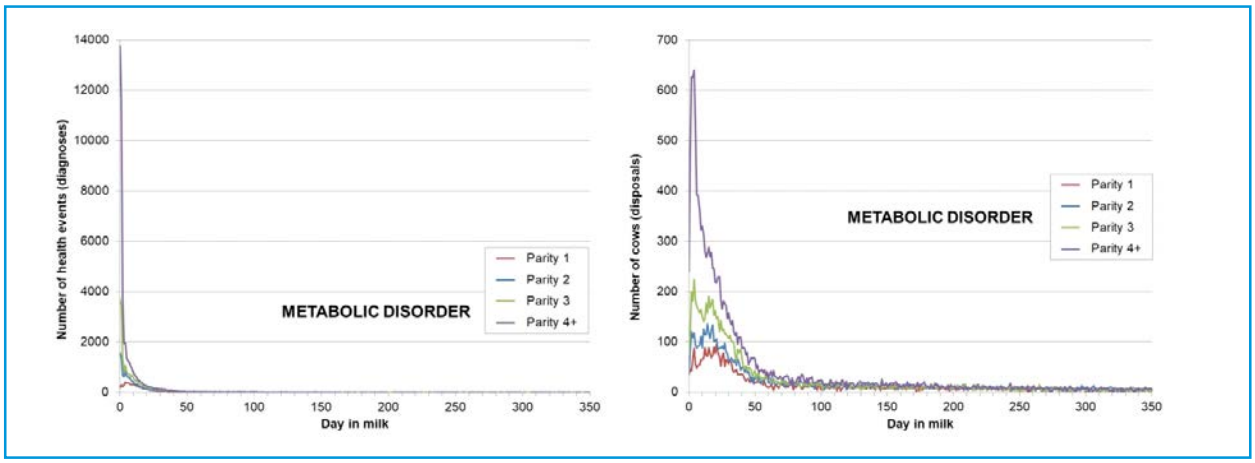

Figure 3. Distribution of recorded health events (diagnoses; on the left) and health-related disposals relative to calving (on the right) for the complex metabolic stability.

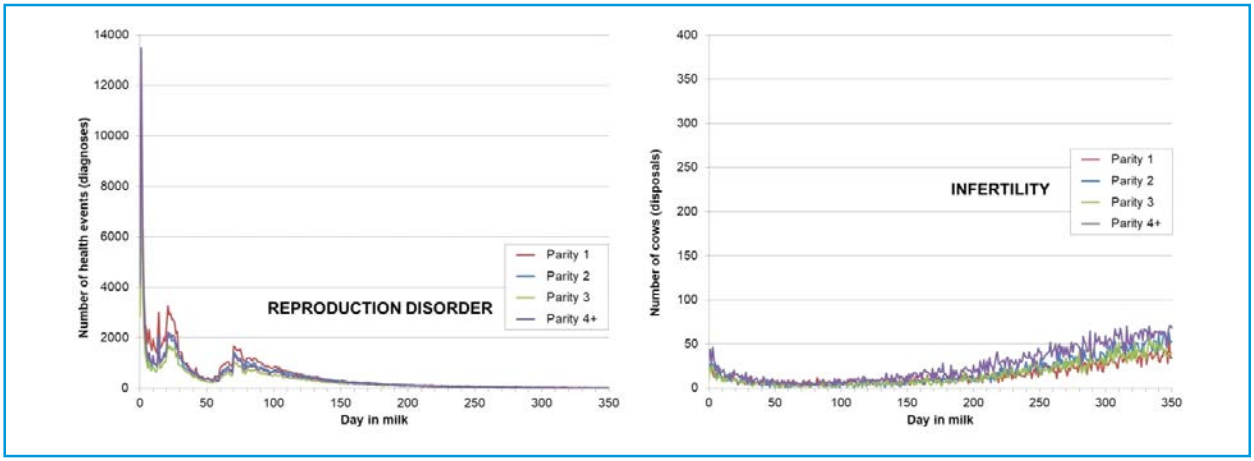

Figure 4. Distribution of recorded health events (diagnoses; on the left) and health-related disposals relative to calving (on the right) for the complex reproduction.

Table 1. Results of analyses of variance with least square mean (LSM) estimates of disposal- and efficiency-related parameter for farms with high diagnosis frequencies (upper quartile within year and region; D1) and the farms with lower diagnosis frequencies (D0)

Parameter	Group	Udder health	Claw health	Metabolic stability	Reproduction
Disposal reason (specific)	D0	22.3	18.7	12.8	20.3
	D1	29.6	22.2	14.7	20.8
Time of disposal [DIM]	D0	188.2	187.9	187.2	185.1
	D1	183.5	183.9	185.7	192.8
Life yield [kg milk]	D0	26,421.4	26,358.1	25,780.4	26,328.7
	D1	25,924.4	26,055.6	27,639.1	26,622.4
Daily life yield [kg milk / day]	D0	12.57	12.61	12.38	12.53
	D1	12.47	12.42	13.04	12.62

DIM = days in milk, kg = kilogram.

typical distribution patterns. Accordingly, they also support the approach of using refined trait definitions and multiple-trait models for genetic evaluation of longevity (Sewalem *et al.*, 2007; Heise *et al.*, 2016).

Reasonable similarities between distributions of health events and corresponding health-related disposal reasons were found for three of the four major health complexes in dairy cattle, indicating the importance of proper herd health management with regard to udder health, claw health and especially metabolic stability in order to avoid premature culling of cows. On the other hand, effects of reproductive disorders tend to become obvious only towards the end of the lactation because they often do not require immediate decisions and allow continued milking of the cows. This makes it plausible that comparisons in this study revealed different shapes of distributions for the fourth of the analyzed health complexes (reproduction).

For optimal integrated use of direct and indirect health data, clear distinction must be made between the sources of information in both management- and breeding-oriented applications supposed to identify and specifically indicate potential for improvement. Separate statistics in health reports and multiple trait approach in genetic and genomic evaluation (indices of increased reliability) allow to maximizing the benefit from all available health-related information while minimizing the risk of misinterpretations.

The high value of applications which support herd health management were illustrated by the comparisons between farm groups. Using lifetime yields for quantification of efficiency, the results indicated reasonable potential for increasing farm efficiency by improved management of udder health and claw health in the dairy herd. At the same time, above-average frequencies of metabolic disorders may not be in conflict with high lifetime yields. However, metabolic stability requires special attention in high yielding herds in order to ensure sustainability of milk production.

The new applications for direct health traits in German Holstein dairy cattle balance the qualitative and quantitative requirements. Tools for farmers which provide comprehensive, consistent and practice-oriented support in management and breeding imply great opportunities for improving animal health and welfare in the dairy herds and by that overall efficiency and sustainability of milk production.

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REPROSCOPE: the observatory of cattle reproductive performances in France

F. Bidan[1], P. Le Mézec[1], P. Dimon[1], P. Salvetti[1], A. Lejard[3], M. Gelé[1] and N. Bareille[4]

[1]Institut de l'Elevage, 149, rue de Bercy, 75595 Paris Cedex 12, FranceCorresponding Author: fabrice.bidan@idele.fr
[2]ALLICE département R&D, Station de phénotypage, Le Perroi, 37380 Nouzilly, France
[3]France Conseil Elevage, 42, rue de Châteaudun, 75009 Paris, France
[4]BIOEPAR, INRA, Oniris, 44307 Nantes, France

Abstract

Reproduction is a key step to ensure proper management and profitability of a farm. The possible use of information from both National System of Genetic Information (SNIG) and National Identification Database (BDNI) offers the opportunity to provide new references to the whole French livestock sector. REPROSCOPE observatory is a web-based interface accessible for free. It allows displaying reproductive performances of 7 million female cattle that have calved in more than 180,000 dairy or beef herds. 20 parameters describe reproductive performances of a selected population in a uniform and exhaustive way using descriptive statistics. This observatory shows a large variability of reproductive performance among herds that highlights the scope for progress. REPROSCOPE observatory facilitates the definition of a consistent objective for a given farm in terms of reproduction, reflecting breeding system specificities and the expectations of cattle breeders.

Keywords: reproduction, livestock, herds, dairy cows, beef cows.

Introduction

Reproduction is the key step of the cattle production success. Calves birth is crucial for every farmer because it reflects the achievement of reproduction process and the farm income depends on it directly (beef herds) or indirectly (dairy herds). Neither milk nor meat production is allowed without animal reproduction. Several studies highlighted the important consequences of decreased reproductive performances on farm income (Coutard *et al.,* 2007; Seegers, 2008; Inchaisri *et al.,* 2010; Inchaisri *et al.,* 2011; Bovins Croissance, 2017). Reproductive disorders are the second production disease behind mastitis in terms of economic impact (Fourrichon *et al.,* 2001). However, this impact is often underestimated. Indeed farmers take into account direct costs due to infertility (additional insemination costs, hormonal treatments…) but they sometimes forget the shortfall due to reduced milk production, reduced calf sales and early culling. Reducing the number of unproductive days of the animals is an important point to increase the profitability of the farm. It means reducing the calving to insemination interval, managing animals culling and reducing age at first calving of the heifers. Few tools exist to help stakeholders to monitor the ongoing reproductive performances of French herds. Even if some existing decision-support tools are very interesting, they have been essentially developed at a regional scale. Stakeholders need widely accessible tools to help them to define reproduction objectives in relation to each

farming system. Supporting stakeholders (farmers, technicians, veterinarians, scientists, teachers…) on reproduction topics in dairy and beef herds is the challenge of REPROSCOPE observatory.

REPROSCOPE observatory

Underlying data

Birth, animal movement and insemination records have been used to provide reproduction data to the observatory. These records come from national databases (National Genetic Information System (SNIG) and National Identification Database (BDNI)) and are provided by Chambers of Agriculture, the National Institute for Agricultural Research (INRA), the French Livestock Institute (IDELE), Milk and Beef Performance Recording Organisations, Breeding Organisations and Insemination Centres. It was decided to provide only anonymous statistics for all the French cattle herds..

A BI (Business Intelligence) solution has been used to process information. After processing, and storage, the data are provided thanks to a free web-based interface: *www.reproscope.fr*.

The calving dates distributions reported in "Chiffres clés bovins, 2015" helped us defining 12-month periods we call campaigns. These campaigns start from the 1st July of the year and end the 30th June of the following year. The observatory counts more than 7 million calvings, 3.5 million inseminated cows and 180,000 cattle herds on average for each campaign (Table 1).

Population selection

REPROSCOPE provides references on reproductive performances at a national scale or for a chosen population. The chosen population is determined by both geographic area and type of production (dairy or beef).

Then, for a chosen campaign, some filters offer to the end-user the possibility to refine the selection:

- At the scale of an animal: performances can be compared between breeds

Table 1. Studied population description, campaign 2016-2017.

		Dairy herds	Beef herds
Number of animals	Cows that have calved	2 258 257	3 017 286
	Heifers that have calved	1 118 248	826 080
	Calves born	3 566 157	3 899 230
	Inseminated cows	2 297 386	402 220
	Inseminated heifers	873 780	212 606
Number of herds	> 10 calvings	58 635	75 666
	< 10 calvings	13 279	28 809
Mean (herds with at least 10 calvings)	Calvings / herd	57	49
	Cows in the herd	62	51

- At the scale of a herd: the choice of the population can be refined according to the main breed, the farm specialisation, the herd size and the dairy production level. Several reproduction management strategies can be taken into account: main calving season, use of artificial insemination and of crossbreeding, replacement rate, and 1st calving age objective.

Reproductive performances can be studied on the population of the females that have calved during the campaign (so the reproductive performances are those of the previous campaign), or on the population of females inseminated by artificial insemination during the campaign.

Available reproductive indicators

Twenty reproductive indicators have been calculated to study reproductive performances. These indicators provide an assessment of fecundity, cows' and heifers' fertility, replacement rate, practice of insemination and cross-breeding, calves mortality and culling (see Figure 1). They are desplayed by descriptive statistics (mean, distribution…) to highlight their variability (see Figure 2). This graphic representation makes it easy to see the expectable margins for improvement.

REPROSCOPE observatory counts 32 different webpages. The combination of twelve filters offer more than 2 billion possibilities of statistical delivery.

Data update

Due to the important volume of data and the IT possibilities of the project, the database is updated currently once a year. The frequency does not allow a real time monitoring of reproductive performances. The role of REPROSCOPE observatory is to provide an ex-post evaluation of reproductive performances.

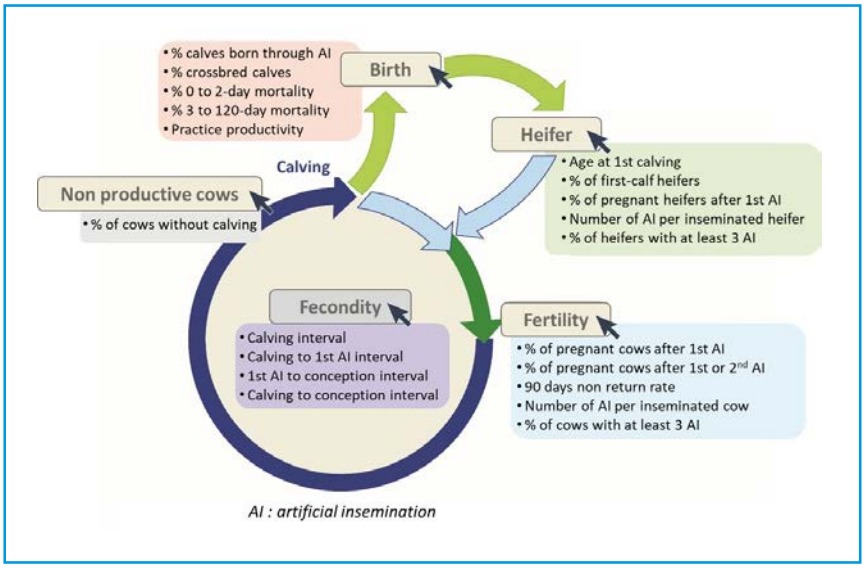

Figure 1. List of available reproductive indicators of REPROSCOPE observatory.

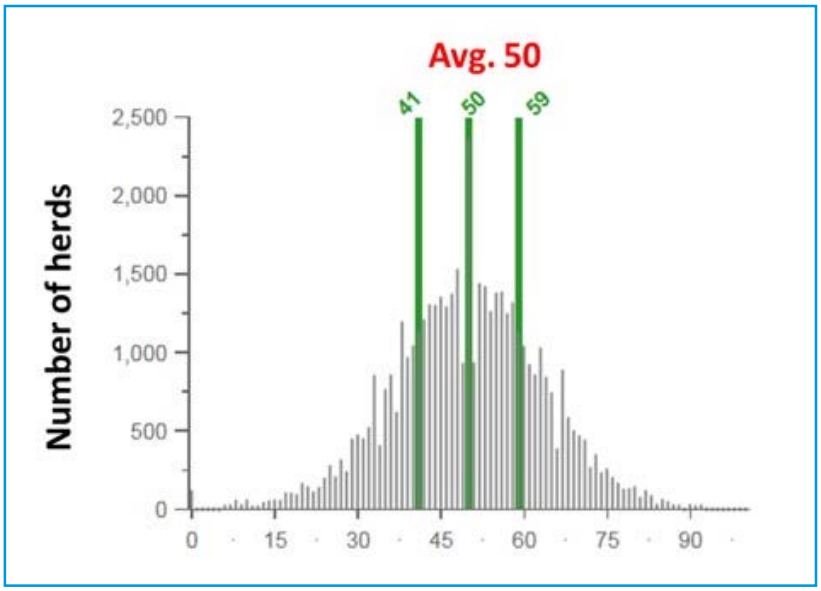

Figure 2. Percentage of pregnant cows after 1st artificial insemination – 48,151 French dairy herds (e" 10 calvings) – campaign 2016-2017.

Reproductive performances exploration

Describing reproduction management strategies

First, the observatory allows describing the different reproduction management strategies by counting the herds that fit selection criteria: main calving season, use of artificial insemination and crossbreeding, replacement rate, 1st calving age objective.

Figure 3 shows the percentage of calves born by AI among all the calves born in the herd during campaign 2016-2017. This information characterise the reproduction method used in the herds: natural mating, AI or both. Among the 51,263 dairy herds, in average 79% of the calves were born from an artificially inseminated cow. 100% of the calves were born from an artificially inseminated cow in 52% of the dairy herds. Only 9% of dairy herds do not use any AI. On the contrary, only 13% of the calves were born from an artificially inseminated cow in the 63,946 beef herds. Only 6% of the beef herds use exclusively AI, whereas 66% of the herds use natural mating only.

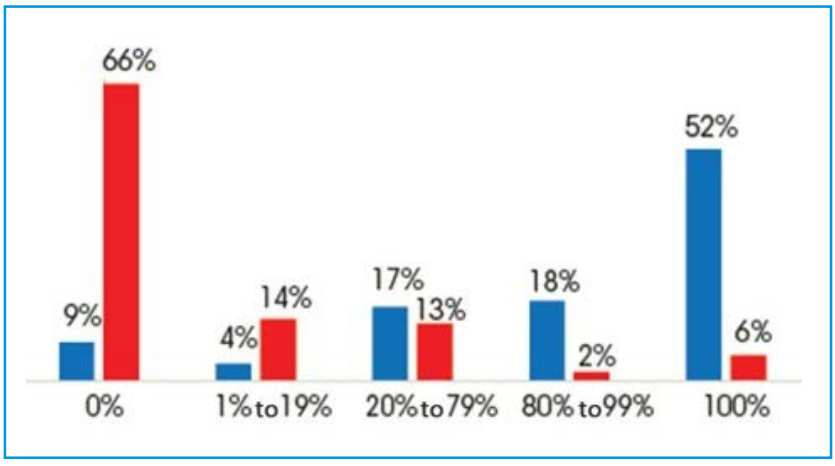

Figure 3. Percentage of calving from AI – 51,263 dairy herds (blue) and 63,946 beef herds (red) – campaign 2016-2017.

Showing performances variability

REPROSCOPE observatory shows the variability of reproductive performances thanks to the chosen graphic representation. Figure 2 and 4 show a difference between dairy and beef herds' performances in terms of percentage of calving after the 1st AI: on average 50% in dairy herds versus 57% in beef herds. Moreover, this representation offers a finer information about the herd performances' distribution around the mean.

The selection filters available offer the possibility to study the reproductive performances according to the reproduction method for example. In this case, the percentage of pregnant cows after 1st AI is higher in the herds where only AI is used exclusively than national mean: +1 percentage point in the dairy herds (51%) and +5 points in the beef herds (62%).

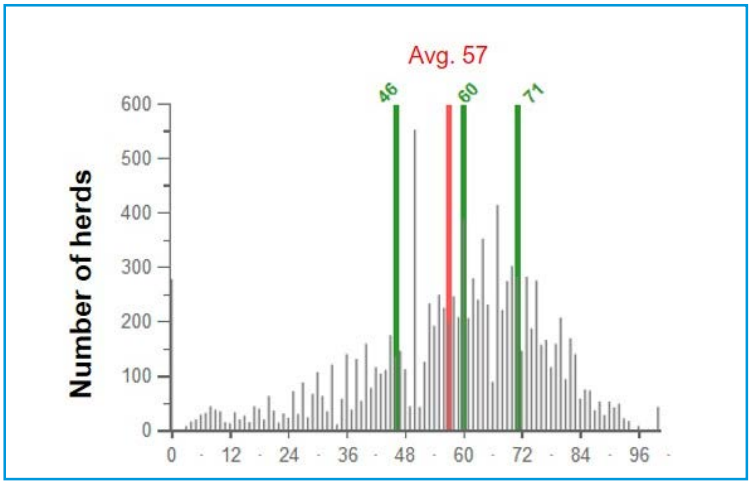

Figure 4. Percentage of pregnant cows after 1st artificial insemination – 11,432 French beef herds (e" 10 calvings) – campaign 2016-2017.

Assessing the differences between breeds, geographic areas, farming systems

Thanks to the selection filters of the observatory, it is easy to compare the reproductive performances of a variety of production systems. Table 2 shows the percentage of pregnant cows after 1st AI for 3 farming systems which vary in terms of the main breed, geographic area (see Figure 5) and calving pattern management.

The smallest percentage of pregnant cows after 1st AI (46%) has been observed in the Holstein dairy herds with spread calving strategy in Bretagne and Grand Est regions. On the contrary the dairy Montbeliarde herds of Auvergne-Rhône-Alpes region with

Table 2. Percentage of pregnant cows after 1st AI (%) for different breeding systems (main breed x calving pattern management) in 3 important geographic areas of dairy production in France.

Geographic area	Breed	Calving pattern management					
		Spread[1]		Semi-grouped[2]		Very grouped[3]	
		%	Number of herds	%	Number of herds	%	Number of herds
Bretagne	Holstein	46%	7 194	48%	538	50%	197
Grand-Est	Holstein	46%	2 698	47%	1 716	49%	354
Auvergne-Rhône-Alpes	Monbeliarde	55%	2 529	57%	734	57%	306

[1] Spread: calving all year long
[2] Semi-grouped: 4 months without any calving
[3] Very grouped: 60% of the calvings grouped on 3 months

Figure 5. Three important geographic areas in dairy production in France.

very grouped calvings have better results (57%). Comparing reproductive performances between different farming systems is also a good way to see that whatever the system, good reproductive performances can be attained.

Conclusion

REPROSCOPE observatory is an easy free tool to obtain updated references of reproductive performances for all the females and herds of bovine supply chain in France (Bidan *et al.,* 2018a). It offers the possibility for stakeholders to update their advisory strategies thanks to system-specific references. The observatory has shown a large variability of the reproductive performances of the herds that impact their profitability (Bidan *et al.,* 2018b), illustrating the expectable margins for improvement in many herds.

Please find all the results on *http://idele.fr/reseaux-et-partenariats/reproscope.html)* and/or visit the observatory on *www.reproscope.fr.*

Acknowledgements

The authors wish to thank UMT maîtrise de la santé des troupeaux bovins, UMT eBIS, UMR PRC, Agrocampus Ouest, Ecole Nationale vétérinaire d'Alfort, Bordeaux Science Agro, Chambres d'agriculture, Entreprises de conseil en élevage, Bovins croissance, Entreprises de sélection et de mise en place, Groupements de défense sanitaire, Groupements techniques vétérinaires, Atol CD.

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A global survey of semen straw bar-coding practices and capabilities at bovine semen collection centers

J. M. DeJarnette[1], O. Gérard2[2], F. Schmitz-Hsu[3], J. Baltissen[4], J. Hooijer[5], L. Morelli[6], R. Spelman[7], L. Journaux[8] and B. Wickham[9]

[1]Select Sires, USA
Corresponding Author: jmdejarnette@selectsires.com
[2]Allice, France
[3]Swissgenetics, Switzerland
[4]Bundesverband Rind und Schwein, Germany
[5]CRV BV, The Netherlands
[6]INSEME spa, Italy
[7]LIC, New Zealand
[8]France Genétique Elevage, France
[9]ICAR, Italy

Abstract

A global survey was conducted to assess straw bar-coding practices, capabilities, and potential hurdles to implementation at bovine semen collection centers (SCC). The survey was distributed to recognized members of ICAR and NAAB. Responses were received from 31 SCC representing 14 countries and ~162 million straws of annual production. Only 8 of the 31 SCC (26%) indicated bar-codes are presently in use representing Europe (5), China (2), and North America (1). The 128 bar-code format was consistent across SCC. Information contained in the bar code varied slightly by SCC. Most SCC included sire identity and collection date (n=7). ICAR code identifying physical/geographic location of semen collection was included by 4 SCC. One organization included a batch number in the barcode which requires connection to central database for interpretation. More than half of SCC (20/31) indicted their present straw printing equipment has the capacity to print bar codes. The perceived lack of demand or need in the industry was viewed as the primary hurdle to implementation by 51% (16/31) of SCC. To a lesser extent, equipment expense (n = 11) and computer programming (n = 10) were also viewed as hurdles to implementation. Sixty-eight percent of SCC (21/31) offer sex-sorted semen but varied in how conventional and sex-sorted were distinguished within sire: 10 SCC used an alpha numeric field, 8 use a separate NAAB marketing code, and 3 reported other methods. In summary, the present capacity for straw bar-coding exceeds the application and the primary obstacle to implementation appears to be the perceived lack of need, utility, and (or) user-friendly application at the farm level. Enhanced efforts at the farm level to facilitate cow-side data capture, transfer, and storage in on-farm record keeping systems are likely necessary to generate producer demand which will in-turn drive global bar-code application by SCC.

Introduction

Accuracy of data recording is an essential component of the integrity and utility of any data management system. In the absence of mandatory requirements or incentive-based programs, easy of data reporting is critical to voluntary user adoption.

The global bovine artificial insemination industry is approaching 80 years of age and annual production is estimated in excess of 250 million straws. In most developed countries, extensive systems are implored for data recording and ultimately reporting to a centralized database for the purpose of comparative herds management analysis, genetic evaluations, and sire fertility evaluation to mention but a few purposes. Computerized on-farm herd management software has greatly enhanced the efficiency of these efforts. More recently, RFID provides a mechanism to enhance both accuracy and efficiency of data reporting for the female being milked, inseminated, evaluated, or treated.

Unfortunately, data recording of service sire information in most countries has progressed very little over time. Though now recorded in computers rather than barn chart, the process remains largely a manual process subject to clerical errors. In addition, tracing sire fertility potential to the freeze batch level has great potential to enhance our understanding of the relationship of semen quality to fertility and thereby enhance the efficiency of the semen quality control program. However, recording of freeze batch is rarely practiced in most countries.

Straw printer with the capacity to include a bar codes on straws have been available since the 1990's. Though several European AI organizations have successful implemented barcoding semen straws, most AI organizations globally have not. The objective of this survey was to assess current bar-coding practices and capabilities at global AI centers regarding straw and identify some of the major hurdles to greater implementation.

Materials and methods

The list of questions for this survey were composed by the 2018 ICAR artificial insemination and related technologies working group. The questions were assembled in an on-line answer format and distributed by the National Association of Animal Breeders to all bovine AI organizations with registered NAAB-ICAR recognized stud code and marketing codes. The survey was conducted during Nov. and Dec. of 2018. Due to the nature of surveys, it was anticipated responses would yield a small sample size of likely biased results and no statistical analysis was intended. Data are simply presented as numeric tallies.

Results and discussion

The global distribution of participants by continent and sum of total annual straw production is presented in Table 1. A total of 31 organizations participated in the survey representing 4 continents and 162,378,000 straws annually. Although South America was not listed as a contributor, at least 4 organizations acknowledged they have production centers in Latin America even though their primary production center was in Europe or North America.

Table 1. Survey participants by continent and total annual straw production.

Continent	No. organizations	Total annual straw production
Europe	10	37,350,000
North America	15	111,178,000
Asia	3	5,000,000
Australia/New Zealand	3	8,850,000
Total	31	162,378,000

Participant responses regarding the capability of existing equipment to print bar-codes and current implementation rates are presented in Table 2. More than half of participant possess equipment capable of printing bar codes but only a fourth actually implement bar-coding at present, with the majority of those residing in Europe.

The information and format of information included in bar codes are presented in Table 3 and clearly illustrate a lack of uniformity that could be problematic to global efforts to standardize data bases and recording.

The perceived primary obstacles to greater implementation are presented in Table 4. Lack of need or demand at the farm level was the predominantly mentioned obstacle though equipment expense and programming requirements were acknowledged as hurdles. Among open form write in comments, space on the straw was noted as an obstacle.

Table 2. Current bar-coding practices and capabilities

Continent	Number of organizations with equipment capable of printing bar-codes	Number of organizations currently implementing bar-codes
Europe (n = 10)	7	5
North America (n = 15)	9	1
Asia (n = 3)	2	2
Australia/New Zealand (n = 3)	2	0
Total (n = 31)	20	8

Table 3. Information included in bar-codes among organizations that presently use of bar-codes.

Organization	Semen collection center	Sire by registration number	Sire by ICAR-NAAB code	Freeze batch format	Batch number
China - A	Yes	Yes	Yes	DDMMYY	
China - B			Yes		
France		Yes		DDMMYY	
Germany (n = 2)	Yes	Yes		YYMMDD	
Netherlands	Yes		Yes	MMDDYY	
Switzerland	Yes				Yes
United States			Yes	MMDDYY	

Table 4. Primary obstacle to greater implementation of bar-coding.

Continent	Lack of need, demand at the farm level	Equipment expense	Programming needs
Europe (n = 10)	4	1	1
North America (n = 15)	10	7	8
Asia (n = 3)	1	2	1
Australia/NZ (n = 3)	1	1	0
Total (n = 31)	16	11	10

Table 5. Is sex-sorted semen offered and how is sex-sorted semen distinguished from conventional semen?

Continent	Offer sex sorted semen	ID by Marketing code	Alpha-numeric field	Other
Europe (n = 10)	8	0	5	3
North America (n = 15)	7	5	2	
Asia (n = 3)	3	1	2	
Australia/NZ (n = 3)	3	2	1	
Total (n = 31)	21	8	10	3

The number of organizations offering sex-sorted semen and the way sex-sorted semen is distinguished from conventional is presented in Table 5. Most organizations offer sex-sorted semen but considerable variation exists in how it is distinguished, with slightly more organization using an alpha-numeric field as opposed to separate NAAB_ICAR marketing codes. Interesting was the tendency for most organizations in North America to use marketing codes while European organizations used alpha-numeric fields.

Summary and conclusion

The capacity to implement bar-coding at global AI organizations presently exceed the implementation rates. Perceived lack of demand at the farm level was the most cited obstacle to implement. Considerable variation presently exists globally in straw identification procedures both within text within bar-codes themselves, which may present considerable challenges to global data assimilation efforts.

Development of a heat-assessment with factors of a cow

L. von Tavel, F. Schmitz-Hsu, U. Witschi and M. Kirchhofer

Swissgenetics, Meielenfeldweg 12, 3052 Zollikofen, Switzerland
Corresponding Author: lvt@swissgenetics.ch

Abstract

A system for a rapid heat-assessment of a cow during insemination was developed based on six factors and an overall score. A field-test with 27 technicians doing 8184 inseminations showed a difference of up to 34.7 %-points in the non-return rate 56 days between score combinations. The proposed system helps considerably to evaluate the cow during the routine insemination process.

Keywords: insemination, heat-assessment, non-return rate

Introduction

The success or failure of an insemination depends mainly on the cow. The heat-assessment of a cow by a technician in the routine process must be done quickly and whenever possible without the need of information from a third party, e.g. the farmer. For this purpose, a simple but effective system is needed to judge the cow in order to predict the success of insemination. We designed a system with which the technician evaluates the relevant data about the cow during the insemination process. The data is recorded using a tablet in the field.

The goal is to collect data in order to derive a more reliable estimate of the bull's non-return rate.

Material and methods

Based on literature (Röthlisberger, 1999; Bühler and Maurer, 2004; Stevenson *et al.*, 1983; Bhat and Bhattacharyya, 2012; Rutten *et al.*, 2016), a set of six factors was chosen to assess the status of the cow and was evaluated in a field test.

- Position of the vulva.
- Quantity of mucus.
- Uterus tonus.
- Size of the uterus.
- Cervix passage.
- Insemination timepoint.

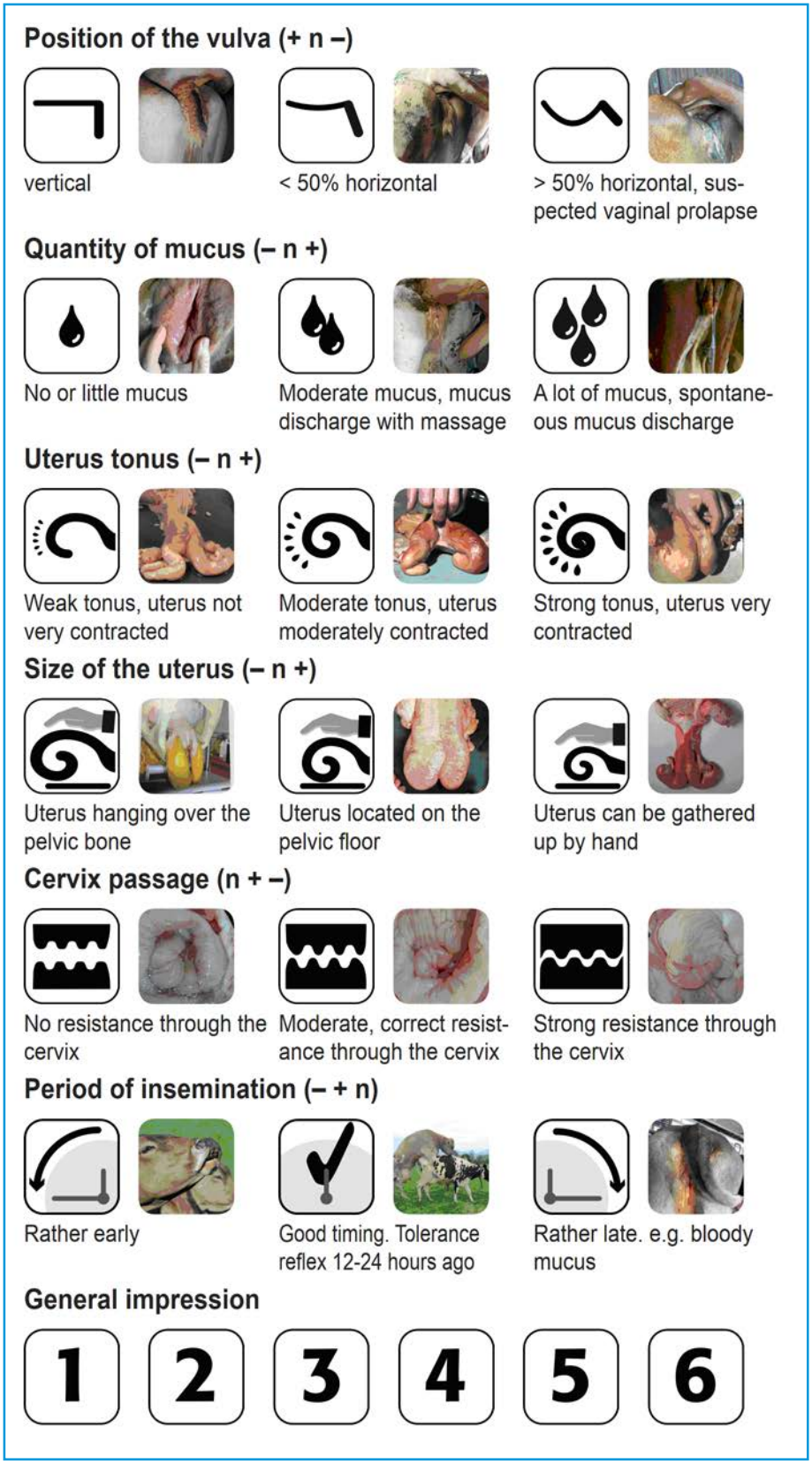

Figure 1. Pictograms and explanatory photos of the heat-assessment system.

These six factors of the cow are scored with three levels each:

+ for good/positive

n for neutral

- for bad/negative.

To simplify data entry and to increase the tangibility for the technician, only pictograms are shown on his tablet. Additionally, the technician is asked to enter a score from 1 to 6 indicating his personal prediction of the probability of success of the insemination. Figure 1 shows definitions and pictograms of the scores plus explanatory photos of the assessment system.

In a field-test for two months, 8184 inseminations done by 27 technicians were evaluated. The heat-assessment was compared with the non-return rate 56 days.

Results

The 27 technicians involved in the field-test accepted the heat-assessment system well after a short training. They used the full range of the scores.

The evaluation of the combination of factors - occurring at least 100 times - showed that the proposed heat-assessment scores are positively associated with the probability of success of the insemination. There was a difference of 34.7 %-points in the NR56 between the inseminations with the best level of all factors and those with the worst level of all factors.

The personal prediction of the technician (1 - 6) at the time of insemination was consistent with the NR56.

Compared to the previous heat-assessment system, the new approach allows a much more differentiated prediction of the success of insemination.

Conclusion

The proposed system helps considerably to evaluate the cow during the routine insemination process. The obtained data also improves the evaluation quality of the bull's NR56, which is essential for AI organisations in terms of quality control of semen straws released to the market.

Swissgenetics introduces the heat-assessment system nationwide (240 technicians) in June 2019.

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Using differential somatic cell count to improve udder health

R.H. Fourdraine, A. Samia Kalantari, J. Amdall and A.D. Coburn

AgSource Cooperative Services, 135 Enterprise Drive, Verona, WI 53593, United States

Abstract

Mastitis continues to be one of the costliest diseases found on US dairy farms. Routine milk analysis for Somatic Cell Count (SCC) has provided a valuable and inexpensive means to monitor udder health. New technologies such as PCR analysis of preserved milk samples have provided additional detail by determining which pathogens may be present allowing a more pinpoint approach in addressing mastitis. Although PCR is a valuable tool the costs for routine analysis of milk samples is too expensive for US dairy farmers. Differential Somatic Cell Count (DSCC) data can now be obtained as part of a regular milk analysis for SCC. Using monthly and weekly collected data AgSource has started the process to determine where DSCC can provide additional value and be incorporated in AgSource information management services. Although several trends have been observed regarding future udder health status, no conclusive results have been obtained using a machine learning approach. To improve the predictive capabilities more weekly milk samples will need to be collected and combined with PCR milk analysis results in order to get more detailed information about the type of infections.

Keywords: Fourdraine, Somatic Cell Count, differential somatic cell count, udder health, prediction, machine learning.

Introduction

Milk recording organizations and milk laboratories have offered individual cow mastitis screening using Somatic Cell Count (SCC) analysis for over 30 years. As management practices have improved so has udder health and herds have seen a decrease in cases of mastitis. US dairy farms have seen a steady decline in bulk tank SCC values. Although significant improvements have been made, mastitis is still one of the costliest disease farms have to deal with. AgSource herds typically use SCC analysis on all cows on a monthly basis and this has proven to be a very cost-effective measurement to monitor udder health. Typically cows are considered at risk for mastitis when the SCC value exceeds 200,000, cows with SCC less than 200,000 are considered healthy and not further diagnosed. Follow up diagnostics for cows exceeding 200,000 such as PCR and bacteriological testing can be used to more accurately pinpoint the specific mastitis causing pathogens. These methods are typically too expensive to use in a whole herd testing scheme. The question therefore is are there other cost-effective methods that can supplement SCC that can be used to easily screen cows and detect onset of mastitis at an earlier point where typically SCC may not have exceeded 200,000.

A possible opportunity may lie in the new Differential Somatic Cell Count (DSCC) measurement that is offered through the Fossomatic 7 DC from Foss Denmark. The DSCC represents the combined proportion of Polymorphonuclear Neutrophils (PMN) and lymphocytes in percent. The percentage of macrophages is 100 - DSCC. DSCC values can be provided for cows that have a SCC value that exceeds 50,000. Past research projects have shown the positive correlation between increased DSCC values as cows are subjected to mastitis causing pathogens. Cows considered healthy typically express low DSCC values (i.e. high percentage of Macrophages). Stage of lactation and parity have also shown to play a factor in DSCC measurements. To date most research was focused on establishing the relationship between changes in DSCC and infection, however little effort has been given to developing a practical application of DSCC in commercial milk testing schemes.

Materials and methods

Little is known about the value DSCC provides above and beyond SCC when included in regular milk recording. In order to build a practical application it was necessary to learn more about the data and any trends we could discover before specific areas of value could be determined. DSCC is only measured on cows with a SCC value of 50,000 or greater, typically in the US dairy industry a SCC value below 150,000 or 200,000 is considered a healthy cow with little concern. As cows exceed 200,000, concerns about infection increases as the SCC value increases. In addition to the magnitude of the SCC value, the duration and frequency of high SCC values is also a concern and typically expressed as new infections, chronic infections, repeat infections and fresh cow infections.

In order to learn more about the value DSCC provides, two tracks of exploration were chosen. The first track involved a preliminary data analysis of regular monthly individual cow milk samples providing insights on potential trends. While the second track involved a six weeks research trial collecting weekly milk samples from a 1,800 cow dairy farm. Cows of interest were selected for follow up PCR to determine if specific pathogens were present. Using cow data from the field trial a machine learning approach was used to determine if the combination of SCC and DSCC has any predictive characteristics to determine the future health status of the cow.

Collected data included, SCC, DSCC, milk composition and individual cow data such a parity, calving date, days in milk, and health events.

For the preliminary data analysis, the monthly sample data set included 124,747 test day milk analysis results, collected since December 2018, that have both SCC and DSCC values. Within this data set there were 39,135 cows at different parity and stages of lactation that had two or more consecutive data points. For the research trial the total number of weekly observations collected was 10,964 records on 2,080 cows from which 1,591 cows had six consecutive weeks of data.

Results

The monthly data analysis is a snapshot of the data that was collected through April 2019. The weekly data used in this analysis only contains data from a single herd. However additional data is being collected on a weekly basis from herds that have milking robots with automated sampling units and will be included at a later date.

Preliminary data analysis

Individual cow SCC data has been the primary tool in the dairy industry to determine if a cow should be considered as potentially infected or not. Past presentations about DSCC values collected by the Fossomatic 7 DC indicated that DSCC has a strong correlation with SCC, if that is the case the first question then becomes what is the correlation and if it is very high, what additional value does DSCC provide over SCC at the individual cow level? Using the monthly data set, the correlation between SCC and DSCC for cows with a SCC value greater than 50,000 was only 0.17 indicating that the relationship is not as high. This should be considered as good news because the combination of DSCC and SCC could point at additional findings that we would not be able to receive from SCC alone. Based on the percent of PMN and macrophages, one of the values DSCC could provide is the early indication that a cow may be potentially infected but has not elevated the SCC value to a level it would raise concern and place the cow on an attention list. A second value would be in determining if an infected cow is healing or responding to treatment that is not captured in the SCC value.

DSCC is measured as a percent of PMN, however little is known about what a normal range would be where the cow is providing an immunity response or is in a healing phase. Based on information gathered from FOSS Denmark, a DSCC value that is greater than 70 should be considered as high on PMN indicating the cow is showing an increased immunity response. Therefore the first interest was to evaluate if healthy cows (SCC score below 200,000) show differences in pathways of becoming infected based on previous month DSCC value. Using the dataset with repeat measures on a single cow, cows were grouped based on DSCC values, results are shown in figure 1. At this time there was not enough data to break out the results by days in milk or parity.

Results in figure 1 show that as DSCC increases a higher percent of cows considered healthy return the next month with a SCC above the threshold of 200,000. This could provide some early insights that cows with SCC <200,000 but DSCC above 70 do not require intervention right away but should be more closely monitored.

The second area of interest involves cows previously listed as infected (SCC>=200,000) and evaluated based on the previous DSCC value if these cows are improving. Figure 2 shows the response from previous to current test day based on the same DSCC categories as Figure 1.

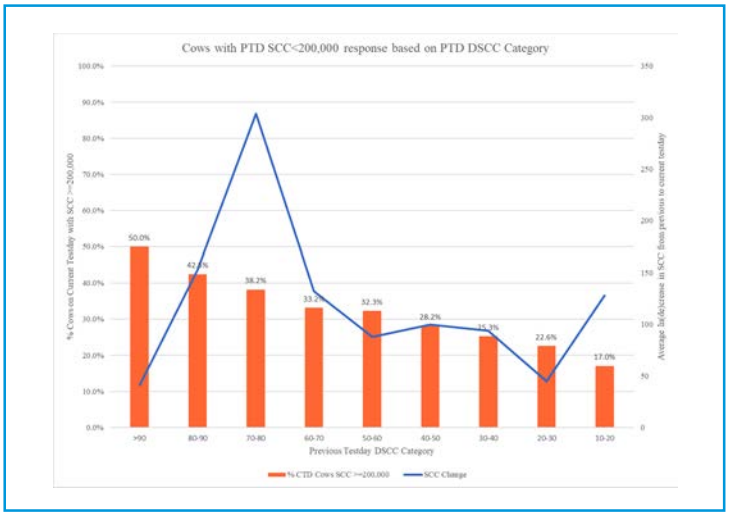

Figure 1. SCC response for clean cows from previous to current test day based on previous test day DSCC

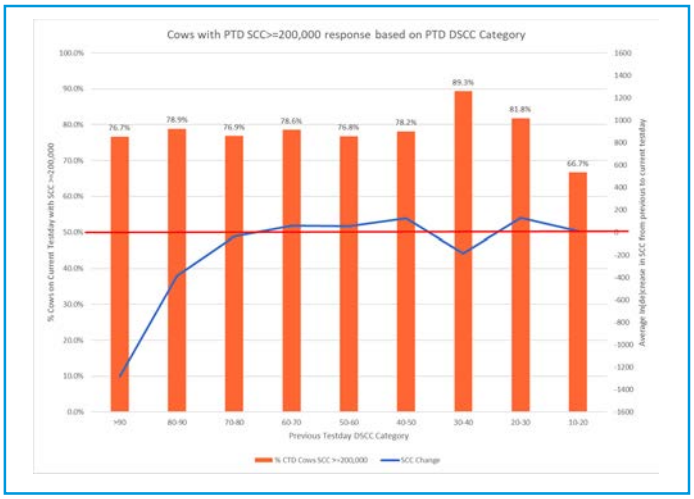

Figure 2. SCC response for infected cows from previous to current test day based on previous test day DSCC

Results shown in figure 2 indicates that regardless of DSCC category almost the same percentage (75%) of cows have SCC greater then 200,000 on the next test day. Although the percent is similar across DSCC categories, the cows that had the highest previous test day DSCC (DSCC greater than 80) showed the greatest reduction in SCC while cows with low DSCC (DSCC less than 70) showed little or no improvement. This raises the question if cows have a SCC of for example 1,000,000 or higher but a DSCC value between 40 and 60, are these cows healing or more likely to return the next month as still infected.

The current AgSource udder health summary provides multiple analysis that look at various groups of cows based on SCC, based on the SCC, the three main groupings of cows are:

- Newly Infected - SCC below 200,000 previously, now above 200,000
- Chronic infected - SCC above 200,000 in 2 consecutive test days
- Cured - SCC above 200,000 previously, now below 200,000

Using the three groupings Figure 3 shows the distribution of cows based on current test day DSCC category.

Results from figure 3 show that cows that are newly infected or chronic have a distribution that has far more cows with DSCC values of 80 or above compared to cured cows. DSCC values between 70 and 80 are somewhat a transition zone while DSCC values below 70 have a greater percentage of cows considered cured. As more data is collected one area to delve deeper into would be the cows considered cured but still exhibiting a high DSCC value and determine if they were truly cured or return to a higher SCC level. A second area are cows listed as newly infected or chronic but exhibiting low DSCC values.

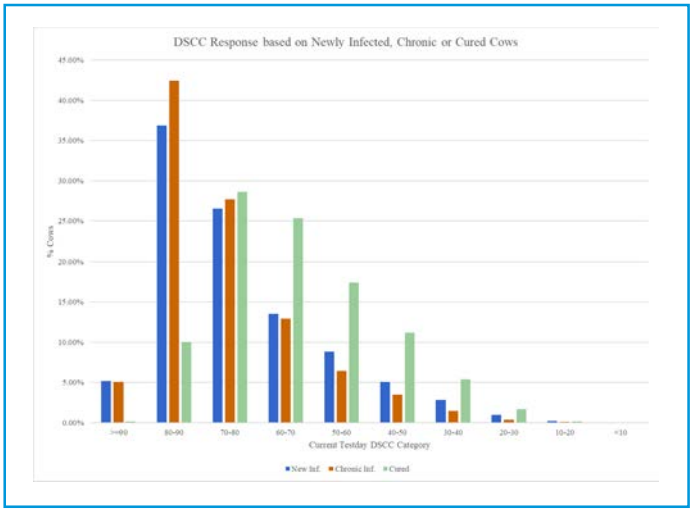

Figure 3. Distribution of cows by current test day DSCC score and infection status.

Research trial results

Utilizing the results from monthly SCC and DSCC data some early insights were gained in regards to which areas DSCC may provide additional value. Correlations between the SCC and DSCC values for the weekly samples were 0.3 which was slightly higher than the correlations observed using the monthly observations but still low enough to indicate there may be opportunity to consider DSCC as additional value over SCC.

Based on this information cows were grouped in several categories. These categories formed the initial starting point that would be used to assess where DSCC might provide possible value as it relates to monitoring udder health. PCR analysis was used to determine if cows in the different categories had any environmental or contagious pathogens present. Table 1 shows a matrix using different categories of SCC and DSCC and impact DSCC may have on udder health. Figure 4 shows the relationship between the weekly SCC and DSCC values for each cow as they fit in the five categories listed in table 1.

The total length of the field trial was 6 weeks and the first couple weeks were used to learn more about the data and identify cows in each of the categories listed above. Tables 2 through 6 show examples of cows with weekly SCC and DSCC values that qualify them for one of the 5 categories mentioned in table 1.

Using week 4 SCC and DSCC data cows were selected based on the criteria in table 1 and using the week 5 samples of those cows PCR analysis was performed on the pooled samples. The process was repeated with cows selected on week 5 and samples

Table 1. DSCC impact matrix.

Category	SCC	DSCC	Possible impact
1	Low (<200,000)	Low (~<70)	Healthy
2	Low (<200,000)	High (~>70)	Early warning
3	Medium (200,000-800,000)	Low (~<50)	Chronic problem
4	High (>800,000)	Low (~<50)	Not responding
5	Medium and High (>200,000)	High (~>70)	Responding to infections

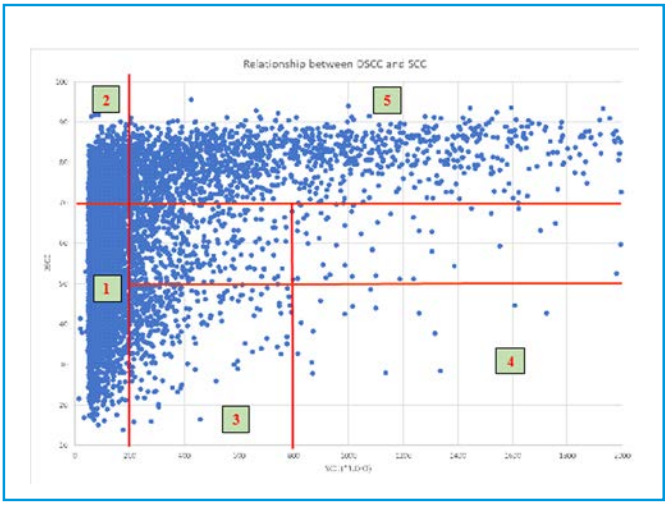

Figure 4. Relationship of DSCC and SCC and udder health category.

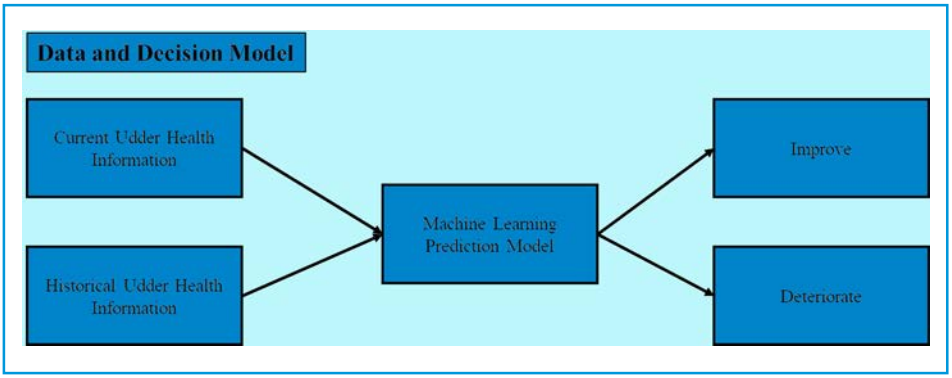

Figure 5. Machine Learning Predictive model.

collected on week 6 were run for PCR analysis. The week 6 samples were pooled and upon detection of any pathogens in the pooled sample individual cows were tested. The goal of the PCR analysis was to determine if any pathogens could be detected and if these were environmental or contagious. Results from week 6 showed that all pools tested positive for *Enterococcus* pathogen. No additional pathogens were found in the cows in category 2. Category 3 had two cows that tested positive for *Strep uberis* and one tested positive for Staph Aureus. Category 4 showed no additional pathogens and category 5 showed cows positive for *Staph aureus* and *Strep uberis*.

Predictive model

Analysis of the monthly and weekly data led the team to consider building a predictive model for future udder health status. Predictions are single cow based and use the most current and prior data on a single cow. The basis of the prediction model is shown in Figure 5.

Table 2. SCC and DSCC values for a cow considered healthy and in category 1.

ID	Date	SCC	DSCC
8892	2/7/2019	9	0
8892	2/14/2019	16	0
8892	2/21/2019	6	0
8892	2/28/2019	17	0
8892	3/7/2019	13	0
8892	3/14/2019	15	0

Table 3. SCC and DSCC values for a cow considered healthy but potentially at risk and in category 2.

ID	Date	SCC	DSCC
5986	2/7/2019	177	86.1
5986	2/14/2019	128	75.3
5986	2/21/2019	200	80.2
5986	2/28/2019	185	79.2
5986	3/7/2019	113	76.1
5986	3/14/2019	144	77.1

Table 4. SCC and DSCC values for a cow that could be chronic infected and in category 3.

ID	Date	SCC	DSCC
527	2/7/2019	379	45.9
527	2/14/2019	259	49.6
527	2/21/2019	217	42.9
527	2/28/2019	343	46.6

Table 5. SCC and DSCC values for a cow that could be infected and not responding in category 4.

ID	Date	SCC	DSCC
1403	2/7/2019	644	46.3
1403	2/14/2019	743	51.9
1403	2/21/2019	932	52.3
1403	2/28/2019	988	42.6
1403	3/7/2019	1725	42.8

Table 6. SCC and DSCC values for a cow considered infected and in category 5.

ID	Date	SCC	DSCC
1136	2/7/2019	1176	84
1136	2/14/2019	2169	83.6
1136	2/21/2019	3021	81.6
1136	2/28/2019	2312	85.1
1136	3/7/2019	2348	85.4
1136	3/14/2019	2140	78.8

Utilizing the field trial data set the number of observations based on the breakdown of the categories listed in Table 1 resulted in some categories having a limited number of observations limiting what can be achieved using a machine learning approach. Several approaches were used with the existing data and shared below.

Weekly observations were used to develop predictive models for flagging animals based on their previous weekly records. This was set up as a classification problem (subset of machine learning methods concerned with learning classes of target variables by provided target from training data). The target variables were created by mapping the observed SCC to 0 and 1. 0 was used for healthy cows (SCC < 200,000) and 1 was used to signal cows at-risk for mastitis (SCC >= 200,000).

After cleaning weekly observations total of 10,763 records were used as the dataset for this classification. From all the available features in the original dataset few were selected as the main features for this study and other features were engineered by transformation of these main features. SCC, DSCC, LACT, DIM, age (days), age at calving were included directly from the dataset, and linear score, Macrophage count, and PMN counts were calculated from the corresponding features. Other features were added to this dataset by merging and adding the number of each health events (abortion, displaced abomasum, ketosis, mastitis, metritis, milk fever, retained placenta) that happened before the current test, with inclusion of the total number of health events. To be able to classify the current SCC category, 3 lagged variables of key features including SCC, DSCC, and linear score was created. These variables were simply the data from the previous records up to 3 weeks prior to the current test. Furthermore, mean and standard deviation of SCC, linear score, DSCC, PMN and Macrophage counts, which include all the previous records of individual animals (excluding the last weekly record), were added to the dataset.

After removing the first week, because of lack of any previous records, and filling the missing values created by generating the lagged variables with the corresponding column median, total of 8,726 data points was divided into 75% train set and 25% test set, randomly. The training and testing sets were created in a way that each set had the same proportion of the target variable (stratifying by target to keep the proportion of target the same in both test and train sets), which was approximately 77% SCC < 200,000 and 23% with SCC >= 200,000. All the models were built on the training dataset and model evaluation was done by 5-fold cross validation, test set was just used to report the performance of the models here.

Different classification algorithms were applied to the training data and the models were evaluated according to their f1-score (weighed harmonic mean of recall (sensitivity) and precision). F1-score was used because for a good classification model both recall (the ability of the model to identify the at-risk cows) and precision (the ability of the model not to incorrectly classify at-risk cows as healthy cows) are important, and F1-score takes both metrics into account. In addition, recall and precision are especially important when there is an imbalanced dataset (as it is in the current dataset 77% healthy vs 23% at-risk cows) and accuracy of the model alone does not prove a good classifier.

From all the models tested the best model was the Gradient Boosting classifier, which is an example of boosting algorithm and subset of broader category of ML models called ensemble models. These are models that could outperform most other models on wide category of datasets by creating series of prediction models (usually tree models in the classification) sequentially. The classification errors at each step are evaluated and more weight is being put on those misclassified records, so the next model could further reduce the misclassification. Predictions of the final ensemble model would be the weighted sum of all the predictions from all individual tree built previously. Another significance of gradient boosting is the fact that it could create a

relative importance of the features for classification. Results showed that the most important features for classifying healthy and at-risk cows in the current model setting, was mean linear score, mean SCC and their standard deviations, which means the cows previous average weekly SCC values is the most significant predictor of its future values (ModelAll). In this case DSCC adds almost nothing to the predictions. However, if we do not consider the mean and standard deviation of previous records in case we do not have it available, previous test SCC alongside PMN counts (generated from DSCC) were important (ModelPart1). Top 10 features sorted by their importance for the above models (ModelAll, ModelPart1) are sorted by their relative importance and can be seen in Table 7.

Based on the relative importance in Table 7 and applying feature selection some features (for example health events and all the categories created by binning the features were excluded) and a model with best subsets were developed.

The model based on the best subsets of features resulted a 79% f1-score with other scores plotted in Figure 6 across both classes. This resulted in a 0.859 area under the ROC curve (AUC), which shows the overall model performance and could be used to compare to other models. This can be compared with a model without any DSCC related features on right panel of Figure 6, which resulted in 0.853 AUC.

Table 7. Relative importance of top 10 features from ModelAll and ModelPart1.

Feature Name	Relative Importance	Feature name	Relative importance
mean_linear_score	0.777	lag_1_Cells	0.616
mean_Cells	0.106	lag_1_linear_score	0.08
sd_Cells	0.028	lag_1_PMN_cnt	0.059
sd_linear_score	0.015	lag_2_Cells	0.056
sd_DSCC	0.007	lag_1_Macrophage_cnt	0.043
lag_1_Cells	0.007	lag_3_Cells	0.023
DIM	0.006	lag_2_PMN_cnt	0.018
lag_3_PMN_MAC_ratio	0.005	DIM	0.017
age_days	0.005	lag_3_Macrophage_cnt	0.015
mean_Macrophage_cnt	0.004	scc_cat_lag_2	0.014

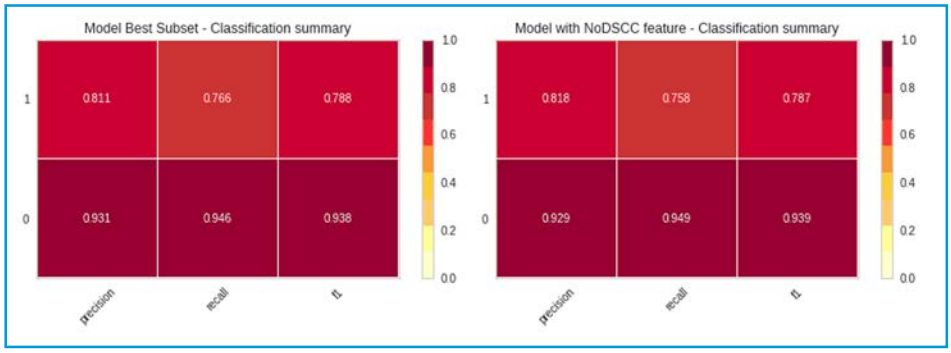

Figure 6. Best performing gradient boosting algorithm (left) vs. Model with no added feature from DSCC. Performance shown is evaluated on the unseen test data separated by respective class 0 as healthy cows (SCC < 200,000) and 1 at-risk cows (SCC >= 200,000)

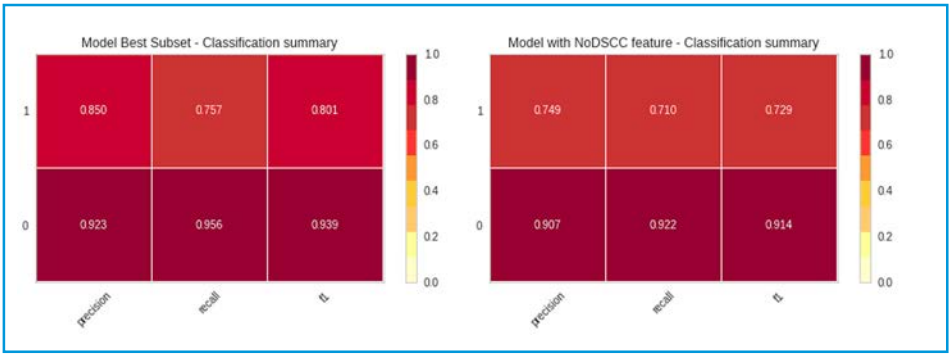

Figure 7. Best performing gradient boosting algorithm (left) vs. Model with no added feature from DSCC. Performance shown is evaluated on the unseen test data separated by respective class 0 as healthy cows (DSCC < 70) and 1 at-risk cows (DSCC >= 70)

A similar analysis was performed predicting DSCC instead of SCC. Therefore, the dataset target variable was changed to use DSCC >= 70 to classify at-risk cows and DSCC < 70 as healthy cows. This showed slightly better F1-score when considering best subset of features in the model and lower F1-score when no DSCC features were used in the model. The AUC of the best subset model, 0.856, was as high as the original models (using the SCC categories as target variables) but the model without any DSCC related features had a lower AUC of 0.817.

Table 8. Relative importance of top 10 features from ModelAll and ModelPart1 when DSCC was used to create target variable.

Feature Name	Relative Importance	Feature Name	Relative Importance
mean_DSCC	0.064	mean_PMN_pct	0.077
sd_DSCC	0.005	sd_PMN_pct	0.007
mean_Cells	0.004	lag_2_Cells	0.003
sd_linear_score	0.002	lag_3_Cells	0.003
lag_2_DSCC	0.002	lag_1_Cells	0.002
lag_1_Cells	0.002	age_days	0.002
age_days	0.001	lag_1_DSCC	0.001
DIM	0.001	DIM	0.001
lag_1_DSCC	0.001	age_at_calving	0.001
lag_3_DSCC	0.000	dim_cat	0.001

Conclusions

Based on the monthly and weekly data analysis, sofar no conclusive results have been reached regarding the use of DSCC. Although patterns in the data suggest that SCC combined with DSCC can identify some cows that may be considered healthy based on SCC alone the addition of DSCC can in some cases point at cows at risk. Using the data collected sofar, a machine learning approach predicting the future status of a single cows was not able to prove that DSCC provides a significant contribution over using SCC only. Future efforts will focus on collecting more weekly milk samples and look for additional relationships between DSCC and health status of the cow. Repeat analysis of monthly milk samples on the same cow will also increase the understanding of SCC and DSCC as it relates to parity and stage of lactation. Further understanding of the impact different environmental or contagious pathogens or impact of other (non-udder) health conditions on SCC and DSCC will be helpful in determining where DSCC can provide additional value.

Assesment of bovine milk fat quality from the view of human health

S. Hadrova[1], A. Vesely[1] and L. Krizova[2]

[1]Agrovyzkum Rapotin, s.r.o., Rapotín, Czech Republic
Corresponding Author: sylvie.hadrova@vuchs.cz
[2]University of Veterinary and Pharmaceutical Sciences Brno, Department of Animal Nutrition, Faculty of Veterinary Hygiene and Ecology, Brno, Czech Republic

Abstract

A desirable fatty acids (FA) profile in milk contributes to the production of milk with higher added value. The aim of this study was to evaluate the quality of milk fat from the view of human health from cow´s milk under on farm conditions. The study was performed on individual milk samples collected from four dairy farms breeding Holstein cows. The diets used on those farms were based on maize silage, hay and supplemental mixtures containing rapeseed oil and cake (Farm 1), extruded full-fat soybean (Farm 2), rapeseed cake + extruded full-fat soybean (Farm 3) or flaxseed + soybean meal (Farm 4). Milk samples were taken from four average yielding cows per herd and were analysed on the content of FA in milk fat. Samples of feedstuffs were taken at the same time as milk samples and were analysed on the content of dry matter (DM) and basic nutrients. Based on the FA profile, sums of SFA, MUFA and PUFA were calculated as well as following selected indices of milk fat quality: atherogenic, thrombogenic, health-promoting indices and hypo-/hypercholesterolaemic ratio. Content of SFA ranged from 61.29 (Farm 1) to 68.36 g/100 g FA (Farm 3). The highest content of MUFA was in milk from Farm 1 (34.71 g/100 g FA) and the lowest in milk from Farm 3 (27.59 g/100 g FA). Content of PUFA was similar in Farms 1 and 3 and higher in Farms 2 and 4. AI ranged from 1.89 (Farm 1) to 2.77 (Farm 3). TI was similar in Farms 1, 2 and 4 ranging between 2.36 and 2.58 and high in Farm 3 being 3.56. The highest HPI was found in milk in Farm 1 and the lowest in Farm 3. HH ratio was high in Farms 1 and 2 being 0.93 and 0.84, respectively and low in Farms 3 and 4 (0.53 and 0.59, respectively).

Keywords: dairy cows, milk, fatty acid profile, milk fat quality, indices.

Introduction

Nutritional value and composition of milk fat can be affected through the nutrition of dairy cows. E.g. it is possible to significantly reduce the content of saturated fatty acids (FA) in milk fat (Shingfield *et al.*, 2008) or increase the content of the n-3 FA and conjugated linoleic acid (CLA) that may have cardiovascular health benefits and anticarcinogenic properties. Diet composition is the main factor that can cause changes in milk FA (Hanus *et al.*, 2018). Feeding oilseed products to lactating dairy cows, as one of the dietary strategies, can modify the FA profile in milk fat to obtain milk rich in unsaturated FA, especially n-3 PUFA and CLA, as e.g. flaxseed. Other oilseeds we could include in the feeding of dairy cows are soybean, rapeseed, sunflower seeds and lupine seeds and their products (Veselý *et al.*, 2009; Chilliard and Ferlay, 2004).

A targeted modification of the FA profile of milk fat can be used for the production of milk with higher added value. For evaluation of milk fat quality, some indices e.g. atherogenic index, thrombogenic index, health-promoting index or hypo-/ hypercholesterolaemic ratio have been proposed (Ulbricht and Southgate, 1991; Chen *et al.*, 2004; Santos-Silva *et al.*, 2002). The aim of this study was to evaluate the quality of milk fat from the view of human health from cow´s milk under on-farm conditions.

Methods

The study was performed on individual milk samples collected from four dairy farms breeding Holstein cows. The diets used on those farms were based on maize silage, hay and supplemental mixtures containing rapeseed oil and cake (Farm 1), extruded full-fat soybean (Farm 2), extruded rapeseed cake + extruded full-fat soybean (Farm 3) or flaxseed + soybean meal (Farm 4). Samples of feedstuffs were taken at the same time as milk samples and were analysed on the content of DM and basic nutrients. The composition of diets that were used on farms are given in table 1.

Table 1: Composition of the diets of dairy cows on individual farms (g/kg DM).

Items	Farm 1	Farm 2	Farm 3	Farm 4
Maize silage	464.1	483.2	508.0	345.0
Meadow hay	79.0	82.0	-	-
Lucerne hay	-	-	92.0	86.0
Barley	121.3	127.6	106.4	198.8
Oat	123.1	129.3	106.4	142.0
Wheat	-	-	-	45.4
Extruded full-fat soya	-	89.4	67.2	-
Soybean meal	-	-	-	39.7
Extruded rapeseed cake	117.6	-	56.4	-
Rapeseed oil	5.5	-	2.1	-
Flaxseed	-	-	-	28.4
Sugar beet chippings	66.1	66.4	49.2	85.2
Sodium chloride (NaCl)	-	-	1.9	2.8
Dicalcium phosphate (DCP)	-	-	4.3	8.5
Limestone ($CaCO_3$)	-	-	4.4	8.5
Sodium bicarbonate ($NaHCO_3$)	-	-	1.1	0.6
Monosodium phosphate	-	-	0.2	1.1
Magnesium phosphate (MgP)	-	-	-	1.1
Premix (sum)[1]	23.3	22.1	-	-
Microelements and vitamin mixture	-	-	0.4	5.7
Rumen protected Met and Lys	-	-	-	1.38

[1]the premix contains (g/kg in supplemental mixture): sodium chloride 6; dicalcium phosphate 17; limestone 16; sodium bicarbonate 1; monosodium phosphate 2; magnesium phosphate 2; microelements and vitamin mixture 6.

Milk samples were taken from four representative average yielding cows per herd and were analysed on the content of FA in milk fat. FA from extracted milk fat were released in the form of fatty acid methyl esters which were separated using a gas chromatograph and detected with the flame ionisation detector as described previously (Veselý *et al.*, 2009). Based on the FA profile, sums of saturated (SFA), monounsaturated (MUFA), polyunsaturated FA (PUFA) were calculated as well as following selected indices of milk fat quality that describe the nutritional value of milk fat:

atherogenic index (AI; Ulbricht and Southgate, 1991):
AI = (C12:0 + 4 x C14:0 + C16:0) / ΣUFA;

thrombogenic index (TI; Ulbricht and Southgate, 1991):
TI = (C14:0 + C16:0 + C18:0) / ((0.5 x ΣMUFA + 0.5 x Σ(n-6) + 3 x Σ(n-3)) + (Σ(n-3) / Σ(n-6)));

health-promoting index (HPI; Chen *et al.*, 2004):
HPI = (ΣMUFA + ΣPUFA) / (C12:0 + 4 x C14:0 + C16:0);

hypocholesterolaemic/hypercholesterolaemic ratio (HH; Santos-Silva *et al.*, 2002):
HH = (C18:1 n-9 + C18:2 n-6 + C20:4 n-6 + C18:3 n-3 + C20:5 n-3 + C22:5 n-3 + C22:6 n-3) / (C14:0 + C16:0).

Results and discussion

Effects of different types of forages and oilseed products on the FA profile in milk fat and nutritional indices are shown in the Table 2. In this study, the content of SFA ranged from 61.29 (Farm 1) to 68.36 g/100 g FA (Farm 3). The highest content of MUFA was in milk from Farm 1 (34.71 g/100 g FA) and lowest in milk from Farm 3 (27.59 g/100 g FA). The content of PUFA was similar in Farms 1 and 3, higher in Farm 4 and the highest in Farm 2 where extruded full-fat soybean was fed to dairy cows. The lipids of soybean are highly unsaturated (Chouinard *et al.*, 1997). Similarly, the content of PUFA in milk fat of cows fed extruded soybean was higher ($P<0.05$) in comparison to groups of cows fed diets supplemented with protected palm fat and rapeseed cake (Kudrna and Marounek, 2006). From the view of human health, a higher content of PUFA in milk fat is desirable. The consumption of n-3 PUFA-rich foods has hypolipidemic, antithrombotic and anti-inflammatory effects (Simopoulos, 1999). Because the milk FA profile can be modified through the animal nutrition, PUFA-enriched milk can have the potential benefits for human health. On the other hand, it can affect the technological properties of milk fat (Hanus *et al.*, 2018).

The high proportions of SFA in milk fat, such as C12:0, C14:0, and C16:0, are related to an increased risk of atherosclerosis (Bobe *et al.*, 2007). To evaluate the risk of cardiovascular diseases we calculated the atherogenic index (AI) that ranged from 1.89 (Farm 1) to 2.77 (Farm 3). Thrombogenic index (TI) showing the tendency to form clots in the blood vessels describes the relationship between the pro-thrombogenic (it is SFA) and the anti-thrombogenic FA (it is MUFA, n-6 PUFA and n-3 PUFA) (Ulbricht and Southgate, 1991; Garaffo *et al.*, 2011), so TI should be low. TI were similar in Farms 1, 2 and 4 ranging between 2.36 and 2.58 where cows were fed a supplemental mixtures containing rapeseed oil and cake (Farm 1), extruded full-fat soybean (Farm 2) and flaxseed + soybean meal (Farm 4) and it was high in Farm 3 being 3.56 where extruded rapeseed cake + extruded full-fat soybean were added to the diet of cows. The health-promoting index (HPI) is inverse of the atherogenic index, thus the highest HPI was found in milk in Farm 1 and the lowest in Farm 3. Further, the hypocholesterolaemic/hypercholesterolaemic ratio (HH) was calculated according to Santos-Silva *et al.* (2002). HH index was high in Farms 1 and 2 being 0.93 and 0.84, respectively and low in Farms 3 and 4 (0.53 and 0.59, respectively). It is supposed that milk fat with high AI and TI values may more likely contribute to development of atherosclerosis or coronary thrombosis in humans, whereas milk with high HPI index and HH ratio may have a protective effect against cardiovascular diseases (Rafiee-Yarandi *et al.*, 2016).

Table 2. Effects of different types of forages and oilseed products on the FA profile in milk fat and nutritional indices

FA and indices	Farm 1	Farm 2	Farm 3	Farm 4
SFA (g/100 g FA)	61.29	62.32	68.36	64.87
MUFA (g/100 g FA)	34.71	32.14	27.59	30.28
PUFA (g/100 g FA)	4.00	5.54	4.05	4.85
AI	1.89	2.07	2.77	2.35
TI	2.36	2.36	3.56	2.58
HPI	0.53	0.49	0.36	0.43
HH	0.93	0.84	0.53	0.59

Conclusion

Using indices for evaluation of milk fat quality allows us deeper insight into the impact of FA on human health. Results of our study showed that health properties of milk fat differed among farms and that dairy nutrition contributed greatly on the variability in milk FA profile.

Acknowledgement

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Comparison of on-line measurements with conventional single-day herd tests

R.G. Orchard[1], A.M. Winkelman[2], G.P.S. Anderson[2], E.M. Steenson[1], V.C. Farr[1], D.M. Gyde[1] and A.F. Yeates[2]

[1]LIC Automation Limited, PO Box 20306, Hamilton 3241, New Zealand
Corresponding Author: rob.orchard@licautomation.co.nz
[2]Livestock Improvement Corporation, Private Bag 3016, Hamilton 3240, New Zealand

Abstract

Previous theoretical studies have shown that frequent tests by on-line milk analysers (OMA) can provide better cow assessments than infrequent laboratory-based tests. This is because the higher test error associated with OMA averages to zero with multiple tests and the true means of traits with high day-to-day variation are better captured using tests taken over several days than with a single-day herd test (1DHT). This theory, however, assumes tests are not affected by cow specific bias (CSB). CSB is a systematic error that causes cows to be consistently under- or over-evaluated relative to the herd, which reduces the accuracy of between-cow comparisons. We compared the precision of data from OMA and 1DHT for milk volume, fat, protein, lactose and SCC, using the 10d average herd test as ground truth. The precision of OMA was better at a cow average level than at an individual test level, but this was dependent on the degree of CSB. CSB was negligible for protein, lactose and somatic cell count (SCC) ≥200 kcells/mL and not negligible for volume, fat and SCC <200 kcells/mL. The precision of the 1DHT estimate of the cow average was numerically similar to the within-cow day-to-day variation of each trait, which is consistent with the theory that day-to-day variation is the primary cause of 1DHT error. For traits with high day-to-day variation (milk volume, fat, SCC ≥200 kcells/mL), OMA provided a statistically equal or better estimate of the cow average than 1DHT. For traits with low day-to-day variation (protein, lactose, SCC <200 kcells/mL), 1DHT provided a significantly better estimate of the cow average than OMA, despite OMA protein and lactose exhibiting negligible CSB. For all milk production traits and for SCC in the range most useful for herd management purposes (≥200 kcells/mL), OMA estimated the cow average with precision and ranking accuracy suitable for herd management.

Keywords: on-line milk analysers, cow-specific bias, day-to-day variation.

Introduction

One argument in favour of on-line milk analysers (OMA), as opposed to laboratory-based herd testing, is that the average of repeated tests provides a good estimate of the true mean (Mein *et al.*, 2000; Clarke and Hannah, 2007). This theory, however, assumes tests are not affected by cow specific bias (CSB). CSB is a systematic error that causes cows to be consistently under- or over-estimated relative to their herd mates. CSB limits the usefulness of the data for between-cow comparisons (Anderson *et al.*, 2016). LIC Automation produces two OMA: *Saber™ Milk* and *Saber SCC*, which between them measure milk volume, fat, protein, lactose and somatic cell

count (SCC). *Saber Milk* fat and protein measurement exhibits relatively high CSB. To address this problem, a new milk composition analyser is being developed by LIC Automation using a technology less susceptible to CSB.

While CSB limits the ability of OMA to average out errors over multiple tests, within-cow day-to-day variation limits the power of a single-day herd test (1DHT) to represent the cow average, no matter how accurate the test. Day-to-day variation for milk volume and fat is typically high (Mackle *et al.*, 1999; Andrée, 2008). Mackle (1999) reported within-cow day-to-day coefficients of variation (CVs) of 8.93% for volume and 5.17% for fat. The current trial compared the ability of OMA and 1DHT to estimate the short-term cow-average milk traits. The aim was to determine whether the advantage of frequent tests by OMA, limited by CSB, outweighed the advantage of the precise tests of the 1DHT, which does not capture within-cow day-to-day variation.

Materials and methods

Data were collected from a herd of 208 cows, milked twice per day in a 24-a-side swing-over herringbone milking system in Waikato, New Zealand. Milk analysers were manufactured by LIC Automation, Hamilton, New Zealand. Prototypes, incorporating a new milk composition analysis technology, were installed at 14 positions, testing milk volume, fat, protein, lactose and SCC. *Saber Milk* and *Saber SCC* were installed at the remaining 10 positions, testing milk volume and SCC. Herd tests were conducted at twenty consecutive milking sessions, from 11 to 21 June 2018. Only milkings with valid results from both the herd test and the OMA (paired milkings) were included in the analysis.

Data from cows that had eight or more paired milkings in the trial period, and at least one day of the middle five days (14-18 June) with both AM and PM paired milkings, were included. The final dataset for volume analysis included 178 cows with data from 2224 milkings, and for SCC included 177 cows and 2209 milkings. The final dataset for milk composition analysis was smaller because the milk composition analysers were only installed at 14 of 24 milking positions, resulting in fewer paired milkings, and included 50 cows with data from 473 milkings. The distribution of tests per cow for these three datasets is illustrated in figure 1.

The final datasets were a mixture of AM and PM results for each cow, depending on which milking positions the cow visited during the trial. It was therefore difficult to determine a ground truth cow average with balanced AM and PM contributions without discarding excessive amounts of data. This problem was addressed by scaling individual AM and PM results to a 24h equivalent result by multiplying by a coefficient derived from the whole herd data. If a cow had both AM and PM results on a day, two 24h values were inferred and both were included in the cow average.

Statistics for SCC were calculated for two ranges using a cut-point of 200 kcells/mL. Precision was quantified using SD of error (SDE) for fat, protein, lactose and SCC (<200 kcells/mL), and SD of relative error (SDRE) for milk volume and SCC (≥200 kcells/mL). Three tests were evaluated: OMA at an individual milking level, OMA at the cow average level, and 1DHT (adjusted for herd day-to-day variation). The 1DHT for each cow was the day closest to the middle day with two herd test results. The ground truth for individual milkings was the herd test, and the ground truth for cow average OMA and 1DHT was the 10-day cow average herd test. Cow averages for SCC were calculated by geometric mean.

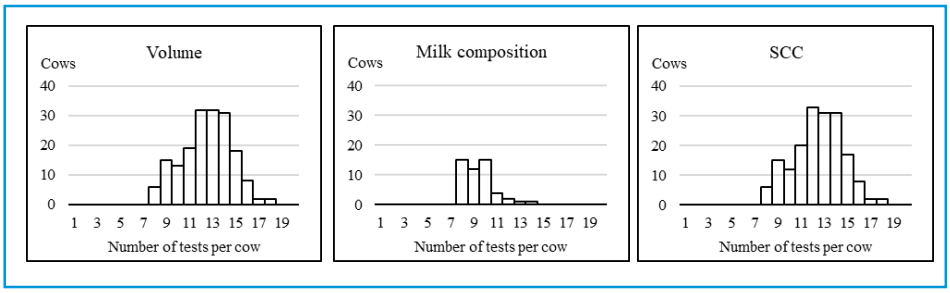

Figure 1. Distribution of tests per cow in the final datasets for evaluating measurement performance.

Within-cow day-to-day variation in the milk traits was quantified as the herd-mean of the cow-SD or cow-CV of 24h herd test results, from cows with at least five 24h values (168 cows). Spearman correlation was used to quantify the ability of a test to correctly rank animals according to milk volume, fat yield, protein yield, lactose yield, SCC less than 200 kcells/mL and SCC greater than or equal to 200 kcells/mL.

Results and discussion

The results of the trial are illustrated in figure 2, where the three types of estimate are plotted against their respective ground truth for each trait. The performance statistics from the trial are shown in table 1. The SDE or SDRE for individual tests and the OMA cow-average, respectively, was 10.6% and 6.0% for volume; 0.36 and 0.18 g/100mL for fat; 0.29 and 0.12 g/100mL for protein; 0.18 and 0.09 g/100mL for lactose; 66 and 42 kcells/mL for SCC <200 kcells/mL; and 52% and 21% for SCC ≥200 kcells/mL. Therefore, OMA had better precision (SDE or SDRE) at the cow-average level than at the individual milking level for all traits, indicating that some of the test error averaged-out with repeated tests. The degree of improvement for protein, lactose and SCC (≥200 kcells/mL) suggests that for these traits, CSB was negligible. For example, the SDE for protein improved from 0.29 to 0.12 g/100mL, whereas the cow average SDE

Table 1. Summary of results.

	Indiv. test			Cow average						
				SDE or SDRE[1]			Spearman correlation[2]			
	Milkings	SDE or SDRE[1]	Cows	OMA	1DHT	p-value	OMA	1DHT	p-value	Within-cow SD[3] or CV
Milk vol.	2224	10.6%	178	6.0%	6.1%	0.855	0.969	0.976	0.226	7.0%
Fat	473	0.36	50	0.18	0.26	0.001	0.957	0.940	0.407	0.31
Protein	473	0.29	50	0.12	0.09	0.028	0.934	0.973	0.027	0.10
Lactose	473	0.18	50	0.09	0.05	0.000	0.935	0.957	0.303	0.07
SCC <200k	1951	66	157	42	26	0.000	0.309	0.948	0.000	21
SCC >200k	258	52%	20	21%	68%	0.000	0.825	0.796	0.430	61%

[1] SDE has units of g/100mL for fat, protein and lactose, and kcells/mL for SCC.
[2] Spearman correlation for fat, protein and lactose was based on kg yield.
[3] Within-cow SD has units of g/100mL for fat, protein and lactose, and kcells/mL for SCC.

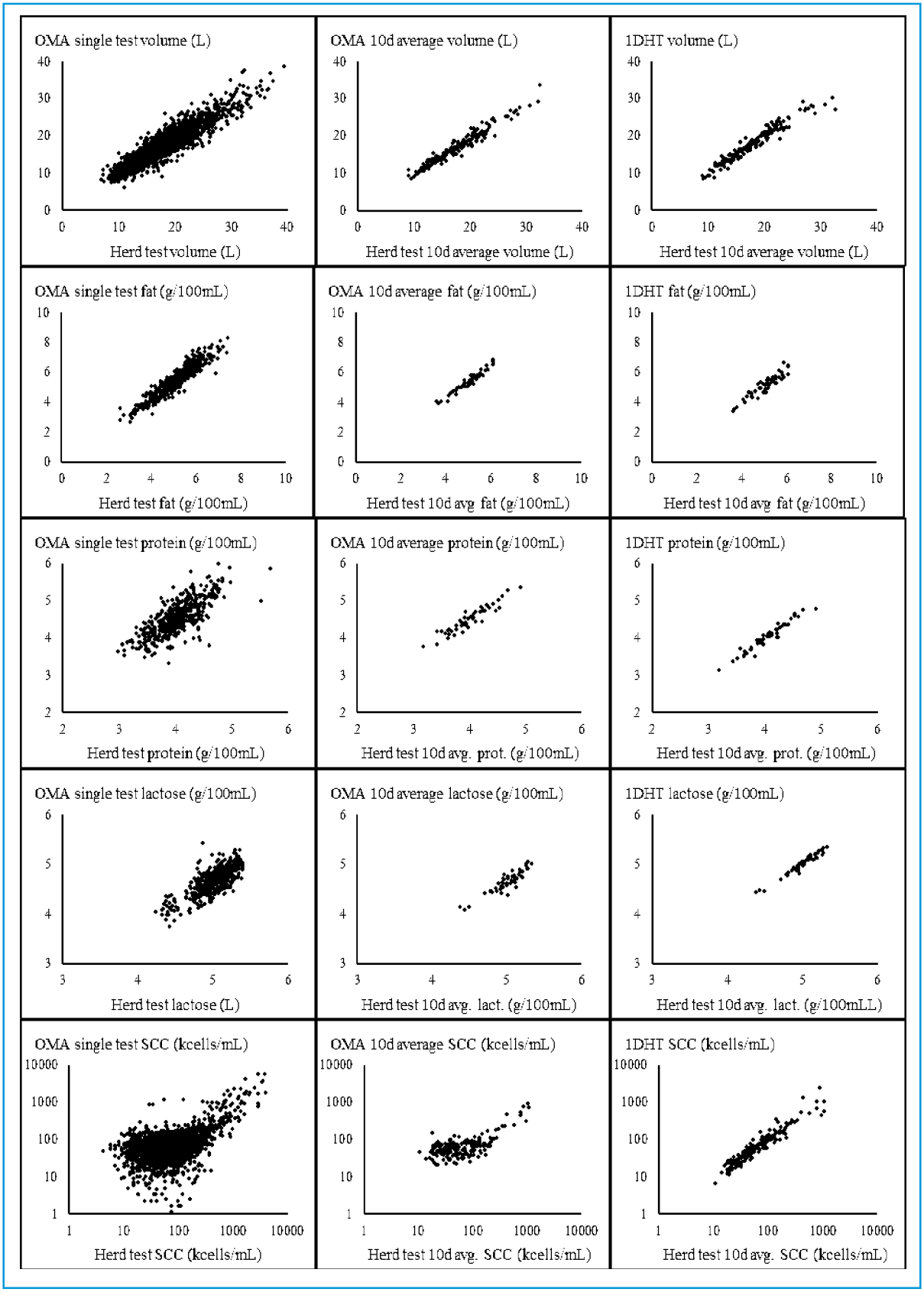

Figure 2. Correlation between the estimate and the ground truth for volume, fat, protein, lactose and SCC; for OMA single tests (left), OMA 10-day average (centre) and 1DHT (left).

expected in the absence of CSB, assuming eight tests per cow, would be 0.10 g/100mL (0.29/$\sqrt{8}$) However, for milk volume, fat and SCC (<200 kcells/mL) the improvement was less than would be expected if there were no CSB.

Day-to-day variation in the production traits was consistent with published work (Mackle 1999, Andrée 2008): relatively high for volume (7.0%) and fat (0.31 g/100mL); and relatively low for protein (0.10 g/100mL) and lactose (0.07 g/100mL). The SDE or SDREs for the 1DHT, compared with the cow average herd test as ground truth, were 6.1% for volume, and 0.26, 0.09 and 0.05 g/100mL for fat, protein and lactose, respectively, which were numerically similar to the within-cow day-to-day SD for these traits. This supports the idea that day-to-day variability inhibits the ability of the 1DHT to provide a result representative of the short term average for a cow. As a result, the OMA provided an equivalent or better estimate of the short term cow average for milk volume, fat and SCC (≥200 kcells/mL) – the traits with high day-to-day variation. For protein and lactose, which had low day-to-day variation, the estimate from 1DHT was significantly better than the OMA. Even so, low SDE and high Spearman correlations (>0.93) for all production traits at the cow average level indicate that the OMA used in this trial is a useful tool for identifying high and low producing cows.

The 1DHT SDE for SCC less than 200 kcells/mL (26 kcells/mL) was substantially smaller than observed in a previous trial (64 kcells/mL, Orchard *et al.*, 2018).The previous trial did not evaluate within-cow day-to-day SD, but the SDE results imply that day-to-day variation was substantially smaller in the current trial. Consequently, in contrast to the previous trial, the 1DHT provided a more precise estimate of the 10-day average than the OMA. The level of CSB exhibited by the OMA in the low SCC range was significant compared with the differences between cows. Accordingly, the OMA had a poor Spearman correlation for SCC <200 kcells/L. The primary uses for an SCC analyser are to detect high SCC animals and those with subclinical mastitis. Neither of these uses require accurate ranking of animals below 200 kcells/mL. In the more important high SCC range, the OMA provided a better estimate of cow average SCC than a 1DHT and had an equivalent Spearman correlation. Therefore, the OMA appears to be a valuable tool for monitoring individual cow SCC.

In summary, this trial has produced experimental data consistent with previous theoretical research that indicated that errors in individual tests from OMA can be averaged-out over multiple tests, but that CSB limits this; and that within-cow day-to-day variation limits the ability of 1DHT to estimate the short-term cow average. For milk volume, fat and SCC ≥200 kcells/mL, the OMA used in this trial provided an equivalent or better estimate of the short-term cow average than a 1DHT. For all traits, the data produced by the OMA provided useful estimates of the cow average for herd management purposes.

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Cow ID-topics related to milking and milk recording

K. de Koning[1], J. Persson[2] and U. Lauritsen[2]

[1]WUR, Boksumerdyk 11, NL- 8912 CA Leeuwarden, The Netherlands
[2]RYK Fonden, Agro Food Park 15, DK 8200 Aarhus N, Denmark

Data is only valid and relevant when linked to an ID

Core value of any registration, whether manual or automatic, is to monitor, control and validate ID. Observing a car running way too fast does not help anyone if numbers and letters on the plate cannot be read. In the same analogy, it doesn't bring the police any further if there is a false ID on the car, or if numbers were made up.

The same counts for using ID systems in animal husbandry. To ensure correct and true data, it is essential to have firm routines and technology to catch cow ID.

Cow ID and data is an issue of great concern

As throughput of cows per time unit increases with larger groups in milking parlours and more automation and constant measurement on a series of parameters moves on to the farms, it gets more and more important to highlight the cow ID topic. Most new milking parlours have rapid exit systems speeding up the process of changing the group being milked to the next group in order to increase the milking capacity of the milking parlour. Many parlours nowadays are equipped with ID at the entrance of the milking parlour (walk-trough ID) – saving costs compared to an ID system at every bail.

In an ideal world the cow is registered at the entrance of the parlor, and software links the cow the right position in the parlor. Finally, data from the cow and the milking flows directly to a database.

Manufacturers often focus on their products ability to read ID when cows pass the antenna. In marketing this is most times expressed as very close to 100%. What seldom is told, is the ability of the system to link cows to the right bail, which is what users of data expect to happen. And taken for granted.

Besides collection of the data mentioned above, the same system is also used to link the sample ID to the Cow. Regarding taking samples, it might happen especially in side by side parlors, that milk meter and sampling device are mounted left or right from the cow, with other words below another cow. However, by correct identification from the meter/sampler and good instructions to the milk recording technician, this can be dealt with. In general it can be concluded that wrong cow ID also will affect the sampling. A good sample can be collected, but when connected to the wrong Cow ID, the data are useless.

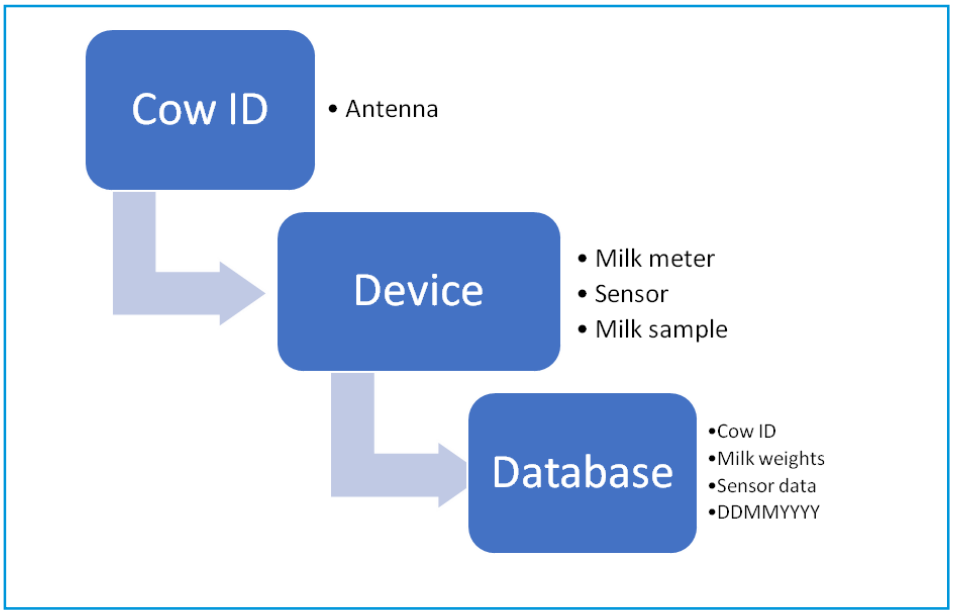


Figure 1. Data from the cow and the milking flows directly to a database (Figure 1).

What can go wrong?

In the everyday situation on a farm, several steps can go wrong with major effects on the quality of data collection. A list of examples is listed below.

Software from various manufacturers

During milking there is only a few seconds to determine cow ID, sequence in the row, link to a bail # and start recording. Especially in large milking parlors (up to 2 times 35 side by side rapid exit parlors) there is very limited time for the first step – determination of the cow ID. If time is too short, it might happen that a cow ID is not measured at all when cows enter, or sometimes when 2 cows are very close to each other, only 1 is identified. The order of cows ID identified is linked to the bails in the milking parlour. So the first cow identified is linked to bail 1, 2nd to bail 2, 3rd to bail 3 and so on.

However, when a cow is not identified, there will be no link to the bail. So if cow at bail 10 in the row is not identified, cow 11 will automatically be linked to bail 10, cow 12 to bail 11 and so on. This will result in one cow not identified and a number of cows linked to the wrong bail.

Most manufacturers have built in options to correct any observed error or mismatch between cow and bail. Often the milker plays an important role in adjusting the cow ID to the right number, however he or she has to see (or g*et al*erted) that something went wrong. To avoid a discussion who is better than others, no brand names is mentioned below.

Errors and the damage these mistakes cause, is slightly different between parlors and rotaries. In parlors one missed cow can result in a full side only errors. On a rotary, errors are in most cased isolated to relatively few cows and bails (normally max 2-3).

What to do during milking – Parlors

Main issue is to avoid cows from backing out of the reading area. This will typically happen for the last part of the row, new cows especially heifers and when sudden noise or abnormal routines is detected by the cows. As explained there are several options delivered by manufacturers.

Alarm

- A light alarm goes in the event the parlor gate is closed and less than a full side is identified.

  The reasons can be:

  - Missed cow. The milker must compare display and identify cows in the row. Correction is made on the panel following instructions and guidance as put forward by the manufacturer. Successful correction depends on the milker.
  - The side is not full. Check for errors as above, correct and/or accept data as they are.

If alarms are left unattended, and cows are not identified, is several cases depending on the manufacturer, these cows will get a calculated milk yield for this milking based on previous milkings.

Locking of data – no correction possible

System A lock cow ID in the moment back gate is closed. From there, no further options to correct ID

System B lock cow in the moment first set of cups is activated. From there, no further options to correct ID

Correction of data, an example

Manufacturers software is to some extend built to deal with errors. A couple of examples below.

System X

Some cow's in a row are not identified. identified. After milking the system pools let's say 5 missing cows in one batch and 5 homeless milk yields in another batch. Based on previous milkings these 2 sets of data will be merged, and a homeless milking with 15 kg, will be added to the file of a cow that likely could have had this amount.

This way of dealing with the subject of missed reading at the entrance, seems on the surface to be pretty smart. Digging into it, it soon reveals that what is looking as a 1 cow error, suddenly shows to be a full row error, because one cow not identified leads to several cows linked to the wrong stall number

System Y

After each milking cows expected to be milking, but not seen, will be subject to a data examination to set an estimated milk yield.

In Denmark we have seen cows in example Y, who for several months did not have a real recording from the meter. Every single milking was predicted.

Help to avoid errors

Some parlors are equipped with a "cow counter". This counter helps to identify number of animals passing the antenna. The counting will correspond with the antenna and leave a "no ID" on the bail where the ID was missed.

This system helps as a backup system but cannot detect everything happening during milking.

Main reasons behind errors

The following examples is from time to time observed in Denmark and Holland:

- Cows without electronic ID.
- User/milker not familiar with the system.
- Cows are pushed from holding pen to parlor.
- Cows passing each other after identification, but before reaching milking point.
- Identification of a cow number in other lane (ID reader not protected quite well).
- Malfunction of installation.
- Lack of maintenance of electronic installation.
- Electronic noise coming from other sources (blowers, LED light etc.).
- Poor installation of electronics and wires. In DK quite a few examples where very basic rules for protection of wires, engines and connections has not been met.
- Any other .....

At the Dairy Campus facilities many selection gates (walk through ID) are used to guide all cows after milking to the right barn and group. The number of correct identifications is now around or above 99%. Just after installation we had variable ID rates from 95 to 98%. Several of the solutions mentioned above were applied to increase accuracy rates.

By mounting Texas gates at the electronic weighing unit positioned at the exit of the rotary, the number of missing readings was also heavily reduced (mix of correct ID and time to weigh the animal).

We know a goat farm in the Netherlands who mounted individual ID antennas at every bail while to his experience identification at the entrance resulted in too many faults (just one example).

A general and well covering reason for errors is that in most situations milkers do not have the time needed to constantly monitor and correct errors.

What to do during milking - rotaries

Milking in a rotary is more "cow oriented" than "row oriented". The milker will immediately notice an empty bail and by experience know there might be a mismatch. Reasons why still things can go wrong:

- Cows without electronic ID.
- Cow expected to walk into bail 1, missed it and end up in bail 2.
- User/milker not familiar with the system.
- Cows passing each other after identification, but before reaching milking point.

- Malfunction of installation.
- Lack of maintenance of electronic installation.
- Electronic noise coming from other sources (blowers, LED light etc.).

Some installations do have cow ID at every bail (like the Dairy Campus rotary), most however do have a Texas gate connected to an ID antenna and the milking platform. This gate is the key to link the right cow to the right bail. If the Texas gate is turned off and cows have direct access to the platform, ID validation does not work either. This also will cause mismatch of cow/bail relation. Some farmers and milkers disconnect the gate to speed up cow traffic. The result will be inaccurate data. Another reason to disconnect the gate, is simply to avoid the noise from airoperated valves and metal scratching when gate opens and close. In some installations it can be a quite frustrating and intensive noise level.

A general and also well covering reason for errors is that in many situations milkers do not have the time needed to constantly monitor and correct errors.

To give an idea, a one-man operated rotary (40 units) will run approximately 180 cows per hour – this is only 20 seconds per cow to do all the things necessary around milking.

Where the antenna is placed

On rotaries antennas can be placed differently.

- Connected to a Texas gate (1-2 meters behind the platform).
- Just outside the platform (“cows last step before jumping”).
- Any of the above combined with an antenna 3-5 bails after entrance for validation of cow ID.
- Antennas mounted at every bail.

Final comments

The above information’s and views are based on sporadic observations plus observations reported by our field- and validation staff. It is not easy to estimate the number of wrong data in the field but estimated on those sporadic observations and the number of faults resulting in bad quality data might be somewhere between 5 and 15%. However as said real field data are missing.

Examples and details are not necessarily fully covering the whole area.

Identification and registration of cattle in the Czech Republic

P. Bucek and L. Nozina

Czech Moravian Breeders' Corporation, Inc., Benesovska 123,
Hradistko, 252 09, Czech Republic
Corresponding Author: bucek@cmsch.cz

Abstract

Identification and registration are prerequisites for milk recording, genetic evaluation, veterinary aspects of cattle breeding, agriculture policy and cattle breeding management on farms. This paper provides updates on this area in the Czech Republic as well as information on the role of the Czech Moravian Breeders' Corporation within the domestic system. The comprehensive and unique identification and registration system used in the Czech Republic employs modern IT technologies, data processing and data flow tools. The identification and registration database is interconnected with milk recording and genetic evaluation databases, incorporating a sophisticated system of plausibility checks and on-farm inspections. As part of this system, cattle breeders have access to the Integrated Agricultural Register (IAR), an administration server for identification and registration. All identification criteria respect EU and national legislations as well as the ICAR Guidelines. A uniform cattle identification eartag system was established in the Czech Republic in the early 1960s, building on a long tradition dating to the establishment of the milk recording industry in 1905. The identification system incorporates eartag distribution and logistics, select control mechanisms, plausibility checks, a supervisory programme and parentage verification.

Keywords: Identification and registration, Czech Republic, database, data processing, eartag, eartag distribution and logistics, Integrated Agricultural Register.

Introduction

Animal identification and registration are the most important prerequisites for successful farm management, milk recording, genetic evaluation and other aspects connected to cattle breeding. This paper summarises the identification and registration system for cattle used in the Czech Republic, detailing its key features and integration with other milk recording systems.

Users, organisations and bodies involved in the identification and registration system and their responsibilities

The following organisations are involved in the identification and registration system used in the Czech Republic:

- The Ministry of Agriculture – administrator of the identification and registration system.
- Czech Moravian Breeders' Corporation – delegated organisation responsible for technical implementation of the system.
- Czech Breeding Inspection and State Veterinary Office – responsible for breeder inspections.
- Various breeders and companies permitted access to the farmer portal.

The Czech Moravian Breeders' Corporation, Inc. oversees all processes related to identification and registration and is authorised by the Ministry of Agriculture. The Integrated Agriculture Register (IAR) (IZR in Czech) is a system used to identify and register livestock animals. The Czech Moravian Breeders' Corporation, Inc. uses IAR to ensure routine aspects of identification and registration are met and also engages in consultancy, testing and development of IAR and its farmer portal.

The Czech Moravian Breeders' Corporation, Inc. was established as a limited liability company for the purpose of privatising the National Breeding Company (State Breeding Institute). The founders of the company are the Czech Fleckvieh Breeders' Association, the Holstein Cattle Breeders' Association of the Czech Republic, and the Union of Breeders. The main goal of privatisation was to ensure all activities carried out on behalf of breeders and their associated organisations are subject to scrutiny, e.g. breeding registration administration, processing milk recording and progeny testing results, animal breeding value evaluation, milk and immunogenetic lab analysis, and technical herd book administration. The Czech Moravian Breeders' Corporation, Ltd. assumed control in the above areas, succeeding the National Breeding Company (State Breeding Institute) in November 1996 and becoming an incorporated company in 1999. Subsequently, the company was joined by other breeding organisations, receiving support from the Ministry of Agriculture of the Czech Republic through the Supporting Guaranteed Agricultural and Forestry Fund (State Government). The objective of these joint efforts was to develop the optimal conditions for the administration of animal identification and registration and to establish a common agricultural policy. The Czech Moravian Breeders' Corporation, Inc. is the sole body responsible for maintaining the dairy cattle identification system, dairy production records and genetic evaluation of dairy cattle. There is a uniform national programme in the Czech Republic.

IAR connects with the following external systems via web services:

- Cattle reproduction system: IAR adds information about animal pedigrees and birth reports to the cattle reproduction system.
- Herd book keeping: herd books document all bulls registered for artificial insemination and natural mating. This information is used for natural mating records.
- State Veterinary Office system: the system of State Veterinary Office use information about the location of animals registered by IAR and overseen by the State Veterinary Office. The State Veterinary Office also uses IAR in case of veterinary problems, e.g. possible infections, etc.
- State Agriculture Intervention Fund: IAR information is used to assess entitlement to subsidies.

- Cattle milk recording: the IAR can be used by breeders to access records and apply for subsidies.
- Record keeping for breeders (breeder system): provides IAR reports about births with IAR information on data processing, pedigree, etc.

Selected technical aspects of IAR

Architecture of IAR is designed in accordance with these requirements:

- High accessibility 365 days per year, 7 days per week and 24 hours a day with minimal accessibility 98%. For 100% of accessibility, assisted running times are considered in uncounted cases. Properly reported interruption times are used where times are shorter than 20 hours per month but no longer than 48 hours over the course of one year
- System security – distinguishes internet and intranet users at the application layer level

The IAR system is based on a three-layer architecture:

- Presentation layer.
- Application layer: servers on the Microsoft .NET platform Framework running on an MS Windows Server environment.
- Data layer: Oracle Database 11g system.

The application layer provides a higher level of security and the options to select scalability split into two parts. Communication between both parts runs from the top down. Technology NET.REMOTING is used. This design splits the application and presentation logics to ensure openness for different type of clients. This architectural design enables future extensions and access to other types of client layers, such as mobile clients. All servers in this platform run on Microsoft .NET Framework 4.0 and Microsoft Windows Server 2012 Standard. The database layer consists of the Oracle Database 11g. To aid recovery in the event of hardware issues with the disk field, the database is also accessible in archive mode and regularly backed up.

The IAR system operates on three environments (operational, testing and development). Each environment has separate application and web servers. The number of servers capable of running is based on the environment, i.e. one for development and another for testing and operation. There is a separate web server in the form of a farmer portal from the internal IAR portal web server.

IAR Testing

IAR replaced an older system used identification and registration of animals. The transition period involved making sure the new system would conform with the original version. Key to this was calculating animal pedigrees (parents and breeds) based on birth reports in the form of official printed accompanying documents. All records needed to be validated against the old system. Animal locations were also maintained from the previous system in order to prepare inventory lists. IAR also took over identification and registration (data migration) data from the original system. All migration was tested in detail based on comparing outputs from both systems in parallel after processing data records from both systems. Any differences were duly accounted for and explained.

Development of IAR

Automated data processing has been routinely used for cattle milk recording and performance recording of other livestock in the CR since 1960s. A modernised identification and registration system was subsequently implemented with the introduction of new EU legislation. In 2006, work began on updating this system with a focus on:

- Detailed analysis and
- Implementation

Timeframe of updates:

01/2008 – migration of data and opening of modules for routine practice

06/2009 – all modules made available for routine practice

01/2010 – breeder module launched

02/2011 – online data processing of identification and registration reports

2015 – breeder module allowing users to request welfare subsidies

2016 – 2018 – breeder module updated

Basic principle of animal registration and identification in the Czech Republic

The breeder sends the report, including eartag number, birth and import details

- The report is then processed and reviewed:
  - Eartag data reviewed for accuracy
  - Pedigree calculated
  - Animal location verified
- Results are sent to the breeders:
  - Successful registration
  - Unsuccessful registration (with reasons given in the report)
- Communication via standard tools

Pedigree calculation

Birth report – all data, including details on natural mating where relevant, sent to breeding database for pedigree calculation

- Pedigree calculation:
  - Pedigree calculated in the breeder database from the identification and registration database + data from the database including details on cattle reproduction (artificial insemination, ET)
- Calculation results returned to the identification and registration database, including:
  - Line and register of father
  - Breed

  - Donor number (in the case of ET)
- Pedigree recorded in the identification and registration database
- Pedigree calculated
- System generates accompanying documents on the animal
- Accompanying documents are printed

Official accompanying documents are protected against falsification. The following protection tools are used:

- Printing below eartag number
- QR includes eartag number, date of birth, breed, breed composition, eartag of mother, line-register of father
- Barcode includes eartag number
- On the reverse side – water mark with ICAR logo

Different aspects of identification and eartag logistics

Several methods are used for animal identification consisting of:

- Plastic eartags
- RFID
- Linkage from farm IDs to official IDs

Eartags (incl. duplicates) can be ordered via the IAR system:

- Breeders can only request eartags for animals registered in the ordering system
- Breeders can only order duplicates for animals in a holding

Czech Cattle ID Structure

Except for horses, donkeys and their crossbreds, animal ID numbers contain a unique alphanumeric code with a maximum of fourteen characters

1. The first two letters denote the country of origin, e.g. CZ for the Czech Republic.
2. These letters are followed by nine digits given a unique numeric sequence.
3. The seventh digit is used to identify bovine animals. The eartag must contain the number 0 for males and the number 9 for females, while the last two digits must be identical to the first two numbers of the registration number of the holding the animal was born in.

Practical example of a cattle ID

CZ999999999KKK is the ID number unique to each cow, where

- CZ = country code
- 999999999 = eartag order number

- KKK = sex and region ID of the animal's birth
- Example
  - CZ000141013**962** = female
  - CZ000645137**062** = male
  - **62** = South Moravian region

Eartag issue procedure, eartag logistics

The following four manufacturers are certified to issue cattle eartags in the Czech Republic:

- Czech Moravian Breeders' Corporation, Inc. (prints and issues DATAMARS eartags)
- HEMA MALSICE (provides Allflex eartags)
- DITA (a disabled community production cooperative)
- EUROPACK, Ltd.

The Czech Moravian Breeders' Corporation, Inc. allocates a unique ID to each individual animal and is authorised to sell and issue eartags upon request by breeders and databases. There is a single national identification scheme. All technical aspects relating to the issuing of eartags are overseen by the Czech Moravian Breeders' Corporation, Inc in respect of EU and national legislation. Each animal's identity is visible, unique and never reused. Animal identification devices and methods comply with legislative requirements.

Eartag logistic process

- The entrusted person (Czech Moravian Breeders' Corporation, Inc.) shall ensure that identification means or duplicates thereof are sent to a keeper within 8 working days upon receipt of the request for means of identification or duplicates thereof.
- The entrusted person shall record the date of the request for means of identification or duplicates thereof.
- For keepers of bovine animals, sheep and goats, the entrusted person shall record the identification device allocated to individual keepers for their holdings within a single region, recording the date of allocation and the number of the allocated identification, including numerical sequences for the region and keeper.
- The entrusted person shall provide keepers of bovine animals, sheep and goats a sufficient number of eartags so that within a single region the supply of such identification sets does not exceed the number requested.
- The entrusted person shall record a duplicate means of identification issued for individual animals in the animal register database, recording the date of issue and the sequence number of the specific duplicate.
- Breeder registration in the central registry is verified based on the breeder's written application for the issue of a number range.
- The breeder's use of the eartags is subsequently verified over the course of the year.
- The breeder can only request a limited number of new eartags depending on the number of cows in the herd.

- A particular number range is issued to the breeder depending on region.
- These eartags may not be used by other breeders, with the issued range of numbers and birth data on all animals recorded in the central registry subject to regular inspections.
- The verified order for a new range of numbers is sent to an eartag manufacturer and chosen by the breeder.
- The breeder may choose from four manufacturers.
- Information about the production and issuing of eartags is then sent by the manufacturer to the Czech Moravian Breeders' Corporation, Inc. for data archiving.

Upon receipt of an application for a duplicate, the animal's data are verified in the central registry. It must also be verified that the animal is alive and owned by the breeder who has applied for the duplicate. Duplicate numbers are entered into a duplicate database, with the required duplicate number then issued by a software application. The order generated is subsequently sent to the manufacturer. The duplicate order is assigned Roman digits, with the confirmed set issued to the Czech Moravian Breeders' Corporation, Inc. with the date of production.

Checks carried out to ensure correct animal identification and avoid duplication

The following inspections are key to ensuring correct animal identification:

- Routine checks
- Eartag issue procedure
- The Czech Moravian Breeders' Corporation, Inc. (CMBC) oversees a system of supervision and quality control, with all inspectors serving as employees of the CMBC
- State supervision
- SNP technology used, replaced by STR during the transition period
- DNA analysis and parentage verification are used for:
    - Breeders
    - Czech Breeding Inspection – checks and supervision
    - Performance recording, herd books
    - Bulls, mothers of bulls, fathers of mothers
- Heifer pedigree – harem mating
- Pedigree verification applies to all animals born and recorded within the system
- Plausibility checks are implemented for reproduction, fertility and in identification and registration datbases

Sample identification

Barcodes are used for 100% identification using milk recording vials, while only electronic data capture (PDA) is used during milk recording.

Conclusion

This presentation summarises the key aspects of identification in the Czech Republic in accordance with EU legislation, national legislation and the ICAR Guidelines. The challenge for ICAR going forward will be to improve automation in all areas, but particularly with regard to identification of big herds (1,000 – 2,000 cows) and to design new modern tools to expedite development in this area. ICAR working groups must continue to collaborate on existing multidisciplinary approaches to automation.

A new standard for using official animal identification schemes for livestock animals in RFID applications worldwide

C.G.C.F. Machado[1], C. Schenk[2] and D. Pachoud[3]

[1]Animalltag Tecnologia em Identificação Ltda., Avenida Dom Carmine Rocco 995, 13568120, São Carlos, Brazil
[2]for AEG Identification Systems GmbH, Hoervelsinger Weg 47, D89081 Ulm, Germany
[3]Datamars SA., Via Industria 16, 6814, Lamone, Switzerland

Abstract

The paper gives the concept of the ISO New Work Item Proposal WD 23636. The basic principle is that official animal identification schemes, which are presently in use, shall be applied in future to RFID based systems. The aim is to avoid the introduction of an extra electronic number. The first part describes how the animal numbers allocated on a national basis are converted into an Animal Identification Number (AIN) that is unique worldwide. It is achieved by adding a “header” to the visible number on the eartag. It contains the ISO 3166 country code and a key for the National Encoding Scheme (NES). The Animal Identification Number, is a worldwide unique number, that will be used for all kind of data processing. However it contains as nucleus the number the farmer is familiar with. The second part describes how the Animal Identification Number is stored in the memory of an ISO/IEC 18000-63 transponder. To characterize the transponder, which are used for animal identification an “Application Family Identifier” is introduced. The AIN is encoded in numeric and alphanumeric characters. In the third part the quality aspects of the UHF technology are discussed and test procedures described.

Keywords: animal identification number, ISO/IEC 18000-63 transponder, ISO 11784, WD 23636, UHF

Introduction

This paper gives the concept of the ISO New Work Item Proposal WD 23636. It includes the following parts:

- Part 1 – Animal Identification Number (AIN). A worldwide unique number that will be used for all kind of data processing. It is based on well established visual schemes.
- Part 2 – Encoding of AIN in Short UII in ISO/IEC 18000-63 Transponder.
- Part 3 – Evaluation of conformance of ISO/IEC 18000-63 Transponder. Quality provisions that shall be fulfilled in order to prove the reliability that is achieved with ISO 11785 Transponder. This part is under development.

Part 1 : The Animal Identification Number AIN

Official Animal Identification schemes have been developed in different countries in different ways. These schemes are used for official identification and registration of livestock animals. They are based on government regulations, are standardized and successfully introduced.

Examples of such livestock identification schemes can be found worldwide: Argentina, Brazil, France, Germany, UK, USA, and so on. These systems make use of visual numbering on ear tags and are the backbone for registration, animal movement, tracing diseases, etc.

Increasing international trade of live animals calls for an Animal Identification Number AIN, that is unique worldwide and based on the existing schemes.

The ISO 11784 Standard: “Radio-frequency identification of animals - Code structure” was published 2 decades ago (1996) without giving consideration to the existing visual schemes.

In the meantime technologies for automatic data capture were developed, which allow for larger transponder memory space than the 64 bit required for ISO 11784. This allows to store the more complex, visual schemes directly in an RFID tag

Using the visual IDs on tags would avoid matching to references via networks and data base access.

The task now is to define an Animal Identification Number AIN based on existing visual schemes and accommodate it in an RFID memory. For economic and availability reasons a 128 bit memory is a preferred solution.

To maintain the uniqueness of the individual Animal Identification Number worldwide is a key issue that shall be standardized.

As stated above, the visual systems used for livestock identification differ from country to country. The legal responsibility is with the national Competent Authority. However there is always an official organization, Issuing Organization, that administers these schemes: i.e. assign the individual animal number to the tag, distribute the tags and records them in a data base.

Examples for bovine animals are given in table 1.

In addition a “Retagging Counter” has to be included in the RFID data of the tag. The retagging counter is an important feature for the traceability of livestock animals – in visual tags some countries use different color for the retagged tag.

Table 1. Examples of visual schemes for bovine animals.

Visual scheme, presently used	Number
NUES 9 (USA, APHIS)	23 ELV 4574
VVO (Germany :Viehverkehrsverordnung)	DE 03 487 70062
SISBOV (Brazil, 2017)	105 51 000001234 5

Procedure

In order to identify the different visual schemes, they have to be translated into a worldwide unique message: the Animal Identification Number (AIN). It is composed of two elements:

- AIN Header, and
- AIN Body.

The message will start with an AIN Header that characterizes the origin of the used scheme. The AIN Header contains the following information:

- Country of the Issuing Organization (NCC = Numeric Country Code).
- National Encoding Scheme (NES) - e.g. according to different species.

It is followed by the AIN Body. The AIN Body contains the following information:

- The Retagging Counter
- A string of alpha numeric characters representing the visual scheme

Such data construct may be used for different high-capacity automatic data capture (ADC) media like RFID according to ISO 18000-63, ISO 18000-M3, NFC, ISO 14223, or optical 2D codes.

The usage in optical codes can rationalize the work with animal passports and documents considerably.

Animal Identification Number AIN

The basis are the visual schemes, administered by Issuing Organizations, which act on governmental regulations.

They are responsible for the unicity of the individual animal number in the relevant country. To relay on that unicity is a key to the new Standard.

Examples of issuing organizations are:

- USA
  Animal and Plant Health Inspection Service (APHIS)
- Germany
  Bundesministerium für Ernährung, Landwirtschaft und Verbraucherschutz
- Brazil
  Secretaria de Defesa Agropecuária (SDA/MAPA)

In practice they delegate the task of administration of the animal numbers to sub entities. These entities are responsible for ordering and distribution of the tags. For example in Germany this is mainly done by the so called LKV (Landes Kontroll Verband) for bovine animals.

Header of the AIN message

In order to keep the unicity of the national animal number on a worldwide level, the origin of the animal number has to be shown. To achieve this target an AIN header is put up in front. It is composed by the following elements:

- Numeric Country Code (NCC) according to ISO 3166;
- National Encoding Scheme (NES) allocated by the Registration Authority.

Numeric Country Code (NCC)

NCC represents the Numeric Country Code and is 10 bits in length. The numbering of NCC is according ISO 3166. The NCC is responsible for maintaining the unicity of the national animal number on a worldwide level.

Examples of NCC are:

- 840 – USA
- 276 – Germany
- 076 – Brazil

National Encoding Schemes (NES)

NES represents the National Encoding Schemes and is 6 bits in length, allowing 64 schemes for each country. According to the country for each species there are different schemes in use (e.g. bovine, swine, caprine). Examples for National Encoding Schemes in the USA are:

- NUES 9 for cattle
- NUES 8 for sheep and swine
- Flock-based number
- Location-based number

Each scheme has to be identified by a key number (NES).

The competent authority, that wants to make use of this Standard has to apply for the National Encoding Schemes (NES) for the different species.

The NES key numbers will be allocated by a Registration Authority (e.g. ICAR) and public access of the allocation has to be guaranteed.

A NES was reserved for non official schemes and tests (NES = 63). It is mandatory to store the country code of the country where the test are performed.

The following keys for NES will be pre-defined in the Standard:

00	NES for official schemes with 64 bits representation without specie definition. The AIN body carries an ISO 11784 type number. This means the 64 bits are allocated as described in ISO 11784. Using an ISO 11784 structure is allowed only with a country code in the AIN header. ISO 11784 numbers containing a manufacturer code instead of Country Code is not allowed.
01..62	NES for official schemes with 16-character alphanumeric representation.
63	NES for unofficial schemes with 16-character alphanumeric representation. In this case the body contains a number wich does not belong to an official scheme and is used in a limited area only. Examples are test transponder or transponder used for farm management or scientific purposes. The transponders using NES = 63 can be reused. Using this key the uniqueness is not guaranteed.

Body of the AIN message

The AIN Body is composed by the retagging counter and the visual number of the animal. The Retagging counter is 1 digit in length and is numeric format. The Visual number of the animal is alphanumeric and the length may vary depending of the technology of the tag used.

Examples of the AIN Body are:

- “0” “23 ELV 4574” – USA
- “1” “DE 03 487 70062” – Germany
- “1” “105 51 0000012345” – Brazil

Composition of the Unique Animal Number (AIN)

NCC,NES,R,PPPPPPPPPPPP
where

- “NCC” is 10 bits Country Code according ISO 3166,
- “NES” is the National Encoding Scheme registered and maintained by the Registration Authority,
- “R” (n1) is the retagging counter
- “PPPPPPPPPPPP” (an12) is the visual animal number

Some examples the data construct for different countries are shown below.

AIN for United States of America

The Issuing Agency that is responsible for identification of bovine animals is Animal and Plant Health Inspection Service (APHIS). This organization has introduced the NUES 9 and the AIN(US) scheme for bovine animals.

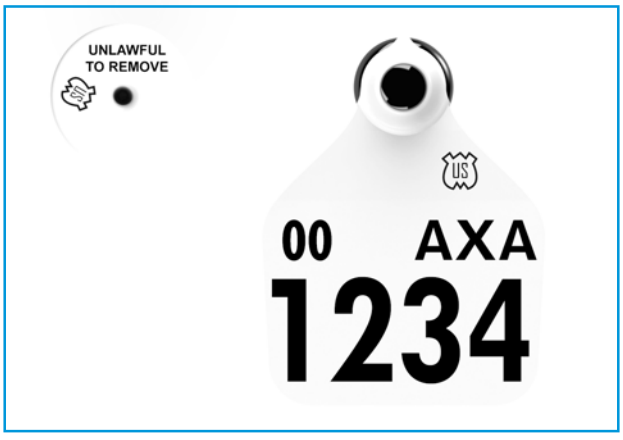


Figure 1. NUES 9 official ear tag.

Table 2. Data construct for encoding the unique animal number from NUES 9.

AIN Header		AIN Body	
NCC	NES	Retagging counter	Animal ID
840	01	0	"00 AXA 1234"

Table 3. Details of data construct for encoding the unique animal number from NUES 9.

Description	Data	Lenght	Type	Remarks
NCC	840	10 bits	Numeric	Country Code according to ISO 3166.
NES	01	6 bits	Numeric	e.g. for NUES9.
Retagging counter	0	1 digit	Numeric	"0" represents the original tag issued and "1" is the first retagging.
Visual number	00 AXA 1234	-	Alphanumeric	Unique animal number as given in the visual scheme. Same as visual animal number.

There is a further scheme used in the US. It is managed by *Animal Identification Number Management System* (AINMS or sometimes shortened to just AIMS) that is used to allocate groups of 840 numbers to approved tag manufacturers.

The AIN(US) starts with 840 (the first three digits are the Country Code for USA) followed by a string of 12 digits. As the AIN(US) always starts with 840 we have a redundancy with the NCC in the AIN Header.

There are 2 options to encode the AIN(US):

- If there is no species information required AIN may use the 64-bit representation of ISO 11784. It includes the country code from bit 17 to 26 and the 12 digit individual animal number from bit 27 to 64 (National Identification Code). In this case the NES shall be "00" and the AIN body will contain 64 bit, or
- If a species information has to be included a different NES has to be allocated. In such a case Aphis has to apply for a new NES (for example "02") for bovine animals containing the visual data, which is a 3 digit country code and the 12 digit individual animal number.

The figures of the AIN(US) scheme will be included in the AIN as reported in table 4 and table 5.

The Competent Authority will have to decide which way to go.

Part 2 : Encoding of AIN in Short UII in ISO/IEC 18000-63 transponder

The aim of the present Part 2 of the standard is to accommodate the AIN in the Short Unique Item Identifier (Short UII) memory format of an ISO/IEC 18000–63 transponder. For economic and availability reasons a 128 bit memory is a preferred solution.

Table 4. Data construct for encoding the unique animal number from AIN(US).

AIN Header		AIN Body	
NCC	NES	Retagging counter	Animal ID
840	00	-	0x8000D200BA2C2B15HEX
840	02	0	"840 003 123 456 789"

Table 5. Details of data construct for encoding the unique animal number from AIN(US).

Description	Data	Lenght	Type	Remarks
NCC	840	10 bits	Numeric	Country Code according to ISO 3166.
NES	00	6 bits	Numeric	64-bit representation of ISO 11784 structure.
Retagging counter	-	-	-	Not applicable.
Visual number	840 003 123 456	64 bits	Numeric	Unique animal number as given in the visual scheme. According with ISO 11784.

Essential features are the introduction of an Application Family Identifier (AFI) and the URN Code 40 encoding rules.

When using ISO/IEC 18000-63 transponders for animal identification, the AIN shall be stored in the UII memory.

General tag features

ISO/IEC 18000-63 transponders have what is known as a segmented memory structure, where four different memory banks are supported and separately addressable. Using binary notation, the memory banks (MBs) are:

- MB00 : RESERVED – for access and login passwords,
- MB01 : UII – for the Unique Item Identifier,
- MB10 : TID – for tag identification (TID), and
- MB11 : USER – for additional user data.

The Memory is organised in a 16-bit word unit for commands to read and write the data. In this concept the UII shall be limited to 128 bit for commercial reasons. Its content is given in Table 6 and Figure 2.

Figure 2. Logical Memory Map as per ISO/IEC 18000-63.

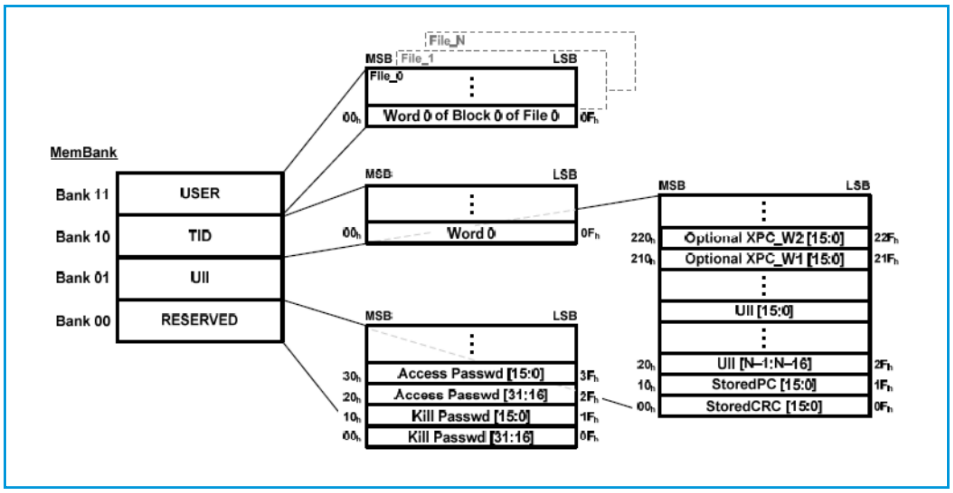


Figure 2. Logical Memory Map as per ISO/IEC 18000-63.

Table 6. Structure of the 128 bit memory UII.

Memory name	Lenght (bits)	Start in (MB 01)	End at (MB 01)
DSFID	8	20_{HEX}	27_{HEX}
AIN Header - NCC	10	28_{HEX}	31_{HEX}
AIN Header - NES	6	32_{HEX}	37_{HEX}
AIN Body	96	38_{HEX}	97_{HEX}
CRC	8	98_{HEX}	$9F_{HEX}$
Total	128		

Structure of MB 01

This memory bank contains the UII and associated syntax.

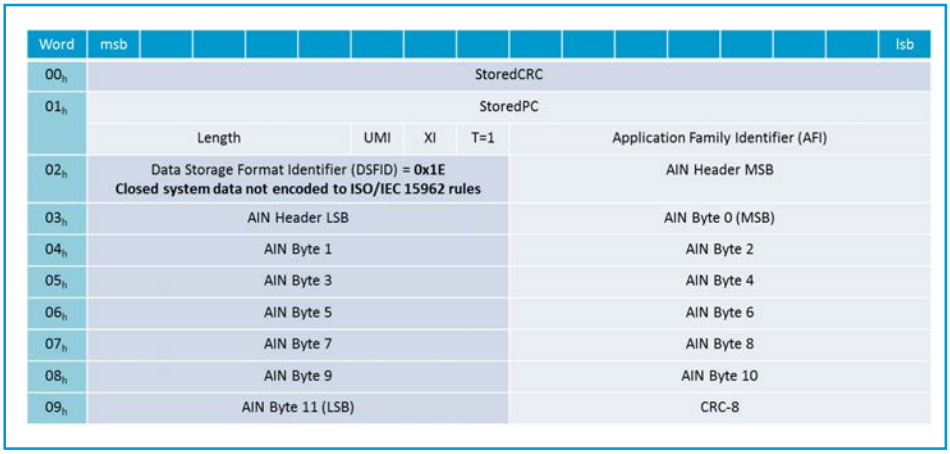
The first word contains a stored CRC-16 (“StoredCRC”). This is automatically generated each time the the tag is power-cycled as per ISO/IEC 18000-63.

The second word contains a Protocol Control word (“StoredPC”) defining among others the length of the UII and the AFI whose value is defined under the authority of ISO.

Figure 3 below illustrates the complete MB01 memory structure for this standard.

AFI

To define an ISO/IEC 18000–63 tag as assigned for animal identification only, an Application Family Identifier (AFI) shall be implemented according to ISO 15962. The AFI is used in UHF and HF RFID technologies to differentiate transponders programmed for the desired application from transponders programmed for other applications that are not relevant for the application in question. This differentiation will accelerate the processing due to a reduced number of tags being considered.



Word	msb														lsb
00_h	StoredCRC														
01_h	StoredPC														
	Length					UMI	XI	T=1	Application Family Identifier (AFI)						
02_h	Data Storage Format Identifier (DSFID) = **0x1E** **Closed system data not encoded to ISO/IEC 15962 rules**								AIN Header MSB						
03_h	AIN Header LSB								AIN Byte 0 (MSB)						
04_h	AIN Byte 1								AIN Byte 2						
05_h	AIN Byte 3								AIN Byte 4						
06_h	AIN Byte 5								AIN Byte 6						
07_h	AIN Byte 7								AIN Byte 8						
08_h	AIN Byte 9								AIN Byte 10						
09_h	AIN Byte 11 (LSB)								CRC-8						

Figure 3. MB 01 Memory Map used by this ISO NWIP.

UII

Encoding and decoding needs to be invoked for complete 16 bit words. The UII is composed of 128 bits. The UII shall contain:

- A Data Storage Format Identifier (DSFID)
- An Animal Identification Number (AIN) , composed by:
  - AIN Header, and AIN Body, that is the Retagging Counter digit plus the Visual IDentification number, as defined in Part 1 .
- CRC 8

The complete structure of the UII is shown in Table 6 and Figure 4 below.

AIN body

AIN body is defined in Part 1. For ISO/IEC 18000-63 RFID tags the UII is 96-bit lenght. If the AIN body has less than 96 bit padding with zero is required.

CRC 8

A CRC-8, resulting from the UII memory. CRC-8 is enough to protect data lengths up to 248 bits. Hence it is suitable to fit the 128 bits memory of the UII memory

URN Code 40

The AIN Body including the Retagging Counter digit in an ISO/IEC 18000–63 transponder must be encoded via URN Code 40.

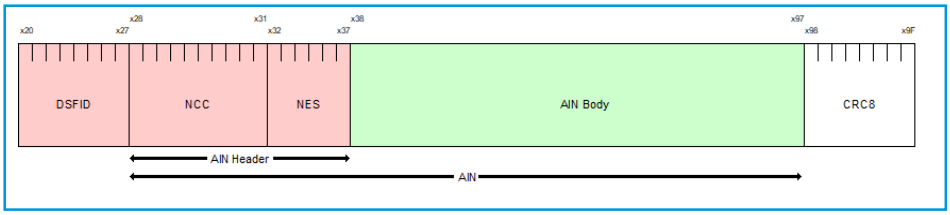


Figure 4. Structure of the 128 bit memory UII.

The URN Code 40 coding stores 3 alphanumeric characters in 16 bits. Applying this code to a memory section (AIN Body) of 96 bits, allows to store 18 alphanumeric characters.

The DSFID, AIN Header and the CRC8 are not encoded via URN Code 40.

By using the URN Code 40 encoding, the last alphanumeric of the string shall be a PAD character. This information will be used by the reader to determine the end of the visual identification number, so we have 17 alphanumeric characters as maximum lenght of the visual identification number.

Use of UHF (Ultra High Frequency) RFID technology in the data capture, traceability and monitoring interface in the official cattle animal identification program

J. Gomes[1] and M. Shimizu[2]

[1] ALLTAGS Solutions in Animal Identification, São Paulo, Brazil
Corresponding Author: .jorge@alltags.com.br
[2] HLA – Hana Latin América, São Paulo, Brasil
Corresponding Author: mshimizu@hanalatinamerica.com

Abstract

The use of radio frequency RFID devices is already widespread in animal identification. The need to adopt new, more flexible and efficient technologies is part of the demand by technicians, farmers, government entities and food companies. Innovative Ultra High Frequency (UHF) technology is a viable alternative, considering its applicability, flexibility and use efficiency in line with good production practices in the food chain.

In 2013, the State of Mato Grosso do Sul, Brazil, in order to maintain and expand its sanitary status at OIE - World Organization for Animal Health, implements a Zone of High Surveillance - ZAV in the regions bordering Paraguay, Argentina and Bolivia. This zone establishes an area of approximately 12,000 km², encompassing 13 municipalities. To guarantee the inventory of animals, control of movement and monitoring of sanitary procedures, the state government establishes the use of individual and inviolable eartags with RFID - UHF technology laser printed with official numbering provided by MAPA - Ministry of Agriculture and Livestock.

Mobile collectors with an internal UHF RFID antenna were used with the ability to read and record electronic eartags information, linking it to the GPS coordinate (Global Position System), data transmission via mobile telephone network using GSM / GPRS technology, and centralizing the storage of data and information in an official database; provided an effective tool for the traceability and individual monitoring of ZAV animals. In addition, the official system of issuing the animal transit guide - GTA, as well as the fiscal documentation for the movement of the animals in the same collector was implemented, thus generating agility and safety in official controls. In the implementation of this project, more than 1,000,000 bovines were identified, thus confirming the viability and efficiency of this technology for animal identification.

Introduction

After an outbreak of foot-and-mouth disease in Mato Grosso do Sul in 2005, and in compliance with the actions advised by the World Organization for Animal Health (OIE), a High Surveillance Zone - ZAV in the border regions between Brazil, Paraguay, Argentina and Bolivia was created resulting of the recommendations made by said organization. This sanitary region covers an area of approximately 12,000 km², involving 13 (thirteen) MS counties, as shown in figure 1.

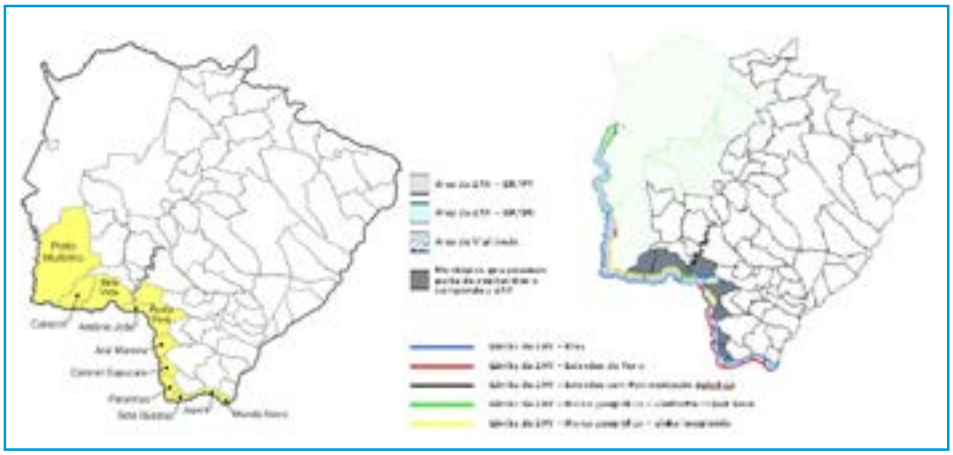


Figure 1. High Surveillance Zone of Mato Grosso do Sul.

The implementation of the ZAV denoted the establishment of an area to strengthen the animal health surveillance system, including the implementation of specific activities such as: individual identification of animals susceptible to foot-and-mouth disease; georeferencing of rural properties; intensive control of animal movement; vaccination against foot-and-mouth disease under the supervision of the official veterinary service throughout the livestock holding, and the direct execution of it, and the intensification of the inspection of the existing livestock holding.

Materials and methods

In this project, a double identification with an inviolable eartag and botton was used, also with RFID - UHF technology, operating between 860 - 960 Mhz, with ISO / IEC 18000-6C protocol (EPC Gen2). The earytags and bottons were laser marked with the official numbering of SISBOV - Brazilian System of Individual Identification of Bovines and Buffaloes, and the activation of the chip was given with the same number as the SISBOV.

Data collection and transmission of information was performed using a HIT 731 collector, which has an integrated UHF reader / antenna, numeric keypad, thermal printer, GPS, and GSM / GPRS / Wi-fi modem; which is accessed through a Smartcard, provided to each producer, and to the technicians involved in the project. Each Smartcard was customized for each user, according to their access permission.

All the information collected was transmitted to an official central system, SIRMA - Integrated Animal Traceability and Monitoring System, which interfaces with the official health system, where it is possible to issue animal transit guides (GTA), as well as to the Secretariat of the State Treasury, thus allowing the issue of the invoices of the animals.

At the time of identification of the animal, the information of the animal's sex, breed, age and owner were recorded on the eartag chip and then sent to SIRMA.

Subsequently, all information on official vaccination, surveillance, and movement was performed on the HIT 731 collector, updating the SIRMA database.

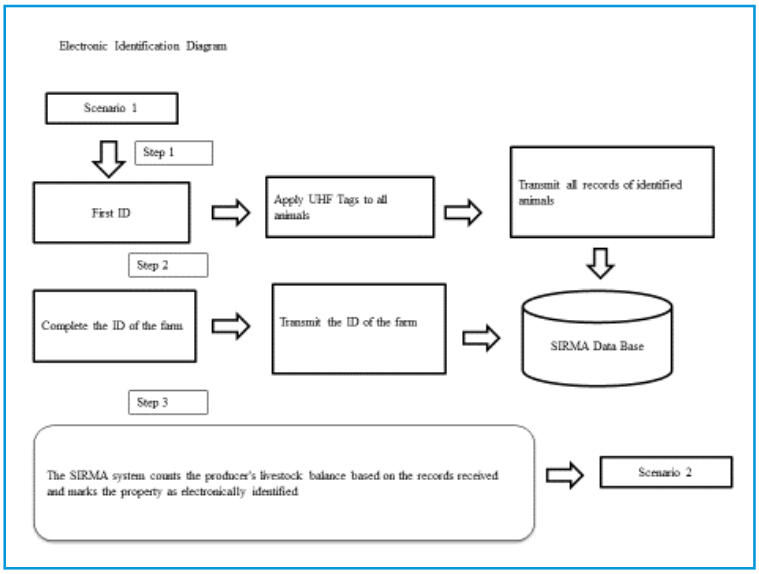


Figure 2. Eletronic Identification Diagram – Scenario 1.

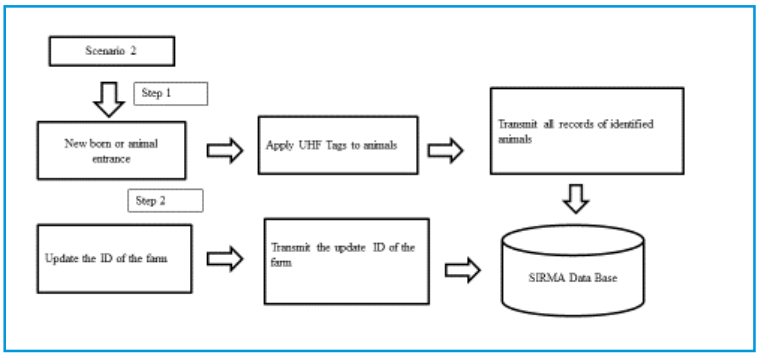


Figure 3. Eletronic Identification Diagram – Scenario 2.

At the beginning of the identification of the animals in the ZAV, the estimated bovine herd was 776.730 animals.

The animal identification work began in October 2013 and ended in September 2017 when it presented the following inventory of live animals in the SIRMA database.

During the 4 years that the identification project was executed, more than 1,000,000 animals were identified electronically.

Conclusion

The animal identification project in the ZAV with the use of UHF-RFID technology demonstrated the technical and operational capacity of this solution in the identification, monitoring and processing of animals, in a safe, efficient and viable way.

Table 1. ZAV Herd - June 2013.

County	Farms	Bovine herd (heads)
Antonio João	336	89.630
Aral Moreira	230	23.350
Bela Vista	901	163.640
Caracol	83	59.840
Coronel Sapucaia	176	46.580
Corumbá	779	22.170
Japorã	570	40.530
Ladário	3	150
Mundo Novo	582	31.170
Paranhos	295	61.060
Ponta Porã	2.721	44.130
Porto Murtinho	265	129.020
Sete Quedas	293	65.460
ZAV Herd	7234	776.730

Table 2. ZAV Herd - September 2017.

County	Bovine herd (heads)
Antonio João	111.851
Aral Moreira	36.119
Bela Vista	103.962
Caracol	70.044
Coronel Sapucaia	85.080
Corumbá	39.881
Japorã	57.842
Ladário	562
Mundo Novo	40.888
Paranhos	60.484
Ponta Porã	50.188
Porto Murtinho	121.175
Sete Quedas	82.304
ZAV Herd	860.380

The UHF-RFID technology allows important advances in the storage of data in the tag, since it has enough memory to store basic information of the animal, besides being more flexible in the reading possibilities.

New advances must be made in the implementation, standardization and regulation of the use of UHF-RFID technology in the identification of animals.

Alternated milk recording – recalculation, results and conclusion for future test planning

K. Kuwan

Vereinigte Informationssysteme Tierhaltung w.V. (vit), Heinrich-Schröder-Weg 1, 27283 Verden, Germany
Corresponding Author: Kai.Kuwan@vit.de

Abstract

Alternating test methods have been offered as an alternative to the standard method for more than 20 years in Germany. A periodic review of correction formulas for milk yield, fat (and protein) is necessary. For test planning it is important to get representative data for the population where the new model should be used. Especially milking interval, herd size should be analyzed before to get a good overview. To get valid data for the milking interval it is useful to extend the test sampling over three or four milking times.

For validation it is necessary to split the data randomly. Two thirds of the data should be used to estimate new formulas. The remaining data should be used as an independent data set to validate the new estimated formulas.

To exclude implausibly data is difficult and needs a lot of experience.

Keywords: Kuwan, alternated milk recording, test planning, validation.

Introduction

Driven by costs for DHI services, problems to require staff for DHI and retention against owner based milk recording, alternated milk recording was introduced in germany in the late 90's.

To develop an own model dedicated and high motivated farmers participated at a large field study. For a period of one year separate samples from every milking time were taken and analyzed. All milk yield from morning and evening milking were separately stored for this research. As the result of this research Liu *et al* published in 2000 a method which also became part of the ICAR guidelines. With the introduction of this method into practice a very controverse discussion about accuracy, comparability of results and the influence of calculating breeding values starts. It ends up that during the first few years alternated milk recording was not allowed for herdbook farms. Nevertheless the proportion of alternated milk recording increased rapidely through the following years up to twenty-five percent. Since 2010 the amount of alternated milk recording is constant in Germany between 24 – 26 % of farms (19 – 20 % of cows).

Based on milk yield from single milkings which were collected with electronic devices on farms with standard methode during the years, in 2006/2007 the formulas for milk yield were recalculated easily. This new formulas for milk yield were introduced into

practice in 2008. The complaints about dubious results for fat and protein content have increased in recent years. New formulas for the calculation of fat (and other ingredients) were also necessary.

Development of DHI farms in the north west and east part of Germany

Table 1 shows the development of the DHI farms over the years from 1995 to 2018. Because of the former historical development the table is divided in two parts, the northwest region with more family based farms and the east part of Germany with much bigger farms based on cooperatives.

As expected and typically for central Europe the number of farms has decreased dramatically. In total the number of farms has fallen by almost more than 60 percent. The slightly decrease of number of cows is influenced by the European milk market policy. While the number of cows per farm in East Germany has risen by 50 percent, it has tripled in the northwest part of Germany.

Over time and both regions we have an increase of milk yield (~ 3.000 kg), a decrease of fat content

(~ 0,38 % point) and a stable protein content. The changes in the ratio milk yield and ingredients may possibly influence the correlations between them. This could be one reason for the complaints about dubious results for fat and protein content. Also large herds mean more employed staff and a changing in milking intervals. In comparison to the data of 1995 the average milking interval between evening and morning milking is more than 20 minutes shorter and we have a higher number of farms now that have milking intervals of 12 hours. This we took into account during test planning.

Test planing

To estimate new formulas we preselected 135 farms with different milking interval and different herd size. The total number of cows was 20,810.

During the test period of three month every four weeks samples were taken at every milking time on two consecutive days starting with the evening milking. This gives us the opportunity to calculate three daily milk yields.

1. Evening milking – Morning milking (First day)
2. Morning Milking – Evening milking (Mix out of first and second day
3. Evening Milking – Morning milking (Second day)

We derive a set of formulas, each formula is estimated for a special situation of the relevant cow and takes into account:

- Herd based milking time (evening/morning).
- Herd based milking interval (8 classes).
- Cow individual lactation (first and higher).
- Cow individual days in lactation (7 classes of 60 days, last class open).

For validation we used a set of 700.000 milkings, collected in Schleswig-Holstein with lactocorder. There we got evening and morning milk yield, two separated sample and for every cow the individual milking time in the evening and the morning.

Table 1. Development of DHI farms

	Northwest Germany						East Germany					
Year	Nr farms	Cows	Cow/farm	Milk kg	Fat %	Protein%	Nr Farms	Cows	Cow/farm	Milk kg	Fat %	Protein %
1995	29.462	961.223	33	6.908	4,27	3,33	4.764	948.510	199	5.702	4,44	3,48
2000	23.686	930.044	39	7.674	4,25	3,38	4.404	850.044	193	7.388	4,26	3,46
2005	18.751	924.470	49	8.118	4,17	3,41	3.794	780.480	206	8.362	4,09	3,42
2010	13.474	814.705	60	8.619	4,13	3,40	3.073	718.806	234	8.900	4,07	3,39
2015	12.797	1.042.037	81	8.705	4,05	3,39	2.496	747.422	299	9.404	3,97	3,38
2018	10.799	1.046.752	97	9.106	4,00	3,42	2.072	672.056	324	9.750	3,93	3,41

Results and conclusion

At first we used the validation data set to check the sequence the cows are milked at the test day. The mean correlation was 0,8 with a wide variation. Farms with tied cows had a correlation near 1.

Particularly bigger herds with milking groups had less correlation (depending on group size and group sequence of milking). In praxis there is less chance to verify the information about the previous milking time and the sequence the cows are milked.

The results of the new formulas are different to the results of the old formulas but show better accordance for cows with high milk yields. More milking interval classes represent better the real situation on farms in germany. The new formulas are used since January 2019 and we have a subjectively smaller saw-tooth-effect for milk yield and fat when changing the milking time (evening/morning) from one testday to the other. Subjectively we also have less reclamation of farmers for unlikely results, after implementing the new formulas.

A correct estimation for extrem yields (for example 10 kg in the evening – 40 kg at the morning milking) is not possible.

It is not appropriate to use more information for derivation of formulas as later in routine application available.

An estimation of formulas every 5-8 years is necessary. Especially if there is a significant increase in average yields or a significant change in correlations between milk yield fat or protein content.

We need data from representative herds, i.e. herds in which we adopt the estimated formulas later.

Data for calculation should cover all environmental subgroups resulting potentially in different formulas, i.e. breeds, regions, milking intervals, lactations, etc.

The dataset should be large enough for splitting into a learning/estimation sample (2/3) and a validation sample (1/3). For estimation the minimum number of observations per subclass should be >1000 (better 2000).

24-hour yield calculations in the Finnish milk recording

J. Kyntäjä[1] and S. Nokka[2]

[1]Mtech Digital Solutions, PL 25, 01301 Vantaa, Finland
Corresponding Author: juho.kyntaja@mtech.fi
[2]Association of ProAgria Centres, PL 251, 01301 Vantaa, Finland

Summary

This paper describes the current status with 24-hour yield calculations in the Finnish milk recording system, as well as the historical reasons behind the choices made. The results of each method are also shortly analysed. The methods are found to be working reasonably well, but not perfectly.

Keywords: milk recording, robotic milking, 24-hour yield calculation

Introduction

In the Finnish milk recording, owner sampling has been common practice since the 1980's, and appr 95% of all herds now record by that method, with their own private recording equipment. At the same time, 90% of all samples are reportedly taken from one milking only. Farmers are also responsible for some 90% of milk recording data capture. In September 2019, 40.0% of all recordings during the previous rolling 12-month period came from automatic milking. This article presents the 24-hour yield calculation methods currently in use.

Historical overview

Up until 2003, the only available sampling method in Finland was proportional sampling. 24-hour yields were simply calculated by adding up milk weights and using the analysed values as they come.

This approach, however, started to be problematic due to three main reasons. Firstly, in a farmer-recording system it became evident that many samples were in fact not exactly proportional between the evening and morning milkings. Secondly, the results showed that a number of farmers were taking samples from one milking only. And the third reason was the advent of automatic milking which made it impossible to continue the old way.

For these reasons, it was decided to allow one-milking sampling starting April 2003.

Currently used methods

In traditional milking systems, milk weights are measured at two consecutive milkings (or three, if the cows are milked thrice per day). Some 10% of all herds claim to take proportional samples, and no correction is applied to their laboratory analyses. For fat content in one-milking samples from traditionally milked herds, the Delorenzo and Wiggans (1986) correction is applied with the received factors.

In automatic milking systems, the milk weights are collected during a 96-hour period and these results are used for calculating a 24-hour yield for each cow (Lazenby *et al*. 2002). In this calculation, the preceding intervals are taken into account to adjust to uneven individual cow measurement periods.

The fat and protein yields, however, are estimated on the basis of a one-milking sample, using data of only two preceding milkings (Peeters and Galesloot 2002). This method was also tried for milk weights but some herds with irregular cow traffic had a lot of problems with that, so the approach was changed in 2016. Also, the original Peeters & Galesloot method was found to produce slightly underestimated fat contents when compared to dairy deliveries, so in 2017, the method was updated by the corrections suggested by Roelofs *et al*. (2006), adding factors like stage of lactation, parity, and hour of the day to the equation.

Evaluation of current methods

To evaluate how the methods are working, a very simple comparison was made with average

24-hour yields produced by each method. The results for the whole Finnish dairy cow population are shown in table 1. In general, the differences between the methods are small.

However, we notice here that the calculation does not entirely cover the difference between fat contents in morning and evening milk. The correction factors used are already 33 years old, and are based on data from a significantly lower yield level. Typical Finnish feeding also produces high milk fat contents which is maybe not entirely in keeping with the data used for making these formulae.

Automatically milked cows also tend to obtain a lower 24-hour fat content than cows from conventional milking systems. This was presumed to be due to higher milk yield, but due to the fact that the automatic milking herds have a significantly higher proportion of Holsteins, the results were recalculated for Holstein breed only (Table 2). Here the difference between morning samples and samples from automatic milking was slightly smaller.

Table 1. Corrected and recorded 24-hour averages by method, all cows.

		Average result			
Sampling scheme	Nr of samples	Milk, kg	Butterfat, %	Protein, %	Cell count
One-milking sample (Z), milking time 4-10 AM	255,461	29.8	4.30	3.58	157
Z sample, milking time 2-8 PM	309,974	30.2	4.51	3.61	187
Proportional (P) sample	112,620	29.6	4.41	3.61	167
Z sample, automatic milking	370,908	33.4	4.23	3.56	214

Table 2. Corrected and recorded 24-hour averages by method, Holstein cows only.

Sampling scheme	Nr of samples	Average result			
		Milk, kg	Butterfat, %	Protein, %	Cell count
One-milking sample (Z), milking time 4-10 AM	116,009	31.3	4.17	3.52	161
Z sample, milking time 2-8 PM	142,204	31.9	4.36	3.56	184
Proportional (P) sample	45,191	31.4	4.25	3.55	167
Z sample, automatic milking	231,346	34.8	4.14	3.52	216

Conclusions

The current 24-hour calculation methods are performing on a satisfactory level. However, it seems that there could be some advantage in recalculating the historical fat correction factors to make the obtained estimates more accurate.

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Global 24-hour calculation trends in automatic milking systems

P. Bucek[1], X. Bourrigan[2], K. Kuwan[3], J. Kyntäjä[4], Y. Lavon[5], F. Reinhardt[3], F.J. Auer[6], B. Dokkebakken[7], K. Haase[8], C. Trejo[9], D. Radzio[10], F. Miglior[11], E. Barras[12], Jere High[13], G. Jóhannesson[14], M. Fioretti[15], Nils-Erik Larsson[16], T. Roalkvam[17], G. Augier[2], Ch. Lecomte[2], C. Lizana[9], F. Rapaioli[18], S. Alday[19], O. Kachanova[20], A. Braun[21], R L Bhagat[22], A B Pande[22], Erna Galvanovska[23], D. Lodina[23], An Pengpeng[24], Sun Xianzhi[24], R. van der Linde[25], A. Pentjärv[26], A. Martins[27], J. Carvalheira[27], U. Lauritsen[28], C. N. Costa[29], B. Coughlan[30], D. Marta[31], P. Rosincinova[31], J. van der Westhuizen[32], A. Coburn[33], R. Cantin[34], J. A. Horst[35], M. Séguin[36], M. Jesús[37], F. Sotelo[38], Á. Kenéz[39], L. Dégen, [40]G. Alain, Bularca Ioan Raul[41], R. Mircea Catalin[41], J. Mathie[42], Z. Ivkic[43], Jianbin Li[44], B. Perisic[45], N. Nayee[46], R.O. Gupta[46], S. Sievert[47], S. Gilheany[48], V. Tytenko[49], G. Fedorova[20], M. Klopcic[50], D. Hambrook[51], ACHA[52], G. Gery[40], R. Fourdraine[33], S. Pinto[27] and D. Snidall[42]

[1]Czech Moravian Breeders' Corporation, Inc., Benesovska 123, 252 09 Hradistko, Czech Republic
[2]France Genetique Elevage, 149, rue de Bercy, 75595 Paris, France
[3]vit (Vereinigte Informationssysteme Tierhaltung w.V) IT-Solutions for Animal Production, Heinrich-Schroeder-Weg 1, 27283 Verden, Germany
[4]Mtech Digital Solutions (ProAgria Group), PO Box 25, 1301 Vantaa, Finland
[5]Israel Cattle Breeders Association, P.O. Box 3015, 38900 Caesaria Industrial Park, Israel
[6]LKV Austria Gemeinnützige GmbH, Dresdnerstraße 89/19, 1200 Vienna, Austria
[7]Minnesota DHIA, 307 Brighton Ave So, 55313 Buffalo, USA
[8]NorthStar Cooperative, P.O. Box 23157, 48909 Lansing, USA
[9]COOPRINSEM, Ramon Freire 980, Osorno, Chile
[10]Polish Federation of Cattle Breeders and Dairy Farmers, 00-515 Warsaw, Poland
[11]Ontario Genomics | MaRS Centre – West Tower, 661 University Ave, Suite 490 Toronto, ON M5G 1M1, Canada
[12]ASR-Switzerland, Schützenstrasse 10, 3052 Zollikofen, Switzerland
[13]Lancaster Dairy Herd Improvement Association, 1592 Old Line Road, 17545 Manheim, USA
[14]The Icelandic Agricultural Advisory Centre, Austurvegur 1, 800 Selfoss, Iceland
[15]Associazione Italiana Allevatori (A.I.A.), Via G. Tomassetti 9, Rome, Italy
[16]Växa Sverige, Box 288, 75105 Uppsala, Sweden
[17]TINE SA, Lakkegata 23, N-0187 Oslo, Norway
[18]Asociación Colombiana de Criadores de Ganado Simmental, Simbrah, Simmcebú y sus Cruces, Calle 85 19C 12OFC 101, Bogota, Colombia
[19]Spanish Holstein Confederation, Carretera de Andalucia KM 23,600, 28320 Pinto, Spain
[20]Plinor Ltd, Russia
[21]CONVIS S.C., Zone artisanale & commerciale, 4, L-9085 Ettelbruck, Luxembourg
[22]BAIF, Development Research Foundation, India
[23]Agricultural Data Centre, Republikas sq. 2, LV1010 Riga, Latvia
[24]Shanghai Dairy Cattle Breeding Center Co., Ltd, 10th Building, 1518 West Jiangchang Rd. Shanghai, China
[25]CRV B.V., Wassenaarweg 20, 6843 NW Arnhem, Netherlands
[26]Eesti Põllumajandusloomade Jõudluskontrolli AS, F. Tuglase 12, Tartu, Estonia
[27]ANABLE, Quinta da Medela – Verdemilho, 3810-455 Aveiro, Portugal
[28]RYK, Agro Food Park 15, DK-8200 Aarhus N, Denmark
[29]Embrapa Dairy Cattle, Rua Eugenio do Nascimento 610, Juiz de Fora, Brazil
[30]ICBF, Ireland

[31]The Breeding Services of the Slovak Republic, S.E., Starohajska 29, Bratislava, Slovakia
[32]South African Stud Book and Animal Improvement Association, 9300 Bloemfontein, South Africa
[33]AgSource, USA
[34]CanWest DHI, Canada
[35]Associação Paranaense de Criadores de Bovinos da Raça Holandesa, Rua Professor Francisco Dranka, 608, Curitiba – Paraná, Brazil
[36]Valacta, Sainte-Anne-de-Bellevue, Canada
[37]Asociación Nacional de Criadores de Ganado Vacuno Selecto de Raza Parda, C/ Profesor Xaime Andrés, 15-B, 24007 León, Spain
[38]Instituto Nacional para el Control y el Mejoramiento Lechero, Uruguay
[39]Állattenyésztési Teljesítményvizsgáló Kft (Livestock Performance Testing LTD), Dózsa György út 58, H-2100 Gödöllõ, Hungary
[40]Association wallonne de l'élevage asbl, Champs Elysées 4, 5590 Ciney, Belgium
[41]Cattle Breeders Association Baltata Romaneasca Simmental Type, Mihai Viteazu Street, No. 382, Harman-Brasov, Harman, Romania
[42]Cattle Information Service, Speir House, Telford, TF3 3BD, UK
[43]Croatian Agricultural Agency, Ilica 101, Zagreb, Croatia
[44]Dairy Cattle Research Centre of Shandong Academy of Agricultural Sciences, No.159, Gongyebei Road, Ji'nan, China
[45]Laboratory for milk quality control, Faculty of Agriculture, University of Novi Sad, Trg Dositeja Obradovica 8, 21000 Novi Sad, Serbia
[46]National Dairy Development Board, Anand, India
[47]National DHIA, 53718 Madison, USA
[48]National Milk Records PLC, Fox Talbot House, Greenways Business Park, Bellinger Close, SN15 1BN Chippenham, UK
[49]State Enterprise Agency of Animal Identification and Registration, 4119, Kyiv, Ukraine
[50]University of Ljubljana, Groblje 3, Domzale, Slovenia
[51]Royal Jersey Agricultural & Horticultural Society-Royal Jersey, Showground Milk Records La Route de la Trinite JE3 5JP Trinity, Jersey, Channel Islands
[52]ACHA. Asociación Criadores de Holando Argentino, Laprida 1818, 1425 Ciudad Autónoma de Buenos Aires, Argentina

Abstract

The ICAR Dairy Cattle Milk Recording WG finished its work on the new version of the ICAR Guidelines in February 2018, with the new version approved at the ICAR General Assembly in Auckland. Changes were made to general aspects of cattle milk recording. Over the short term, it was decided that priority be given to improving the 24-hour calculations section of the Guidelines: Procedure 1, Section 2 – Computing 24-Hour Yields. The work comprises several research projects, technical analyses and policy discussions. Central to these efforts, the ICAR Dairy Cattle Milk Recording WG is committed to engaging in discussion with various milk recording organisations and ICAR members working in this sector. To that end, the group is holding a milk recording workshop and technical session at ICAR 2019 in order to stimulate discussion on the types of changes needed in this field.

The ICAR Dairy Cattle Milk Recording WG (DCMRWG) is currently researching current practice toward improving the 24-hour calculations section of the Guidelines: Procedure 1, Section 2 – Computing 24-Hour Yields. Before any changes are made, however, it is vital that the current situation is assessed comprehensively, delving into key aspects related to methodologies, processes, trends and the opinions of milk recording organisations. The DCMRWG conducted a survey of relevant organisations to address these issues, shed light on the level of harmonisation among players, and set a future

direction and strategy on 24-hour calculations for the cattle milk recording sector. One of the goals of the project is to strengthen communication and encourage the exchange of information between working groups and MROs alike. The survey consists of 90 questions and uses solely aggregated data to reflect global practice. Data was obtained from 52 organisations worldwide, giving a representative example of different situations, needs and the specific problems faced.

This part of the project examines the use of automatic milking systems (milking robots) and gauges the general requirements and opinions of milk recording organisations in this area. It considers the impact of automatic milking systems on the milk recording sector, the different options available when milking herds, methodologies (particularly in related to those recommended in the Guidelines), calculation of fat and protein production, impacts of data quality indicators, sampling schemes, and milk yields from multiple numbers of days. The survey reveals how various organisations use their own factors and coefficients, providing information on how they are estimated. It provides information on data collection periods, how animals and herds are chosen for analysis, how are data edited and how organisations work with data before analysis, how factors are used in particular countries (are they unique or specific according to the region and/or breeds, comparison which is used for results, how results are evaluated from estimations or recalculations (method Z, M...) and which statistical indicators are used. A very important part of the project is to establish a future policy and set out practical recommendations for the future.

The results of the survey will prove invaluable when making changes to the ICAR Guidelines. The group wishes to thank all of the organisations that took part in the survey. Central to these efforts, the ICAR Dairy Cattle Milk Recording WG is committed to engaging in discussion with various milk recording organisations and ICAR members working in this sector. Crucially, however, before any changes are made to the Guidelines, the situation among ICAR members and non-members must be assessed. The group is now conducting a detailed overview on methodologies and practical trends in order to gauge opinion and identify the most pressing issues affecting milk recording organisations.

Introduction

The survey is an official project of the Dairy Cattle Milk Recording Working Group comprising two surveys of global milk recording organisations on the topic of 24-hour calculation trends in automatic milking systems and classical milk recording systems. This part of the project summarises the data provided for automatic milking systems (milking robots). The main aim of the project is to use the results to improve Procedure 1, Section 2 of the ICAR Guidelines for Dairy Cattle Milk Recording – Computing 24-Hour Yields. Before any changes are implemented the group decided that the current situation among ICAR member and non-member organisations would need to be monitored and evaluated. The opinions and needs of milk recording organisations as well as the problems they face are detailed here. Covering all aspects of 24-hour calculations in automatic milking system, the survey should provide a benchmark in this field for MROs toward improving their methodologies.

Materials and methods

Data were obtained from 52 organisations from around the world. The participating organisations representing the various countries are listed in Figure 1, with all collaborators credited as authors of the project. Consisting of 90 questions, the survey provides an analysis of all data, which were submitted between December 2018 and

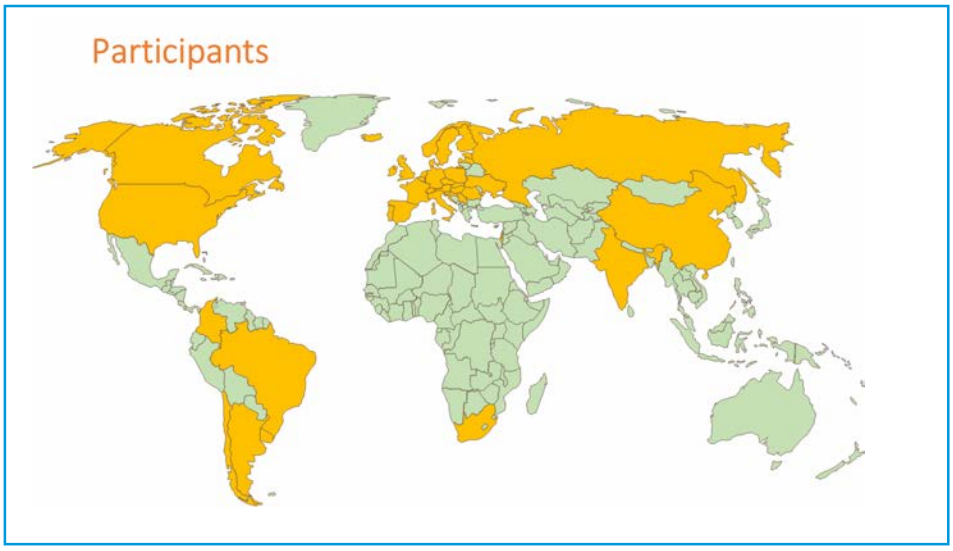

Figure 1. Countries taking part in the project

March 2019. It is expected that the results presented – detailing the different needs, problems and situations faced by MROs – will assist in making improvements to the ICAR Guidelines.

Results: General aspects of 24-hour AMS calculations

Impact of AMS on milk recording

The survey documents the prevalence of automatic milking system use among MROs (Table 1). Figures are compiled based on data provided by 39 organisations, with 13 organisations choosing to skip this question. The number of milking robots has increased, with 28.2% organisations stating that 5 to 20% of their records were AMS-based, 20.5% of organisations stating a share of 20 and 50%, and 7.7% organisations specifying more than a 50% share from AMS. This trend is seeing MROs start to create new services and additional value for customers. Data are also being combined from different sources toward future integration. Harvesting sensor data, simplifying the milk recording process as a whole, and using only one sample for AMS are all key areas to be discussed. At any rate, new services being rolled out by MROs must be reflected in the ICAR Guidelines, a key issue for the Dairy Cattle Milk Recording Working Group.

What recording methods do you use for AMS?

The majority of MROs take milking data from a multiple number of days, mostly including the sample day (Table 2), with only some MROs excluding the sample day. Only seven organisations use data from one day, while, less commonly, four organisations calculate the milk total automatically using robot software. The DCMRWG recommends using raw data calculations from data processing centres as opposed to calculating directly from software. Calculations of data from 4 days are preferred to those taken from just one day.

Table 2 indicates most MROs use one method to calculate AMS milk yields (83.9%), while, for perhaps practical reasons, only 16% combine two as follows:

- Milking data from a multiple number of days + from one day
- Milking data from a multiple number of days + robot software total

Based on responses, milk yields are not taken beyond a period of 7 days, with very few MROs stating they record beyond one week. Most MROs record between 4 and 7 days.

- 2 days: 13.0% of organisations
- 3 days: 4.3% of organisations
- 4 days: 30.4% of organisations
- 5 days: 4.3% of organisations
- 6 days: 4.3% of organisations
- 7 days: 39.1% of organisations

Do you use the Lazenby (2002) method described in the Guidelines

Lazenby (2002) is used by 11 organisations, with 2 organisations used an adaptation of the method (Table 3).

Lazenby (2002) is approved for calculating milk yields over a multiple number of days. The following additional comments were also provided:

- Currently we take into account the last 2 days
- In 2019, we tried to implement a 4-day (96-hour) system
- Overall good
- It is working well
- It seems to work well. We have yet to encounter any problems.
- The method seems to be pretty accurate. We have validated and compared recorded milk with delivered milk to the dairy, with the difference in cases where no cows were missing and calvings were correctly registered coming in at around 1-2%.
- Our experience is that it works well enough! We compared it with milk delivered to dairy companies, where the farmer estimates the milk consumed or wasted on the farm, and consider it reasonably correct.
- We haven't carried out any scientific study of this.

How do you calculate fat and protein yields using AMS?

Fat and protein yields should be calculated on the sampling day (Table 4) based on milk analysis results for that day and milk yield production. There can be discrepancies between test day milk analysis and 24-hour milk yield production, which is calculated over a multiple number of days. Most MROs only use milk yield from the sampling day

Table 1. What is the importance of AMS within your organisation ?

Answer options	Response	
	Number of organisations	Percentage
None of our recorded herds are from AMS	8	20.5
Less than 5% of our records are from AMS	9	23.1
Between 5 and 20% of our records are from AMS	11	28.2
Between 20 and 50% of our records are from AMS	8	20.5
More than 50% of our records are from AMS	3	7.7
Total	**39**	**100.0**

Table 2. What recording methods do you use for AMS?

Answer options	Number of organisations
We use milking data from a multiple number of days, including the sample day	22
We use milking data from a multiple number of days, excluding the sample day	3
We use milking data from one day	7
We use an automatically calculated milk total based on robot software	4

Table 3. Do you use the Lazenby (2002) Method described in the guidelines (see guidelines p 12, Procedure 1, Computing 24-hour yields)?

Answer options	Number of organisations
Yes	11
Yes, but with adaptations	2

Table 4. How do you calculate fat and protein yields using AMS?

Answer options	Number of organisations
We use milk yield from several days, including the sampling day, to calculate the fat and protein yields	13
We use milk yield from several days, excluding the sampling day, to calculate the fat and protein yields	3
We only use milk yield from the sampling day to calculate the fat and protein yields	17

Table 5. What data quality indicators do you monitor when extracting data from the robot software?

Answer options	Number of organisations
Interrupted milkings	11
Data format	13
Milking speed	2
Milk secretion rate	3
Milk yield per milking	22
Milking interval – Missing milkings, 4 hours sampling	12
Recognised data loss	6
Other	4

to calculate fat and protein yields, as recommended by the ICAR Guidelines. Calculations over several days, excluding the sampling day, of fat and protein yields are less accurate. This will again be discussed in advance of the Guidelines.

What data quality indicators do you monitor when extracting data from robot software?

Table 5 shows that MROs mostly use the following quality indicators: milk yield per milking, data format, milking interval and interrupted milkings. The number of combined indicators are summarised in Table 6. Interrupted milking has an influence on fat percentage as do data formats. However, harmonising one format is complicated. The quality of raw data should be accounted for before calculation.

The following comments were provided:

- Comparison to bulk tank
- Milking interval lower than 4 hours. Consistency indicator between consecutive milking for protein % and SCC
- The cow must have a 24-h average from 7 days
- All milking yields for the test day

One indicator is most common (Table 6), but some use more than one indicator. Raw data must be evaluated in advance of 24-hour calculations.

Most indicators are used to exclude individual milkings from data processing (11 organisations). Alternatively, data alerts are generated (5 organisations); seven MROs employ indicators for information purposes only (Table 7).

Checks, data quality and the amount of data available should be reviewed thoroughly.

Below are further comments:

- 24-hour milk production is calculated in comparison with actual/expected milk production.
- For the calculation of expected milk production per minute, the lactation period is divided in parts of 14-days, starting with day 1.
- Expectations per period are made in 3 steps in which wrong milk weighings are detected and neglected for making estimations. A milk weighing can be wrong if the interval is unknown, the deviation is too big compared to surrounding milk weighings, provided the minute-production exceeds the allowed maximum of 70 gr/min, or if the interval exceeds the allowed 1,200 minutes (except for milk recording with just one available milk weighing). In step 1, only milk weighings that meet the roughest criteria of <70 gr/min and < 1,200 minutes interval pass. In step 2, only milk weighings that meet the standard deviation criterion pass. In step 3, only milk weighings deviating only slightly from expected values pass.
- Currently we do not account for: milking intervals under 4 hours, non-consistency between consecutive milkings for protein % and SCC
- We total recorded yields for the test day, and then analyse fat and protein in proportionally mixed samples from the test day

- Milkings with a secretion rate of more than 70g per minute are excluded, as the total yield equates to more than 100kg per day

Do you use the Bouloc et al (2002) method described in the ICAR Guidelines?

This method is designed for calculating milk yield production over one day. Implementation is low with only 5 MROs stating they use the method. Most MROs calculate over a multiple number of days, with one MRO using an adaptation of the method.

What sampling schemes do you use for AMS?

The most common practice is to use scheme Z only (27 MROs), which involves sampling and recording from one milking per cow (Table 8). Prevalence of one-milking sampling has increased with an eye on reducing costs, an important area for future discussion. Schemes E & P that employ all samplings are less common due to the high costs and labour overheads associated with test day preparations. Schemes in which all samples are taken and analysed separately should be used as the golden standard, and represents the most accurate method when using automatic milking systems. Some MROs specified both schemes Z and M are used in cases where the customer prefers higher accuracy (method Z in particular). The industry will need to strike a balance between accuracy and mounting costs going forward. Practice is fairly uniform in this area.

Most MROs use only one sampling scheme for AMS (Table 9). Only a few MROs merge two systems, e.g. Z and M. Merging schemes may particularly benefit herds from which bulls are chosen for artificial insemination, while also aiding management and accuracy.

Do you use the Galesloot and Peeters (2000) method described in the ICAR Guidelines

In cases where only one sample is taken, fat % must be corrected. A total of seven MROs stated they used the Galesloot & Peeters (2000) method (Table 10), with four specifying different methods. A large proportion of MROs do not correct data. The preference is to estimate in-house coefficients, the original Dutch coefficients, or second-generation Dutch coefficients (Table 11).

The DCMRWG recommends correcting fat % to ensure accuracy.

Descriptions of coefficients will need to be updated in the Guidelines.

One-milk sampling and fat corrections are recommended.

Please evaluate how well this method is working in your experience, providing links to any scientific studies you may have conducted:

- Good but we suspect that milking hours should be accounted for
- In France, the Peeters & Galesloot method has been in use since 2018.
- We use the methods established by DRMS
- Customers seem satisfied, but their main interest is SCC

Table 6. Number of combined indicators used by MROs

Number of combined indicators	% of organisations that use combined indicators
1	61.5
2	9.6
3	17.3
4	7.7
5	3.8

Table 7. Do these indicators affect calculations?

Answer options	Number of organisations
No, but they are used for generating user alert messages	5
No, they are only informative	7
Yes, they are used, excluding individual milkings from data processing	11

Table 8. What sampling scheme do you use for AMS?

Answer options	Number of organisations
Scheme Z – sampling from one milking per cow and recording	27
Scheme M – separate samples from several milkings, all analysed separately	6
Scheme E – samples from several milkings joined in equal amounts for analysis	3
Scheme P – samples from several milkings joined proportionally for analysis	2

Table 9. Number of sampling schemes used by MROs

Number of sampling schemes used by MROs	Number of organisations
1	23
2	6
3	1

Table 10 Do you use the Galesloot and Peeters (2000) method described in the guidelines (see overview document: p14, Procedure 1, Computing 24-Hour Yields)?

Answer options	Number of organisations
No, we use a different correction method for one-sample milking	4
No, we use no correction	16
Yes but with adaptations	2
Yes to correct fat content	5

- There is the suggestion that fat percentages tend to be underestimated, especially in cases where sampling starts in the morning.
- Our methods seem to work well though could probably do with improving. That is on the other hand always a question of time and money versus gain.
- Our experience is that it works well enough! We compared it with milk delivered to dairy companies, where the farmer estimates the milk consumed or wasted on the farm, and consider it reasonably correct.
- We have yet to conduct a scientific study in this area.

When analysing several samples or combining them in a non-proportional way, how do you calculate daily fat and protein yields?

Options shown in Table 12 are less common. Most MROs use milk weights to generate a weighted average, as recommended in the Guidelines.

The following comments were provided on various sampling schemes:

- Good
- Where only one fat sample is available, we use the formula described in *https://doi.org/10.3168/jds.S0022-0302(02)74124-6* to calculate the 24-hour fat percentage.
- Indications whether the robot has been successful or not are used for calculations. Samples of non-successful milkings are excluded from calculations.
- No comments
- The method is described in the national guidelines
- *https://infothek.die-milchkontrolle.de/* (ADR-Empfehlung 1.8: MLP AMS)

Sampling schemes M and E are less commonly employed due to high costs. Interval lengths can vary at either 12, 14, or 24 hours (Table 13). In cases where all samples are taken, the sample-taking period can be shortened to decrease costs.

Reducing the sampling period has some advantages, but efforts should be made to ensure enough samples are provided. If it is shortened too much, there is the risk that some cows will go unsampled.

The following additional comments were provided:

- Kg/milk measurements for herds are always based on a period of at least 24 hours or longer for AMS
- The sample taken in herds with automatic milking systems might be shorter than 24 hours. But for all cows at least one sample is taken. The period used for taking samples in a herd during milk recording is often 16 to 20 hours, due to the time needed to transport the equipment from one farm to the other.
- In France, the sampling period is between 12 and 24 hours by robot (for one box), M scheme.

Table 11. What coefficients do you use?

Answer options	Number of organisations
We estimate our own national coefficients	6
We use coefficients from a third organisation	2
We use the original Dutch coefficients	1
We use second-generation Dutch coefficients	3

Table 12. When analysing several samples or combining them in a non-proportional way, how do you calculate daily fat and protein yields?

Answer options	Number of organisations
We use a simple average of all samples analysed	1
We carry out a direct analysis of combined samples	2
We use milk weights to generate a weighted average	5
We use a formula to calculate 24-hour yields from a non-proportionally combined sample	0

Table 13. How long does the sampling period last when using schemes M and E (hours).

Answer options	Number of organisations
12	3
14	1
24	3

Table 14. Over what period do you collect data for estimations or recalculations?

Answer options	Number of organisations
Use one-year data	2
2-5 years	4
5-10 years	2
Irregularly, as required	1
N/A, never	1

Table 15. How are herds and/or cows selected for estimations or recalculations?

Answer options	Number of organisations
All data available	15
Randomly chosen	2
Independently defined criteria	3
Statistical analysis	0
Other criteria	3

Table 16. Do you edit or exclude raw data?

Answer options	Number of organisations
Yes	8
No	2

Results – estimating independent factors and coefficients for AMS

Some organisations estimate their own factors and coefficients, an important topic for the new version of the ICAR Guidelines. Very important will be discussion about minimal number of the animal, herds, etc. which are necessary for accurate estimates (minimal requirements on data).

Survey summarises how many records were used for estimations or recalculations of factors and coefficients. There are differences among MROs that estimate or recalculate their own factors. The following numbers were provided:

- Number of herds from 3 to 13,300
- Number of cows from 360 to 400,000
- Number of milkings 14 to 1,779,324
- Number of lactations 5,000 to 1,200,000

Recommendation in this field could be valuable.

Over what period do you collect data for estimations or recalculations?

Most MROs collect data for estimation or recalculation over a period of 2 to 5 years. Two MROs stated 5 to 10 years, two other over only one year, and one other on an irregular basis (Table 14).

How are herds and/or cows selected for estimations or recalculations?

The most common practice is to select herds and/cows for estimations/recalculations based on all available data (Table 15). = Statistical analysis is not carried out for automatic milking systems.

Do you edit or exclude raw data?

Most MROs edit/exclude raw data when estimating or recalculating coefficients for AMS (Table 16).

Editing raw data is recommended. Two MROs provided the following information:

- Animals with incomplete lactation data from sold, deceased or transferred animals
- We employ the following 5 criteria:
  - Permitted range of daily recorded values
  - Records with missing information
  - Days in milk between 7 and 360 days
  - Milking intervals under 4 hours
  - Number of lactations over 9

Which types of data do you exclude?

Table 17 summarises types of excluded data. Duplicate records or entries with missing information are most commonly excluded.

- Interval between milkings under 4 hours
- Maximal lactation between 5 and 7
- Lactation stage 330 or 360 days

For the number of exclusion criteria applied, see below:

- 1 criterion: 8 organisations
- 2 criteria: 7 organisations
- 3 criteria: 3 organisations
- 4 criteria: 2 organisations

Multiple exclusion criteria are recommended.

Do you use uniform, national factors/ coefficients?

Uniformly applied factors/coeffecients are most common, while those based on regional or production systems are less usual (Table 18).

The same factors are generally used for all breeds. Only two MROs use different factors due to costs and logistics (Table 19).

One MRO stated they collect field data for crossbreed animals as part of a sponsored project.

What type of comparative analysis is used for AMS estimations/ recalculations?

Concerning comparative analysis using AMS, the recommended method of analysing samples separately (24-hour, golden standard) is most common; only two MROs differed in approach (Table 20).

Simple indicators are most commonly applied (Table 21). Clearer definitions of minimum requirements for indicators are required. Some MROs use overly complex indicators.

Table 17. Which types of data do you exclude?

Answer options	Number of organisations
Duplicate records	15
Records with missing information (IDs, lactation figures, dates, weights)	13
Intervals between milkings	2
Excessive differences in milk yield production between milkings	3
Lactation stages (days in milk)	2
Other	4

Table 18. Do you use uniform, national factors/coefficients?

Answer options	Number of organisations
Yes	7
No, based on region/production system	2

Table 19. Are there any differences in factors/coefficients between breeds nationally?

Answer options	Number of organisations
Yes, different factors/coefficients are used	2
No, the same factors/coefficients are used for all breeds	7

Table 20. What type of comparative analysis is used for AMS estimations/recalculations?

Answer options	Number of organisations
All samples are analysed separately (24-hour, golden standard)	4
Different approach	2

Table 21. How do you evaluate results based on estimations/recalculations (method Z, M) and which statistical indicators do you use?

Answer options	Number of organisations
Correlation between estimated/predicted daily yields and actual/true daily yields (from reference method, golden standard)	5
Comparison of means, standard deviations and maximum difference (overall, within subgroups)	4
Systematic bias, SD for differences and accuracy (R^2)	2

Who is responsible for developing and implementing new methods?

Most MROs develop and implement new methods themselves, but less commonly in collaboration with research institutes. The following other responses were also provided:

- Ministério Agricultura – Brazil
- Sponsoring agency
- Dairy records providers
- ICAR

Conclusions, recommendations and future policies

- 52 organisations took part in the survey, comprising 90 questions
- A very important part of the project is to establish a future policy and set out practical recommendations for the future
- Impact of AMS on milk recording
    - This trend is seeing MROs start to create new services and additional value for customers
    - Data are also being combined from different sources toward future integration
- As the number of milk recording organisations increases worldwide, customer services need to be improved
- Data is mostly applied based on a multiple number of days for calculating 24-hour milk yields
- Most of the organisations use milk yield from the sampling day to calculate the fat and protein yields which is recommended practice
- Data quality systems are routinely used when handling AMS
- Raw data should always be used
- The prevalence for calculating 24-hour milk yields based on one day has decreased
- The most common practice is to exclusively use scheme Z
- There is a general trend toward simplification with a view to cutting costs
- Fat % should be factored in when taking only one sample, with some MROs stating corrections are not always applied
- Not all MROs estimate their own factors and coefficients
- There is general consensus on the areas in the Guidelines that need to be prioritised

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Global 24-hour calculation trends in classical milk recording systems

X. Bourrigan[1], P. Bucek[2], K. Kuwan[3], J. Kyntäjä[4], Y. Lavon[5], F. Reinhardt[3], F.J. Auer[6], B. Dokkebakken[7], K. Haase[8], C. Trejo[9], D. Radzio[10], F. Miglior[11], E. Barras[12], Jere High[13], G. Jóhannesson[14], M. Fioretti[15], Nils-Erik Larsson[16], T. Roalkvam[17], G. Augier[1], Ch. Lecomte[1], C. Lizana[9], F. Rapaioli[18], S. Alday[19], O. Kachanova[20], A. Braun[21], R.L. Bhagat[22], A.B. Pande[22], E. Galvanovska[23], D. Lodina[23], An Pengpeng[24], Sun Xianzhi[24], R. van der Linde[25], A. Pentjärv[26], A. Martins[27], J. Carvalheira[27], U. Lauritsen[28], C. N. Costa[29], B. Coughlan[30], M. Dianova[31], P. Rosincinova[31], J. van der Westhuizen[32], A. Coburn[33], R. Cantin[34], J.A. Horst[35], M. Séguin[36], M. Jesús[37], F. Sotelo[38], Á. Kenéz[39], L. Dégen, [40]G. Alain, Bularca Ioan Raul[41], Rotar Mircea Catalin[41], J. Mathie[42], Z. Ivkic[43], Jlanbin Li[44], B. Perisic[45], N. Nayee[46], R. O. Gupta[46], S. Sievert[47], S. Gilheany[48], V. Tytenko[49], G. Fedorova[20], M. Klopcic[50], D. Hambrook[51], ACHA[52], G. Gery[40], R. Fourdraine[33], S. Pinto[27] and D. Snidall[42]

[1]Czech Moravian Breeders' Corporation, Inc., Benesovska 123, 252 09 Hradistko, Czech Republic
[2]France Genetique Elevage, 149, rue de Bercy, 75595 Paris, France
[3]VIT (Vereinigte Informationssysteme Tierhaltung w.V) IT-Solutions for Animal Production, Heinrich-Schroeder-Weg 1, 27283 Verden, Germany
[4]Mtech Digital Solutions (ProAgria Group), PO Box 25, 1301 Vantaa, Finland
[5]Israel Cattle Breeders Association, P.O. Box 3015, 38900 Caesaria Industrial Park, Israel
[6]LKV Austria Gemeinnützige GmbH, Dresdnerstraße 89/19, 1200 Vienna, Austria
[7]Minnesota DHIA, 307 Brighton Ave So, 55313 Buffalo, USA
[8]NorthStar Cooperative, P.O. Box 23157, 48909 Lansing, USA
[9]COOPRINSEM, Ramon Freire 980, Osorno, Chile
[10]Polish Federation of Cattle Breeders and Dairy Farmers, 00-515 Warsaw, Poland
[11]Ontario Genomics | MaRS Centre – West Tower, 661 University Ave, Suite 490 Toronto, ON M5G 1M1, Canada
[12]ASR-Switzerland, Schützenstrasse 10, 3052 Zollikofen, Switzerland
[13]Lancaster Dairy Herd Improvement Association, 1592 Old Line Road, 17545 Manheim, USA
[14]The Icelandic Agricultural Advisory Centre, Austurvegur 1, 800 Selfoss, Iceland
[15]Associazione Italiana Allevatori (A.I.A.), Via G. Tomassetti 9, Rome, Italy
[16]Växa Sverige, Box 288, 75105 Uppsala, Sweden
[17]TINE SA, Lakkegata 23, N-0187 Oslo, Norway
[18]Asociación Colombiana de Criadores de Ganado Simmental, Simbrah, Simmcebú y sus Cruces, Calle 85 19C 12OFC 101, Bogota, Colombia
[19]Spanish Holstein Confederation, Carretera de Andalucia KM 23,600, 28320 Pinto, Spain
[20]Plinor Ltd, Russia
[21]CONVIS S.C., Zone artisanale & commerciale, 4, L-9085 Ettelbruck, Luxembourg
[22]BAIF, Development Research Foundation, India
[23]Agricultural Data Centre, Republikas sq. 2, LV1010 Riga, Latvia
[24]Shanghai Dairy Cattle Breeding Center Co., Ltd, 10th Building, 1518 West Jiangchang Rd. Shanghai, China
[25]CRV B.V., Wassenaarweg 20, 6843 NW Arnhem, Netherlands
[26]Eesti Põllumajandusloomade Jõudluskontrolli AS, F. Tuglase 12, Tartu, Estonia
[27]ANABLE, Quinta da Medela – Verdemilho, 3810-455 Aveiro, Portugal
[28]RYK, Agro Food Park 15, DK-8200 Aarhus N, Denmark
[29]Embrapa Dairy Cattle, Rua Eugenio do Nascimento 610, Juiz de Fora, Brazil

[30]ICBF, Ireland
[31]The Breeding Services of the Slovak Republic, S.E., Starohajska 29, Bratislava, Slovakia
[32]South African Stud Book and Animal Improvement Association, 9300 Bloemfontein, South Africa
[33]AgSource, USA
[34]CanWest DHI, Canada
[35]Associação Paranaense de Criadores de Bovinos da Raça Holandesa, Rua Professor Francisco Dranka, 608, Curitiba, Paraná, Brazil
[36]Valacta, Sainte-Anne-de-Bellevue, Canada
[37]Asociación Nacional de Criadores de Ganado Vacuno Selecto de Raza Parda, C/Profesor Xaime Andrés, 15-B, 24007 León, Spain
[38]Instituto Nacional para el Control y el Mejoramiento Lechero, Uruguay
[39]Állattenyésztési Teljesítményvizsgáló Kft (Livestock Performance Testing LTD), Dózsa György út 58, H-2100 Gödöllõ, Hungary
[40]Association wallonne de l'élevage asbl, Champs Elysées 4, 5590 Ciney, Belgium
[41]Cattle Breeders Association Baltata Romaneasca Simmental Type, Mihai Viteazu Street, No. 382, Harman-Brasov, Harman, Romania
[42]Cattle Information Service, Speir House, Telford, TF3 3BD, UK
[43]Croatian Agricultural Agency, Ilica 101, Zagreb, Croatia
[44]Dairy Cattle Research Centre of Shandong Academy of Agricultural Sciences, No.159, Gongyebei Road, Ji'nan, China
[45]Laboratory for milk quality control, Faculty of Agriculture, University of Novi Sad, Trg Dositeja Obradovica 8, 21000 Novi Sad, Serbia
[46]National Dairy Development Board, Anand, India
[47]National DHIA, 53718 Madison, USA
[48]National Milk Records PLC, Fox Talbot House, Greenways Business Park, Bellinger Close, SN15 1BN Chippenham, UK
[49]State Enterprise Agency of Animal Identification and Registration, 4119, Kyiv, Ukraine
[50]University of Ljubljana, Groblje 3, Domzale, Slovenia
[51]Royal Jersey Agricultural & Horticultural Society-Royal Jersey, Showground Milk Records La Route de la Trinite JE3 5JP Trinity, Jersey, Channel Islands
[52]ACHA. Asociación Criadores de Holando Argentino, Laprida 1818, 1425 Ciudad Autónoma de Buenos Aires, Argentina

Abstract

The ICAR Dairy Cattle Milk Recording WG (DCMR WG) is currently rolling out changes to the dairy cattle milk recording section of the ICAR Guidelines, which were approved in Auckland at the beginning of 2018. The core activities of the group are to improve 24-hour calculations used in classical milk recording and automatic milking systems. It was decided that preparations would be given over in the short term to improving the 24-hour calculations section of the Guidelines: Procedure 1, Section 2 – Computing 24-Hour Yields. Before any changes in the Guidelines, is necessary to monitor and analyse current situation in milk recording organisation, their needs and problems. The DCMRWG invited various organisations from around the world to take part in a survey. Data was obtained from 52 organisations in total. The survey consisted of 90 questions. The survey presents an overview of the current situation and is the basis for all planned changes. As well as monitoring the current situation, the survey aims to establish a future policy and set out recommendations as a way of harmonising practice worldwide. It is also hoped that the survey will serve as a springboard for instigating discussion among milk recording organisations and assessing needs. This was one of the main goals of the project is to strengthen communication and encourage the

exchange of information between working groups and MROs alike. As the survey will deliver aggregated data, practice will be benchmarked for respective organisations to reflect common practice in this field worldwide.

The first part of the study consists of several sections: a general overview, practical experiences with methods recommended in the ICAR Guidelines, problem areas MROs wish to address, priorities and needs, and processes used to estimate coefficients and factors. Some organisations estimate their own factors and coefficients and survey gave an overview on the following areas: number of organisations which estimate own factors and coefficients, problems with estimations, number of animals and herds used for estimations (different indicators used), time period between estimations or recalculations, how cows and herds are chosen, criteria used for selecting herds and cows, data editing and criteria for data exclusion, factors and coefficients used nationally or differences between breeds and regions, estimations and recalculations of conventional methods (not from AMS), what comparisons are used, results from estimations or recalculations (am/pm, method Z, etc.) and the types of statistical indicators used.

The results of the survey should prove invaluable when making changes to the ICAR Guidelines and for benchmarking MROs in a global context, adapting methodologies among organisations where relevant.

Acknowledgements: The ICAR Dairy Cattle Milk Recording WG wishes to thank all of the organisations that took part in the survey.

Introduction

This project analyses trends in 24-hour calculations. The ICAR Dairy Cattle Milk Recording Working Group surveyed ICAR member and non-member organisations in order to summarise and evaluate the needs of milk recording organisations and the challenges faced. Covering all aspects in this area, the survey should be useful as a benchmark for milk recording organisations toward improving their methodologies. It provides an overview on methods recommended in the Guidelines, moving toward a better understanding of all processes and practicalities associated with 24-hour calculations while evaluating the practice of estimating/recalculating factors and coefficients. The analysis should prove invaluable for improving the ICAR Guidelines in this area, namely Procedure 1, Section 2 of the ICAR Guidelines – Computing 24-hour Yields. It is hoped the outcomes of the survey will help inform future practice among MROs.

Materials and methods

The project consists of a survey totalling 90 questions. Data was obtained from 52 organisations from around the world. Countries of origin are shown in Figure 1, with all participants credited as authors of the paper. Data used for the analysis was collected between December 2018 and March 2019.

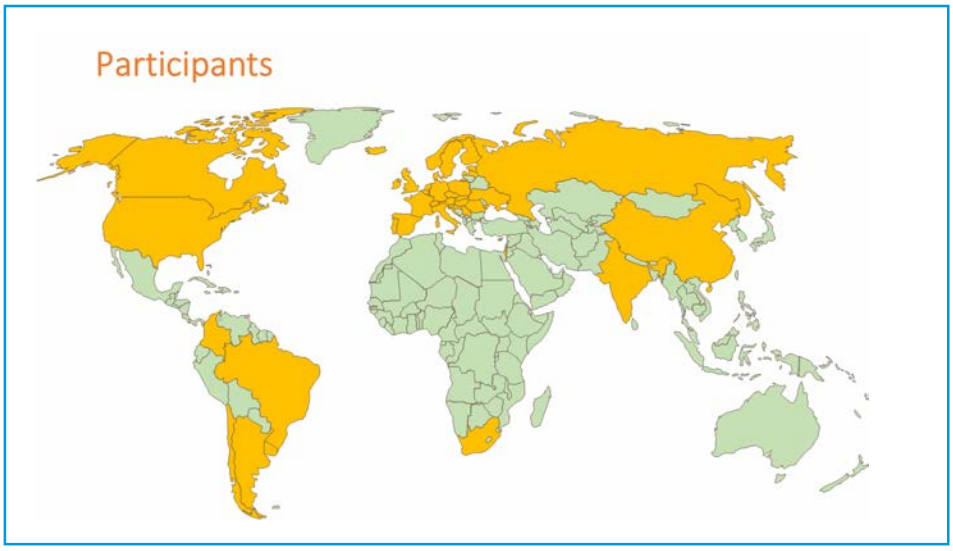

Figure 1. Countries involved in the project

Results – General aspects: 24-hour calculations for classical milk recording systems

Which of the following options does your organisation use for manually operated milkings?

Table 1 shows options for using manually operated milking settings. It is evident that there is a trend toward simplification, with the aim of reducing costs and the overheads, especially for big herds. The standard among organisations is to take one sample. Only seven organisations take more than one milking for both samples. Improving milk recording in big herds (more than 1,000 cows) is a major challenge for the industry. The introduction of new sampling services is required.

Do you use the DELORENZO AND WIGGANGS (1986) METHOD described in the guidelines (see overview document: p 5, Procedure 1, Section 2)?

All information on the DeLorenzo and Wiggans (1986) method is given in Table 2 to Table 6.

Methods in the Guidelines are based on 24-hour calculations. Table 2 shows that this method used 13 organisations and 3 organisations use this method with adaptations. The big advantage of this method is that it is simple and easy to understand and use in principle.

Most of the organisations use factors and coefficients from the Guidelines and some from other countries (Table 3). The problem is that it is difficult to collect data from large data sets, which requires accumulated experience and knowledge. This is probably one of the main reasons why coefficients from the Guidelines are mostly used. Where coefficients and factors are estimated, the recommendation is to use equipment to cover the times of morning and evening milkings.

Table 1. Which of the following options does your organisation use for manually operated milkings?

Answer options	Number of organisations
Complete one-milking recording (milk weight + sample)	35
One-milking sample	21
We always take more than one milking for both samples	7
We only record in AMS	1

Table 2. Do you use the Delorenzo and Wiggangs (1986) method described in the guidelines (see overview document: p 5, Procedure 1, Section 2)?

Answer options	Number of organisations
Yes	13
Yes, but with some adaptations or changes	3

Table 3. What is the origin of the factors you use for this method?

Answer options	Number of organisations
We use factors and coefficients from other countries	2
We use factors and coefficients from the guidelines	11
We use our own factors and coefficients	0

Table 4. Which sampling schemes do you use for this method (see overview document: p 13 and 14, Overview Cattle Milk Recording)?

Answer options	Number of organisations
T	11
C	0
Z	7

Table 5. Which milking frequencies do you use this method for?

Answer options	Number of organisations
2x per day milking	12
3x per day milking	9
4 to 6 per day milking	0

Table 6. How do you define milking times when using this method?

Answer options	Number of organisations
Milking start time on the herd level	12
Middle point of milking time on the herd level	3
Milking start time on the milking group level	1
Middle point of milking time on the milking group level	0
Individual milking start time on the cow level	2

DeLorenzo and Wiggans (1986) is mostly used for methods T and Z. Organisations in the survey do not use this method in the case of method C (Table 4).

Table 5 shows DeLorenzo and Wiggans (1986) is used in for 2 milkings per day and 3 milkings per day, but not for 4 to 6 milkings per day. This is according to the recommendation in the ICAR Guidelines.

Milking times influence accuracy. The survey also analysed how milking times are defined when using the DeLorenzo and Wiggans (1986) method. It will be valuable to add some comments relevant for Table 6 in the new version of the ICAR Guidelines. All organisations use only one option from Table 6 and do not combine them. Most common option in classical milk recording is milking time on the herd level.

Some organisations provided other comments for evaluating their experience:

- We have no scientific studies.
- We have seen a saw teeth effect with AM/PM sampling, This increases with shorter or longer periods between milkings (12 hours for 2X or 8 hours for 3X minimising the saw teeth effect).
- This works well as long as we get accurate times form the dairy farm.
- Works very well on most herds, but there are some problems with 3x herds where am milkings are sampled.
- The present correction still creates a situation where 24-hour fat from evening samples is somewhat higher than from morning samples.
- We have a lot of issues with the calculation of fat (and also SCCs). We get a regular up-and-down fat levels at herd level and the SCC records are not useful.
- I don't think it works particularly well in the case of big herds.
- Our experience is that it works well enough. We compare delivered milk to dairy companies, and the farmer estimates milk consumed or wasted on the farm, amounts which seem to be reasonably correct.
- We have not performed any scientific study of this.
- Useful for 3 milkings. Liu method is not used for 3 milkings.
- It might be valuable to discuss development of the Liu method for 3 milkings. Update Guidelines in this specific case.
- Three milkings should be a discussion item for the ICAR Dairy Cattle Milk Recording WG.

Analysis for three milking based on DeLorenzo and coefficients for this case are available.

Do you use the LIU ET AL. (2000) METHOD describe in the guidelines (see overview document: p10, Procedure 1, Section 2)?

Table 7 shows that the Liu method (2000) is used by 6 organisations, with 3 organisations adapting some equations and 2 making other adaptations. In cases where organisations want to estimate their own coefficients there are insufficient records in some classes. Importantly, new coefficients are estimated for this method, the results of which will be presented at the ICAR Conference in Prague.

The Liu method was used for more sampling schemes (Table 8). It is evident that different practices are used for 24-hour calculation methods. Interestingly, this method is also used for sampling scheme C, a point that should generate discussion on sampling scheme C among the group. Clear recommendations in this field are needed.

The survey also analysed which milking frequencies are used for the Liu method. Most of the organisations use this method in case of 2 milkings per day. Interestingly, 4 organisations used this method in case of 3 milkings per day (Table 9).

The most accurate approach is to define milking times as individual milking start times on the cow level. But this is difficult because it is frequently unavailable in classical milk recording systems (Table 10). The most common option used in milk recording organisations is milking start times on the herd level.

Experiences with using the Liu method are summarised below:

- It can work well, but milking start times are not recorded accurately, so can't be used all the time.
- The Liu method has been used in France since 2011.
- In the French model, we added another class of milking interval.
- Due to changes in milk yield and fat content over the last 15 years, a new model will be established in 2019.
- No problems.
- Very good.
- Will be available for the public.
- A new version will be presented in Prague.
- The ICAR Guidelines will be updated once new coefficients are presented at the ICAR Conference in Prague.

Are there recorded herds where the regular milking intervals do not create a 24-hour recording day?

Some organisations specify that regular milking intervals are not created for a 24-hour recording day (Table 11). This was the case for 5 organisations in less than 10 % of all herds and in 2 organisations in case of more 10 % of all herds (Table 11). This approach can be useful for automatic milking systems and calculations for protein and fat production.

Do you use milk yield data from more than one day when using electronic milk meters (HAND ET AL., 2006) (see Guidelines p 16, Procedure 1, Section 2 - Computing 24-hour Yields)?

There were different situations when using data from more than one day for calculating milk yields with electronic milk meters. In classical milk recording, most organisations use data from one day for calculating 24-hour milk yields (Table 12). This is completely different in comparison with automatic milking systems where the common standard is to use data from multiple numbers of days for calculating 24-hour milk yields. One of the problems when using multiple numbers of days for 24-hour calculations is identification, an issue that needs to be discussed.

The most common method is to add the sampling date to the measurement (Table 13). Excluding the measurement is less common.

Table 7. Do you use the Liu et al. (2000) method described in the guidelines (see overview document: p10, Procedure 1, Section 2)?

Answer options	Number of organisations
Yes	6
Yes but we adapt some equations	3
Yes but we employ adaptations, e.g. different parities, milking intervals and stages of lactation classifications, intercept, slope, different numbers of formulae	2

Table 8. Which sampling schemes do you use this method for (see overview document: p 13 and 14, Overview Cattle Milk Recording)?

Answer options	Number of organisations
Scheme T	10
Scheme C	5
Scheme Z	3

Table 9. Which milking frequencies do you use this method for?

Answer options	Number of organisations
2x per day milking	10
3x per day milking	4
4 to 6x per day milking	0

Table 10. How do you define milking times when using this method?

Answer options	Number of organisations
Milking start time son the herd level	8
Middle point of milking times on the herd level	1
Milking start times on the milking group level	3
Middle point of milking times on the milking group level	0
Individual milking start times on the cow level	1

Table 11. Are there recorded herds where the regular milking intervals do not create a 24-hour recording day?

Answer options	Number of organisations
Yes, less than 10% of all herds	5
Yes, more than 10% of all herds	2

Table 12. Do you use milk yield data from more than one day when using electronic milk meters (Hand et al., 2006) (see guidelines p 16, Procedure 1, Section 2 - Computing 24-hour yields)?

Answer options	Number of organisations
We only use one-day milking data	33
We use data from several days as described in the guidelines	8
We use data from several days but with adaptations	0
We calculate 24-hour yields from a number of days differently	1

Most common standard is to have only one option from the options = listed in Table 12 for the 24-hour period. Combined options (see Table 12) are less common.

Where multiple numbers of days to calculate milk yield production, the common option is 7 days. Organisations using multiple numbers of days are harmonised in this indicator. Only one organisation uses 2 days.

The survey also analysed the connection of milk analysis results with milk yields (Table 14). Half of the organisations used connections between results of milk analysis and the test day and the other half multiple numbers of days. It is recommended to connect data from milk analysis with the test day.

The survey evaluated experiences with Hand et al., 2006. These were the additional comments from some organisations:

- Milk yield is fairly stable at an average of 7 days, with sample components is corrected by milking start times and intervals between milkings. This method should be improved in the future.
- Overall doing well.
- Seems to be OK for management purposes.
- Very limited use, overwhelming use of only test day milk yield.

Do you use other methods not mentioned in the Guidelines?

The survey gave an opportunity to review other methods not recommended in the ICAR Guidelines. There were 4 cases of methods not described in the Guidelines (Table 15) being used. These cases will be discussed, checked and analysed by the ICAR Dairy Cattle Milk Recording Working Group. There were 2 cases in the case of method T, 1 case for milking robots, and 1 case for other cases.

The following comments were provided:

- For calculating 24-hour fat percentages, if there is only one sample available, we use the method described in: *https://doi.org/10.3168/jds.S0022-0302(02)74124-6*
- Canadian AM/PM factors; revised factors in 2016; applies for non-robotic systems
- We note that in Brazil a new regulation has being applied, which stipulates different types of sampling taken with electronic meters
- In France, the Liu method in respect of the T, Z and C schemes is currently used, with Peeters & Galesloot's method used for robots.

Estimating independent factors and coefficients in classical milk recording systems

Results for the independent factors and coefficients in classical milk recording systems summarised in Tables 16 to 24.

Do you estimate your own factors and coefficients?

Most organisations used their own factors and coefficients. The Dairy Cattle Milk Recording Working Group is planning to add a new part to the ICAR Guidelines outlining recommendations for estimations of factors, coefficients, derivations of equations, and a calculation policy.

Table 13. In your measurement period, how do you treat the sampling date?

Answer options	Number of organisations
The sampling date is excluded from the measurement	2
The sampling date is added to the measurement	6

Table 14. How do you connect milk yields with milk analysis results?

Answer options	Number of organisations
With the milk yield from a longer measurement period	4
With the milk yield on the sampling day only	4

Table 15. Do you use other methods not mentioned in the Guidelines?

Answer options	Number of organisations
Yes for sampling scheme T	2
Yes for sampling scheme Z	0
Yes. For sampling scheme C	0
Yes. For milking robots where only one sample is taken (adjusting milk contents from one sample)	1
Yes. For other cases	1

Table 16. Do you estimate your own factors and coefficients?

Answer options	Number of organisations
Yes	20
No	18

Table 17. How long does it take to calculate basic data for estimating/recalculating coefficients?

Answer options	Number of organisations
2-5 years	4
5-10 years	3
Irregularly, as required	3
Within 1 year	2
Over 10 years	2
N/A	1

Table 18. How do you choose herds and/or cows for estimations/recalculations?

Answer options	Number of organisations
All data available	13
Randomly chosen	3
We set our own criteria	5
Statistical analysis	3

Table 19. Do you edit and exclude raw data?

Answer options	Number of organisations
Yes	14
No	3

The following comments point to some issues MROs face when defining formulas, coefficients and factors:

- Poor data collection on milk quality coefficient estimation
- Lack of availability of international consultants with experience in factor development
- Different production systems, i.e. seasonal grazing systems have quite different lactation curves
- Differences between irrigated and unirrigated areas where pasture is the main forage
- We have devised our own formula for predicting 24-hour fat percentages
- Obstacles to deriving factors for converting milk composition from a subsample of a milk recording. For economic reasons, abbreviated sampling is used for a sample from a control day with a dual or triple daily milking regime. Identical and uneven intervals can occur between individual milkings. The major problems are:
    - The relatively high frequency of different variants of non-standard intervals in two or three daily milkings
    - Although same-day intervals typically differ by no more than ± 0.5 hours and are considered equal, it can occur that 3.5 hours are unaccounted for or 10/14 in twice-daily milkings
    - Different milking rates in one herd (part of the herd three times a day, part of the herd twice a day, according to the stage of lactation) for the estimation and practical use of recalculation factors in milk recording
- Milking interval times
- Collecting very large reference data sets (with one sample by am and pm milking) from different breeds to define regression formulas for each breed
- Not yet, we are collecting data.
- Proper participation in different environments and production levels.
- Transfer of data from commercial milking software to certain fields for use in calculations.
- Time and farmers who support the experiment
- Very large reference data set – to define regression formula, breeds, season – most important problem

There was considerable variability among organisations which estimate own factors, coefficients in number of data available. The following data on intervals are for different indicators:

- Number of herds: from 2 to 542. One organisation stated that it varies per breed: different for Holstein and Jersey. One organisation wrote that it is 1-3% of all herds
- Number of cows from 500 to 80,000. One organisation stated Holstein and Jersey breeds differ. One organisation stated 1-3% of all cows.
- The number of milkings also proved highly variable, as previous indicators were between 9,000 and 7,496,476. One organisation used data from 3-6 test days, with another stating figures from 6 to 36 depending on the frequency of the variations of different time intervals between milkings (two to three times a day)

- The number of lactations also varied, with the maximum at 185,600
- Some organisations limit the number of lactations per cow, with 3 or 4 lactations the norm.
- There were also other comments:
    - Coefficients (conversion factors) are used for short-term sampling results (a single milk sample on a control day). The number of cases (herds, cows, milking, lactations) is practically lower the more the intervals there are between milkings, which differs from the same intervals (equal intervals)
    - In France we define the regression formula for the Liu method in 2011 and recalculated and checked the accuracy of the coefficients in 2015
    - We use data as required

The ICAR Dairy Cattle Milk Recording Working Group will add recommendations to the new version of the ICAR Guidelines on minimum and optimum numbers of herds, cows, milkings and lactations. All criteria need be defined.

How long does it take to calculate basic data for estimating/recalculating coefficients?

How do you choose herds and/or cows for estimations/recalculations?

The majority use all available data (Table 18) given the complexity of collecting data for estimating factors and coefficients.

The following criteria were specified:

- Multiple samples per cow over following herd test dates
- Different milking time groups
- Different milking interval groups

Further comments were also added:

- Herd sampling covers all national territories
- We calculate coefficients randomly for half the population and validate them against the other half
- Also different milking interval groups

Do you edit and exclude raw data?

The majority of organisations edit and exclude raw data (Table 19).

Some organisations specify criteria use for data editing and data excluding:

- Completeness of data according to the purpose of the research, outliers detection.
- Few milkings are recorded, lactations started by abortion, long period from calving to first milk recording
- In practice, herds are selected with intervals between milking when estimating factors for the appropriate interval (e.g.14 hours at twice daily milkings or 6 hours, three milkings per day, or the same 12/12 and 8/8/8 intervals). Several control days (months, once a month) are measured (kg, milk), sampled and analysed (% of milk components) for the whole day's milking and all milkings. Reference values

(kg and %) are then calculated from the database. The regression method is used to compute recalculation equations for the whole control day results from one-day milking result according to the length of the interval. This does not apply to the breed milked or their hybrids, nor the order/stage of the lactation. Coefficients are updated approximately after 6 to 10 years. The most important factor (which includes breed, order and lactation stage) is the milking weight (milk yield, kg), included in the form of weight (kg of milk) during reference value calulations (milk, fat, protein, lactose and somatic cell count for the whole control day).

- We use 5 criteria:
  - Permitted range of daily recorded values
  - Records with missing information
  - Days in milk between 7 and 360 days
  - Number of lactation grower than 9
  - Overly large differences in milk yield production between milkings
- Outliers
- Coefficients calculated using BLUES as described by Vollema and Olori
- We exclude milk samples with fat content above 9% or lower than 1.5% and protein above 7% and below 1%.
- Milk yield, fat and protein content

What types of data are excluded?

Excluded data are given in Table 20. The following criteria were given:

- Interval between milkings less than 26 or 6 or 8 hours.
- Interval between milkings greater than 33 or 18 or 16 hours.
- Number of lactations less than 5 or 7.
- Stage of lactation 305 or 360 or 365 days.

Do you use national factors and coefficients?

The majority use national factors and coefficients (Table 21)

Are there any national differences between breeds?

The majority of responses specified no differences (Table 22). Reference data for breeds with small numbers of animals are typically unavailable. One country had reference data for Montbeliarde from an electronic milk meter, estimating coefficients based on milking times at an individual level, which is the best approach.

Table 20. Which data are excluded?

Answer options	Number of organisations
Duplicate records	17
Records with missing information (ID, Lact., Dates, Weights…)	18
Intervals between milkings	3
Overly large differences in milk yield production between milkings	10
Lactation stage (days in milk)	5

Table 21. Do you use national factors and coefficients?

Answer options	Number of organisations
Yes	12
No. We use different factors, coefficients and/or production system for different regions	5

Table 22. Are there any national differences between breeds?

Answer options	Number of organisations
Yes, different factors and coefficients are used for different breeds	5
No	13

Table 23. Where estimations or recalculations of conventional methods (not from AMS) are analysed, what comparisons are used?

Answer options	Number of organisations
A4	10
Different approaches (methods)	1

Table 24. How do you evaluate results from estimations or recalculations (am/pm, method Z…) and which statistical indicators do you use?

Answer options	Number of organisations
Correlation between estimated/predicted daily yields and actual/true daily yields (from reference method, golden standard)	13
Comparison of means, standard deviations and maximum differences (overall, within subgroups)	8
Systematic bias, SD of differences and accuracy (R^2)	6

Where estimations or recalculations of conventional methods (not from AMS) are analysed, what comparisons are used?

With the exception of one organisation, the general consensus is to use comparison method A4 (Table 23) as recommended in the Guidelines and the DCMRWG.

How do you evaluate results from estimations or recalculations (am/pm, method Z...) and which statistical indicators do you use?

The majority of responses indicate a preference for simple indicators. Recommendations in this area will be added to the new version of the ICAR Guidelines. Some organisations combine indicators from more groups (see Table 24).

Conclusion

- Comprising 90 questions, the survey obtained responses from 52 organisations from around the world.
- A trend toward simplifying the milk recording process and reducing the number of samples, especially in big herds, is evident.
- Methods in the ICAR Guidelines are based on 24-hour calculation practice among MROs.
- Precise recording of herd milking times is crucial.
- There are new coefficients for the Liu method.
- In comparison with milking robots results from multiple numbers of days, where they are not commonly used, most organisations use one-day milk recording data. Where not, the time period is mostly 7 days.
- Four organisations stated they used methods not contained in the Guidelines, an area that will be discussed within the DCMR WG.
- The general trend is for MROs to calculate their own factors and coefficients. Calculation policy in this area needs to be addressed.
- Coefficients and factors are regularly recalculated.
- Mostly, all of the available data is used for estimating factors and coefficients.
- Most of the organisations edit and exclude raw data when estimating factors and coefficients.
- Most milk recording organisations that estimate independently use unique factors and coefficients, which also applies to breeds.
- Organisations prefer to use simple statistical indicators .

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Additional value of cell differentiation in the course of DHI testing

E. Gass[1], F. Onken[1], A. Bartel[2], C. Baumgartner[3], F. Querengässer[2] and M.G. Doherr[2]

[1]German Association for Performance and Quality Testing, DLQ, Irmintrudisstraße 15, 53111 Bonn, Germany
Corresponding Author: folkert.onken@dlq-web.de
[2]Institute for Veterinary Epidemiology and Biostatistics, Freie Universität Berlin, Königsweg 67, 14163 Berlin, Germany
[3]Bavarian Association for raw milk testing, mpr, Hochstatt 2, 85283 Wolnzach, Germany

Abstract

As a well-established parameter in monthly DHI testing, somatic cell count (SCC) is being used to monitor udder health and to support management decisions on dairy farms.

The aim of this study was to evaluate, whether the additional analysis of cell differentiation in the course of DHI testing could further enhance the informative value of DHI results, e.g. in the form of prognostic key figures for udder health. Using a new generation of high throughput devices, SCC and cell differentiation index (CDI) were analysed simultaneously. The CDI essentially reflects the proportion of macrophages in the total SCC. Cell differentiation was routinely performed from DHI samples taken over a period of 1.5 years from approximately 920,000 animals, partly from robot farms in two different German federal states. Additionally, an experiment including 2,500 animals was conducted over a period of up to 6 months: DHI samples were analysed with regard to SCC and CDI. Simultaneously, SCC, CDI, and the bacteriological status were assessed from udder quarter level samples of the same animals. The data set was supplemented by additional information in regard to diagnosis and treatment of animals.

Statistical analysis of the collected data reveals a complex interaction of cell count and CDI, making it difficult to directly generate additional value from cell differentiation separately from somatic cell count results. Furthermore, it is impractical to model acute inflammatory processes of the udder due to the common interval of four weeks in between DHI testing dates. Nevertheless, two statistical models including CDI and additional DHI parameters could be established in order to predict cell counts in the future. In the case of currently > 100,000 cells/ml, the probability for elevated cell counts in the next two months can be predicted. Whereas in the case of currently < 100,000 cells/ml, the probability for stable udder health with low cell counts in the next two months is predicted. By providing the probability for different outcome scenarios, farmers would be able to rank their animals according to high or low risk and prioritize their effort. The data from quarter milk samples including the bacteriological status is currently being evaluated and preliminary results will be available soon. They will serve as reference to DHI samples and give more detailed insight into actual processes in the udder and the potential further value of CDI.

Keywords: udder health, DHI data, cell differentiation, somatic cell count, statistical models, prognostic key figures, bacteriological status.

Introduction

Mastitis is still one of the most common diseases in dairy farms, influencing not only animal welfare adversely but also the economic performance. Checking the somatic cell count (SCC) routinely in the course of DHI testing is the best way to indirectly assess the current udder health status of cows. Additional knowledge on how udder health is likely to develop in the future will be beneficial to farmers in order to establish even more effective udder health monitoring.

Differential somatic cell count in milk is described as a method to identify intramammary processes in the udder more precisely (Pilla *et al.*, 2013). The aim of the German ZellDiX project is to enhance the informative value of DHI results by evaluating the additional value of differential somatic cell count (DSCC) and by establishing statistical models that reliably predict future udder health.

Material and methods

Since the introduction of a new generation of devices (Fossomatic 7 DC, FOSS, Denmark) (Damm *et al.*, 2017), not only the total SCC, but also the differential somatic cell count (DSCC) can be analysed routinely in a high throughput manner allowing the assessment of the cell differentiation index (CDI). The CDI essentially reflects the proportion of macrophages in the total SCC. DHI data sets of 920,000 animals were routinely obtained on 19,000 different farms in Germany over consecutive months. The data set consisted of highly diverse farms in respect to size and management type. In the first step of the data analysis we fitted two statistical models, one for chronic SCC elevations and one for stable good udder health. Chronic elevations were defined as cell counts above a defined threshold in the next two DHI measurements. In order to meet different farmers' needs, results were derived for SCC thresholds between 200,000 and 700,000 cells/ml. Cows with stable good udder health had SCC values below 100,000 cells/ml in the next two DHI measurements. For mathematical modelling, we used generalized additive models (GAM) (Wood, 2008) with penalized cubic regression splines. Both models were 10-fold cross-validated and tested using internal and external validation data. In addition to these predictions, GAMs allowed us to identify biases in the underlying data set and the impacts of individual parameters.

In an initial step, a descriptive analysis of the data pool was done in order to characterize the correlation of cell count and CDI using the software "R" (Version 3.52, R Foundation Vienna). Heat maps were used to visually describe the probability for a cell count increase in the next month in relation to CDI and cell count in the initial month (Figure 1).

In a second step, models were established in order to predict individual risks for stable udder health (Figure 2) and for chronic udder impairment considering different initial SCC values (Figure 3). The additional value of CDI was evaluated for SCC-only models and full models (Figure 4).

Results

The descriptive analysis shows, that for animals with an already elevated current cell count above 200,000 SCC/ml the combination of cell count and CDI has good potential for predicting a sustained cell count elevation (next 2 months above 200,000 SCC/ml). This can be seen in Figure 1 where we have both a vertical and horizontal color gradient. Especially for current cell counts between 300,000 and 3 million SCC/ml lower CDI are associated with lower probabilities and with a rising CDI the probability of sustained cell count increases (up to 80%).

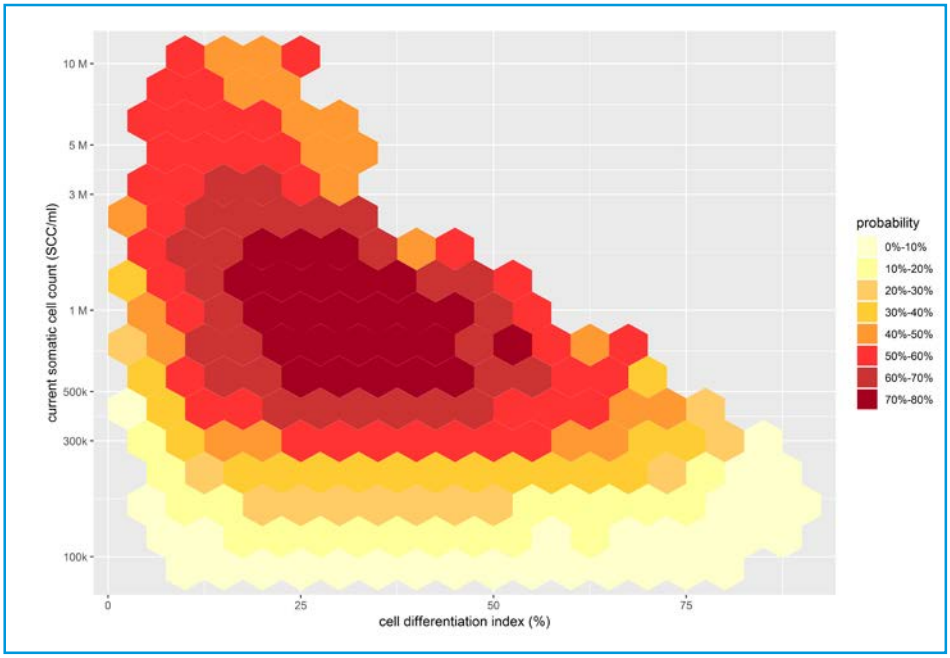

Figure 1. Probability of chronic udder impairment. Cell count above 200,000 cells/ml in the next two months, depending on cell differentiation index (CDI %) and initial cell count above 100,000 cells/ml.

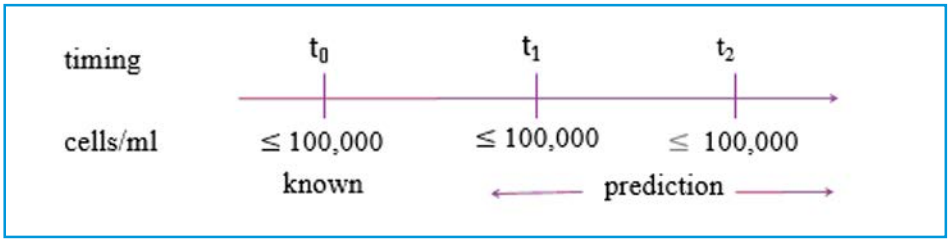

Figure 2. Model for stable udder health: For every animal with a current SCC d" 100,000 cells/ml, the probability for low cell counts in the next two months is calculated.

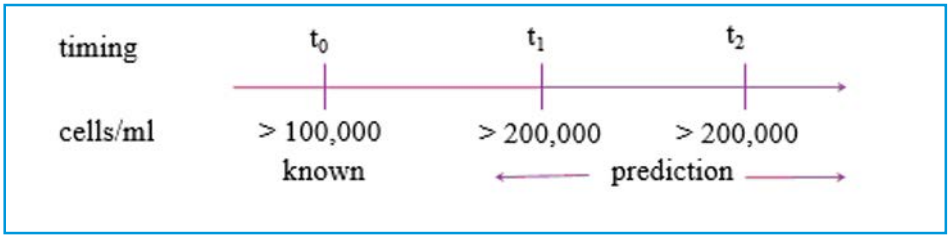

Figure 3. Model for chronic udder impairment: For every animal with a current elevated SCC > 100,000 cells/ml, the probability for high cell counts in the next two months is calculated.

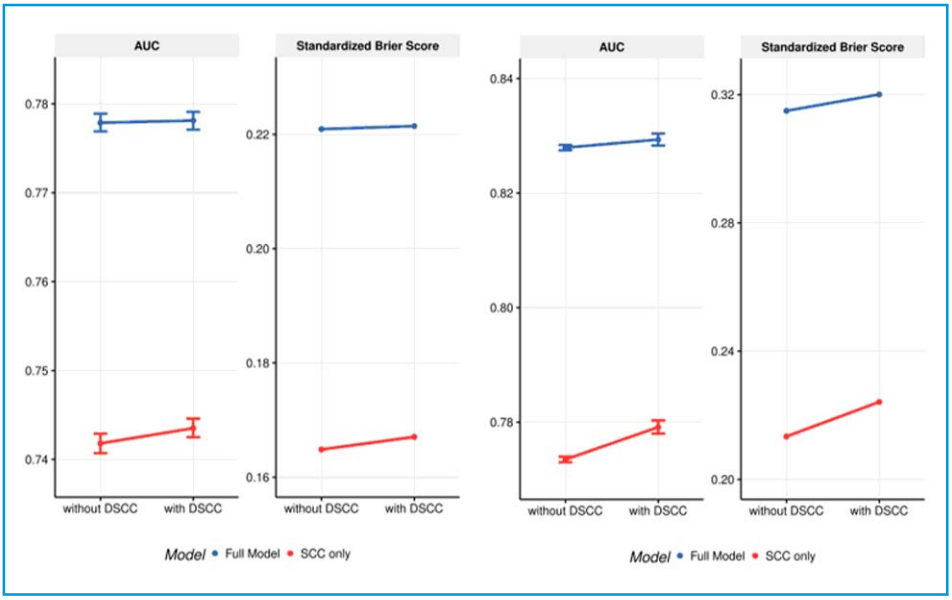

Figure 4. Comparison of model accuracy for different models for (left) stable udder health (Figure 2) and (right) chronic udder impairment (Figure 3) with and without CDI. SCC-only models (red) include current and historic cell counts. Full models (blue) include additional DHI information such as: milk yield, DIM, age, lactose content, fat:protein ratio, proportion of udder healthy cows and new infection rate on the farm.

The predictions of the models accurately reflected the real probability, independent of region, size and breed composition of a farm as tested by multiple validation approaches. The AUC of the chronic udder health model at a SCC threshold of 400,000 cells/ml was 0.868 [95% CI 0.866 – 0.870] with a calibration slope of 0.995 [95% CI 0.983 – 1.006]. For the stable udder health model, the AUC was 0.780 [95% CI 0.779 – 0.781] and the calibration slope was 0.993 [95% CI 0.990 – 0.996].

Conclusion

As shown in Figure 1, the probability for cell counts > 200,000 cells/ml in the next two months can depend on the level of CDI, especially for animals with current cell counts between 300,000 and 3 million cells/ml. This additional value can be confirmed by values for AUC and standard brier score for the SCC-only model (Figure 4, red). However, when improving the overall model performance by including other available DHI results, the additional value of CDI is minimal (Figure 4, blue).

Recently the full models for stable udder health and for chronic udder impairment were presented and discussed among pilot farms. They were described to be a helpful tool in order to rank animals with different individual risks and to facilitate management decisions, such as the treatment with antibiotics. With these pilot farms a practical evaluation was started in April 2019.

Outlook

As reference for udder health, an experiment including 2,500 dairy cows was conducted over a period up to 6 months: SCC and cell differentiation were analysed from DHI samples as well as from quarter level samples of the same animals. Additionally, mastitis pathogens were identified from quarter level samples. The data of this experiment will be analysed shortly, allowing to better characterize the additional value of CDI.

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"KetoMIR2" - modelling of ketosis risk using vets diagnosis and MIR spectra for dairy cows in early lactation

A. Werner[1], F. Gollé-Leidreiter[1], K. Droessler[1], F. J. Auer[2], M. Mayerhofer[3], A. Köck[3], C. Egger-Danner[3]and L.M. Dale[1]

[1]*Regional association for performance testing in livestock breeding of Baden-Wuerttemberg (LKV - Baden-Wuerttemberg), Heinrich Baumann Str. 1-3, 70190, Stuttgart, Germany*
Corresponding Author: ldale@lkvbw.de
[2]Regional association for performance testing in livestock breeding of Austria (LKV - Austria), Dresdner Straße 89/19, A-1200 Wien, Austria
[3]ZuchtData EDV-Dienstleistungen GmbH, Dresdner Str. 89, 1200 Wien, Austria

Abstract

Ketosis is a problematic disease in dairy cattle and it is a metabolic disorder in ruminants, it is producing indigestion and decreasing food consumption; as well it may increase milk fat percentages and ketone bodies and induces a rapid decrease in milk yield. Because ketosis is associated with a wide range of characteristics that can be measured in milk and with recent advances in the estimation of milk components using mid-infrared (MIR) spectrometry, now exists the possibility to determine the composition of several additional milk or blood components such as: negative energy balance or ketone bodies: acetone and â-hydroxybutyrate and citrate milk components, or blood components, such as: BHB, NEFA, glucose und IGF1, etc. The underlying idea is currently to build spectrometric tools, for dairy cows' ketosis risk determination based on veterinary diagnosis and milk MIR spectra from routine milk recording.

The first approach, KetoMIR1, was based on milk components predicted from standardised milk MIR spectra and is routinely applied by LKV Baden Württemberg and LKV Austria since 2015 respective 2017. The objective of this study was to improve the KetoMIR1 model by directly using the milk MIR spectra and other modelling approaches. The trial data set contains around 810,496 spectral data from around 10,079 LKV Baden Württemberg and LKV Austria herds participating in health monitoring programs. The spectral data set was first pre-processed by Savitzky-Golay first derivative to remove the offset differences between samples for baseline correction, before performing Legendre polynomial modelling. To identify the main variables that were positively or negatively associated with ketosis determination, the data was submitted to logistic regression in combination with lasso parameter optimization using the "glmnet" R package. For the non-healthy group the spectral data recorded within $\pm$14 days around a ketosis diagnosis was used. For the healthy group only spectra which had no diagnosis associated within $\pm$60 days were used.

Furthermore, the sampling moment, lactation stage and important breeds and the Legendre polynomial data based on days in milk correction for the 212 OptiMIR selected wavenumbers of spectral data were input variables for KetoMIR2 model. The validation approach was first 10 fold cross validation and an external validation set from a lot of 11 representative farms was selected. The KetoMIR2 calibration model showed medium sensitivity (0.72) and good specificity (0.84). It has to be underlined that no information

could be found in the literature of direct use of spectral data to predict the ketosis threat. The ketosis was usually detected using ketostix, blood analysis or by modelling of BHB, acetone or citrate in milk.

The KetoMIR2 model shows better classification as KetoMIR1. KetoMIR2 model probability shows high correlation with NEB, BHB and milk yield. KetoMIR2 provides three classes of ketosis warning such as not, moderately and severely endangered. The moderately endangered class is a signal for the farmer. In that case the farmer would contact the veterinary and a control would be made in order to prevent the ketosis diseases in time. The KetoMIR2 prediction can also be used in herd management to detect general feeding deficiencies in the late and early lactation transition period at herd level.

Keywords: KetoMIR, ketosis risk, ketosis detection, early lactation, MIR milk spectra, dairy cow, dairy farming

Introduction

Because ketosis is associated with a wide range of characteristics that can be measured in milk and with recent advances in the estimation of milk components using mid-infrared (MIR) spectrometry, now exists the possibility to determine the composition of several additional milk or blood components such as: negative energy balance or ketone bodies: acetone and beta-hydroxybutyrate and citrate milk components, or blood components, such as: BHB, NEFA, glucose und IGF1, etc. The underlying idea is currently to build spectrometric tools, for dairy cows' ketosis risk determination based on veterinary diagnosis and milk MIR spectra from routine milk recording. The first approach, KetoMIR1 (Hamann et al . 2017), was based on milk components predicted from standardised milk MIR spectra and is routinely applied by LKV Baden-Württemberg and LKV Austria since 2015 respectively 2017. The objective of this study was to improve the KetoMIR1 model by directly using the milk MIR spectra and other modelling approaches. Furthermore a more robust and transnationally applicable MIR model was envisioned by combining reference data and standardized spectra produced by different FTIR analyser models in different milk recording organisations.

Material and methods

The trial data set contained 810,496 spectral data from 10,079 LKV Baden Württemberg and LKV Austria herds participating in health monitoring programs at least for one year. Since ketosis is a mainly a problem in early lactation only days in milk ranging from 5 to 120 days in milk (DIM) were taken into account. The spectral data set was first standardized by applying the OptiMIR/EMR method (Grelet *et al.,* 2015) and pre-processed by Savitzky-Golay first derivative to remove the offset differences between samples for baseline correction, before performing Legendre polynomial modelling. To identify the main variables that were positively or negatively associated with ketosis determination, the data was submitted to logistic regression in combination with lasso parameter optimization (Friedman *et al.* 2010) as implemented in the "glmnet" R package. For the non-healthy group the spectral data recorded within $\pm$14 days around a ketosis diagnosis was used. For the healthy group only spectra which had no diagnosis associated within $\pm$60 days were used. The sampling moment, lactation stage and important breeds together with the Legendre polynomial data based on days in milk correction for the 212 OptiMIR selected wavenumbers of spectral data were input variables for KetoMIR2 model. The calibration was performed with 10 fold

cross validation on a subset of 1.472 non-healthy and 793.976 healthy data records. For external validation a subset of 18 representative farms was selected consisting of 166 non-healthy records and 14.882 healthy records.

Since logit binomial classification provides a sigmoid linear probability with a standard threshold of 0.5 there is the option of using this probability as a quasi linear index for risk of ketosis. The plausibility of this ketosis risk probability has been assessed by correlating it to standard milk components, new milk MIR components like ketone bodies (Grelet C. et al. 2016), fatty acids (Grelet C. et al. 2014), minerals (Soyeurt H. et al. 2009) and MIR based blood components (BHB, NEFA, Glucose, IBF1, Insuline, Calcium) (Dale L. et al. 2019 not yet published) or traits like energy balance (NEL and ME) (Dale L. et al. 2019) with the help of the R package “corrplot”.

Results and discussions

The KetoMIR2 calibration model showed medium sensitivity (0.72) and good specificity (0.84).in the external validation set. It also shows a better accuracy than KetoMIR1.

The application of the model to the LKV-BW and LKV-AT test subsets showed nearly equal accuracy supporting the assumption that transnational model creation and application is feasible. The accuracy of the breed test subsets showed comparable results for the single purpose breeds Holstein (HOL) and Brown-Suisse (BSW) but a lower sensitivity and higher specificity for the mixed purpose breed Simmental (SIM) which can be explained by the lower prevalence of Ketosis diagnosis in the Simmental calibration set.

Table 1. KetoMIR calibration and validation statistics.

Model	Calibration Set		Test Set	
	Sensitivity	Specificity	Sensitivity	Specificity
Final Model	0,76	0,84	0,72	0,83
LKV-AT	0,76	0,84	0,72	0,81
LKV-BW	0,76	0,85	0,72	0,84
SIM	0,73	0,86	0,58	0,88
BSW	0,79	0,79	0,72	0,81
HOL	0,79	0,82	0,76	0,83

As a result of the correlation analysis of the ketosis risk probability against different milk components the probability shows high positive correlation with blood NEFA (0.79), blood BHB (0.6), aceton (0.65) and the fatty acid C18-1Cis9 (0.73) but only medium positive correlation with fat/protein ratio (0.46) and Citrate (0.25). High negative correlations were found with energy balance (EB NEL and ME) (-0.78), glucose in blood (-0.67), IGF1 in blood (-0.66) and insulin in blood (-0.55) whereas medium negative correlations were found with middle chained fatty acids C12 (-0.44) and C10 (-0.44). However for the short chained fatty acid C4 a positive correlation of 0.4 was found.

The correlations fit well with the usual metabolic effects of extreme body fat mobilisations e.g. an increased concentration of NEFA, ketone bodies and long chained unsaturated fatty acids and the concentration decrease of middle chained fatty acids and an extreme negative energy balance. (Overton T.R. 2017) The positive correlation of the short fatty acid C4 could not be explained by a special physiological role as counterpart to

long chained fatty acids in order to stabilise the melting point of the milk fat. The lower correlation of the fat protein ratio shows that negative energy balance is better linked to fatty acid and ketone body profiles than to fat protein ratio.

The strong correlation with the main ketosis indicators justified the construction of a multi class scheme based on thresholds applied to the ketosis risk probability in order to overcome the restrictions of a binary classification in the central region of probability. As already done in KetoMIR-1 the probability was divided into three areas, a traffic light scheme, defining the classes as not, moderately and severely endangered associated with the colours green, yellow and red.

Since the shape of the sigmoid probability curve changes with increasing weeks in milk the probability thresholds were chosen per week of milk based on the assumption that the share of the medium and high risk classes is constantly shrinking from 5 to 120 DIM. Based on these class definitions further analysis was done showing that the prevalence of ketosis and other related diseases like displaced abomasum as well as fertility problems is higher in the endangered classes than in the not endangered class.

Conclusions

It has to be underlined that no information could be found in the literature of direct use of spectral data to predict the ketosis risk. The ketosis was usually detected using ketostix, blood analysis or by using thresholds of BHB and Acetone concentration in milk and BHB and NEFA concentration in blood. The KetoMIR2 model shows better classification as KetoMIR1. The KetoMIR2 model probability predictions show high correlation with common ketosis indicators like NEFA, BHB, Acetone and fatty acids and a stagnation and drop of the milk yield with higher probability values. KetoMIR2 provides three classes of ketosis warning such as not, moderately and severely endangered with room for a local adaption of the thresholds. The moderately endangered class is a signal for the farmer. In that case the farmer would contact the veterinary and a control would be made in order to prevent the ketosis diseases in time. The KetoMIR2 prediction can also be used in herd management to detect general feeding deficiencies in the late and early lactation transition period at herd level. KetoMIR2 has been developed in the international big data project D4Dairy – P2.2 Disease Detection with Milk Spectral Data (*https://d4dairy.com/en*, 2018 - 2022). Within this project the model will be further evaluated and optimized for use in routine herd management and breeding.

Acknowledge

This work was conducted within the COMET-Project D4Dairy that is supported by BMVIT, BMDW and the provinces of Lower Austria and Vienna and developed within the framework of the EMR standardisation of MIR spectral data (European Milk Recording EEIG).

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From new milk-testing parameters to new DHI services. The view of an instrument manufacturer

D. Schwarz

FOSS Analytical A/S, Foss Alle 1, Hilleroed, Denmark
Corresponding Author: das@foss.dk

Abstract

FOSS has a long history in developing analytical solutions and introducing new parameters to the industry. The objective of this study is to provide an overview on the implementation of new milk-testing parameters in practise and how they can become new DHI services that can be offered and utilised by the dairy industry. Specifically, examples on quality assurance as well as the actual practical application for the parameters differential somatic cell count (DSCC), beta hydroxybutyrate (BHB) and acetone (i.e. ketosis screening), and fatty acid profiling, respectively, will be presented.

Mastitis is still the most costly disease in dairy farming. DSCC represents the proportion of specific immune cells (neutrophils (PMN) and lymphocytes vs. macrophages) and thus provides more information about the actual udder health status of dairy cows. The results of a recently concluded study clearly demonstrate that the test performance (i.e. sensitivity) for identification of mastitis increases applying the combination of DSCC and SCC as compared to SCC alone. This, in turn, opens up the possibility to develop new tools for improved management of mastitis such as more targeted mastitis screening as well as selective dry cow therapy, which are both currently tested under practical conditions.

Ketosis is a costly metabolic disorder, which usually occurs in dairy cows during the early lactation period when energy demands for milk production exceed energy intake. Milk BHB and acetone in regularly available DHI samples can be predicted using Fourier transform infrared (FTIR) technology. Quality assurance procedures for ensuring generation of reliable data have been developed and documented. The application of the data is different among DHI laboratories/organisations. While ketosis screening services are based on milk BHB results only in some countries, the data is incorporated in decision trees in other countries.

The milk fatty acid profile contains a lot of information about the processing properties of milk as well as the nutritional status of dairy cows. Various different practical applications and quality assurance tools are used around the world.

In conclusion, milk samples harbour a lot of information and, besides the traditional parameters, new tools as well as services that can be offered to the dairy industry help to increase the value of milk testing. However, dairy farmers and farm advisors are rather in need of meaningful information than in need of raw data. It is therefore clearly in the interest of FOSS to share global experiences on new parameters as well as actively participate and contribute to the development of new milk-testing based DHI services.

Keywords: milk analysis, mastitis, ketosis, fatty acid profile

Introduction

Production related diseases in dairy cows (e.g. mastitis, ketosis) often remain undetected or untreated given their subclinical character and thus cause significant economic losses to dairy farmers as well as adversely impact animal welfare.

Mastitis, the inflammation and/or infection of a cow's udder typically caused by bacteria, is still causing tremendous losses of •32 billion to the dairy industry worldwide and thus the most costly disease in milk production (Seegers *et al.*, 2003; Halasa *et al.*, 2007).

Ketosis, a metabolic disorder in high yielding dairy cows, where energy demands exceed energy intake is another issue causing significant economic losses on dairy farms nowadays. The incidence of ketosis has been estimated to be 25-60% in dairy herds with costs of •260 per case (Mc Art *et al.*, 2013, 2015; Mahrt *et al.*, 2015).

Milk samples on individual cow and herd level are available regularly through dairy herd improvement (DHI) and payment testing, respectively, and it is thus convenient to utilise such readily available samples for determining more parameters than SCC, fat, protein, and lactose.

The objective of this study is to provide an overview on the implementation of new milk-testing parameters in practise (particularly through DHI testing) and how they can become new DHI services that can be offered and utilised by the dairy industry.

Mastitis

Somatic Cell Count (SCC), representing the total number of cells in milk, is a well-accepted and broadly used indicator for mastitis and milk quality (e.g. Schukken *et al.*, 2003). Since its introduction in the 1970s the regular and inexpensive determination of SCC on individual cow level as well as the implementation of incentives in terms milk prices depending on the actual quality of milk (e.g. SCC level) have contributed significantly to the improvement of udder health. Data from the Netherlands illustrate this positive development: average bulk tank SCC dropped from 600,000 cells/ml in 1971 to 200,000 cells/ml in 2002 (Figure 1).

Differential Somatic Cell Count (DSCC) is a new parameter indicating the percentage of individual immune cells (i.e. PMN combined with lymphocytes) in milk (Damm *et al.*, 2017; Schwarz, 2017a). DSCC is known to increase significantly as a results intramammary infection (i.e. mastitis) as described elsewhere (Schwarz *et al.*, 2018; Wall *et al.*, 2018).

The combination of SCC and DSCC leads to an improvement in the identification of mastitis cases through DHI testing (unpublished data). This, in turn, can serve as basis for improved mastitis management in the frame of DHI testing and as a result to further improvements regarding udder health on dairy farms.

Besides providing the industry with innovative analytical solutions, FOSS actively helps in the establishment of SCC for improving milk quality in developing countries by sharing best practises etc. in dedicated seminars. Furthermore, the implementation of (new) services for mastitis management based on SCC (and DSCC) is performed in close cooperation with the industry.

Ketosis

Milk beta-hydroxybutyrate (BHB) and acetone can be predicted from milk samples and used as indicators for ketosis. The possibility of using DHI samples and FTIR

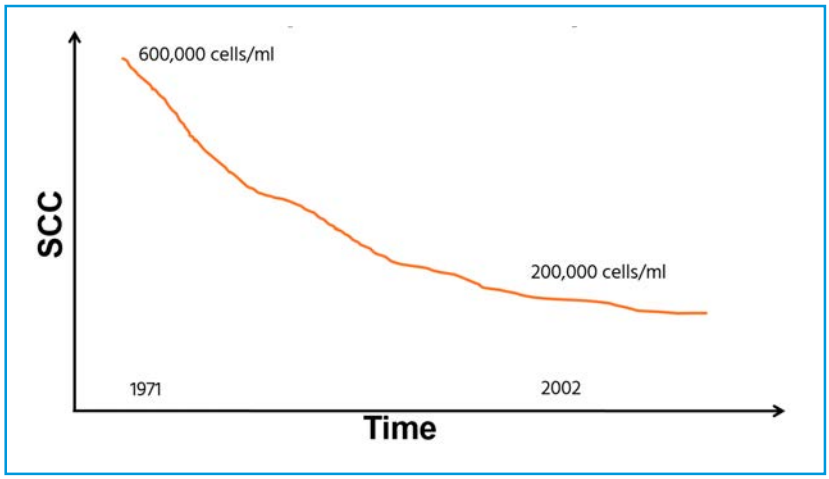

Figure 1. Development of average bulk tank SCC over time based on data from the Netherlands (according to Sampimon et al., 2005)

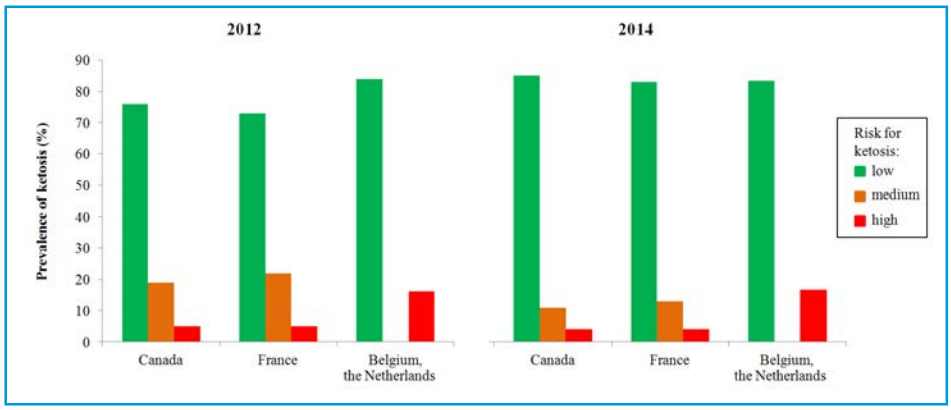

Figure 2. Prevalence of ketosis (low, medium, high risk) in Canada (Valacta), France (CLASEL) and Belgium (region Flanders) and the Netherlands (Qlip and CRV) in 2012 (left) and 2014 (right), respectively. Data for Belgium and the Netherlands are expressed as ketosis yes (high risk) or no (low risk).

technology for herd level ketosis screening with good values for sensitivity and specificity has been described elsewhere (de Roos *et al.*, 2007; Denis-Robichaud *et al.*, 2014).

Best practise cases on quality assurance procedures in laboratories (Schwarz *et al.*, 2015; Schwarz, 2017b; IDF, 2019) as well as the practical application of milk BHB and acetone results were described in various publications (e.g. Santschi *et al.*, 2016; Renaud *et al.*, 2019). Briefly, it is a practical and highly-valuable service that can be offered through DHI testing to help reducing the incidence of ketosis (Figure 2).

FOSS has documented best practise cases from around the world and, e.g., contributed to respective activities within IDF (preparation of IDF Bulletin on new IR applications). In close cooperation with the industry in terms of implementing ketosis screening as a new milk-testing service, FOSS is working on making ketosis screening available to more dairy farms worldwide.

Other applications

The milk fatty acid profile contains a lot of information about the processing properties of milk as well as the nutritional status of dairy cow.

Milk fatty acids can be determined differently, e.g. according to the degree of saturation, the chain length, and their origin (FOSS application notes 64 and 5465). While the focus of working with milk fatty acid profiles was mainly on improving dairy products (e.g. elevated content of unsaturated fatty acids) in the past, work in more recent years was rather focused on utilising the results for improving the nutrition of dairy cows (e.g. Jensen, 2002; Palmquist, 2006).

FOSS is actively involved in the development of quality assurance procedures to secure the reliability of the generated milk fatty acid data. Beyond that, various activities regarding the development of actual practical applications of milk fatty acid results are currently running. Any new developments will be shared in dedicated seminars.

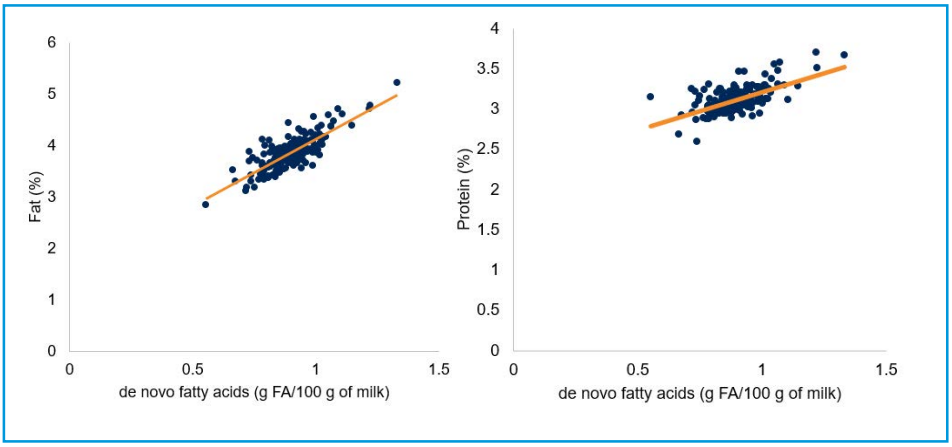

Figure 3. Exemplary data describing the interrelation between the de novo fatty acid content and milk fat (left) and milk protein (right), respectively.

Conclusions

Milk samples harbour a lot of information and, besides the traditional parameters (i.e. SCC, fat, protein, lactose), FOSS has developed new innovative parameters serving as basis for new services that can be offered to the dairy industry and help to increase the value of milk testing. However, dairy farmers and farm advisors etc. are rather in need of meaningful information than in need of raw data. Hence, it is clearly in the interest of FOSS to support the industry by sharing global experiences/best practise cases on the application of new parameters (e.g. through dedicated seminars) as well as actively participate and contribute to the development of new milk-testing based services.

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Wall, S.K., O. Wellnitz, R. Bruckmaier & D. Schwarz. 2018. Differential somatic cell count in milk before, during, and after artificially induced immune reactions of the mammary gland. J. Dairy Sci. 101:5362–5373.Fig 2. Interrelation between the de novo fatty acid content and milk fat (top) and milk protein (bottom), respectively.

Hyperketolactia occuring before or after artificial insemination and monitored in milk samples is associated with a decrease in conception in lactating dairy cows

M. Jattiot[2], A. Albaaj[1], L. Manciaux[2], S. Saille[2], C. Julien[1], G. Foucras[1], and D. Raboisson[1]

[1]IHAP, Université de Toulouse, INRA, ENVT, Toulouse, France
Corresponding author: A. Albaaj, Email: ahmad.albaaj@yahoo.com
[2]Bretagne Conseil Elevage Ouest, 1 rue Pierre et Marie Curie, CS 80520, 22195 Plérin Cedex, France

Abstract

The reproductive performance of dairy cows is a key parameter of profitability and sustainability, affected by many factors, such as a Negative Energy Balance (NEB). NEB leads to ketosis, characterized by an excessive production of circulating ketone bodies, like acetone and beta-hydroxybutyrate (BHBA) after calving. Estimation of milk Acetone and BHBA concentrations are now routinely available through new algorithms developed on the mid infrared spectroscopy profiles (MIR spectrum), providing large datasets. This offers new opportunities to study the changes in conception rates, in relation to hyperketolactia (HKL) around artificial insemination (AI). In this study, data were collected from a Milk Recording Program in West part of France during years 2013 to 2016.

Lactation characteristics and test-day milk results for all lactations has been included, as well as milk concentrations of acetone and BHBA, and data on artificial insemination. For each AI, conception was considered as a binary trait and defined as successful if it was followed by a calving after a referent pregnancy period. Many thresholds were considered and tested as positive test to define cows with HKL, which were then categorized into four classes according to the HKL dynamics before and after AI.

A two-step statistical analysis was performed, using R software. First, the best thresholds to define the categorical variables SCC, DIM (Day In Milk) and 305d MY (Milking Year) to be included in the final logistic regression (second step) were obtained through generalized additive models. Then, a logistic regression with a Poisson correction was performed, using a step-by-step procedure to include explanatory variables. The final model included the HKL categorical variables defined by the different Acetone and BHBA thresholds and was adjusted by the variables DIM, parity, and 305d MY, and herd as a random variable. SSC dynamics, DIM, 305d MY and parity were significantly associated with conception success in all models. No interaction between the above mentioned variables or with HKL was detected.

HKL defined by Acetone or BHBA concentrations before or after AI was significantly associated with a decrease in conception, depending on the threshold, the milk component and the class (HL, HH, LH). High milk BHBA values were associated with a 4 to 14% less likely conception compared to low ones, whatever the BHBA increase is seen before AI, after AI or both. High Acetone after AI was associated with a more

than 10% less likely conception for all thresholds > 0.10 mM, but not before AI. The significant association between HKL after AI and conception has never been reported before.

The negative association between HKL and reproductive performance is consensual and based on pathophysiological and epidemiological evidence. However, the potential physiological mechanisms to explain such association remain not completely defined. The present results suggest that ketosis should be considered as a risk factor for deteriorated reproduction performances and consequently should be of interest for farm advisors.

Key words: hyperketolactia, conception, BHBA, acetone, dairy cows.

Introduction

The reproductive performance of dairy cows is a key parameter of profitability and sustainability. Many factors affect reproductive performance, such as a Negative Energy Balance (NEB). NEB leads to fat mobilization characterized by an excessive production of circulating ketone bodies, like acetone and beta- hydroxybutyrate (BHBA) after calving (Duffield *et al.*, 1998), which defines Ketosis. Two recent meta- analysis highlighted that a decrease in reproduction performance were associated with hyperketonemia (Raboisson *et al.*, 2014, Abdelli *et al.*, 2017).

Estimation of milk Acetone and BHBA concentrations are now routinely available through new algorithms developed on the mid infrared spectroscopy profiles (MIR spectrum). Large datasets available on milk ketones offer new opportunities to study outcomes associated with subclinical ketosis or hyperketonemia. The aim of this presentation is to quantify the changes in conception rates, in relation to hyperketolactia (HKL) around artificial insemination (AI).

Materials and methods

Data and variables

Data were collected from a Milk Recording Program in West part of France (BCEL Ouest; *http://www.bcel- ouest.fr*) during years 2013 to 2016. Lactation characteristics and test-day milk results for all lactations has been included. Data on artificial insemination were available and collected using MySQL software (MySQL, version 5.0, Oracle Corp., Redwood City, CA). For each AI, conception was considered as a binary trait and defined as successful if it was followed by a calving after a referent pregnancy period.

Milk concentrations of acetone and BHBA were measured during 4 months after calving in the local official laboratory for milk analysis (Mylab *http://www.labo-mylab.fr/,* with a MilkoScan®-FOSS analyzer, using the Fourier transform mid-infrared (FT-MIR) spectrometry, after a specific calibration to predict acetone and BHBA contents. Many thresholds were considered and tested as positive test to define cows with HKL, which were then categorized into four classes according to the HKL dynamics for each AI and each threshold of Acetone or BHBA.

Table 1. Classes defining the HKL dynamic before and after AI.

	Dynamic after AI (acetone or BHBA)	
Dynamic before AI (acetone or BHBA)	Low	High
Low	LL	LH
High	HL	HH

Statistical analysis

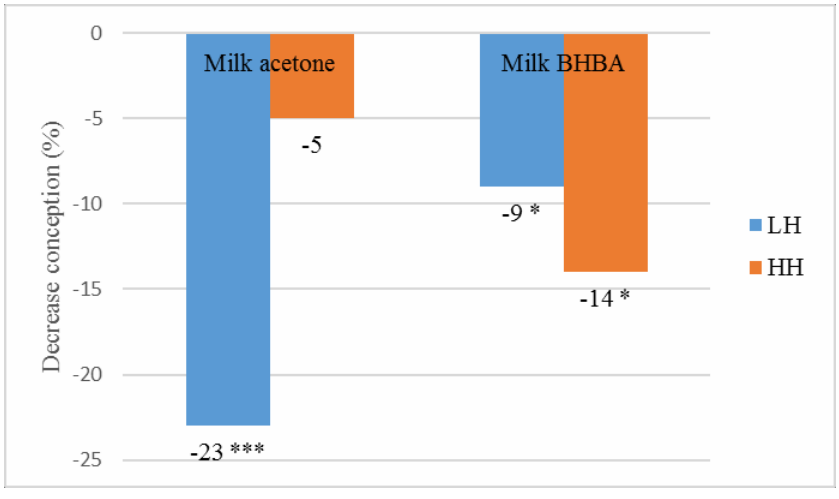
Data were analyzed using R (version 2.10.1, 2009–12–14, The R Foundation for Statistical Computing, Vienna, Austria). A two-step statistical analysis was performed. First, the best thresholds to define the categorical variables SCC, DIM (Day In Milk) and 305d MY (Milking Year) to be included in the final logistic regression (second step) were obtained through generalized additive models (GAM, package gam). Then, a logistic regression with a Poisson correction was performed using the package nlme, using a step- by-step procedure to include explanatory variables. The final model included the HKL categorical variables defined by the different Acetone and BHBA thresholds and was adjusted by the categorical variables DIM and parity, and the continuous variable 305d MY. All models included herd as a random variable and were applied either to the first AI following each calving or to all AIs.

Results

SSC dynamics, DIM, 305d MY and parity were significantly associated with conception success in all models. No interaction between the above mentioned variables or with HKL was detected. HKL defined by Acetone or BHBA concentrations before or after AI was significantly associated with a decrease in conception, depending on the threshold, the milk component and the class (HL, HH, LH). High milk BHBA values were associated with a 4 to 14% less likely conception compared to low ones, whatever the BHBA increase is seen before AI, after AI or both. High Acetone after AI was associated with a more than 10% less likely conception for all thresholds > 0.10 mM. Acetone before AI and conception were not associated.

Discussion

The negative association between HKL and reproductive performance is consensual and based on pathophysiological and epidemiological evidence (Raboisson *et al.*, 2014, Abdelli *et al.*, 2017). These associations are lower than the ones reported in previous trials. However, previously published models did not always include



*Significance: * p<0.05; *** P<0.001*

Figure 1. Percent decrease conception in case of HKL, compared to the LL class (threshold=0.2 mM).

co-variables, which strongly influences the coefficient value of the subclinical ketosis variable (Raboisson *et al.*, 2014). The lack of association between high Acetone before AI and conception remain unexplained.

The significant association between HKL after AI and conception has never been reported before. However, the potential physiological mechanisms to explain such association remain not completely defined.

Conclusion

The present work confirmed the link between high ketones in dairy cows and conception success, and highlight the association between HKL after AI and conception rate, what has never been demonstrated up to now. High ketones in advanced lactation are likely to be consecutive from various

primary disorders (secondary ketosis). Even if these situations are not primary ketosis, the present results suggest that it should be considered as a risk factor for deteriorated reproduction performances and consequently should be of interest for farm advisors.

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qPCR kits for fecal samples to identify the shedders of Paratuberculosis or Salmonella dublin among highly ELISA-positive cows

J. Katholm[1], D.B. Holt[2], A. Petersen[2] and T.W. Bennedsgaard[3]

[1]DNA Diagnostic A/S, Voldbjergvej 14, 8240 Risskov, Denmark
Corresponding Author: jk@dna-diagnostic.com
[2]DNA Diagnostic, Voldbjergvej 14, 8240 Risskov, Denmark
[3]Veterinarians Himmerland Cattle, Markedsvej 6A, 9600 Aars, Denmark

Abstract

The use of ELISA tests in milk and blood is a common way to find cows infected with Paratuberculosis (MAP), and in Denmark, Salmonella dublin as well. Because of the need for repeated sampling for MAP (due to low specificity of the ELISA test) the cost is relatively high. The results are a decreasing participation in the Danish MAP control program.

Among herds ELISA-positive for Salmonella in bulk tank milk, it is common to look for highly ELISA-positive cows, but often many cows are antibody positive, even infection-free animals, which makes it difficult to locate cows shedding the Salmonella. Therefore, in both disease complexes, there is a need for a test that enables farmers to find the right cows to cull, in order to reduce the presence of the pathogens in the herds.

DNA Diagnostic A/S, Risskov, Denmark, has developed two new qPCR tests, 'ParaTB', and 'Salmonella 4 Cows', both of which can be coupled to the same fecal extraction protocol, also developed by DNA Diagnostic A/S.

For the fecal test for MAP, a total of 46 cows listed as high ELISA-positives and 58 control cows (low ELISA signal) in the Danish control program, from the same herds, were tested by the ParaTB qPCR test. Only 26 (57%) of the high ELISA-positive cows was found to be high shedders of MAP bacteria in the fecal samples (Ct values <33). Of the 58 control cows 5 (9%) were shedding high numbers of MAP bacteria. Also, 169 cows from an assumingly negative herd were tested and all tested negative. Finally, fecal samples from 5 cows with diarrhea and clinical signs of MAP were tested, of which all tested positive (Ct values from 21,4 to 32,6).

For the fecal test for Salmonella dublin, a total of 55 high Salmonella ELISA positive (OD>100) cows, were tested, and only 7 (13%) were positive shedders of Salmonella bacteria. Among 402 cows with lower ELISA-positive Salmonella antibodies measurements in milk or blood, two extra shedders were found. All shedders were culled immediately. During the six months after the last PCR positive cows were culled, all newly introduced heifers where checked by milk ELISA at first test day. None of the animals showed seroconversion. This indicates that new infections seem to have stopped. On this farm, this is the first period in two years, that newly introduced heifers have not seroconverted for Salmonella dublin in the ELISA test before first test day.

The newly developed qPCR for MAP, 'ParaTB', and the qPCR for Salmonella (Salmonella spp. + Salmonella dublin), 'Salmonella 4 Cows', have shown to be highly effective in finding cows shedding the bacteria in fecal samples, and thereby motivating the farmers to effectively reduce the shedding of bacteria by culling shedding cows immediately.

Keywords: Paratuberculosis, Salmonalla dublin, ELISA, qPCR, culling strategy

Introduction

The use of ELISA tests in milk and blood is a common way to find problem cows with Paratuberculosis (MAP), and in Denmark, Salmonella dublin as well. Because of the need for repeated sampling for MAP (due to low specificity of the ELISA test) the cost is relatively high. It is common knowledge among farmers, that even high antibody-positive cows for MAP, are not going to show symptoms right away. Saxmose & Kirkeby (2016) found that 29% of cows listed as highly positive cows in Denmark, calved after being listed as high ELISA positives and stayed in the farm for an average of 1.4 years (max. 6.9 years). The results are a decreasing participation in the Danish MAP control program.

Among herds positive for Salmonella in bulk tank milk, it is common to look for highly ELISA-positive cows, but often many cows are antibody positive, which makes it difficult to locate cows shedding the Salmonella. Therefore, in both disease complexes, fecal qPCR is a tool to find the right cows to cull, in order to reduce the presence of the pathogen in the herds.

Material and methods

MAP trial

Fecal samples were collected in nine Danish dairy herds, between October 2018 – April 2019. In total 46 cows listed as high MAP ELISA-positives in the Danish control program and 58 control cows (ELISA negatives) from the same herds, was tested by the ParaTB qPCR test, DNA Diagnostic A/S, Risskov, Denmark. In addition, 169 cows from an expected complete negative herd (found negative in the Danish control program), as well as 5 cows from three different herds, of animals showing clinical symptoms of MAP, such as reduced weight and diarrhea, were tested.

Salmonella trial

In total 55 cows with high Salmonella ELISA signal (OD>100), and 402 cows with lower ELISA-positive measurements in milk or blood, was tested by the Salmonella 4 Cows qPCR test, DNA Diagnostic A/S, Risskov, Denmark.

Sample treatment, DNA extraction and qPCR

Fecal samples were collected in 'Faeces Tube 76mm x 20 mm' (Sarstedt, O/N 80.734) using the accompanied lid scoop, and stored at 4 °C until DNA extraction, for a maximum of four days. DNA extractions were performed according to supplier protocol ('ParaTB' / 'Salmonella 4 Cows', DNA Diagnostic A/S). Briefly, 7 mL 'Buffer F' was added to the Sarstedt Feces Tube containing the feces samples, and mixed. The tubes were centrifuged at 1000x *g* for 1 minute and 250 µL supernatant transferred to the supplied 2 mL 96-deep-well plate containing 'Beads solution'. The deepwell plate was centrifuged at 5000x *g* for 5 minutes, supernatant removed and pellet washed with 1 mL 'Wash

Buffer', followed by a second centrifugation step. 120 µL 'Lysis-I mix' was added to the pellets, and samples homogenized. The samples were transferred to supplied 0.2mL tubes (8-well-strips), and incubated at 37°C for 20 min, 95°C for 15 min and 4°C for 5 min. The resulting lysate was centrifuged at 5000x *g* for 5 minutes, and 4 µL supernatant transferred to a well in either a 'ParaTB' qPCR plate or a 'Salmonella 4 Cows' qPCR plate, containing all necessary components for the qPCR reaction. qPCRs were performed on a CFX96 Touch (Bio-Rad), an ABI 7500 Fast (Thermo Fisher), or a MX3005p (Agilent). qPCR analysis according to supplier protocol ('ParaTB' / 'Salmonella 4 Cows', DNA Diagnostic A/S)

Results

In table 1 it is shown that only 26 (57%) of the ELISA-positive cows was found to be high shedders of MAP bacteria in the fecal samples (Ct values <33). Of the 58 control cows, 5 (9%) were shedding high numbers of MAP bacteria. In the 169 fecal samples from cows in an assumingly negative herd all tested negative. Finally, fecal samples from the five cows with clinical signs of MAP all tested positive (Ct values from 21.4 to 32.6).

Table 2 shows that among the 55 high ELISA positive (OD>100) cows only 7 (13%) were positive shedding Salmonella bacteria.

Among the 402 cows with lower ELISA-positive measurements in milk or blood, two extra shedders were found. All shedders culled immediately after test results. None of the new introduced seronegative ELISA heifers showed seroconversion over a now 6-month period. This indicates that new infections seem to have stopped.

Table 1. Fecal qPCR and ELISA results from 46 positive cows and 58 control cows in the Danish MAP control program. Also 169 cows from expected negative herds tested negative in both test (not shown).

qPCR Para Tb

	ELISA in milk	
Fecal sample	**Pos**	**Neg**
Pos<33	26	5
Neg >33	20	53

Table 2. Fecal qPCR and ELISA milk and blod. Results from 55 high positive ELISA cows and 402 ELISA low positive or negative cows

qPCR Salmonella 4 cow

	ELISA in milk or blood	
Fecal sample	**Pos**	**Neg**
Pos < 37	7	2
Neg >37	48	400

Conclusion

The newly developed qPCRs for MAP, ParaTB, and the qPCR for Salmonella dublin, 'Salmonella 4 Cows', have shown to be highly effective in finding cows shedding bacteria for these two infections in fecal samples, and thereby motivating the farmers to effectively reduce the shedding of bacteria by culling these cows immediately.

Follow up test in the Salmonella positive farm in the six months after the last PCR positive cows were culled, all newly introduced heifers where checked by milk ELISA at first test day. None of the animals showed seroconversion. This indicates that new infections seem to have stopped. For this farm, it is the first time in two years, that newly introduced heifers have not seroconverted for Salmonella (ELISA test) before the first test day.

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Scoring animal welfare

B. Luntz[1] and D. Krogmeier[2]

[1]Institut für Tierzucht, Germany
[2]Department of Animal Science, Michigan State University, East Lansing, USA

Animal welfare and animal protection are essential criteria for our society in the qualitative assessment of food. The consumer combines healthy food from a food production according to the requirements of animal welfare. This requirement also applies to the keeping of our animals in stables.

Farmers are obliged to keep documentation on the condition of their herd. Farmers must already record animal welfare indicators as part of their own on-farm controls. In order to properly classify the results of the self-check, the livestock owner must be provided with evaluation criteria (target and threshold values). From these requirements it was interesting to carry out a screening of the current state of the Bavarian dairy farms. For this purpose, the classifiers of the Bavarian State Institute for Agriculture recorded in the year 2017 over a period of eleven months the characteristics of integument damage to the ankle joint, locomotion and contamination of the animal. The recording took place within the routine of linear type classification, on a five-step scale. The data were collected from cows for the linear exterior evaluation and were thus taken from a random sample. Within the project 29636 Fleckvieh cows in 6068 farms were evaluated according to these animal welfare criteria. The classification takes place according to the specifications of the definition in the classes.

In addition, information on farm management was also related via the LKV. An important aspect of this investigation was the type of stable. A total of 20 different stable construction variants were distinguished. For a simplified presentation, the walking stables were grouped together according to the high boxes or deep boxes systems and the various forms of fixed stables were also grouped together. The influences of the herd size and the milk yield of the farm were also investigated.

The existing systems of linear description in Fleckvieh and Braunvieh are based on the influence of life time. Therefore, it was interesting to investigate the relationship to the standard characteristics in the available data.

The evaluation of the stable construction variants shows clear differences. The critical evaluations of the features Integument and Locomotion with the numbers 1 and 2, are clearly lower in barns with deep boxes, compared to the variant high box. Planar floors have advantages over clafted floors. With the Integument feature, the conditions in the fixed stalls are no worse than in the barns with high boxes. The critical scores are about the same here. The characteristic contamination shows a worse picture in the fixed stables than in the walking stables. Here, the proportion of scores 1 and 2 is almost 50%. With increasing number of cows and herd performance, the animal welfare criteria were evaluated with a higher score.

An examination of the animal welfare criteria locomotion and integument in connection with the traits feet and legs shows that the breeding procedure also leads to more animal welfare. All individual characteristics and the main trait for feet and legs have positive correlations to the experimental characteristics. The Locomotion trait, which is officially recorded in the Holstein breed, is indirectly improved in Fleckvieh breeding. Animals with correct and functional legs show less Integument damage and run better. A breeding improvement of the foundation already has positive effects on animal health and welfare.

The collection of animal welfare indicators in the context of linear scored type traits makes it possible to produce comprehensive data material in a relatively short period of time. This provides a good overview of the situation in the various husbandry and production methods as well as in the various intensity levels in milk production. The clear separation of control tasks or even sanctions is important here, as in this case an objective and comprehensive performance test for exterior characteristics would be considerably more difficult.

Supporting German dairy farmers: establishing a monitoring system based on health key indicators extracted from existing control systems

S. Hachenberg[1], M. Au[1], B. Behr[1], J. Brinkmann[2], J. Braunleder[3], S. Carrasco[4], J. Duda[4], D. Doepfer[5], S. Gruber[6], H. Karatassios[7], M. Kussin[7], R. Mansfeld[6], S. March[2], K.F. Stock[3], M. Tremblay[5] and F. Onken[1]

[1]*German Association for Performance and Quality Testing, DLQ, Irmintrudisstraße 15, 53111 Bonn, Germany*
Corresponding Author: sabrina.hachenberg@dlq-web.de
[2]Thuenen-Institute of Organic Farming, Federal Research Institute for Rural Areas, Forestry and Fisheries, Trenthorst 32, 23847 Westerau, Germany
[3]*IT-Solutions for Animal Production (vit), Heinrich-Schroeder-Weg 1, 27283 Verden (Aller), Germany*
[4]*Landeskuratorium der Erzeugerringe für tierische Veredelung in Bayern e.V., Landsberger Straße 282, 80687 Munich, Germany*
[5]*University of Wisconsin, 2015 Linden Drive, Madison, WI 53706, United States of America*
[6]*Ludwig-Maximilians-Universitaet, Clinic for Ruminants with Ambulatory and Herd Health Services, Sonnenstraße 16, 85764 Oberschleißheim, Germany*
[7]*Osnabrueck University of Applied Sciences, Faculty of Agricultural Sciences and Landscape Architecture, Oldenburger Landstraße 62, 49090 Osnabrueck, Germany*

Abstract

German farmers are required by law to regularly self-assess the welfare of their animals. The project Q Check is aiming at developing a system that will assist farmers to objectively assess animal health and welfare in dairy cows. For this reason, a quarterly report will be compiled from animal-based key indicators to give an overview of the on-farm situation. The anonymised and aggregated reports can also be used for national animal welfare monitoring: Continuous collection of these key indicators enables the summary and publication of figures reflecting the current animal health and welfare status and progressions at federal state and at national level. Q Check is based on four data recording and analysis systems, which are already established in Germany and implemented on a national level. Out of these systems, the most suitable indicators to describe herd health have been selected by 215 experts within a two-stage Delphi study. In addition, over 50 face-to-face interviews with stakeholders related to the German dairy sector have been performed in order to take into account the socio-scientific point of view. To complete the process, the selected indicators are currently being checked against mass data and hence tested for suitability regarding monitoring purposes. An automatic farm-specific evaluation of animal health, based on verified indicators, will provide support to farmers in fulfilling their legal requirements and in identifying weak points on the individual farms. A benchmarking system will be set up which will allow tracking the individual herd health indicators in the same farm in their course over time and compared with similar farms. These routinely provided horizontal and vertical statistics will facilitate targeted intervention and support objectified management decisions, implying that dairy farmers can benefit in several respects. In the course of the project, new tools for determining the risk of ketosis in the scope of milk recording will also be validated and implemented at national level to

enhance monitoring of this major disease complex. The results of these nationwide, systematic investigations will contribute substantially to objectifying the discussion about the health and welfare situation of dairy cows.

Keywords: animal health, animal welfare, key indicators, self-assessment, national monitoring system, German dairy sector.

Introduction

Animal welfare is a multidimensional concept comprising health, behaviour and the emotional state of an animal (Fraser, 2008). In 2014, a farm-internal self-monitoring requirement has been added to the German animal welfare act. Consequently, dairy farmers are legally bound to self-assess and evaluate the welfare of their cows based on key indicators (see §11 article 8 TierSchG). Additionally, the Federal Ministry of Food and Agriculture aims at developing a national animal welfare monitoring system in order to collect animal welfare data on a regular basis (BMEL, 2019). While the legal regulations meet the consumers' and retailers' growing demands for milk production under high welfare standards, the regulations are challenging for dairy farmers, especially since there are neither definitions of suitable and reliable indicators nor appropriate documentation schemes which would safeguard legally proper implementation of monitoring routines in the dairy farms.

The aim of Q Check was the development of a set of on-farm indicators that is suitable and reliable for self-assessment of animal health and welfare based on existing data recording and analysis systems and minimizes the need for additional documentation. The intention was to identify indicators with additional value for the dairy herd health management. Furthermore, a benchmarking system (Turland & Slade, 2018) will be established in order to compare herd health status over time or between similar farms. The study design supports the transfer of anonymized individual animal welfare assessment results on an aggregate level into a national animal welfare monitoring system.

In order to cover another major disease complex, Q Check validates new tools for determining the risk of ketosis in the scope of dairy herd improvement (DHI) for the implementation on national level.

Methods and material

Q Check is based on four data recording and analysis systems, which are already established and implemented in Germany. The fully automated systems collect standardised animal related data:

1. DHI – with a coverage of up to 3.7 million cows or 89% of the German dairy cow population
2. Milk quality testing
3. National database for animal identification (HI-Tier)
4. Auditing system for quality management (QM-Milch)

Data collected by the systems above generally provide robust information. Data were pooled and cross-linked for the development of an overview with key indicators, in order to simplify the procedure of self-assessing animal welfare on-farm. Indicators had to be easily and automatically collected and supported by the dairy sector on a broad scale. A team of scientists, farmers and cattle veterinarians derived a set of

53 potentially suitable indicators from the systems mentioned above. The final selection and evaluation of the indicators has been performed following an interdisciplinary approach:

1. Two-stage Delphi survey: 215 Practitioners, scientists, vets and further stakeholders have been asked about their opinion on 53 preselected indicators, regarding their suitability for on farm self-assessment and/or national welfare monitoring.
2. Statistical validation: those indicators meeting approval from a two thirds majority of respondents in the Delphi survey have been determined using DHI mass data.
3. Stakeholder analysis: 51 face-to-face interviews have been conducted in order to gather differentiated points of view on the topic animal welfare.

Additionally, Q Check investigates new DHI analysis tools to detect poor metabolic adaptation syndrome, with the focus on early lactation. Based on machine learning algorithms prediction models are being applied, systematically optimized and automatized. The aim is to set up a nationwide routine analysis that enables farmers to react to metabolic malfunction at an early stage in terms of an early-warning system.

Results

On-farm self-assessment of animal health

Detailed analysis of the available data recording and analysis systems revealed the need to focus on health parameters. Q Check determined 13 relevant key indicators for describing animal health on dairy farms. Both normative and status quo based evaluation of selected indicators have been compared (see table 1). As shown in table 1, there is only a slight deviation within the two methods. In order to implement a framework for the evaluation of indicators, normative and status quo based evaluation will be aligned and further investigated.

Benchmarking system

In order to enhance the motivation of dairy farmers, the implementation of a benchmarking system is under progress. Due to major structural differences between dairy farms within Germany, all farms are classified by farm size and breed. This allows horizontal benchmarking next to vertical comparison. Access to an individual documentation and benchmarking report will be provided to every farm. The report will be published every three months and, respectively, once a year and contained a horizontal as well as a vertical comparison.

National animal welfare monitoring

Anonymized and aggregated results of the Q Check report will be used to picture the animal welfare status on national and federal state level on a yearly base. National animal welfare monitoring will reflect farm size and main breed as classified in the Q Check report.

Tool for early detection of poor metabolic adaptation

The development of a tool to detect poor metabolic adaptation at an early stage is still under progress. Results are expected until end of project in summer 2020.

Table 1. Results of welfare indicators and target values (tv) selected via Delphi survey (column one) and statistical analysis of DHI mass data (column two) for each indicator of the relevant set.

	Delphi[1]	Statistical Analysis[2]			
Indicator	tv	++	+	Median	-
Amount of cows with SCC ? 100,000/ml milk [%]	75	71	64	56	47
Amount of cows with SCC >400,000/ml milk [%]	5	5	8	11	15
Amount of heifers with SCC >100,000/ml milk [%]	12.5	0	17	27	38
New infection rate in the dry period [%]	10	13	16	20	25
Cure rate in the dry period [%]	75	81	70	58	44
New infection rate during lactation [%]	15	8	17	29	41
Amount of cows with chronically infected udders with poor cure prospects [%]	1.4	0	2	5	10
Amount of cows with a fat-protein-ratio ? 1.5 within 100 days p.p. [%]	10	4	7	11	17
Amount of cows with a fat-protein-ratio <1.0 within 100 days p.p. [%]	7.5	2	5	9	14
Culling rate [%]	25	18	23	29	37
Mean productive life time [months]	48	56	46	38	32
Calf mortality within 12 weeks [%][3]	5				
Cow mortality [%][3]	2.6				

[1]

Conclusion

The identified indicators represent only a selection within the wide range of animal welfare indicators suitable for cattle. Q Check is not limited to these indicators. Future developments might well add additional automated evaluations to the report as well as to the national monitoring.

Q Check proactively approaches major current challenges in German dairy farming: the four existing data systems form a validated basis while the selection process described above is scientifically approved to identify indicators that are suitable to illuminate important aspects of animal health in dairy farming. Additionally, the anonymized results in form of a national animal welfare monitoring can help to objectify the debate on welfare of dairy cows.

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Investigations on the relationship of dry matter intake and energy balance to health in German dairy cattle using conventional and genomic breeding values

N. Krattenmacher[1], E. Stamer[2], I. Harder[1], W. Junge[1]and G. Thaller[1]

[1]Kiel University, Institute for Animal Breeding and Husbandry, Hermann-Rodewald-Straße 6, 24118 Kiel, Germany
Corresponding Author: nkrattenmacher@tierzucht.uni-kiel.de
[2]TiDa Tier und Daten GmbH, Bosseer Straße 4c, 24259 Westensee/Brux, Germany

Abstract

The implementation of genomic selection has enabled selection for difficult-to-measure traits, like dry matter intake (DMI) or energy balance (EB). To improve health traits like metabolic stability, a less pronounced energy deficit postpartum is considered to be a key challenge. On the other hand, feed efficiency is gaining economic importance possibly leading to conflicts in the design of breeding goals.

Although several significant phenotypic associations between health and EB traits were reported in the literature, little is known about their genetic relationship as datasets containing the necessary information are still scarce and usually small.

For first lactating Holstein cows of the Karkendamm research herd it could be shown that animals belonging to the best 20 % of the herd with regard to classically estimated breeding values for EB represented the only group with positive average breeding values for metabolic stability.

Karkendamm data from 336 cows have recently also been used within the project “optiKuh”. The aim of this project was to build a German reference population for the traits DMI and EB. The total data set contained DMI records from 1,341 cows and EB records from 1,322 cows, respectively. 1,163 cows were also genotyped. Applying a random regression model and using the Single Step method, genomic breeding values for DMI and EB were estimated. In April, vit (Verden) published for the first time genomic breeding values for direct health traits (RZudderfit (mastitis resistance), RZhoof (- health), RZrepro (-duction), RZmetabol (-ic stability), RZhealth (total)) and this opens up the possibility to investigate the relationship of DMI and EB to health using genomic breeding values. A subset of 269 Karkendamm cows had genomic breeding values for both, EB traits and health traits. On average, the cows in the optiKuh reference population exhibited a negative EB during the first 75 days. Thus, health breeding values were correlated with both, the average lactation day 1 to 75 breeding values for DMI and EB (hereinafter referred to as “BV1-75”) and the average lactation day 1 to 350 breeding values for DMI and EB. Correlations were all positive and generally stronger if the BV1-75 were considered. The closest relationship was found between the BV1-75 for EB and RZhealth ($r=0.41$, $P < 0.0001$). RZmetabol was most closely correlated with BV1-75 for DMI ($r=0.35$, $P < 0.0001$ vs. $r=0.27$ ($P <0.0001$) with BV1-75 for EB), indicating that selection for decreased DMI might have detrimental effects on metabolic stability. This is especially relevant if DMI can be considered in the breeding

goal, but genomic evaluation for health traits is not (yet) possible. International collaboration (e.g. within the framework of the global Dry Matter Initiative II) is necessary to further enhance our knowledge on the associations between DMI, EB, and health traits.

Keywords: energy balance, dry matter intake, health

Introduction

The application of genomic selection has opened up the possibility to select for difficult-to-measure traits, like DMI or EB. However, selection for these traits has to be seen in the context of conflictive requirements regarding animal health and efficiency (Tetens *et al.*, 2014). To improve health traits (e.g. metabolic stability), a less pronounced energy deficit postpartum is supposed to be an important challenge. On the other hand, feed efficiency is gaining importance due to economic and ecologic reasons. Although several significant phenotypic associations between health and EB traits were reported in the literature (e.g. Collard *et al.*, 2000), little is known about their genetic relationship as datasets containing the necessary information are still scarce and limited in size. With exception of the Nordic countries, which have been recording health traits for many years, large-scale recording of health traits is limited to auxiliary traits or recording of direct health traits has only recently been implemented (Boichard and Brochard, 2012). The impact of selection for improved feed efficiency should be carefully considered to avoid potential negative consequences (Spurlock *et al.*, 2012; Veerkamp *et al.*, 2013), especially in countries where DMI can be considered in the breeding goal, but genomic evaluation for health traits is not yet possible. In this study, the relationship of DMI and EB to health in German dairy cattle was examined using both, conventional and genomic breeding values. The results give a first indication on whether undesirable genetic associations exist that should be considered and further studied.

Material and methods

Three different datasets provided the basis for the investigations. A summary of the datasets and used methods is given below.

Analyses based on conventional breeding values

1,589 Holstein Friesian primiparous cows were studied during their first 180 days in milk at the dairy research farm Karkendamm of the Institute of Animal Breeding and Husbandry, Kiel University, Germany. Within the observation period a bull dam performance test was run and all Karkendamm bull dam candidates had to complete a test period under commercial conditions until day 180 in milk. Non-qualified cows left the herd afterwards. Therefore, only records from the first 180 days in milk were used.

Disease data were recorded between 2000 und 2010. All medical treatments by veterinarians or farm staff were recorded and allocated to disease classes. Three disease categories were analysed: mastitis, claw and leg diseases, and metabolic disorders. Disease codes were generated in an analogous manner for all three categories. Each observation day was allocated a code, “1” if the cow showed a disease and “0” otherwise. For mastitis, the day of the treatment and the following five days in

milk were coded with "1". An 8-day disease period was considered for claw and leg diseases and metabolic disorders. Breeding values were estimated applying a threshold model.

Individual DMI, milk yield and live weight per day were recorded for day 11 to 180 in milk between 2006 and 2009. EB was calculated as the difference between energy intake and estimated energy requirements for milk output and maintenance. The results provided the basis for the estimation of EB breeding values for 526 cows using a random regression model.

Data and models were described in detail by Buttchereit *et al.* (2010).

On average, cows exhibited a negative EB during the first 42 days in milk, therefore, daily relative breeding values for EB from day 11 to 42 were averaged, grouped and related to relative breeding values for the three health traits.

Analyses based on genomic breeding values

Recently, data from the German project "optiKuh" have been successfully used to estimate sufficiently accurate genomic breeding values for DMI and EB. These breeding values were correlated to the newly available official genomic breeding values for health estimated by vit (Verden, Germany). The Pearson correlations between breeding values, albeit not as informative as genetic correlations, provide new insights into the genetic relationship among EB, DMI, and several health traits.

Breeding value estimation for DMI and EB

Karkendamm data from 336 cows were used within the project "optiKuh". The aim of this project was to build a German reference population for the traits DMI and EB. Data were recorded from 2014 to 2017 on eight German research farms (Braunschweig, Dummerstorf, Futterkamp, Hohenheim, Iden, Karkendamm, Neumühle, and Riswick). Feed intake data recording was standardized across farms. EB was estimated using phenotypic information on milk yield, milk ingredients, live weight, gestation stage, and feed intake. The total data set contained average weekly DMI records from 1,341 cows and average weekly EB records from 1,322 cows, respectively. 1,163 cows were also genotyped. Applying a random regression model and using the Single Step method, genomic breeding values for DMI and EB were estimated. The optiKuh dataset and the effects considered in the random regression model were described in detail by Harder *et al.* (accepted).

Breeding value estimation for direct health traits

In this year, vit (Verden) has introduced genomic breeding values for direct health traits. The data basis (n=676,508 cows and 1,490,285 lactations) came from animal health recording in herds (veterinarians, farmers, claw trimmers). The definition of the health traits was based on the German version of the ICAR Health Key. For the evaluation, 13 health traits were considered which can be assigned to four complexes: udder health, claw health, reproduction, and metabolic stability. The respective number of disease events within lactation was evaluated for all traits. An animal without any recorded information for a trait was defined as a healthy animal for this trait, provided that it was present in herd at least 75% of the trait specific time span without having a diagnosis. The time span for most traits included the entire lactation (day of calving to day 305 in milk). For mastitis, data from 10 days before calving were taken into account.

For traits predominantly occurring at the beginning of lactation, only records until day 50 in milk (retained placenta, (endo)metritis) or day 100 in milk (left-displaced abomasum, milk fever) were considered. For ovary cycle disorders, the risk period was defined as lactation day 51 to 305. Cows with health data collected in multiple lactations were considered as repeated observations. For "udder health", "reproduction" and "metabolic stability" breeding values were estimated within the respective trait complex using a multi trait animal model including repeated measures. Only for claw health traits the breeding values were estimated based on a single trait model including repeated measures. Comprehensive information on the genetic parameters, the statistical model and additional information traits (culling reason information of all cows under milk recording born from 1995 onward) can be found in the description of the genetic evaluation published at the vit-Homepage (VIT, 2019).

Considering the 336 Karkendamm cows with genomic breeding values for DMI and EB, a subset of 269 cows also had genomic breeding values for health traits and was used for further analyses.

Results and discussion

The relationship of DMI and EB to health was studied using conventional and genomic breeding values. These breeding values were estimated using distinct datasets. The analyses based on conventional breeding values were performed using only data from the pre-genomic era. For the analyses based on genomic breeding values, the data basis was more up-to-date and comprehensive, especially for the health traits. Therefore, we have placed greater emphasis on the results from the analyses based on genomic breeding values.

Analyses based on conventional breeding values

Figure 1 shows the average breeding values for claw and leg health, udder health and metabolic health plotted against breeding value classes for EB depending on the average breeding values from day 11 to 42. Primiparous cows with very low EB breeding values also had the worst average breeding values for claw and leg health. Udder health seems to be unaffected by EB, which is, however, not in line with the results from the analyses based on genomic breeding values. Most noticeable, the group of primiparous cows with the best EB breeding values was the only group with positive average breeding values for metabolic health.

Analyses based on genomic breeding values

On average, the cows in the optiKuh reference population exhibited a negative EB during the first 75 days, which was 33 days longer in comparison to the energy deficit period observed in primiparous Karkendamm cows recorded earlier (2006 to 2009 (dataset used for conventional breeding value estimation) vs. 2014 to 2017 (optiKuh dataset used for genomic breeding value estimation)). The duration of the negative EB found for the optiKuh reference population is in line with the results of Coffey *et al*. (2002) who reported that cows in lactation 1 to 3 returned to positive EB between day 72 and day 95 in milk. Moreover, studying primiparous cows of the Karkendamm herd, von Leesen *et al.* (2014) have already shown that the duration of the energy deficit postpartum has increased over time (42 days (Buttchereit *et al.*, 2010; data recording from 2006 to 2009) vs. 55 days (von Leesen *et al.*, 2014; data recording from 2006 to 2012)). Accordingly, the longer duration of the energy deficit period was considered

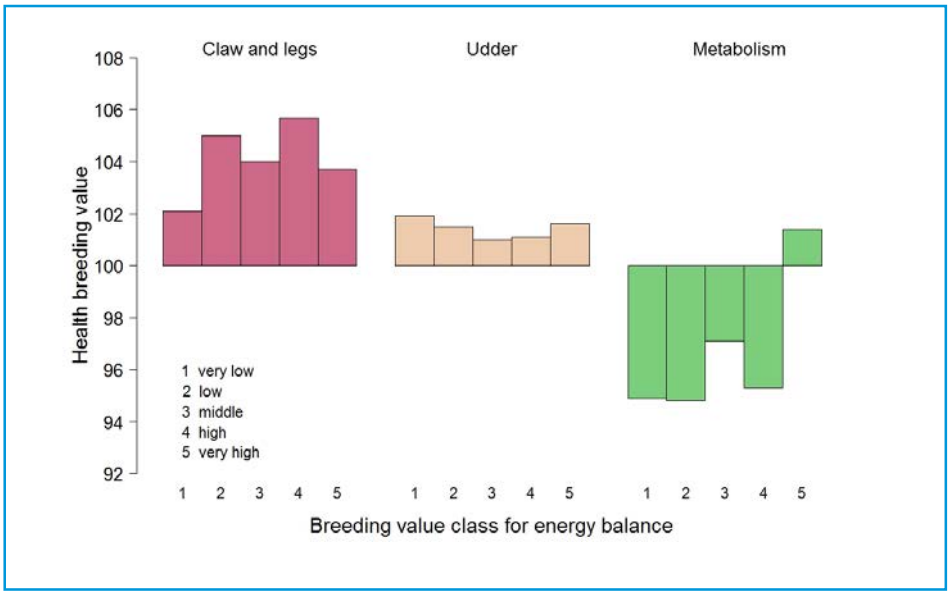

Figure 1. Average relative breeding values for health traits plotted against breeding value classes for energy balance (EB). All breeding values were derived from conventional breeding value estimation using threshold and random regression models, respectively, on data from cows recorded within the first 180 days in milk; on average, cows exhibited a negative EB during the first 42 days in milk, therefore, daily relative breeding values for EB from day 11 to 42 were averaged and used for grouping. Figure adapted from Figure 2 in Buttchereit et al., 2010 (n=526 Holstein Friesian cows).

for all analyses described below. Health breeding values were correlated with both, the average lactation day 1 to 75 breeding values for DMI and EB (hereinafter referred to as “BV1-75”) and the average lactation day 1 to 350 breeding values for DMI and EB. Correlations were all positive and generally stronger if the BV1-75 were considered (see Table 1), meaning that cows with a higher feed intake, especially in early lactation, are less prone to health problems. The most pronounced relationship was found between the BV1-75 for EB and RZhealth ($r=0.41$, $P < 0.0001$). RZmetabol was most closely correlated with BV1-75 for DMI ($r=0.35$, $P < 0.0001$ vs. $r=0.27$ ($P <0.0001$) with BV1-75 for EB), indicating that selection for decreased DMI might have detrimental effects on metabolic stability. This was in line with the findings from the analyses based on conventional breeding values, also suggesting that selection for a higher feed intake in the beginning of lactation would have favourable effects on metabolic health. Correlations with non-health traits including the total merit index are also given in Table 1. The results indicate that a selection for a less pronounced energy deficit postpartum would have no negative side-effects.

Analogous to the analyses based on conventional breeding values, the daily genomic breeding values for DMI and EB from day 1 to 75 were averaged, grouped (3 vs. 5 classes due to the smaller dataset) and related to the genomic breeding values for health traits (see Figure 2 and 3). The use of the genomic breeding values resulted in a clearer picture which is most probably due to the better data basis and more reliable breeding value estimation for the health traits. The findings indicate that a higher feed intake is beneficial with regard to all health traits. However, selection against severe energy deficits would be even more helpful in this context as the group differences were generally more pronounced.

Table 1. Pearson correlations between official genomic enhanced breeding values (gEBV) estimated by vit (Verden) and genomic breeding values for dry matter intake (DMI) and energy balance (EB) from the optiKuh-project (n = 269 Holstein Friesian cows).

Official gEBV for ...	Average lactation day 1 to 350 genomic breeding value for ...		Average lactation day 1 to 75 genomic breeding value for ...	
	DMI	EB	DMI	EB
Mastitis resistance	0.13	0.26	0.22	0.32
Claw health	0.26	0.30	0.30	0.32
Resistance to reproductive disorders	0.12	0.18	0.27	0.32
Resistance to metabolic disorders	0.27	0.20	0.35	0.27
Total health	0.23	0.32	0.34	0.41
Production	0.54	0.10	0.50	n.s.
Longevity	0.23	0.29	0.33	0.41
Reproduction	n.s.	n.s.	n.s.	0.14
Conformation	0.16	0.15	0.15	0.16
Total merit index	0.57	0.24	0.56	0.24

n.s. = not significant (p-value ? 0.05).

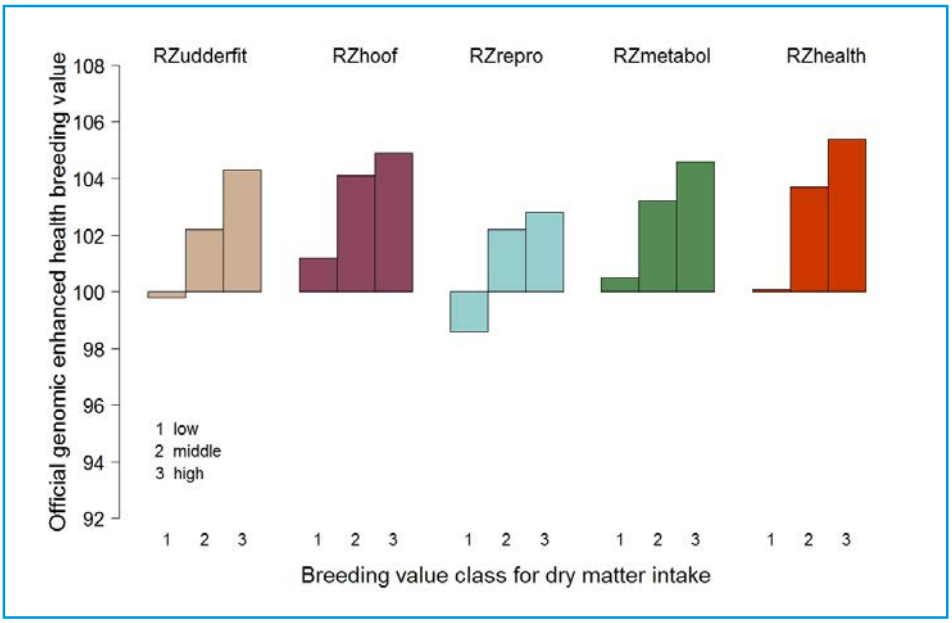

Figure 2. Official genomic enhanced breeding values for health traits (RZudderfit (mastitis resistance), RZhoof (- health), RZrepro (-duction), RZmetabol (-ic stability), RZhealth (total)) plotted against breeding value classes for dry matter intake (DMI). The DMI breeding values were derived from a genomic breeding value estimation using a random regression model and the Single Step method; on average, cows exhibited a negative energy balance during the first 75 days in milk, therefore, genomic breeding values for DMI from day 1 to 75 were averaged and used for grouping (n=269 Holstein Friesian cows).

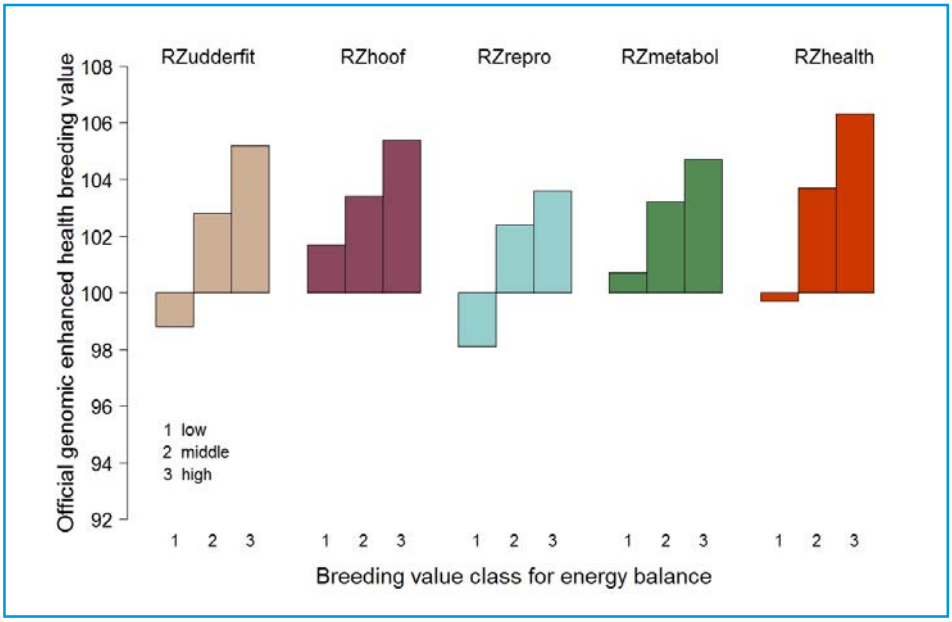

Figure 3. Official genomic enhanced breeding values for health traits (RZudderfit (mastitis resistance), RZhoof (- health), RZrepro (-duction), RZmetabol (-ic stability), RZhealth (total)) plotted against breeding value classes for energy balance (EB). The EB breeding values were derived from a genomic breeding value estimation using a random regression model and the Single Step method; on average, cows exhibited a negative EB during the first 75 days in milk, therefore, genomic breeding values for EB from day 1 to 75 were averaged and used for grouping (n=269 Holstein Friesian cows).

Conclusions

The results suggest that, with regard to health traits, selecting for higher feed intake or a less severe energy deficit in early lactation would be beneficial. This complicates the current efforts to improve feed efficiency. International collaboration (e.g. within the framework of the global Dry Matter Initiative II) can help to further enhance our knowledge on the genetic relationships between DMI, EB, and health traits, thereby enabling the design of balanced breeding goals aiming to avoid unwanted correlated responses, which is especially relevant for countries without a genomic evaluation for health traits.

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Measures to monitor and improve claw health, lameness and animal welfare in Austrian dairy farms

M. Suntinger[1], J. Kofler[2], R. Pesenhofer[3], C. Winckler[4] and C. Egger-Danner[1]

[1]ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria
[2]University Clinic for Ruminants, Department for Farm Animals and Veterinary Public Health, University of Veterinary Medicine, Vienna, Austria
[3]Federation of Austrian Claw Trimmers, Hitzendorf/Styria, Austria
[4]Department of Sustainable Agricultural Systems, Division of Livestock Sciences, University of Natural Resources and Life Sciences (BOKU), Vienna, Austria

Summary

Good claw health is a prerequisite for safeguarding animal welfare as well as efficient and economic dairy production. In Austria, since 2006, veterinary diagnoses related to claw alterations and diseases of the lower limb are routinely recorded in the central cattle database (RDV) together with other production disease diagnoses. However, different studies showed that the veterinarian diagnoses mostly cover records of cows with severe claw disorders. In contrast, data from claw trimming proved to be a valuable source of information to map claw health in a more comprehensive and continuous way. With the aim to improve claw health and animal welfare efficiently, data pipelines for claw trimming data, cow individual data on lameness and other animal-based welfare indicators related to leg health in Austrian dairy herds are currently being established within the project “Klauen-Q-Wohl”. This program was initiated by the Federal Association of Austrian Cattle Breeders (ZAR) in cooperation with the Federal Association of Austrian Claw Trimmers (AÖK).

Data logistics are being established that allow a detailed documentation by the claw trimmers as well as recording claw trimming information on a more general way by the farmers. This information is incorporated in a scheme to monitor welfare and to advice on measures for improvement.

The tool to improve claw health and welfare with focus on claw health and lameness related welfare aspects is based on farm individual risk factors and results from benchmarking. The so far established infrastructure for ICAR-standardized, electronic documentation of claw trimming data enables claw trimmers to send claw disorders by a single click via an interface to the RDV. Next to this, the infrastructure allows claw trimmers to recall animal information covering animal-ID, lactation number and stage of their supervised farms to their claw documentation software before trimming. This feature accelerates electronic documentation and ensures correct animal identification. So far, forty trained and certified claw trimmers have joined the project.

First experiences indicate that the advice provided to farms as well as farm management gains in quality. Once the data has been stored in the RDV, the farmer has access to this data via online herd management programs and/or a mobile app at all times. Claw health and other welfare-related data will be used to provide practical herd management solutions for farmers to promote the improvement of animal health as well as for breeding value estimation for claw and claw-related health traits.

Keywords: claw health, animal welfare, lameness, claw trimming, herd management, decision support, data logistics, advisory tool, risk factors.

Introduction

Good claw health is a prerequisite for safeguarding animal welfare as well as efficient and economic dairy production. In Austria, claw diseases rank among the most frequent causes of culling in dairy cows, i.e. about 8% in 2018 (ZuchtData, 2019). Costs of lameness have been estimated to amount to up to 450 Euros per lame cow and year (Kofler, 2015). Healthy claws are thus not only important for animal welfare, but also of economic significance. An important success factor for targeted measures to improve claw health and welfare are data. Data from claw trimming has proved to be a valuable source of information to map claw health in a comprehensive and continuous way (Heringstad *et al.*, 2018). Lameness records are valuable auxiliary traits for early detection of claw health problems, but can also be used for genetic improvement of claw health (Koeck *et al.*, 2019). Digital programs for the documentation of claw trimming events offer an important basis for monitoring of claw health in cattle. The immediate analysis of the data brings benefits for claw trimmers and their supervised farms (Kofler, 2013). In Austria, various educational institutions offer certified training programs for claw trimmers. Electronic documentation of the findings has already become a fixed part of these training programs. However, the acceptance of these software solutions has lagged behind the potential so far. As a response to the increasing consumer awareness regarding animal welfare and health, on-farm assessments are of high significance to safeguard animal well-being. The choice of the parameters plays an important role in the quality of the assessment of the animals' welfare status (Winckler, 2019). The project "Klauen-Q-Wohl" has been initiated to set up national data pipelines and to develop targeted tools to improve claw health and animal welfare in Austrian dairy farms. The paper describes the steps taken to achieve these aims.

Approach: the Project Klauen-Q-Wohl

In 2017, the Austrian project "Klauen-Q-Wohl" started. The title represents the two main working areas focusing on claw health and claw health related animal welfare indicators in dairy cattle. The aim of the project is to develop an infrastructure for electronic documentation of ICAR-standardized claw trimming data, lameness and claw health related animal welfare indicators and new practical tools and benchmarks for herd management and animal welfare. The multi-disciplinary project team builds a bridge between science and practice: Representatives from the Federal Association of Austrian Cattle Breeders, Federal Association of Austrian Claw Trimmers, performance recording organisations, animal health organisations, provider of software solutions as well as practitioners (claw trimmers, farmers). The participative approach aims at achieving the highest possible practicability, dissemination and acceptance of the results.

Measures

Central database

To enable comparisons between farms and genetic evaluation, it is important that data are centrally available. For improvement of claw health in terms of prevention, herd management and genetics as well as for monitoring of claw health and welfare, it is important that the claw health data can be linked to production data from the central cattle database (RDV). As the RDV is the common comprehensive cattle database in

Austria, the logistics for recording claw health and welfare within Klauen-Q-Wohl and agreements for data processing, according to the general data protection regulation, is based on the RDV.

Documentation and data recording of claw trimming data

Claw trimmers

An interface has been set up between the RDV and the claw trimming software program Klauenmanager. At the same time, ICAR-standardized definitions of claw disorders have been established on both sides. In order to advance documentation, claw trimmers are being financially supported in purchasing hardware and software. In return, they send the documented claw trimming data to the RDV. In the beginning of 2019, the project involved nearly 40 certified claw trimmers, who actively provide documentation to their farmers. To ensure data quality, regular training sessions including comparison of observers are held. The Klauenmanager program offers very precise documentation of foot and claw disorders (all ICAR claw lesions) covering severity and location on cow, leg and claw zone level as well as trimmed cows without disorders (scored healthy).

Farmers

A large number of farmers in Austria trim their cows' claws by themselves. Furthermore, there are claw trimmers who are not interested in the documentation, even if their farmers demand it. For this group of farmers the performance-testing organisation offers a herd management app and computer program with access to the animal list, which can be used to record claw trimming information at a more general level (main ICAR claw lesions). Data processing takes place directly within the central cattle database. A more attractive online and offline app especially for claw trimming practice is currently being developed.

Veterinarians

Veterinary diagnoses related to claw diseases are routinely recorded in the central cattle database (RDV) either electronically by the veterinarian or by the performance recording organisations. The diagnosis code currently covers only four claw-related diagnoses. The integration of the ICAR claw lesions in the RDV will also enable veterinarians to document claw diagnoses in a more precise way.

Documentation and data recording of lameness and claw health related animal welfare indicators

The measures to monitor claw health related animal welfare indicators cover the following areas:

- Animal-based welfare parameters: This includes parameters such as lameness scoring, BCS, claw position score, alterations of integument, cleanliness of upper and lower limb and production traits like fat/protein ratio.
- Management- and resource-based parameters which are also referred to as risk factors cover parameters such as stocking density, claw trimming interval, hygiene, feeding regime, access to pasture as well as descriptors of the housing equipment (e.g. cubicles, floor properties).

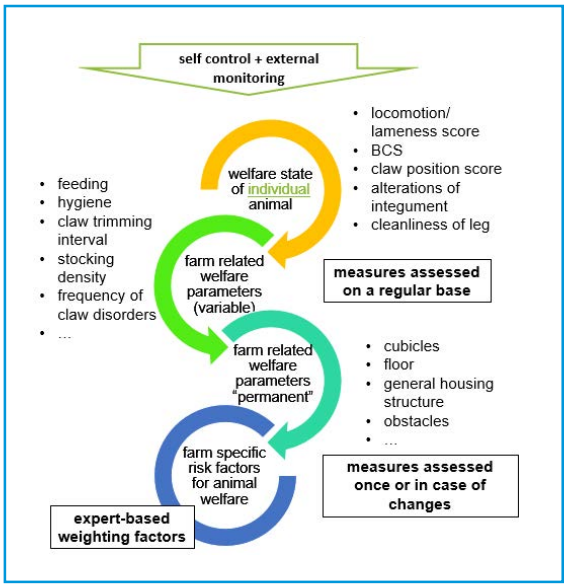

Figure 1. Different measures and factors aimed at assessing and improving animal welfare.

Some of the welfare measures mentioned above are assessed regularly while others are assessed only once or in case of changes (see Figure 1). For some welfare measures, existing data stored in the central cattle database are going to be used. Data logistics are being established that allow assessing animal welfare and other farm related parameters via mobile app and software programs.

Tools to improve claw health and welfare

Based on the recorded information the current situation of the farm in regard to claw health and animal welfare can be assessed and monitored. Benchmarks to compare farms and claw trimmers across their trimmed herds will be provided in near future. A tool supporting analysing risk factors and developing targeted measures for improvement is under research.

Current state

The data flow shown in Figure 2 shows that the efforts in the project are successful. In March 2019, approximately 5000 claw-trimming records have been submitted to the RDV, and the trend is increasing. The main seasons for claw trimming are autumn and spring, which is well indicated by the shape of the curve. With increasing public relations activities and the provision of technology for documentation, the willingness of farmers for electronic documentation also increases.

The data interface described above is not a one-way street. Claw trimmers have the possibility to recall the daily updated animal-ID list of their farms. Benchmarks between claw trimmers and across their trimmed herds will be provided in near future. Once the data has been stored in the RDV, the farmer has access to this data via online herd management programs and the mobile app at any time. A claw health module embedded in the existing herd management program for farmers and veterinarians,

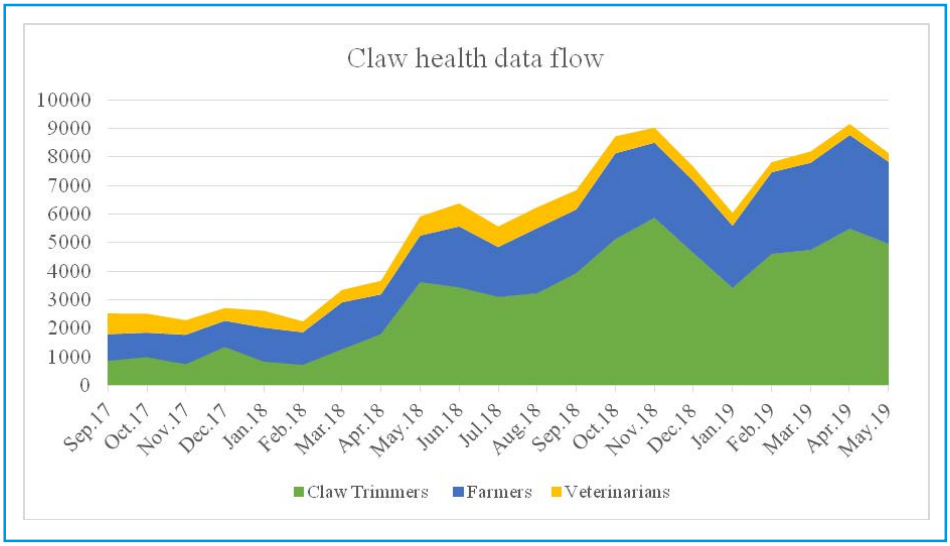

Figure 2. Monthly claw health data flow electronically documented by claw trimmers (including historic data), farmers and veterinarians, and sent to the Austrian central cattle database (RDV) since the start of the project "Klauen-Q-Wohl".

processing data from various sources, with evaluations within and across herds is already being programmed. Based on literature findings and expert opinion, a risk factor tool has been developed, which is currently being tested using the data from several pilot farms. As visualised in Figure 1, the state of individual animal welfare as well as farm related welfare parameters and benchmarks feed into this tool. In order to be able to better reflect the individual farm situation (strength/weakness), the evaluations take the results of claw trimming (predominantly infectious or non-infectious diseases) into account. This practical herd management solution, designed for farmers (self-control) and advisors (external monitoring), is intended to promote the improvement of claw health and animal welfare in Austrian dairy farms. The valuable data basis generated within the framework of project "Klauen-Q-Wohl" will be used for breeding value estimation for claw and claw related health traits to additionally support long-term improvement of animal health.

Conclusion

Considering the frequency of claw disorders in dairy herds worldwide, prevention and early detection of claw disorders is an important welfare topic. Documentation and central recording is the precondition for monitoring claw health and animal welfare. Central availability of data is needed for benchmarking and very valuable for targeted prevention and improvement programs. Above all, central data processing avoids double recording and enables synergies in use of data e.g. data for claw health and welfare assessment can also be used for genetic evaluation.

Acknowledgement

Special thanks is given to all project partners especially the claw trimmers, (pilot) farms and performance recording organizations for their cooperation within the project Klauen-Q-Wohl. The project is supported by the Federal Ministry Republic of Austria

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The ICAR "Artificial Insemination and Related Technologies" Working Group: its goals and current projects

F. Schmitz-Hsu[1,2], O. Gérard[1,3], J. Baltissen[1,4], J. M. DeJarnette[1,5], J. Hooijer[1,6], L. Journaux[1,7], L. Morelli[1,8], R. Spelman[1,9] and B. Wickham[1, 10]

[1]Artificial Insemination and Related Technologies Working Group, ICAR, Via Savoia 78, esc.A, int.3, piano 1, 00198 Rome, Italy
Corresponding Author: fsc@swissgenetics.ch and olivier.gerard@allice.fr
[2]Swissgenetics, Meielenfeldweg 12, 3052 Zollikofen, Switzerland
[3]Allice, 149 rue de Bercy, 75012 Paris, France
[4]Bundesverband Rind und Schwein e.V., Adenauerallee 174, 53113 Bonn, Germany
[5]Select Sires, Inc., 11740 U.S. 42 North, Plain City, OH 43064, USA
[6]CRV, Wassenaarweg 20, 6843 NW Arnhem, The Netherlands
[7]Institut de l'Elevage, 149 rue de Bercy, 75012 Paris, France
[8]INSEME SpA, Via Cadiane 181, Saliceta San Giuliano, 41126 Modena, Italy
[9]LIC, Private Bag 3016, Hamilton 3240, New Zealand
[10]ICAR Secretariat, Via Savoia 78, esc.A, int.3, piano 1, 00198 Rome, Italy

Abstract

The "Artificial Insemination and Related Technologies" Working Group (AI & RT WG) is a body of ICAR. Its task is

- to maintain, update, promote and extend universal guidelines for recording data associated with artificial breeding (for both male and female gametes, primarily in cattle) and its use to assess reproductive success;
- to conduct and report the results of international surveys in this context;
- to identify and specify services that can be provided by Service ICAR;
- to stimulate and facilitate international collaboration in research and development on all aspects of recording artificial breeding data and its use to assess reproductive success

Currently the AI & RT WG consists of 7 ordinary members, 2 associated members representing the industry supplying instruments etc. for AI, plus 2 members representing ICAR Board and ICAR Secretariat.

An overview of the recent and planned activities of the Working Group is given.

Keywords: artificial insemination, embryo transfer, guidelines

Introduction

Annually in cattle breeding several hundred million semen units are produced worldwide. Additionally, several hundred thousand embryos are transferred per year. The intensive international trading of semen and embryos asks for guidelines, among

others on how to produce and label semen units, how to record data in the context of artificial insemination (AI) and embryo transfer (ET) and on how to assess fertility. To address these tasks, ICAR established a specific working group, called “Artificial Insemination and Related Technologies Working Group” (AI & RT WG). In this document the recent activities of the AI & RT WG are summarized, and an overview of the planned actions is given.

The ICAR Guidelines on AI and ET data and fertility analysis

The AI & RT WG is responsible to maintain, update, promote and extend the section “06 AI and ET Data and Fertility Analysis” of the ICAR Guidelines. These guidelines are openly accessible under *www.icar.org*. Section 06 covers the following subjects:

1. Bovine Semen Straw Marking
   Information to be printed on the straw, barcoding, breed codes
2. Bovine Embryo Production and Transfer
   Recording of relevant data, parentage assessment, quality control
3. Fertility Reporting for AI organisations
   Measurements/definitions, rules of calculation
4. Annexes
   - Incidence of the chosen option for the exclusion of short returns
   - Consideration of cattle reproductive physiology
   - Embryos storage and movements
   - Validation of data
   - Survey results

Recent activities of the Working Group

Besides of its own constitution, the AI & RT WG addressed in the recent time the following subjects:

1. Maintain the guidelines.
2. Update the information on what is printed by large AI organisations on semen straws.
3. Conduct a worldwide survey on barcoding semen units.
4. Initiate a project for establishing an International Database for Semen Information.

There are separate reports are given at the ICAR Congress 2019 on the activities 3 and 4.

Planned activities

Within the next months the AI & RT WG plans - besides maintaining the guidelines - to address the following topics:

- Establish the International Database for Semen Information, starting with a proof of concept.

- Evaluate the relevance and impact of new technologies (RFID etc.).
- Collaborate closer with:
    - Other bodies of ICAR (Interbull, Animal Data Exchange, etc.).
    - The International Embryo Technology Society (IETS).
    - The industry.

With its activities, the AI & RT WG endeavours to contribute significantly to the needs of all stakeholders in the field of artificial breeding.

International data exchange for the recording and traceability of worldwide artificial inseminations: a new and modern concept

O. Gérard[1,2], L. Journaux[1,7], F. Schmitz-Hsu[1,3], J. Baltissen[1,4], J. M. DeJarnette[1,5], J. Hooijer[1,6], L. Morelli[1,8], R. Spelman[1,9], B. Wickham[1, 10]

[1]Artificial Insemination and Related Technologies Working Group, ICAR, Via Savoia 78, esc.A, int.3, piano 1, 00198 Rome, Italy
Corresponding Author: olivier.gerard@allice.fr and fsc@swissgenetics.ch
[2]Allice, 149 rue de Bercy, 75012 Paris, France
[3]Swissgenetics, Meielenfeldweg 12, 3052 Zollikofen, Switzerland
[4]Bundesverband Rind und Schwein e.V., Adenauerallee 174, 53113 Bonn, Germany
[5]Select Sires, Inc., 11740 U.S. 42 North, Plain City, OH 43064, USA
[6]CRV, Wassenaarweg 20, 6843 NW Arnhem, The Netherlands
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Abstract

The "Artificial Insemination and Related Technologies" Working Group (AI & RT WG) is a body of ICAR. One of its main missions consists in maintaining, updating, promoting and extending universal guidelines for recording data associated with artificial breeding (for both male and female gametes, primarily in cattle) and its use to assess reproductive success (*F. Schmitz-Hsu, 2019).* Within this frame, the Group is working on a new concept of AI data exchange platform which is described in the present document.

Key words: Data exchange platform, traceability, proof of concept.

Introduction

Big Data can provide new efficient decision making tools for helping agricultural development as well as biodiversity protection.

In the sector of Artificial Insemination (AI), semen production from the semen collection center to the field and then insemination of cows require reliable recording and strict traceability. During the last 20 years, many countries have developed national barcodes printing systems on straws in order to provide such a rigorous traceability. Unfortunately, these technologies only work at a national scale and are hardly usable in other technical environments. On the other hand, worldwide trade of semen has regularly increased and safe traceability has become a main issue, especially when considering sanitary security issues and reliable origin of genes.

In the frame of its missions, the ICAR Artificial Insemination and Related Technologies Working Group (AI&RT-WG) is aiming at implementing an international data exchange system gathering all information regarding any proven bovine sire used anywhere in

the world and whatever the Semen Collection Centre (SCC) where the semen was produced. The goal is to provide reliable statistics and information about genes exchanges all around the planet and to secure linked sanitary issues.

This document aims at describing the different steps that have to be followed and achieved before this project can be fully implemented. It is also a call to good wills who would be interested by it and would like to join the AI&RT-WG.

Ins and outs of the project

As a first step, the following concept has to be proven:

- Any AI technician in the fields inseminating a bovine female can connect himself to the international query system from a mobile connected device.
- Key entrance code to the international database will be three digits NAAB code identifying any SCC in the world added to the current barcode used by the SCC.
- Any SCC will be free, in addition to the information printed on straw, to include various information within its own file using dedicated application programming interfaces (API) in the exchange system: genetics, genomics, sanitary, genealogy,…
- Connection from the fields to the databases will be done thanks to an API giving access to individual SCC information.
- Minimum information will be the full deciphed content of the printed barcode.
- Maximum information available will have no limit and will be property of the SCC owner of the sire.

The second step will consist in:

- Finding partners to develop and evaluate the technical feasability of the concept: two or three different countries (not limited) representatives from different continents (if possible).
- Evaluating the total costs, advantages and drawbacks of the system.

The third step will deal with the funding of such a project, if possible, via official international institutions like regional funding agencies, European Bank for Reconstruction and Development : EBRD, ICAR or Interbull.

However, we have to keep in mind that the success of a digital project depends as much on technological mastery as on the willingness of the teams to implement it.

And as a conclusion:

“When you’re trying to reach a goal, data not only tells you if you’re succeeding, but it also suggests which activities you should do more of in order to improve your results.”
(Bill Gates)

Factors affecting pregnancy rate after cervical insemination in dairy sheep flocks

S. Priskas[1], S.A. Termatzidou[1], S. Garganis[2] and G. Arsenos[1]

[1]Faculty of Veterinary Medicine, Aristotle University of Thessaloniki, Greece
Corresponding author: stpriskas@vet.auth.gr
[2]Institute of Molecular Biology and Genetics, Biomedical Sciences Research Center
Alexander Fleming, Vari, Greece

Abstract

The objective was to assess the factors affecting the success of cervical artificial insemination (CAI) with chilled semen in intensively reared dairy ewes in Greece. The study involved 1,242 adult ewes from 14 flocks in northern Greece (Lacaune, n=885 and Chios, n=357). A typical estrous synchronization protocol (intravaginal progestogen sponge×14 d and 400-500 IU of equine chorionic gonadotropin after sponge removal) was applied in ewes during mating period (May to November). All ewes were cervically inseminated 53-56 h after sponge removal. Semen was collected from 10 fertile (mass motility >4) adult purebred Lacaune rams using an artificial vagina. Each ejaculate was approved for CAI after evaluation of viability, sperm membrane integrity and kinematic parameters by a computer assisted sperm analyzer (CASA). Semen was diluted with skimmed milk to 1.6×10^9 spermatozoa/mL and kept at 15°C until insemination. Pregnancy diagnosis (PD) was performed by trans-dermal ultrasonography at 35-40 d after service.

The following data were available for each ewe: breed; parity; previous lambing date; body condition score at onset of synchronization (BCS_s), at the day of CAI (BCS_i) and at the day of PD (BCS_p); presence of rams during synchronization and number of previous synchronizations. Recordings during the CAI procedure included: onset of synchronization to CAI interval; semen collection to CAI interval; semen deposition depth; cervical mucus presence; duration of CAI. Housing conditions (bedding space; air volume and ventilation) and dietary management were also recorded in each farm. The association between CAI success and categorical variables was assessed with Chi-square independence test. The difference in the mean values of continuous variables between pregnant and non- pregnant ewes was tested through the application of one-way analysis of variance (SPSS v.25.0).

The results showed that breed, parity, semen deposition depth, time from semen collection to CAI and presence of rams during the synchronization period significantly affected CAI success ($P<0.05$). Pregnancy rate in farms with poor ventilation was significantly lower ($P<0.05$) compared to farms with adequate ventilation (40.0% vs. 53.4%). Ewes in medium condition at synchronization (BCS_s: 2.50-3.25) showed significantly higher ($P<0.01$) pregnancy rates compared with under-conditioned (BCS_s <2.50) and over-conditioned (BCS_s >3.50) ewes (51.4% vs. 33.0%).

Similarly, ewes at good condition at the time of CAI (BCS_i: 2.50-3.25) had a significantly higher ($P<0.01$) pregnancy rate than the rest (52.2% vs. 31.8%). Positive energy balance following the onset of synchronization seems to benefit under-conditioned and ewes at medium condition.

Instead, weight gain after sponge placement in over-conditioned ewes resulted to significantly lower (P<0.05) pregnancy rates (14.0% vs. 54.8%). In conclusion, selection of appropriate ewes, BCS recording prior to synchronization and evaluation of dietary management and housing conditions are key factors dictating pregnancy rates following CAI.

Keywords: sheep, insemination, factors, fertility.

Introduction

Assisted reproductive technologies have been implemented in livestock systems to respond to the demand for higher productivity and better quality. The use of artificial insemination (A.I.) has a significant impact on sheep breeding industry, as it enables the rapid introduction of valuable genes to improve production traits and prevents disease transmission (Faigl *et al*, 2012).

However, in comparison with other food producing animals, the implementation of A.I. in sheep is relatively limited. The only exception is France, where more than 410 000 inseminations are performed annually in both nucleus and commercial flocks of the dairy Lacaune breed (Barillet *et al*., 2001). The structural complexity of the ewe cervix prevents deep deposition of semen in uterus and leads to poor fertility rates when frozen- thawed semen is used for cervical A.I. (Salamon and Maxwell, 1995). Fertility rates can be enhanced by the application of laparoscopic insemination; however, increased cost, welfare concerns and the requirement of technical skills are some limitations that have affected negatively the demand of this procedure. Using chilled semen for cervical AI enhances fertility, but increases semen production cost, has time limitations during transportation and often gives irregular results, since the success of the method is affected by many factors. Environmental conditions, management factors, health of males and females, physiological status of ewes are among the factors that need to be controlled before AI implementation. (Donovan *et al*., 2006; David *et al*., 2008; Santolaria *et al*., 2011).

Our objective was to carry out an artificial insemination programme to study the factors affecting the success of cervical artificial insemination (CAI) with chilled semen in intensively reared dairy ewes in Greece. It is the first study that assesses the effect of female, ram, AI procedure conditions and farm nutrition program at the same time on fertility rates after AI on intensively reared dairy sheep in the area.

Materials and methods

Animals

The present trial was conducted during the usual breeding season in Greece, from May to November, for two consecutive years (2017-2018). For the purpose of the study, 1,242 adult ewes (885 Lacaune and 357 Chios) were used from 14 commercial flocks located in North and Central region of Greece. The selected ewes belong to the most common intensively reared breeds in Greece and were born and raised in the above regions. During the study, the animals were at the 5-7th month of their lactation.

Estrous synchronization and CAI procedure

Each ewe was treated with a typical estrous synchronization protocol including intravaginal placement of a sponge containing 20 mg fluogestone acetate (FGA) (Chronogest CR®, MSD Animal Health) for 14 days. At the day of sponge withdrawal,

500 IU (Lacaune) or 400 IU (Chios) of equine chorionic gonadotropin (eCG) (Gonaser®, Hipra) were intramuscularly injected to the ewes.

Semen was collected from 10 Lacaune rams that were located in the same semen collection center (Ovis PC, Thessaloniki), using an artificial vagina. Immediately after collection, motility and concentration of the undiluted semen were assessed. Only ejaculates with concentration greater than 3 x 10^9 spermatozoa/ ml and mass motility greater than 4, on the 0-5 scale described by Evans and Maxwell (1987), were used for the study. After this evaluation, semen was diluted to concentration of 1,6 x 109 spermatozoa/ ml using skimmed milk supplemented with antibiotics, gradually cooled at 15^{o}C and loaded into 0,25 ml mini straws (IMV Technologies, France) (400x106 spz/ dose). The straws were transported on farm for use inside thermos flasks with acetic acid ampoules at 15^{o}C.

Cervical fixed-time AI was performed on each farm 53-56 hours after the sponge removal. Ewes were immobilized by two assistants, with hind legs lifted. In case of mucus presence inside vagina, the animal was put again in horizontal position and the mucus was removed using a speculum. AI was performed afterwards with the help of a speculum equipped with light source and an ovine AI gun (IMV Technologies, France). All artificial inseminations were carried out by the same technician within 8 hours after semen collection. During the procedure, ewes were kept on a restrained area and released to their boxes after insemination, or they were head-locked in feed alley whenever this was applicable Ultrasonography was performed 35-40 days after AI for pregnancy diagnosis (PD) using 5MHz transducer with sector probe (Animal Profi, Draminski, Poland).

Data collection

For all inseminated ewes, data concerning breed, parity, previous lambing date and number of previous synchronizations were recorded. Body Condition Score (BCS) was assessed for each ewe at the time of sponge placement (BCS_s), CAI (BCS_i) and PD (BCS_p). BCS was assessed by palpation in the lumbar region by the same experienced evaluator. Scores assigned to the ewes were based on the existing scale of Russel *et al.* (1969) ranging from 0 to 5, according to which score (0) represents extremely emaciated animals, while the highest score (5) represents obese ones; 0.25 and 0.5 unit increments were used. Changes of BCS between sponge placement and pregnancy diagnosis (51- 56 days) were evaluated to determine whether the animals were in negative, zero or positive energy balance during that period.

At the time of AI, the following data were collected for each ewe: semen collection- AI interval, sponge removal- AI interval, time required per AI, presence of mucus in vagina, presence of rams near the females during synchronization period and semen deposition site. The latter was distinguished in 3 classes depending on the deposition depth of the catheter and retrograde flow of semen: vaginal deposition, external cervical os deposition with partial semen backflow or deeper cervical placement without semen backflow.

Housing conditions of females were assessed in each farm with the calculation of stocking density (m^2 of available floor space/ ewe), available air volume (m^3 of shed volume/ ewe) and available feed space (cm/ ewe). Quality of ventilation was subjectively distinguished in 3 classes by the same evaluator: 1) Good: absence of odour, open type building with functional characteristics that ensure adequate air renewal, side and ridge openings; 2) Moderate: not very good ventilation conditions, presence of odour at tolerable levels, constructions that couldn't always ensure the adequate air

renewal, absence of roof ridge opening; 3) Inadequate: buildings where air renewal was always inadequate or impossible, absence of ridge and side openings, odour at non- tolerant level.

Statistical analysis

The association between CAI success and categorical variables was assessed with Chi-square independence test. The difference in the mean values of continuous variables between pregnant and non- pregnant ewes was tested through the application of one-way analysis of variance (SPSS v.25.0, IBM). Significance level was set at P= 0.05.

Results and discussion

The results of the study are presented on Table 1. Ewe breed, parity, BCS at sponge placement and CAI, as well as BCS change was found to have effect on fertility of the ewes. Overall pregnancy rate was 43.4 %. Lacaune ewes had significantly higher conception rate (48.9%) than the Chios ewes (29.7%). Fertility was higher at animals on 2nd and 3rd lactation period (51.3% and 48.3%) and declined on older ewes, a finding that agrees with studies of Arranz *et al.* (2008) and Palacin *et al.* (2012). Lower conception rates of primiparous ewes could be attributed to their inclusions with older ewes that usually lamb earlier, or to nutritional deficiencies as a result to their larger requirements for growth compared with older ewes (Anel *et al.*, 2005).

Females at moderate BCS (2.5-3.25) exhibited better results in our study, as ewes in good condition have greater ovulation rate than thinner ewes. However, there seems to be a plateau on the effect of BCS on fertility as there is no benefit of increased BCS beyond a point, and conception rates decline in animals with BCS> 3.5. Our study agrees with many authors ending up that ewes should have a BCS of 2.5-3.25 at mating period (Kenyon, 2013; Fukui, 2010) The animals that retained or increased their body weight at the time around CAI, had higher pregnancy rates compared to the animals that lose weight, as it seems that low feed intake and BCS reduction at mating period, results to lower ovulation rate, decreased embryonic growth and increased fetal losses. However, the effect of BCS increase on fertility was not the same for every ewe. Animals with BCSe" 3.5 at onset of synchronization that continued to gain weight had significantly lower conception rates than thinner animals on positive energy balance (Table 2). We suggest that weight gain should be discouraged in fat sheep as can cause high ovulation rates and increase embryonic losses (Rassu *et al.*, 2004).

Regarding to the factors related to the procedure of CAI, deposition of semen inside cervix also increased significantly chances of conception compared to vaginal or external cervical os deposition (46.4% vs. 36.3 and 33.5% respectively). The deeper deposition allows more semen to reach the fertilization site and increases pregnancy chances. In our study, the site of semen placement was found to differ between the 2 breeds, as deposition inside cervix was more frequent on Lacaune than Chios ewes (80.5% vs. 61.9%) (Table 3). This must be a reason for the difference on conception rates among the breeds.

The presence of rams in the area near the synchronized ewes is a factor that could affect pregnancy rates. In farms where the rams were kept apart from the area of the ewes, pregnancy rates were higher in our study. According to Contreras- Solis *et al.* (2009), exposure of females to rams before sponge removal could reduce ecG administration- onset of estrous interval and reduce the success of classic fixed time insemination protocols. That could be overcome by inseminating the ewes earlier.

Table 1. Description of risk factors assessed in the analysis.

Risk Factors	N	Mean	Pregnancy (%)	Sig
Breed				**
Lacaune	885		48.9[a]	
Chios	357		29.7[b]	
Parity		3.11 ± 1.18		**
1	96		43.8[a,c]	
2	339		51.3[b]	
3	308		48.1[a,b]	
4	326		38.3[c]	
>4	173		28.9[d]	
Months from calving		6.02 ± 0.68		n.s.
5	272		46.3	
6	668		44.3	
7	302		38.7	
BCS_s				**
Low (<2.5)	228		35.1[a]	
Moderate (2.5-3.25)	700		51.4[b]	
High (>3.25)	314		31.5[a]	
BCS_i				**
Low (<2.5)	220		30.9[a]	
Moderate (2.5-3.25)	707		52.2[b]	
High (>3.25)	315		32.4[a]	
BCS change				**
BCS decrease	297		30.3[a]	
BCS retain	409		43.8[b]	
BCS increase	536		50.4[b]	
Semen deposition depth				**
Vagina	67		36.3[a]	
External os	242		33.5[a]	
Cervix	933		46.4[b]	
Mucus presence				n.s.
No	886		43.6	
Yes	356		43	
Previous eCG administration				n.s.
No	1179		44.0	
Yes	63		31.7	
Sponge removal to A.I. interval		54.98 ± 0.73		n.s.
Semen collection to A.I. interval		4.79 ± 1.02		**
A.I. duration (min/ animal)		1.15 ± 0.22		n.s
Presence of rams				**
No	1013		46.4[a]	
Yes	229		30.1[b]	

n.s.: Not significant *P*? 0.05; *: *P*< 0.05; **: *P*< 0.01.

Each superscript letter denotes a class of each factor that does not differ significantly from other at the 0.05 level.

Table 2. Effect of BCS increase on fertility of ewes with different BCS.

	BCS at sponge placement		
	<2.5	2.5-3.25	>3.25
BCS increase	48% (61/126) [a]	57% (201/351) [a]	14% (8/59) [b]

Different superscripts between different columns indicate significant differences (*P*< 0.05).

Table 3. Semen deposition site in Lacaune and Chios ewes.

Breed	Semen deposition site % (No. ewes)		
	Vagina	External os	Cervix
Lacaune	3.4% (30)[a]	16.2% (143)[a]	80.5% (712)[a]
Chios	10.4% (37)[b]	27.7% (99)[b]	61.9% (221)[b]

Different superscripts within same column indicate significant differences ($P < 0.05$).

Table 4. Effect of housing conditions on fertility.

Risk Factors	N	Mean	Pregnancy rates (%)	Sig
Bedding space (m2/ ewe)		1.55± 0.15		n.s.
Air volume (m3/ ewe)		9.22± 1.32		n.s.
Feed space (cm/ewe)		35.69± 6.71		n.s.
Ventilation				**
Good	238		53.4[a]	
Moderate	679		41.5[b]	
Inadequate	325		40.0[b]	

n.s.: Not significant P? 0.05; *: $P < 0.05$; **: $P < 0.01$

Each superscript letter denotes a class of each factor that does not differ significantly from other at the 0.05 level

Fertility was found to be decreased in farms where ventilation conditions were inadequate or moderate (40% and 41.5% respectively). On contrast, animals that lived in environment with good ventilation, exhibit higher pregnancy rates. This finding indicates the need of evaluating the micro- environmental conditions inside a farm, in order to achieve better productive and reproductive performance, especially in areas with high temperatures during summer. No other studied factor related to the housing of ewes was found to affect conception rates of CAI (Table 4).

Conclusion

In conclusion, ewe breed and parity, BCS and its changes and semen deposition site inside females reproductive canal, are factors affecting fertility after CAI on intensively reared dairy sheep of Greece. Conception rates can also be affected by time interval from semen collection to CAI and presence of rams near the ewes during synchronization period. Between housing parameters, ventilation seems to play crucial role in the success of the method. Targeted selection of ewes, evaluation of farm's management practices and nutrition program, as well as improvement of housing conditions, could lead to better and more consistent results of CAI, contributing to its application in greek intensive flocks in larger scale.

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Milking control operation: A very important tool for the development of dairy cattle breeding in Morocco

N. Belkadi

National Cattle Breeders Association of Morocco

Introduction

Since 1975 national dairy plan, Morocco took actions to improve the genetic of cattle breeding.

The actions consisted on the heifer importation operations, the popularization of the artificial insemination on the local breed and moreover, the development of the milking control activity.Started with state farms and reached the private farms later, this last activity Carried out at the beginning by the regional services of the Ministry of Agriculture to be ceased since 2006 to the professional organizations,

The main objective of this activity was the local production of purebred heifers.

With the outbreak of mad cow disease in Europe in 2000, the heifer's importation stopped. Thus , to substitute the importation, the government launched local heifer's production in cattle farms under milking control operation. This activity has been reinforced by the genetic improvement actions contained in the Green Morocco plan strategy launched in 2009.

History of dairy control activity

This activity has evolved through several steps summarized as follows:

- 1968: launch of dairy control for the first time in cattle farms managed by a state company and then extended to private dairy farms in two irrigated areas (Gharb and Doukkala).
- 1973: opening of the standard genealogical books for the four breeds at the Ministry of Agriculture : Holstein, Pie Noire, Pie Rouge and Tarentaise
- In the 1980-1990 decade until the end of 2000: the number of farms under milk control decreased from 390 farms for 11,000 dairy cows to 120 farms for 5,000 controlled dairy cows, respectively.
- Since 2000, because of mad cow disease outbreak in Europe, heifer's importation was stopped. Meanwhile, the cattle farms under milking control operation launched local heifer's production.
- From 2000 to 2008, the operation of the dairy control knew an irregular evolution because of shutdown of some farms and the opening of new farms.
- Since 2009, the Green Morocco plan has been introduced and the dairy control activity has been strengthened by the following concrete actions:
    - The establishment of an Operational Specifications for the dairy control plan,

- Transfer of the dairy control activity to the professional organizations operated by a ministerial regulations
- Publication of a decree concerning the modalities of public aid for the animal production intensification included heifers production
- Edition of an Operational Specifications related to the organization of the dairy control and to the selection of purebred cattle breeders.

Current situation and development prospects for milk control

The Government has accompanied and encouraged the operation of milk control by granting subsidies accorded to local heifer's production. The amount of these subsidies has begun from 1500 DH (140 Euros) in 2008 to reach 5000 DH (450 Euros) during the last 5 years until now. This operation was a great success during the decade 2010 to 2018 with a very positive evolution as can be shown in the following table:

Year	Cattle Farms	Controlled Dairy Cows	Locql Selected Heifers	imported heifers
2009	200	1500	600	13297
2010	250	2500	1500	26700
2011	300	8000	4300	16500
2012	350	8500	3400	9100
2013	350	9000	4500	8500
2014	400	11000	6000	14000
2015	500	33500	7500	3800
2016	470	33000	8000	13400
2017	644	44500	12000	20300
2018	728	49000	16300	21190

The number of cattle farms under dairy control increased from 200 units and 1,500 cows in 2009 to 728 units (including 14 large farms) and 49,000 cows. The number of selected heifers increased from 600 to 16,300, respectively.

In parallel with this evolution of farms units, the milk productivity has improved to pass for 305 days standard lactations on average from 4000 - 6000 in 2010 to 6000- 7500 liters per dairy cow in 2018.

This evolution shows the success of the milk control strategy, boosted by the Green Morocco Plan , that enhanced local production of heifers in cattle farms. Less acclimated than the local heifers, the imported heifers will see their number decrease since the subsidy granted by the Green Morocco plan for this matter is eliminated in 2019.

Conclusion

In the short term, Morocco intends to focus on the development of national production of heifers in the cattle farms under milk control operation. This strategy helps to create a local market, which meets the needs of the country on heifers, in minimizing heifers importation, increasing the milk productivity and improving the milk quality.

The estimation of the genetic parameters for conformation traits in the Romanian Spotted cattle breed

H. Grosu, M.C. Rotar and M.A. Gras

National Research&Development Institute for Biology and Animal Nutrition,Calea Bucuresti, 077015, Balotesti, Romania
Corresponding Author: rotar.mircea.catalin@gmail.com

Abstract

Improving the global genetic potential of cattle, involves the consideration of several groups of characters, such as milk production, longevity, conformation, reproduction and others. An economical milk and meat production are sustained by superior longevity which is influenced by a harmonious conformation. Among the character groups enumerated above, in the present paper were analysed the conformation traits from the genetic point of view (heritability, genetic and environmental correlations). The genetic parameters were estimated for a number of 18 conformation traits, using as phenotypic information the linear score from the conformation traits appreciation of cows at first calving from the Romanian Spotted breed. In total, 2387 animals were analysed, of which 1193 were parents and 1194 were animals with performance. In order to optimize the running time and genetic parameters computation, we used the canonical transformation method, applied to a multi-trait animal model. The fixed effects of the model were: year-month, age at first calving and stage of lactation, and random effects were herd-year-season and animal. The obtained results revealed that the values of heritability, and genetic and environmental correlations are within the normal range of variation, specific to the conformation traits, similar for other cattle populations.

Keywords: canonical transformation, conformation, genetic parameters.

Introduction

For a more productive cattle population and a long and productive life, we must be sure of what animals will be removed from the herd. For that we try to preserve animals with good conformation and that will ensure us a sustainable production (Bertipaglia *et al.*, 2012). The exterior of an animal is associated with the production and in that case, it is necessary for us to make a conformation evaluation (Liu *et al.*, 2014). The purpose of the conformation evaluation is to discover the ideal animal. The managerial target of a herdsmen is to be efficient from financial point of view, and from that perspective, the conformation evaluation not imply high costs (Zink *et al.*, 2014; Satola *et al.*, 2017). It can be done very easy, also being good for exterior traits inclusion in total breeding value evaluation. All the country in the world were cattle breeding have an important share in economy, estimate genetic parameters for conformation traits, estimates that will help in cattle genetic evaluation (Mindur *et al.*, 2014; Akinsola *et al.*, 2018). Because the exterior evaluation includes a lot of traits, and also the number of evaluated animals is high, mathematical methodology must be involved into solving the mixed model equation in a short time and with fewer computer resources (Misztal

I. *et al.*, 1995). In the presenting paper canonical transformation was applied. This procedure analyses traits one by one and in the end gives results like in simultaneous analysis.

Material and methods

2387 animals were analysed, 1193 of them were parents and 1194 were offspring with measured performances. Each animal with records had scores for all 18 analysed traits, resulting a total number of 21492 scores, used in the analysis. For this study, all the data were provided by Romanian Spotted Simmental-type Breeding Association from Brasov, Romania. Like any other evaluation system found in other countries, the classical visual evaluation was performed, by 5 referees. For each trait the score was between 1 and 9 scores. In the genetic evaluation, in order to have a fare hierarchy, scores were transformed in points from 50 to 90, each trait being adequately customized.

In order to solve the mixed model equation, finalized with genetic parameters, the traits were grouped in four categories: height at cross, rump length, hip width, rump angle, body depth were introduced in type traits group. Muscularity was introduced in muscle group. Hook angularity, hook development, pasterns, height hoof traits were introduced in feet and legs group. Udder traits: fore udder length, rear udder length, fore udder attachment, central ligament, udder depth, teat placement, teat length, teats thickness traits were introduced in udder group.

For estimating genetic parameters, was applied B.L.U.P. methodology to a multi-trait animal model with canonical transformation. The analysis was performed by R software, version 3.5.1. (R Core Team (2018). R: A language and environmental for statistical computing. R Foundation for Statistical Computing, Vienna, Austria (URL *https://www.R-project.org/*).

The biometric model used was:

$$y_{ijklm} = B_i + DIM_j + AGE_k + YM_l + HYS_m + a_{ijklm} + e_{ijklm} \quad (1)$$

Where,

y_{ijklm} - recorded performances;
B_i - fixed effect of the referee;
DIM_j - fixed effect of days in milk for each cow in the scoring moment;
AGE_k - fixed effect of age;
YM_l - fixed effect of the combination month-year of calving;
HYS_m - random effect of the combination herd-year-season;
a_{ijklm} - random effect of the animal;
e_{ijklm} - error.

Results and conclusions

First step was to perform an analysis for descriptive statistics, for both scores and points. For each trait mean, mean error and standard deviation were calculated (Table 1). Scores ranged from 3.84 up to 7.08 with the general average 5.62, it can be observed. The traits from feet and legs group has majority of values around the average. If we look at the points number, we can observe that the means ranged between 75.8

and 87.2, with the general average of 82.39. In terms of standard deviation, for scores was obtained values from 0.87 to 1.66. On the other hand, for points number, the variation was between 3.75 and 9.18. For both scores and points the trait with the highest standard deviation was in udder group and the lower value was in feet and legs group, also for both scores and points.

Table 1. Standard deviation, Mean and standard error of mean for conformation traits.

Body region	Trait	Mean + Standard Error		Standard Deviations	
		Scores	Points	Scores	Points
Type traits	Height at Cross	6.41 + 0.04	79.1 + 0.40	1.47	6.77
	Rump Length	5.09 ± 0.05	76.2 ± 0.34	1.58	6.51
	Hip Width	4.95 ± 0.04	75.8 ± 0.34	1.45	5.78
	Rump Angle	5.30 + 0.03	85.6 + 0.25	0.97	3.95
	Body Depth	5.73 ± 0.04	78.9 ± 0.25	1.22	4.86
Muscle	Muscularity	5.14 + 0.04	83.6 + 0.31	1.24	5.83
Feet and Legs	Hock Angularity	5.28 ± 0.03	84.5 ± 0.28	0.93	4.04
	Hock Development	6.73 + 0.03	86.2 + 0.21	1.04	4.24
	Pasterns	5.74 + 0.03	81.5 + 0.24	0.87	4.05
	Hoof Height	6.14 ± 0.03	82.3 ± 0.20	0.95	3.75
Udder Traits	Fore Udder Length	6.58 + 0.04	80.1 + 0.24	1.55	6.19
	Rear Udder Length	5.87 ± 0.05	79.8 ± 0.23	1.66	6.64
	Fore Udder Attachment	5.95 + 0.03	83.6 + 0.21	1.14	4.55
	Central Ligament	6.20 + 0.04	87.2 + 0.31	1.36	6.40
	Udder Depth	7.08 ± 0.03	86.8 ± 0.26	1.09	4.53
	Teat Placement	5.16 + 0.03	83.6 + 0.26	1.14	5.29
	Teat Length	3.93 + 0.03	86.6 + 0.37	1.15	8.03
	Teat Thickness	3.84 ± 0.03	81.7 ± 0.36	1.07	9.18

The purpose of this study was to estimate genetic parameters and in table 2 it can be observed genetic variance, phenotypic variance and heritability. In terms of genetic variance, table 2 shows that the values ranged from 2.01 up to 16.64. Feet and legs group has the lowest values for genetic variance and the biggest value was 38.37 for teat thickness trait. Also, for the phenotypic variance it can be observed that the highest value was for the same trait like the genetic variance. The values for phenotypic variance ranged between 11.94 and 89.51.

In term of heritability we can observe that the values ranged from 0.13 up to 0.54, with the lowest value for fore udder length trait and the highest for rump length. Other authors show similar values for heritability (Nemcova *et al.*, 2011). Higher heritability for conformation traits was observed by other authors (Rotar *et al.*, 2019), but in general terms all the values ranged from 0.12 to 0.60.

It can be observed in Figure 1 that for one animal all 18 breeding values were grouped in four major groups and in the end, all of that was centralized in a global index. If the animal were retained at reproduction only by hierarchy from one group, the evaluation can be biased. Animal 4 had the highest breeding value for group Muscle and if the hierarchy were performed only by that group, in the end the evaluation is not correct. When the global index was calculated, animal 4 was disqualified because for udder traits and type traits it obtained low breeding values.

Table 2. Heritability for conformation traits.

Trait	Genetic Variance	Phenotypic variance	h^2
Type traits			
Height at cross	16.28	38.87	0.42
Rump length	10.29	37.85	0.54
Hip width	9.99	30.06	0.33
Rump angle	4.34	16.85	0.26
Body depth	7.55	24.98	0.30
Muscle			
Muscularity	12.31	31.27	0.39
Feet and legs			
Hock angularity	2.11	14.37	0.15
Hock development	2.31	15.92	0.15
Pasterns	2.76	14.34	0.19
Hoof height	2.01	11.94	0.17
Udder traits			
Fore udder length	3.94	31.03	0.13
Rear udder length	7.68	37.16	0.21
Fore udder attachment	2.48	18.17	0.14
Central ligament	14.24	36.31	0.39
Udder depth	4.57	20.05	0.23
Teat placement	6.85	27.82	0.25
Teat length	16.64	62.51	0.27
Teat thickness	38.37	89.51	0.43

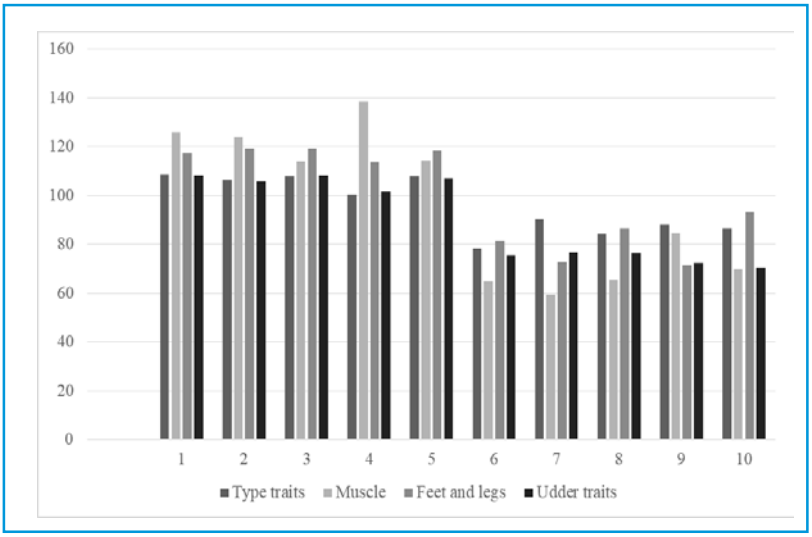

Figure 1. Relative Breeding Values for best/worst five cows

In terms of genetic and environmental correlation, in the presenting paper correlation were from highly negative to highly positive. In table 3 it can be observed that the lowest genetic correlation was obtained between teat length and rump length (-0.13), also negative correlation was obtained in general terms between udder traits and type traits. At the opposite, the highest genetic correlation was obtained between rump length and hip width (0.69). Regarding environmental correlation, the trend was similar with that from genetic correlations.

Table 3. Genetic correlation (above diagonal) and Environmental correlation (below diagonal).

Trai	HC	RL	HW	RA	BD	M	HA	HD	P	HH	FU	UL	UA	CL	UD	TP	TL	TT
HC		0.47	0.49	-0.02	0.47	0.2	0	-0.01	-0.03	0.08	0.13	0	0.03	0.03	-0.12	-0.07	0.07	0.11
RL	0.45		0.69	-0.08	0.51	0.17	-0.02	0.07	0.04	0.1	0.25	0.2	0.12	0.09	0.02	-0.07	-0.13	-0.04
HW	0.48	0.71		-0.01	0.49	0.26	0	0.06	0.02	0.11	0.27	0.22	0.16	0.12	-0.04	-0.09	-0.06	0.03
RA	-0.04	-0.1	-0.03		0	0.02	0.01	0.01	0	-0.04	-0.05	-0.06	0.01	0.04	0.04	0.06	0.07	-0.02
BD	0.47	0.5	0.5	0.03		0.21	0.02	0.08	0.06	0.13	0.23	0.19	0.17	0.06	-0.02	0	-0.08	-0.02
M	0.23	0.15	0.25	0	0.24		0.1	0.18	0.1	0.18	0.4	0.35	0.32	0.36	0.09	0.06	0.23	0.38
HA	-0.01	-0.02	-0.02	0.02	-0.03	0.15		0.23	0.16	0.11	0.05	0.04	0.11	0.12	0.16	0.07	0.06	0.07
HD	0.07	0.12	0.09	0.05	0.13	0.19	0.3		0.26	0.25	0.2	0.3	0.32	0.26	0.29	0.11	0.08	0.09
P	0.01	0.08	0.05	-0.02	0.08	0.12	0.26	0.32		0.31	0.11	0.16	0.14	0.15	0.28	0.14	0.03	0.01
HH	0.15	0.14	0.15	-0.04	0.19	0.2	0.2	0.3	0.37		0.26	0.23	0.18	0.2	0.21	0.11	0.09	0.13
FU	0.22	0.3	0.31	-0.04	0.26	0.41	0.07	0.24	0.15	0.29		0.68	0.5	0.51	0.16	0.13	0.1	0.26
UL	0.07	0.25	0.27	-0.07	0.22	0.31	0.05	0.31	0.16	0.26	0.73		0.59	0.57	0.24	0.16	0.07	0.22
UA	0.11	0.16	0.21	0.03	0.21	0.34	0.11	0.35	0.14	0.23	0.59	0.67		0.5	0.25	0.2	0.11	0.2
CL	0.06	0.09	0.11	-0.02	0.01	0.35	0.11	0.26	0.12	0.21	0.54	0.58	0.54		0.33	0.18	0.18	0.31
UD	-0.07	0.05	0.02	0.02	0.01	0.07	0.14	0.3	0.24	0.19	0.19	0.28	0.3	0.34		0.22	0.06	0.05
TP	-0.05	-0.08	-0.1	0.04	0	0.14	0.1	0.11	0.14	0.12	0.16	0.16	0.23	0.13	0.23		0.14	0.05
TL	0.05	-0.14	-0.08	0.08	-0.08	0.18	0.09	0.05	0.01	0.05	0.05	0.02	0.08	0.18	0.05	0.16		0.61
TT	0.08	-0.09	-0.03	0	-0.07	0.32	0.12	0.08	0	0.11	0.23	0.18	0.2	0.33	0.08	0.07	0.64	

As resulting from the presented study, the values of heritability, and genetic and environmental correlations are within the normal range of variation, specific to the conformation traits, similar for other cattle populations.

Genetics an environmental correlations are stronger inside the grouped traits, especially in udder traits group.

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Practical applications to improve udder health: a pathogen-specific approach

M. Suntinger[1], W. Obritzhauser[2], B. Fuerst-Waltl[3], C. Firth[2], M. Mayerhofer[1] and C. Egger-Danner[1]

[1]ZuchtData EDV-Dienstleistungen GmbH, 1200 Vienna, Austria
[2]Unit of Veterinary Public Health and Epidemiology, Institute of Food Safety, Food Technology and Veterinary Public Health, Department for Farm Animals and Veterinary Public Health, University of Veterinary Medicine, 1210 Vienna, Austria
[3]Division of Livestock Sciences, Department of Sustainable Agricultural Systems, University of Natural Resources and Life Sciences (BOKU), 1180 Vienna, Austria

Abstract

Due to advancing technology on dairy farms, data integration is becoming increasingly important with regard to professional herd management. The aim of this study was to develop pathogen-specific udder health evaluations to upgrade the web-based udder health program and allow a proactive improvement of udder health in Austrian dairy herds. Investigations were preceded by data harmonization and the integration of the results of bacteriological milk cultures from laboratories into the Central Austrian Cattle Database. Udder health status can be assessed using various factors. In this study, test-day somatic cell count records, the veterinarian-reported diagnoses of acute and chronic mastitis, as well as the results of milk sample cultures, were combined. Research and development was based on data collected during an observational study conducted in cooperation with 250 farms, 17 veterinarians, 6 milk laboratories and research institutions.

Almost 6,900 quarter milk samples collected from lactating dairy cows with (suspected) udder health problems were available. Pathogen-specific udder health reports on individual cows, current and previous herd infection reports, and parameters allowing benchmarking both within and across herds were developed and subsequently displayed in clearly arranged charts. Such evaluations provide vital information on farm-specific pattern(s) of pathogens annually or even over a predefined period of time. In addition, the combination of bacteriological data and routinely-recorded animal production and health data provide details on period(s) of risk of infection as well as the cow group(s) at risk.

The pathogen-specific program allows a step-by-step analysis of animal and herd udder health status. Management issues and possible reservoirs of infection can therefore be identified more easily and eliminated at an earlier stage. Assessing the infection status of the udder, by means of milk culture results, can assist in decision-making processes leading to more precise control and prevention measures to improve udder health. One of the main challenges regarding this tool is the availability of quarter milk samples on a regular basis to ensure good quality and a high informative value of the evaluations.

Apart from supporting management decisions, results of bacteriological milk cultures may also be used in genetic evaluations of udder health. Thus, practitioners need to be motivated and trained accordingly in order to achieve sufficient data availability. The more information available, the more targeted a treatment can be: this tool could,

therefore, play a crucial role in the prudent use of antimicrobials on dairy farms. Results are in routine use in the herd management program within the Central Cattle Database in Austria and Germany (RDV) to assist veterinarians and farmers.

Keywords: pathogen-specific, culture milk samples, udder health, herd management, preventive control.

Introduction

In the field of udder health, where good herd management is essential, a web-based udder health module is available for farmers and veterinarians in Austria. Up to now, it was based on test-day SCC and veterinary diagnoses. An assessment of needs regarding data use in dairy farming in Austria showed that the electronic availability of the results of bacteriological testing of milk samples from laboratories was a particularly high priority for both farmers and veterinarians (Perner *et al*. 2016; Weissensteiner *et al*. 2018). A standardised diagnostic code for results of bacteriological milk analyses has been developed and an interface for data exchange between the central cattle database (RDV) and milk laboratories was established while taking international state-of-the-art field research into account (Obritzhauser *et al*., 2019). These efforts ensure well-prepared and harmonised data. Obtaining causative pathogens by sending milk samples for culture to external laboratories gives more detailed information for mastitis diagnostics and enables treatment specific to the pathogen involved (Cha *et al*. 2016). Therefore, the objective of this study was to develop an udder health management tool to be made available to dairy farmers and herd veterinarians in Austria considering pathogen information.

Material and method

Data collection took place within the framework of the ADDA project "ADvancement of Dairying in Austria" between 1 October 2015 and 30 September 2016 in which a total of 250 farms, 17 veterinarians and six laboratories participated. A total of 6,892 quarter milk samples collected from 1,382 lactating cows with (suspected) udder health problems from over 200 farms were available for the investigations. In most cases, all four udder quarters, even healthy quarters, were sampled. Approximately 450 samples had to be discarded because of contamination, sour milk, or empty or broken tubes. In the majority of the milk samples analysed (72.2%), no pathogens could be detected. A total of 1,533 (22.2%) samples were culture positive. Among the most common bacteria were *CNS, Staphylococcus aureus, Streptococcus uberis, Streptococcus dysgalactia* and other *Streptococci, E. coli* and other *Enterobacteriaceae.* Data were analysed at cow and quarter level and merged with calving, lactation and udder health data, such as mastitis diagnosis and test-day somatic cell counts.

Results and discussion

Examples of pathogen- specific evaluations for udder health herd management

Selected results used for a pathogen-specific udder health herd management tool are presented below. Based on some examples, the intended use and the informative value of the evaluations are described. They are intended to assist in answering questions such as: Which mastitis pathogens can be found predominantly (leading bacteria) at farm level? How many of the cows being sampled demonstrate symptoms of infection? Can infections be assigned to a particular cattle group? What is the most likely path of infection? Where is the main source of infection? Does the infection incidence and situation change over time?

Pathogen-specific udder health reports on individual cows

Figure 1 shows an example of a daily individual cow report covering production, reproduction and health data, complemented by the date of milk sampling and the bacteriological culture result at quarter level. In the example given, the cow was infected by the pathogen *Staphylococcus aureus* in both hind udder quarters. No pathogens have been found on the fore udder quarters. The linkage with other animal data stored in the RDV also enables us to determine the stage of lactation in days at the time of sampling.

Data storage in this kind of format allows results to be assessed online at any time and repeatedly by farmers and their veterinarian(s). This comprehensive animal-specific view helps to analyse the situation more rapidly, identify chronically infected animals with poor prognosis, assisting veterinarians in selecting an appropriate therapy, and dry off strategy.

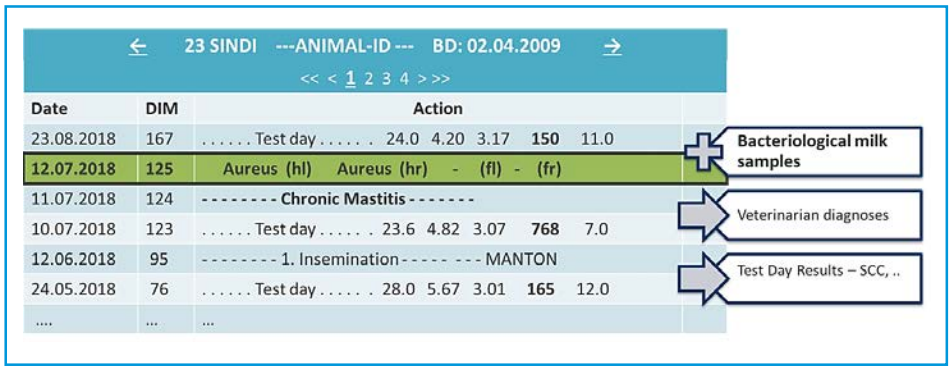

Figure 1. Report at individual cow level based on current and historic pathogen-specific and further udder health information.

Report on farm-specific pattern of pathogen

Figure 2 shows an example of a summary of the pathogen spectrum in the herd. The report is intended to show which pathogens are responsible for the majority of infections in a defined period. Ideally, a leading pathogen can be identified. The pattern of pathogen is always herd-specific as it only considers pathogens sampled from milk at this specific farm. The frequencies of pathogens sampled are displayed in the bar chart with decreasing frequency from left to right. By showing the number of cows with at least one positive culture sample for the specific pathogen, the extent of infected cows in the herd can also be assessed.

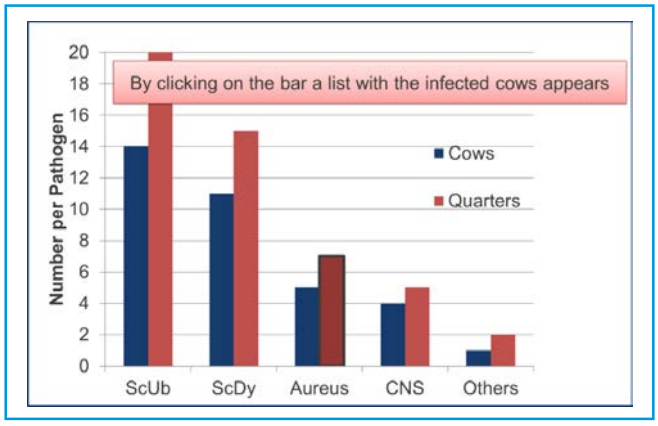

Figure 2. Report on farm-specific pattern of pathogen annually or over a predefined period of time.

The number of infected quarters for these cows is shown in the second bar. If a leading pathogen can be identified, an appropriate pathogen-specific therapy and prevention concept can be developed in consultation with a veterinarian.

Herd report 2 - Pattern of pathogen per lactation

Figure 3 shows an example of the summary of the pathogen spectrum per lactation in the herd. The combination of bacteriological data and routinely recorded animal identification, production and health data may facilitate the detection of period(s) of risk of infection as well as the cow group(s) at risk, amongst other things.

As there may be pathogen-specific differences in first or higher lactating cows, the same report can be displayed separating cows per pathogen by lactation number. Once the cow group-at-risk is known, deficiencies in certain areas (e.g. hygiene in the calving box, milking hygiene, feeding, management at drying off) might be identified.

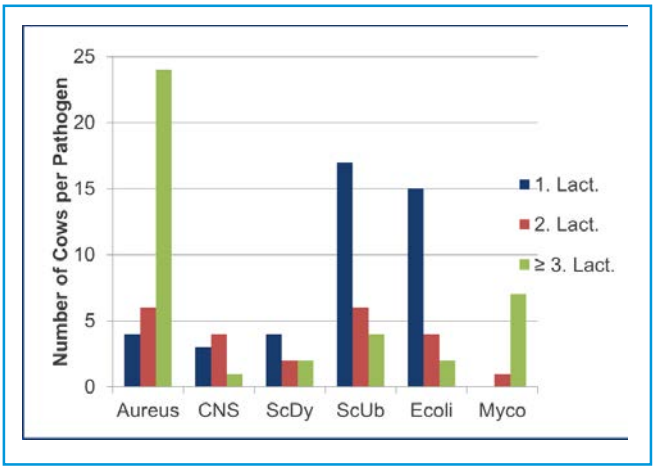

Figure 3. Example of annual herd report - Pattern of pathogens per lactation (1st, 2nd, and 3rd or higher).

		contagious pathogens						environmental pathogens			
		MYCO	SCAG	AUREUS	SCDY	CNS	SCUB	ECOLI	ENBA	STREP	OTHER
Farm current state	Nr. of Cows	0	0	7	5	3	3	4	0	2	1
Farm previous year	Nr. of Cows	4	0	16	12	4	7	6	1	3	2

Figure 4. Reservoir of infection given in number of cows per pathogen. Example of herd management report which shows the pathogen occurrence from culture positive milk samples expressed in number of infected (at least once) cows per pathogen over a period of 12 months.

Figure 4. Reservoir of infection given in number of cows per pathogen. Example of herd management report which shows the pathogen occurrence from culture positive milk samples expressed in number of infected (at least once) cows per pathogen over a period of 12 months.

Herd report – Reservoir of infection

Figure 4 shows an example of the pattern of pathogens on a farm when dividing the pathogens into their reservoir of infection. The detection of the reservoir of infection may provide information on management mistakes. The frequency of pathogens may give more insight into the possible reasons for occurrence of udder health problems. The pathogen groups differ in their way of transmission and require different preventive and control measures. Line two ("farm previous year") illustrates the pattern of pathogens from the year before. This might be beneficial to farmers in allowing them to check the effect of implemented management strategies/ steps.

Conclusions

The pathogen-specific program allows a step-by-step analysis of animal and herd udder health status. By integrating the results of bacteriological culture milk samples into the existing udder health tool, management issues and possible reservoirs of infection can be identified more easily and therefore eliminated at an earlier stage. Assessing the infection status of the udder, by means of milk culture results, can assist in decision-making processes leading to more precise control and prevention measures to improve udder health. This tool, which now allows a more comprehensive picture of udder health in dairy cows, could play a crucial role in the prudent use of antimicrobials. Professional udder health management with targeted use of antimicrobials is vital in times of increasing antimicrobial resistance. Within the D4Dairy project, further research will focus on of the harmonisation of sensitivity testing of antimicrobials and the development of targeted dry-off strategies (Obritzhauser *et al.* 2019).

Acknowledgement

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Abbreviations

MYCO = *Mycoplasma* spp, SCAG = *Streptococcus agalactiae*, AUREUS = *Staphylococcus aureus*; SCDY = *Streptococcus dysgalactiae*, CNS = Coagulase-negative *staphylococci*. SCUb = *Streptococcus uberis*, ECOLI = *Escherichia coli*, ENBA = *Enterobacteria* spp, STREP = *Streptococci* spp, others = pathogens not listed separately, hl/hr/fl/fr = hind/front left/right

French regional genetic collaborative projects to improve welfare and resilience of dairy cows

H. Leclerc[1], I. Croué[2], R. Vallée[1], A. Baur[2], A. Barbat[3], S. Fritz[2], M. Philippe[4], M. Brochard[5], F. Guillaume[4], G. Thomas[1], L. Manciaux[6], J.B. Davière[7], L Voidey[8] and N. Gaudillière[9]

[1]IDELE, UMT eBIS, 78352 Jouy-en-Josas, France
Corresponding Author: helene.leclerc@inra.fr
[2]ALLICE, UMT eBIS, 78352 Jouy-en-Josas, France
[3]INRA GABI, UMT eBIS, 78352 Jouy-en-Josas, France
[4]EVOLUTION, 35538 Noyal sur Vilaine, France
[5]MO3 - UMOTEST, 01250 Ceyzériat, France
[6]BCEL-Ouest, 22195 Plérin Cedex, France
[7]SEENERGI, 53942 Saint Berthevin Cedex, France
[8]Apporteur Grand-Est, France
[9]MO3 - Conseil Elevage 25-90, 25640 ROULANS, France

Abstract

Two collaborative projects, GENOSANTE and MO3SAN, considering Holstein (HOL) and Normande (NOR) breeds on the one hand, and Montbéliarde (MON) breed on the the other hand, bring together French companies (breeding companies, milk recording and herd support organizations in HOL and NOR; breeding companies, milk recording and herd support organizations and Livestock health protection groups (GDS) in MON) and research organizations (INRA, Allice, and IDELE). The aim of those projects is to provide selection tools for new traits to improve dairy herd profitability and cow welfare. The two projects focus on three areas of research: ketosis, claw disorders and heath data through events recorded by farmers.

Ketosis is one of the most common disorders in dairy cows due to energy deficit in early lactation. Its prevalence reaches 4% for its clinical form and 12-20% for the subclinical form. Analysis of beta-hydroxybutyrate (BHB) and acetone through MIR spectrum in milk collected since 2012, from 7 to 120 days in milk, were used. Heritability estimates of acetone were 0.12 in HOL, 0.15 in NOR and 0.11 in MON and 0.10, 0.16 and 0.14 for BHB. Genetic and genomic breeding values for ketosis have been estimated routinely since 2016 in HOL and NOR and are under development in MON.

Claw lesions are the 3rd most important health issue in dairy cattle, after mastitis and fertility issues. They impact herds both economically and in terms of animal welfare. 21 lesions are routinely recorded by professional trimmers on touch screens. Seven lesions (Digital Dermatitis (DD), Heel Horn Erosion (HHE), Interdigital Hyperplasia (IH), Sole Hemorrhage Circumscribed (SHC), Sole Hemorrhage Diffused (SHD), Sole Ulcer (SU) and White Line Fissure (WLF)), with prevalence ranging from 7 to 53% on trimmed cows (depending on the trait and breed), were studied. Heritabilities ranged from 0.02 to 0.08 in HOL, 0.04 to 0.22 in NOR and 0.05 to 0.11 in MON. Genetic correlations revealed two distinct genetic groups for claw lesions: infectious (DD, HHE, and IH) and noninfectious (SHC, SHD, WLF, and SU) lesions. Genetic correlations among lesions of the same group were moderate to high. Genetic evaluation for claw health was implemented late 2017 in HOL, and is under development in NOR and MON.

Common health disorders registered on farm (metritis, retained placenta, milk fever…) are currently under study in HOL.

All these developments aim at improving dairy cow welfare and resilience through genetic and management and are only possible with efficient data flows from phenotype collection in herds to genetic evaluations and management tools for breeders.

Keywords: Collaborative project, dairy cow, ketosis, claw health, health, genomic evaluation.

Introduction

Genetic selection of dairy cattle, initially based on production traits, has been gradually completed by functional and health trait. Presently, genomic selection development brings new perspectives. Genetic trend is expected to increase, thanks to the reduction in generation interval, particularly for low heritability traits such as those related to animal health. To enlarge the panel of traits genetically evaluated, different strategies can be used: 1/ better use of existing information, such as MIR spectra, or 2/ building a new reference population from scratch, by collecting new phenotypes (eg. claw disorders); this second option is of course much more expensive than the first one.

Genosanté and MO3SAN are French collective achievements initiated by the Evolution breeding company in 2015 on the one hand and Umotest breeding company in 2018 in the other hand. To meet these challenges of developing selection tools for new traits to improve dairy herd profitability and cow welfare, they brought together partners representing stakeholders of the whole dairy sector, from upstream (milk recording and herd support organizations (DHI), Livestock health protection groups (GDS) and breeding companies) to downstream (milk processing industry) and R&D partners. It aims at improving animal health by proposing new tools both for management and for selection. The project should also help the milk industry to better answer consumer's requests for less veterinarian treatments and for animal welfare. This project is based on the complementarity of the partners skill's: new phenotypes recording, herd management and health support with DHI, new phenotypes recording and health support with GDS, genotyping and selection with breeding companies, genetic evaluation with joint technology unit (UMT eBIS) (gathering INRA, IDELE and Allice).

Those projects focus on 3 groups of traits that have a significant impact on herd health, animal welfare and herd profitability: Ketosis, Claw health traits and other health traits (metritis, retained placenta, displaced abomasum, milk fever…), this latter group of traits being still under study.

Ketosis: a first trait, with a large phenotyped population available through MIR spectra

GénoSanté project deals with Holstein (HOL) and Normande (NOR) dairy breeds, respectively the 1st (1.5 millions of lactation per year in DHI) and 3rd (190 000 lactation per year in DHI) breed in France, and MO3SAN project deals with Montbéliarde (MON) breed, the 2nd breed (425 000 lactations per year in DHI) in France.

Ketosis is a metabolic disorder of dairy cows at early stage of lactation. It is due to a lack in energy intake relative to the energy required for milk production. In France, its prevalence is estimated at 3 to 4 % for clinical ketosis and at 12 to 20% for subclinical cases. A main impact of this disorder is a decrease in milk production by 300 to 500 kg milk per lactation. Moreover, it is associated to reproduction disorders (delay in cyclicity, lower conception rate) and to other disorders such as mastitis. In 2012, the tool Cetodetect® was implemented, thanks to the European program Optimir (2011-2015),

in order to help farmers and technicians to detect early cases of ketosis (Schwartz *et al.*, 2015). This tool is based on a decision tree from beta hydroxybutyrate (BHB) and acetone (acet) concentrations estimated from MIR spectra on milk samples. Lactating cows receive a score between 0 and 5, with 0 corresponding to healthy cows; 1 to 2 to subclinical cases, 3 to 5 to clinical ketosis. This indicator helps farmers to prevent ketosis by adapting the feeding or through treatments in case of clinical ketosis. Génosanté and MO3SAN aim at completing the panel of tools with a genetic evaluation.

A large database

Phenotypes used for the genetic evaluation are milk BHB and milk acetone contents predicted from MIR spectra since 2012 for GénoSanté and 2015 for MO3SAN. These concentrations were log-transformed in order to obtain a normal distribution, assuming that the risks have a multiplicative effect. Only data from the farms working with the DHI participating to those projects were used. The analysis was based on test days of pure breed cows recorded between 7 and 120 days of lactation and in 1st to 5th parity. Contemporary groups of less than 5 animals per herd x test-day were excluded from the analysis. Almost 2.3 million of HOL cows, 400 000 NOR and 178 000 MON cows meet all these requirements (table 1).

Development of a genetic evaluation (polygenic, genomic or single-step)

The model used was a multiple-trait animal model, using each test day as repeated data within and between lactations. It includes fixed effects of herd x year, month x year, stage of lactation x parity (3 classes: 1, 2, 3 to 5), age at 1st calving for nulliparous cows and days dry x parity for multiparous ones, and an effect of the laboratory within year.

The estimated heritabilities (table 2) were 12, 15 and 11 % for acetone concentration in HOL (based on 800 000 cows), NOR (based on 140 000 cows) and MON breeds, respectively, and 10, 16 and 14% for BHB. The estimated repeatabilities were 22, 24 and 20% for acetone, 22, 24 and 20% for BHB.

The heritabilities of these traits are moderate, as for other functional traits such as somatic cell score (Rupp and Boichard, 1997). They are consistent with those estimated in other countries, such as in the Netherlands (Van der Drift *et al.*, 2012), slightly lower than those obtained with models using different lactations as different traits (around 20%, Koeck *et al.*, 2014; Vosman *et al.*, 2015).

In HOL and NOR breeds, a genomic evaluation was performed using a reference population including all females and males with performances and genotyped by one of the partner breeding companies of Génosanté. Performances of females were Yield Deviations, those of males were DYDs computed from YDs of ungenotyped daughters.

Table 1. Description of the data available for ketosis traits in three breeds in spring 2019.

	Holstein	Normande	Montbéliarde
#cows with phenotypes	2 291 428	408 182	178 360
#genotyped cows with phenotypes	121 872	31 801	33 699
#genotyped sires with DYD of ungenotyp. daught.	18 945	2 461	3 439

Table 2. Estimated genetic parameters in three breeds for ketosis traits: log(acetone) and log(BHB) (heritabilities (h^2) and repeatabilities in bold; genetic correlations (rG) above the diagonal and correlations between permanent environment (rPE) below the diagonal).

		Holstein		Normande		Montbéliarde	
		log(acet)	log(BHB)	log(acet)	log(BHB)	log(acet)	log(BHB)
h^2 and rG	log(acet)	**0.12**	0.85	**0.15**	0.89	**0.11**	0.85
	log(BHB)		**0.10**		**0.16**		**0.14**
Repeat	log(acet)	**0.18**		**0.24**		**0.20**	
and rPE	log(BHB)	0.88	**0.22**	0.91	**0.26**	0.66	**0.20**

The size of the reference population was quite large, with more than 140 000 animals in HOL, and 35 000 animals in NOR (Table 1). The model of genomic evaluation was similar to the one used for the French official genomic evaluations. It is based on a MarkerAssisted BLUP, using from 250 to 3000 QTL according to the breed and the trait. These QTLs were first pre-selected with the BayesCπ methodology and then traced with 4-SNP haplotypes. The first evaluation for ketosis was published in August 2016.

In MON breed, due to more recent development (spring 2019) the genetic evaluation will be implemented with a single-step model where all genotype, pedigree, performance and progeny data available through MO3SAN project are analysed simultaneously. Routine evaluation are planned in 2021.

For each animal, a ketosis index was computed, with a 50% weight for BHB and acetone. As expected, a reduction of the risk of ketosis (clinical and subclinical) was observed for cows with a higher GEBV. For instance, in HOL, the average percentage of testdays corresponding to ketosis cases was 9% for cows with a GEBV between +1 and +2, while it reached 33% for cows with a GEBV between - 1 and -2, i.e. a 3.5 times lower risk of ketosis.

Claw health traits: a reference population to be built

Claw lesions are one of the most important health issues in dairy cattle. Hoof and leg disorders are a major welfare problem in dairy farming, often causing pain and lameness in cows (11% of cows with lameness – Delacroix, 2000). Their origin is multifactorial: infectious, traumatic, housing/hygiene, nutrional… Hoof disorders are also associated with high cost and have been identified as the third most costly pathology after mastitis and fertility troubles (Enting *et al.*, 1997; Van der Waaij *et al.*, 2005). Even without being responsible for clinical lameness, some studies describe that more than 50% of cows show at least one lesion (e.g., Van der Linde *et al.*, 2010; Van der Spek *et al.*, 2013). Reducing the prevalence of claw lesions is therefore of major interest in dairy farms.

Data collected

Twenty-one claw health traits are collected as described in ICAR Atlas (ICAR, 2015) by professional trimmers on touch screen. Seven of them, having a prevalence of at least 5% were studied: sole hemorrhage circumscribed (SHC), sole hemorrhage diffused (SHD), sole ulcer (SU), white line fissure (WLF), digital dermatitis (DD), heel horn erosion (HHE) and interdigital hyperplasia (IH). Each trait is described by a severity

score from 1 to 3, except for DD having a 4th level. The traits DD, HHE, and IH can be classified as infectious traits and SHC, SHD, SU, and WLF as non-infectious traits. Data collection started in April 2014. The trimmers visited farms when called by farmers to trim their cows. Croué *et al* (2017) investigated effect of preselection of cows for trimming because including untrimmed cows as healthy caused bias in the estimation of genetic correlations. A trimming status trait to account for preselection have been used, as it allows consideration of the exhaustive population of cows present at a time a trimmer visited a farm without causing bias in genetic parameters.

Due to the non-exhaustive collection of information on the herd (preselection of cows for trimming) and the limited number of herds using the trimming services proposed by DHI and GDS, the population available to estimate genetic parameters and construct a reference population for genomic evaluation is limited in size. In our studies, we do not considered a severity degree of the lesion. A cow was given a score of 1 for a lesion if the lesion was observed by the trimmer, 0 if it was not. Only data from the farms working with the DHI participating to those projects were used. The analysis was based on data collected from purebred cows recorded between days in milk 1 to 550 of lactation in 1st to 3rd parity for HOL (1 to 5th parity for NOR and MON). Contemporary groups of less than 5 animals per herd x test-day were excluded from the analysis for HOL (4 animals per herd x test-day in NOR and MON). Only hind claw information was kept because front hooves were not often trimmed and showed fewer lesions than hind hooves, the two hind claw must be trimmed. Only the first trimming record of each cow was kept. The model will be updated when the proportion of cows trimmed several times is higher. In spring 2019, almost 120 000 million of HOL cows, 17 000 NOR and 15 000 MON cows me*et all* these requirements (table 3). For genetic parameters estimation, only 46 787 trimmed cows (+ 54 090 contemporary non trimmed cow) where used in HOL, and the complete population available in spring 2019 in NOR and MON.

Development of a genetic evaluation

The model used was a multiple-trait animal model. It includes fixed effects of herd-date of trimming, parity, stage of lactation (10 classes). The model include a heterogeneous residual variance on trimmer-year effect.

In the HOL population trimmed cows, 82% of the cows had at least one lesion (Croué *et al*, 2017). The HHE and SHD were the most frequent lesions, with prevalence of 53 and 43%, respectively (Table 4a). The least frequent lesion was SU, with a prevalence of 7%. In NOR, the most frequent lesions is still HHE, and in MON, it is SHD with 35 (Table 4b) and 45% (Table 4c) respectively. Some difference between breeds need to be noticed. For DD, MON seems to be less concerned with only 16% of cows whereas 29 and 32% in HOL and NOR respectively. For IH, NOR is more concerned with a prevalence of 21% of cows while 9% or less in HOL and MON. For WLF, the prevalence is variable between breed: 9% in NOR, 16% in HOL and 24% in MON.

Table 3. Description of the data available for claw health traits in three breeds in spring 2019.

	Holstein	Normande	Montbéliarde
#cows with phenotypes	118 816	17 350	14 985
#genotyped cows with phenotypes	16 982	5 618	2 078
#genotyped sires with DYD of ungenotyp. daught.	3 183	409	662

Table 4a. Prevalence (%) of claw lesions and estimated genetic parameters in Holstein breed for 7 claw health traits: (Digital Dermatitis (DD), Heel Horn Erosion (HHE), Interdigital Hyperplasia (IH), Sole Ulcer (SU), White Line Fissure (WLF), Sole Hemorrhage Circumscribed (SHC) and Sole Hemorrhage Diffused (SHD), heritabilities (h^2) in bold on the diagonal with standard errors in bracket; genetic correlations (rG) above the diagonal with standard errors in bracket).

		Infectious traits			Non infectious traits				
	Preval.	DD	HHE	IH	WLF	SU	SHC	SHD	TRIM
DD	29	**0.07** (0.01)	0.63 (0.07)	0.68 (0.05)	-0.21 (0.08)	-0.04 (0.09)	-0.23 (0.09)	-0.10 (0.11)	0.43 (0.08)
HHE	53		**0.04** (0.01)	0.51 (0.08)	-0.05 (0.09)	0.36 (0.09)	0.15 (0.11)	0.02 (0.12)	0.55 (0.09)
IH	8			**0.08** (0.01)	-0.16 (0.08)	-0.02 (0.08)	-0.01 (0.10)	-0.15 (0.10)	0.37 (0.08)
WLF	14				**0.06** (0.01)	0.51 (0.08)	0.35 (0.10)	0.23 (0.11)	0.10 (0.09)
SU	7					**0.05** (0.02)	0.86 (0.05)	0.26 (0.11)	0.36 (0.09)
SHC	16						**0.03** (0.00)	0.49 (0.11)	0.45 (0.10)
SHD	43							**0.03** (0.01)	0.13 (0.12)
TRIM									**0.02** (0.00)

Table 4b. Prevalence (%) of claw lesions and estimated genetic parameters in Normande breed for 7 claw health traits: (Digital Dermatitis (DD), Heel Horn Erosion (HHE), Interdigital Hyperplasia (IH), Sole Ulcer (SU), White Line Fissure (WLF), Sole Hemorrhage Circumscribed (SHC) and Sole Hemorrhage Diffused (SHD), heritabilities (h^2) in bold on the diagonal with standard errors in bracket; genetic correlations (rG) above the diagonal with standard errors in bracket).

		Infectious traits			Non infectious traits				
	Preval.	DD	HHE	IH	WLF	SU	SHC	SHD	TRIM
DD	32	**0.10** (0.02)		0.86 (0.05)	-0.44 (0.17)	0.02 (0.15)	-0.17 (0.19)		0.30 (0.12)
HHE	35				Not converged				
IH	21			**0.22** (0.03)	-0.46 (0.15)	-0.08 (0.13)	-0.34 (0.17)		0.25 (0.10)
WLF	17				**0.04** (0.01)	0.51 (0.17)	0.36 (0.23)		0.34 (0.16)
SU	11					**0.08** (0.02)	0.70 (0.15)		0.21 (0.13)
SHC	9						**0.04** (0.01)		0.17 (0.18)
SHD	29								Not converged
TRIM	43								**0.16** (0.02)

Table 4c. Prevalence (%) of claw lesions and estimated genetic parameters in Montbéliarde breed for 7 claw health traits: (Digital Dermatitis (DD), Heel Horn Erosion (HHE), Interdigital Hyperplasia (IH), Sole Ulcer (SU), White Line Fissure (WLF), Sole Hemorrhage Circumscribed (SHC) and Sole Hemorrhage Diffused (SHD), heritabilities (h^2) in bold on the diagonal with standard errors in bracket; genetic correlations (rG) above the diagonal with standard errors in bracket).

		Infectious traits			Non infectious traits				
	Preval.	DD	HHE	IH	WLF	SU	SHC	SHD	TRIM
DD	16	**0.05**	0.71	0.77	-0.12	0.50		-0.30	0.53
		(0.01)	(0.14)	(0.12)	(0.17)	(0.17)		(0.19)	(0.13)
HHE	34		**0.07**	0.55	-0.08	0.60		-0.46	0.50
			(0.02)	(0.14)	(0.16)	(0.13)		(0.17)	(0.12)
IH	9			**0.08**	0.15	0.51		-0.08	0.49
				(0.02)	(0.15)	(0.14)		(0.18)	(0.12)
WLF	24				**0.11**	0.46		0.25	0.22
					(0.02)	(0.14)		(0.16)	(0.12)
SU	8					**0.08**		-0.14	0.59
						(0.02)		(0.18)	(0.11)
SHC	14							Not converged	
SHD	45							**0.07**	-0.41
								(0.02)	(0.13)
TRIM	53								**0.29**
									(0.03)

The estimated heritabilities (table 4a, 4b, 4c) are low to moderate, according to the breed and the trait: 0.02 to 0.08 in HOL, 0.04 to 0.22 in NOR and 0.05 to 0.11 in MON. In general, genetic correlations among lesions of the same group (infectious vs non infectious) were moderate to high (between 0.50 to 0.68 and 0.55 to 0.77 in HOL and MON respectively for infectious traits – between 0.23 to 0.86 and 0.36 to 0.70 in HOL and NOR respectively for non-infectious traits). Heritabilities and correlations estimated are consistent with those estimated in other countries, such as in the Netherlands (Van der Spek *et al.*, 2013).

A genomic evaluation (Croué *et al.*, 2019) was performed for the 3 breeds using a reference population including all females and males with performances and genotyped by one of the partner breeding companies of Génosanté and MO3SAN. Performances of females were Yield Deviations, those of males were DYDs computed from YDs of ungenotyped daughters. In spring 2019, the size of the reference population was around 20 000 animals in HOL, 6 000 animals in NOR and 2 700 animals in MON (Table 3). For the last two breeds, these population sizes need to be further increased to make genetic evaluations more reliable and to estimate missing traits (HHE and SHD for NOR and SHC for MON). The genomic evaluations are based on GBLUP. In HOL genome wide association studies (GWAS) have been carried out and have shown a large number of QTL (Croué *et al*, 2019).

For each genotyped animal, an index for RLI (resistance to infectious lesions) and for RLNI (resistance to non-infectious lesions) were computed. In HOL, RLI has a 50% weight for DD, 25% for HHE and 25% for IH, and RLNI has a 40% weight for WLF, 40% for SU and 10% each for SHC and SHD. As expected, whatever the traits (DD figure 1A, IH figure 1B, SU figure 1C and WLF figure 1D) and the breed, animals with poorer index (lower than -1) have a 80% risk of presenting the lesion, while animals with an index of +1 have a risk lower than 10%.

Routine evaluation are available since 2017 for HOL, winter 2019 for NOR and planned for 2021 in MON, with an enlarge reference population in order to improve genomic prediction equation.

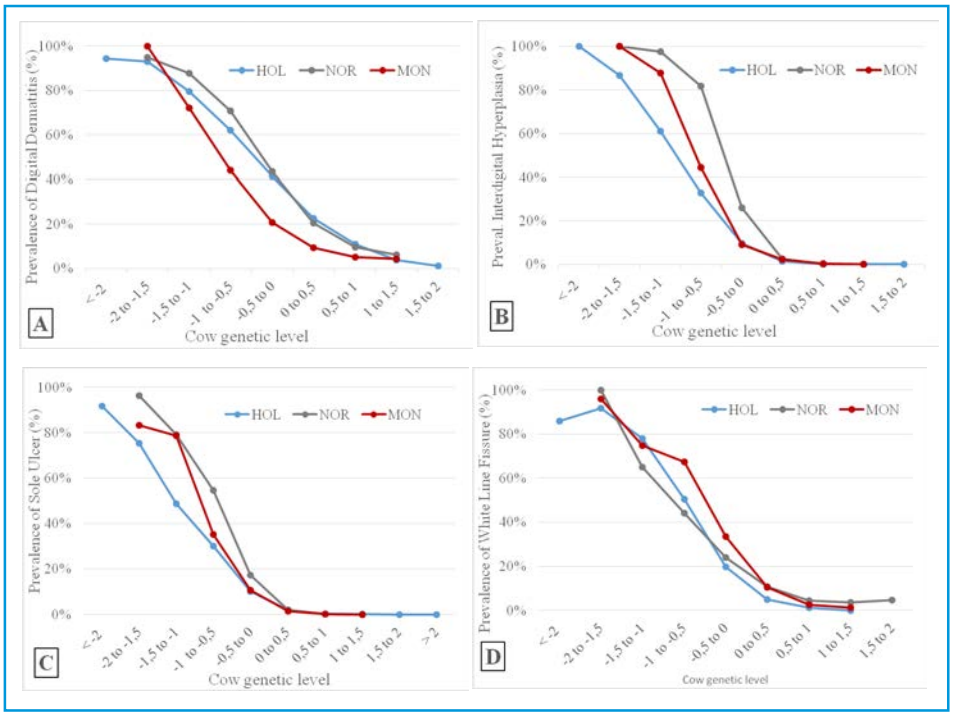

Figure 1. Prevalence of claw traits (A: Digital Dermatitis ; B: Interdigital Hyperplasia ; C: Sole Ulcer; D: White Line Fissure) in function of cow genetic index (minimum number of 10 cows per class).

Conclusion

Génosanté and MO3SAN are collective achievements of partners sharing a common goal, improving the productive health of dairy cows. Evaluations of other new traits are expected over the coming years. All the partners of the program share the benefits. Breeders and AI companies will be able to account for these traits in their breeding process. Genetic evaluations brings also useful information for DHI, which can better understand the major risks for disorders through the estimated environmental effects (eg. herd x year).

Genomic selection is a promising tool to increase resistance to new health traits such as ketosis or claw lesions in dairy cows.

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Conditions of mechanical milk meters through in a Uruguay test platform

D. Hirigoyen[1,2], M. Calvo[3], A. González-Revello[2] and R. de los Santos

[1]Instituto Nacional de Investigación Agropecuaria (INIA), La Estanzuela, Ruta 50, km 11, Uruguay Corresponding Author: dhirigoyen@inia.org.uy
[2]Dpto. ciencia y Tecnología de la leche. Facultad de Veterinaria, Udelar, Uruguay
[3]Cooperativa Laboratorio Veterinario de Colonia. COLAVECO, Uruguay

Abstract

This paper attempts to present levels of functionality and accuracy of 193 milk meters (MM), verified and tested in a basic milk meters test platform (MMTP) in Uruguay. The MMs belonged to 8 dairy producers and 9 independent controlling companies, which specialize in offering milk control services in the country. The universe evaluated, corresponding to 2 of the main brands in the market, used in permanent milking cycles in different dairy farms to estimate milk production of each animal. The results obtained showed that 50,8% of MM, was above 3% error, being classified as “unfit” to perform measurements at dairy farm level by following the recommended criteria of the International Committee for Animal Recording (ICAR). MM admitted to MMTP, had never been valued by an independent body; only 26% of them were evaluated for a second time and 4% for a third, in the period covered by this evaluation from 2008 to 2012.

The results of the checks carried out, allow to the conclusion that it is necessary and indispensable, created in Uruguay, a regulatory body that establishes limits of error and technical requirements, following international standards. The MM had been experiencing intense wear and tear for the continuous and permanent use, between dairy farms, leading an author to suggest following up a verification year, ensuring the accuracy used to establish management measures in the herd and making productive, reproductive, nutritional and genetic management.

Keywords: Milk meter, Accuracy, Verification.

Introduction

In Uruguay, the productivity of dairy farms in terms of the ratio of “milking cows/cows’ mass” has been above 72%. (DIEA,2018). With practically the same number of animals per herd (approximately 425,000 cows’ mass and 308,000 milking animals), the production went from 1,073 million litters remitted to plants in the financial year 1994/ 1995, to 1,900 million in the first 9 months of 2018. (INALE,2018). The increase in individual milk production per cow has been the main factor in the growth of milk production in the country in recent decades, and annual litters per cow are increasing at a rate of 2% per year. The evaluation of productivity within each herd and estimation of milk production per animal requires measurements and production databases, which, together with the genetic background of the production of the animals and their parents, allow to select the animals genetically superior and drive progress in certain features of economic importance (Mark, T.2004; Madouasse A. et al., 2010).

Nowadays in Uruguay, the measurement of milk production per cow is carried out mostly by portable mechanical instruments and to a lesser extent by fixed electronic devices. Both are designed to be added to any type of milking system and quantify the individual milk production, without affecting milk output time or udder health as established by the Dairy Herd Information Association, (DHIA,2011). They are used to control milk production, establish management measures in the herd (productive, reproductive, nutritional and genetic). The equipment is inserted between the collector and the milk pipe, in each of the descents, permanently or only during the milk control, they can be their own or belong to independent controlling companies, which specialize in offering this service.

The MM are basic instruments composed of at least 5 fundamental parts: cover plastic, base assembly, flask, tap with strap and rubber gaskets (Figure 1).

The operating conditions lead to MM wear due to which, like any instrument or equipment used to quantify a quantity, must be subjected to calibration and verification procedures, to limit the uncertainty of the measurements, within a field of acceptable tolerance. (ISO: 5725-6,1994) and the International Committee for Animal Recording (ICAR) advises, to be verified at least once every 12 months. In Uruguay, most of the meters used to belong to the brands Waikato® (Hamilton, New Zealand) and Tru Test® (Palmerston Norte, New Zealand) and have similar characteristics of operation and use (Photo 1).

In this sense, the verification process in control banks is carried out reproducing the milking conditions to which the MM or lactometer is subjected, using water instead of milk, verifying by weight the precision of the sample contained inside it. Because the monthly and regular measurement is decisive for the proper management of the farm's milk production, the precision and correct functioning of these lactometers, during their useful life is essential for efficient use. It is necessary to have independent organizations that qualify and evaluate the status of these instruments, whether owned by private control operators or by the producers themselves.

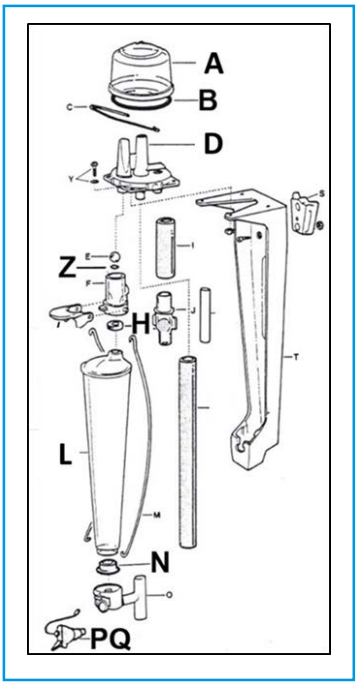

Figure 1. Basic scheme of milk meter (Waikato). Parts: Cover Plastic (A), Base Assembly (D), Flask (L), Tap with strap (P-Q), rubber gaskets (B, Z, H y N).

Figure 2. Main brands of mechanical milk meters used in Uruguay, Waikato® (left), Tru Test® (right).

The main objective of this work was to determine the fitness of 193 MM mechanics used in our country to quantify the dairy production of animals. At the same time, the level is described in terms of functional acceptability reached by them when verified for 5 years, in an independent evaluation platform that was installed in Uruguay in 2008 and the main causes of malfunction of MMs at a structural level. and the way of use.

.

Material and methods

Work was carried out on a basic MMTP, located in a laboratory situated in Nueva Helvetia, Colonia, Uruguay, at the end of 2008. It consisted of a room, with a group of vacuum motor pump SAC, of 1.5 Hp set at 50 kPa, (15 “Hg), 20 L stainless steel vacuum and interceptor lines, dead weight type vacuum regulator, 30 L stainless steel bucket, an inlet tube, a vacuum gauge (indicates Vacuum level) and a shut-off valve To perform the mass adjustment, a MercoCity scale, model ACS-L2 III, with a range between 0.2 - 30 Kg, and an accuracy of 0.010 Kg was available. A MM analysed corresponded to the brands Waikato (75%) and Tru Test (25%). All MMs that entered the MMTP was evaluated following the procedure followed by (DHIA, 2011), and approved by (ICAR, 2016). There were 193 instruments traced at the level of 251 records made in the MMTP during the period n study was recorded if the use of MMs was individual or shared.

The structural reason for the MM malfunction was sought and the frequency with which they were found in the instruments was established, considering also the brand of the same.

The instruments to evaluate belonged to 17 owners of different sites of the dairy basin, who attended by only, 2 and 3 times, in 70%, 26%, and 4% respectively.

Prior to each measurement, the instruments were disassembled and cleaned with citric acid and industrial detergent. Then, each MM was mounted on the test platform, verifying by a level, its vertical position (within ± 0.5 degrees). The suction hose of the MM was carried to an open bucket (30 L), directly below the meter. An air intake restrictor was used, to guarantee a flow of 3.5 to 4.0 L / min., At the level of available vacuum. Drinking water was used at a temperature of 19 ± 5 ° C.

Each meter was subjected to 3 consecutive test measurements, expressing the readings according to criteria established by ICAR, (2016), and the manufacturers of Waikato Milking System, (2002), where the acceptance range is ± 3%, on the average of the readings made. The MMs that did not pass the test were classified as “unfit use”, and they underwent repair, replacement of parts and recalibration, being delivered to their owner in conditions of aptitude. Of the 193-equipment verified in the MMTP, 2 MM were discarded, due to severe deterioration of some of its parts, not being able to be replaced, and its disposal recommended. In general, if it could not be repaired, it was suggested that the service be withdrawn.

The data were analysed and presented as an average ± standard deviation.

Results and discussion

When using different types of instruments or equipment, to measure any type of quantifiable quantity, it is convenient to have a series of key concepts, which belong to the field of metrology, of course. For this, it is necessary to distinguish the management of two concepts, which are closely related, such as verification and calibration, but which are different (JCGM 200, 2012). The calibration applies only and exclusively to measuring instruments; of any kind of quantifiable magnitude when compared with values of a previously established pattern. On the other hand, in the Verification, the instrument is compared, but not done with the previous reference standards, but it is “compared” directly, with another instrument, (previously calibrated, of course), to verify that the calibration of The first instrument is the correct one.

In relation to the study that motivates this communication, it is possible to say that the certificates issued by the MMTP inform the users in relation to the verification of the MMs, giving objective evidence that this instrument complies with the requirements specified by the manufacturers or the rules. (UNIT-ISO 10012, 2003).

Verification should not be confused with a calibration where it has been adjusted and if it should have been calibrated.

Of the 193-equipment verified in the MMTP, 2 MM was discarded, due to severe deterioration of some of its parts, not being able to be replaced, and its disposal recommended. Of the MMs verified belonging to 17 owners who participated in the evaluations, 100% had never been valued by an independent organization, MMTP type, as created in 2008. Once the evaluation system began to operate in the MMTP, only 9 owners of MM batches checked their equipment a second time, and only 2, for a third time. This frequency of verification is not enough, and it departs from the international recommendations to undergo evaluation between periods of 12 months (ICAR, 2016). In relation to the fitness of the total equipment verified, it was found that 50.8% was above 3% error, being classified as “unfit” measurements at the dairy level.

Table 1. Deviation values in the measurement (%) with respect to the reference method in the mechanical milk meters.

	Ranges (%) *	N° Equipment
Fit	0-2,9	95
	03-may	49
Unfit	5,1-10	44
	>10	3
Total		191

* *Deviation from the value of the reference method, according to the criteria of IRAM 8042 which establishes the fitting as ≤ 3%.*

97% of MMs classified as unfit presented a deviation with respect to the reference measurement, in values between 3 and 10%, with 3 instruments having higher values than the latter. This means that when they are used at the dairy farm level to measure production, there are animals that are being poorly qualified.

The percentages of the diversion of MMs in relation to the reference measurement are illustrated in Table 1.

The achievement of this situation gave rise to erroneous indicators, which influenced the making of wrong decisions at the level of the owners of the animals, with erratic economic implications based on results above or below their real value.

The standards of IRAM standard 8042, (1989) and DHIA, (2011), establish that MMs must be tested every 12 months, subject to inspection and maintenance at least once a year. The acceptance ranges for both establish satisfaction when the result ranges between 1.5 and 2.5%, being somewhat more demanding than the one used in this work. If so, it would increase the percentage of MM outside working conditions. Surely the nonconformity of the lots is since 100% of the equipment entered in this MMTP did not receive a regular verification that complied with the provisions of ICAR, (2016).

The results obtained give objective evidence that 50% of the instruments used at the national level, to evaluate the dairy herd and to analytically grade milk at the laboratories level, do not satisfy the specified requirements nor the internationally approved standards. If it is taken into account that in Uruguay approximately 140,000 animals/ month, are subject to the official and private milk control system, using these instruments, it is possible to say that: with the range of error found, almost 45% of the estimates made were able to be a sub or overvalued. These non-conformities generate more impact if we consider that the individual milk samples collected with these MMs were sent mainly to central analysis laboratories, for the improvement test of dairy herds. These instruments that estimate the production of milk and serve to obtain the sample to qualify for the parameters of fat, protein, urea nitrogen, and somatic cell count, etc., should provide producers with a guarantee of accuracy in the operation.

The figures handled at the country level indicate that 25-30% of all dairy cows participate in the monthly milk yield record and are the basis for making decisions on components such as herd management (health services of the udder, feeding, etc.) and genetic improvement.

The system of a monthly contract to independent control operators, who transfer the MMs between establishments, leads to mechanical wear of the pieces due to the frequency of operation and impacts caused by the displacement between sites. Additionally, there are no established error limits, nor specific technical requirements approved at the national level, which assess the precision with which these instruments

Table 2. Frequent defects observed in milk meters which cause incorrect measurements (n = 127)

	N° Equipment (%) /Brand	
Error´s Cause	Waikato	Tru-Test
Wear of Gaskets	62 (49%)	27 (21,1%)
Wear of Gaskets + Tap with strap	0	9 (7,1%)
Wear of Gaskets + Flask	11 (8,6%)	0
Wear of Gaskets + Cover plastic	18 (14,2%)	0

are measuring. This takes on a greater dimension if we consider that the producer makes a genetic improvement, supported by the selection of superior animals based on productive merits that are valued through these instruments.

The MM as any measuring instrument, requires maintenance, cleaning, and regular adjustment. Being manually operated devices for daily, weekly or monthly milk registration, the components of these have a limited shelf life, subject to use and handling; since they experience wear of some pieces, which, when not replaced when required, generate incorrect measurements, such as those found in this period, in the MMTP.

If we analyze in detail which was the pieces that showed the greatest wear and tear, as can be seen in Table 2, it is possible to say that failure errors are the most frequent wear of joints, followed by breakage of caps and measuring cup. In most cases, (except for the 2 instruments eliminated), once the altered parts were evaluated and detected, the spare parts were replaced, the error was solved and returned in “fit “conditions to the users and owners.

The shared use of MMs by more than one controller and between different properties leads to greater wear of the equipment that causes severe failures in the measurements. MMs that have a single owner, unlike the property shared by a group of producers, translate into a better state of the instruments, probably due to better care and

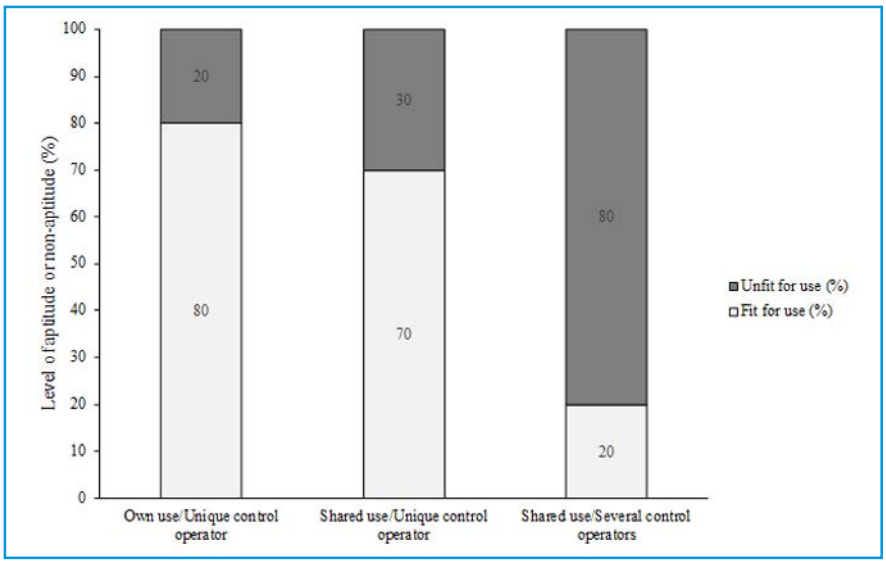

Figure 2. Level of aptitude or non-aptitude (%) of mechanical milk meters according to the type of uses.

conservation of these. On the other hand, the use in a single property reduces the assemblies in the milk lines, as well as the transfer of the equipment, which leads to lower levels of wear and tear of key pieces.

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Dairy cattle milk recording working group update. Short-term prospects for cattle milk recording

Pavel Bucek

Czech Moravian Breeders' Corporation, Inc., Benesovska 123, 252 09 Hradistko, Czech Republic

Introduction

This introduction to the ICAR Dairy Cattle Milk Recording WG was presented at the panel discussion during the ICAR Conference in Prague in June 2019. Entitled *What Next?*, the discussion involved representatives of several working groups and subcommittees including the Dairy Cattle Milk Recording Working Group, the Functional Traits Working Group, the Recording and Sampling Devices Sub-Committee, the Sensor Devices Task Force and the Animal Data Exchange Working Group. The panel discussed the future direction of the milk recording industry, approaches to the organisation of ICAR working groups, subcommittees and task forces, and how milk recording organisations (MROs) can respond to new trends and challenges.

Membership

Dairy Cattle Milk Recording Working Group members specialise in different fields, comprising technical personnel as well as practitioners employed by MROs involved in daily administration activities and herd management. The group is represented by all of the important geographic areas, informing the group's understanding of the needs of different territories around the world. Specialising in all aspects of dairy cattle recording, the group covers current and prospective farm systems, lactation calculation, sample transportation, databases, plausibility checks and quality management. Members:

- Pavel Bucek – Czech Republic
- Franz Josef Auer – Austria
- Xavier Bourrigan – France
- Bruce Dokkebakken – USA
- Kai Kuwan – Germany
- Juho Kyntäjä – Finland
- Yaniv Lavon – Israel
- Filippo Miglior – Canada
- Danuta Radzio – Poland
- Friedrich Reinhardt – Germany
- Carlos Trejo Jimene – Chile

Priorities

The group is currently in the process of making improvements to content in Section 2 of the Dairy Cattle Milk Recording Guidelines. The section is composed of three parts: Section 2 - Guidelines for Dairy Cattle Milk Recording, Procedure 1 – Computing 24-hour Yields and Procedure 2 – Computing Accumulated Lactation Yields. The most recent update of the Guidelines – approved in February 2018 at the ICAR Conference in New Zealand – was general in focus. Attention has now switched to developing Procedure 1. Significant progress is expected to be made in time for ICAR 2020, with the final version delivered at ICAR 2021. The goal is to make content more customer-oriented, clearer, and more practical toward assisting the daily practice of MROs. There will be a particular emphasis on providing practical recommendations to make 24-hour calculation methods more applicable for farmers.

Key projects

The group is committed to monitoring practice among milk recording organisations worldwide. To that end, group members recently carried out a number of projects, notably a number of extensive global surveys:

- 24-hour calculation surveys of automatic and classical milk recording systems (52 organisations)
- World trends in cattle milk recording (3 parts/46 organisations)
- South American project
- Plausibility checks project (25 organisations)
- Management of milk recording organisations – current problems and future challenges (41 organisations)
- KPI development for the ICAR Certificate of Quality
- Big data project (milk recording x feeding)
- Special interdisciplinary projects
- Collaboration with ICAR WGs, SCs & TFs (Accuracy Task Force & Sensors Device Task Force), etc.

Key Guidelines Research

With regard to 24-hour calculations, a number of the group's research projects have been aimed at simplifying methods used by cattle farmers. A new 24-hour calculations policy is due to be published, with recommendations for estimating coefficients and factors and evaluating methods. Below is a list of projects recently conducted:

- Recalculation of the Liu method – AM/PM sampling as the industry standard
- Research project on sampling scheme C calculations
- Detailed technical analysis of 24-hour calculations
- Comparing different 24-hour calculation methods
- Recalculation of coefficients for automatic milking systems (Galesloot method)
- Earmarking improvements for the Liu method adaptation of sampling scheme Z, a method that provides several benefits
- AfiLab Project – in-line analysis
- Comparison of different 24-hour calculation methods

Collaboration with Industry

Members continue to engage with MROs and stakeholders in the cattle MR industry, having established contact with 52 organisations globally. Members regularly liaise with experts outside the group at ICAR congresses and other events, including at:

- Technical sessions, where information is exchanged with MROs
- Practical workshops such as at ICAR 2019 (involving more than 140 participants)
- Meetings where advisory services are offered to resolve technical MR problems
- Meetings to discuss changes to the Guidelines
- Promotional events organised by ICAR and the WG abroad, e.g. trainings in Iceland, China, Poland, etc.
- Consultancy meetings for organisations from the UK, Russia, Romania, Afghanistan, etc.

The Future of Milk Recording

The group is actively seeking new approaches to MR data processing and to innovating 24-hour calculations. Big data, artificial intelligence, deep learning, and new software are all being explored, with a number of projects in the works.

AMS and MRO internal data are also becoming increasingly available from milk labs, including conformation data and other types of data from automatic milking systems (milking robots). The big challenge is to combine all of the data from different sources. Higher value is achieved when data is analysed in unison toward creating new services for milk recording customers. Proper ways of combining data from AMS with other animal information will be a very important task for milk recording organisations in the future.

The following indicators will also need to be measured: weights, feed intake, feed efficiency, metabolic problems, etc. As more and more information is set to be processed and analysed by MROs, suitable technologies will have to be integrated as part of the suite of services offered by MROs.

The efficiency of the milk recording process must be improved to aid daily practice on farms. More tests could be introducing at the beginning of lactations and less at the end of the process. Metabolic problems most commonly occur at the beginning of lactations. Accordingly, an innovative solution in this area could yet yield significant positive outcomes.

Needs Analysis of MROs | 24-hour Calculations

Analysing the needs of MROs worldwide, the group carried out a recent survey – 24-Hour Calculation Methods: Global Trends – gathering data from 52 organisations. Consisting of 90 questions, the survey covered the period December 2018 – March 2019. The responses from the survey participants are considered crucial to developing an updated version of the 24-hour calculations section of the Guidelines. Below are a series of statements by MROs in relation to the Guidelines ranked according to priority on a scale of 1 to 10 (1=low, 10=high):

- We need detailed descriptions of equations and examples (8.1)
- We need descriptions to be clearer and easier to use (7.8)
- We need practical examples on deriving factors and coefficients (7.3)

- We need practical comments and recommendations for use (7.2)
- We need new methods to be included in the Guidelines (5.5)
- We want a completely different approach to 24-hour calculations and would like to see a new method introduced (4.6)

It is most common for MROs (18 organisations) to devise new methods internally or in collaboration with research institutes (15 organisations). Others collaborate with research institutes as well as commercial companies or, less commonly, with commercial companies exclusively.

New 24-Hour Calculation Guidelines

Resulting from the group's discussions concerning the new version of Procedure 1, the following key issues were identified:

- Not all areas can be unified nor is it necessary to standardise all areas
- There are differences in the implementation of methods among MROs
- A degree of unity must be established
- Most MROs follow the ICAR Guidelines, but minor differences remain
- Future policy
  - Ø Calculation – collaboration – sharing factors and coefficients, problems with calculations and estimating factors
  - Ø Estimating coefficients: possible international project among ICAR members
  - Ø New services for herds using AMS
  - Ø New technologies, screening and possible additions
  - Ø Do we need new ICAR services in this field? A new laboratory for verifying the quality of estimated factors, coefficients?
  - Ø Lend support to countries in need, advisory services
  - Ø Some MROs are unable to derive equations, providing an opportunity for ICAR to offer data check and outsourcing services in this field

Consumer Focus

The group must improve the services offered to consumers. BV health traits are an important source of consumer data and welfare and there are various ways of meeting these requirements.

Further discussion items

- Future innovations of the ICAR Guidelines, e.g. individual lactation qualification in France
- Project milk recording outputs and outcomes
- Daily milk recording
- New services for herds using AMS

- New technologies
- Quality Management Systems for Dairy Farming – Opportunities & Challenges for Recording Organisations. New services for MROs.
- Validation and certification, development of quality indicators, plausibility checks for multiple data sources; checks/validations
- Standardisation and calibration are expected to play a big part
- Data storage strategies
- Accuracy of different methods and intervals in milk recording
- Big data, integrating deep learning within MR practice
- Possible innovative approach in calculation for 24-hour on the base of big data
- For Dairy Cattle Milk Recording Working Group is resolving current problems & priority points for the MR Workshop in these field which were discussed during the milk recording workshop in Prague:
    - Ø How do we keep AMS customers happy?
    - Ø Whose milk is in the vial?
    - Ø How complex exactly is it to calculate daily yields?

Executive summary from the discussion at the milk recording workshop

A milk recording workshop organised by the ICAR Dairy Cattle Milk Recording WG took place on Tuesday 18/06/2019 in Prague (ICAR 2019). It was attended by more than 140 registered participants, representing milk recording organisations, manufacturers, universities, research institutes, and other bodies from around the world. The aim of the workshop was to shift from a science perspective toward resolving commonly encountered practical issues, and to explore the day-to-day business concerns of milk recording organisations with a view to stimulating discussion and improving practice. The workshop consisted of introductory presentations followed by discussion on each topic, with the main focus centred on engaging participants in meaningful and in-depth discussion.

Key discussion items during the workshop

The milk recording workshop, which was chaired by Juho Kyntäjä and Xavier Bourrigan, revolved around three core topics.

1. How to keep AMS customers happy?

Four presentations, 15 minutes each.

- Denmark, Jonas Persson
- France, David Saunier and Xavier Bourrigan
- Switzerland, Eric Barras
- Norway, Tone Roalkvam

Group discussion (15 minutes in groups, 15 minutes conclusion):

What steps can we take to improve services for AMS customers?

2. Whose milk is in the vial?

Three presentations, 15 minutes each.

- Poland, Danuta Radzio
- Canada, Richard Cantin
- Sweden, Nils-Erik Larsson

Group discussion (15 minutes in groups, 15 minutes conclusion):

What steps can we take to secure the cow-vial link?

3. How complex is it to calculate daily yields?

Two presentations, 15 minutes each.

- USA, Angie Coburn
- Italy, Mauro Fioretti

Group discussion (15 minutes in groups, 15 minutes conclusion):

What steps can we take to arrive at better 24-hour yield estimates?

How to keep AMS customers happy?

The following points were considered most pressing:

- Data from different sources should be integrated.
- All data should be available online.
- The advantage milk recording organisations have is that they store data not typically accessible from automatic milking systems.
- Simplicity.
- Outputs should be standardised.
- Big data and machine learning are challenges for the future in terms of creating new services.
- Added value of services is very important, e.g. benchmarking (including data not accessible from AMS)
- New breeding values can be gleaned from robot data.
- Easy-to-use services.
- Added value can improve innovation and the interpretation of results.
- Robots are excluded from MR practice in Israel.
- Slovenia saw a reduction in customers implementing automatic milking systems.
- Comfort of service and control.
- Cross contamination is relevant for the discussion and continues to pose a problem.
- Less samples, more user-friendly milk recording system.
- One exchange format could be valuable.
- Maintenance.

- Deep benchmarking based on all data available, graphic design.
- Improving 24-hour estimation of milk content.

2. Whose milk is in the vial?

Key items discussed during this part of the workshop:

- Minimise human error; well-trained staff specialised in the use automatic milking systems; training is very important.
- Cow IDs in parlours are not always 100% accurate.
- Improvements in software.
- Samples and barcodes should be scanned in one step (automatic scanning) simultaneously in the milking parlour (barcode, QR code). Reduce steps and human error.
- Milk DNA is another option, but is costly.
- Vial identification (barcode, RFID) and time stamps could be introduced.
- Connecting IDs with vial RFIDs.
- Eliminating human influence = less mistakes.
- Electronic support is very important in terms of reducing risk.
- Animal identification in milking parlours – individual cows should be identified on site at the milking parlour.

How complex is it to calculate daily yields?

Summary of the discussion:

- Milk yields are based on a 96-hour period in the case of automatic milking systems.
- Fat should be corrected when using automatic milking systems.
- Sharing factors and encouraging collaboration between milk recording organisations remain a challenge and an opportunity for the future (data is not always readily available, costs, etc.).
- There is an opportunity to share experiences and knowledge in this field.
- Unifying different methods and identifying synchronicity in this area need to be prioritised.
- Large amounts of data are often required when estimating coefficients.
- For some methods, old coefficients can be consulted.
- ICAR should nurture in-house collaboration on the issue of 24-hour calculations.
- Calculations from sensors, where data is taken over multiple days, should be discussed.
- Calculation is a very complex and difficult task contingent on a range of influencing factors.

Conclusion

Farmers need faster access to results and data processing centre delays need to be reduced. Farmer services need to be improved across the board and MROs need to create more value for customers, particularly in the area of herd management. The group recommends introducing just-in-time services to minimise delays, e.g. upload data one week and deliver results the next. The expectations on MR management need to be more clearly defined. We must give farmers reason to be involved in the milk recording system we advocate. We need to provide more benefits to MROs than to AMS manufacturers. Only with better services can we align ourselves with future development.

List of participants

Ansgar Adriany
LKV Bavaria e.V.
Germany

Felix Adrion
Agroscope c/o DLZ FI EFD
Switzerland

Kaie Ahlskog
Association of ProAgria Centres
Finland

Clément Allain
Institut de l'Elevage
France

Olena Alshanova
Ministry of agrarian policy and food of Ukraine
Ukraine

Christian Ammon
Leibniz-Institute for Agricultural Engineering and Bioeconomy
Germany

Roozen Antonius
SLU Faktura Mottagning
Sweden

Michel Astruc
Institut de l'Elevage
France

Franz Josef Auer
LKV Austria
Austria

Andreja Babiæ
Croatian agency for agriculture and food
Croatia

Cecilia Bagenvik
DeLaval International AB
Sweden

Pat Baier
AgSource Cooperative Services
United States

Jens Baltissen
Bundesverband Rind und Schwein e. V.
Germany

Cuthbert Banga
Agricultural Research Council
South Africa

Anastasiia Baranova
Anastasiia Baranova
Russian Federation

Eric Barras
ASR Switzerland
Switzerland

Michal Basovnik
Breeding Cooperative Impuls, cooperative
Czech Republic

Christian Baumgartner
Milchprüfring Bayern e.V.
Germany

René Baumont
Institut National de la Recherche Agronomique
France

Carsten Behrens
Landeskontrollverband Sachsen-Anhalt
Germany

Daiva Beinorienë
State Enterprise Agricultural Information and Rural Business Centre
Lithuania

Haifa Benhajali
SLU Faktura Mottagning
Sweden

Carlo Bertozzi
Awé
Belgium

Ernst Bohlsen
LKV Niedersachsen e.V.
Germany

Renzo Bonifazi
Netherlands

Lizzie Bonsall
Holstein UK
United Kingdom

Ondøej Borský
MILCOM servis a.s.
Czech Republic

Lot Bos
Nedap
Netherlands

Xavier Bourrigan
Institut de l'Elevage
France

Monika Brandt
Landeskontrollverband Schleswig-Holstein e.V.
Germany

Armand Braun
CONVIS s.c.
Luxembourg

Pierre Broutin
Bentley Instruments
France

Alex Brown
Agriculture and Horticulture Development Board
United Kingdom

Sabine Büchel
WMB AG
Germany

Pavel Bucek
Czech Moravian Breeder's Corporation Inc.
Czeck Republic

Javier Burchard
Council on Dairy Cattle Breeding
United States

Pamela Burger
Financial Department Vetmeduni Vienna
Austria

Martin Burke
Ireland

Maksym Bykhovtsov
Zorya Animal Id (Jsc "Kyiv Polygraphic Factory "Zorya")
Ukraine

Richard Cantin
CanWest DHI
Canada

Fernando Cardoso
Embrapa Pecuaria Sul
Brazil

Emma Carlen
Växa Sverige
Sweden

Michaela Cerná
Výzkumný ústav •ivoèišné výroby, v. v. i.
Czech Republic

Alicia Chaigheau
Evolution
France

Noureddine Charfeddine
CONAFE
Spain

Valentin Charrier
Seenovia
France

Mohsen Chebbi
EAAP
Italy

Emilia Ciurescu
Romanian Breeding
Romania

Patrick Clark
Patrick Clark
United States

Angie Coburn
AgSource
United States

Kevin Coffey
Munster Bovine
Ireland

Joanne Conington
SRUC
United Kingdom

Andrew Cooke
Rezare Systems
New Zealand

Elena Couto
Italy

Andrew Cromie
Irish Cattle Breeding Federation
Iceland

Brad Crook
Agricultural Business Research Institute, University of New England
Australia

Laura Monica Dale
Regional association for performance testing in livestock breeding of Baden-Wuerttemberg (LKV - Baden-Wuerttemberg)
Germany

Rui Dantas
ANABLE, Associação Nacional para o Melhoramento dos Bovinos Leiteiros
Portugal

Jean-Bernard Daviere
SEENERGI
France

Yvette de Haas
Wageningen University and Research
Netherlands

Gerben de Jong
CRV B.V.
Netherlands

Suzanne de Roo
EuroGenomics Cooperative
Netherlands

László Dégen
Livestock Recording LTD. Hungary
Hungary

Frédéric Dehareng
CRA-W
Belgium

Kees DeKoning
Wageningen Livestock Research - Dairy Campus
Netherlands

Franziska Dettmann
LKV Niedersachsen e.V.
Germany

Andie Dimitriadou
Italy

Mark Doornink
VAS
United States

Lothar Döring
Landeskontrollverband Sachsen-Anhalt
Germany

Klauss Droessler
Regional association for performance testing in livestock breeding of Baden-Wuerttemberg (LKV - Baden-Wuerttemberg)
Germany

Jean-Francois Duckerts
Belgium

Andrew Dungey
National Milk Records plc
United Kingdom

sebastien Duroy
Institut de L'Elevage
France

Iva Dvorakova
Spolecnost pro kontrolu uzitkovosti, spol. s r.o.
Czech Republic

Christa Egger-Danner
ZuchtData EDV-Dienstleistungen GmbH
Austria

Ross Evans
Irish Cattle Breeding Federation
Ireland

Laurence Feeney
Progressive Genetics
Ireland

Mauro Fioretti
Associazione Italiana Allevatori (A.I.A.)
Italy

Mike Fletcher
Shearwell Data
United Kingdom

Marina Foa' Gips
Israel Cattle Breeders' Association (ICBA)
Italy

Robert Fourdraine
AgSource Cooperative
United States

Johannes Frandsen
SEGES
Denmark

Justin Frankfort
National Milk Records
United Kingdom

Darryl Samuel Fynn-williams
Darryl Samuel Fynn-williams
Ghana

Alain Gastebled
Institut de l'Elevage
France

Edvardas Gedgaudas
The Chamber of Agriculture of the Republic of Lithuania
Lithuania

Martin Gehringer
LKV Niederösterreich
Austria

Marine Gele
Institut de l'Elevage
France

Nicolas Gengler
ULiege-GxABT
Belgium

Olivier Gérard
Allice
France

Marc Gerschwiler
Switzerland

Ann Gladwell
Eurofins DQCI, LLC
United States

Hubert Göft
FOSS
Germany

Fritz Gollé-Leidreiter
Regional association for performance testing in livestock breeding of Baden-Wuerttemberg (LKV - Baden-Wuerttemberg)
Germany

Jorge Andrade Gomes
Brazil

Sarah Görlich
Qualitas AG
Switzerland

Florian Grandl
LKV Bayern e.V.
Germany

Mihail- Alexandru Gras
Romanian Breeding
Sweden

Clément Grelet
CRA-W (Walloon Agricultural Research Center)
Belgium

Laurent Griffon
Institut de l'Elevage
France

Amel Guellouz
OEP
Tunisia

François Guillaume
Evolution
France

Leszek H¹dzlik
Polish Federation of Cattle Breeders and Dairy Farmers
Poland

Zoltan Haller
Romanian Breeding
Romania

Leon Ham
Lely International N.V.
Netherlands

Frido Hamoen
CRV B.V.
Netherlands

Soren Hansen
Eurofins Milk Testing
Denmark

Suzanne Harding
World Holstein Friesian Federation
United Kingdom

Bevin Harris
LIC
New Zealand

Stephan Hartwig
Landeskontrollverband Mecklenburg-Vorpommern eG
Germany

Marie Haskell
SRUC
United Kingdom

Teija Hellberg
ProAgria Keskusten Liitto ry
Finland

Pera Herold
Landesamt für Geoinformation und Landentwicklung Baden-Württemberg
Germany

Jere High
Lancaster Dairy Herd Improvement Association
United States

Tilman Hoefelmayr
WMB AG
Switzerland

Pieter Hogewerf
Pieter Hogewerf
Netherlands

Bruce Holmquist
World Simmental-Fleckvieh Federation
Canada

Dino Holmquist
Eurofins Milk Testing Denmark A/S
Denmark

Miel Hostens
Miel Hostens
Belgium

Marleen Houthuijs
Plastifran B.V.
Netherlands

Jeng-Fang Huang
Livestock Research Institute, Council of Agriculture, Executive Yuan
Taiwan

Peter Huijsmans
Qlip
Netherlands

Cahrl Hunlun
South Africa

Lelior Iacob
Romanian Breeding
Romania

Daria Iakovishina
Ksivalue
Russian Federation

Kaivo Ilves
Eesti Põllumajandusloomade Jõudluskontrolli AS
Estonia

Zdenko Ivkiæ
Croatian Agency for Agriculture and Food
Croatia

Dobrila Jankovic
Agriculture faculty Novi Sad, Serbia
Serbia

Manon Jattiot
BCEL OUEST
France

Laurent Journaux
France genetique elevage
France

Josef Jungwirth
LKV Bayern
Germany

Alexandr Kalashnikov
NTSAU, Nothern Trans-Ural State Agraricultural University
Russian Federation

Dariusz Kamola
Polish Federation of Cattle Breeders and Dairy Farmers
Poland

Fredrik Karlsson
DeLaval International AB
Sweden

Karolina Kaseja
SRUC
United Kingdom

Eva Kasna
Institute of Animal Science
Czech Republic

Jorgen Katholm
DNA-Diagnostic
Denmark

Gil Katz
afimilk LTD
Israel

Mike Keane
Irish Cattle Breeding Federation
Ireland

Junsoo Kim
Korea Animal Improvement Association
Korea (the Republic of)

Sandra Kipp
VIT, IT-Solutions for Animal Production
Germany

Marija Klopcic
UL - Biotechnical Faculty
Slovenia

Ihor Klymenok
State Enterprise “Agency of animal Identification and registration”
Ukraine

Markus Koblmüller
LKV Austria
Austria

Kirill Kosodurov
Agroplem LLC
Russian Federation

Anita Kranjcevicová
Institute of Animal Science
Czech Republic

Nina Krattenmacher
Kiel University
Germany

Dorota Krencik
Poland

Liga Kubulina
Sigulda’s Stock Breeding and Artificial Insemination Station
Latvia

Josef Kucera
Czech Republic

Sophie Kunz
Qualitas AG
Switzerland

Kai Kuwan
IT Solutions for Animal Production (vit w.V.)
Germany

Jindøich Kvapilík
Czech Republic

Roman Kwasiborski
FOSS North America
Canada

Juho Kyntäjä
Mtech Digital Solutions Ltd
Finland

Anne-Sofie Ladekjaer-Mikkelsen
Eurofins Milk Testing Denmark A/S
Denmark

Jorge Lama
COOPRINSEM
Chile

Arjan Lamers
JoinData
Netherlands

Nils-Erik Larsson
Växa Sverige ek. för.
Sweden

Antti Latva-Rasku
Faba osk
Finland

Dalia Laureckaite-Tumeliene
State Food and Veterinary Service
Lithuania

Yaniv Lavon
Israel Cattle Breeders Association
Israel

Julie Leblois
Walloon Breeding Association
Belgium

Hélène Leclerec
Institut de l’Elevage
France

Christophe Lecomte
France Conseil Elevage
France

Daniel M. Lefebvre
Valacta
Canada

Pierre Lenormand
SEENOVIA
France

Kirsi Leppikorpi
ProAgria Keskusten Liitto
Finland

Chengzhu Liang
Technical Center of Qingdao Custom
China

Bianca Lind
Bundesverband Rind und Schwein e. V.
Germany

David Lipovský
Czech Republic

Betka Logar
Kmetijski inštitut Slovenije/ Agricultural Institute of Slovenia
Slovenia

Bernhard Luntz
Institut für Tierzucht
Germany

Yan Luo
GS1 China
China

Mike Lynch
Irish Cattle Breeding Federation
Ireland

Beate Maassen-Francke
GEA
Germany

Monnye Mabelebele
University of South Africa
South Africa

Carlos Machado
Animalltag Europa Lda.
Portugal

Ákos Maróti-Agóts
University of Veterinary Medicine Budapest
Hungary

Stu Marsh
Y-TEX Corp.
United States

Burke Martin
Ireland

António Martins
ANABLE
Portugal

Jon Massey
University of Bristol
United Kingdom

Janette Mathie
The Cattle Information Service
United Kingdom

Kim Matthews
Agriculture and Horticulture Development Board
United Kingdom

Jane Mättik
Animal Breeders Association of Estonia
Estonia

Jay Mattison
National DHIA
United States

Raffaele Mazza
Agrotis srl
Italy

Matthew McClure
ABS-Global
United States

Kevin McDermott
Irish Cattle Breeding Federation
Ireland

Arsim Memaj
Ministry of Agriculture Forestry and Rural Development
Albania

Alexis Michenet
SLU Faktura Mottagning
Sweden

Viggo Mikalsen
TINE SA
Norway

Michal Milerski
Institute of Animal Science
Czech Republic

El Kharroussi Mohamed
ANEB Maroc
Morocco

Laura Monkman
defra
United Kingdom

Attila Monostori
Livestock Recording LTD. Hungary
Hungary

Robert Moore
Valacta
Canada

Rui Moreira
EABL - Estação de Apoio à Bovinicultura Leiteira
Portugal

Romy MorrinODonnell
Weatherbys Scientific
Ireland

Cesare Mosconi
ICAR
Italy

Lina Moussa
FOSS
Denmark

Andrew Munro
Weatherbys Scientific Australia
Australia

Solomon John Muchina Munyua
IGAD Centre for Pastoral Areas and Livestock Development
Kenya

Hannu Myllymäki
Faba osk
Finland

Niall Naughton
Irish Cattle Breeding Federation
Ireland

Donata Navickienë
State Enterprise Agricultural Information and Rural Business Centre
Lithuania

Riccardo Negrini
AIA, Associazione Italiana Allevatori
Italy

Timothée Neuenschwander
Holstein Switzerland
Switzerland

Niels Henning Nielsen
RYK/Danish Catlle Federation
Denmark

Hugh Nivison
ABRI
Australia

Dan Nodolf
National DHIA
United States

Adéla Nosková
Institute of Animal Science
Czech Republic

Belkadi Noureddine
ANEB Maroc
Morocco

Folkert Onken
DLQ
Germany

Silvia Orlandini
Italy

Thierry Pabiou
Irish Cattle Breeding Federation
Ireland

Lorenzo Pascarella
AIA, Associazione Italiana Allevatori
Italy

Parth Balkrushnabhai Patel
Hari Om Dairy Farm
India

Josipa Paviciæ
Croatian agency for agriculture and food
Croatia

Kalle Pedastsaar
Eesti Põllumajandusloomade Jõudluskontrolli AS
Estonia

Jonas Persson
RYK Fonden Denmark
Denmark

Neil Petreny
CanWest DHI
Canada

Natasa Pintic Pukec
Center for Quality Control of Livestock Products
Croatia

Klemen Potocnik
University of Ljubljana, Biotechnical Faculty
Slovenia

Irmantas Povilauskas
JSC Animal milk recording
Lithuania

Pavlína Prášilová
Czech Republic

Axel Prediger
WMB AG
Switzerland

Stergios Priskas
Aristotle University of Thessaloniki
Greece

Lukáš Prýmas
Czech Republic

Jiansheng Qiu
Neogen
United States

Joanne Quigley
Integrity Systems Company Ltd
Australia

Danuta Radzio
Polish Federation of Cattle Breeders and Dairy Farmers
Poland

Reinhard Reents
VIT IT Solutions for Animal Production
Germany

Othon Reynoso-Campos
SIINIGA, Confederacion Nacional de Organizaciones Ganaderas-
Mexico

John Rhoads
John Rhoads
United States

Christian Riede
LKV Rhineland-Palatinate-Saar e.V
Germany

Siobhan Ring
Irish Cattle Breeding Federation
Ireland

Tone Roalkvam
TINE
Norway

Saintilan Romain
GenEval
France

Sergio Roman Ponce
INFAP
Italy

Toine Roozen
SLU Faktura
Sweden

Mircea-Catalin Rotar
Baltata Romaneasca Simmental Type
Romania

Hubert Rothfuss
LKV Niedersachsen e.V.
Germany

Hergen Rowehl
Landeskontrollverband Schleswig-Holstein e.V.
Germany

Freddie Ruijs
Lely International
Netherlands

Wolfgang Ruten
VIT IT Solutions for Animal Production
Germany

Ieva Rutkovska
Latvian Holstein Association
Latvia

El¿bieta Rybicka
Polish Federation of Cattle Breeders and Dairy Farmers
Poland

El Mouatassim Said
Appolon Bioteck
France

Yosuke Sasaki
University of Miyazaki
Japan

David Saunier
FCEL
France

Simone Savoia
SLU Faktura Mottagning
Sweden

Brendan Scanlon
Progressive Genetics
Ireland

Sven Schierenbeck
VIT IT Solutions for Animal Production
Germany

Thomas A. Schmidt
BRS e.V. - Germany
Germany

Fritz Schmitz-Hsu
Swissgenetics
Switzerland

Jort Schutte
Nedap Livestock Management
Netherlands

Andrew Scott
LIC
New Zealand

Tamás Sebõk
Hungarian Holstein Association
Hungary

Olle Selander
Delaval International AB
Sweden

Eli Sellem
ALLICE
France

Joanna Sendecka
SLU Fakturamottagning
Sweden

Mathew Shaffer
Datagene Ltd
Australia

Feroz Sheikh
High Mountain Arid Agriculture
India

Jen Wen Shiau
TaiwanLivestock Research Institute
Taiwan

Steven Sievert
Steven Sievert
United States

Simona Sillingová
MILCOM servis a.s.
Czech Republic

Mojca Simcic
University of Ljubljana, Biotechnical Faculty
Slovenia

Anurag Singhal
Engineering
India

Steven Skinner
Agricultural Business Research Institute
Australia

Evija Skujina
Agricultural Data Centre
Latvia

Inguna Slice
Agricultural Data Centre
Latvia

Olesya Smirnova
NPO Holstein Breeders' Association of Russia
Russian Federation

Dena Snidall
CIS, Cattle Information Service
United Kingdom

Hélène Soyeurt
Gembloux Agro-Bio Tech, University of Liège
Belgium

Marija Spehar
Croatian Agency for Agriculture and Food
Croatia

Erwin Speybroeck
CRV B.V.
Netherlands

Kathrin F. Stock
VIT IT Solutions for Animal Production
Germany

Eva Stormwall
Växa Sverige
Sweden

Svenja Strasser
Mutterkuh Schweiz
Switzerland

Anna Strzy¿ewska
Polish Federation of Cattle Breeders and Dairy Farmers
Poland

Pei Chung Sun
Today's Instruments Co., Ltd.
Taiwan

Marlene Suntinger
ZuchtData EDV-Dienstleistungen GmbH
Austria

Alena Svitakova
Instutite of Animal Science
Czech Republic

Peter Tongel
Research Institute of Animal Production Nitra
Slovak Republic

Sne•ana Trivunoviæ
University of Novi Sad, Faculty of Agriculture
Serbia

Volodymyr Tytenko
State Enterprise "Agency of animal Identification and registration"
Ukraine

Danguole Urbsiene
JSC Animal milk recording
Lithuania

Laima Urbsiene
Pieno Tyrimai, UAB
Lithuania

Mikko Utriainen
VTT Technical Research Centre of Finland
Finland

Darius Valkauskas
State Enterprise Agricultural Information and Rural Business Centre
Lithuania

Harrie van den Bijgaart
Organisation: Stichting Kwaliteitszorg Onderhoud Melkinstallaties (
Netherlands

Japie van der Westhuizen
SA Stud Book and Animal Improvement Association
South Africa

Brian Van Doormaal
CDN, Canadian Dairy Network
Canada

Wim van Haeringen
VHLGenetics
Netherlands

Mathijs van Pelt
CRV B.V.
Netherlands

Bert Van 't Land
CRV B.V.
Netherlands

Elsa Vasseur
McGill University
Canada

Roel Veerkamp
Wageningen University and Research
Netherlands

Jana Velechovská
Czech Republic

Eric Venot
France Génétique Elevage
France

William VerBoort
Holstein Association USA dba AgriTech Analytics
United States

Zdeòka Veselá
Výzkumný ústav •ivoèišné výroby
Czech Republic

Martin von Allmen
swissherdbook
Switzerland

Lubos Vostry
Institute of Animal Science Prague, Uhøínìves
Czech Republic

Dereje Wakjira
Intergovernmental Authority on Development, Center for Pastoral Areas and Livestock Development
Kenya

Andrew Warne
NMR
United Kingdom

Harald Oscar Wenzel Ubilla
COOPRINSEM
Chile

Fredrik Westerberg
Eurofins Milk Testing Sweden AB
Sweden

Brian Wickham
Ireland

Hans Wilmink
HwConsultancy
Netherlands

Ming Che Wu
Taiwan Livestock Research Institute
Taiwan

Ludmila Zavadilová
Institute of Animal Science
Czech Republic

Lei Zhang
University of Liège - Gembloux Agro-Bio Tech
Belgium

Nan Zhang
GS1-China
China

Jing Zhao
GS1 China
China