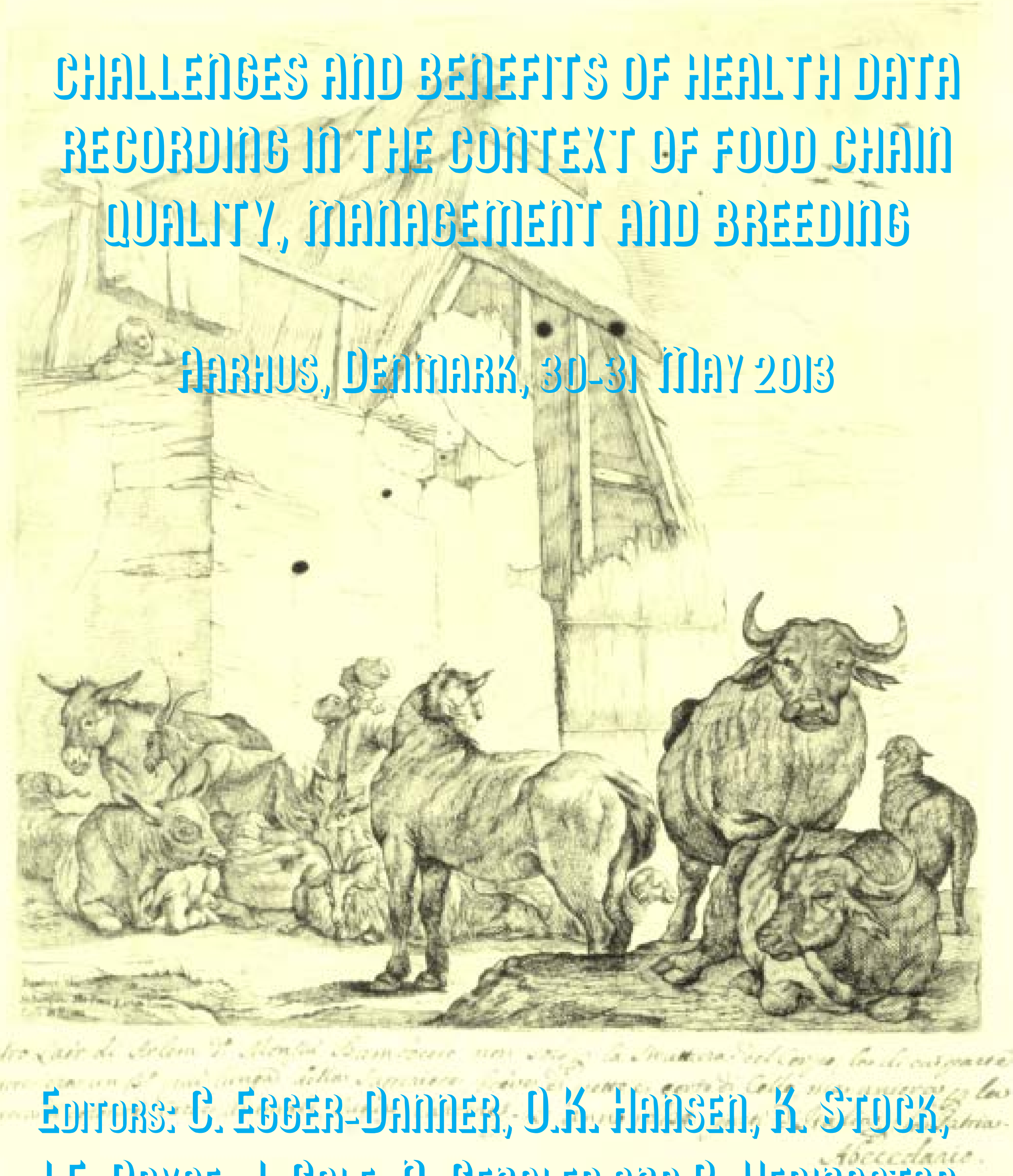
ISSN: 1563-2504
ISBN: 92-95014-13-8

ICAR Technical Series no. 17



CHALLENGES AND BENEFITS OF HEALTH DATA RECORDING IN THE CONTEXT OF FOOD CHAIN QUALITY, MANAGEMENT AND BREEDING

Aarhus, Denmark, 30-31 May 2013

Editors: C. Egger-Danner, O.K. Hansen, K. Stock, J.E. Pryce, J. Cole, N. Gengler and B. Heringstad

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

Title of the Series: ICAR Technical Series
Title of the Volume: Challenges and benefits of health data recording in the context of food chain quality, management and breeding
Editors: C. Egger-Danner, O.K. Hansen, K. Stock, J.E. Pryce, J. Cole, N. Gengler and B. Heringstad
Publisher: ICAR, Via G. Tomassetti 3, 1/A, 00161 Rome, Italy
Responsible for ICAR Technical Series: Cesare Mosconi
ISSN: 1563-2504
ISBN: 92-95014-13-8

ICAR and the Organisers wish to thank the following company for sponsoring the workshop:

- Arbeitsgemeinschaft österreichischer Fleckviehzüchter, Austria
- GENO SA, Norway
- Holstein Australia
- ITW Reyflex France
- Vereinigte Informations systeme Tierhaltung w.V. (VIT), Germany

A special thank must be addressed to Knowledge Centre for Agriculture for their kind availability and the given assistance during the organisation and the meeting

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Challenges and benefits of health data recording in the context of food chain quality, management and breeding

Proceedings of the ICAR Conference
held in Aarhus, Denmark, 30-31 May 2013

Editors: C. Egger-Danner, O.K. Hansen, K. Stock, J.E. Pryce,
J. Cole, N. Gengler and B. Heringstad

October 2013

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Introduction

Improved animal health is becoming increasingly important worldwide, because of its effect on farm economy, animal welfare and food safety. The precondition for monitoring, elaboration and implementation of measures to improve animal health and reduce the use of antimicrobials are reliable health data. The main difficulty in setting up such systems is that many different parties are involved and need to cooperate. Precondition of success is the benefit of the parties involved. Systems set up in cooperation with the legal bodies as well as different parties offer the possibility to use synergies and be of higher effectiveness. The aim of the International Committee for Animal Recording (ICAR) is to promote the development and improvement of the activities of performance recording and the evaluation of farm livestock. As an international, non-profit body ICAR can serve as a platform to share information and knowledge. The main emphasis within this conference was on aspects of logistics of data recording as well as motivation and benefit of different parties and the community.

The Organizing Committee of the ICAR
Functional Traits Working Group

Christa Egger-Danner, Ole Klejs Hansen, Kathrin Stock, Jennie Pryce, John Cole, Nicolas Gengler and Bjorg Heringstad b

Summary and main outcomes

More than 145 participants from 30 countries all over the world

In conjunction with the ICAR Technical Workshop, the ICAR 2013 Health Data Conference organized by the ICAR Functional Traits Working Group was held in Aarhus, Denmark from 30 to 31 May, 2013. There were more than 145 participants from over 30 countries representing different disciplines - farmers, veterinarians, representatives of research and dairy industry, breeding and recording organizations, advisory services, administrators.

The popularity of this conference demonstrates that the topic of health data recording has been addressed at the right time. Mr. Sergio Pavon from the EU Commission DG Health and Consumer Protection stressed the increased focus on animal health in the context of animal welfare, food safety and environmental aspects. The program included many other well know experts covering data legislative aspects, recording, logistics, processing, data quality and validation, benefits as well as challenges of working with health data. The delegates exchanged their views and experiences ranging from countries with experience in health data to countries that are in the planning or start-up phase.

Main outcomes

- Easy care, healthy, "invisible" cow is what farmers want.
- The aim is to have minimum effort for recording with maximum benefit for herd improvement.
- Multidisciplinary use of farm and veterinary data will help to achieve this aim.
- Clear agreements concerning data ownership and use are needed.
- Legal regulations may be supportive for establishing health monitoring systems, but motivation of the stakeholders involved is the key factor for long-term success.
- Disease information such as mastitis, infertility, lameness, metabolic disorders are necessary for targeted improvement of animal health which is in accordance with the EU-strategy "Prevention is better than cure".
- Data quality and data quantity assurance measures are very important.
- There is a need for international standardization.
- Electronic devices and automated systems may contribute to future solutions.
- Each country has to find solutions fitting their circumstances.
- We can do better when we work together (multidisciplinary, multi-country approaches)!

The PDF files of the presentations are available on the web at:
www.icar.org/Documents/Aarhus_2013/PowerPoint/index.htm

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Session 1

General aspects - Part I

Future challenges concerning animal breeding and health

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Animal breeding and health

The EU animal health strategy[1] is mainly aimed at transmissible animal diseases, and it does not specifically address health problems linked to animal breeding practices. Besides, the European Commission has in place a number of initiatives in the field of animal breeding which also contributes to protect the health of individual animals. For instances, the Commission is funding several research projects dedicated to research in livestock production, contributing to develop animal breeding and health via projects funded by DG Research. The following are examples of research projects funded by the European Commission: Quantomics (2010-2013: *http://www.quantomics.eu* / and 6 million Euros), Gene2farm (2012-2016: 3 million Euros), Low Input Breed (2009-2014: http: / / *www.lowinputbreeds.org* / and 6 million Euros) or NextGen (2010-2014: *http://nextgen.epfl.ch* / and 3 million Euros biodiversity oriented).

In addition, the European Commission supports the EU reference laboratory responsible for rendering uniform the testing methods and the assessment of the results for pure-bred breeding animals of the bovine species (Interbull, which is a permanent Sub-Committee of ICAR: *www.icar.org*).

One of the main objectives of the Commission with these initiatives is to ensure that trade in bovine genetics and their imports from third countries are harmonised and based on reliable information. This goal is being achieved via several activities like: to investigate and to provide standard methods for both national and international genetic evaluation of bovine populations, to perform regular international comparisons of what performance of pure-bred bovine animals for breeding , to provide methods and perform regular validation of national genetic evaluations of bovine populations and to provide technical assistance to Member States in matters related to assessing the genetic merit of bovine populations.

This will help to provide important information which can be used for Veterinary medicines, Scientist on animal diseases, Veterinary preventive medicine and Genetic diseases and to bring valuable information on issues like the role of the genes in predisposition to diseases caused by different pathogens, metabolic disorders, development / physiological disorders, information on the effects of genetic resistance to diseases, medication and vaccination and genetic resistance against pathogens

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[1] Reference COM (2007) 539 final

In the EU, at present bulls of dairy breeds are selected based on balanced criteria which considers not only high level of milk and milk component productions but also on criteria like: longevity, mastitis resistance, female fertility, calving difficulty, cow temperament and conformation traits related to fitness. The starting of the development of genetic evaluations for these traits in the EU is relatively recent.

Animal breeding and welfare

The Treaty on the functioning of the European Union refers explicitly to Animal welfare as follows: "In formulating and implementing the Union's agriculture, fisheries, transport, internal market, research and technological development and space policies, the Union and the Member States shall, since animals are sentient beings, pay full regard to the welfare requirements of animals, while respecting the legislative or administrative provisions and customs of the Member States relating in particular to religious rites, cultural traditions and regional heritage." .

Several elements have contributed to animal welfare become a major and legitimate concern in the EU : the new cultural approach to animal welfare, new interests of society and policy makers in promoting compliance with welfare standards and -appropriate information is disseminated-. Consumers are concerned about the humane and responsible treatment of animals. The latter was highlighted in the "Attitudes of EU citizens towards Animal Welfare", during the Eurobarometer Survey, March 2007. In this survey, it was noted that 62% of European consumers stated that they would change their shopping habits and purchase products which are more animal welfare-friendly.

The EU has a wide range of legislative provisions concerning the welfare for animals. Council Directive 98 / 58 / EC concerning the protection of animals kept for farming purposes states: "natural or artificial breeding procedures which cause or are alike to cause suffering or injury to any animal concerned must not be practised" or "No animal shall be kept for farming purposes unless it can reasonably be expected on the basis of its genotype or phenotype, that it can be kept without detrimental effect on its health or welfare". The European Food Safety Authority's (EFSA) Animal Health and Welfare panel provides independent scientific advice to the European Commission, the European Parliament and EU Member States. Its scientific opinion focuses on helping risk managers to identify methods to reduce poor welfare and to improve health. While EFSA has no mandate to give advice on ethical or cultural issues related to welfare, it has produced scientific report on the effects of farming systems on dairy cow welfare and disease (July 2009; EFSA-Q-2006-113). Some of the main conclusions of this study are that leg disorders, mastitis and reproductive disorders are considered major components of poor welfare in dairy cows. The panel concluded that long term genetic selection for higher milk yield is one of the major factors affecting the health of dairy cows as well other aspects of their welfare.

On the request of the Commission EFSA has produced in 2012 a series of scientific opinions on the use of animal-based measures to assess the welfare of dairy cows, pigs and broilers.

Animal health law

The Commission launched during 2013 new legislative proposal for a Regulation on Animal Health (herein after referred as: Animal Health Law (AHL)). The new AHL tends to pass from a fragmented legislation of circa 40 Directives and Regulations into a single and robust legal framework for animal health. It will lay down the overarching principles for prevention and control of transmissible animal diseases. The new AHL will extend the scope of disease prevention and control to kept and wild animals (not only production animals) and their products, terrestrial, aquatic and other animals. It will bring clearer definitions on responsibilities for keepers, operators, veterinarians, competent authorities and a sound risk based approach by introducing categorization / prioritisation of diseases for EU intervention. Other major elements introduced in this AHL include the improvement of the response to emerging diseases as well as more prevention (Biosecurity at farms, in transport, assembly, at borders), disease notification and reporting, enhanced surveillance and a clearer policy for the use of vaccines and in relation to disease control & diagnosis. The above-mentioned will also contribute to easier and safer trade via an enhanced convergence with international standards on animal health (OIE), and by introducing provisions on compartmentalisation and requirements for exports, while at the same time adding more flexibility to adjust to elements like climate changes and other emerging risks.

Animal breeding & international trade

Certain EU breeder's organisations complain that genomic selection in the EU is on disadvantage in relation to third countries due to a policy of governmental subsidies policy. The last consequence of this allegedly unfair competition leads to an advantageous situation of imported products at lower prices in the EU market.

The EU has always been a major exporter of genetic material and technology-related. Recently, new trade barriers imposed by third countries based on animal health grounds are emerging making international trade in genetic material more difficult. For some of those agents emerged pathogens, there would be a lack of international standards making it more difficult to set up safe international trade recommendations or guidelines. In addition, barriers having an "administrative" nature have also appeared as a major problem for international trade. Not least, environmental and biodiversity reasons have occasioned unjustified trade restrictions in this sector. In some cases those restrictions have as main objective, the protection of national / domestic production against imports from EU Member States. It seems to be a legal gap in the Agreements concluded in the framework of the World Trade Organisation (WTO). For instances, it is not clear whether this type of restriction would fall under the SPS (Sanitary and Phytosanitary) or the TBT (Technical barriers to trade) Agreements or any other. Till the above-mentioned questions are not solved, it will be difficult to challenge these types of trade barriers at international level, resulting on incertitude & unpredictability for operators in terms of international trade.

Genetic erosion and biodiversity

One of the major challenges for the Commission when trying to set an EU policy on animal breeding is how to address Biodiversity. Representatives of EU breeders organization tend to defend the line of having as many traits as possible (e.g. via genomic selection)in order to avoid the risk to fall under the so called "Genetic erosion". One of the major risks of genetic erosion is that less market-oriented breeds may be left behind in favour of more commercial breeds. This brings us to the main question: how to preserve and to ensure genetic biodiversity? And how animal breeding organisations can play a positive role in the preservation of genetic biodiversity? Local initiatives are not by themselves able to cope since a bigger infrastructure is needed (e.g. human & financial resources). Also there would be a need for the European Commission to actively participate in the work of international bodies (UN and WTO) on this issue. At the moment the EU treaty provides in this field, shared competences between the European Commission and EU Member States, making more difficult to have a single voice at international level. Others like Nagoya Protocol (still to be ratified by COM-DG ENV and MS). Finally, the Commission have additional instruments supporting the conservation of agricultural genetic resources such as the Rural Development Policy (Rural Development Council Regulation (EC) No 1698 / 2005).

Cloning and genomic selection

The European Commission plans to produce during 2013 a legislative proposal with measures on cloning technique in the EU for main farm animals. This has been particularly requested by the European Parliament. Cloning technique is rare in sheep, goats and pigs and it is more advanced in particular in dairy cattle and sport horses. .In this proposal, the use of cloning for scientific / research purposes will not be affected.

There are several open questions on the application of measures to imports from third countries, in particular for imports of genetic material.

From the genetic perspective, it is important to have access to as many traits as possible. This could somehow contradict the final aim of the cloning technique as the latter tends to encourage the use of a limited number of traits. Other breeding techniques like genomic selection if used in a responsible manner could provide economically viable alternatives to cloning without compromising genetic diversity.

The future legislation on zootechnia

The European Commission is currently working on a new revision of the existing legislation on zootechnical standards applicable to breeding animals which is scheduled for adoption in 2013. This new proposal aims at simplifying and to improving the wording of the existing legislation. It will also address points of controversial interpretation of the existing legislation e.g. cross-border activities of approved breeding organisations and those points which because of lack of clarity have been the source of complains by competent authorities and operators. It is the duty of the Commission to create the enabling environment for the free circulation of breeding animals and their germinal products on the internal market and the freedom to provide services.

With these objectives EU Member States, operators and competent authorities shall ensure that activities like intra-EU trade in pure-breed animals, their germinal products the establishment of herd-books and the recognition of organisations and associations maintaining herd-books should not be prohibited, restricted or impeded on zootechnical grounds.

Other challenges

There are future challenges concerning animal breeding and consumer protection in the European Union. One is the issue of intellectual property rights, but another more important is how best to approach the consumer. Not least, there would be a need to set up more official channels of communication with consumer's associations such as the civil society dialogue.

The use of health data: perspective of a Ministry

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The health of farm animals has strongly become the focal point of the awareness of our society in recent times. Animal health is also present on the political agenda as a result. Helmut Brunner, Bavarian Minister of State for Food, Agriculture and Forestry, has set his sights on improving animal health and enhancing animal welfare in Bavaria (Brunner 2012) – and as one of his colleagues I support him to the best of my ability. That is why I am pleased and thankful that I may present the view of the Bavarian agricultural ministry on the use of health data.

The Free State of Bavaria is one of 16 federal states in the Federal Republic of Germany – and the most important agricultural state among these federal states. In Bavaria there are 93 700 farms (> 5 ha), which cultivate 32 hectares of agricultural area on average.78% of them keep farm animals, for one thing because over 1 million hectares of permanent grassland can only be usefully exploited by means of animal husbandry, and on the other hand because the marginal area configuration of many farms necessitates higher added value from animal husbandry to secure a livelihood. The cattle population encompasses 3.3 million head of cattle (kept by 56 000 cattle farmers), of which 1.2 million are dairy cattle (kept by 40 000 dairy cattle farmers). The pig population of 3.5 million animals is distributed on 7 100 farms.

The *Landeskuratorium der Erzeugerringe für tierische Veredelung in Bayern e.V.* (LKV; Bavarian Association for Animal Production) is responsible for the implementation of milk recording. Approx. 1 million dairy cattle have been tested annually somewhat constantly for over 30 years. If we look at a few indicators which result from milk recording, then the following picture ensues and described in table 1.

In the period from 1982 to 2012, the average herd size doubled from 20 to 40 cows. The milk yield was increased from 4 906 to 7 349 kg per cow and year. The somatic cell count is overall on a level that indicates good udder health. The trend is even slightly positive. The age of culling as an indicator of productive life span has noticeably decreased from 6.1 to 5.5 years. The percentage of cullings tends to be declining, but particularly the disease-related cullings have substantially increased. The cullings in 2012 were most frequently because of udder disease (16.3%), claw disease (9.7%) and metabolic disease (2.5%).

Table 1. Results of milk recording in Bavaria 1982 – 2012.

	1982	1992	2002	2012
Herd size (dairy cows)	20.6	24.0	29.7	39.8
Milk yield, kg	4 906	5 437	6 424	7 349
Somatic cell count, n / ml	204 000	197 000	197 000	191 000
Culling age, years	6.1	5.8	5.5	5.5
Culling percentage, %	29.9	26.6	28.1	25.2
of which:				
- udder disease, %	6.7	11.1	13.0	16.3
- claw disease, %	5.8	10.2	9.5	9.7
- metabolic disease, %	0.9	1.5	1.5	2.5

The genetic trends for health-relevant characteristics such as the breeding values for fitness, somatic cell count and productive life span mainly show a positive trend for the past 12 bull age groups with Fleckvieh cattle, whereas the breeding value for maternal fertility has at least remained stable (Emmerling 2012).

Another level of consideration is the economical level. The scientific evaluation of accounting data for Bavarian dairy farms is the basis for the *Milchreport Bayern* (Bavarian Milk Report), which has existed in this classification since 2004 (Table 2).

Germany, for instance. But there are also several small hotspots in Bavaria. The lower life expectancy of farm animals, the increased diseases and increased loss rates are discussed by consumers as problems. Intensive animal husbandry be only controllable with massive use of medication. In particular, antibiotics are feared as increasing resistances, which ultimately threaten the health of people. In addition to the economic concerns, demands for an improvement of animal health due to ethical responsibility, i.e. because of the avoidance of suffering and pain for the animals, are increasingly emphatic. However, not only consumers demand healthier

Table 2. Costs for veterinarians and medications.

	2004	2006	2008	2010	2011
Number of farms	185	499	515	290	279
Dairy cows	50	54	58	65	68
Milk yield, kg ECM/cow	7 560	7 413	7 529	7 723	7 974
Somatic cell count, x 1.000/ml	176	175	178	180	178
Losses of calves, %	11.8	11.7	10.5	10.4	11.5
Losses of cows, %	2.2	3.5	3.2	2.9	3.0
Costs for veterinarians and medications, •/cow/year	97	99	101	107	111

animals, but also farmers themselves. For instance, a survey of cattle breeders (Steininger 2013) in Austria and Germany revealed that farmers themselves want healthier animals. This is expressed with the personally pursued breeding objective. The order of preference there is: 1. fertility; 2. udder health; 3. productive life span. Moreover, farmers call for support in their breeding work through new breeding value characteristics, in the following order of preference:1. metabolic stability; 2. claw health; 3. feed / energy efficiency. In particular, they have asserted the need for additional information with the following priorities: 1. fertility and animal health; 2. effective bull selection; 3. planning for mating.

The demand for improving the health of farm animals is not fundamentally new for many animal breeders and animal farmers. In this regard they can oppose the current political and societal demands to a certain degree. For this purpose I would like to mention two examples from Bavaria.

In 2010 we started the project **PROGESUND**, which is financed with state subsidies amounting to 764 000 Euros. The comprehensive and routine acquisition of disease diagnoses in cattle farms has now been in progress since November 2012 (Zeiler 2012). Diagnoses are stored in a central database and systematically evaluated in conjunction with the master data and performance data of animals. In addition, observations such as milk fever or parturient paresis, placental retention and umbilical hernia with calves are reported by animal owners to the central database of the Bavarian “Identification and Information System for Animals” (HITier) in conjunction with the obligatory birth registration and included in the evaluations insofar as they originate from PROGESUND participants. Although participation is voluntary, in the period of 15 months (status as of 3 May 2013) 65 % of Bavarian cattle farmers have already reported observations for more than 1 million births (Carmanns 2013). All farmers and veterinarians participating in **PROGESUND** can retrieve health reports online at any time, which can be utilised for better herd management and for better livestock support. As soon as a sufficient data volume is available, these data will also be utilised for an estimation of breeding value characteristics such as mastitis, fertility disorders, cysts and milk fever. Austria is several years ahead of us with regard to health monitoring. The penetration in the area is already very high there, and official breeding values for health traits are already routinely available.

QUALIFOOD is an information platform which was initiated in 2008 and developed with state support (246 000 euros) by *Fleischprüfring Bayern e.V.* (Bavarian Association for Meat Inspection) together with the Bavarian meat industry. Farmers, suppliers, slaughterhouses and other stakeholders have the opportunity here to view and retrieve their participant related data regarding slaughters, veterinary findings and control measures recorded by slaughterhouses and production establishments. Data is permanently available to them for documentation purposes, for evaluations and for promotion of their operational success. In the “slaughter data” module, the weight and classification data ascertained daily

by the participating slaughterhouses are uploaded immediately after slaughter and provided for evaluations and as a download for acquisition in inventory control or other IT systems. In the “veterinary data” module, detailed evaluations of the diagnostic data collected on the animals for slaughter are provided during the meat hygiene inspection. **QUALIFOOD** is quite actively utilised in the pork sector. For example, an accumulation of conspicuous lung examination findings is taken as a reason to inspect the climate of the stable in the production establishment.

These two examples are certainly merely a modest start. But they are proof that the conviction and willingness to record and intent to use health data exists and continues to increase. Health data can contribute towards detecting health problems at an early stage. “Organisational blindness” can sometimes only be overcome through industrywide comparisons in the sense of benchmarking. Because many diseases are also caused or intensified through deficiencies in husbandry or management, diseases, and thereby also treatments, can be reduced through preventive measures. And with that we once again come one step closer to producing healthier foodstuffs through healthier animals.

I am convinced that it is worthwhile to utilise all data sources with health indicators such as performance test data, claw trimming data, veterinary data, slaughterhouse data and – to an increasing extent – also livestock farming data which arise due to increasing automation and are systematically utilised much too seldom. Ideally, all data should be compiled and the knowledge generated from this should be made available to all authorised users on one platform.

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Presentation of Danish system of registration and use of health data (registration, database, data security, herd health contracts,...)

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Abstract

Knowledge Center for Agriculture in Denmark – owned by the farmer's organizations – has a long tradition for developing and operating a central cattle database. The central cattle database has over the years been growing with more and more data in all different areas for breeding evaluation, for feeding management, for production management and for documentation of the production. In the nineties agreement was made with the authorities that the central cattle database should deliver the mandatory cattle data to the authorities database

The result is that today there is one central database with all cattle data. There is high degree of validation. Data are delivered from very many sources around the dairy production; farmer, veterinarians, advisory services, milk recording, AI technician, other services, Dairies, Slaughter houses etc.

Health data in the central Danish Cattle database

Health data can be recorded by the farmer, by the Veterinarian and others with special obligations concerning health topics on the cattle farm. Due to the regulation about medicine usage there has to be clinical symptoms registered, to do the treatment. This gives a high rate of registration of diseases and health traits on dairy cows.

Claw health has over the last years got a high focus in Denmark, but there has been a leach of registrations in that area. To improve that a tool do registration during claw trimming has been developed. The tool is today used by 60% of the claw trimmers, and has increased the registration dramatically for the benefit of breeding evaluation and production management.

All in all it gives us a very solid basic of data within the health area with a high registration rate and high data security, and data that can be combined with other data for breeding and production management

Introduction

Data recording in central data systems in Dairy Production in Denmark started almost 50 years back in connection with milk recording. It started with a lot of manually recording involving a lot of man power. Increasing requests for data for breeding evaluation and later management purposes increased the data that got recorded. Over the years the amount has increased dramatically to a very complete system.

With stronger focus on food safety and traceability "the public" introduced laws for the dairy farmer for mandatory registrations concerning the single animal. Since these data already were recording in the already existing central cattle databases the Dairy Business (the farmers union) suggested the Danish Ministry to do this in cooperation. After long negotiations and some changes along the road it has led to that today all mandatory registrations are done in the Central Danish Cattle Database

Disease recordings have for many years been of high interests for breeding evaluation and later also management tools. The big challenge has been to get it systematically registered. Back in the nineties the Dairy Business made an agreement with Veterinarians Union – veterinarians in Denmark are independent business – about registration. Systems were made to transferee disease registration to the Central Cattle Database in connection with the monthly invoice from the veterinarian to the farmer. In that way the data came in without extra work. In the beginning the 2000s agreement were made with the authorities so the farmer were allowed to make treatment with medicine him selves. In the agreement demands about registration of diseases in the Central Cattle Databases

The data sources to day

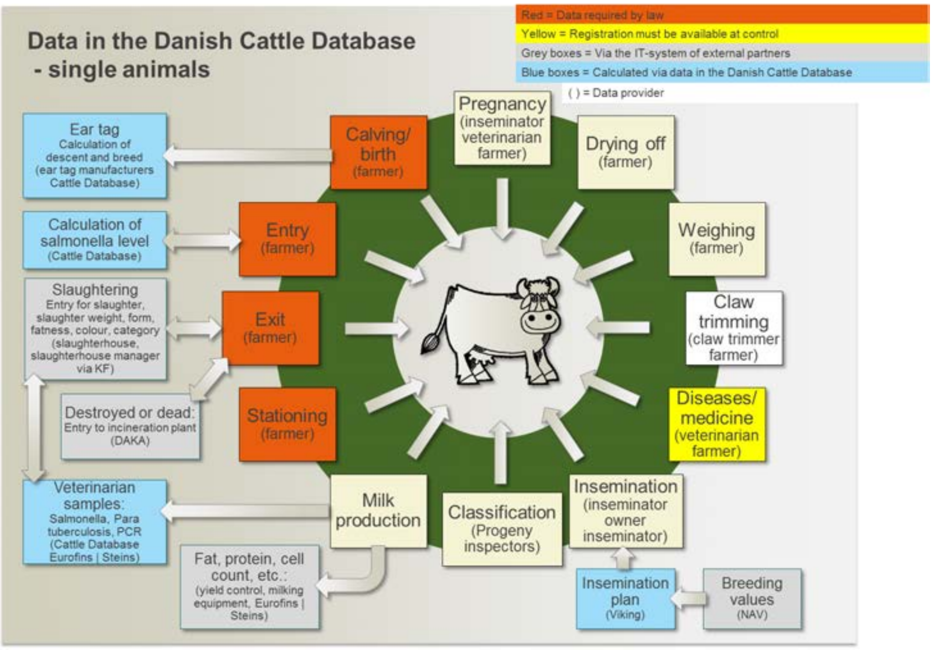
Data are delivered to the Central Cattle Database from very many sources around the dairy production:

- Mandatory recordings due to EU regulations
- Voluntary recordings
    - Milk recording
    - Reproduction
    - Health management
    - Feeding
- Recordings from service suppliers
    - AI Technicians
    - Veterinarians
    - Hoof trimmers
- Dairies
- Slaughter houses
- Etc.

In the following figures we have tried to illustrate data sources, and how the directly and indirectly deliver data to the Danish Cattle database. The illustrations are split into the two types of data; Figure 1, Data on the single animal level and Figure 2, Data on herd level

Some remarks on data completeness and data reliability

Some data are compulsory for the farmer to report to the DCDB/CHR, such as movements (including deaths and slaughters) and calvings. Since these data are under the control of the authorities and are regularly checked the data are considered to be close to 100% correct information regarding this data for cattle. The relationship between herds, farms and owners are registered by the Danish Veterinary and Food Administration using data from databases of other Danish authorities, e.g. Danish Commerce and Companies Agency. The agreement with the ministry about the registration in the Central Cattle Database also demands I high degree of validation rules on the registered data, which again gives a high reliability on the data



Data in the Danish Cattle Database - single animals

Red = Data required by law
Yellow = Registration must be available at control
Grey boxes = Via the IT-system of external partners
Blue boxes = Calculated via data in the Danish Cattle Database
( ) = Data provider

Ear tag
Calculation of descent and breed
(ear tag manufacturers Cattle Database)

Calculation of salmonella level
(Cattle Database)

Slaughtering
Entry for slaughter, slaughter weight, form, fatness, colour, category
(slaughterhouse, slaughterhouse manager via KF)

Destroyed or dead:
Entry to incineration plant
(DAKA)

Veterinarian samples:
Salmonella, Para tuberculosis, PCR
(Cattle Database Eurofins | Steins)

Calving/ birth
(farmer)

Entry
(farmer)

Exit
(farmer)

Stationing
(farmer)

Pregnancy
(inseminator veterinarian farmer)

Drying off
(farmer)

Weighing
(farmer)

Claw trimming
(claw trimmer farmer)

Diseases/ medicine
(veterinarian farmer)

Milk production

Fat, protein, cell count, etc.:
(yield control, milking equipment, Eurofins | Steins)

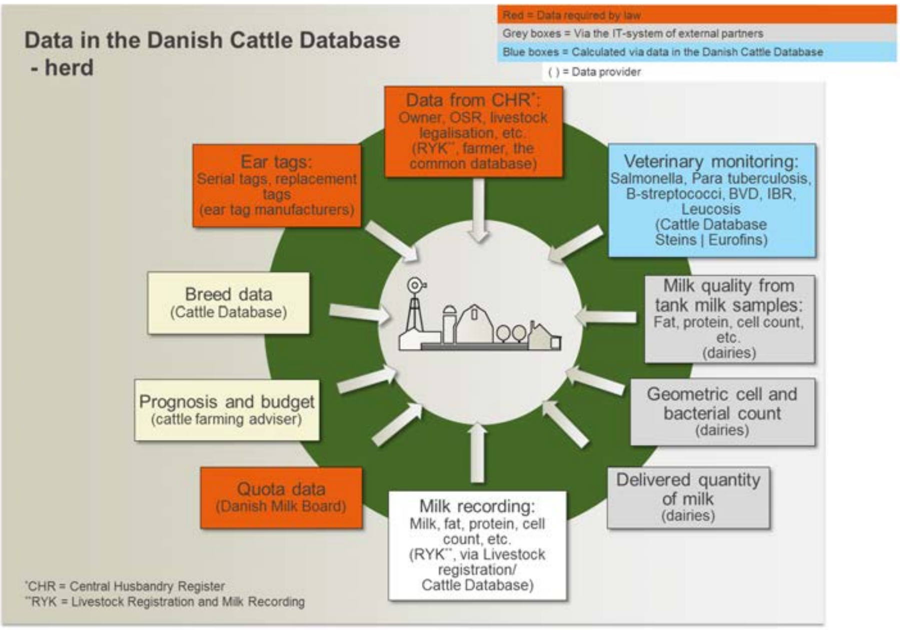
Classification
(Progeny inspectors)

Insemination
(inseminator owner inseminator)

Insemination plan
(Viking)

Breeding values
(NAV)

Figure 1. Data on the animal level.



Data in the Danish Cattle Database - herd

Red = Data required by law
Grey boxes = Via the IT-system of external partners
Blue boxes = Calculated via data in the Danish Cattle Database
( ) = Data provider

Data from CHR*:
Owner, OSR, livestock legalisation, etc.
(RYK**, farmer, the common database)

Ear tags:
Serial tags, replacement tags
(ear tag manufacturers)

Veterinary monitoring:
Salmonella, Para tuberculosis, B-streptococci, BVD, IBR, Leucosis
(Cattle Database Steins | Eurofins)

Breed data
(Cattle Database)

Milk quality from tank milk samples:
Fat, protein, cell count, etc.
(dairies)

Prognosis and budget
(cattle farming adviser)

Geometric cell and bacterial count
(dairies)

Quota data
(Danish Milk Board)

Milk recording:
Milk, fat, protein, cell count, etc.
(RYK**, via Livestock registration/ Cattle Database)

Delivered quantity of milk
(dairies)

*CHR = Central Husbandry Register
**RYK = Livestock Registration and Milk Recording

Figure 2. Data on the herd level.

Reporting of data concerning reproduction is on a voluntary basis. But a major part of the milk producers report this data. Since it is used for the daily management of the herd, and some validation rules on the Central Cattle Database these data are also close to 100%, and almost daily updated. Milk recording data are reported for all herds in the milk recording. These herds include approx. 95% of all milk producers. Most data concerning laboratory result are transferred from the laboratory, in most cases being Eurofins | Steins. From Eurofins | Steins we receive data concerning milk quality and disease surveillance results from blood and milk samples

All data registrations have an "owner". The user always has to identify him selves to the system, and that username is always put on the registration, and is visible. This gives other user with access to the data and especially the farmer a good possibility to follow up on possible errors in the registration

Health data Registration

Health data can enter the Central Cattle database from different sources and for different purposes. The Veterinarian will automatically get his registration transferred to the Database when invoicing the farmer in the case where the farmer doesn't have to use the mandatory Health Advisory Agreement and in the case when other data is registered. The Farmer has to record if he wants to tread animal him selves with medicine.

The Danish Herd Health Advisory Agreement is agreed between the Ministry and the Danish Dairy Business. The motivation from the dairy farmer has been to be allowed to do treatment with medicine by him selves without calling the veterinarian. To control that it demands regularly advisory visits from the veterinarian, once a week or once every second week depending on the number of animals. The agreement is visualized in figure 3

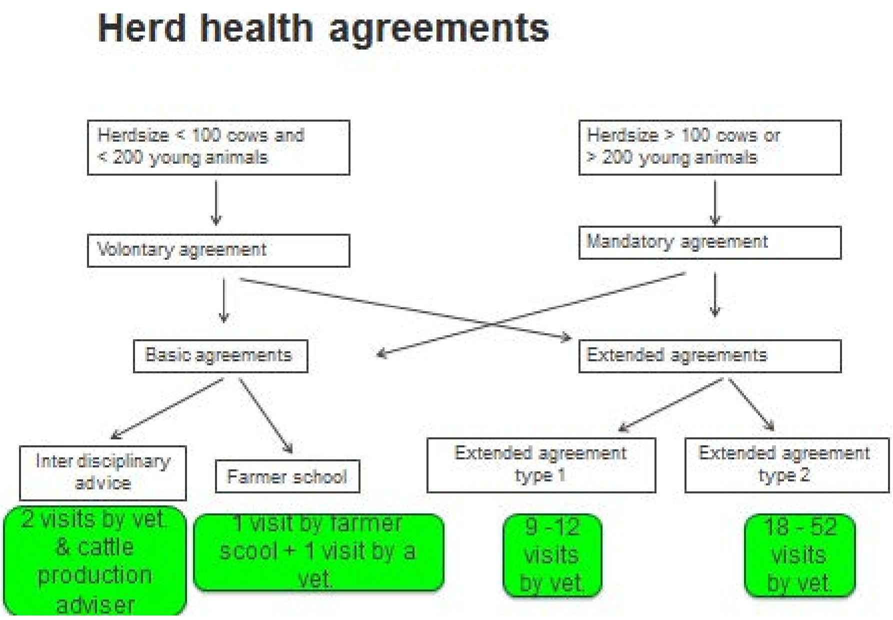


Figure 3. The Danish herd health agreement.

A special area in Health registration in Denmark is the claw health. Historically it has been very difficult to get farmer and the Hoof trimmer to do any registration. The veterinarian has to some extent done some registration on claw health. But due to the increasing development in claw diseases it some years ago got very high focus also in Denmark. One of the recognition was that we needed and easier registration way than paper. To solve that, a pc program was developed to be used on a touch screen. The program was released in 2010 and today the program is used by nearly 60% of the Hoof trimmers in their daily routines. This has generated registrations on claw diseases on more than 40% of the dairy herds with high benefits for breeding evaluation and a new advisory area; Claw Health Management.

Ownership of data

Data in the Danish Central Cattle Database are owned by the farmer. This has been strongly emphasized by the board of the Cattle Department. This means that all access to the data demands a signed authorization from the farmer. The only exception from that is data for research projects approved by the board. The rules are:

1. It is not allowed to use data for other purposes than for this specific project. No patents can be applied for without involving Knowledge Centre for Agriculture, Cattle.
2. Knowledge Centre for Agriculture, Cattle, will receive a report or similar on the survey / analyses, for which the data have been used.
3. Data are not to be published in such a way as to identity a single herd or farmer, e.g. *the* farm with highest number of cows.
4. Individual farmers or herd owners should not be contacted directly on the basis of the delivered data.

Appendix 1. Examples of data on herd and animal in the Danish Central Cattle Database

Example: Data from one (or two) cow(s). Data from screen in *www.glr-chr.dk*

Basic information from one animal

Animal no.	12345-67890
Male / female	Cow
Breed	DHF, Danish Holstein
Date of birth	31-03-2007
Mother's no.	DK-023521-00199
Nationality	DK, DANMARK
Herd no.	12345
Type of herd/code for usage	1202 Dairyherd
Bluetongue basic vaccination	1. vaccination 19-08-2008 2. vaccination 14-09-2008
Latest BT-vaccination	21-04-2009
Herd's level in Salmonella Dublin surveillance programme	04-11-2009 Niveau 1b,
Farm no. in CHR	67890
Herd owner:	
Name	Farmer Hansen
Address	Dairy Road

Calving (related to animal)

Date of birth	Animal no.	Calving no.	Sex	Condition of calf	Present farm no.	Present herd
16-01-2010	12345-67890	1	Kvie (heifer)	Levende kalv Live calf	67890	67890

Movement of one animal

Date	Farm no.	Herd no.	Reason (in, out, birth)	Farm no. to/from
05-05-2007	67890	67890	1, Indgang	45678
05-05-2007	45678	45678	16, Afgang levebrug	45678
31-03-2007	45678	45678	3, Fødsel	

Further information from another cow: Animal no: XXXXX-12345

(Internal DB_id = 10073XX144)

Insemination, calving and other 'incidents' – data from 'Dyreregistrering'

Date	'Incident' (Danish: hændelse)	male/ female calf	Progress	Size	Animal no. of calf
15-09-2007	Insemination				
11-06-2008	Calving	female	easy	2	XXXXX-02540
17-06-2008	'Sterile test' (Danish: steril prøve)				
02-09-2008	Insemination				
23-09-2008	Insemination				
07-11-2008	Bluetongue vaccination				
11-12-2008	Bluetongue vaccination				
03-07-2009	Calving	male	easy	-	XXXXX-02672
16-09-2009	Insemination				
19-06-2010	Calving	male	easy	3	XXXXX-02779
24-06-2010	'Sterile test'				
06-09-2010	Natural insemination start (Danish: løbning start)				
07-09-2010	Natural insemination end (Danish: løbning slut)				

Milk yield of the selected animal

Date	Milk (kg)	Fat (g)	Protein (g)	Somatic cell count (x 1000)
14-06-2008	18.0	545	713	226
31-07-2008	16.6	627	554	429

Vetstat - Monitoring usage of antimicrobials in animals

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Abstract

Following increasing focus on antimicrobial (AM) usage and risk of bacterial resistance, an on-going, national monitoring system of all veterinary drug use was implemented in Denmark in 2000. Information is reported by veterinarians and pharmacies and stored in a central database, Vetstat. Information includes prescribing veterinarian, receiving herd, product name, amount of product, animal species, age group and diagnostic group. Based on this information, various estimates of the Danish AM usage for production animals are regularly presented. The estimates may include conversion from amount of active compound to "Animal Daily Doses" (ADD) and different means of adjusting for number of animals available for treatment. Consequently these conversions introduce risks of inconsistency, misclassification and disagreement when reporting AM consumption.

The aim of this paper is: 1) to describe the structure and content of Vetstat, 2) to discuss possible pitfalls when designing a system as Vetstat and 3) briefly present the overall AM usage in Danish cattle herds from 2007 to 2011, including a discussion of the main sources of errors.

Results: In 2011 an estimated 13.7 tons AM were prescribed for cattle equivalent to 8.7 grams AM per live cattle in 2011. The total amount of AM resembles approximately 18.7 million ADD, which would imply that 3.4% cattle>2 years of age and 5.2% of cattle <1 year of age were treated daily. The most used AM for systemic treatment in 2011 were narrow spectrum penicillins. Diseases related to the mammary glands were the predominant indication for AM treatment (29% of treatments).

Keywords: antimicrobial consumption, surveillance system, pharmaco-epidemiology, Vetstat

Introduction

The association between resistant bacteria strains and use of antimicrobials (AM), especially growth promoters for production animals is well established (Agersø and Aarestrup, 2013; Lathers, 2001; Martel *et al*., 2001; Aarestrup *et al*., 2001). The possibility of such resistant bacteria entering the human food chain caused growing concern in Europe during the 1990s. Consequently, an EU conference ("The Microbial Threat") was held in Denmark in 1998. One of the recommendations issued was to monitor the veterinary use of AM more closely. In order to comply with these recommendations, Denmark instigated an on-going surveillance program in 2000 of the medical consumption for (production) animals, collecting all data in a national database, Vetstat (Stege *et al*., 2003).

The aims of this on-going Danish program are:

1. monitor veterinary usage of drugs in animal production;
2. help practitioners in their work as farm advisors;
3. provide transparency as a basis for ensuring compliance with 2 rules and legislation and
4. provide data for pharmaco-epidemiological research." (Stege *et al.*, 2003).

The purpose of this paper is to:

1. describe the structure and content of Vetstat;
2. discuss possible pitfalls when designing a system as Vetstat and
3. briefly present the overall AM usage in Danish cattle herds from 2007 to 2011, including a discussion of the main sources of errors when reporting AM consumption.

Vetstat - structure and content

Vetstat is a relational database on an Oracle platform and is owned and managed by the Ministry of Food, Agriculture and Fisheries. During the nineties many legislative regulations were passed by the Danish government to curb AM sale. The regulations included limits on veterinary profits from sale of AM and a ban on use of growth promoters in production animals (Aarestrup *et al.*, 2010). All AM and the largest majority of all other veterinary therapeutic drugs are prescription-only in Denmark. Virtually all sale of veterinary medicine are made through pharmacies, veterinary practitioners or feed mills. Data on medicine consumption are therefore submitted to Vetstat by these three entities (Figure 1). Pharmacies and feed mills purchase drugs directly from the drug manufacturers. Veterinary practitioners purchase drugs for use in practice from pharmacies. All pharmacies, veterinary practitioners, veterinary practices and feed mills have a unique ID. Content of entries to Vetstat are shown in figure 2.

Vetstat's definitions of animal species, age group and diagnostic group are shown in table 1.

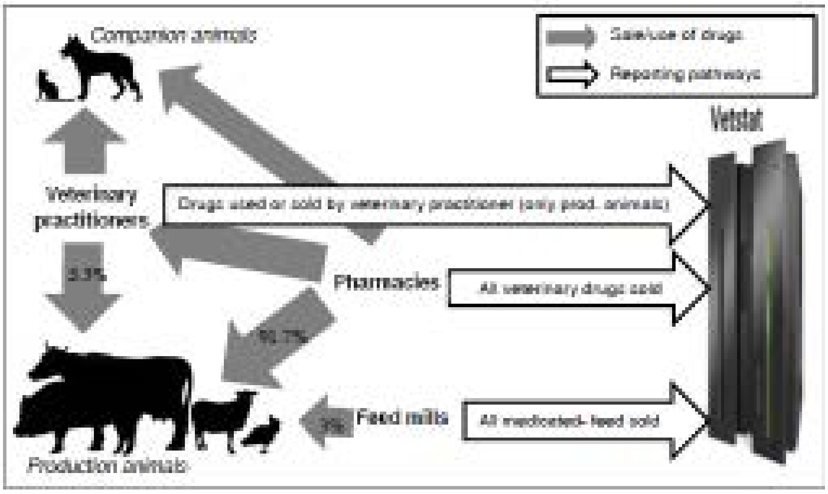
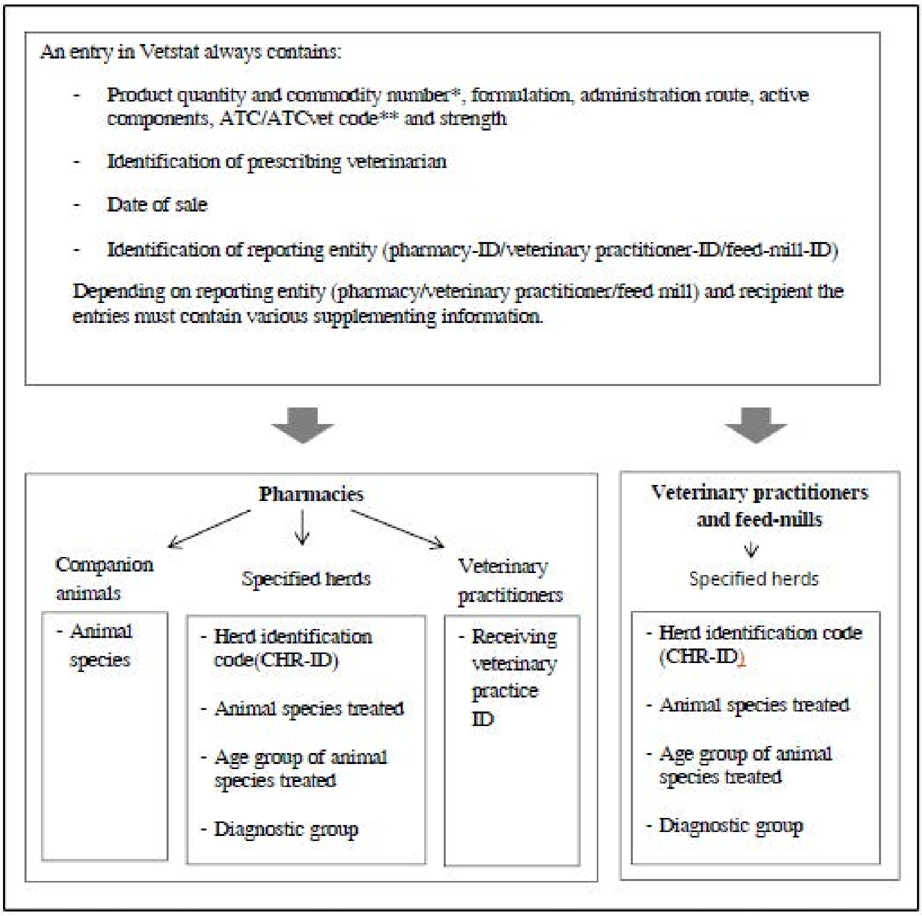


Figure 1. Reporting pathways- Vetstat and percentage of total kg AM active compound reported for production animals in 2011.



An entry in Vetstat always contains:

- Product quantity and commodity number*, formulation, administration route, active components, ATC/ATCvet code** and strength
- Identification of prescribing veterinarian
- Date of sale
- Identification of reporting entity (pharmacy-ID/veterinary practitioner-ID/feed-mill-ID)

Depending on reporting entity (pharmacy/veterinary practitioner/feed mill) and recipient the entries must contain various supplementing information.

Figure 2. Content of entries according to reporting entity and recipient of drug.

**The Nordic commodity number identifies name of medicinal product, strength, form and size of packaging.*

***The Anatomical Therapeutic Chemical classification system identifies all human drugs in a five-digit hierarchical system. Products with the same active substance in the same pharmaceutical formulation are given the same ATCcode. The ATCvet system is the veterinary counterpart (Dahlin et al., 2001).*

Submission of data to Vetstat

All Danish pharmacies have electronic and standardized billing systems. These are linked to Vetstat, which ensures automatic transfer of data on all veterinary drug purchases. This improves the validity of data on quantity and commodity number of drugs sold.

Electronic journal systems are used by most Danish veterinary practices[1]. These softwaresystems automatically transfer data on all treatments regarding production animals to Vetstat in connection with billing. The software-systems are developed and distributed by private companies and there are no official guidelines or

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[1] TANG-dyrlægeløsning(TANG data) and Vetvision(Novasoft).

Table 1. Vetstat definitions of animal species, age group (including according standard weight) and diagnostic group.

Animal species	Age group (standard weight -kg)	Diagnostic group
Pigs	Breeding animals, gilts, suckling pigs (200) Weaners (15) Finishers (50)	Reproduction, urogenital system Udder Gastro-intestinal system Respiratory system Joints, limbs, hooves, CNS, skin Metabolism, digestion, circulation
Cattle	Bulls, cows (600) Calves <12 months (100) Heifers, steers (300)	
Sheep, goats	>12 months (50) <12 months (20)	
Mink	Not recorded (1)	Other (mink only)
Aquaculture	Not recorded (1)	Red mouth disease Furuncolosis Brood syndrome Other
Poultry	Broilers (0,2) Layers (1) Rearing flocks (1)	Abdominal organs Coccidiosis Enteritis Hepatitis Salpingitis Other Respiratory system / organs
Other production animals*	Not recorded (1)	
Horses	Not recorded (500)	Not recorded
Pets	Not recorded (not given)	

**Llamas, rabbits, deer, ostriches*

legislation on the setup. A few veterinarians choose to report data directly into Vetstat, either manually on the Vetstat webpage or by discs sent to the Ministry of Food, Agriculture and Fisheries. According to Danish legislation veterinarians must report drugs used for production animals at least once per month.

Only few substances are approved for pre-mixed medicated feed for production animals. Thepurchases are reported directly to Vetstat by the feed-mills.

Herd identification code- system

Since 1993 all Danish herds have been legally required to register in the Central Husbandry Register (CHR-register). The CHR-register is, as Vetstat, owned and managed by the Ministry of Food, Agriculture and Fisheries. All herds are given a unique identity code (CHRID) relating to the geographical coordinates of the herd in question (Madec *et al.*, 2001). In addition to information on geographical location the register also contains data on production type and number of animals present in the herd (animal species, age group) and contact information on the herd owner

(Mousing *et al*., 1997). By law all changes in number of animals must be reported to the CHR-register no later than 7 days after the event for cattle and once per year for pigs[2].

List of veterinary products

All Danish drugs, both human and veterinary, must be approved either by the Danish Health and Medicines Authority or the European Medicines Agency. Newly approved veterinary drugs are registered into Vetstat every second week manually by a ministry employee. Information must include:

- Commodity number
- Active component(s)
- Strength
- Package size
- Formulation
- Administration route
- ATC / ATCvet code
- Average daily maintenance dose per kg live animal for the main indication according to relevant animal species (DMDkg)

Standard values on recommended dosage are published yearly by the Danish Health Authorities.

Quantification of drug consumption

Several units have been proposed to quantify AM drug consumption for production animals (Callens *et al*., 2012; Chauvin *et al*., 2001; Eagar *et al*., 2011; Timmerman *et al*., 2006). In the Danish surveillance of AM consumption usage for production animals is mostly reported as:

- kg active compound AM consumed
- (number of) Animal Daily Doses (ADD)
- ADDs per 100 animals per day (percentage treated per day)

Calculation of Animal Daily Dose (ADD)

ADD is defined as the daily maintenance dose per live animal for the main indication. Therefore ADD provides a measurement that takes potency of drugs into account. ADD enables reports on AM consumption to adjust for differences in dosage regimens depending on animal species and size. To account for the large variation between weights in production animals, the parameter standard weight was introduced in Vetstat. Standard weight is the estimated average weight at treatment assigned to all major production animal species according to age group (Table 1). ADD is the veterinary equivalent to the human measurement "defined daily dose" (DDD) (Wertheimer, 1986). DDD is an international standardized measurement defined by WHO (Anonymous, 2009), whereas ADD is still calculated differently across borders. In Vetstat ADD is calculated as:

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[2] For herds with more than 300 sows, 3000 finishers or 6000 weaners, information on animal numbers must be updated biannually.

$$ADD = \frac{Total\ amount\ of\ active\ compound\ AM\ sold/used(mg)}{dosage\ pr\ kg\ live\ animal(DMDkg) * standard\ weight\ of\ animal}$$

Calculation example:

100 mL of EthacilinVet. containing 300 mg benzylpencillinprocain / mL for use in cows (600kg)

$$ADD = \frac{(100mL\ product * 300mg/mL)}{15mg/kg\ * 600kg} = 3{,}33ADD$$

Adjustment for population size

To enable adjustment for herd size when reporting AM consumption, the parameter "percentage animals treated per day" (or ADD per 100 animals per day) was introduced by the Danish authorities. The number of "pen places", presumably resembling live animals at any given time, is currently used as denominator. Data on number of pen places (animals present in herd) are automatically derived from the CHR-register.

ADD per 100 animals per day is calculated as:

$$ADD\ pr\ 100\ animals\ pr\ day = \frac{ADD\ used}{number\ of\ pen\ places * days\ in\ period} \times 100$$

Calculation example:

150 ADD (cows / bulls) used in a herd with 400 pen places in January (31 days).

$$ADD\ pr\ 100\ animals\ pr\ day = \frac{150\ ADD\ used\ (total\ in\ 31\ days)}{400\ pen\ places * 31\ days} \times 100\ =\ 1{,}2$$

Equaling an estimate of 1,2% of cows treated per day during January.

User-access to Vetstat-data

Data on overall national AM consumption for all animal species and for pigs specified are presented online on the webpage of the Ministry of Food, Agriculture and Fisheries.

Detailed data on all entries into Vetstat are accessible to veterinarians and farmers on Vetstat's webpage vetstat.dk. Farmers can monitor all entries regarding their own herds. Veterinarians can monitor all entries submitted by themselves. Veterinarians can monitor all entries on herds with whom they have a Health Advisory Agreement (HAA)[3]. Automated graphic reports can be made on AM consumption for each individual herd reported as ADD per 100 animals per day.

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[3] HAA’s are mandatory for Danish herds of a certain size (>100 cows or >200 heifers and steers. They cover rules on frequency of veterinary visits, treatment schemes and management.

Since spring 2012 it has been possible for any member of the public to obtain access to detailed data excerpts from Vetstat. Possible pitfalls when designing a system as Vetstat

Possible pitfalls when designing a system as Vetstat

Presently there is no automatic linking of animal species, age group and diagnostic group. This makes it possible to make an entry containing logically diverging values e.g.: animal species "cattle", age group "broilers" and diagnostic group "furunculosis". In 2011 1.4% entries reported by pharmacies on drugs for use in cattle herds either stated an invalid age group, diagnostic group or both.

Furthermore cases of erroneous data on prescribing veterinarian-ID are known to the authors. A validation process was introduced in 2003 (Jensen *et al*., 2004), where prescribing veterinarian-ID is checked against the Danish veterinary authorities' list of registered veterinarians. Despite this, entries still occur where the entered veterinarian-ID does not correspond with the ID of the actual prescribing veterinarian. The authors speculate this might be due to typing errors by the reporting entity or misreading of the veterinarian-ID on handwritten prescriptions.

Vetstat only incorporates data on consumption submitted by the three reporting entities (pharmacies, veterinary practitioners, feed-mills). Reporting procedures have improved much since Vetstat was first implemented in 2000. This is important to keep in mind, especially when evaluating consumption over time. An increase in AM consumption according to Vetstat might not be a true increase in consumption, but rather a reflection of increased registration of consumption. Data registrations by pharmacies are considered complete. Since the 1980s all Danish pharmacies have employed a standardized IT-based reporting system, reporting all purchases of drugs to the Danish Health and Medicines Authority. The same cannot be said for data from veterinary practitioners. It is estimated that registrations on up to 25% of AM used in cattle practice were missing for several years following the launch of Vetstat (DANMAP, 2003). From 2010 to 2012, the estimate has been that 10% of AM used in veterinary cattle practice were not registered into Vetstat by the veterinary practitioners (DANMAP, 2012).

The lack of consistency in registrations by veterinary practitioners might be due to many factors, such as lack of entries being submitted by veterinary practitioners or due to rejection by the Vetstat database procedures[4]. Veterinary practitioners also had the drawback that they did not already utilize an existing, automatic reporting system when Vetstat was implemented, such as the pharmacies did.

In 2011 36% of the AM registered for use in cattle were purchased through veterinary practitioners (Figure 3). Contrary to this, less than 0,1% of the AM purchase for pigs were directly through veterinary practitioners. Therefore data validity on Danish pig AM consumption is considered better than that on cattle Am consumption.

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[4] Until 2011 entries submitted by veterinary practitioners lacking information on any of the required parameters were allocated to en error table in Vetstat for correction.

Effect of calculation routines on AM consumption reports

Data on the Danish AM consumption for cattle are published yearly by DANMAP - the Danish Integrated Antimicrobial Resistance Monitoring and Research Programme (DANMAP, 2012). To adjust for potential missing registrations by veterinary practitioners, DANMAP calculates AM consumption for cattle (kg active compound) as:

$$\begin{aligned} &\textit{DANMAP cattle AM} \\ &\qquad = \textit{AM sold directly for use in cattle herds from pharmacies} \\ &\qquad + \textit{AM sold for use in cattle practice from pharmacies} \end{aligned}$$

By applying this method, AM consumption is estimated relying solely on data registered by pharmacies. Registrations by pharmacies on AM sold for use in veterinary practice do not include information on animal species (figure 2). Therefore this method is not without flaws as:

1. AM used in mixed practice for cattle are not included.
2. AM used for non-cattle are included if used by veterinarians employed in cattle practice.

An alternative to the DANMAP method is solely to include data where animal species have been explicitly specified as "cattle". This method does not adjust for missing registrations by veterinary practitioners.

When comparing AM consumption according to these two methods there is a discrepancy of 4-15% (Table 2) (DANMAP, 2008, 2009, 2010, 2011, 2012).

This comparison highlights the importance of meticulous description of calculation routines when publishing numbers on AM consumption. DANMAP reports can be accessed at *www.danmap.org*.

Antimicrobial consumption in Danish cattle according to Vetstat data

All Vetstat data were assessed for entries where animal species "cattle" were given. The reported AM consumption for Danish cattle increased from 12.7 tons in 2007 to 13.7 tons in 2011 equivalent to 7. 9 and 8.7 grams AM per live cattle respectively. In 2011 AM reported by pharmacies for cattle constituted 64% of total reported AM kg consumption for cattle (Figure 3).

Table 2. AM consumption (kg active compound) for cattle 2007-2011 according to Vetstat and DANMAP respectively.

	Vetstat	DANMAP	Discrepancy (kg active compound AM)	Discrepancy in %
2007	12741	15000	2259	15.1
2008	12923	14500	1576	10.9
2009	13232	15000	1768	11.8
2010	14027	14636	608	4.2
2011	13671	14678	1006	6.9

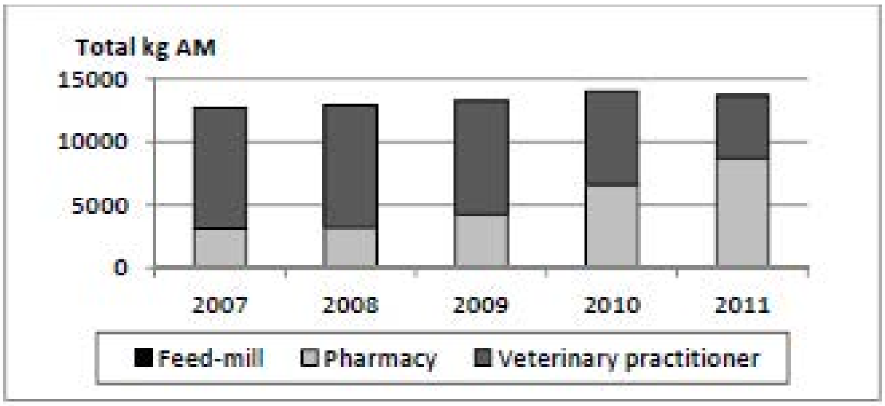

Figure 3. AM consumption reported for use in cattle 2007-2011, shown as total kg active compound AM per year according to reporting entity. Feed mills account for less than 0,1% of consumption)

Figure 4 and 5 depicts the AM consumption in the different cattle age groups, reported as kg active compound and ADDs, respectively. The effect of adjusting for animal standard weight is obvious as the AM consumption for use in cows and bulls constitutes roughly 80% of the total amount of active compounds, whereas it constitutes about 45% % of the total ADDs.

Figure 5 also shows the total Danish cattle population, which has increased slightly with 1.5% from 2008 to 2011. Due to changes in reporting methods reliable numbers on cattle population were not available before 2008.

The AM consumption for cattle in 2011 resembles approximately 18.7 million ADDs, which would imply 3.4% cattle>2 years of age and 5.2% of cattle <1 year of age were treated daily. This implies a 5% decrease since 2007 in AM consumption measured as ADD. This decrease may be even larger, due to an increase in cattle population and a decrease in lacking registrations from veterinary practitioners.

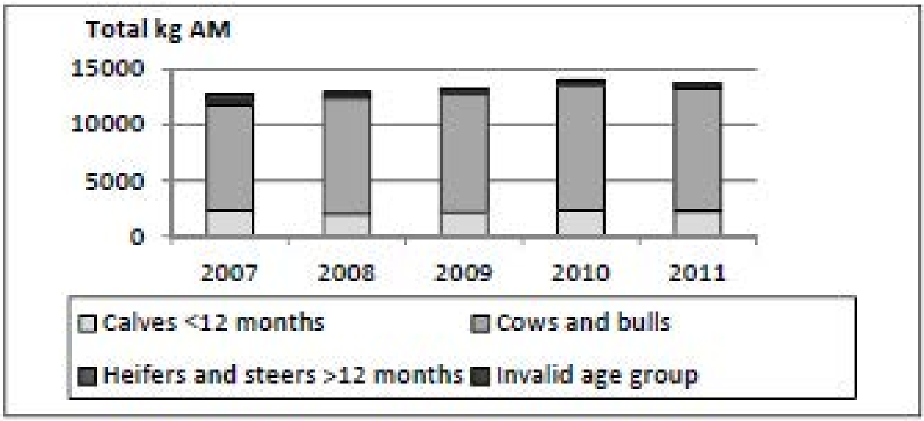

Figure 4. AM consumption reported for use in cattle 2007-2011, shown as total kg active compound AM per year according to age group.

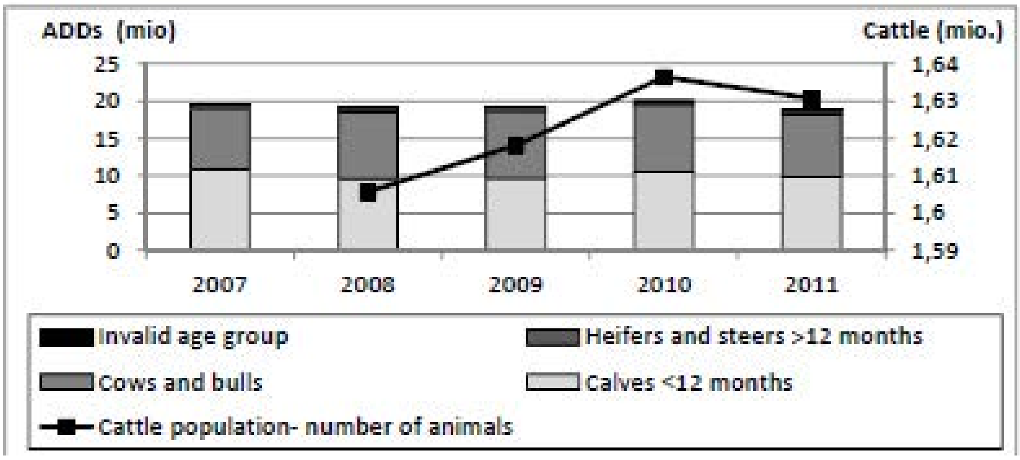

Figure 5. AM consumption reported for use in cattle 2007-2011, shown as ADD per year, according to age group and number of pen places from 2008-2011.

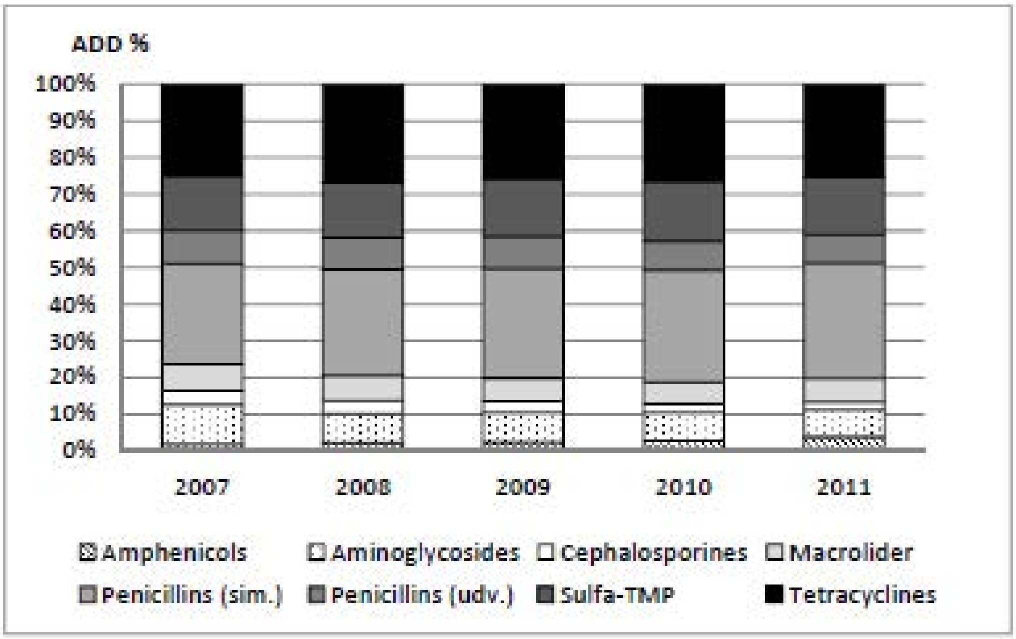

Figure 6. AM consumption reported for use in cattle 2007-2011, shown as percentage of ADD distributed according to ATC main group (Fluoroquinolones, lincosamides and pleuromutilins are not presented, as they each account for less than 1% of the consumption.

Pattern of AM consumption according to ATC main group has been relatively stable since 2007. The most used AM for systemic treatment in 2011 were narrow spectrum penicilllins (figure 6). Diseases related to the mammary glands were the predominant indication for AM treatment (29% of treatments) (Figure 7).

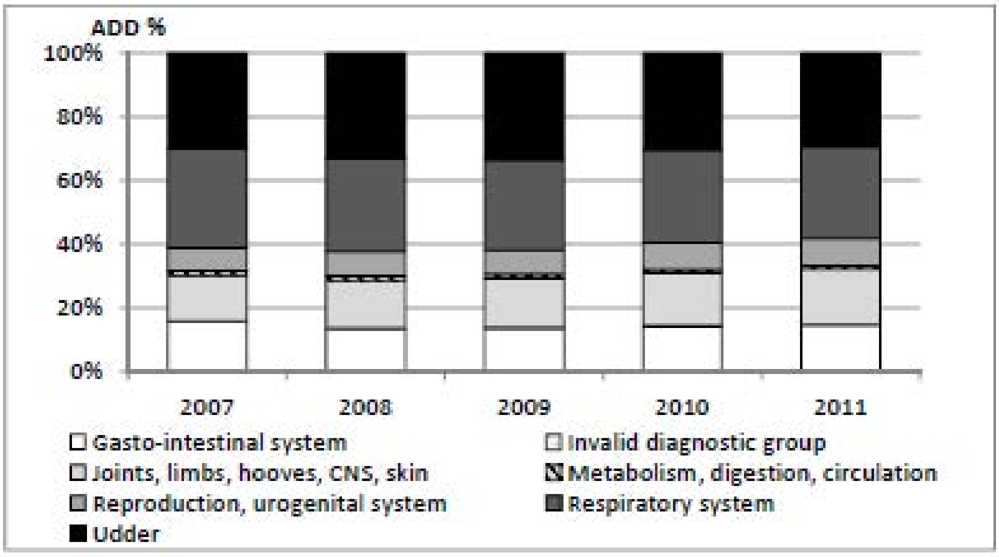

Figure 7. AM consumption reported for use in cattle 2007-2011, shown as percentage of ADD distributed according to diagnosis group.

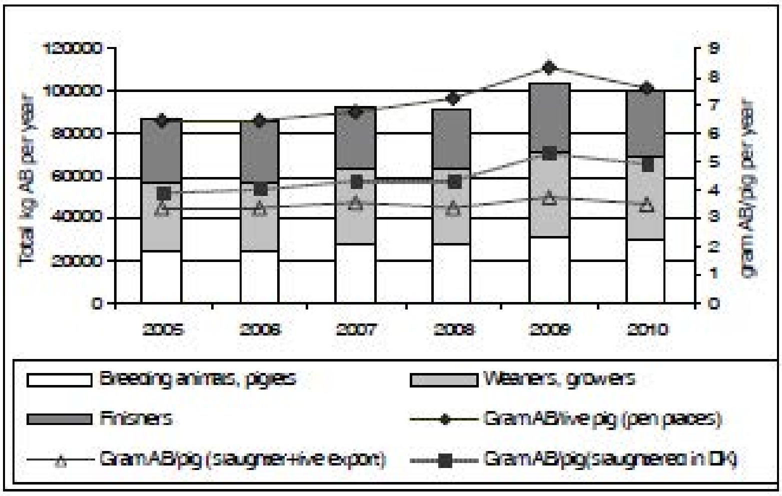

Figure 8. Danish consumption of AM for pigs 2005-2010. Measured in total amounts and as g/pig/year, using 3 different denominators

It is important to realize, that what holds true for DDD also applies to ADD ((Norway), 2012)). ADD does not necessarily reflect the prescribed-, used- or recommended daily dose. Drug consumption data presented as ADD only gives an estimate of consumption and not an exact picture of actual use.

AM consumption reports - Effect of animal population

To enable adjustment for population size when reporting AM consumption, Danish authorities presently use "number of pen places", presumably resembling live animals in herd at any time. This does not pose a large problem in the dairy industry, as turnover of animals per year is quite low (mortality rate of Danish cows in 2011 was 5.4% (Anonymous, 2012). But for herds with a large turnover of animals, such as fattening pig facilities, this may not be an accurate measure, as several generations pass the stable facilities each year.

When making international comparisons, it is also important, how number of animals produced each year are measured (e.g. with or without exported finishers). Pigs>30 kg that are exported for slaughter outside Denmark should be included, since they have received most of their AM treatment before export (measured in ADDs, the usage for weaners and growers constituted 77% of total usage in 2010). The export is especially important to take into consideration, when evaluating consumption over time as it increased 146% (3,1 to 7,8 million live pigs) from 2005 to 2010.

Many different takes on population estimation exists (Chauvin *et al.*, 2008; MacKenzie and Gould, 2005; Merle *et al*., 2012). Figure 8 illustrates the pig AM consumption as gram active compound / pig / year from 2005-2010 applying three different population measurements:

1. Number of pen places.
2. Number of pigs slaughtered in Denmark.
3. Number of pigs slaughtered in Denmark + number of exported growers and finishers.

Data on number of pen places were collected from Statistics Denmark. Data on number of pigs produced were collected from Statistics - PIGMEAT including number of pigs slaughtered in Denmark and the number of pigs>30 kg, exported from Denmark each year. Student's t-test was used to test the difference between mean AM consumption / pig / year for 2005 and 2010.

Without adjusting for number of pigs, the consumption increased from 86.932 in 2005 to 100.066 kg in 2010 (i.e. 15%, p<0,05). Table 3 shows consumption / pig / year applying the three different measurements of pig population. The increase from 2005 to 2010 constituted 1.14g (17,7%), 1.0g (25,6) and 0.1g (3,9%) / pig / year, respectively. From 2005 to 2010 there was a significant increase in consumption / pig / year (P<0,001) when using "number of pen places" and "number of pigs slaughtered in Denmark". But the increase was not significant when measuring population as "pigs slaughtered in Denmark + number of exported growers and finishers".

Table 3. Danish consumption of AM/pig in 2005 & 2010 using 3 different denominators.

	Year		
	2005	**2010**	**P- value**
Gram AB / pen place	6.46	7.60	<0.001
Gram AB / pig slaughtered in DK	3.94	4.94	<0.001
Gram AB / pig slaughter+live export	3.40	3.51	0.3069

The authors conclude that population always should be included when reporting the AM usage. Also, there is an obvious risk of misclassification if the productivity is not taken into account.

Conclusions

In conclusion, Vetstat data offers a great opportunity to assess AM usage both at a national level and a herd level. But these data must be used with caution. One must consider potential erroneous data, lacking registrations and changes in population, especially when evaluating AM consumption over time.

Acknowledgement

We thank the Danish Pig Levy Fund for financial support of the study.

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Session 2

General aspects - Part 2

More than 30 years of health recording in Norway

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Abstract

Data from the health recording system are used for many purposes, including genetic evaluation, herd management and research. The health records provide useful information for farmers, veterinarians and advisors in their daily work. Data from many years makes it possible to monitor trends of the most important diseases and estimate genetic and environmental factors affecting diseases.

Health records are crucial for improvement of animal health via genetics, preventive measures, epidemiological research, and environmental improvements.

Introduction

The aims of this presentation were to describe the Norwegian Cattle Health Recording System, illustrate how this information is used for genetic evaluation in Norwegian Red and to improve health management at herd level, present phenotypic- as well as genetic trends for important health traits, and discuss present and future possibilities and challenges regarding dairy cattle health recording.

The Norwegian Cattle Health Recording System

Health recording for dairy cows is well established in Norway, where each case of veterinary treatment has been registered on an individual cow basis since 1975. Figures for 2012 shows that 98% of the dairy cows participate in the Norwegian Dairy Herd Recording System (NDHRS), where individual health recording is integrated. Each animal has an individual "health card" where veterinarians record diagnoses by disease codes, and describe symptoms and treatment. This record follows the animal from birth to slaughter. Only veterinarians are allowed to distribute or prescribe medicine for animals, but they are not allowed to sell medicine, only pharmacies can do that. All veterinary treatments of individual dairy cows, calves and young animals are recorded, and veterinarians use these notes in their daily work to look at previous symptoms and treatments on the same animal.

The health recording system has been updated and revised several times since 1975 (Østerås *et al*., 2007). The first system included 10 traits or disease codes. This was extended to 46 traits in 1978. A new organ-related health code system was introduced in 1989, the number of disease codes increased to approximately 300, and the 90 most

Table 1. Summary of diagnoses and disease treatments reported to the Norwegian Cattle Health recording system in 2011. Total number of records (n) including cows, calves, and young animals, for disease codes with more than 100 recorded cases in 2011. For each group % of all treatments are given in parenthesis[1] (From Tine, 2012).

Diagnoses	No.	Diagnoses	No.
		Reproductive system/obstetrical	
Infectious diseases (1 %)		**conditions (8 %)**	
Erlichiosis	110	*Uterus prolapsed*	344
Piroplasmosis	127	*Torsion of the uterus*	466
Contagious diarrhea	197	*Prolonged gestation*	369
Contagious respiratory disease	393	*Dystocia*	2449
		Vaginal prolapsed	589
Respiratory, cardiovascular and			5992
hematopoietic systems (3 %)		*Retained placenta*	
Unspecific respiratory disease			
		Reproductive and urinary	
	4220	**systems(13 %)**	
Digestive system (6 %)		*Abortion*	401
Indigestions	2422	*Aneastrus*	3566
Colic/gastrointestinal			3770
dislocation/abomasal dislocation	588	*Heat synchronization*	
Traumatic gastritis	1401	*Silent heat*	2998
Gastritis/enteritis	2969	*Metritis,vaginitis and salpingitis*	2086
Parasitic diseases	553	*Cystic ovaries*	2519
Bloat	159	*Castration*	568
		Repeated breeding	492
Skin and claw (7 %)			
		Nervous system and sense organs	
Dehorning due to injury		**(0.2 %)**	
Laminitis	142	*Eye infection*	111
Hoof diseases	899		
Lice infection	3675	**Musculo-skeletal system (3 %)**	
Scab	2495	*Tendinitis and bursitis*	385
Wounds, injuries	135	*Fractures*	162
	837	*Arthritis*	3070
Mammary system (41 %)		*Paresis due to pelvic and muscular injury*	275
Agalactia			
Severe/moderate clinical mastitis	129	**Non-organ related (16 %)**	
Mild clinical mastitis	30689	*Abscesses/phlegmons*	1402
Subclinical mastitis	15920	*Hypomagnesaemia/grass tetany*	249
Teat injuries	1826	*Ketosis*	6855
Dry cow therapy	2219	*Milkfever*	11284
	4512	*Paresis – except parturient paresis*	425
Prophylactic treatment[2]		*Deficit of vitamins or minerals*	420
Vaccination			
Dehorning	2681		
Prophylactic treatment of parasites	57345		
Milk fever	18351		
Mastitis	633		
	226		

[1] In 2011 the total number of recorded treatments was 132,358, of these 112,503 were treatments of dairy cows, the total number of dairy cows was 334,104, and the number of cow-years was 220,965.

[2] Total number of prophylactic treatment was 85,133, of these 95 % were treatments of calves/young animals.

used codes where printed on the health card. Prophylactic treatment can be noted for each disease code by adding 500 to the code number. Individual health cards for calves and young animals have been available since 1989. Some new disease codes for mastitis and reproductive disorders were introduced in 1999, when the mastitis codes where adapted to the International Dairy Federation (IDF) recommendations (1999).

Table 1 shows a summary of diagnoses and disease treatments reported to the Norwegian health recording system in 2011. The diseases codes are grouped in 10 organ-related groups. Disease codes with more than 100 recorded cases in 2011 were included in the table. For a complete overview see Østerås (2012). Clinical mastitis, milk fever, ketosis and retained placenta were the 4 most common diseases in dairy cows, and accounted for 61% of all veterinary treatments of cows in Norway.

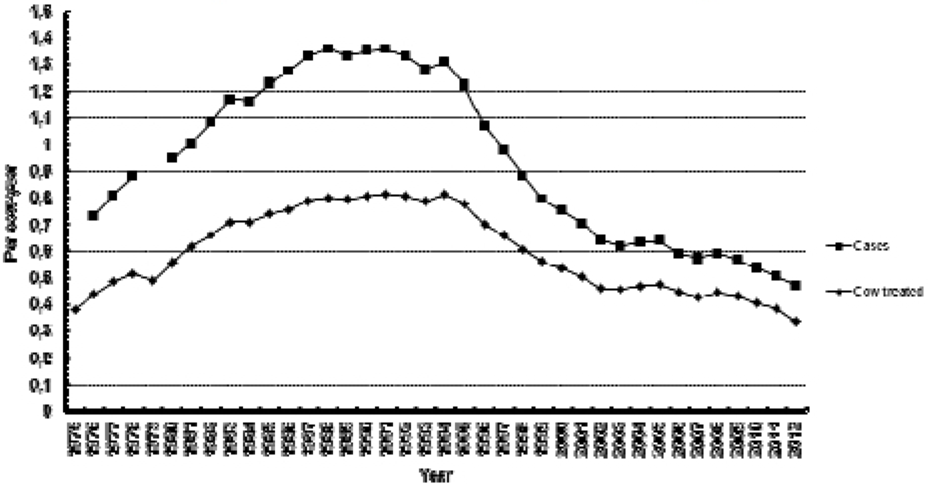

Figure 1. Total no of veterinary treatments and no of cows treated per cow-year from 1975 to 2012 (from Tine, 2012)

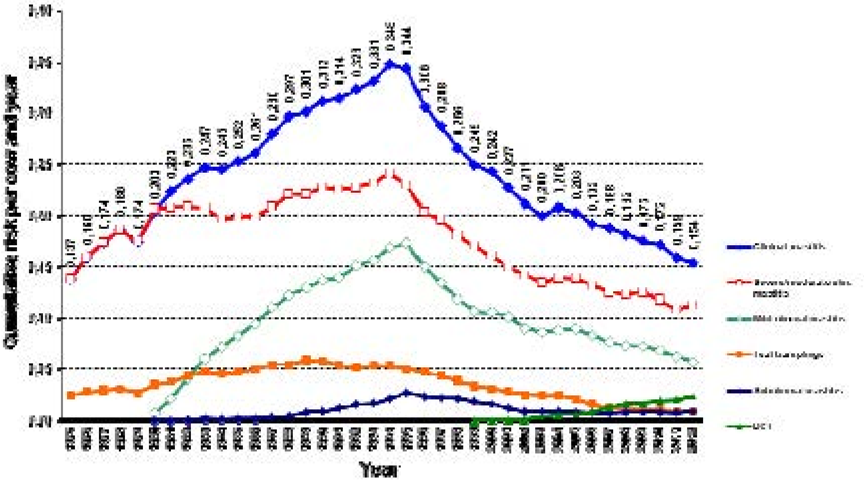

Figure 2. Veterinary treatments of mastitis per cow-year year from 1975 to 2012 (from Tine, 2012)

These 4 were the only diseases with more than 2 records per 100 cow-years at risk, while claw diseases, teat injuries, dry cow therapy, dystocia, aneastrus, silent heat, and cystic ovaries had 1-2 records per 100 cow-years at risk (Tine, 2012).

Phenotypic trends

Figure 1 show that the total number of veterinary treatments and number of treated cows per cow-years increased from 1975 to around 1990, and then decreased gradually since 1994. The main reason was changes in clinical mastitis treatments as shown in Figure 2.

Figure 2 shows that the incidence of clinical mastitis decreased gradually since 1994 while the incidence of veterinary treated subclinical mastitis and dry cow therapy increased slightly in recent years. Approximately 30% of the reduction in clinical mastitis is a result of genetic improvement of Norwegian Red cows (Heringstad *et al.*, 2003). The rest is due to an action by the farmer's organizations to reduce the unnecessary use of antibiotics which changed the treatment strategies, establishment of Norwegian Cattle Health Service, and development of mastitis control programs, advisory- and herd management tools. The health periodicals generated from the NDHRS with information about key figures on the epidemiological aspects of mastitis dynamics in each herd is one example.

The overall treatment rate of Norwegian dairy cows was reduced by 61% from 1994 to 2011 (Tine, 2012). The health records have been a crucial tool for this achievement, as they are the basis for development of herd management tools and for genetic improvement.

Data quality

Because antibiotics and other drugs can be prescribed only by veterinarians in Norway, these

health records are viewed as good quality. This was confirmed by a recent project finding that only 10-12% of the health events were unreported (Espetvedt *et al.*, 2013). Comparisons of retail sales of intramammary antibiotics used for mastitis therapy and the incidence rate of clinical mastitis over 30 years revealed parallel curves and ensures that the trend shown in Figure 2 is a true reduction in mastitis treatments (Østerås *et al.*, 2007)

Recent developments

Veterinarians report directly to central database. It has been possible for veterinarians to report health data directly to the central database, NDHRS, since 2008. From January 1st 2012 veterinarians are obliged by regulations to report all use of medication to the Norwegian food authorities. This can easily be done by combining electronic journals and reporting health data to NDHRS. Since autumn 2012 more than 60% of the health data are reported directly from veterinarians to NDHRS. This has increased the number of recorded calf- and young stock health events, and reduced the lag-time from the day of treatment to the event is recorded in the central database.

Health recording for calves and young animals. Health recording for calves and young animals has improved during recent years. Gulliksen *et al.* (2009) indicated that about 60% of the health events for calves were reported to NDHRS in 2004-2007. This has increased and year 2012 was the first year with more reported health data from calves and young stock than from dairy cows. Dehorning and prophylactic treatment for parasites were the most frequent health events reported for these groups of animals (Tine, 2012). Respiratory disease is the most frequent disease in dairy calves in Norway.

Claw health. A system for recording of claw health was introduced as part of NDHRS in 2004 (Sogstad et al., 2007). The claw trimmers record whether the cow has normal (healthy) claws or if one or more of 9 claw disorders are present. More than 70,000 claw health records from 3,000 herds were reported to NDRHS in 2012. The first genetic analysis of claw health based on these data was presented by Ødegård *et al*. (2013) and Geno, the breeding organization for Norwegian Red, aim to implement genetic evaluation based on claw health data. Systems for electronic recording and direct transfer of data from claw trimmers to the central database will soon be available, based on the same system as in the other Nordic countries.

Mastitis pathogens. Bacteriological milk sample results from the mastitis laboratories have been recorded routinely into the NDHRS since 2001. This development made studies of pathogen specific mastitis possible (Whist *et al*., 2007; Haugaard *et al*., 2012).

Health data used for genetic evaluation of Norwegian Red

Mastitis and other diseases have been included in the breeding objective of Norwegian Red since 1978. In the current total merit index the relative weight on mastitis is 21% (Geno, 2013). Routine genetic evaluation of mastitis and other diseases are based on information from the health recording system. All data from 1978 onwards are available and used for genetic evaluation. Health traits have generally low heritability, so large daughter groups are needed in progeny testing to obtain reliable breeding values for these traits. In Norway a 7- trait model is used for genetic evaluation of mastitis (Svendsen and Heringstad, 2006), where clinical mastitis is defined as a binary trait within 7 defined periods of the first 3 lactations based on whether or not the cow had at least one recorded treatment of clinical mastitis. The trait "other diseases" has 2 % weight in the total merit index and includes milk fever, ketosis and retained placenta (Geno, 2013).

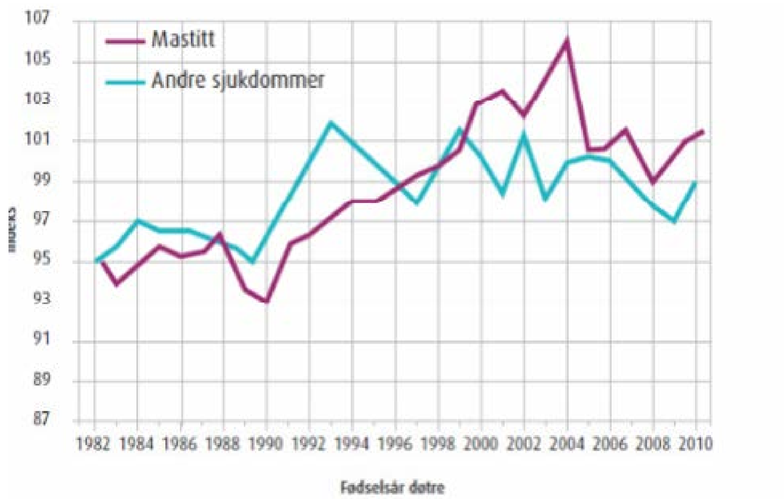

Figure 3. Genetic trends for mastitis and other diseases in Norwegian Red, given as mean index for mastitis (red) and other diseases (green) by birth year of daughters (From Geno, 2013b)

The Norwegian Red breed has been selected for improved mastitis resistance over the longest time period worldwide and represents one of few cattle populations where assessment of effects of long-term selection against mastitis is possible in a large scale. Figure 3 shows genetic trends for mastitis and other diseases in Norwegian Red (Geno, 2013b). The genetic change for mastitis from 1990 to 2010 was on average 0.4 index points per year. Despite unfavorable genetic correlations between milk yield and mastitis it is possible to obtain genetic improvement of both traits if estimated breeding values are precise (traits recorded for large enough daughter groups), and if selection is sufficiently intense, i.e. traits receive an appropriate weight in the total merit index used for selection of sires.

Results from a Norwegian selection experiment illustrate that it is possible to obtain large selection response for clinical mastitis if enough weight is put on the trait, and that selection for increased milk production will result in an unfavorable correlated increase in mastitis incidence, if resistance to the disease is ignored in the breeding program (Heringstad *et al*., 2007). After 5 cow generations the genetic difference between the 2 lines, selected strongly for high protein yield and low mastitis incidence, respectively, were about 10%-units clinical mastitis (Heringstad *et al*., 2007).

Implementation of genomic selection in dairy cattle breeding programs will not change the need for large scale recording of health traits. Genomic breeding values can be predicted with reasonably good reliability for production traits but so far with much lower reliability for traits with low heritability like health and fertility (Luan *et al*., 2009). Therefore reliable phenotypic data for large reference populations are needed for these traits.

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Challenges of health data recording - an Australian perspective

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Abstract

Australian dairy farmers record health data for 3 main reasons:

1. farm management decisions at an individual cow and a herd level;
2. to comply with farm quality assurance schemes (e.g. drug usage and withholding periods); and,
3. genetic evaluations.

There are at least 10 different farm management software packages available for recording farm data. Standard data interchange formats (DIF) are used for transferring data from the farm software to the Australian Dairy Herd Improvement Scheme (ADHIS) which uses the data for estimating breeding values. Currently, the only data uploaded to ADHIS are from herds that are enrolled in milk-recording and participation in this is relatively low (capturing approximately 46% of cows). There are many reasons for this, including a long drought through the 2000s which resulted in many farmers cost-cutting by stopping herd-testing; another is the move to in-line recording systems where data is currently not captured centrally. However, not participating in milk-recording does not have to exclude Australian dairy farmers from having health or fertility events incorporated in genetic evaluation runs. The main challenge to integrating health data from non-milk-recording herds into the central database is unique animal identification and identifying ancestry. New tools, such as cheap parentage identification could help ensure that integrity of pedigree is maintained, although there is obviously still a cost involved. The Australian dairy industry has laid the foundations for a new central database that will store and integrate data from multiple sources; the expectation is that the number of users and data providers will be much broader than for genetic evaluations. It is hoped that the new central database will enable data capture on a greater variety of traits and from many more farms than previously. Currently somatic cell count and survival are the only aspects of herd health that breeding values are estimated for in Australia. Data capture is again an issue for diseases such as mastitis and lameness. Understanding their genetic control is the first task, as lameness and mastitis may have a different genetic basis in Australia compared to housed production systems in the Northern hemisphere. For example, lameness is often a result of pressure on the hoof resulting from walking long distances.

Keywords: Data recording, genomics, mastitis, lameness.

Introduction

There are around 1.6 million dairy cows in Australia of which 46% (731,082) participate in herd-testing (ADHIS, 2012). The average herd-size is 222 and the average milk yield is 6,930 litres (ADHIS, 2012). Seventy eight percent of dairy cows are Holstein, 12% are Jersey, 5% are Holstein-Jersey crosses and 4% are red breeds (Figure 1).

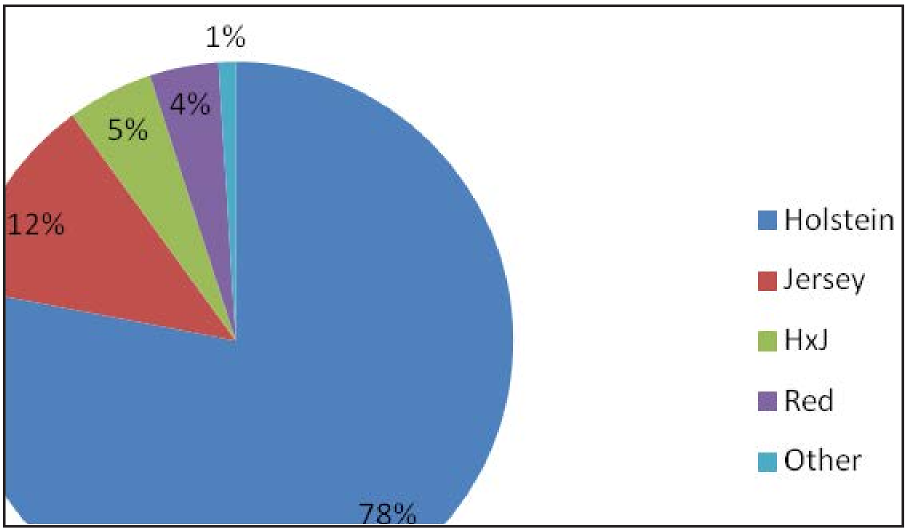


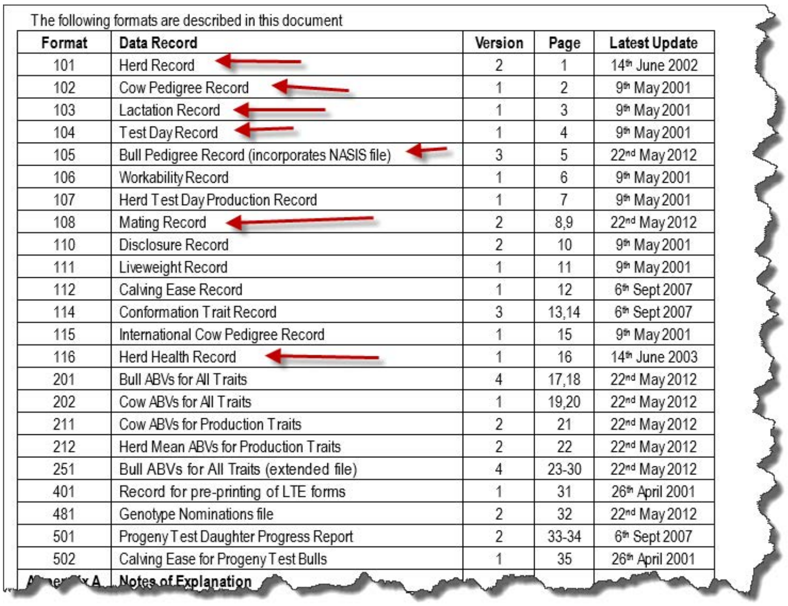
Figure 1. Breed composition of the Australian dairy population.

Recording system overview

Data Processing Centres (DPCs; that are generally part of milk recording organisations) provide data to the Australian Dairy Herd Improvement Scheme (ADHIS) for genetic evaluation purposes. There are 11 DPCs located across Australia. Farmers have an agreement with the DPC to allow their data to be used for research and genetic evaluations. Data is provided in standard data interchange format (DIF) as fixed length flat files. A snapshot of DIF format files is shown in Figure 2. For example, the DIF101 file includes information on the farm and owner, while the DIF102 includes cow information, such as animal identification, birth dates and sire identification. Approximately 1/3 of cows do not have their sire identification recorded which renders data from these cows useless for genetic evaluations. The health data DIF file (DIF116) has not been updated for around a decade, although there are plans to work on developing this file. DIF116 data are not currently used for genetic evaluations by ADHIS, as the proportion of herds recording health data is low. Currently the somatic cell count breeding value (a proxy for mastitis resistance) and longevity breeding value (for overall health and well-being) are the only "health" breeding values estimated by ADHIS.

As DIF files are transferred to ADHIS prior to a genetic evaluation run,this database can be considered to be static, but regularly updated.

The domestic farm data software providers generally comply with the DIF formats, meaning that data collected on most farms can be used for genetic evaluations. One of the main challenges for Australia is ensuring that data collected on farm actually reaches ADHIS. For example, there are logistical reasons why some fertility (mating information and pregnancy test results) does not reach ADHIS.



The following formats are described in this document

Format	Data Record	Version	Page	Latest Update
101	Herd Record	2	1	14th June 2002
102	Cow Pedigree Record	1	2	9th May 2001
103	Lactation Record	1	3	9th May 2001
104	Test Day Record	1	4	9th May 2001
105	Bull Pedigree Record (incorporates NASIS file)	3	5	22nd May 2012
106	Workability Record	1	6	9th May 2001
107	Herd Test Day Production Record	1	7	9th May 2001
108	Mating Record	2	8,9	22nd May 2012
110	Disclosure Record	2	10	9th May 2001
111	Liveweight Record	1	11	9th May 2001
112	Calving Ease Record	1	12	6th Sept 2007
114	Conformation Trait Record	3	13,14	6th Sept 2007
115	International Cow Pedigree Record	1	15	9th May 2001
116	Herd Health Record	1	16	14th June 2003
201	Bull ABVs for All Traits	4	17,18	22nd May 2012
202	Cow ABVs for All Traits	1	19,20	22nd May 2012
211	Cow ABVs for Production Traits	2	21	22nd May 2012
212	Herd Mean ABVs for Production Traits	2	22	22nd May 2012
251	Bull ABVs for All Traits (extended file)	4	23-30	22nd May 2012
401	Record for pre-printing of LTE forms	1	31	26th April 2001
481	Genotype Nominations file	2	32	22nd May 2012
501	Progeny Test Daughter Progress Report	2	33-34	6th Sept 2007
502	Calving Ease for Progeny Test Bulls	1	35	26th April 2001
Appendix A	**Notes of Explanation**			

Figure 2. A snap-shot of the data interchange format files document from an ADHIS manual. The DIF records with arrows next to them are required for genetic evaluation of health and fertility traits.

Examples of software used in Australia

There are at least 10 farm software programs that are used to record cow and health data. However, the 3 most popular are Mistro, EasyDairy and DairyData. Mistro and EasyDairy are farm software providers, while DairyData was designed and is sold by veterinarians. Therefore, in DairyData some extra attention is paid to recording of reproduction and health data.

Health data recording in Australia

Health data is voluntarily recorded in Australia. A record consists of a cow's health event and a date of occurrence. Most of the data recorded is for preventative measures such as vaccination, drenching, dry cow therapy etc. There are 340 codes that farmers can use to enter treatments and health events. Having a large number of codes may make it difficult for the farmer to decipher the correct code to use. Also, the incidences of a lot of the categories are low. For this reason, in estimating genetic parameters for health disorders, Haile-Mariam and Goddard (2010) summarised the data as:

1. Udder health including mastitis - clinical, teat injury, sore teats, black spots on teat.
2. Reproductive disorders including abortion -early (no new lactation), ovarian cysts, uterine prolapse, uterine infection / metritis, uterine irrigation, anoestrus-inactive ovaries, retained foetal membranes, deformed calf.
3. Leg problems including dislocated hip, downer cow, paralysis at calving, arthritis, lameness.
4. Data on all disorders including all recorded treatments (excluding dry cow therapy, vaccination and drenching) and disease events to investigate whether there is a genetic component to overall disease resistance. A summary of health events recorded in 2007 and 2008 is presented in table 1. Additionally heritability estimates are also presented, which are consistently low, but comparable to other studies of similar data estimated in other countries.

Table 1. Incidences of health disorders and heritabilities with standard errors in brackets (adapted from the study of Haile-Mariam and Goddard, 2010).

	Udder		**Reproductive**		**Leg**		**'All disorders'**	
Year	**2007**	**2008**	**2007**	**2008**	**2007**	**2008**	**2007**	**2008**
Herds	91	112	99	154	45	58	203	225
Records	18291	14928	20810	19874	9695	7192	40256	45356
Incidence	0.142	0.129	0.056	0.058	0.053	0.055	0.31	0.214
Heritability	0.035 (0.009)		0.006 (0.004)		0.013 (0.009)		0.016 (0.004)	

Capturing extra data

Currently, Dairy Futures CRC in conjunction with ADHIS and Warrnambool Vet Clinic are collaborating on a project to increase the capture of fertility data (mating information and pregnancy test results) that would not normally be uploaded to the ADHIS database. It is expected that data for other traits, such as health and disease, capture of data will also increase as a result of this project. With some effort it should be possible increase the amount of data available to estimate breeding values.

Currently, the proportion of herds contributing valid fertility data to genetic evaluations is fairly low. However, this varies by state. For herds where data was provided to ADHIS (via their Data Processing Centre; DPC), 49.8% of Victorian herds have some mating data used for fertility ABV calculation in 2008, 2009 or 2010. The percentage of herds with mating data used in ABV calculation in other States is lower. There are some logistical reasons why the proportion of data is low, for example incomplete data capture from some of the herd-management software.

The current status of software systems is as follows:

- MISTRO - data transfer with most DPC's is working well
- EASY DAIRY / DAIRY DATA / DAIRY ID - We have tested the manual transfer of fertility & mating data from Farm to DPC to confirm the process will work. Once the fertility & mating data reaches the DPC it is then routinely transferred to ADHIS. Testing has now been completed and automation of data transfer has recently started for Easy Dairy users. Early results have been most encouraging with up to 9 years of farm fertility data with over 9 000 records moved from a single farm to DPC with the click of the on-farm software button.
- VETERINARY HELD FERTILITY DATA - A partner in the project is Warrnambool Veterinary Clinic, who own the popular Dairy Data software used by many veterinary practices and some farms to closely monitor fertility levels. Pregnancy test data is important because it can be used to calculate pregnancy rate, which is one of the traits in the multi-trait model. We can split the vet clients data into those herds that are herd testing and those herds that are not.
- FULLY AUTOMATED DAIRY PLATFORMS - High tech platform systems will be also studied to see what current data can be transferred from these systems in a suitable format to the Herd Improvement DPC platforms. These high tech systems are collecting massive amounts of cow and herd data 365 days of the year so it becomes important to see how we can include their data and make full use of their data .

By comparing exactly the same herds over the same period of time, an extra 18% of cows had valid fertility data in March 2013 compared to August 2012.

New central data system

In Australia, data relevant to farms is collected by multiple private businesses using many different systems and formats. There is a lot of duplication with the same information being entered in multiple systems and farmers are responsible for coordinating information from different sources. Information needed for day-to-day management and strategic decisions of the farm business is often not readily accessible. For this reason, a Central Data System (CDS) has been proposed for Australia. In contrast to the ADHIS database, the CDS is live rather than static. The overarching objective of the CDS for animal performance data is to provide a unified, authoritative dairy data system for supporting on-farm decision making, providing data for improved genetic evaluation, herd improvement and industry analysis. The key beneficiaries of the CDS will be Australian dairy farmers and organisations that innovate in response to the improved data-infrastructure. Its purpose is to enhance the adaptive capability of the dairy supply chain to improve farm margins and growth opportunities. The CDS is currently in the planning phase, with deployment expected in 2017.

Genomic reference population

One risk of replacing progeny-testing with breeding schemes that screen large numbers of young bulls and only select a small number of these for widespread use, is that fewer bulls will be added to the reference population on an annual basis than in the past. This would decrease the reliability of genomic prediction as the distance between the current dairy population and the majority of animals in the reference population increases (Lillehammer *et al.*,2010). Countries with small populations may be more affected by this issue than larger populations (McHugh *et al*., 2011). Considerable effort has gone into increasing the size of current reference populations and this effort must continue to ensure reference populations remain relevant to selection candidates. One of the strategies used to increase reference populations is to share genotypes with other countries.

Genotyping of cows is another way that the reference population can be grown. Genotyped females need to be incorporated cautiously, as there could be a risk that some of them are preferentially treated and therefore their phenotypes could be biased. Instead, directly targeting a group of randomly selected cows may be more beneficial. In Australia, the size of the male reference population is around 3000 Holstein males, so adding genotyped females to the reference population could improve the reliability of breeding values.

Recently, the Australian Dairy Futures Cooperative Research Centre's 10 000 Holstein Cow Genomes project and Jer-nomics project embarked on collecting DNA samples and genotyping 10 000 Holstein and 4 000 Jersey cows (from commercial herds). In April 2012, this information has become part of the Australian reference population. This has led to a 4-8% improvement in the reliability of breeding values depending on trait. Table 2 shows the increase in reliability of genomic breeding values for 437 young Holstein bulls achieved by adding close to 10 000 cows to the reference population.

Table 2. The reliability of genomic breeding values of 437 young bulls when bulls only were included in the reference population and when cows were also included

Trait	Bulls only	Bulls + cows	Change
Protein	54	61	7
Fat	54	61	7
Milk	54	61	7
Survival	30	36	6
Fertility	33	37	4
Somatic cell count	43	51	8
Milking speed	49	53	4
Temperament	49	53	4
Likability	49	53	4
Mammary system	39	44	5
Overall type	38	44	6
Udder depth	38	43	5
Udder texture	33	38	5

The 10 000 Holstein Cow Genomes project and Jer-nomics project were one-off genotyping events. We now intend to establish a more permanent genomic reference population that comprises around 100 herds.

Having the entire sequences of bulls may help to increase the accuracy further. The idea behind sequencing key ancestors of cattle breeds, is that we will have the causative mutations in the data set, i.e. we will be able to capture more of the genetic variation in a trait. The 1 000 bull genomes project has started with an aim to provide researchers with a large database for genomic prediction and genome wide association studies in all cattle breeds (*http://1000bullgenomes.com*).

Genomic reference populations may assist with difficult to measure traits, such as health, as efforts to record and evaluate these traits can happen in a small reference population and the benefits used by the entire population i.e. prediction equations are based on cows in the reference population that have phenotypes on a range of traits, possibly also including health traits.

Conclusions

Health data for dairy cows is sparsely recorded in Australia. However, through our endeavours to increase the amount of data collected for fertility, it is anticipated that more health data will also become available. A new central data system is planned which should help by connecting farmers with their data. Prediction of breeding values can be enhanced, especially for difficult to measure traits, such as health traits, in dedicated resource populations that are genotyped.

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Lillehammer M, T.H.E. Meuwissen & A.K. Sonesson (2011) A comparison of dairy cattle breeding designs that use genomic selection. J. Dairy Sci. 94: 493-500.

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Use of automated systems for recording of direct and indirect data with special emphasis on the use of MIR milk spectra (OptiMIR project)

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Abstract

A current tendency in developing tools to support farm management is to make use of advanced sensors closely associated to animals, facilitating the collection of large quantities of data ideally at a low cost without perturbing the animal itself. On a dairy farm level, sensors measuring milk conductivity or pedometers measuring mobility are often cited as examples. This introduces the concept of "precision livestock farming" where a given "bioresponse" captured by a "biosensor" allows the creation of feedback to adjust the "bioprocess". Such on-farm systems are often restricted to a given farm and they are mostly strictly separated from standard performance recording systems. In dairy cows, a particular rich source of information to detect a "bioresponse" is milk and its (fine) composition. Standard milk analysis undertaken in milk recording schemes by mid infrared spectroscopy (MIR) generates spectral data that reflects the milk characteristics. Therefore, spectral data directly reflects the metabolic (e.g., energy balance) and health (e.g., udder health) status of the cow. The use of MIR spectral data to predict fine milk components (e.g., fatty acids) is now becoming commonplace. However the use of MIR spectral data could provide an even more direct method to assess the "bioresponse" in relation to health, fertility, feeding, milk quality and even rejection of pollutants. For this reason, 12 EU milk recording organizations and milk laboratories together with 6 EU research groups have joined forces to develop the North-West Europe INTERREG IVB Project OptiMIR (*www.optimir.eu*). As a first step to use spectral data for developing decision support tools, the project includes the development of methods to standardize spectral data generated by various apparatuses in different laboratories. Through the OptiMIR project, health indicator traits from milk analysis either through the prediction of milk components (i.e. lactoferrin) or through the direct assessment of the health status of the cow (i.e. clinical mastitis) will become available. These data can then be generated in routine milk recording and can be stored in a central database. Because generating MIR data at the on-farm level is still difficult and expensive, the use of near infrared (NIR) spectroscopy is currently also under investigation by other groups. For a comprehensive use of fine milk composition, as for other automated sensors, the optimum would be a close and bi-directional interaction between in-line on-farm systems and central databases in order to contribute to the successful implementation of powerful health monitoring systems and decision support tools.

Keywords: milk composition, milk spectra, indirect health data.

Introduction

The use of direct milk yield meters and similar sensors in robotic milking units within fully computerized milking parlours linked to farm computers and herd management systems, is often seen as a classical case of "precision livestock farming" in dairy cattle. A current tendency in developing tools to support farm management is to make use of advanced sensors, often closely associated to animals, facilitating the collection of large quantities of data. On dairy farms, sensors measuring milk conductivity or pedometers measuring mobility are often cited as examples. A very comprehensive review was recently published by Rutten *et al.* (2013). The concept of "precision livestock farming" can then be summarized where a given "bioresponse" is captured by a "biosensor", which allows the creation of feedback by using the collected data in an appropriate model to adjust the "bioprocess". (e.g., Aerts *et al.*, 2003). Figure 1 shows a typical set up.

Based on their review Rutten *et al.* (2013) distinguished four levels of use of sensor data: I) technical, II) data interpretation, III) integration of external information and IV) decision making. They identified that in dairy cattle the available systems are generally poor when considering levels III) and IV).

In contrast to many other species and production systems, dairy farming has also another, well-developed historic dairy herd management approach which relies on classical performance recording, mostly supervised by technicians, on centralized milk testing and on centralized databases (ICAR, 2012). These data are also the primary source of dairy cattle data used in animal breeding (Interbull, 2012). Recent research has extracted additional information from these performance data (e.g. Mayeres *et al.*,2004) and to improve advisory tools based on standard performance recording data.

Currently the uses of on-farm computers based systems and centralized performance-recording based tools are considered as two opposite "worlds" for dairy cattle management. However, in practice, the use of automated systems for

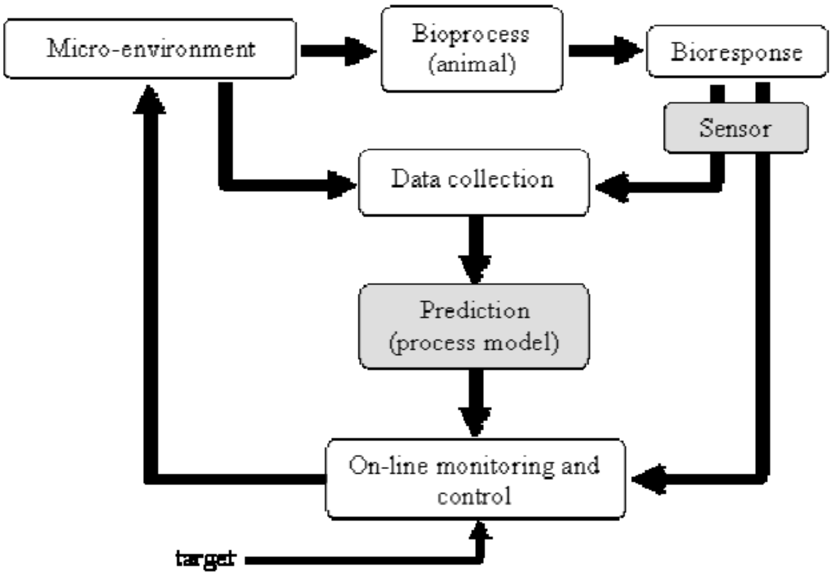

Figure 1. Typical set up of model-based process control (from Aerts et al., 2003).

recording of direct and indirect data is becoming very important, especially for novel traits. An additional source of information could be available by maximizing the potential of already existing off-farm analysis tools. Only through the availability of these novel traits research and development are possible leading to their application in management and breeding. The present paper focuses on the use of milk composition and especially the use of mid infrared (MIR) milk spectra as a rich source of new information. Particular emphasis will be given to the new OptiMIR project (e.g. Massart, 2011) its rationale for the innovative collection of health data, the use of this data for research, and the dissemination of the results of this research to the farmers.

Milk composition and animal health

It is well known that milk composition, and in particular, milk fat, protein content and fatty acid profiles may be significantly altered due to a variety of factors, one being metabolic or health status of the animal. Therefore changes in milk composition are considered potential indicators for the status of a given animal (e.g., Hamann & Krömker, 1997). Milk becomes a potentially particular rich source of information if the "bioresponse" in milk can be captured through its (fine) composition. Standard milk analysis undertaken through milk recording schemes by mid infrared spectroscopy (MIR) generates spectral data that reflects the overall milk composition. The prediction of animal health from milk MIR spectra can be through two approaches:

1. first predict specific milk components (indicator traits) from milk MIR and then, using regression models including these milk composition traits, predict animal health, or
2. predict animal health directly from the milk MIR (Figure 2). Alternatively indicator traits as defined in approach (1) are currently studied as alternative and additional sources of information for health traits as fatty acids in milk for fertility

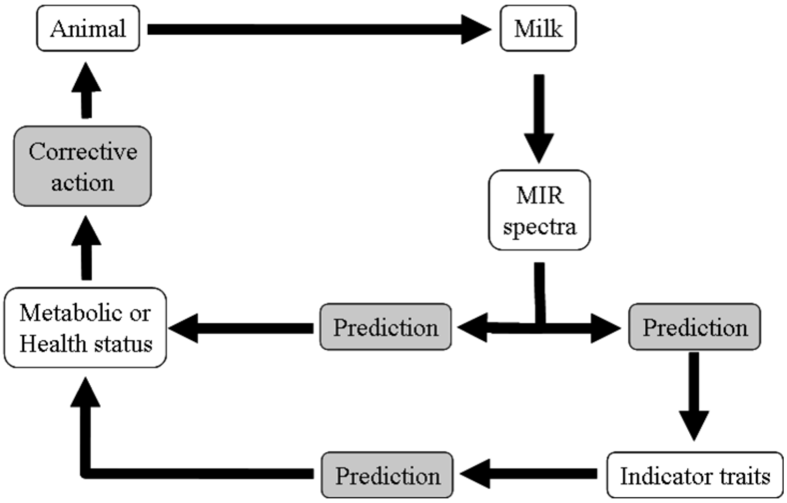

Figure 2. Pathway for direct and indirect prediction of metabolic or health status traits.

(e.g. Bastin *et al.*, 2011). The use of somatic cell count in conjunction with mastitis is another well-known example even id somatic cell count is a component not predicted from MIR spectra.

Predicting health relevant milk components from MIR spectra

A powerful tool to detect milk composition is the use of MIR spectra to determine fat, protein, urea and other major components. Soyeurt *et al.* (2006) also proved that minor milk components can also be predicted from MIR spectra as long as a calibration data set can be created with reference values that reflect the underlying variability and the variation in the component under investigation is reflected in variability in the associated spectrum.

A well-known example of the indirect use of milk composition is the detection of ketosis. Research showed the feasibility of predicting of β-hydroxybutyrate (BHB) and acetone in milk from MIR (de Roos *et al.*,2007). However de Roos *et al.* (2007) also reported, which was later confirmed by van der Drift *et al.* (2012), that indirect detection of subclinical ketosis with BHB and acetone was associated with large prediction errors. A contributing factor to reduced accuracy of prediction of animal health from MIR predicted indicator traits, is the accumulation of prediction errors as shown in Figure 2. In this context the prediction errors reported by de Roos *et al.* (2007) remained rather large and as shown in their results the relationships between predictions and reference values were not clearly linear.

Similarly novel indicator traits for animal robustness or udder health were recently made available [i.e., lactoferrin, (e.g., Soyeurt *et al.* 2007)]. Again even, when predictions of the traits can be made reasonably precise the accurate relationship between these derived traits and animal health is more difficult. Based on these two finding (avoiding cumulating estimation errors), the new direct approach, featured inside the OptiMIR project, was developed.

The OptiMIR project

The basic novel scientific idea underpinning the OptiMIR project is that direct use of MIR spectral data could provide more informative "bioresponse" to relate to health, fertility, feeding, milk quality and even rejection of pollutants. For this reason, 12 EU milk recording organizations (MRO) and milk laboratories together with 6 EU research groups have joined forces to develop the North-West Europe INTERREG IVB Project OptiMIR (*www.optimir.eu*) as equal partners around the topic of direct use of MIR spectra for management use. The first novel component of OptiMIR is therefore that this project was built around a clear path from the acquisition of data towards to the dissemination of results, this last point becoming a major priority in many European research framework projects. A second novelty of this project is the concept of management information traits (MIT). A good example is that instead of trying to use an indirect trait as lactoferrin with an a priori cut-off level, a directly useful MIT as "probability of having a subclinical mastitis" was defined. As these MIT are directly describing status, they can be easier used in a decision making tool.

In order to use directly MIR spectra, in a first step the OptiMIR project includes the development and use of methods to standardize spectral data generated by various apparatuses (Grelet *et al.*, 2012) across spectrometers used in the project. The third originality of the project is the creation of a transnational research data base that allows collating relevant data from different partners in order to increase its relevance for research and development. Respecting the original data ownerships, this data base will also continue to exist and the stored data, at least partially, potentially contribute to further projects which can in exchange use the OptiMIR partnership as dissemination channel. Finally, by developing expertise and some joint tools, OptiMIR will help create and disseminate the acquisition of health indicator traits from MIR milk analysis either through the prediction of milk components or through the direct assessment of the health status of the cows. These data can then be generated in routine through milk recording and can be stored in their central databases.

Current status of interaction between on-farm and off-farm systems

Very early with the first sensors (classical milk yield meters) becoming available performance recording agencies have started to develop ways to recover this on-farm data. Basically two strategies were pursued. The first strategy is the development of own on-farm management systems, the PCDART program (Dairy Records Management Systems, Raleigh, NC, USA) being an example. Unfortunately this limits the choice for herd owners and is considered not necessarily optimal by them because of their preference for another system. A second strategy was to develop methods to export the data from the farms to central databases independently from the manufacturers of the different on-farm systems. Again the natural limit that appeared was the need or, unfortunately, the lack of common exchange standards. Therefore in many countries different customized tools are under development or already deployed to get access to this data. In the Walloon Region of Belgium the Walloon Breeding Association (AWE) is currently implementing Ori-Automate, a tool developed in collaboration between France Conseil Elevage (FCEL) and Valacta (Dairy Production Center of Expertise Quebec-Atlantic, Canada) based on Valacta's Trans-D software. Ori-Automate is a bi-directional interface tool that links farm management software to performance-recording databases, being multi-manufacturer and able to be pluged-in directly into on-farm data bases (Saunier *et al.*, 2012).

There are two other hidden advantages in a bi-direction approach for health data acquisition. First on-farm sensor-based tools need to access basic animal data in order to operate. By linking up with the recording agencies farmers no longer need to enter this information, potentially even several times, as it is readily available in the central databases. This obviously limits potential errors especially in animal identification and improves health data quality. Also current on-farm systems when provided by different manufacturer are seldom designed to exchange data. By communicating with Ori-Automate or similar systems, the exchange between on-farm tools is, indirectly, established which will improve quantity and quality of health data.

Use of on-farm data and interaction with OptiMIR

Because generating MIR data is still difficult and expensive, alternative techniques have been proposed (Rutten *et al.*, 2013). The use of near infrared (NIR) spectroscopy is also under investigation (e.g., Nguyen *et al.*, 2011) to relate the generated spectra to milk composition. Initial results are promising; however off-farm MIR measurements are still more reliable and, as shown in the OptiMIR project, they can be harmonized and standardized among apparatuses. Stability of on-farm sensors in general over time is still uncertain and rarely reported. Experience with MIR showed that this could be an issue that has to be considered by manufacturer of sensors. For a comprehensive use of fine milk composition, as for other automated sensors that are generating relevant data, the optimum would be a close and bi-directional interaction between in-line on-farm systems and central databases. These databases should contain also data obtained by off-farm methods (e.g. MIR spectra) that allow to benchmark and correct on-farm systems. Optimal would be the use of both data sources for health monitoring system. By their open conception the tools developed in OptiMIR can take advantage of additional on-farm measurements as soon as they become available. It can also provide useful feedback as soon as a bi-directional exchange

Conclusions

Currently, many automated sensors are used on-farm to record health related data. Interaction between these automatic sensors, off-farm systems and centralized databases is still weak and highly depending on powerful data exchange protocols and tools. Off-farm systems based on MIR spectral data are currently being developed inside the OptiMIR project. This project has a certain number of specific features including the close association between MRO and scientific partners, the building of a transnational data base and the joint development of advisory tools. By their open conception tools developed in OptiMIR can take advantage of on farm measurements, but can also provide useful data back to farms as soon as bi-directional data exchange can be organized. Finally the use of automated systems for recording of direct and indirect data on-farm and off-farm will be a major source of health relevant data in the future.

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Use of health data for research

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Abstract

Animal health issues are of increasing importance to all animal breeding sectors, by raising health and welfare issues and causing major production costs, but also to citizens, by affecting possibly their own health and lifestyle choices. So far, traditional selective breeding approaches have been applied successfully to enhance production and reproduction traits; but the inclusion of animal health related traits are scarcely considered because of a clear lack of easy measurable and relevant health phenotypes and associated genetic markers which could be integrated in running breeding programs. Though, there have been numerous studies in the past showing evidence of genetic variability of responses to various diseases of economic interest. New opportunities have been arising thanks to major advances in animal genomics and related technologies. Most research strategies are now developed, combining structural, population and functional genomics approaches. The objectives of this research studies using health data are two-fold: 1-identification of genes, gene products and regulatory networks involved in host pathogen interactions which could be used in selection and 2- better understanding their functions and the underlying mechanisms. Applications of such research using health data may cover areas like vaccine development, improved diagnosis and treatment, epidemiology, in addition to breeding. Likely, integrated strategies using several approaches will be more successful to combat diseases. Thus, research and development aiming at understanding health related mechanisms and implementing integrated strategies for improved health of livestock requires large use of recorded health data, collaborative multidisciplinary programs and efficient technology transfer between research and industry. Improving recording systems of health data would benefit both research and industry in an ultimate goal of breeding more "robust" animals for a sustainable production.

Keywords: Animal disease, animal health, genomics, health data, phenotypes, recording.

Introduction

In the context of intensification and specialization of all livestock sectors, animal welfare and animal health are given an increased emphasis in current breeding objectives. Indeed, animal health issues are raising health and welfare problems but also causing major production costs, but also to citizens, by affecting possibly their own health and lifestyle choices. So far, traditional selective breeding approaches have been applied successfully to enhance production and reproduction traits; but the inclusion of animal health related traits are scarcely considered because of a clear lack of easy measurable and relevant health phenotypes and associated genetic markers which could be integrated in running breeding programs. To gather all this necessary information, acquisition of relevant health data is crucial and can be organized and exploited at different complementary levels, as presented in this paper.

Need of health data for an integrated approach of disease control

Clearly, animal health issues may be better tackled in animal breeding by developing integrated approaches than by applying single disease control strategies. Integrated animal health management involves both prevention and cure of diseases, potentially important decisions on the animals, like selection, culling, and developing vaccination programmes. It concerns also the pathogen and its environment when applying chemotherapy or biosecurity measures.

Integrated disease control therefore comprises important steps with potentially major effects for the animal populations and their environments. Thus, it needs a prior critical evaluation of the disease targets and the optimal control means, requiring necessarily health data in quality and quantity.

Need of health data for validating disease resistance phenotypes

Among most promising approaches for prevention and control of animal diseases are - breeding for disease resistance and - development of novel vaccines. Developing breeding for disease resistance strategies for any given disease requires jointly identifying genetic markers and underlying mechanisms related to the disease resistance phenotypes. And there is, to date, a clear lack of disease phenotypes. This is a problem, well known as the "phenotypic gap", but which appears as an even more important bottleneck for health related traits as it is often more difficult to find easy to measure and relevant health traits.

An example of a classical approach to identify the desirable set of disease resistance traits is given. This example applies to a parasitic disease in poultry, but can be transposed to any other disease and animal species. Implementation of selection for disease resistance to coccidiosis is hampered by a lack of easily measurable, repeatable and relevant disease phenotypes. A two-fold implementation has been processed: from large to small set of phenotypes, and from experimental to commercial lines (Figure 1; Hamzic *et al.*, 2014).

Firstly, a large panel of disease phenotypes has been measured and analysed (repeatability, variability, correlations...), on experimental chicken lines showing large individual variability for the response to coccidiosis. Secondly, most pertinent measures have been validated, in pilot study, then in large scale challenge of commercial animals. Ideally, this small set of validated phenotypes, which can be automated, will be sufficient to exploit the genetic variability for further selection.

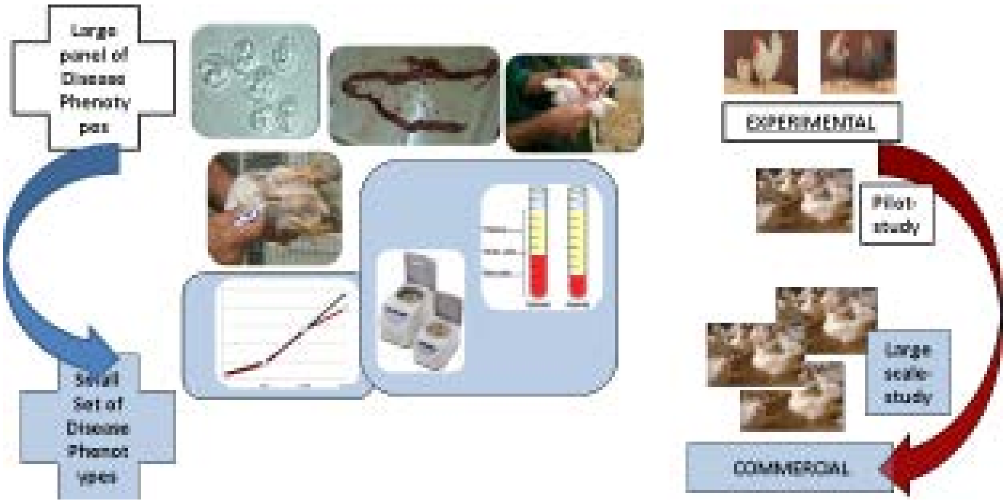
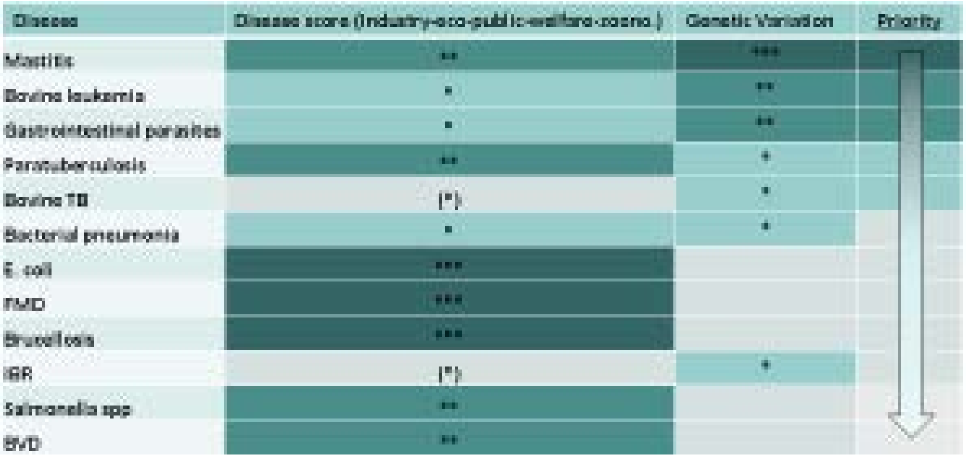


Figure 1. A classical approach to validate disease resistance phenotypes, from a large panel to a smaller set, from experimental to commercial.

Need of health data for breeding for disease resistance. For which diseases?

Prior starting measuring a number of health related phenotypes to initiate a breeding for disease resistance strategy, a critical evaluation of the diseases is needed. A pertinent choice will look first at a "genetic variation" score, which includes 1- a well documented genetic variability for the diseases of interest and 2- the availability of genomic tools to measure and further exploit this variability. This latter criterion is likely to evolve fast as genomic tools become more sophisticated for each species and more information becomes available. But to prioritize diseases, once should consider also other criteria, without which practical interest of developing a breeding strategy is minimal, such as industry concern, economic impact, public concern, threat to food safety or zoonotic potential, impact on animal welfare…, making up a "disease score". The "genetic variation" score and the "disease" score" may be combined to establish a list of "priority diseases" (Figure 2; Davies *et al.*, 2009). This



Disease	Disease score (industry-eco-public-welfare-zoono.)	Genetic Variation	Priority
Mastitis	**	***	
Bovine leukemia	*	**	
Gastrointestinal parasites	*	**	
Paratuberculosis	**	*	
Bovine TB	(*)	*	
Bacterial pneumonia	*	*	
E. coli	***		
FMD	***		
Brucellosis	***		
IBR	(*)	*	
Salmonella spp	**		
BVD	**		

Figure 2. Priority list of infectious cattle diseases, with disease scores taking into account industry and public concern, economic and zoonotic potential, animal welfare impacts. (Simplified from Davies et al., 2009).

ranking of diseases needs of course to be updated regularly within our changing environments and adapted to different international contexts if needed. This approach can very well be used to rank diseases from other perspectives than breeding, like in terms of disease control strategies.

Idntification of genetic markers and underlying mechanisms of health traits

Once 1- disease resistance phenotypes have been identified and validated, these well characterized phenotypes are essential to identify 2- genetic markers and 3-underlying mechanisms, in a process of developing breeding for disease resistance strategies (Figure 3).

Though efforts in genome sequencing and SNP discovery are still needed, denser chips are now developed, allowing, through whole-genome association analysis, the identification of genetic markers associated with disease traits (e.g., identification of SNP associated with resistance to paratuberculosis in Holstein cattle, figure 4; Kirkpatrick *et al.*, 2011). Making use of high throughput technologies, individual genome sequences allow now the identification of the causal mutations associated with health traits and the generation of SNP which can be used in population-wide studies in order to identify animals with improved health related traits (Bai *et al.*, 2012). This new refine knowledge in the genetic control of health traits can bring additional understanding to a "black box" genomic selection process of livestock and can turn into novel tools for control and diagnostic of animal diseases (Figure 3).

The same advanced genome enabled technologies offer new opportunities to better understand regulation of the disease process, (e.g. immune responses, molecular dialogue between the host and the pathogen) by greater insight into transcriptomics and now sequencing of transcripts. Whereas QTL approaches aim at identifying mutations underlying genetic variations seen between hosts for the given health traits, transcriptomics approaches aim at identifying genes being transcribed in a particular tissue at a particular time of the disease process. Thus, both are essential

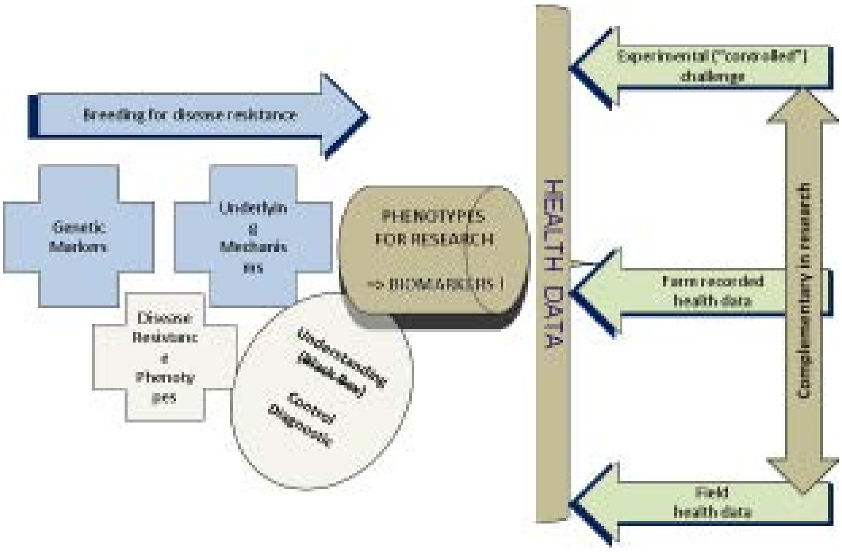


Figure 3. Use of health data, from complementary sources (experimental, farm, field), as novel phenotypes for research (indentifying genetic markers, underlying mechanism, disease resistance phenotypes).

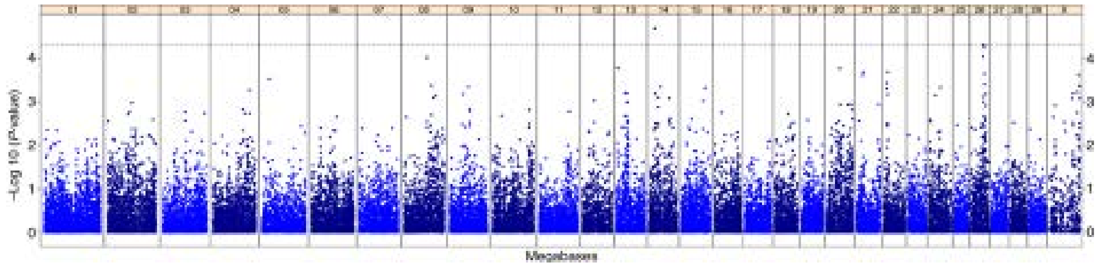


Figure 4. Whole-Genome association analysis of susceptibility to paratuberculosis in Holstein cattle (Kirkpatrick et al., 2011).

and complementary approaches, giving tools to dissect, understand and utilize host genetic variation, using health data towards identification of genetic and functional biomarkers, the ultimate goal (Figure 3).

Need of using complementary sources of health data

Because of the obvious need of developing integrated strategies to control diseases, not only complementary tools are needed (see above), but also complementary sources of large-scale health data are necessary, from 1- experimental "controlled" challenges, 2- farm and 3- field levels (Figure 3).

Experimental "controlled" challenges may allow the initial screening of health phenotypes (see § "Need of health data for validating disease resistance phenotypes"), as many measurements necessitate in the first steps to deliberately infect animals with control doses for instance. These health data will be highly complementary to measurements obtained in farms or accessed from the field by collecting veterinary records or history of naturally infected animals' episodes.

Use of large scale multi farm data will give the unique opportunity to have access to health data obtained in different environments, husbandry or management conditions, allowing to make use of differences to gain in standardization of the health phenotypes of interest. Ultimate goal, of prime interest for the breeders, is identifying health data as indicators of robustness, i.e., the ability of animals to cope with variable environments. Thus, having access to detailed health records and animal performances from a variety of environments, using these production traits as proxy for health is likely the only way to make a significant step towards pertinent definition of robustness and identification of usable markers for breeding. Maximizing animal resources can be then achieved through trusted collaboration between actors and facilitated dialogue between disciplines.

Field health data are often found to be complementary to farm recorded data, for example by making use of outbreaks happening in the field with health data recorded in cohorts in farms. Such complementary source of health data is applied on the PRRS (Porcine Reproductive and Respiratory) syndrome in pigs exampling a stakeholder cooperation with data used from cohorts of growing pigs from different breeding companies (Boddicker *et al.*, 2012). Epidemic field data can be also envisaged to be more efficiently used as done so far, for example to calibrate genomic predictions, as in the case of bovine tuberculosis (Bishop *et al.*, 2012). Finally, field health data from animals exposed to recurrent disease threats or extreme environments, like in developing countries, offer often underexploited richness in terms of reservoir of phenotypes and genotypes.

Best use of health data by collaborative research

Significantly advances in knowledge in the field of animal health can best come from use of health data from different sources, but also from different species, combining multi-disciplinary expertise and eventually multi-national projects. Such an example of collaborative research aiming at sharing tools and optimizing animal resources and health data has been conducted in a large animal disease genomics network (*www.eadgene.info*).

As an illustration, an original joint research programme on transcriptomic studies on mastitis in ruminants has been conducted, combining heterogeneous microarray data realized with different ruminant host species and infected with different mastitis-causing pathogens (Table 1; Genini *et al*., 2011). For the first time, a meta-analysis combined experiments and time points to create the four main responses to mastitis infection. Such an analysis showed that it could fit well with the high heterogeneity of health data representing the different biological systems, being a proof of principle for studies combining health data from diverse sources. But most importantly, the results reinforced previous findings but also revealed several new

Table 1. Combination of experiments and time points to create the 4 main responses to mastitis infection (from Genini et al., 2011).

	Time after infection							
Experiment #	**2 h**	**3 h**	**6 h**	**8 h**	**12 h**	**24 h**	**36 h-72 h**	**72 h**
1A: *E. coli* in cattle (*in vivo*)			{1} I, II, IV		{2} I, IV	{3} I, III, IV		
1B: *S. aureus* in cattle (*in vivo*)			{4} I, IV		{5} I, IV	{6} I, II, IV		
1C: *S. aureus* in cattle (*in vivo*)					{7} I, II, IV			{8} I, III, IV
2: *S. uberis* in cattle (*in vivo*)							{9} I, IV	
3: *S. aureus* in cattle macrophages (*in vitro*)	{10} I, II, IV		{11} I, III, IV					
4: *S. aureus* in goat (*in vivo*)					{12} I, II	{13} I, III		
5: *S. aureus* in sheep dendritic cells (*in vitro*)		{14} I, II		{15} I, III				
6: *S. aureus* in goat (*in vivo*)						{16} I		

http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3118214/table/T2/?report=objectonly

Combination of microarray data from a total of 6 different experiments and 16 different time points {in parentheses} to analyse 4 different responses to mastitis infection: (I) overall response, (II) early stage response, (III) late stage response, and (IV) cattle-specific response.

themes, including the involvement of genes and pathways that were not identified in individual studies, using limited set of health data. These results pave the way for the development of novel therapeutics and vaccines for mastitis in ruminants.

Combination of microarray data from a total of 6 different experiments and 16 different time points {in parentheses} to analyse 4 different responses to mastitis infection: (I) overall response, (II) early stage response, (III) late stage response, and (IV) cattle-specific response.

What are the best health data?

Best health data for general health issues are likely those which can allow the best means of describing host genetic effects. However, the following dilemma will be soon faced, namely, the most precisely defined health phenotypes will allow a better detection power of genetic factors involved in the related health traits, but as shown previously, these narrowly defined health phenotypes are often the most difficult to measure and collect.

Collection of health data thus needs to be optimized, also by carefully assessing an optimum timing for the different measures. Advance knowledge in the kinetics of different process of the host responses (e.g. immune responses) and the individual variability of the host in mounting the responses will have to be acquired (e.g. in prior pilot studies) to make best use of health data.

Best health data may be also indirect trait data, for example in case of stress induced immune suppression like some subclinical mastitis cases, where collecting stress data might be as informative as direct pathological data.

Prospects for using health data

Several research areas needing health data are emerging or finding new prospects with the availability of high throughput technologies. Developing novel vaccines is one of them: ideally, integrated approach to disease control aims at identifying genes responsible for the genetic variation, both of disease resistance and of response to vaccination. Such research is developed for viral diseases in cattle like bovine respiratory disease (Glass *et al*., 2012) and can provide novel tools to select more resistant animals and more efficient vaccines. If early step of vaccine development may use controlled experiment data, further measures of vaccine effectiveness will necessarily need sufficient field health data.

Another emerging field is the analysis of the microbiota. There is increasing interest in studying not only the interactions between the host and the pathogen, but also to include the microbiota in this continuous interactive process. Measuring and analyzing microbiota data, as an integrated picture to monitor the health status of animals will become essential, especially for gut or respiratory health.

Conclusion

Research and development aiming at understanding health related mechanisms and implementing integrated strategies for improved health of livestock require large use of recorded health data, collaborative multidisciplinary programs and efficient technology transfer between research and industry.

If we look towards innovation, the key challenges for collecting and using health data will be likely among the following recommendations:

- Integrate health related traits in existing multi-trait selection programmes,
- Aim to use the same health traits for breeding and management,
- Develop cost effective tools to analyse field disease outbreaks and develop predictive diagnostics,
- Support initiatives integrating genomic approaches to vaccine development,
- Facilitate research including collaborations between animal health research institutions, commercial breeding and pharmaceutical companies,

with a common objective of joint acquisition of health data in order to generate new knowledge and innovation.

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Session 3

Logistics of recording of health data (standardization and data exchange, data security, data ownership, database,..)

Standardization of health data. ICAR guidelines including health key

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Abstract

Systematic improvement of animal health requires knowledge about the status quo and reliable measures to characterize it. In dairy herds, health monitoring has gained importance to ensure sustainable and cost-efficient milk production in accordance with public expectations. In this context, standardized recording of health data is essential for comparability and interpretability of health-related analyses, implying the need for generally accepted and clear guidelines.

To assist implementation of health monitoring and convey harmonization, the ICAR Functional Traits Working Group has compiled the ICAR guidelines for Recording, Evaluation and Genetic Improvement of Health Traits, which were approved in June 2012. Disease diagnoses and observations of impaired health can be classified as direct health data, providing the basis for targeted approaches to improve the animal health status. Data sources need to be taken into account because of their impact on information content and specificity. The key for health data recording is characterized by a hierarchical structure that makes it possible to record on different levels of detail and includes comprehensive recording options with coverage of all organ systems and types of diseases. Important features are compatibility with other recording systems and broad usability as a reference regardless of specific intentions and contexts of health data collection. Input can range from very specific diagnoses of veterinarians to very general diagnoses or observations by producers, and the unique coding of clearly defined health incidents minimizes the risk of misinterpretations and facilitates analyses of different types of health data. The overall quality and success of health monitoring is substantially influenced by appropriate use of standards and available recording tools, implying the need for tailored support particularly in the implementation phase. In integrated concepts, specific qualifications of professions can be used synergistically to further standardize recording of health data and thereby benefit efficiency of animal health improvement on farm and at the population level.

Keywords: direct health data, veterinary diagnoses, integrated health monitoring concepts.

Introduction

Animal health aspects have gained enormous importance in the livestock sector and its public reputation. Society is increasingly requesting transparency with regard to production conditions along the whole food chain, with particular demands for high standards of animal welfare and health (Egger-Danner *et al.*, 2012). Furthermore, the dairy industry has recognized that with the increasing progress in production traits, the health of the dairy cow is increasingly challenged, and the ability to cope with these challenges may impact sustainability and profitability of milk production. Accordingly, more and more weight is placed on collection and use of health- related information today, with the aim to improve health and longevity in dairy cattle (Stock *et al.*, 2012b).

Approaches to improve health may be either based on disease diagnoses and direct observations of impaired health (direct health data) or on health indicators, i.e. traits correlated with health and disease (indirect health data). Although the former promise maximum efficiency of health-oriented optimizations on individual farms and of breeding programs, large- scale implementation of such health monitoring has not yet been possible in many countries. Heterogeneity of documentation is one of the major factors which may delay or frustrate setting-up routine work with direct health data. Without harmonization of trait definitions and recording, there is no basis for analyses across farms, benchmarking and genetic evaluations, so monitoring efforts are unlikely to pay off. However, examples of national health initiatives exist in which documentation standards of different size and format have been installed and successfully tested (e.g. Appuhamy *et al.*, 2009; Egger-Danner *et al.*, 2012; Fourichon *et al.*, 2001; Koeck *et al.*, 2012; Østeras *et al.*, 2007; Stock *et al.*, 2012a; Zwald *et al.*, 2004). In the Scandinavian countries, nationwide dairy health recording systems exist for decades, with a pioneer role of Norway (start of the Norwegian Cattle Health Recording System in 1975; Østeras *et al.*, 2007). Data collection approaches had necessarily impacted the trait spectra, and although stakeholders are aware of the benefits of flexible systems where specific expertise can contribute to long-term success, there are worldwide still only a few routine integrative health monitoring systems for dairy cattle (Stock *et al.*, 2012b).

Animal health within ICAR

Health indicators like somatic cell score have been included in international standards for recording and evaluation published by ICAR since the 1990s, providing the basis for considering health aspects in breeding. To further health monitoring and targeted improvement of dairy health, new guidelines specifically addressing the direct health traits were to be compiled under the responsibility of the ICAR working group for functional traits. In 2012, the ICAR guidelines for

Recording, Evaluation and Genetic Improvement of Health Traits got approved, providing recommendations regarding best practices for working with health data (ICAR, 2012).

General aspects to be considered when working with direct health data include the possible data sources with their specific characteristics concerning information content, pros and cons of their involvement. Furthermore, data security is an important issue to be addressed from the very beginning of planning infrastructure development for health data. Standardization of recording, control of data quality and continuity of data flow require particular attention because of the rather limited options for forcing complete and detailed health documentation for all animals. Because motivation of all parties involved is the major determinant, ways to long-term success of health monitoring are disclosed in the health guidelines addressing early feedback as well as long-term perspectives and both management and breeding. The comprehensive health key, given exemplarily as an appendix of the guidelines, can be considered extremely helpful for setting up health monitoring systems in dairy cattle. In the following, this key will be outlined with its main characteristics, illustrating its suitability for a broad range of applications.

Health key

The central key for health data recording has been referred to in the ICAR health guidelines as kind of gold standard (ICAR, 2012). Its compilation was driven by practical demands and carried by collaborations between science and dairy industry, with fundamental contributions of the German bovine specialist R. Staufenbiel. Apart from the large number of diagnoses included, it is the hierarchical structure of the key which makes it compatible with a variety of recording systems and very flexible in use.

The veterinary diagnoses or disease observations and further health-related information are grouped into nine categories: organ diseases; reproduction disorders in females; reproduction disorders in males; infectious diseases; parasitoses; metabolic diseases and deficiencies; poisoning; behavioral disorders and general findings; and health-related information not representing diagnoses. In each of these categories, subcategories or disease groups and individual items are listed with varying specificity, from low to high (Table 1).

In the health key, most space is devoted to the organ diseases, with some consistent entry options for each organ system: hereditary diseases and malformations are followed by tumors, injuries and various other acquired diseases. Rare diagnoses or observations of impaired health which are not explicitly listed can be entered as 'others' under the respective sub-category.

Depending on who had under which conditions acquired health information on some animal (e.g. clinical observation of farm staff vs. specific veterinary examination) and who had entered this information into the system, the comprehensive health key includes items appropriate for a broad spectrum of users. Providing entries with varying levels of detail, it is up to the user to decide how much information can and should be stored. The two examples given in Table 2 illustrate the user-dependent specificity of health data. After an injury with substantial blood loss the shock condition may be documented under 'organ diseases' as 'Diseases of the cardiovascular system' (1.05.) or specifically as 'Hypovolemic shock' (1.05.06.02.01.). After infertility-related cycle control, results

Table 1. Disease categories and major sub-categories with respective numbers of more specific items in the key for health data recording included as annex in the ICAR guidelines for Recording, Evaluation and Genetic Improvement of Health Traits (version 1.2, April 28, 2013).

Code	Technical term	No. of items
1.	Organ diseases	539
1.01.	Diseases of skin, subcutis and coat	27
1.02.	Diseases of the trunk	22
1.03.	Horn diseases	11
1.04.	Diseases of the lymphoid system	8
1.05.	Diseases of the cardiovascular system	49
1.06.	Diseases of the respiratory tract	46
1.07.	Diseases of the digestive tract	108
1.08.	Diseases of the urinary tract	23
1.09.	Diseases of the locomotory apparatus	63
1.10.	Claw diseases	56
1.11.	Diseases of the central nervous system and the sensory organs	40
1.12.	Diseases of the udder (other than mastitis)	37
1.13.	Mastitis (inflammation of the mammary gland)	36
2.	Reproduction disorders in females	116
2.01.	Diseases of the female reproductive system	23
2.02.	Pregnancy disorders	17
2.03.	Diseases related to calving	24
2.04.	Disorders in the postpartal period	16
2.05.	Female infertility	30
3.	Reproduction disorders in males	44
4.	Infectious disease and other microbe-related diseases *	103
5.	Parasitoses (parasite infestations)	42
6.	Metabolic diseases and deficiencies	73
7.	Poisoning	35
8.	Behavioral disorders and general findings	14
9.	Health-related information not representing diagnoses	45

* except local infections of udder and claws

referring to 'reproduction disorders in females' may be documented unspecifically as 'Female infertility' (2.05.) or specifically as 'Luteal cystic ovary disease' (2.05.02.04.02.). Information on a comatose cow with severe milk fever may be documented under 'metabolic diseases and deficiencies' as 'Disturbances of calcium and phosphorus balance' (6.03.01.) or most specifically as 'Parturient coma / Stage 3 of parturient paresis' (6.03.01.01.02.).

The unambiguous definitions of items and the clear structure of the health key point at the options for future combination of health data from different sources. Different recording options exist for example for clinical mastitis in the keys used for health data recording in German and Austrian dairy cattle, but the comprehensive reference key is providing the common denominator for joint analyses of mastitis data. Depending on how many details have been saved in the least specific of the contributing systems, the level of specificity of trait definitions may be considerably

Table 2. Examples for health data recording with different specificity via the comprehensive key for health data recording included as annex in the ICAR guidelines for Recording, Evaluation and Genetic Improvement of Health Traits

Code	Technical term
1.	Organ diseases
1.05.	Diseases of the cardiovascular system
1.05.06.	Disorders of blood vessels
1.05.06.02.	Shock (acute circulation insufficiency)
1.05.06.02.01.	Hypovolemic shock
2.	Reproduction disorders in females
2.05.	Female infertility
2.05.02.	Ovarial infertility
2.05.02.04.	Ovarial cysts
2.05.02.04.02.	Luteal cystic ovary disease
6.	Metabolic diseases and deficiencies
6.03.	Disturbances of mineral balance
6.03.01.	Disturbances of calcium and phosphorus balance
6.03.01.01.	Parturient paresis (milk fever)
6.03.01.01.02.	Parturient coma / Stage 3 of parturient paresis

lower in joint analyses. However, the increased amount of available data with respective impact on reliabilities may outweigh the loss of details when compared to specific single-source analyses.

With the first release of the ICAR health guidelines, version 1.1 of the health key was published (ICAR, 2012) which was recently updated to allow active recording of absence of certain diseases. Accordingly, standardized documentation is now also possible for extended health-documentation for instance in connection with claw trimming, 'Examination of the claws with no abnormality detected' (1.10.00.), or some gynecological herd screening, 'Examination of the female reproductive system with no abnormality detected' (2.01.00.). With this extension of the key, development towards data structures of test-day-model type is enabled, which is particularly relevant for farms with already established routines and desirable from the analysts point of view. Compared to the recording of only cases which requires assumptions regarding animals without disease records and at-risk periods (Koeck *et al*., 2012) the picture of the health status of the herd is much more complete when using data from herd screens. However, it is unlikely that broad use will be made of active recording for healthy cows in the near future.

Use of the comprehensive health key

In addition to the expertise of the user of some documentation system, the intention of health data collection is an important factor for how many details are to be saved. To survey herd management, broad and simple documentation may be easiest to implement, so a subset of diagnoses with few details could be used in standard software solutions (Østeras *et al*., 2007). Optionally, farmers may extend this set by items referring to their herd-specific focus of health disorders in order to obtain information for targeted optimization. Professions like claw trimmers collect data on only relatively small subset of traits, but are interested in options for very detailed recording. Finally veterinarians require solutions for detailed documentation for the full spectrum of traits, covering all organ systems and types of diseases. With the choice of items from the comprehensive hierarchical health key, recording systems can be designed which reflect user-demands and at the same time facilitate data flow in integrative systems. Cross- referencing between a simplified key for veterinary medical layman (observations of impaired health from farmers) and some specific expert keys (general or organ-specific veterinary key, claw trimmers' key etc.) is avoided, facilitating combination of health data from different sources.

Availability of a single clear and comprehensive reference for health data recording can become the key factor for long-term success of integrative health monitoring concepts, because it maximizes the chances of fruitful collaborations between all parties involved. The hierarchy can guide users and analysts in data recording and processing as well as results interpretation. If needed, focuses can be defined and re-defined with shifts towards more detailed documentation for some disease(s) or disease complex(es) than for others, keeping the same key for coding. Analyses of appropriate depth can be run with maximum information and minimum risk of misinterpretation due to linking of different keys. Experiences with the central key for health data in Germany have shown that harmonized definition and coding of health data can be considered as first step towards an integrative concept of health monitoring in dairy cattle. The central key for health data recording is today equally used in herd management software for farmers, claw trimmers' software and veterinary software, implying that the requirements for an integrative health monitoring system have been fulfilled.

In the era of genomics, international collaborations have become extremely important, implying the need for internationally harmonized definition of phenotypes. With the ICAR health guidelines the standard has been set for international efforts to improve dairy health in a targeted manner and using the full range of available methodologies.

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Health data recording in Finland

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Abstract

Health recording in Finland started in 1982 according to a Norwegian model and slightly earlier than in Sweden and Denmark. Its principle is that veterinarians write treatments down on an individual cow health card and AI technicians collect the data at their next visit. Herd owners can also enter these data to the database by themselves. No party has a duty to enter treatment data into the register, so it is a voluntary system. Yet, about 89 % of all herds sent in at least one treatment during 2011, and the total number of registered treatments reached 55 % of the number of recorded cows. The data belongs to the farmer but carries with it an automatic authorisation for use by Faba, NAV and Viking Genetics for breeding purposes. Each year, summary statistics are made by Faba and the data about the health status of dairy cows in the municipality to respective authorities. Farmers receive a health summary in the annual report from milk recording.

Keywords: veterinary, data, Finland.

Introduction

In Finland, veterinary treatment data has been recorded for breeding purposes since 1982. Around that time, the need for progeny testing for health had arisen in all Nordic countries and each one was putting up their own system while Norway was the first to actually start it and Finland was the second.

From the beginning, the system has been working on a voluntary basis. Keeping the records or sending them to the database is voluntary. Yet in 2011, 89 % of herds sent in at least some data and the total number of treatments equaled 55 % of the total cow number. According to Virtala (2012), some 83 % of all treatments are captured in the database.

The data is owned by each individual farmer but Faba, NAV and Viking Genetics are allowed to use it for breeding purposes.

Two databases

Treatment data exists in two separate databases. The older one is the advisory database that was established for breeding purposes. Apart from veterinary treatments, it also gathers data on preventive measures, hoof treatments and self-medication done by farmers. It has 195 different treatment codes.

Apart from the advisory database, the so-called Naseva database was established in 2006. It is a voluntary food safety register whose main focus is medication and withdrawal periods before slaughter.

Data capture methods

Treatment data is collected through seven different channels. The oldest system is based on individual cow cards that are sent out to the farms twice per year after the heifer calves reach the age of 6 months. These cards are kept on the farm and presented to the veterinarian and the AI technician every time they visit. Each time, they make notice of what they have done to which cow. Apart from that, the AI technician collects both kinds of data on the computer and sends them to the central database after a day's work.

The farmer can enter data into the advisory database through the Ammu on-farm software. Hoof trimmers have their own mobile software that they use when treating the animals, or some still send in data on sheets.

The farmer can also enter data into the Naseva database through a software solution but this option is mainly used for cows that are being slaughtered. Apart from that, some veterinarians transfer data from their clinical software to the Naseva database.

Table 1. Relative use of different data capture methods and capture delay per method.

Data capture method	Percent of all entered data	Average delay, days
Veterinarian	12.6	38
Farmer through Naseva	18.1	64
Farmer through Ammu	5.6	55
Advisor through Ammu	4.6	98
Hoof trimmer on sheets	0.8	232
Hoof trimmer	16.7	2
AI technician	41.5	84

Table 2. Treatment prevalences in the Finnish cow population in 2011 (Faba, 2012).

Breed	Fertility treatment	Milk fever	Ketosis	Nutritional disorder	Udder disease	Hoof disease	Total
Ayrshire	17.8	3.2	0.9	1.7	16.2	1.2	50.8
Holstein	20.4	4.6	1.7	2.3	20.9	1.7	63.0
Finncattle	13.7	4.1	2.3	1.7	16.3	1.1	47.8
All cows	18.7	3.7	1.2	2.0	17.9	1.4	

Data use

Treatment data is used for breeding purposes: each animal receives breeding values for udder health, hoof health and other treatments. Genetic trends show that Finland has managed to keep these on a rather steady level while selecting for production traits.

The data is also summarised on farm level and reported back to the farmers. The summaries are available in management software. There is also a web service where farmers can look at individual cow treatments for their own animals and their ancestors.

Treatment statistics are also prepared annually.

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Challenges and opportunities for farmer-recorded data in health and welfare selection

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Abstract

With an emphasis on increasing profit through increased dairy cow production, a negative relationship with fitness traits such as health has become apparent. Decreased cow health impacts herd profitability because it increases rates of involuntary culling and decreases milk revenues. Improvement of health traits through genetic selection is an appealing tool; however, there is no mandated recording system for health data in the US. Producer-recorded health information provides a wealth of information for improvement of dairy cow health, thus improving the profitability of a farm, yet several challenges remain. The broad definition of 'direct health' does not truly reflect the heterogeneity and complexity of these traits. While there is a virtually endless pool of phenotypes potentially considered for selection, it is paramount to identify a few key parameters for which a consistent and demonstrable improvement can be achieved. We have demonstrated how farmers' recorded events represent a credible source of information with reported incidences matching most of the epidemiological evidence in literature, with calculated incidence rates ranging from 1.37% for respiratory problems to 12.32% for mastitis. Furthermore, we have demonstrated that relationships among common health events constructed from on-farm data provide supporting evidence of plausible interconnection between diseases and overall data quality. The results of our analyses provide evidence for the feasibility of on-farm recorded health base breeding programs. Nevertheless, there is an intrinsic heterogeneity of players, and a complex infrastructure in the collection and flow of information connected to health traits, and among the reasons for the slow implementation of health selection programs, data privacy concerns are at the top of the list in the US.

Keywords: diseases, data validation, US Holsteins.

Introduction

Throughout the past fifty years or more, there has been a focus on increased profit through increasing dairy cow production. With this focus on production, a negative relationship with fitness traits including health and fertility traits, has become apparent (Rauw *et al*., 1998). An alternative to increasing net profit of producers is to decrease management costs by improving the overall health of the cows. Declining health of cows can impact the profitability of a herd by affecting several aspects including additional culling, decreased and lost milk, veterinary expenses, and additional labor. Kelton *et al.* (1998) estimated the cost of several common health events ranging from $39 per lactation with an incidence of cystic ovaries up to $340 per case of left displaced abomasum. Over the past fifteen years, however, these economic costs may have drastically changed.

Improvement of health traits by genetic selection is an appealing tool. Difficulty is encountered, however, because there is no mandated or consistent recording system of health traits throughout the United States (Maltecca, 2013). The potential for genetic improvement in health-related traits has been demonstrated in cattle breeds (Abdel-Azim *et al.*, 2005; Appuhamy, 2009). Genetic improvement of clinical mastitis incidence has also been demonstrated in Norwegian cattle (Heringstad *et al.*, 2003) (more recent). The lack of health-related phenotypes in the US creates an obstacle in achieving genetic improvement of health traits. Several previous studies have confirmed the possibility of using on-farm recorded health information for genetic improvement. (Zwald *et al.*, 2004a,b; Miglior, 2009, 2013). In prior research we investigated whether US producer-recorded data reflected the true incidence of health events from epidemiological studies. Further investigation of relationships among occurrences between common health events were compared and corroborated the use of on-farm data as a viable strategy (Parker Gaddis *et al.*, 2012).

The use of survey data still poses challenges in terms of data quality and appropriate use. A deeper understanding of causes and distribution for these data is needed. While there is a virtually endless pool of phenotypes that could be potentially considered for selection, there needs to be an effort in identifying a few key parameters for which a consistent and demonstrable improvement can be achieved (Maltecca, 2013). Within this framework an alternative perspective could be used when analyzing health data that aims to extract the underlying health function of a cow. A principal component analysis (**PCA**) may be able to distinguish between groups of health events in order to further elucidate the complex nature of these traits. It could be hypothesized that some cows are more susceptible to a common type of disease, such as reproductive or metabolic due to an underlying disruption in ordinary function. Because of the binary nature of the data, a principle component analysis cannot be directly applied to health event incidence data; however it could be performed on pseudo-phenotypes, such as sire de-regressed breeding values. Alternatively, a multiple correspondence analysis (**MCA**) can be performed directly with binary data (Greenacre and Blasius, 2006). Furthermore, while selecting remains an overarching goal, the nature of disease traits implies a large role in the managing elements of dairy operation, and benchmarking management practices and herd characteristics related to disease incidence can be used to both perform data quality control and risk assessment. In this paper, as part of a larger effort, we provide a preliminary characterization of both individual disease and herd characteristics related to disease incidence.

Material and methods

Data

Voluntary producer-recorded health event data were available from Dairy Records Management Systems (Raleigh, NC) from US farms from 1996 through 2012. The health events included in the analyses were mastitis (MAST), metritis (METR), cystic ovaries (CYST), digestive disorders (DIGE), displaced abomasum (DSAB), ketosis (KETO), lameness (LAME), reproductive problems (REPR), and retained placenta (RETP) from cows of parities one through five. Previous editing was applied to the data for common health events as described in Parker Gaddis *et al.* (2012). Minimum and maximum constraints were imposed on the data by herd-year in order to avoid using records from herd-years that were deemed as either over- or under-reporting. Lactations lasting up through 400 days postpartum were included in the analyses, considering that cows with extended lactations are likely to be those that have not become pregnant.

Table 1. Summary statistics for each health event of interest.

Health event	**Number of records**	**Number of cows**	**Number of herd-years**
Cystic ovaries	222 937	131 194	3 369
Digestive disorders	156 520	97 430	1 780
Displaced abomasum	213 897	125 594	2 370
Ketosis	132 066	82 406	1 358
Lameness	233 392	144 382	3 191
Mastitis	274 890	164 630	3 859
Metritis	236 786	139 818	3 029
Reproductive disorders	253 272	151 315	3 360
Retained placenta	231 317	138 457	2 930

Grouped analyses

Individuals

Several analyses were performed to investigate disease data clustering at an individual level. A MCA was performed using the FactoMineR package (Husson *et al.*, 2012) of R (R Core Team, 2012). Many records in the dataset did not have complete observations for all the included health events. The missMDA package (Husson and Josse, 2012) of R was used to impute missing health event observations within the dataset before performing the MCA (Husson and Josse, 2012). A PCA was also performed. Because PCA requires quantitative variables, phenotypes used for this analysis were sire de-regressed estimated breeding values. Estimated breeding values were obtained from a multiple-trait threshold sire analysis using the pedigree-based relationship matrix A. De-regression was performed based on the methodology described by Garrick (2009). The PCA was completed using the FactoMineR package (Husson *et al.*, 2012) of R (R Core Team, 2012). Grouped analyses could be considered either from the susceptibility of individuals to certain diseases or with an interpretation stemming from the hypothesis that certain diseases tend to occur together. To determine the optimal number of clusters when considering individual observations, several preliminary analyses were performed. A scree plot was produced to indicate an optimal number of clusters at the inflection point. A hierarchical cluster analysis based on k-means was then performed on the de-regressed sire breeding values as pseudo-phenotypes. The analysis was performed using the fpc library (Hennig, 2013) of R (R Core Team, 2012). Clustering was also performed based on Ward's minimum variance criterion applied to Euclidean distances (R Core Team, 2012).

Herds

Herd summary information was available for four time points throughout each year from 2000 through 2011 for March, June, September, and December. The production, income, and feed cost summary included data such as total number of cows in milk, milk, fat, and protein amounts for the herd, as well as amounts of silage, forage, and concentrates used. The reproductive summary of the current breeding herd included variables such as total number of cows in the breeding herd and voluntary waiting period. A reproductive summary of the total herd included data on percentage of successful services total number of pregnant cows. A stage of lactation profile described data such as number of milking cows by parity group (1st, 2nd, 3+, and all lactations) as well as average daily milk production by parity group. The genetic summary provided data such as the genetic profile and number of service sires used. The production by lactation profile contained descriptive statistics of milk, fat, and protein production split by parity group. A current somatic cell count summary included variables for the percent of cows with a specified SCC level by parity group. The dry cow profile contained the number of days dry for cows in each parity group as well as the number of cows dry for less than 40 days, between 40 and 70 days, and greater than 70 days. Lastly, a yearly summary of cows that entered and left the herd included with data split by parity group.

For this analysis, health information was edited using previously developed criteria to be applied to on-farm recorded data in order to ensure a high quality of the data. The edited health data were then merged with the herd summary data. This resulted in 954,519 records from 266,174 cows across 1,021 herds representing 15,169 sires. A preliminary analysis of the herd variables was conducted in R (R Core Team, 2012) using the caret package (Kuhn, 2013). A function to find any linear dependencies was used to ensure that none of the information provided by the herd summary was completely redundant. After confirming no linear dependencies among the variables, correlated variables were analyzed. The mean overall correlation among the variables was 0.09 with a standard deviation of 0.21. Given that three standard deviation units added to the mean correlation was equal to 0.72, a cut-off for highly correlated variables was designated as 0.75. Variables were removed to minimize the number of highly correlated variables within a dataset. Following this edit, 89 variables pertaining to herd characteristics remained.

Results and discussion

Individuals

In order to investigate how individuals cluster based on their disease liability, hierarchical clustering was performed based on k-means with a k value of 4 based on a scree plot assessment. The results of this analysis are shown in table 2.

In general, the groups tended to be negative for MAST, negative for all events, negative values for metabolic and reproductive events, and positive values for all events. A dendrogram showing the hierarchical clusters based on the pseudo-phenotypes is shown in Figure 1 along with a scatter plot of the individuals using the first two principal components.

When analyzing from the perspective of the health events, LAME and MAST separate very clearly in both the MCA and PCA results. The PCA results indicate that KETO and METR tend to cluster together as well as DSAB and RETP This separation can be seen in Figure 2 showing the variable representation of the PCA. The multiple-trait analysis also estimated a moderate correlation between KETO and METR. The MCA results have a cluster of positive incidences of several health traits including METR, KETO, RETP, DSAB, and DIGE as shown in figure 2. The clear separation of

Table 2. Results of hierarchical clustering based on k-means applied to de-regressed breeding values for sires with estimates for all health events. CYST = cystic ovaries; DSAB = displaced abomasum; KETO = ketosis; LAME = lameness; MAST = mastitis; METR = metritis; RETP = retained placenta.

Cluster	CYST	DSAB	KETO	LAME	MAST	METR	RETP
1	-0.31	1.27	1.06	-0.01	-0.19	0.58	0.42
2	0.22	-0.62	-0.40	0.08	-0.09	-0.14	-0.11
3	0.60	-2.16	-1.33	0.16	0.09	-0.67	-0.53
4	0.02	0.30	0.18	-0.05	0.05	0.06	0.01

CYST in the PCA is not seen in the MCA results. However, if imputed data is not included when performing the MCA, the separation of CYST is observed. This may indicate that the separation of CYST in the PCA, as well as the MCA without imputing missing data, is an artifact resulting from having incomplete records. In general, the MCA and PCA results indicate that several of the health events do tend to cluster together. This indicates that there is the possibility of creating broad health event definitions while not losing a large amount of information. For example, based on biological knowledge as well as the MCA and PCA results, groups of events could be formed for mastitis or other udder-related disorders, lameness and foot or leg problems, reproductive disorders, and metabolic disorders. This reduces the details that are needed from producers while still allowing informative health data to be collected.

Herds

A principle component analysis was performed on the 89 herd variables to determine if certain characteristics tended to occur together. Eleven components explained about 50% of the total variation explained by the herd variables while twenty-eight components explained 75% of the total variation. A description of the dimensions was also inspected. Based on the results, somatic cell counts in first and second lactation cows and the number and average age of cows across all lactations were the most characteristic of the first dimension. The second dimension most highly reflected production traits such as rolling average of milk pounds, summit milk of first lactation cows, average daily milk production from 1 to 40 DIM for all cows, and fat yield. The third dimension reflected the number of cows dry over seventy days, the number of cows entering the herd, and the number of cows dry less than forty days.

Herd variables were clustered in regard to the crude incidence of common health events. Each health event was analyzed individually. The optimum number of clusters for the data was estimated and observations were split into the optimum number of clusters "around medoids". For each event, the optimal number of clusters was two. Following clustering, the average of select herd characteristics are given for each health event in table 3. The number of second lactation cows entering the herd was greater in the cluster with lower incidences of mastitis, ketosis, and retained placenta. Herd characteristics that involved number or percentage of cows leaving the herd were among the characteristics that were most different between the clusters of herds for mastitis, metritis, ketosis, and retained placenta. The herds

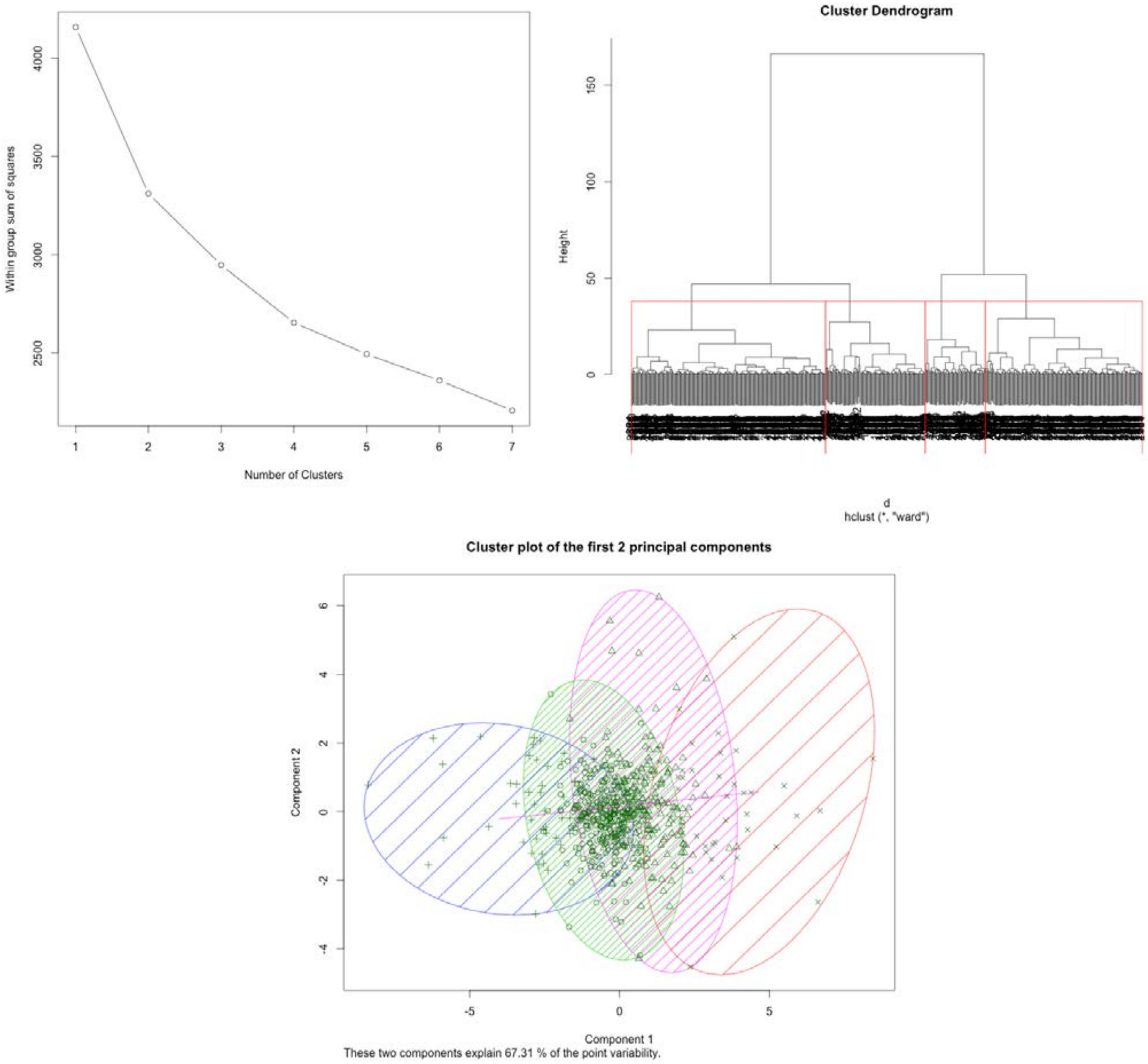

Figure 1. Panel A: Scree-like plot indicating within-group sum of squares with each number of clusters using scaled de-regressed sire estimated breeding values as pseudo-phenotypes. Panel B. Cluster dendrogram showing hierarchical clustering results using de-regressed sire breeding values as pseudo-phenotypes for sires with estimates for all health events. Red rectangles indicate the optimal four clusters. Panel C Cluster plot of individuals against the first two principal components determined based on pseudo-phenotypes of de-regressed sire estimated breeding values for all health events. Each cluster is shown by an ellipse with each individual depicted by either a circle, square, cross, or x.

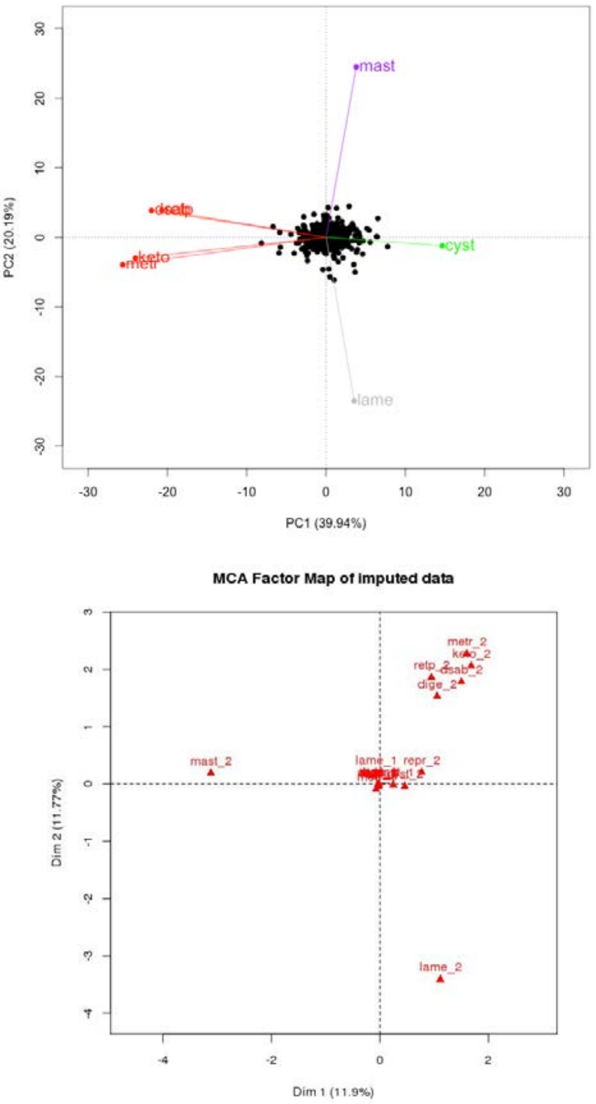

Figure 2. Panel A: Principle component analysis variable factor map using de-regressed sire estimated breeding values for sires with estimates for all events. The first two components (Dim 1 and Dim 2) are displayed, explaining 39.94% and 20.19% of the variance, respectively. CYST = cystic ovaries; DSAB = displaced abomasum; KETO = ketosis; LAME = lameness; MAST = mastitis; METR = metritis; RETP = retained placenta. Panel B: Multiple correspondence analysis factor map from imputed data portraying the first two dimensions (Dim 1 and Dim 2) which explain 11.9% and 11.77% of the total variance, respectively. No incident = 1, Incident = 2. CYST = cystic ovaries; DIGE = digestive disorders; DSAB = displaced abomasum; KETO = ketosis; LAME = lameness; MAST = mastitis; METR = metritis; REPR = reproductive disorders; RETP = retained placenta.

clustered with lower incidences of the analyzed diseases had fewer cows leaving the herd, whereas herds clustered with high incidences had a greater number of cows leaving the herd. Herds that were clustered in the low incidence groups for metritis, mastitis, and ketosis all reported having higher numbers of total cows and milking cows on pasture. Total number of services was a herd characteristic that

Table 3. Average of select herd characteristics based on clustering results.

Health Event	Incidence (Group)	Total cows (RA)	Milk lbs. (RA)	Fat lbs. (RA)	Protein lbs. (RA)	Avg. days to 1st service	Actual calving interval	Avg. % successful services	Total number calving	Avg. daily milk production	Body weight
RETP	0.005 (Low)	333	20884	792	653	84	13.9	36	561	66.6	1270
	0.10 (High)	444	22113	834	687	82	13.8	34	892	70.1	1306
MAST	0.008 (Low)	263	20872	794	652	85	14.0	36	349	66.5	1273
	0.16 (High)	554	21269	805	663	83	13.9	36	1110	68.3	1286
METR	0.01 (Low)	322	21026	803	660	86	14.0	35.3	445	66.8	1274
	0.14 (High)	578	21582	813	667	83	14.0	34.5	707	69.0	1310
KETO	0.006 (Low)	370	21744	833	681	79	13.8	32.7	427	69.3	1270
	0.10 (High)	441	22569	853	701	78	13.8	31.3	682	72.5	1311

RA = rolling yearly herd average; RETP = retained placenta; MAST = mastitis; METR = metritis; KETO = ketosis.

Table 4. Herd variables with greatest relative importance by health event.

Health event	Variable 1	Variable 2	Variable 3
Ketosis	Milk yield (all cows)	Avg. days to 1st service (2nd lactation cows)	Services per pregnancy (pregnant 1st lactation cows)
Mastitis	Average total pregnant cows	Voluntary waiting period	Total cows
Metritis	Voluntary waiting period	Total cows	Feed cost per cwt milk
Retained placenta	Average total pregnant cows	Average percentage heats observed	Pounds concentrate consumed

was among those most different between the two clusters for several diseases. Herds with low incidences of retained placenta, ketosis, or mastitis had less total number of services than herds with high incidences of those diseases.

Conclusions

Opportunities exist to improve disease prediction and overall herd disease management by making use of patterns observed at both individual and herd level. Grouped information can be used in data editing and herd benchmarking, as well as a way to increase selection efficacy. Further evaluations of more comprehensive predictive models are nonetheless required.

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MediRund: Example of database and data exchange for health data used by farmers and veterinarians in the Netherlands

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Abstract

In 2011 the dairy and beef sector in the Netherlands decided to establish a sectorial database for monitoring the use of antibiotics by dairy and beef farms. The national product board for livestock and meat is in charge of the regulations and the overall reports about the use of antibiotics to the Dutch authorities.

The goal of this system is to make the use of antibiotics transparent for all chain partners and reduce the usage of antibiotics. At the same time there should be no extra administrative workload for farmers. To achieve this, only data which is already being captured is used in the national database. It is not based on individual treatments, but it is based on deliveries from vet to farm.

Veterinarians are required to send all deliveries of medicines containing antibiotics to the central database "MediRund". The data from the national identification and registration system (I&R) is used for calculating the rolling average number of animals per category on the farm.

The SDa (Dutch veterinary medicines authority) has determined the antibiotic content of the available medicines and defined bench mark indicators for responsible use of antibiotics.

MediRund is producing quarterly new figures for every farm. Those figures are used by the certified quality organizations to monitor and sanction farms if the usage is above the allowed level. Quality organizations are established by the dairy- and beef industry and combine the work on monitoring antibiotics with other activities to guarantee the quality of milk and beef.

This system is now operational from January 1st 2012. Farmers had to choose a veterinarian and a quality organization responsible for monitoring their farm, especially the use of antibiotics.

Keywords: Antibiotic, sectorial database, transparent use.

Introduction

In the years 2005-2010 Infections caused by resistant microorganisms often failed to respond to conventional antibiotic treatment, resulting in prolonged illness and greater risk of death by humans and animals. In particular the human aspect meant that there came a lot of political pressure on the dairy and beef industry to enforce less, better and more transparent use of antibiotics.

MediRund

The national Dutch product board for livestock & meat was asked to develop and implement regulations. They decided to establish a sectorial core database for monitoring the use of antibiotics by dairy and beef farms. CRV is asked to support the sectorial system. The product board has the ownership of the data and is responsible for reporting to the authorities. CRV is the owner of the software and responsible for the operational part. Initial investment is paid by the national product board. Operational costs and revenues are for CRV. Revenues are only obtained by paid helpdesk. Information services are for free.

The goal of this system is to make the use of antibiotics transparent for all chain partners and reduce the usage of antibiotics. At the same time there should be no extra administrative workload for farmers. To achieve this, only data which is already captured is being used in the national database. Veterinarians are sending all deliveries of medicines containing antibiotics to the central "MediRund" database. The national Identification and registration system is used for the number of present animals on the farm and the authorities provide the antibiotic content of the medicines in "animal-daily-dosages". With all this information MediRund is producing quarterly new figures. Those figures are used by the certified quality organizations to monitor and sanction farms if the usage is above the allowed level. Quality organizations are established by the dairy- and beef industry.

Operational experiences

The system is now operational from January 1st 2012. Farmers are happy with the transparency of the system. They had to choose a veterinarian and a quality organization who are responsible for the antibiotics use on their farm. Besides those two stakeholders, they can give access to the data to all people they want. The use of antibiotics has become transparent for chain partners and politics. Only by making the use transparent the use of second and third choice antibiotics was reduced enormously. Transparency creates awareness to farmers and veterinarians.

The key figure DD / DJ is a value known by many participants. It gives the use of antibiotics a measurement.

The costs of the monitoring system are relatively low, meanwhile the quality of the data is fairly good. To improve management: the registration of diseases and treatment of individual cows is still necessary.

Session 4

Data validation

Validation of the Nordic disease databases

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Abstract

The Nordic disease databases have been in operation for several decades, but only limited efforts has been made to validate them. In 2007 a joint Nordic project was initiated with the aim to validate each national database and to compare the data validity between countries. Validation was made by "patient chart reviews" and by using a second source of data collected on-farm. The intention to treat sick cows also affects the completeness of the records, and this was evaluated by investigating attitudes of farmers and veterinarians. The results showed that the correctness of the data was high, but that completeness was less than 100% and it varied by disease complex and country. Standardization of disease registrations is necessary for valid between country assessments, but adjustments for incompleteness can meanwhile be used. There were also differences between countries in the attitudes to treat sick cows, which also influences the comparability of disease records between countries.

Keywords: validation, database, disease, dairy.

Introduction

Systems for recording of diseases in dairy cattle have been in operation in the Nordic countries for several decades. The system in Norway (NO) started already in the mid 70'ies (Østerås *et al.*, 2007), while the systems in Finland (FI), Sweden (SE) and Denmark (DK) started in 1982, 1984 and 1991, respectively (Gröhn *et al.*, 1986; Emanuelson, 1988; Bartlett *et al.*, 2001). A unique feature with these systems is that the data is integrated with information from the milk-recording scheme, AI activities and routine maintenance claw trimmings in a comprehensive database on the individual animal level. The main purpose of the systems is to monitor the prevalence and incidence of endemic diseases. However, the animal databases are also used for herd health activities, genetic evaluations and for research.

Originally the disease data was only used within one country, but they have increasingly been used also for across country comparisons and for the Nordic genetic evaluations. The systems have much in common, which would make comparisons across countries reasonable. The most significant aspect is that dairy farmers in all Nordic countries have very limited access to prescription drugs, such as antibiotics, without consulting a veterinarian. Moreover, the systems also involve the veterinarian, one way or the other, in the recording of diseases, even if the technical solutions differ somewhat (Figure 1).

However, formal comparisons of disease incidences, where data were analyzed based on identical inclusion / exclusion criteria and methods, found large differences in disease incidences between the Nordic countries that were difficult to explain (Valde *et al*., 2004). These differences raised concerns about data quality and comparability, and in 2007 a joint Nordic project, DAHREVA, was initiated with the aim to validate each national database and to compare the data validity between countries. The aim of this paper was to briefly summarize some major components of DAHREVA.

DAHREVA - Assessment of the validity of the dairy health recording systems in the Nordic countries

The ultimate goal of DAHREVA, financially supported by NKJ (Nordic Joint Committee for Agricultural and Food Research), was to get a better understanding of the true disease situation in Nordic dairy herds and to create a basis for quality improvement measures. The project leader was Anna-Maija Virtala (FI) and involved several project partners in each Nordic country. The project has resulted in a large number of publications - not the least one PhD-thesis focusing on locomotor disorders (Lind, 2013), one on mastitis (Wolff, 2012), one on metabolic disorders (Espetvedt, 2013) and one on reproductive disorders (Rintakoski, 2013). The project addressed several parts in the data flow from a diseased cow until a record is found in the database (Figure 2). More specifically the goals of DAHREVA were to study

1. Discrepancies between "true disease occurrence" and health records.
2. data flow from farm to the registry.
3. Attitudes of farmers and veterinarians towards treatments and using the recording systems.

Actual versus recorded diseases

This component of DAHREVA concerned the steps 3 to 9 in Figure 2, i.e. we wanted to evaluate what proportion of diseased cows that the farmers observed ended up in the database. Herds were therefore asked to record all clinical disease in their dairy cows that they observed during their normal routine work. Recording was made on a recording sheet specifically designed for the purpose, and focus was on mastitis, reproductive disorders, locomotor disorders and metabolic diseases. Herds were provided with detailed definitions of the respective disease conditions, and were also asked to identify if the case was attended by a veterinarian or not. The study was conducted during two 2-month periods during the spring and in the autumn of 2008. A random sample of 1000, 900, 800 and 400 dairy herds with ? 15 cows in DK, FI, NO and SE, respectively (representing between 8 and 25% of the herds), were asked to participate, but in the end data was available from between 105 and 179 herds per country. Data were retrieved from the national cattle databases and matched against the data recorded in the herds, and completeness, i.e. the proportion of actual disease cases that were also found in the database, was calculated.

Completeness was calculated separately for several diseases and separately for cases that were veterinary attended and not. A few examples are presented in table 1. The low completeness for locomotor disorders in Sweden can be explained by the fact that only few cases are actually attended by a veterinarian; most (mild) locomotor disorders are handled by claw trimmers. The explanation for the low completeness

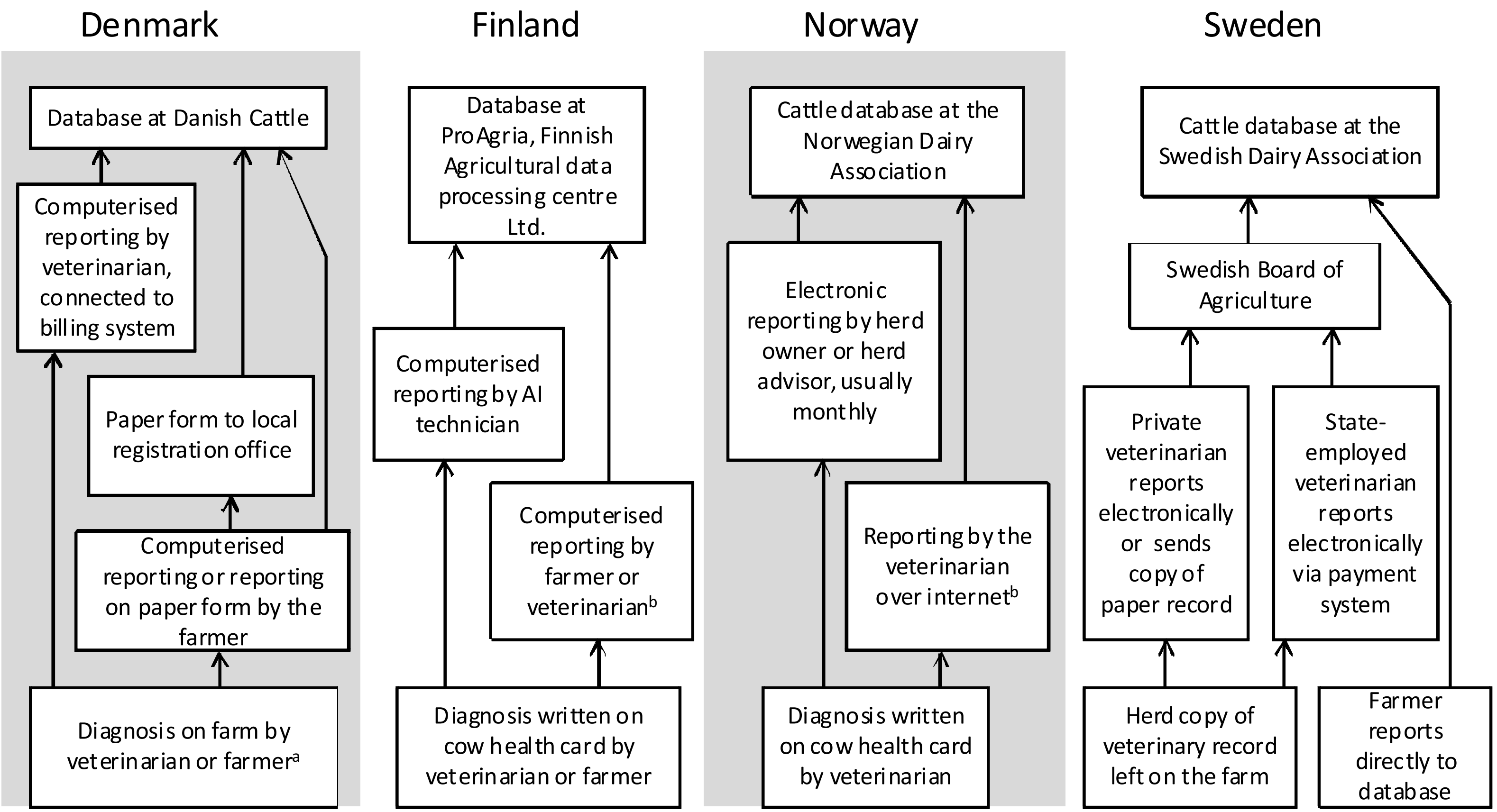
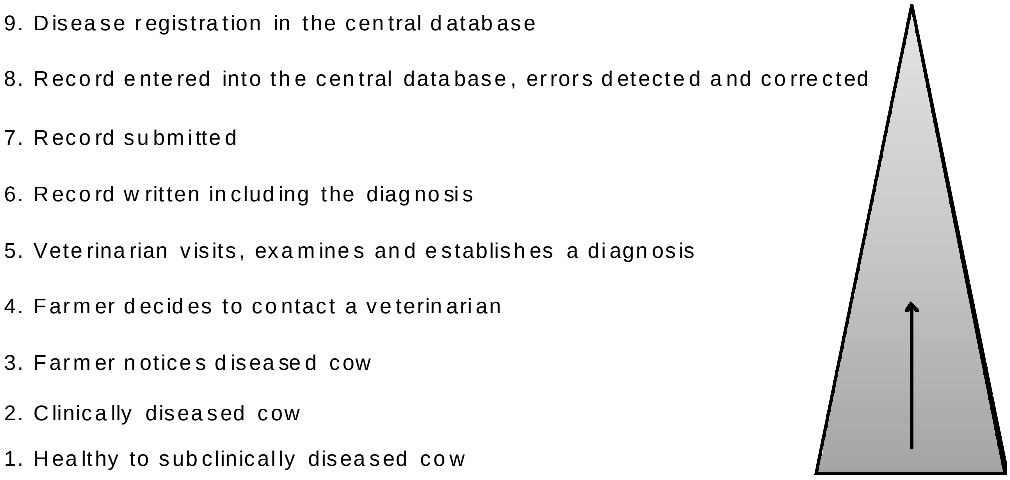


Figure 1. Data flow for disease records from the herd to the central cattle database in the four Nordic countries (Wolff, 2012).
[a]Farmers with a certain herd health contract, bIntroduced in 2008.



9. Disease registration in the central database
8. Record entered into the central database, errors detected and corrected
7. Record submitted
6. Record written including the diagnosis
5. Veterinarian visits, examines and establishes a diagnosis
4. Farmer decides to contact a veterinarian
3. Farmer notices diseased cow
2. Clinically diseased cow
1. Healthy to subclinically diseased cow

Figure 2. Data flow from a diseased cow to database (Wolff, 2012).

Table 1. Completeness for veterinary attended cases of clinical diseases observed by farmers in Denmark (DK), Finland (FI), Norway (NO) and Sweden (SE).

Disease	**DK**	**FI**	**NO**	**SE**
Locomotor disorders	0.88	0.56	0.60	0.33
Mastitis	0.94	0.56	0.82	0.78
Milk fever	0.88	0.71	0.80	0.82
Oestrus disturbances	0.96	0.93	0.85	0.85

for mastitis in Finland is that the "normal" action of a farmer at a suspected case of mastitis is to send a milk sample for bacteriological analysis and a veterinarian is usually only contacted if the sample is positive.

Completeness for all cases, i.e. both veterinary treated or not, was lower than the completeness's presented in Table 1, because cases that are not attended by a veterinarian can be reported to the database but is reported to a much lower extent. This completeness was, for example, 0.90, 0.51, 0.75 and 0.76 for mastitis, but the difference between the completeness for all and veterinary treated cases varied with disease complex. Please see publications by Lind, Rintakoski, Espetvedt and Wolff for complete results and discussions about the differences in completeness between countries and diseases.

Problems that this part of DAHREVA had to deal with were a) underreporting by the farmers; b) mismatch of dates; c) the variety of disease codes. The underreporting became obvious, because a number of disease cases that were treated by veterinarians were found in the national databases, but were still not recorded by the farmers on the recoding sheets. However, including only "good reporters", i.e. farmers with few cases from the database not found in their recording sheets, in the calculations of completeness did not affect the results to a large extent. Many cases of diseases could not be matched between database and farm records on the exact date. This could be due to a misunderstanding of farmers in the study of what date should be reported, i.e. day of discovery of a diseased cow, day of contacting the veterinarian or day of visit of the veterinarian, or due to ambiguousness in the recording systems. Allowing for a discrepancy of ±4 (for some diseases ±7) increased the completeness significantly, but an increase to ±30 days did not increase the completeness further. Finally, we realized that there was a huge difference in the amount of disease codes used, and how specific they were, in the national databases. As an example the system used in Sweden had about 250 codes related to locomotor disorders while there were about 20 codes in each of the other countries. Also, there were 43 codes related to mastitis in Sweden, but only between 9 and 18 in the other countries. The project had therefore to create dictionaries to translate the national codes to a common code, and it is obvious that some degree of specificity was lost in that process.

The conclusion from this part of the study was that there was underreporting for all diseases in all Nordic countries and that there were significant differences in the degree of underreporting between the countries and between diseases.

Data loss

A common approach for validation of secondary data is a "patient chart review" (Emanuelson & Egenvall, 2013), and this was applied in DAHREVA to quantify the loss of data from steps 6 to 9 in Figure 2. In such an approach the on-farm records, e.g. receipts, the herd ledger, cow cards, notes in the herd-management software, etc., are compared in detail with what can be found in a database. The design of this part of DAHREVA differed between the countries, mostly due the differences that existed in procedures to record and collect the data (Figure 1). In general, treatment records on-farm was retrieved either by sending digital photos by email or sending originals or photocopies by mail services. The total number of records varied between approximately 1200 (SE) to 30,000 (DK). Completeness was calculated as the proportion of on-farm records that could be found in the database. In FI and NO also correctness, i.e. the proportion of events in the database that were correct diagnostic events, was calculated.

The average completeness was 0.80, 0.83, 0.85 and 0.84 in DK, FI, NO and SE, respectively, but the variation was substantial within country. For instance, the completeness of records made by certain kinds of veterinarians in Sweden was almost 100%, while it was lower overall. The completeness was generally affected by age of the animal (poorer for young animals), disease complex, origin of the animal (poorer for purchased animals, due to id problems) and region (at least in FI and SE). The correctness of the records in the database in Finland varied between 0.84 and 0.96 and was in Norway 0.97-9.98. Complete results and discussions can be found in the publications by Bennedsgaard, Rintakoski, Espetvedt and Wolff.

Mismatching of cow identities was a major reason for discrepancies between on-farm and database records. Part of the explanation for this problem was poor handwriting and transcription errors, but was a particular situation for cows that were not born on the farm in which case dual and ambiguous identities could give the veterinarians problems to know what to record. Another problem the project had to deal with was again discrepancies in the dates of the recorded events. It is worth noting that also auxiliary data, such as sex, age, breed, should also be subject for assessment of correctness in studies such as these.

A conclusion from this part of DAHREVA was that information is lost in the recording process in all Nordic countries, but the degree of correctness of data that is found in the database is generally very high.

Attitudes

The third major component of DAHREVA was to evaluate attitudes towards diseases from both a farmer and a veterinary perspective, i.e. steps 3-5 in Figure 2, because the decision making process may have a significant effect on the difference between actual and recorded diseases. This part was based on the Theory of Planned Behaviour (TPB) from social psychology, where the behavioural intention (BI) is assessed rather than the actual behaviour. The BI, in turn, is determined by constructs such as a person's attitude, subjective norm and perceived control regarding the behaviour. A TBP study is very time consuming and the DAHREVA project was therefore limited to actions related to cases of mild clinical mastitis (MCM) in a lactating dairy cow. For farmers we investigated their intent to contact a veterinarian on the same day as detecting signs of MCM, and for veterinarians we investigated their intention to start medical treatment of a dairy cow with MCM on the same day as making the diagnosis. The study was a combination of face-to-face interviews and questionnaires and aimed to capture both the BI as well as the underlying constructs.

The results showed that there were significant differences in the BI of farmers between all countries except DK and NO, and that SE farmers had the weakest BI and FI farmers the strongest (Table 2). Attitude was the construct that explained most of the variability in BI in all four countries. The most important driver in all countries was to achieve a quick recovery for the cow. The BI's of veterinarians also differed between the countries (Table 2) and, assuming the intention scenarios presented to the veterinarians in this study to be equally common in the countries, the result means that the DK veterinarians would treat seven cases of MCM out of ten while veterinarians in FI would only treat four. Again, attitude was the most important component of BI in DK, NO and SE, while perceived control was most important in FI. Please see publications by Lind, Rintakoski, Espetvedt and Wolff for complete results and discussions.

Table 2. Median behavioural intention score (range 0-1) for a farmer to contact a veterinarian on the same day as detecting signs of mild clinical mastitis (MCM), and for a veterinarian to start medical treatment of a dairy cow with MCM on the same day as making the diagnosis in Denmark (DK), Finland (FI), Norway (NO) and Sweden (SE).

	DK	**FI**	**NO**	**SE**
Farmer	0.50	0.63	0.50	0.38
Veterinarian	0.71	0.42	0.58	0.50

The conclusion from this part of DAHREVA was that the threshold for action on signs or diagnosis of a case of mild clinical mastitis differs significantly between the countries. These differences in attitudes will also affect the proportion of cases of mastitis observed on-farm that will be recorded in the national databases, and thus also affect comparisons of disease frequencies. Similar analyses on other disease complexes are needed to be able to verify if the differences are general or specific for cases of mild clinical mastitis.

Conclusions

DAHREVA has provided a good understanding of the differences in the Nordic disease databases. It became obvious that completeness of the recordings were less than 100%, because there was underreporting and loss of data in the systems. The completeness differed between countries and between diseases; facts that can be used to adjust apparent incidences to make them more comparable between countries. The correctness of the data in the disease databases was reassuringly high. There were significant differences in attitudes towards treatments of mild clinical mastitis between the countries, which will affect comparisons of disease frequencies.

Electronic data recording and transfer is now being implemented in Finland and Norway, which may positively affect the completeness in the future. A process to harmonize disease codes between the Nordic countries has also started, partly as a result of DAHREVA, but no harmonization can ever remove differences that are due to differences in attitudes to act on observed diseases. The potential effect of differences in attitudes is important to realize for any across-country comparisons of disease frequencies.

Acknowledgements

All colleagues within DAHREVA are gratefully acknowledged for the fruitful and fun collaboration we had over several years. Thanks also to the Nordic Joint Committee for Agricultural research (NKJ), e.g. via the Swedish research council Formas, for financial support and to the participating farmers.

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Comparison of different methods to validate a dataset with producer-recorded health events

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Abstract

This study is part of a larger project whose overall objective is to develop genetic evaluations for resistance to mastitis and other diseases in Canada. Health data recorded by producers were available from the National Dairy Cattle Health System. Eight diseases are recorded by producers on a voluntary basis: mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries and lameness. Data validation is an important part of analysis of producer-recorded health data. The objective of this study was to investigate the impact of 5 data validation methods on genetic evaluations for mastitis resistance in first lactation Canadian Holstein cows. As expected the number of usable herds and the number of records were increased with a less stringent data validation, whereas mastitis frequency was decreased. For genetic analyses, univariate and bivariate linear sire models were fitted. Heritability of mastitis was decreased with a less stringent data validation with estimates ranging from 0.013 to 0.026. Lactation mean somatic cell score was highly correlated with mastitis (0.65-0.69) independently of the applied data validation method for mastitis. Pearson correlations between sire breeding values for mastitis resistance based on the different data validation methods were all higher 0.95. Overall, the present study showed that genetic evaluations for mastitis resistance stay similar independently of the applied data validation method. However, there is evidence for some underreporting of mastitis cases in the Canadian health recording system. Therefore, future work is necessary to increase data quality in the Canadian health recording system.

Keywords: mastitis, data validation, Canadian Holsteins.

Introduction

In Canada, a national dairy cattle health and disease data management system started in 2007. The main objectives of this initiative are to provide information to dairy producers and their veterinarians for herd management and to establish a national genetic evaluation system for genetic selection for disease resistance. Eight diseases that are known to affect herd profitability are recorded by producers on a voluntary basis: mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries and lameness. The feasibility of using producer recorded health data for genetic evaluations for disease resistance in Canada has been previously shown by Neuenschwander *et al.* (2012) and Koeck *et al.* (2012).

In order to obtain reliable and accurate genetic evaluations, recording of disease cases should be as complete as possible on all participating farms. However, data quality can vary among farms and even for a given farm over time.

In the Scandinavian countries and Austria disease recording systems are implemented on a large scale and genetic evaluations for health traits are carried out routinely. Norway has a mandatory disease recording system for dairy cattle and, therefore, it is assumed that all herds report complete health data. Previously only herds with at least 1 recorded mastitis case per herd and year were considered for routine genetic evaluation in Norway. However, due to small herd size and declining disease frequencies in recent years, this data edit is not applied anymore (B. Heringstad, personal communication). Also, in Sweden, disease recording is mandatory and records from all cows are included in routine genetic evaluation (NAV, 2012). In contrast, Finland and Denmark include only records from herds that participate actively in health recording. In Finland only herds with at least 1 veterinary diagnose per herd and year are included (Y. Pösö, personal communication). In Denmark the herd is considered to be participating if the number of treatments is greater than or equal to 0.3 per calving in the period from calving to 4 or 9 months after calving. In the 9-month period, it is not allowed to be a 3 month period after birth, where there is no reported disease diagnosis in the herd. It is also a requirement that there is at least 7 and 10 calvings in the following 4 - and 9-month period, respectively (U. S. Nielsen, personal communication). In the routine genetic evaluation in Austria, only farms with a minimum average of 0.1 first diagnoses per cow and year are considered. Besides, continuous submission of health data by veterinarians or performance recording technicians is checked (C. Egger-Danner, personal communication).

In the present study the impact of 5 data validation methods on genetic evaluations for mastitis resistance in Canadian Holsteins is presented. The results should lead to a better understanding of data quality in the Canadian health recording system.

Material and methods

Health database

Health data from April 2007 to January 2013 were obtained from the Canadian Dairy Network (Guelph, Ontario). Summary of current data in the database is given in Table 1. The database consisted of 633,876 disease cases from 6,327 herds. Recording of mastitis was done in the majority of herds (88%), followed by displaced abomasum (66%) and retained placenta (62%).

The number of reported disease cases per year and month has shown a continuous increase from 2007 to 2010 and stabilized in the year 2011 (Figure 1). In contrast, the total number of herds recording health data remained almost unchanged in the last 5 years (Figure 2). In 2012, about 4,000 herds recorded health data, which accounts for 42% of all herds under milk recording.

Table 1. Summary statistics of the health traits database.

Health category	**Health event**	**% of disease cases**	**% of herds**
Mastitis	Mastitis	42.1	88
Displaced abomasum	Displaced abomasum	4.7	66
Ketosis	Ketosis	3.0	39
Milk fever	Milk fever	3.6	51
Retained placenta	Retained placenta	8.4	62
Metritis	Acute metritis	5.9	41
	Purulent discharge	3.9	22
	Endometritis	1.4	11
	Chronic metritis	2.4	23
Cystic ovaries	Cystic ovaries	12.1	49
Lameness	Lameness	12.1	57
	Foot rot, laminitis, sole ulcer and other claw disorders	0.4	7

Figure 1. Number of reported disease cases per year and month (dashed line represents delay in data delivery).

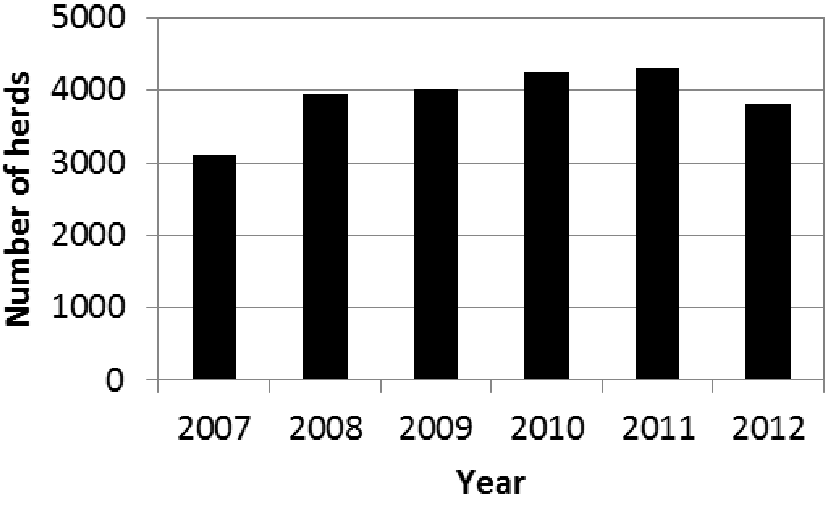

Figure 2. Number of herds recording disease cases per year.

Data validation and editing

For investigating the impact of data validation on number of records, mastitis frequency and genetic parameters 5 different data validation methods were analyzed. In the first 4 scenarios only herds with at least one recorded mastitis case were considered. The first recorded mastitis case was defined as the beginning of the data recording period. Additionally minimum mastitis frequencies per herd and year were applied for data validation methods A, B and C:

- Minimum mastitis frequency of 5% per herd and year (**Method A**)
- Minimum mastitis frequency of 3% per herd and year (**Method B**)
- Minimum mastitis frequency of 1% per herd and year (**Method C**)
- No minimum mastitis frequency per herd and year (**Method D**)

In the last scenario all herds with at least one recorded disease case (any disease) were considered. The first recorded disease case was defined as the beginning of the data recording period. To ensure a continuous data recording a minimum disease frequency of 5% per herd and year was also considered (**Method E**).

Holstein is the most common dairy cattle breed in Canada (constituting up to 90% of the dairy cows) and, therefore, almost all health records were from Holstein cows. For this reason, analyses were carried out for this breed only. For the analyses, only records from first parity cows were considered.

Trait definition

In Canada clinical mastitis cases are recorded by producers. Mastitis is defined as visually abnormal milk (e.g. clots, flakes, or watery) from one or more quarters, that may also include inflammation of the udder (e.g. heat, swelling, or discoloration) and systemic illness of the cow (Kelton *et al.*, 1998).

For analyses, mastitis was defined as a binary trait (0 = no mastitis, 1 = mastitis) based on whether or not the cow had at least one mastitis case in the period from calving to 305 d after calving. Test-day records between 5 and 305 DIM were considered for SCC. Test-day SCC was $\log_2$ transformed to SCS ($\mathrm{SCS} = \log_2(\mathrm{SCC}/100{,}000) + 3$) and averaged over lactation (**LSCS**).

Pedigree

The sire pedigree file was generated by tracing the pedigrees of sires and maternal grandsires back as far as possible.

Model

Linear sire models were fitted using the AI-REML procedure in the DMU package (Madsen and Jensen, 2008). Initially univariate models were run for mastitis. Subsequently bivariate models were run between mastitis and LSCS. In matrix notation, the model was:

$$y = X\beta + Z_h h + Z_s s + e$$

where **y** is a vector of observations for mastitis and LSCS; β is a vector of systematic effects, including fixed effects of age at calving and year-season of calving; h is a vector of random herd-year of calving effects; s is a vector of random additive genetic sire effects; e is a vector of random residuals; and X, Z_h and Z_s, are the corresponding incidence matrices. Random effects were assumed to be normally distributed with zero means, and $\mathrm{Var(s)}=A\sigma_s^2$, $\mathrm{Var(h)}=I\sigma_h^2$, $\mathrm{Var(e)}=I\sigma_e^2$, where σ_s^2, σ_h^2 and are the additive genetic sire, herd-year, and residual variances, respectively, I is an identity matrix, and A is the additive genetic relationship matrix.

Age at first calving had 16 classes, in which <22 and >35 months were the first and last class, respectively, and other classes were single months. Four seasons of calving were defined from January to March, April to June, July to September and October to December.

Results and discussion

Descriptive statistics

Table 2 gives an overview of the data validation methods. As expected the number of usable herds and the number of records were increased with a less stringent data validation, whereas mastitis frequency was decreased. Mastitis frequency was 12.7% based on the most stringent data validation method (A) and in agreement with previous studies. In a literature review, Kelton *et al.* (1998) found a mastitis frequency of 14.2% across studies. A higher mastitis frequency of 20% was obtained by Zwald *et al.* (2004) in US Holstein cows. In a more recent study, Mrode *et al.* (2012) reported a mastitis frequency of 13.5% in first lactation UK Holstein cows.

Mastitis frequencies based on data validation methods B, C, D and E were lower, which possibly indicates underreporting of mastitis cases in the Canadian health recording system.

Table 2. Impact of data validation on number of usable herd, records and mastitis frequency in first lactation Holstein cows.

	Data validation method				
	A[1]	B[2]	C[3]	D[4]	E[5]
Total herds, n	5,076	5,076	5,076	5,076	5,728
Usable herds, n (%)	2,995 (59)	3,342 (66)	3,697 (73)	5,076 (100)	4,110 (72)
Records, n	129,091	151,575	181,405	295,673	217,196
Sires with • 1 daughter, n	5,042	5,426	5,924	7,406	6,301
Sires with • 30 daughters, n	509	634	818	1,626	1,142
Mastitis frequency, %	12.7	11.4	10.0	6.5	8.6
LSCS	2.2	2.2	2.2	2.2	2.2

[1] A: At least one recorded mastitis case and a minimum mastitis frequency of 5% per herd and year.
[2] B: At least one recorded mastitis case and a minimum mastitis frequency of 3% per herd and year.
[3] C: At least one recorded mastitis case and a minimum mastitis frequency of 1% per herd and year.
[4] D: At least one recorded mastitis case.
[5] E: At least one recorded disease case (any disease) and a minimum disease frequency of 5% per herd and year.

Genetic parameters

Heritabilities and genetic correlations for mastitis and LSCS from bivariate analyses are given in Table 3. Generally, heritability estimates of mastitis (0.013 to 0.026) were in the range of previously published studies (e.g. Carlén *et al.*, 2004; Mrode *et al.*, 2012). Heritability of mastitis was decreased with a less stringent data validation method, whereas heritability of LSCS was nearly constant in the different analyses. The decreasing heritability estimate of mastitis can be partly explained by the decreasing mastitis frequency, as heritability estimates are frequency-dependent when applying linear models to binary data. However, heritability of mastitis was also decreased when transformed to the underlying scale using the classical formula of Dempster and Lerner (1950).

Lactation mean somatic cell score was highly correlated with mastitis (0.65-0.69) independently of the applied data validation method for mastitis.

Table 3. Impact of data validation on genetic parameters from bivariate linear sire models.

	Data validation method				
	A	B	C	D	E
Heritability, Mastitis	0.026	0.022	0.020	0.013	0.017
Heritability, Mastitis_DL[1]	0.067	0.060	0.059	0.049	0.054
Heritability, LSCS	0.123	0.125	0.123	0.122	0.124
Genetic correlation	0.69	0.66	0.65	0.66	0.68

[1] Heritability estimates were transformed to the underlying scale using the formula of Dempster and Lerner (1950).

Estimated breeding values

Pearson correlations between sire breeding values for mastitis resistance based on the different data validation methods are shown in Table 4. The correlations were all higher 0.95 showing that genetic evaluations stay similar across the data validation methods. Although in method E data validation was done across all diseases, genetic evaluation based on this method was highly correlated with the other evaluations. This can be expected, as mastitis is recorded in almost all participating herds.

Table 5 presents the number of top 100 bulls based on data validation method A that are in common with the other methods. Selecting the top 100 bulls based on any data validation method would not have major consequences on selection decisions. As expected the number of top 100 bulls that are in common with method A was slightly decreased with a less stringent data validation.

Conclusions

Data validation is an important part of analysis of producer-recorded health data. Less stringent data validation led to a lower mastitis frequency, indicating that possibly there is some level of underreporting in the Canadian health recording system. Although genetic evaluations stay similar across the investigated data validation methods, future work is necessary to increase data quality in the Canadian health recording system.

Table 4. Pearson correlations between sire breeding values for mastitis resistance from univariate linear sire models, only sires with at least 30 daughters in all data sets were considered (n = 509).

Data validation method	B	C	D	E
A	0.986	0.976	0.957	0.962
B		0.990	0.972	0.973
C			0.984	0.976
D				0.973

Table 5. Number of top 100 bulls in common with data validation method A, only sires with at least 30 daughters in all data sets were considered (n = 509).

Data validation method	Number of top 100 bulls in common with data validation method A
B	91
C	90
D	86
E	85

Acknowledgments

All dairy producers recording health data are gratefully acknowledged. This study was funded by the DairyGen council of Canadian Dairy Network (Guelph, Ontario, Canada) and the Natural Sciences and Engineering Research Council of Canada (Ottawa, Ontario, Canada).

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Aspects of validation and data quality based on veterinarian diagnoses

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Abstract

In Austria a health monitoring system for cattle was established between 2006 and 2010. Meanwhile registration of veterinarian diagnoses has been implemented into routine genetic evaluation as well as animal health programs. Presently from about 12.500 farms veterinary diagnostic data subject to documentation by law (Law on the Control of Veterinary Medicinal Products [*Tierarzneimittelkontrollgesetz*]) is standardized, validated and recorded in a central database.

Precondition for efficient use is correct health data. Therefore plausibility checks and data validation are of importance. For use and interpretation the data source and logistics of data recording have to be considered. By working with field data anybody has to be aware that the real incidence of disease will probably not be the same as the observed incidence based on the recorded diagnoses especially in subclinical diseases and disorders. Not all diseases will involve treatment or are treated depending on different herd management strategies and therefore lack recording. Additionally the challenge is to distinguish between farms with low frequencies of disease and incomplete documentation and recording. These limitations make data validation a key issue in health monitoring systems. Nevertheless data from broad health monitoring systems are very valuable for genetic evaluations, for surveillance purposes and herd health management.

The present paper covers aspects of data validation based on Austrian experiences with veterinary diagnoses for genetic evaluation, herd health management and the overall monitoring of the health status. Reasons for incomplete data and measures to improve data quality are presented as well.

Introduction

Health traits are becoming more and more important in breeding, herd management and in the context of prevention of diseases. Good data quality is necessary if any benefits are to be gained from health data. Experiences from different countries showed that it is challenging to establish a system of registration of veterinarian diagnoses. It is important that the system is adjusted to the existing circumstances and requires a minimum of additional work for farmers and veterinarians. The benefit for the stakeholders involved is essential.

Field data have the advantage of a big quantity of data from a wide range of different farms, but do not always provide complete data. Different validation studies from different countries showed different degrees of completeness (Bartlett *et al.*,2001, Mörk *et al.*,2010, Gaddies *et al.*,2012, Espedvedt *et al.*,2012). Field data do involve high emphasis on monitoring of the registration including plausibility checks and validation. Depending on the use of data different restrictions and criteria have to be applied. The present paper describes the aspects of data validation based on the Austrian circumstances and experience.

Material

The study is based on veterinary diagnoses in dairy cattle in Austria. Between 2006 and 2010 an Austrian wide health monitoring system was established. The overall aims were the development of a genetic evaluation for health traits, the provision of information for herd management und preventive work for farmers and veterinarians as well as benchmarks for monitoring the health status for the Austrian Ministry of Health and the Austrian Animal Health Organizations. A detailed description is found in Egger-Danner *et al.*,2012.

Registration of veterinarian diagnoses

The precondition for the recording of diagnoses is the availability of standardised data. By legal obligation, diagnoses and treatments have to be documented in Austria (Law on the Control of Veterinary Medicinal Products [*Tierarzneimittelkontrollgesetz*]). These documents have to be kept for 5 years by the veterinarians as well as the farmers. However, these data have neither been collected nor stored in a database. A standardized code consisting of 65 diagnoses divided into 10 categories was developed for the project and was published by the Ministry of Health before the start of the project in 2006. This coding system only includes diseases, which can be diagnosed on site by the veterinarians, but currently no laboratory results. A two-digit code for the standardized diagnosis was added to the receipt form for the documentation of medication (Law on the Control of Veterinary Medicinal Products).

Diagnostic data is recorded into the Austrian central cattle database. This has the advantage that validation checks can be done using the information gathered from identification and performance recording. Within the course of each disease the diagnosis is only recorded once (course diagnosis).

The diagnoses are collected by the performance recording organisations or may be sent electronically to the database by the veterinaries. The data are stored within the central cattle database (Rinderdatenverbund, RDV) in Austria.

Participation of farms in health monitoring in Austria

The project was based on voluntariness so that each farmer under performance recording was free to take part. Since 2011 recording of direct health traits is compulsory for the breeding program of most of the breeding organizations in

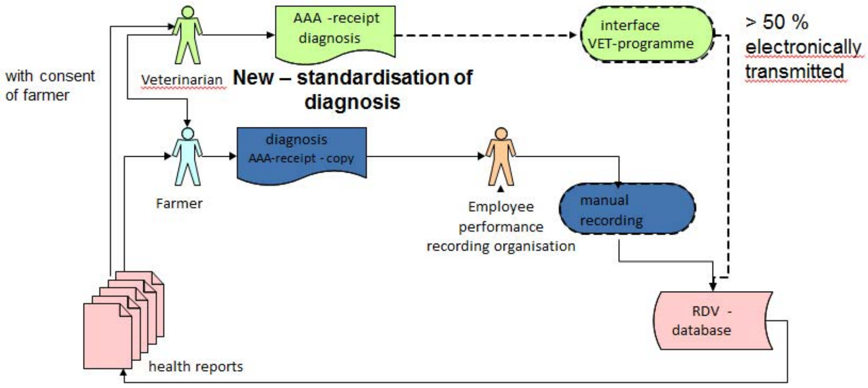

Figure 1. Data logistics for recording of veterinary diagnoses into the central cattle data base in Austria.

Austria. Figure 2 shows a marked increase in participation in 2011 and 2012 due to the decisions of the Cattle Breeding Organisations. The number of farms providing diagnostic data is increasing continuously but is lagging behind the decision of compulsory registration of health data. Big differences exist between federal states. There are some who have achieved an extent of above 90% of veterinary diagnoses, others are substancially lower.

Impact of data recording on frequency of diagnoses

Table 1 shows the incidence rates of the most frequent diagnoses in Austrian cattle depending on the type of data recording. VET means that more than 75% of the diagnoses of a farm are sent to the central cattle data base directly by the veterinarian. The other group includes farms where diagnostic data are recorded either by the employees of the performance recording organisations (PRO) and some farms where there is a mixture of types of recording. Table 1 shows that incidence rates of fertility disorders are higher if calculated with data electronically transmitted. The reason

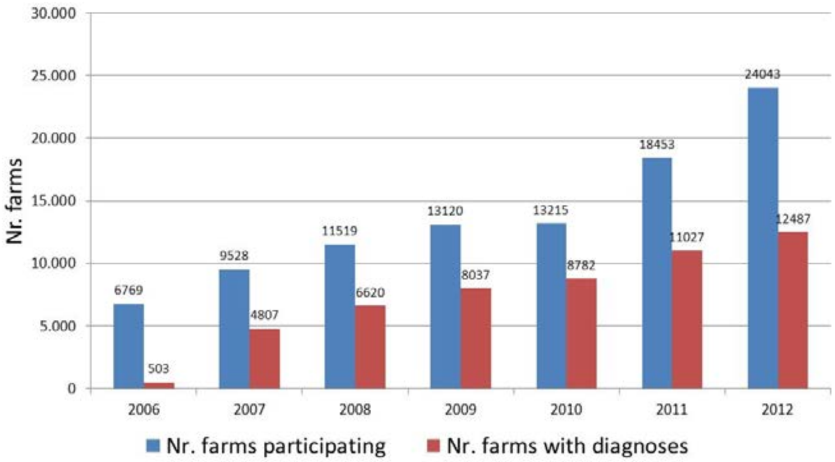

Figure 2. Participation of farms in health monitoring and nr. of farms with diagnoses.

Table 1. Incidence rates based on different data registration methods (more than 75% of diagnostic data submitted electronically (VET), and recording by employee of a performance recording organization or mixture (RPO)) for dairy cows under observation in 2012

Traits	VET	PRO	Diff
Validated dairy cows	36,756	110,597	
Metabolic disorders	**5.65**	**4.08**	**-1.57**
Milkfever	4.36	3.10	-1.26
Ketosis	1.06	0.78	-0.29
Reproductive disorders	**26.14**	**18.54**	**-7.60**
Metritis	5.34	3.36	-1.97
Anoestrus	9.59	6.50	-3.09
Cystic ovaries	9.90	6.57	-3.33
Prolapse of vagina	0.13	0.08	-0.04
Retained placenta	3.34	3.49	0.15
Puerperal disorders	2.05	1.10	-0.95
Udder disorders	**18.16**	**15.73**	**-2.43**
Acute mastitis	12.72	11.37	-1.35
Chronic mastitis	5.84	4.65	-1.19
Hoof and claw disorders	**4.12**	**3.48**	**-0.64**
Panaritium, DD	2.30	1.78	-0.52
Hoof ulcer	0.92	0.96	0.04

might be that if there is no waiting period for drugs used the documentation might not be complete. Due to the fact that veterinarians using electronic devices usually document all treatments irrespective of drug use because of internal organisational reasons. Another reason for the higher incidence rates might be that veterinarians who are using electronic devices are more active in prevention and routine checks.

Methods

The challenge of validation is to differentiate farms with low frequency versus farms with incomplete health data recording. One important precondition before storage of the data in the cattle data base are plausibility checks.

Plausibility checks

The plausibility checks applied before storage in the cattle data base include checks for correct ID of the animal, checks concerning plausibility of date (the animal has to be at the respective farm at the day of the diagnosis) and code of diagnoses. As only first diagnoses are recorded there is also a check concerning the respective time period for first diagnoses per code. More detailed information is found under Austrian Ministry of Health (2010).

Another important plausibility check is by farmer and veterinarian directly by provision of health reports und use within animal health programs. The inclusion of the registered veterinary diagnoses in the health reports facilitates a check for the correctness of the data by farmers and veterinarians. An incorrect documentation and recording of diagnostic data can be recognized and corrected.

Aspects of validation

Only validated data are used for genetic evaluation and the calculation of different benchmarks. Criteria for validation are continuous data recording and the definition of a valid observation period, the incidence rate per farm and the coding of the diagnoses.

Valid observation period

A valid observation period is defined per farm and per animal. In the first step a valid observation period with compulsory recording of diagnoses is calculated taking the date of joining the health monitoring program, the data of the first diagnoses per farm and information concerning start of data transmission into account. As farms do have very small herdsizes it is possible that for a certain period the farm is already providing reliable data, but no case of diagnoses occurred. Continuity of data recording and an eventual ending of health data registration is checked as well. Based on that information for all dairy cows the valid observation period is defined.

Incidence rates of farms

A minimum requirement of 0.1 first diagnoses per cow and year are applied. Only time periods fulfilling these requirements are considered. The incidence rate of first diagnoses validated for genetic evaluation was on average 0.5 diagnoses per cow and year. For electronically transmitted data the incidence rate is 0.7 first diagnoses per cow.

Coding of diagnoses

In Austria diagnoses are standardized by codes for 65 diagnoses. In Egger-Danner *et al*. (2012) the distribution of the different codes of diagnoses per lactation is shown. On average about 40% of the diagnoses are due to fertility disorders and around 35% are due to udder health problems. Veterinarians working with practice management software often use a more detailed list of diagnoses for their own documentation. To link this to the standard codes of diagnoses published by the Austrian Ministry of Health in 2006 a list of synonyms is provided. For genetic evaluation complex traits definitions are used e.g. acute and chronic mastitis are combined to clinical mastitis. Therefore variations in coding of specific diseases between the veterinarians do not cause major problems for genetic evaluation presently, for calculation of incidence rates and monitoring of specific diseases it matters much more. Figures 3 to 7 show the variation in codes of diagnoses by veterinarians restricted to veterinarians with a minimum of 500 diagnoses. The reasons might be that some vets are more specialized in certain diseases or that some veterinarians are working in prevention and e.g. ultrasound examinations

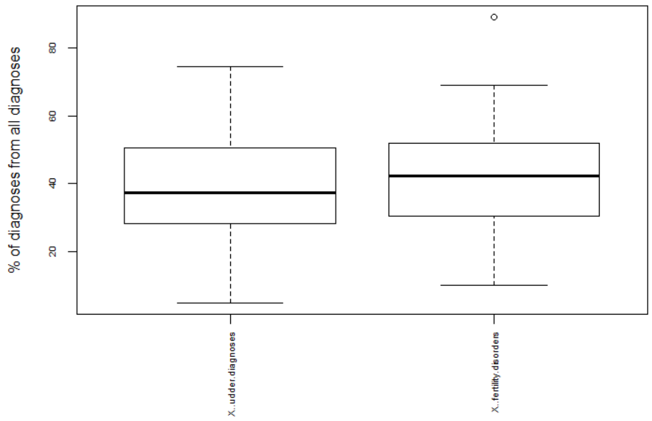

Figure 3. Variation in the percentage of fertility disorders and udder diseases per veterinarian of farms validated for genetic evaluation in 2012.

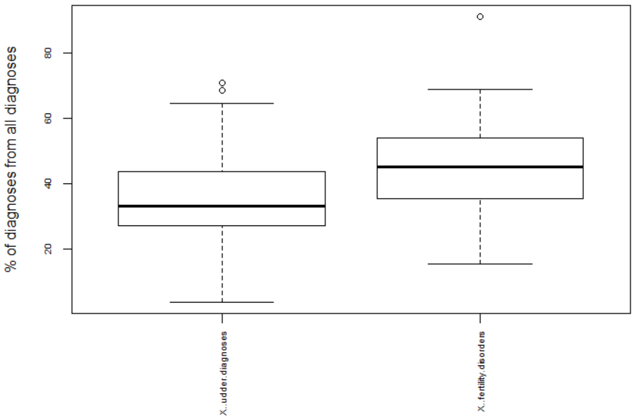

Figure 4. Variation in the percentage of fertility disorders and udder diseases per farm validated for calculation of benchmarks in 2012 (elect. data transmission).

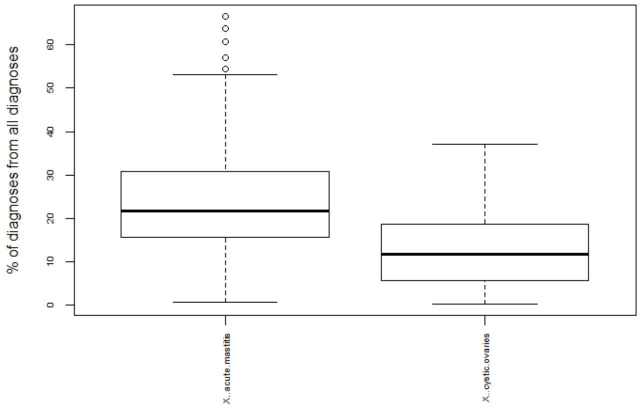

Figure 5. Variation in the percentage of acute mastitis and cystic ovaries per veterinarian of diagnoses from farms validated for genetic evaluation in 2012.

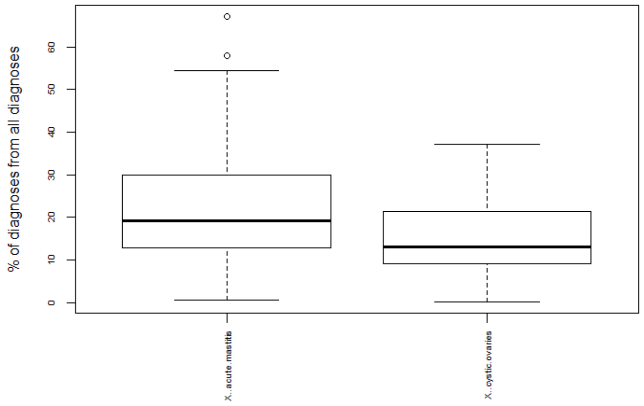

Figure 6. Variation in the percentage of acute mastitis and cystic ovaries per veterinarian of diagnoses from farms validated for calculation of benchmarks in 2012 (elect. data transmission).

are standard. Incorrect coding or mistakes in linkage of codes of diagnoses according the list of synonyms might also be reasons as well as a higher incidence of specific diseases in certain farms or regions by time. Future studies are needed to assess differences in coding in detail.

Other aspects of validation

The completeness of recording of diagnoses could be validated by the usage of additional information. Since 2012 in Austria additional health relevant observations are recorded together with recording of calving ease. This information will be considered in the future to achieve a higher degree of completeness of information.

Use of data

The requirements for validation are depending on the use of data. For herd management only plausibility checks are applied. For genetic evaluation less stringent validation is applied compared to the calculation of benchmarks. The statistical models used in genetic evaluation account for different environmental effects (effect of farm, year *season and type of recording) (Fuerst *et al.*,2010). As a huge amount of data is needed, there is the question about more stringent validation and higher heritabilities or a higher amount of data and lower heritability (Egger-Danner *et al.*,2009). One aspect is that due to low frequencies of certain diagnoses and the requirement of stable breeding values very often a combination of different diagnoses is used for estimation. Koeck *et al.* (2010) shows that the correlation between different fertility disorders are very high and that e.g. early fertility disorders are more stable than single traits like retained placenta, puerperal disorders and metritis. Therefore she recommends the aggregation of different single fertility disorders to early and late fertility disorders. If this is done the conditions concerning coding are not that strict. The conditions for the calculation of benchmarks and the monitoring of diseases are different. The benchmarks should reflect the real incidence to a high degree. Therefore the requirements on the data quality are higher and more stringent validation criteria are applied. The amount of farms participating is not that important.

Results and discussion

As shown in Egger-Danner *et al.* (2012) about 30% of the farms with diagnoses are excluded for genetic evaluation. The percentage varies between regions. Studies from other countries (e.g. Neuenschwander (2010), Gaddies *et al.* (2012)) also show that high percentages of farms are excluded. If producer-recorded health data are used the fact that a farm is working one year more on e.g. udder health is of higher relevance compared to documentation systems based on the legal documentation requirements connected with the application of drugs. Nevertheless it has to be considered that there are differences in documentation of diseases requiring the application of drugs with waiting period or not.

For the calculation of benchmarks for the Austrian Ministry of Health and the Austrian Animal Health Organizations only data from farms where at least 75% of the diagnoses are transmitted electronically by the veterinarians are used. Further work on validation is in progress.

Three different levels of validation were applied. Restrictions on herdsize were the same for all three levels. Figure 7 shows the distribution of farms according to the percentage of cows with diagnoses in 2012.

No validation/loose (LOOSE). There was no emphasis put on the definition of a valid observation period per farm. The first recorded and last recorded diagnoses per farm were relevant for the calculation of the percentage of animals per farm with certain diagnoses. This group includes 6,111 farms.

Validation for genetic evaluation (EBV). Due to the small herd sizes in Austria the first recorded and last recorded diagnoses per farm might not be the reliable factor for determination of the observation period. Therefore additional information from the veterinarian and the employee of the performance recording organization was used. Incidence rates per farm and year were calculated and only years where the incidence rate was above 0.1 first diagnoses per cow and year were considered. This group consists out of 4,579 farms.

Validation for the calculation of benchmark (VET75)s. Additional to the criteria for genetic evaluation the dataset was restricted to farms where more than 75% of the diagnostic data ware sent electronically by the veterinarian. 1,522 farms are included.

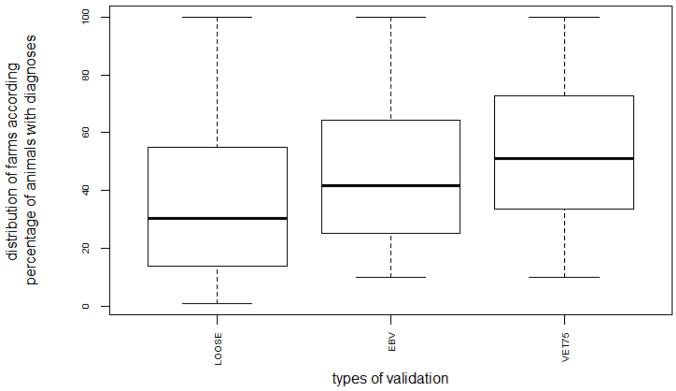

Figure 7. Distribution of farms according to percentage of animals with diagnoses in 2012.

Evaluation of reasons for incomplete data

To improve data quality it is important to know about the reasons of incomplete data. In 2010 a survey based on 600 farms, which were excluded due to validation criteria, was carried out. The survey showed that despite promotion, not all farms or their veterinarians are providing reliable health data. The main reasons for incomplete data mentioned were missing documentation of treatments in general, missing standardization, or that not all available receiptswere provided by the farmer. However, with awareness-building activities and regular information, data quality could be improved.

Measures to improve data quality

Monitoring of recording

Continuous monitoring and evaluation of measures to improve health data quality is done regularly. There is need for further improvement of validation and the provision of regular feedback.

Recording of health data

To improve completeness of data additionally to the registration of veterinarian diagnoses and the possibility for the farmers to record health observations in the data base, recording of health observations around calving by the EPO was started in 2012. Some federal states have already reached a completeness of recording of 95%.

The first priorityare veterinarian diagnoses. Legal documentation requirements are existing. The veterinarian diagnoses are the precondition for the use of synergies and the collaboration of farmer and veterinarian in prevention of diseases.

Continuous information and motivation

Precondition for implementation and maintaining a health monitoring system is the motivation of farmers and veterinarians for documentation and provision of information. The benefit of use of the data is essential. The Austrian experiences show that information and motivation is more challenging than technical aspects.

Further development of benefits of recording

To increase the benefit of health data recording further developments together with partners from the German federal states Bavaria and Baden-Württemberg are in elaboration. These include further work on genetic evaluation and further services for herd management for farmers and veterinarians. An online-platform for veterinarians has been developed. Features for easier documentation of drug use on a voluntary basis are in elaboration..

Real incidence and observed incidence

If diagnostic data based on a nationwide health monitoring system are used it has to be considered that the observed incidence will not necessarily reflect the real incidence of diseases. It depends on the decision of the farmer whether a veterinarian is consulted. Some farmers react earlier others do not consider e.g. a SCC above a certain level a problem Nevertheless field data have the advantage that a huge amount of data is available at low costs. But, high emphasis has to be put on validation.

Conclusions

A good data quality is the precondition for benefit out of health data recording. To motivate farmers and veterinarians to put emphasis on documentation and recording of diagnostic data, additional benefit has to be provided to farmers and veterinarians. Benefits can be breeding values, information for herd management and prevention or easier documentation requirements. Constant monitoring of the registration as well as feedback to the people involved is important to assure a good data quality continuously. Emphasis has to be put on validation especially when a system of health data recording is newly established. The requirements for validation may depend on the use of data. Field data offer the chance that a huge amount of data with limited effort of recording is available. Nevertheless data from broad health monitoring systems are very valuable for genetic evaluations, for surveillance purposes and herd health management.

Acknowledgement

The authors gratefully acknowledge the collaborative work of the project partners in Austria (Federation of Austrian Cattle Breeders, ZuchtData EDV-Dienstleistungen GmbH, University of Natural Resources and Life Sciences Vienna, University of Veterinary Medicine, Chamber of Agriculture, Chamber of Veterinaries, animal health organizations, performance reporting organizations, breeding organizations) to establish a “Health monitoring system in cattle”, and also wish to thank all participating dairy farmers and veterinarians. The project was financed by the Federal Ministry of Agriculture, Forestry, Environment and Water Management (BMLFUW) of Austria, the Ministry of Health and the Federation of Austrian Cattle Breeders (ZAR). Validation and provision of benchmarks are especially supported by the Austrian Ministry of Health. The authors thank the partner organizations from the German federal states Bavaria and Baden-Württemberg for the good cooperation in developing a health monitoring system.

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Validation, use and interpretation of health data: an epidemiologist's perspective

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Abstract

The Canadian National Animal Health Project was launched in 2006 in an attempt to stimulate the consistent recording of important health events on Canadian dairy farms, and to move these event data into the national milk recording database. In 2005, the year prior to the launch, just over 14% of herds nationally were contributing health event data to the national database. The contributing herds increased to almost 50% in 2007 and reached a peak of just over 70% in 2011. The primary use of these event data is at the farm level, where dairy producers and their veterinarians and other advisors use these data to monitor health and productivity, to motivate changes in management and to measure the outcomes of these changes. Moving these data into a central system for surveillance, benchmarking and genetic evaluation is a secondary use and still does not get much attention from many producers. As a consequence, there are issues with variability in disease definition and in the consistency of recording across various disease conditions. The most frequently recorded health event across the country is mastitis. Based on data from 6,438 herds of 10,021 enrolled in milk recording in 2008, we estimated that the incidence of clinical mastitis in Canadian dairy herds was 19 cases / 100 cow-years. A very intensive farm level study involving 91 herds from across Canada as part of the Canadian

Mastitis Research Network National Cohort of Dairy Herds program reported a clinical mastitis incidence of 26 cases / 100 cow-years. A comparison of these data would suggest that we still have an under-reporting of health events, even in those herds who are actively recording and forwarding health event data. Nonetheless, these data have been used to generate genetic parameters for health traits in Canadian Holstein cattle, and continue to increase in quantity and quality.

Keywords: health data, validation, incidence, monitoring.

Introduction

Dairy herd improvement (DHI) organizations have a longstanding history of recording production data, event data and some regularly assessed health data on dairy farms for fuelling the record of performance and genetic evaluation processes. While there are challenges to collecting and validating these data, they have the advantage that they occur regularly on every farm for every animal. For instance, every cow must calve to produce milk, hence she will have a calving date. Every lactating cow should produce milk on DHI test day, the milk will have an associated weight, composition (fat, protein, lactose) and can readily be assessed for subclinical mastitis by measuring the somatic cell count (SCC). Issues around the accuracy of animal inventories, measurement instruments and animal identification are the primary focus of data validation.

Sporadic health events (diseases that occur irregularly, if at all, to some animals at certain stages of lactation / life) have been recorded by dairy farmers on dairy farms since the earliest days of organized herd health (Harrington, 1979) and likely well before that. These data have value at the farm for managing animal health, for sorting and segregating individuals and groups, for making therapeutic and preventive treatment decisions and for deciding which animals to keep and to breed. These data also have potential value beyond the farm, aggregated at the local, regional, national or international level for the purposes of benchmarking, surveillance, documenting health status for international trade and genetic evaluation (Koeck, 2012). The Canadian National Animal Health Project was launched in 2006 in an attempt to stimulate the consistent recording of important health events on Canadian dairy farms, and to move these event data into the national milk recording database. In 2005, the year prior to the launch, just over 14% of herds nationally were contributing health event data to the national database. The contributing herds increased to almost 50% in 2007 and reached a peak of just over 70% in 2011. Recording of 8 diseases that are believed to have an effect on herd profitability are recorded voluntarily by dairy farmers. These diseases are mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries and lameness. These data have been used to generate genetic parameters for health traits in Canadian Holstein cattle (Neuenschwander *et al.*, 2012; Koeck *et al.*, 2012), and continue to be the source of research investigators nationally and regionally.

For disease data to be useful for benchmarking (a collection of summary statistics for all herds within an appropriate group based on farm type or geographic location that a member of that group can compare themselves to) and surveillance (the routine of collection and reporting of disease data for the purpose of identifying unusual patterns, either the emergence of a disease that has not been present previously or an increase in the frequency or severity of endemic disease), they must be readily aggregated and transformable into summary statistics. Disease data are most commonly presented as prevalence proportions (proportion of diseased individuals at a point in time) or incidence rates (number of new cases per animal unit time at risk) (Dohoo *et al.*, 2009). Generating these summary values depends upon being able to accurately count the number of individuals affected (the numerator), the number of individuals at risk (the denominator), and the duration of time that each individual or group are at risk and are being observed. Recommendations for these in the context of the diseases of major significance in dairy cattle have been published (Kelton *et al.*, 1998). Given the quality of inventory data in most milk recording databases, the denominator and time components are relatively easy to generate. The most difficult element to estimate accurately at either the animal or aggregate level is the numerator.

There are many challenges to aggregating these disease numerator data beyond the farm, including variability in disease definition at the farm, inconsistency in case definition and regular accurate data validation.

The Numerator: disease definition

Since diseases of dairy cattle vary from the simple to the complex, the identification and recording of these disease events also varies. A number of approaches to disease recording have evolved and these may vary dramatically among farms in the same geographical region. These disease classification systems can be based on aetiology, severity, epidemiology, duration and target body system. In some cases diseases are subdivided by etiologic agent (mastitis), while in other instances diseases are combined based on a belief that they have a shared causal pathway (ketosis and displace abomasum). Ultimately, it is important to understand and refine the level of classification relative to the intended use of the disease data, especially if these data are being aggregated across farms.

Consider the decision to record cases of ketosis on a dairy farm. This is based on agreement among the herd owner / manager, farm staff and perhaps the herd veterinarian, that the disease is of importance and knowing which cows had the disease is useful in guiding treatment or prevention. If the disease is not considered of importance, then the disease will not be routinely recorded. The absence of ketosis events in a farm data file does not mean the disease is absent, only that the disease was not considered important enough to identify and recored.

The challenge in agreeing upon a consistent disease definition is not small. For example, will ketosis be recorded simply as a binary event (yes / no) or on the basis of clinical progression (no ketosis, sub-clinical ketosis, clinical ketosis)? Does there need to be a distinction between primary ketosis and ketosis secondary to disease conditions such as displaced abomasum? Will the recording of ketosis be based on a definitive diagnosis of the disease condition by the herd veterinarian or the treatment of a putative ketosis case by the herd owner / manager or farm staff? Will the diagnosis be based on cow-side tests (milk or urine tests) or laboratory tests (blood or milk)? Which cow-side test(s) will be used (breath, powder, tablet, reagent strip) and what do we know about the sensitivity and specificity of the test(s)? Which ketone body (acetone, acetoacetate or beta-hydroxybutyrate) will be measured and which body fluid will be used (urine, milk or blood)? Should there be a distinction between a mild case (off-feed) and a severe case (nervous ketosis)? Will the diagnosis be based on human observation or on in-line sensors that are becoming more common in milking systems (Rutten, 2013). The answers to these questions will determine the disease definition for ketosis on one farm, but may be dramatically different on a neighbouring farm. Aggregating these disparate ketosis cases into a common database can be problematic and will add to the variability and perhaps inaccuracy of the summary data produced for benchmarking, surveillance and genetic evaluation.

Disease coding and standardization of nomenclature is an important area of discussion both in human and veterinary medicine (Case, 1994). Less attention has been directed towards the standardization of disease definitions and recording protocols. The International Dairy Federation (IDF) has established a set of international guidelines for bovine mastitis (Osteras *et al*., 1996), the American Association of Bovine Practitioners has made recommendations for reproductive performance (Fetrow *et al*., 1994) and standard definitions for eight clinically and economically significant diseases of dairy cattle are currently under discussion in Canada (Kelton *et al*., 1997). While some classification guidelines are being developed, there is still a general lack of utilized standard disease definitions and recording guidelines.

The Numerator: case definition

One of the greatest challenges in aggregating disease data and calculating incidence is deciding what constitutes a disease event, and do we count all disease events for a cow or just the first one in a lactation (a common practice when calculating a lactational incidence rate or risk). If we consider the ketosis example once more, is the recording of a case being triggered by a diagnosis and treatment, or simply by the preventative treatment of a cow considered at risk for developing ketosis? Should all treatments be recorded and counted as unique and individual events, or should only the first in a string of treatments for a unique case be recorded? How does one distinguish when a second diagnosis of ketosis, in the same animal, during the same lactation is a new case as opposed to a relapse or continuation of an existing case? The challenge becomes greater when we consider mastitis, which can be differentiated both by udder quarter and by etiologic agent or pathogen. Do we count only the first case of mastitis, regardless of quarter or pathogen, in a lactation? Do we enumerate each uniquely infected quarter and further distinguish by pathogen? These issues may seem trivial, yet they are critically important to consider when we summarize data from multiple sources. It is important to realize that there is no one correct answer to each of these questions, but it is important that our methods are recorded and that when we compare among regions or groups, that we use the same protocols.

The Denominator: Time at risk

In order to generate appropriate summary statistics that account for the number of animals at risk of either having or developing disease, we need to have accurate inventory numbers and we need to consider the dynamics of the population or herd. When we calculate disease prevalence, the denominator is simply the total number of animals that could be diseased that are present at that point in time. To calculate an incidence rate however, the denominator becomes considerably more difficult as we are seldom dealing with a closed population. Even in herds of static size that do not buy and sell cattle for commercial purposes, the average herd turnover of 35% means that one third of the cows will leave in a 12 month period, and will be replaced by new individuals. The matter becomes more complex when we consider that the period of risk varies by disease. Let us consider the ketosis example once more. When summarizing the data do we consider all cows equally at risk of developing ketosis, or is there a parity consideration? Should all lactating cows be considered at risk of developing disease, or are cows only at risk for clinical ketosis during the first 4 weeks post-partum? All of these questions must be asked and answered before a uniform and consistent estimate of cow time at risk can be developed for a herd. In addition, if the data are to be pooled or compared across farms, then there must be consistency of definition across all herds contributing to the system.

Disease event validation

The final challenge in using aggregated health data from many herds is validating the accuracy and consistency of recording. Moving the health data into a central system for surveillance, benchmarking and genetic evaluation is a secondary use for these records and as such does not get much attention from many producers. As a consequence, there are issues with variability in disease definition and in the consistency of recording across various disease conditions (Wenz, 2012). The most frequently recorded health event across Canada is mastitis. Based on data from

6,438 herds of 10,021 enrolled in milk recording in 2008, we estimated that the incidence of clinical mastitis in Canadian dairy herds was 19 cases / 100 cow-years. A very intensive farm level study involving 91 herds from across Canada as part of the Canadian Mastitis Research Network National Cohort of Dairy Herds program reported a clinical mastitis incidence of 26 cases / 100 cow-years. A comparison of these data would suggest that we still have an under- reporting of health events, even in those herds which are actively recording and forwarding health event data.

Under reporting is a common issue and can have many component causes, including; the starting and stopping of recording of a particular disease event at unpredictable and undocumented times; failure to transcribe all events to a repository (farm computer for instance) from which the records move up the data chain (Figure 1); the many individuals or technologies responsible for identifying and generating the disease event data; and seasonal variation in the intensity and consistency of animal observation needed to identify disease events.

Data validation varies in complexity depending on the types of data being captured. For instance, in traditional milk recording data it is relatively easy to identify a missing milk weight or SCC value if the cow has a record at the preceding test and the following test. Having identified that the data element is missing, one can move ahead and determine how to deal with the missing value. With health data, one does not know if the lack of a disease event is because the event did not happen (the cow did not experience the disease), if it was missed (failure to identify or correctly attribute the disease event), if it was not recorded by the observer, if it was not transcribed correctly into the farm record (paper or computer), or if it was not transferred to the central database. In this case the absence of a single case of ketosis on a 50 cow dairy might be indicative of a healthy herd (a good thing) or the failure to recognize and record a potentially important health event (not so good). The time and effort involved in validating health records is substantial, and in most cases well beyond the resources of most organizations. Even in well established systems with a strong history of support, deficiencies have been indentified (Espetvedt, 2013).

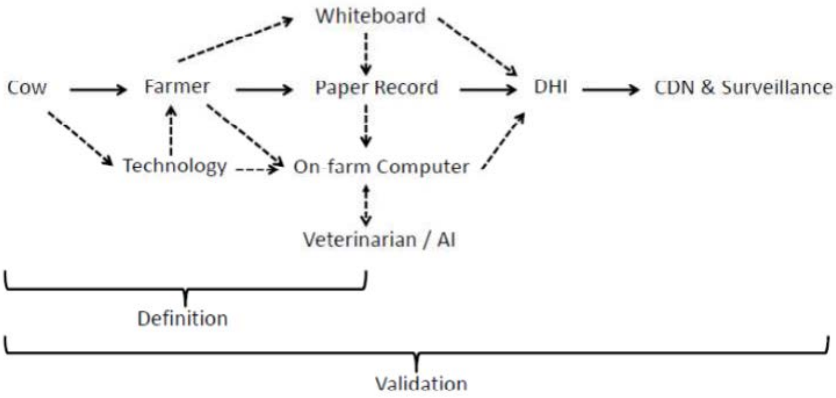

Figure 1. Disease data flow incorporating issues of definition and validation.

Conclusions

There are many good reasons to aggregate health data from many dairy farms into a single database, including benchmarking, surveillance and genetic evaluation. In the ideal world, we would choose to establish standardized disease definitions, use standardized case definitions, count animal time at risk in a consistent manner and then generate well defined summary statistics from accurate and consistent data. Our attempts in this area have been only partially successful at best. Recognizing that the aggregating of disease events represents a secondary use of these data (the primary use is at the farm level), we must decide how important the inevitable variability will be, the impact it will have on our benchmarks or genetic evaluations, and hence whether the degree of error in the system is acceptable.

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Session 5

Benefits of health data recording

The value of health data from dairy farmers in the United States

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Abstract

In the United States, most dairy farmers who use on-farm dairy management systems voluntarily record health incidences to facilitate effective cattle management. However, there is no national effort to organize or regulate the recording of health data such as enforcing standard or consistent definitions of health conditions. But when the data have been aggregated into experimental databases, several researchers have been able to compute lactation incidence rates, heritabilities and reliabilities at levels that are relatively comparable with other studies. PCDART from DRMS is one of three primary on-farm software systems that service dairy farmers and provide typical methods for data recording such as flexible health definitions, unlimited number of events and assistance with consistent within farm recording. There are 3250 herds (845K cows) that are managed by producers using PCDART and also enrolled on DHIA. Herds are representative of U.S. herd sizes and breeds. Of these herds, 44% deliver health incidences for off-farm backup at DRMS. Another 45% of herds also record health incidences at a lower rate, but these herds do not routinely deliver data files for off-farm backup at DRMS. Data recording histories for 'backup' herds were assessed for calving years 2009 through 2011 for entry of 34 recognized mature cow conditions of varying value to the dairy industry. Lactation incidence rates were similar to those found in earlier studies under more controlled environments. Additionally, the rates of entry of health events for large 'non-backup' herds were comparable to those of large 'backup' herds. 'Backup' herds recorded a mean of 123 events per 100 cows per year and 65% of herds recorded a minimum of 10 usable events per 100 cows per year. Larger herds (number of cows>500) recorded useful data at almost twice the rate of smaller herds. The most prevalent conditions were mastitis, lameness, metritis, cystic ovaries, other reproductive problems, retained placenta, Johne's and ketosis. There is sufficient potential in both volume and quality of U.S. health data to contribute to computation of meaningful genetic measures for selection using conditions of concern to producers.

Keywords: health events, farmer input, on-farm.

Introduction

Efforts in the United States to coordinate the collection of health event data from dairy farmers have not been successful for two primary reasons: lack of a mandated and structured system and expected vulnerability of information from private dairy farms when data are placed under the control of governmental agencies. However in the U.S., most dairy herd managers rely on one of just a few different on-farm dairy herd management software systems to record dairy cattle health events in a within-herd structured manner. The incentives for farmers to record health incidences are rooted in their desire to quantify incidence rates, manage treatments and minimize financial losses resulting from impacts of disease and threats of contaminated milk or meat. This presentation will describe the breadth, depth and current availability of health events from U.S. dairy producers to be used in a national Genetic Evaluation Program.

Dairy Records Management Systems (DRMS) is one of four dairy records processing centers in the United States and, as of January 1, 2013, DRMS centrally processed DHIA records for 13,432 herds with 2,109,684 cows, 48.7% of the cows enrolled on DHIA. Currently, 3,250 herds use the DRMS' PCDART on-farm dairy herd management software. Cows in these herds represent approximately 40% of the cows serviced by DRMS.

In PCDART, dairy farmers may assign their own 4-character mnemonic codes and 12-character description that fits their management schema of disease management. Although this allows personal customization and a wide range of terms to describe identical diseases, it also makes it difficult when using these data for genetic assessment. Attempts to standardize within the U.S. dairy industry have proven futile but recent research at North Carolina State University (Parker Gaddis, *et al.*, 2012) has affirmed that these data as currently reported can be used effectively to predict genetic value of breeding animals.

This presentation will address the current potential and availability of health events from on-farm dairy herd management systems, numbers of herds, the rates of reporting and the resulting volume of data that might be available to contribute to a U.S. national evaluation of dairy health events.

Data evaluated

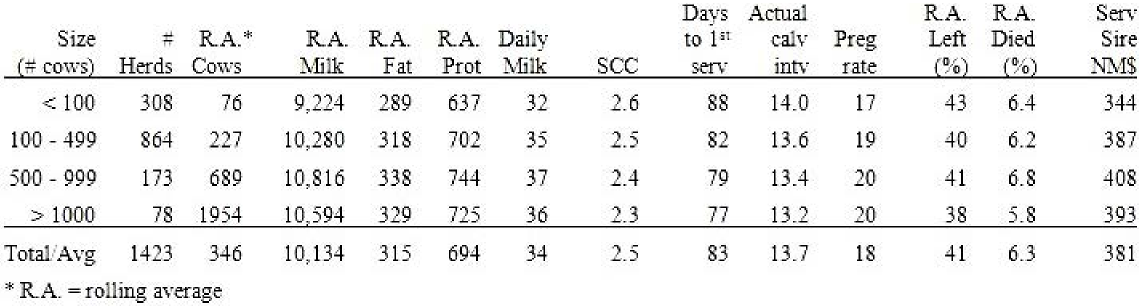
Data included lactation records and health events from herds that were enrolled on PCDART for a minimum of two calendar years during the period of January 1, 2009 and December 31, 2012. Corresponding lactation records were edited to include those initiated during January 1, 2009 through December 31, 2011 for cows in parities one through five with complete and valid animal identification and cows not terminated during the lactation. There were 549,393 cows with 841,604 lactations in 1423 herds. Breed distribution was 89.8% Holstein, 5.8% Jersey, 3.1% crossbred and 1.2% others.

Geographically, there were herds in 42 of the 48 continental states with a fairly even distribution in most regions except for a lower concentration in the western dairy states of California and Washington.

Table 1 characterizes several herd metrics by herd size. On average, smaller herds produced less milk, produced milk with slightly lower quality, had lower reproductive performance, had a greater rate of herd turnover, experienced cows dying at a higher rate and used lower quality service sires as measured by Net Merit.

Health event data were standardized using 4-character mnemonic codes and 12-character descriptions as defined by each dairy farmer and were corrected for inconsistency and improper spelling. Table 2 lists example 4-character mnemonic codes and illustrates the variety of classification across herds. Health events totaling 4,659,600 from the four-year period were edited to include only events from adults within parities one through five and recorded within 365 d of calving. Data were further edited to include only events from one of 34 targeted categories yielding 2,029,263 health events. This included additional edits to eliminate events of dystocia and retained placenta greater than 7 days within calving.

Table 1. Average herd characteristics by herd size.



Size (# cows)	# Herds	R.A.* Cows	R.A. Milk	R.A. Fat	R.A. Prot	Daily Milk	SCC	Days to 1st serv	Actual calv intv	Preg rate	R.A. Left (%)	R.A. Died (%)	Serv Sire NM$
< 100	308	76	9,224	289	637	32	2.6	88	14.0	17	43	6.4	344
100 - 499	864	227	10,280	318	702	35	2.5	82	13.6	19	40	6.2	387
500 - 999	173	689	10,816	338	744	37	2.4	79	13.4	20	41	6.8	408
> 1000	78	1954	10,594	329	725	36	2.3	77	13.2	20	38	5.8	393
Total/Avg	1423	346	10,134	315	694	34	2.5	83	13.7	18	41	6.3	381

* R.A. = rolling average

To be included, herd-years were required to have a minimum of at least one reported incidence of the targeted health event and a minimum of 5 cows. To eliminate excessive reporting levels, herd-years were excluded when the reporting frequency exceeded 2 standard deviations above the mean reporting frequency for that health event.

Records were excluded when the herd was not enrolled on PCDART for two complete calendar years. Although such a restriction may not necessarily be relevant, it afforded expeditious data assessment but more importantly it eliminated initial partial years when dairy producers were learning the system and final partial years when dairy farmer attention may be waning.

Seventy-nine percent of the herds (n=1094) contributed data for the entire four years; 8 percent (117 herds) contributed data for three years and 13 percent (179 herds) contributed data for two years. The average annual turnover of herds on PCDART for the past five years has been 12% enrolling herds and 8% withdrawing herds so

Table 2. Examples of mnemonics used to denote health events.

Health event and associated mnemonics
CYST=cystic ovary: 2CYS,3BRD,CFLO,CFRO,CLO,CLO1,CLO2,CRO,CSTO,CSTR,CY L, CY R,CY-L,CY-R,CYL,CYR,CTLN,CYBO,CYEX,CYLO,CYLR,CYRO,CYRT,CYS,CYSL, CYSR,CYST,CYVE,FCLU,LCST,LCY,LCYS,LOCY,OPCS,OVCO,OVCY,PO3X,POLY, RCY,RCYS,ROCY,STAT,CYST,CIST
KETO=ketosis: ACET,ACID,ACIT,ACTI,FEKE,IV,KE,KET,KET1,KET2,KET3,KETD,KETH, KETO,KITO, KTOS,NVKT,KETO,KET5,KET.,KETS,KET+
LAME=lameness: BDFT,BLCK,BLK,BLKF,BLOC,BLOK,F-RT,FEET,FINJ,FOOT,FROT, FTAB,FTLG,FTR,FTRT,HOBB,HOCK,HOOF,HROT,LAME,LEG,LEGS,ROT,WRAP,LAME, LIMP,LAMN
MAST=mastitis: EMAS,FREM,M +2,M +3,M 4Q,M GG,M HF,M LF,M LR,M RF,MRR,M.F., M-?,M+,M-1,M-2,M-3,M-4,M4QT,MAS,MAS4,MASR,MAST,MBAG,MLF,M-F,MLFQ,MLR, M-LR,MLRQ,MMQ,MRF,M-RF,MRFQ,MRR,M-RR,MRRQ,M-E,MST1,MST2,MST3,MSTA, MT,MT2+,MTRE,Q.MA,QMSR,QTMS,QTMT,QUAR,QUTR,STAP,STAR,STPH,STPQ, STRP,TOX,TOXI,TOXM,TX,TXCQ,TXIC,MYCO,DUMP,MAS1,MLFQ,MBRQ,MBLQ, MA2+,MFRQ,MAST
METR=metritis: ECP,MET,METR,MTRI,PUS,PUSS,PYMO,PYO,PYOM,UTME,METR, ENDO,MET1,MET+
RETP=retained placenta: RETP,NCLN,R.P.,REPT,RETA,RETP,RFM,RFS,RMAB,RP,RPIN, RPL,RPRE,RTFM,RTPL,UTRP

the current effective availability of data will probably persist or increase. As new dairy farmers become accustomed to the system and how to capitalize on the opportunities of recording health events they will probably add increasing numbers of health events.

Health events were initially chosen for inclusion based on prevalence in the database. It is acknowledged that it will be important to apply additional criteria when deciding whether a health event should be targeted for genetic evaluation. Kelton, *et al*. (1998) advised that diseases must meet “most, if not all, of the following criteria”:

1. the disease was currently recorded and reported;
2. the median reported frequency of occurrence of the disease in adult dairy cows was 5% or greater;

3. the disease had a documented economic significance; and
4. the disease manifested itself clinically such that a discrete case definition, which could be used by a producer or veterinarian without the need for laboratory confirmation, could be established.

The rate of occurrence of the edited health events was 37.4% in first lactation cows, 28.2% in second lactation, 19.6% in third lactation, 10.2% in fourth lactation and 4.6% in fifth lactation. After assessing the rate of occurrence for the targeted 34 traits, nine health events were eliminated because of each of them were represented in less than 20 herds. These events included adhesion, cancer / tumor, bloat, coliform mastitis, E. coli, foot ulcer, stillbirth / mummy fetus, uterine infection / injury and vaginal / uterine prolapse.

Table 3 illustrates the summary statistics for the 25 remaining events and includes number of herds, lactations and cases. As expected from previous studies, the highest number of cases occurred with mastitis and metritis which are two of the more common ailments on dairies. There also was a high concentration of lameness in many herds. Although there was a substantively lower concentration of the health events abortion, hypocalcemia, cystic ovary,

displaced abomasum and retained placenta than the top three conditions, there are a high number of herds affected.

Table 3. Numbers of herds, lactations and cases by health event code and name.

Health event	Herds	Lactations	Cases
ABCS = abscess	45	58 721	1 967
ABRT = abortion	456	334 214	2 462
BLDM = bloody milk	24	35 667	664
CALC = hypocalcemia	455	361 183	7 339
CLOS = clostridium	20	21 971	1 720
CYST = cystic ovary	563	322 887	18 254
DIAR = diarrhea / BVD	47	63 480	4 298
DIGE = digestive problems	336	318 106	9 653
D.A. = displaced abomasum	439	409 836	5 859
DOWN = downer	42	53 057	242
DYST = dystocia	191	179 551	3 134
EDEM = udder edema	49	60 564	1 525
INFU = mammary infusion	34	18 733	2 738
JOHN = Johne's	68	60 160	10 748
KETO = ketosis	269	290 329	10 536
LAME = lameness	550	468 274	59 922
MAST = mastitis	758	570 225	59 660
METR = metritis	654	540 991	45 740
PEYE = pink eye	63	56 544	286
PNEU = pneumonia	42	53 585	713
REPR = other reproductive problem	141	155 100	14 427
RESP = respiratory	354	342 985	6 439
RETP = retained placenta	530	436 138	11 638
SULC = stomach ulcer	20	28 039	1 248
WART = hairy heel wart	56	80 811	7 458

Results - incidence of health events

The relative impact of a specific disease on dairies was expressed by its frequency of occurrence and computed using lactation incidence rates (LIR) in the following manner:

$$\text{LIR} = \frac{\text{number of first occurrences of a specific health event in lactations}}{\text{number of lactations at risk}}$$

Table 4 lists LIRs for the 25 targeted health events by lactation number, mean across lactations and standard error of the mean. The final column includes mean incidence rates and 95% incidence range of each health event that were available from literature and were compiled by Parker Gaddis, *et al*. (2012). At least 10 citations were found for most diseases listed in this column with the exception of health events that are more typically reported in calves, such as diarrhea, digestive problems and respiratory problems.

Notice that LIRs were not found in the literature for thirteen diseases, most of which have much lower numbers of cases relative to other diseases. Exceptions were Johne's, other reproductive

problems and hairy heel wart, each of which had a relatively high number of occurrences and a relatively high LIR. However, 'other reproductive problems' is a combination of reproductive diseases so LIRs from literature would be irrelavent.

For diseases with corresponding literature citations, calculated LIRs were within the 95% incidence range from literature. With three exceptions, the mean LIRs were somewhat lower than the mean incidence from literature. For digestive problems, displaced abomasums and ketosis, the LIRs were only slightly higher than literature LIRs.

These results generally agree with findings from Parker Gaddis, *et al.* (2012) which were also derived PCDART data. LIRs for several diseases in the current study were markedly higher than the prior study. In fact, LIRs for hypocalcemia, cystic ovary, diarrhea / BVD and respiratory problems were double. This might reflect changes in importance or prevalence of these diseases in more recent years.

Additionally, the health events from Parker Gaddis, *et al*. (2012) were from a more extended

time period (thirteen years versus four years) with only a one-year overlap with the current study. The current study also used dates of enrollment and withdrawal from PCDART to edit inclusion to complete calendar years. This edit allowed more time for some new users to become accustomed to PCDART before their data were included and it truncated inclusion for herds that withdrew from PCDART .

With the exception of bloody milk, the rate of incidence increased with lactation number which also generally agrees with Parker Gaddis, *et al.* (2012).

Table 4. Lactation incident rates by lactation, mean across lactations, and mean incidence from literature with 95% range.

Health event	**Lactation**	**Incident Rate LIR %**	**Mean (S.E.)Across lactations lactations (%)**	**Mean literature incidence[1] (95% range) [no. citations**
ABCS = abscess	1	2.50	5.03 (2.53)	
	2	3.34		
	3	5.19		
	4	5.03		
	5	9.08		
ABRT = abortion	1	1.41	1.89 (0.53)	
	2	1.47		
	3	1.78		
	4	2.08		
	5	2.70		
BLDM = bloody milk	1	2.73	3.15 (0.71)	
	2	2.58		
	3	3.26		
	4	2.84		
	5	4.33		
CALC = hypocalcemia	1	2.05	5.20 (3.44)	7.44
	2	2.33		(1.49, 21.75)
	3	4.43		[18]
	4	6.98		
	5	10.24		
CLOS = clostridium	1	5.74	7.67 (1.81)	
	2	6.59		
	3	6.84		
	4	9.68		
	5	9.53		
CYST = cystic ovary	1	5.02	7.32 (2.01)	9.05
	2	5.99		(0.76, 21.70)
	3	6.93		[21]
	4	8.64		
	5	10.02		
DIAR = diarrhea/BVD	1	3.09	5.27 (2.64)	5.88
	2	3.45		(2.77, 11.22)
	3	5.42		[5]
	4	4.71		
	5	9.69		
DIGE = digestive problems	1	2.53	3.84 (1.29)	2.60
	2	2.91		(0.20,6.89)
	3	3.47		[8]
	4	4.60		
	5	5.67		
DOWN = downer	1	0.71	1.53 (0.81)	
	2	0.84		
	3	1.40		
	4	2.04		
	5	2.63		

(to be continued ...)

(... to be continued)

Health event	Lactation	Incident Rate LIR %	Mean (S.E.)Across lactations lactations (%)	Mean literature incidence[1] (95% range) [no. citations
D.A. = displaced abomasum	1	2.08	3.18 (0.93)	2.67
	2	2.35		(0.56, 8.85)
	3	3.37		[11]
	4	3.87		
	5	4.20		
DYST = dystocia	1	1.91	2.82 (1.34)	5.29
	2	1.86		(0.80, 13.34)
	3	2.35		[14]
	4	2.89		
	5	5.09		
EDEM = udder edema	1	1.47	2.47 (0.96)	
	2	1.64		
	3	2.31		
	4	3.53		
	5	3.40		
INFU = mammary infusion	1	8.19	10.14 (2.34)	
	2	8.66		
	3	8.46		
	4	12.46		
	5	12.92		
JOHN = Johne's	1	9.39	11.88 (2.82)	
	2	10.27		
	3	9.88		
	4	14.44		
	5	15.41		
KETO = ketosis	1	3.96	6.27 (2.31)	5.07
	2	4.21		(0.32, 19.50)
	3	6.04		[21]
	4	7.78		
	5	9.34		
LAME = lameness	1	6.64	8.98 (2.41)	9.27
	2	7.27		(2.54, 30.44)
	3	8.12		[17]
	4	10.37		
	5	12.47		
MAST = mastitis	1	8.62	12.00 (2.97)	17.98
	2	10.18		(0.96, 39.13)
	3	11.56		[29]
	4	13.35		
	5	16.30		
METR = metritis	1	6.54	8.17 (2.14)	12.34
	2	6.23		(1.77, 35.50)

(to be continued ...)

(... to be continued)

Health event	Lactation	Incident Rate LIR %	Mean (S.E.)Across lactations lactations (%)	Mean literature incidence[1] (95% range) [no. citations
PEYE = pinkeye	1	0.90	1.28 (0.63)	
	2	0.79		
	3	1.01		
	4	1.39		
	5	2.33		
PNEU = pneumonia	1	1.43	2.09 (0.85)	
	2	1.89		
	3	1.54		
	4	2.05		
	5	3.54		
REPR = other reproductive problems	1	3.80	6.27 (2.58)	
	2	5.06		
	3	4.86		
	4	7.36		
	5	10.26		
RESP = respiratory	1	1.89	2.72 (0.84)	3.30
	2	2.13		(0.21, 7.11)
	3	2.46		[12]
	4	3.20		
	5	3.93		
RETP = retained placenta	1	3.04	5.49 (1.96)	8.02
	2	4.35		(2.33, 17.94)
	3	5.24		[30]
	4	6.80		
	5	8.00		
SULC = stomach ulcer	1	3.41	6.60 (3.11)	
	2	4.42		
	3	6.71		
	4	7.01		
	5	11.45		
WART = hairy heel wart	1	5.95	7.64 (2.59)	
	2	4.99		
	3	6.94		
	4	8.83		

[1] Calculated from Appuhamy *et al.* (2009); Barker *et al.* (2010); DeGaris and Lean (2008); Dubuc *et al.* (2010); Emanuelson *et al.* (1993); Faye (1992); Fleischer *et al.* (2001); Frei *et al.* (1997); Gay and Barnouin (2009); Groehn *et al.* (1992); Gröhn *et al.* (1989, 1995); Hamann *et al.* (2004); Heringstad *et al.* (1999); Miller and Dorn (1990); Mörk *et al.* (2009); Olde Riekerink *et al.* (2008); Stevenson (2000); Toni *et al.* (2011); Yániz *et al.* (2008).

Additional sources of data

The 1 423 herds that were evaluated are enrolled on a PCDART backup feature that sends data to DRMS servers to enable DRMS staff to assist in rebuilding the dairy farmer's entire database in the event of a disaster. Additionally, DRMS has permission to provide data from these farmers to advisors or consultants. Prior to edits, these 'backup' dairies represented 39% of PCDART users.

Other dairy farmers who are enrolled on PCDART rely on 'backup' systems that are on-farm, primarily because their communications systems are incapable of high-speed delivery of large disaster recovery data files to DRMS. However, health entries during the most recent test period are delivered from these 'non-backup' farmers to DRMS with other test day data that have been entered to accomplish test day processing. DRMS does not have complete definitions of the health events (only 4-character mnemonic) and DRMS does not have permission to deliver these data to advisors or to use for other purposes..

But an assessment of data from these 'non-backup' dairies found that they enter health events at a more modest rate when compared to similar sized 'backup' herds. Backup herds recorded a mean of 123 events per 100 cows per year and 65% of herds recorded a minimum of 10 usable events per 100 cows per year while 'non-backup' herds recorded a mean of 52 events per 100 cows per year.

For both types of herds, larger herds (number of cows>500) recorded useful data at almost twice the rate of smaller herds.

Table 5. Rate of recording for 'backup' herds and 'non-backup' herds in the centralized database.

Size (# cows)	Backup (# herds)	Backup rate of recording	Non-backup # herds	Non-backup rate of recording
< 100	308	106	462	36
100 - 499	864	102	880	49
500 - 999	173	191	84	126
> 1000	78	246	26	179
Total / avg.	1 423	123	1 452	52

Rate of recording the 34 targeted health events.

Conclusions

Based upon data from DRMS' PCDART on-farm herd management system, health incidence data that have been recorded by dairy farmers have LIRs similar to previous studies. However, the quality and quantity of available data probably could be improved by promoting and supporting the adoption and use of clear clinical signs for each disease.

In the past, dairy farmer leaders in the U.S. have objected to the delivery of their health data to centralized databases under the control of the federal government. But recent changes to transition the operational elements of the U.S. Genetic Evaluation Program to be under the auspices of the Council on Dairy Cattle Breeding, a private industry non-profit entity, should remove this impediment to centralized storage and use of health data from U.S. dairy farmers.

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Benefits of recording of diagnostic data. A veterinarian perspective

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Abstract

In 2006 a health monitoring system for cattle in Austria was started. Since 2011 monitoring of health data is integrated into the breeding programs of Austrian cattle breeders and therefore compulsory for all breeding herds. Veterinarian diagnoses are standardized, validated and recorded in a central cattle database.

Besides the use of diagnostic data for routine evaluation of health traits, the information obtained can be used for management decisions to improve the health status in cattle herds. Veterinarians receive health reports for the herd management to consult their farmers. These health reports include all already existing information from performance recording as well as diagnostic data. Health reports are used by veterinarians for auditing the member farms of the Austrian animal health organisations.

Using the experiences from the health monitoring system recordings of treatments and the use of veterinary medicinal products shall be implemented into the health monitoring system on a voluntary basis. As a result, the central cattle database will serve as a register for treatment data and therefore simplify the documentation of treatments by farmers and veterinarians.

From the end-consumer´s perspective the food safety and the health risks caused by drug resistant bacteria are increasingly of particular interest. There is growing demand for consumer confidence in animal health and drug use. Associating diagnostic data with treatment data can give valuable information on prudent use of veterinary drugs and serve as a basis for further research on the impact of drug use in cattle production on antimicrobial resistance.

Keywords: health monitoring system, consultancy, health reports, animal health, drug use

Introduction

As a result of vast changing conditions of production in the livestock industry and after the eradication of classical infectious diseases, diseases caused by various environmental conditions are responsible for major production losses in livestock. A modified veterinary approach to the problems is therefore necessary. The treatment of the individual animal loses importance compared to the care of the herd.

The cost pressure in animal production led to an increased use of veterinary medicinal products without adequate diagnostics, instructions by a veterinarian and documentation in livestock. With the Law on the Control of Veterinary Medicinal Products (2002) a new legal framework for the use of veterinary drugs by veterinarians and farmers in Austria was created. The Animal Health Service (AHS) aims to give advice and supervision on farmers and their livestock. This in turn should minimize the use of veterinary drugs and prevent diseases caused by farming conditions in animal production. Within the scope of the AHS farmers may use veterinary drugs in their animals, however only with close guidance, supervision and written documentation by the veterinarian.

The contracted veterinarian has to perform regular audits on the farms. The frequency, the content and the way of documentation of the audit are determined by the Animal Health Service Regulation (2009). In cattle farms the audit needs to be carried out at least once a year by the contracted veterinarian. The central point of the audit is to assess the health status of the herd. After the diagnosis of existing problems, a plan of action has to be determined. The veterinarian is obliged to evaluate the measures taken and to accurately document these. The final reports of each audit have to be submitted to the AHS office.

To assess the health status of dairy cattle, the analysis of data from the milk performance recordings, the indicators of the herd's fertility and the evaluation of the frequency of clinical conditions are essential. The milk performance recordings, calving and insemination data and the somatic cell counts are collected in farms under performance recording. Data is then stored in the central cattle database. The basis for the documentation of diagnoses is the receipt that is created by the veterinarian for any drug application or drug release. The receipts also have to be added to the medication documentation of the farm (Egger-Danner *et al.*, 2010).

In 2006 a health monitoring system for cattle in Austria was established (Egger-Danner *et al.*, 2012). Since then, any diagnosis stated on the drug receipt is to be completed with a 2- digit diagnostic code. The identity of the animal as well as the identity of the farm, the diagnostic code and the date of the diagnosis is recorded. Diagnoses are validated and saved in the central cattle database.

Management decisions to improve the health status

The data analysis is performed by the Association of Austrian Cattle Breeders. Reports are made available for the veterinarians.

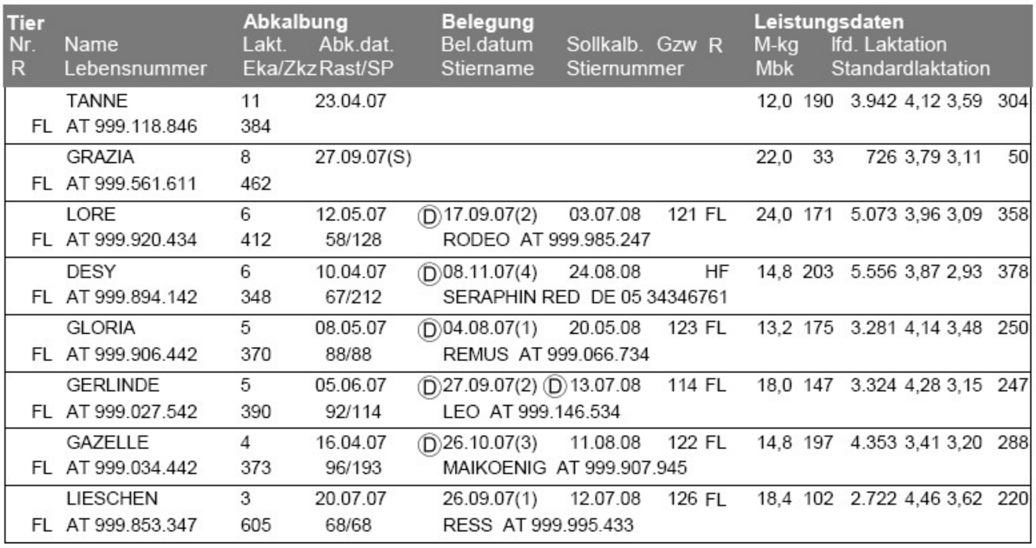
Since January 2008, data of the health monitoring is integrated into reports that are available to farmers after each milk recording (Egger-Danner *et al.*, 2010). The information obtained can be used for management decisions to improve the health status in cattle herds. Veterinarians receive health reports for the herd management to consult their farmers. These health reports include all already existing information from performance recording as well as diagnostic data. Health reports are provided in accordance to the performance recording in a 5-week interval (Obritzhauser *et al.*, 2008).

Fertility

Health reports present information on calving (age at first calving, calving to calving interval, calving ease, premature births). For each cow of the herd the calving to first service interval, the calving to conception interval and the number of AI´s are given. Diagnoses are marked with "D" (Figure 1).

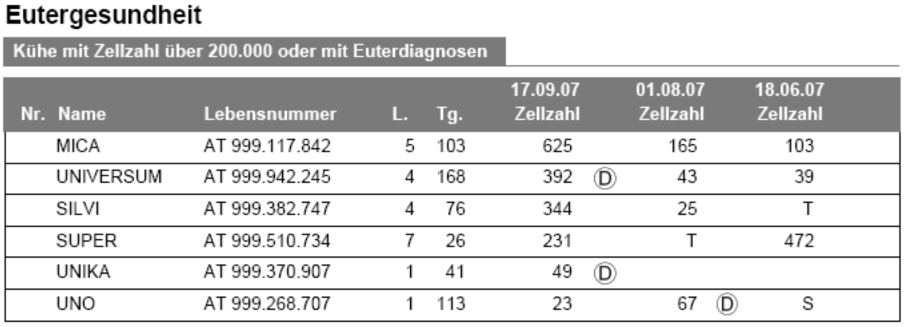
Udder Health

In addition somatic cell count (SCC) of individual cows measured, the distribution of SCC in the herd during the past year is graphically shown on the health report. Cows with an increased SCC and cows with a recorded udder disease are then summarized in a list (Figure 2).



Tier Nr. R	Name Lebensnummer	Abkalbung Lakt. Eka/Zkz	Abk.dat. Rast/SP	Belegung Bel.datum Stiername	Sollkalb. Stiernummer	Gzw	R	Leistungsdaten M-kg Mbk	lfd. Laktation Standardlaktation				
	TANNE	11	23.04.07					12,0	190	3.942	4,12	3,59	304
FL	AT 999.118.846	384											
	GRAZIA	8	27.09.07(S)					22,0	33	726	3,79	3,11	50
FL	AT 999.561.611	462											
	LORE	6	12.05.07	Ⓓ17.09.07(2)	03.07.08	121	FL	24,0	171	5.073	3,96	3,09	358
FL	AT 999.920.434	412	58/128	RODEO	AT 999.985.247								
	DESY	6	10.04.07	Ⓓ08.11.07(4)	24.08.08		HF	14,8	203	5.556	3,87	2,93	378
FL	AT 999.894.142	348	67/212	SERAPHIN RED	DE 05 34346761								
	GLORIA	5	08.05.07	Ⓓ04.08.07(1)	20.05.08	123	FL	13,2	175	3.281	4,14	3,48	250
FL	AT 999.906.442	370	88/88	REMUS	AT 999.066.734								
	GERLINDE	5	05.06.07	Ⓓ27.09.07(2)	Ⓓ13.07.08	114	FL	18,0	147	3.324	4,28	3,15	247
FL	AT 999.027.542	390	92/114	LEO	AT 999.146.534								
	GAZELLE	4	16.04.07	Ⓓ26.10.07(3)	11.08.08	122	FL	14,8	197	4.353	3,41	3,20	288
FL	AT 999.034.442	373	96/193	MAIKOENIG	AT 999.907.945								
	LIESCHEN	3	20.07.07	26.09.07(1)	12.07.08	126	FL	18,4	102	2.722	4,46	3,62	220
FL	AT 999.853.347	605	68/68	RESS	AT 999.995.433								

Figure 1. Health report provided in a 5-week interval - fertility



Eutergesundheit

Kühe mit Zellzahl über 200.000 oder mit Euterdiagnosen

Nr.	Name	Lebensnummer	L.	Tg.	17.09.07 Zellzahl	01.08.07 Zellzahl	18.06.07 Zellzahl
	MICA	AT 999.117.842	5	103	625	165	103
	UNIVERSUM	AT 999.942.245	4	168	392 Ⓓ	43	39
	SILVI	AT 999.382.747	4	76	344	25	T
	SUPER	AT 999.510.734	7	26	231	T	472
	UNIKA	AT 999.370.907	1	41	49 Ⓓ		
	UNO	AT 999.268.707	1	113	23	67 Ⓓ	S

Figure 2. Health report provided in a 5-week interval – udder health.

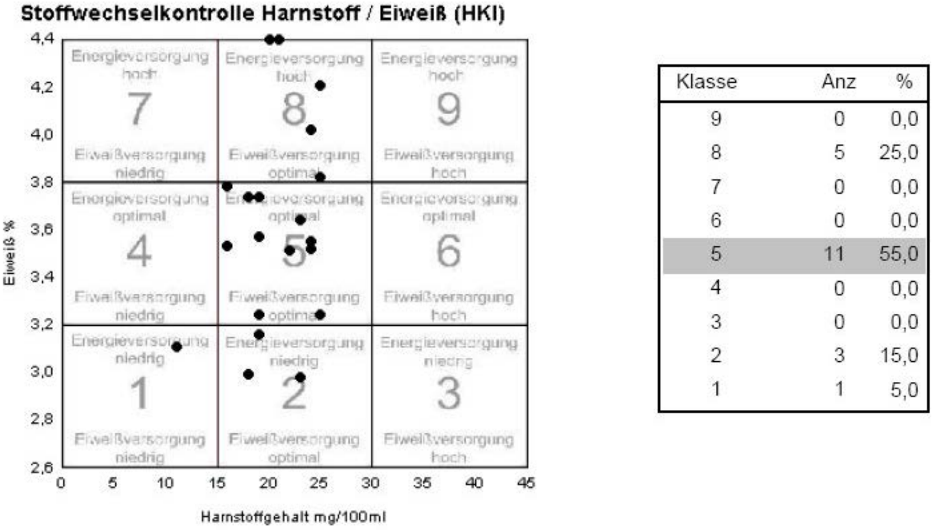
Metabolism

To evaluate the energy and protein supply of the cows in the herd (especially in the first lactation) the milk yield as well as the fat-, protein- and urea contents have to be assessed. Deficiencies in the nutritional management of the cows are easily recognizable through the graphical presentation of the results of the performance recordings (Figure 3).

Auditing the member farms of the Austrian animal health organisations

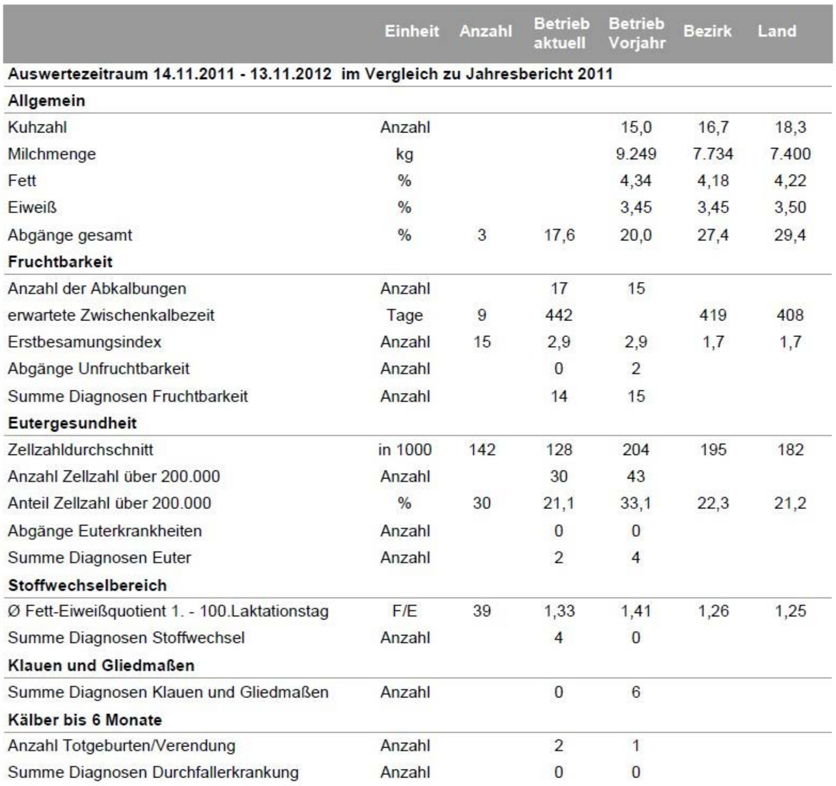
In accordance with the provisions of the Animal Health Service Regulation (2009), audits need to be conducted by contracted veterinarians in member farms of the Austrian Animal Health Service (Obritzhauser, 2012). The health status of the cattle of supervised farms can be evaluated on the basis of diagnoses and performance parameters that were collected since the last audit. The annual reports of health monitoring provide the basis for evaluating the general health situation of the herd.

Annual reports summarize the results of milk performance recordings and diagnostic monitoring collected throughout the period of one year (Figure 4).



Klasse	Anz	%
9	0	0,0
8	5	25,0
7	0	0,0
6	0	0,0
5	11	55,0
4	0	0,0
3	0	0,0
2	3	15,0
1	1	5,0

Figure 3. Health report provided in a 5-week interval – energy and protein supply.



	Einheit	Anzahl	Betrieb aktuell	Betrieb Vorjahr	Bezirk	Land
Auswertezeitraum 14.11.2011 - 13.11.2012 im Vergleich zu Jahresbericht 2011						
Allgemein						
Kuhzahl	Anzahl			15,0	16,7	18,3
Milchmenge	kg			9.249	7.734	7.400
Fett	%			4,34	4,18	4,22
Eiweiß	%			3,45	3,45	3,50
Abgänge gesamt	%	3	17,6	20,0	27,4	29,4
Fruchtbarkeit						
Anzahl der Abkalbungen	Anzahl		17	15		
erwartete Zwischenkalbezeit	Tage	9	442		419	408
Erstbesamungsindex	Anzahl	15	2,9	2,9	1,7	1,7
Abgänge Unfruchtbarkeit	Anzahl		0	2		
Summe Diagnosen Fruchtbarkeit	Anzahl		14	15		
Eutergesundheit						
Zellzahldurchschnitt	in 1000	142	128	204	195	182
Anzahl Zellzahl über 200.000	Anzahl		30	43		
Anteil Zellzahl über 200.000	%	30	21,1	33,1	22,3	21,2
Abgänge Euterkrankheiten	Anzahl		0	0		
Summe Diagnosen Euter	Anzahl		2	4		
Stoffwechselbereich						
Ø Fett-Eiweißquotient 1. - 100.Laktationstag	F/E	39	1,33	1,41	1,26	1,25
Summe Diagnosen Stoffwechsel	Anzahl		4	0		
Klauen und Gliedmaßen						
Summe Diagnosen Klauen und Gliedmaßen	Anzahl		0	6		
Kälber bis 6 Monate						
Anzahl Totgeburten/Verendung	Anzahl		2	1		
Summe Diagnosen Durchfallerkrankung	Anzahl		0	0		

Figure 4. Annual health report – Summary of indicators.

Current annual reports can be accessed at any time from the central cattle database. These summarize data that demonstrate fertility, udder heath and metabolic status of the herd in tabular and graphical form (Schwarzbacher *et al*., 2010). Statistics on the frequency of diseases are important for the farm manager to ensure accurate strength-weakness analysis in comparison to historical operating data (vertical comparison) and in comparison to other farms with similar production conditions (horizontal comparison). With these figures, the health and performance can be assessed (Figure 5).

The audit itself must not be misunderstood as a formal control measure. The contracted veterinarian may not control the herd supervised by himself. The contracted veterinarian however has to assess the animal health situation of the farm in terms of a self-evaluation process together with the farmer. The AHS audit is an essential element of the legally obligatory self-monitoring (Food Safety and Consumer Protection Act 2006).

Information about the health status of the population

A summarized analysis of performance and health indicators of the population is provided to AHS offices and the Austrian veterinary authorities once a year. The data is used to monitor the population in order to detect long-term negative trends and as an early warning system. The information about the health status is used for the elaboration of training programmes, the identification of target groups and the development of animal health policies. The overviews contain health indicators for

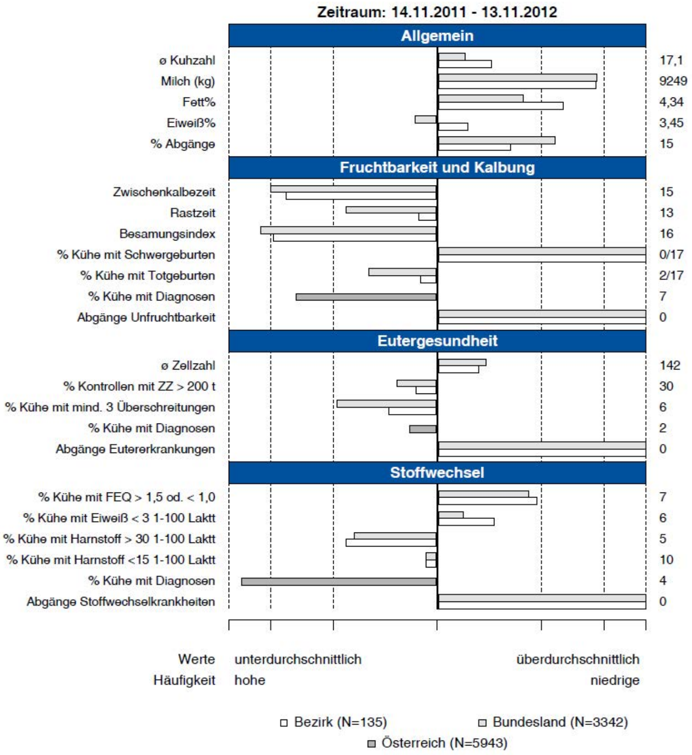
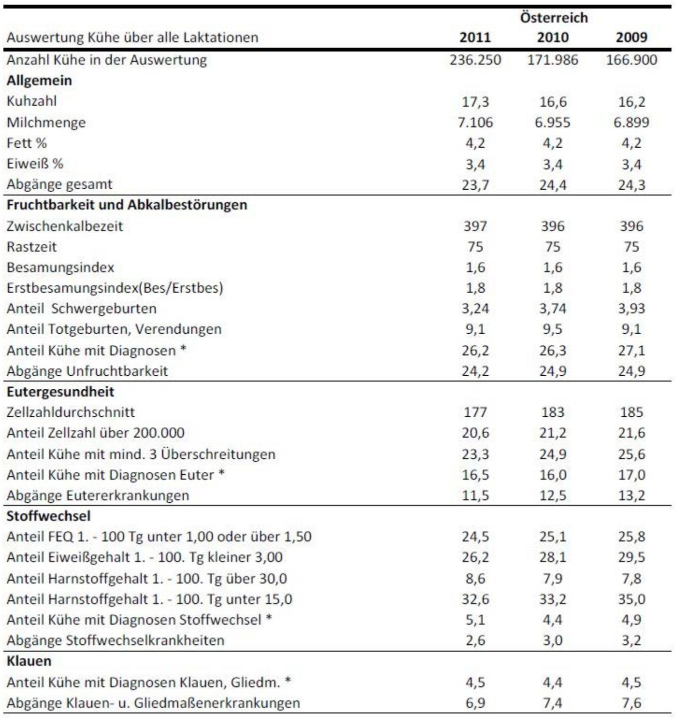


Figure 5. Annual health report – graphical summary of indicators.



Auswertung Kühe über alle Laktationen	2011	Österreich 2010	2009
Anzahl Kühe in der Auswertung	236.250	171.986	166.900
Allgemein			
Kuhzahl	17,3	16,6	16,2
Milchmenge	7.106	6.955	6.899
Fett %	4,2	4,2	4,2
Eiweiß %	3,4	3,4	3,4
Abgänge gesamt	23,7	24,4	24,3
Fruchtbarkeit und Abkalbestörungen			
Zwischenkalbezeit	397	396	396
Rastzeit	75	75	75
Besamungsindex	1,6	1,6	1,6
Erstbesamungsindex(Bes/Erstbes)	1,8	1,8	1,8
Anteil Schwergeburten	3,24	3,74	3,93
Anteil Totgeburten, Verendungen	9,1	9,5	9,1
Anteil Kühe mit Diagnosen *	26,2	26,3	27,1
Abgänge Unfruchtbarkeit	24,2	24,9	24,9
Eutergesundheit			
Zellzahldurchschnitt	177	183	185
Anteil Zellzahl über 200.000	20,6	21,2	21,6
Anteil Kühe mit mind. 3 Überschreitungen	23,3	24,9	25,6
Anteil Kühe mit Diagnosen Euter *	16,5	16,0	17,0
Abgänge Eutererkrankungen	11,5	12,5	13,2
Stoffwechsel			
Anteil FEQ 1. - 100 Tg unter 1,00 oder über 1,50	24,5	25,1	25,8
Anteil Eiweißgehalt 1. - 100. Tg kleiner 3,00	26,2	28,1	29,5
Anteil Harnstoffgehalt 1. - 100. Tg über 30,0	8,6	7,9	7,8
Anteil Harnstoffgehalt 1. - 100. Tg unter 15,0	32,6	33,2	35,0
Anteil Kühe mit Diagnosen Stoffwechsel *	5,1	4,4	4,9
Abgänge Stoffwechselkrankheiten	2,6	3,0	3,2
Klauen			
Anteil Kühe mit Diagnosen Klauen, Gliedm. *	4,5	4,4	4,5
Abgänge Klauen- u. Gliedmaßenerkrankungen	6,9	7,4	7,6

Figure 6. Annual health report population – Summary of indicators.

the Austrian dairy cattle population for the last three years and are further broken down by province. To ensure the validity of the data, only information from farms with more than 10 cows and farms whose diagnostic data are transmitted electronically from the veterinarians are used (Figure 6).

Further developments

Internet platform for veterinarians

All data from the milk performance recordings and health monitoring are available at any time via the Internet (RDV4M) for the farmer. Currently, an internet platform is being developed to always give access to the current performance and health information to the contracted veterinarians too. Additionally, management aids (action lists), and vet-specific evaluations for the herd management will be available for the veterinarian.

Central register for treatment data

An overall aim of the health monitoring system is a contribution to food safety. The increased attention to health traits in cattle breeding and to improved animal health through management measures shall result in a minimization of the use of veterinary medicines. In particular, the use of antibiotics in animal production is under growing criticism. Which antibiotics are going to be approved for veterinary use in the future essentially depends on the prudent use of these substances. Critically important antimicrobials may only be used for specific veterinary needs and the use must be justified by objective diagnostic measures.

In Austria, the documentation of treatments is obligatory by law. With each application of veterinary medicinal products the identity of the farm and the animal, the date of application, the drugs applied or dispensed and the withdrawal period have to be documented by all veterinarians and farmers. A pilot project to estimate the amounts of antibiotics used in the Austrian cattle, pig and poultry production was completed in 2010 (Obritzhauser *et al.*, 2011). With this project, the methodological basis for the compulsory documentation of the type and quantity of antimicrobials used in livestock production was created.

Using the experiences from the health monitoring system recordings of treatments shall be implemented on a voluntary basis. As a result, the central cattle database can serve as a register for treatment data and therefore simplify the documentation of treatments by farmers and veterinarians. The documentation of treatment data along with diagnostic data can be done by the veterinarian with reasonable effort. The use of electronic devices will be prerequisite, as it simplifies and minimizes administrative work. The benefits of the easy access to performance recordings and health reports outweigh the costs for the participating veterinarian.

Preliminary results of use of antibiotics in dairy cattle

The Austrian Agency for Health and Food Safety was assigned by the Austrian Ministry of Health to develop methods with which the quantity of antimicrobials, applied or dispensed by veterinarians to livestock, can be determined and monitored. Within this project an attempt for the assessment and statistical evaluation of the consumption of antimicrobial substances in dairy cattle farms

Table 1. Prescribed daily doses of antibiotics used per year in dairy farms associated with different diagnoses

ATCvetCode	Antibiotic	Infertility, diseases ass. with parturition		Udder diseases		Diseases of claws and legs		Diseases of the respiratory tract		Other diseases		Antibiotics total	Critically important antibiotics total	
		PDD/LU	%	PDD/LU	%	PDD /LU	%	PDD/LU	%	PDD /LU	%		PDD/LU	%
QJ01A	Tetracyclines	0,005		0,001		0,001		0,004		0,001		0,013		
QJ01B	Amphenicoles	0,000		0,000		0,000		0,001		0,000		0,001		
QJ01C	Beta-LactamAntibacterials, Penicillins	0,001		0,032		0,002		0,000		0,008		0,045		
QJ01D	Other Beta-Lactam Antibacterials	0,004		0,010		0,042		0,003		0,012		0,074		
QJ01E	Sulfonamides and Trimethoprim	0,002		0,002		0,004		0,002		0,004		0,022		
QJ01F	Macrolides, Lincosamides and Streptogramins	0,000		0,042		0,000		0,001		0,002		0,046		
QJ01G	Aminoglycoside Antibacterials	0,000		0,002		0,000		0,001		0,001		0,003		
QJ01M	Quinolones and Quinoxaline Antibacterials	0,001		0,025		0,000		0,010		0,007		0,048		
QJ01R	Combinations of Antibacterials	0,001		0,001		0,008		0,078		0,025		0,196		
QJ51C	Beta-Lactam Antibacterials, Penicillins for intramammary use	0,012		0,379		0,000		0,000		0,003		0,392		
QJ51D	Other Beta-Lactam Antibacterials for Intramammary use	0,001		0,137		0,000		0,000		0,004		0,143		
QJ51F	Macrolides, Lincosamides and Streptogramins for Intramammary use	0,000		0,002		0,000		0,000		0,000		0,002		
QJ51R	Combinations of Antibacterials for Intramammary use	0,000		0,280		0,000		0,000		0,002		0,283		
QJ51X	Other Antibacterials for Intramammary use	0,000		0,002		0,000		0,000		0,000		0,002		
Total QJ01		0,016	3,5	0,115	25,6	0,057	12,7	0,099	22,2	0,058	13,0	0,448	0,169	37,6
Total QJ51		0,012	1,5	0,800	97,4	0,000	0,0	0,000	0,0	0,009	1,1	0,822	0,145	17,6
Total QJ		0,028	2,2	0,914	72,1	0,057	4,5	0,099	7,8	0,067	5,3	1,271	0,313	24,7

under performance recording in Austria was made. The data is derived from 8.234 treatment records and prescriptions acquired from 8 veterinary practices active in dairy cattle farms between 2008 and 2010. As units of antimicrobial consumption, the amount of active substances (g) per livestock unit (LU) per year applied and the number of prescribed daily doses (PDD) per LU per year was considered. This parameter was estimated applying Monte Carlo simulation techniques, where uncertainties in the annual working hours in the veterinary practices, in the number of produced animals and in the proportion of the non-treated population were taken into account.

3.29 g / LU (median) of active antimicrobial substances per year were applied to cattle in dairy cattle farms. Correspondingly, a median of 1.69 PDD / LU per year (quantiles: 1.28 – 2.13) were used. Three quarters of the consumed doses (median of 1.27 PDD / LU) belonged to the ATCvet group QJ (antiinfectives for systemic use). Antibiotics ranked as critically important antimicrobials (3rd and 4th generation Cephalosporines, Macrolides and Quinolones) were used by the participating veterinarians (median of 0.31 PDD / LU). Cephalosporins of the 3rd and 4th generation (median of 0.22 PDD / LU) were most frequently applied to dairy cattle in the therapy of udder diseases and diseases of claws and legs.

From the end-consumer´s perspective the food safety and the health risks caused by drug resistant bacteria are increasingly of particular interest. There is growing demand for consumer confidence in animal health and drug use. Associating diagnostic data with

treatment data can give valuable information on prudent use of veterinary drugs and serve as a basis for further research on the impact of drug use in cattle production on antimicrobial resistance (Table 1).

Conclusion

Since 2011 monitoring of health data is integrated into the breeding programs of Austrian cattle breeders and therefore compulsory for all breeding herds. The health monitoring in cattle is thus part of a surveillance programme for cattle health. The cooperation of representatives of agriculture, veterinarians and science for the development of the health monitoring programme has proven well. New benefits for the participating farmers and veterinarians are created through the further development of an electronic data exchange platform for performance, diagnostic and treatment-data. The health monitoring is important for improving health and productivity in cattle husbandry. It provides a valuable contribution to the safety and the quality of food products from cattle production. This in turn is only achievable with a well working partnership between farmers and veterinarians, and the voluntary self-commitment to consumer demands for comprehensive health surveillance and disease prevention as well as for the maximum possible transparency in food production.

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Benchmarking for health from the perspective of consultants

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Abstract

Benchmarking for health offers the consultant an opportunity to compare performance both between and within farms over time. As well as a 'formal' process it should also be an ongoing 'informal' process in any herd health planning consultancy. Benchmarking can prove to be a useful tool to illustrate the need for improvement, the potential benefits such improvement might offer, as well as a means to motivate producers to change both on an individual basis and in a group setting. By benchmarking over time one can also identify 'added value' by looking at both the absolute and relative change in performance. However, the benchmarking process is also fraught with pitfalls; if used inappropriately it can engender 'despair' amongst the poorest performers who may be constrained by their management systems, encourage complacency in those who are apparently the 'best' and a feeling of 'adequacy' in the remainder. Often a single parameter does not provide an appropriate benchmark, and indices based on a basket of parameters may provide a better marker of overall performance. To avoid these and other pitfalls the aim of the benchmarking process should be determined early on. The consultant needs to take care in the selection of appropriate benchmarking parameters, ensure robust data capture and identify an appropriate benchmarking group. Thereafter a gap analysis can be undertaken and process differences identified with absolute or relative targets set for future performance. Communication is key to the whole process in encouraging implementation and ensuring compliance with recommendations. Central to any success is the need for a continuous process encompassing regular review, adjustment of goals and recalibration. One should not benchmark for benchmarking's sake, the aim of any health benchmarking process should be to result in an overall improvement in cow health and welfare; this paper will attempt to outline a process which can be used to facilitate that outcome.

Keywords: animal health, dairy, benchmarking.

Introduction

Benchmarking is a process that has been utilized in the business sector for many years and is used to compare performance and determine best practice. Overall performance can be compared within industry sectors, or similar processes can be benchmarked and compared between industry sectors. Even when comparing within industry sectors it is important to take into account different approaches to management; whilst for instance at the highest level one could compare overall profitability to determine what is potentially the most profitable system, when certain systems and process are inherent then further comparison needs to take into account different systems of management. For example, when comparing within the dairy industry, whilst it would be valid to compare overall performance between herds to determine the most efficient management system (at a given point in time), further analysis and understanding of where improvements can be made can only come through comparison of farms with similar management systems. For instance, high input intensive systems farms need to be compared with each other and not with low input extensive systems; similarly it is difficult to compare family owned and run businesses with large agri-business enterprises.

In recent years there has been an increasing interest in the use of benchmarking in the dairy industry, in no small part facilitated by the easy access to data, personal computers and the internet. Whilst 'health' benchmarks have been periodically published for several decades in the UK (Kossaibati & Esslemont, 1995) they have necessarily been restricted to relatively small cohorts of well recorded herds. More extensive benchmarking has been attempted, but as outlined later becomes increasing vulnerable to inadequacies and inconsistencies in data recording – a shortcoming of which the consultant / practitioner need to be aware.

The benchmarking process

Whilst benchmarking can be performed in a variety of ways and with different objectives, the overall process is similar irrespective of the chosen approach. An overview of a generic benchmarking process is outlined in figure 1 and described below. The process can be subdivided into two phases, a planning phase and an implementation phase. As the name suggests, the planning phase encompasses the initial set up of the process whilst the implementation concerns the process of continual review and hopefully improvement. Whilst the process of improvement and implementation can continue indefinitely, a periodic review and re-planning is essential as the benchmarking group and objectives may change and different metrics may be required as herd performance improves. For instance, in the early stages of a mastitis control program monitoring using somatic cell counts may be appropriate (and easy), but as the process develops the concurrent monitoring and planning around clinical mastitis data may become essential.

Whilst the planning stage is shown in a stepwise manner, it is likely that this will also be an iterative process involving the benchmarking group in the process (especially when used in small groups as a consultant), rather than the process being developed before the group involved is engaged.

Determine objective(s)

The first step in any benchmarking process should be to determine the objectives of the process. In the context of animal health this could be at a relatively high level such as an improvement in mastitis and milk quality, fertility performance or lameness, or in a more focussed way such as to improve dry period mastitis control. The objectives need to be relevant and achievable to the group to be benchmarked and will evolve over time. For example, a group may decide their objective is to

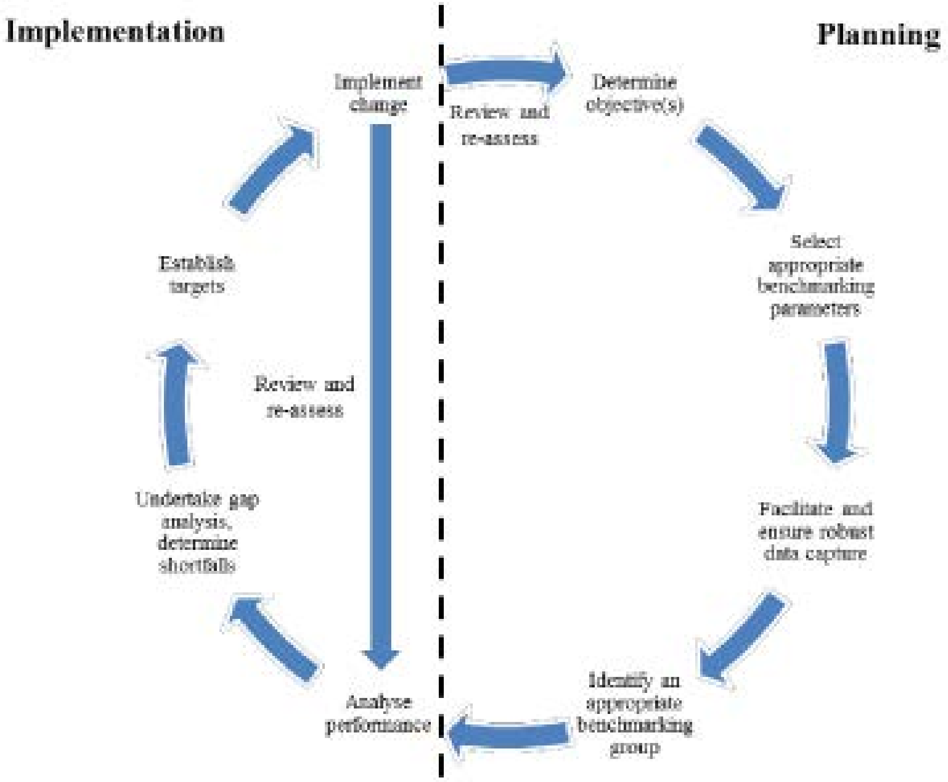

Figure 1. Outline of the benchmarking process.

improve mastitis and milk quality. The initial objective may be the reduce bulk milk somatic cell count (SCC), however the approach to achieving this aim will necessitate monitoring and benchmarking by more than the outcome measure alone.

Select appropriate benchmarking parameters

The ultimate success of any benchmarking process will depend on the selection of appropriate metrics. If we take the example cited above of a desire to reduce bulk milk SCC; this 'high level' parameter is easily manipulated (cows withheld from the bulk tank) and easily influenced by culling. In addition this outcome could be measured via the quality of milk sold or as a calculated value from individual cow recordings. Whilst the second measure is preferable, this is again influenced by cows not recorded.

When one considers these factors then it becomes evident that whilst the objective is to reduce bulk milk SCC this will only be achieved through measurement of the 'inputs' rather than the 'outputs'. A calculated bulk milk SCC will determined primarily by the contribution of high SCC cows, but the proportion of high SCC and chronically infected cows whilst of interest does not provide an insight into how to improve the current situation. For this reason, in this instance appropriate benchmarking measures would be the rate of new infection and therefore rate of 'evolution' of high SCC cows, though this again needs further sub-division into the relative contribution of the dry and non-lactating periods (Bradley & Green, 2005; Green *et al.*, 2007). So in order to achieve the group objective of reducing bulk milk SCC, what is required are benchmarks that reflect factors that influence that output, these can then be compared within the group to determine how each may affect the outcome on each enterprise within the group. In the case of this example, appropriate benchmarking parameters would need to at least include average days in milk, exit rate, proportion of the herd infected and chronically infected, lactation new infection rates and the proportion of cows freshening with a high SCC (ideally subdivided into new infections and failures to cure) amongst others.

The importance of such diverse measures when benchmarking for health is illustrated in figure 2 which illustrates the dry period and lactating period new infection rates of one unit compared to a large benchmarking dataset using the TotalVet software (www.total-vet.co.uk). In this example the herd has one of the highest rates of new infection in lactation, and yet is in the 90th percentile with respect to new infection in the dry period illustrating that poor performance in one aspect of SCC control does not necessarily correlate with poor performance in another. More importantly it is only through this detailed knowledge that appropriate farm level interventions can be put in place.

Another example of a popular benchmarking parameter which can be misleading when applied in different herds is the 100 day in calf rate - ie the proportion of cows calved (eligible for service) that have conceived by 100 days post calving. Whilst this may appear to be an attractive overall measure of herd fertility performance encompassing both submission and conception rates it is unduly influenced by management decisions such as the voluntary waiting period (VWP). A herd with the VWP of 42 days has 2.76 oestrous cycles within which to get a cow pregnant, whereas a herd with a VWP of 60 days only has 1.9 oestrous cycles. A simplistic view suggest this can be overcome by using a calving index as this will be less affected by the VWP, but this does not reflect fertility culling.

Therefore, when measuring and monitoring some outcomes more complex approaches are required encompassing a variety of measures generating indices such as the Transition Cow Index (Noorland & Cook, 2004). These provide a useful overview of performance to select the best performing herds whereas benchmarking within the index can identify areas for improvement.

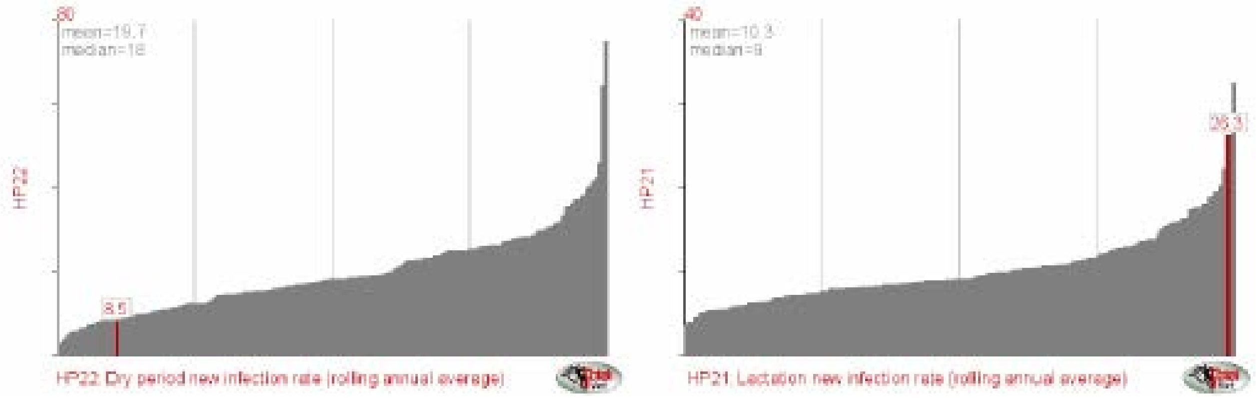

Figure 2. An illustration of dry period and lactating period new infection rate on a single unit when compared to a large benchmarking dataset.

Facilitate and ensure robust data capture

'Garbage in - Garbage out'….. Accurate and efficient data collection is essential if any benchmarking process is going to be robust. Careful selection of the necessary data and facilitation of data capture is essential. In principle, the closer this data capture can get to the 'farmer' the better as this is likely to facilitate data capture. This can only be achieved if the farmer can see the benefit in the associated effort and therefore integration of analysis and meaningful feedback is essential. When concurrent farm and central databases exist 'drift' between the datasets overtime will inevitably occur which can erode confidence in the recording process.

Any process must incorporate means to screen for missing data. Even in herds which are identified as containing 'good quality' data further scrutiny can reveal substantial shortfalls (Hudson *et al.*, 2012); of 468 herds identified by practitioners as having 'good quality data' only 105 were subsequently identified as having sufficiently robust data for the purposes of research into the interaction between mastitis and fertility. Recommendations and practices for data collation such as those outlined by the Functional Traits Working Group (ICAR, 2012) are essential if robust data is to be collated that can be used on a larger scale.

Identify an appropriate benchmarking group

Also crucial in the benchmarking process is the creation of appropriate benchmarking groups. These can be matched in a number of ways, dependant on the objective and purpose of the exercise. In large bench marking exercises it is useful to match based on production systems or perhaps by herd size, geographical location or level of production. In cases where the aim is to work collectively towards a common goal then perhaps more important is the shared aim than the exact herd parameters *per se* as there is a great deal of scope to transfer knowledge and skill between quite diverse farming business models.

Analyse performance

Analysis of performance is dependent on the selection of the correct benchmarking parameters. However, even when these have been selected, careful analysis and scrutiny is required. The use of both means, median and inter-quartile ranges is crucial to enable appropriate targets to be determined. Appropriate periods of analysis need to be selected to allow meaningful comparison which will be determined by seasonal variations and herd size as well as disease incidence / prevalence.

Undertake gap analysis, determine shortfalls

Once performance has been analysed it is possible to determine differences within the benchmarking group and attempt to correlate these with differences in management strategies and techniques. In a small group setting discussion around management strategies can be invaluable with transfer of knowledge between farmers to determine best practice associated with each management system.

Establish targets

Targets need to be relevant and achievable. Whether targets are based on values within a small benchmark group or a wider population will depend on the smaller benchmarking group. Arguably it is better to aim for a long term goal, but with a shorter term target aiming for a 'relative' improvement compared to current performance. It is important n this stage of the process not to engender complacency of despair in different members of a benchmarking group and this is why 'going forward' it is often useful to not only look at absolute benchmarks but also at relative improvements over time.

Implement change

Any change should be based on evidence derived from the benchmarking process and based on current knowledge and literature such as that envisaged and implemented as part of the DairyCo Mastitis Control Plan (*www.mastitiscontrolplan.co.uk*) (Green *et al.*, 2007). As time progresses the impact of change needs to be assessed and the impact of any change fed back into the system to allow control measures and management to be refined.

Review and re-asses

Any benchmarking process must encompass and ongoing process of review and re-assessment of past and current management practices. As any control strategy progresses it will be necessary to periodically review both the targets and the metrics used for analysis. This continuous process of re-assessment and re-calibration is essential if any process is to remain relevant.

Benchmarking in the Dairy Industry

There are number of schemes and mechanisms available in the UK and elsewhere that have been developed with the aim of facilitating benchmarking in the dairy industry. One such mechanism in the UK Milkbench+ has been developed and managed by the levy-funded organization, DairyCo (*http://www.milkbenchplus.org.uk/Public/Content.aspx?id=1*). This draws upon data from many aspects of a farm enterprise with the aim of allowing an independent assessment of the financial performance of the business. It inevitably draws on measures of animal health and performance, but does not look at these aspects in detail.

Health Benchmarking

Compared to schemes such as Milkbench+ outlined above, benchmarking for health is far more challenging

Benchmarking as part of a national scheme

Benchmarking can play a role in national schemes allowing producers to compare their performance with that of their peers as illustrated in Figure 3 and utilized as part of the DairyCo Mastitis Control Plan initiative in the UK. In this scheme, farmers and their advisers can input a small number of parameters to allow comparison of their performance with other herds nationally. This approach is relatively crude and can only allow comparison at quite a 'high level'. However it does allow an insight for the producer into what is potentially achievable and in the case of the DairyCo initiative also allows an estimate of disease costs to be made thereby providing a further motivation for change.

Inevitably this approach does not enable detailed analysis or the creation of herd specific targets and gap analysis. For this reason the robustness of the data is relatively less important and the aim is to use this as a motivational tool rather than the basis of an evidence based approach to improvement.

Benchmarking small groups

The authors probably make most use of benchmarking in this context. Benchmarking actual performance and relative performance over time can prove to be both a useful motivational tool and way to understand best practice. In the 'small group' context there is a greater opportunity to undertake a meaningful gap analysis and for framers to help each other in implementation of best practice. In this context it is also much easier to promote and support good data capture and consistent recording which ensures any decisions and interventions are likely to be made from a more robust evidence base.

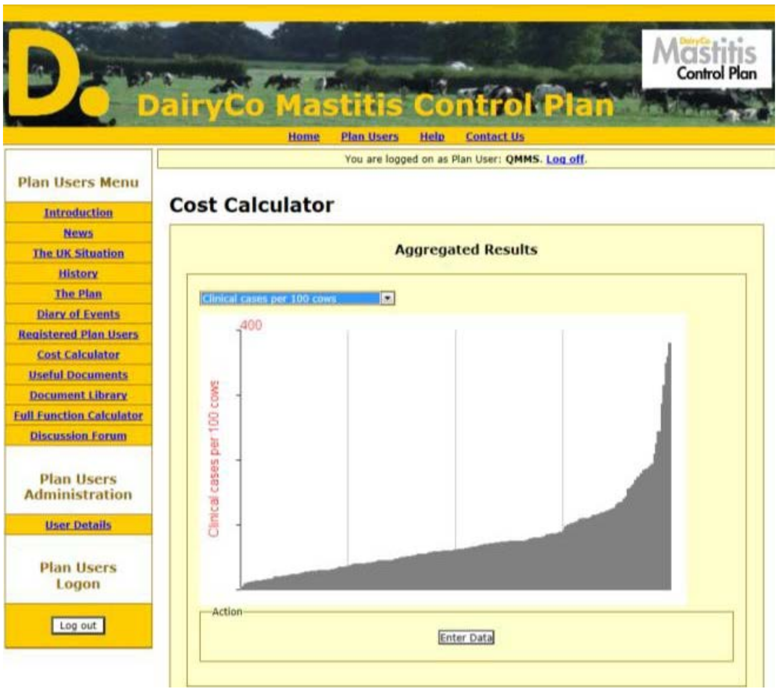

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Figure 3. An illustration of the use of data from a large cohort of herds to allow farmers to compare performance of a 'high level' benchmark.

Benchmarking individual herds

In the opinion of the authors this is arguably the 'purest' and most appropriate use of benchmarking. Any business (and probably even some so with an agricultural business) is only comparable to itself and comparison of historic with current performance is the ultimate benchmark for the individual producer. Whilst it is useful to understand performance relative to others, the ultimate aim is to determine performance in the individual unit and whether this is improving and deteriorating. What is appropriate and achievable in one management unit is likely to be very different from another and progress over time is the ultimate goal.

Conclusions

Whilst the whole process has many potential pitfalls, benchmarking offers the consultant and practitioner alike a useful means by which to compare herds and also to monitor progress within herds over time. Benchmarks can provide a useful focus for discussion around individual herd management in one to one consultancy, but are also a useful tool for use in the context of discussion groups and meetings. One should not benchmark for benchmarking's sake, there should be clear objectives of the benchmarking process, which in the case of health benchmarking should be an overall improvement in cow health and welfare.

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Genomic evaluation of health traits in dairy cattle

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Abstract

There is growing interest from dairy producers in traits related to health and fitness of cattle, which often have low heritabilities but high economic values. Traits with low heritability can be improved by genetic selection, but large numbers of daughter records are required to produce predicted transmitting abilities with high reliability. Producer-recorded health event data collected from on-farm computer systems were used to estimate variance components and compute traditional predicted transmitting abilities (PTA) for several health traits (digestive problems, displaced abomasum, ketosis, lameness, mastitis, metritis, reproductive problems, and retained placenta) using single-trait threshold sire models. Heritabilities ranged from 0.01 for lameness to 0.30 for displaced abomasum using only first lactation data. Results were similar when only first lactation or first through fifth parity data were used. Multiple trait models also were used to estimate genetic correlations among those traits, which ranged from -0.29 (ketosis, lameness) to +0.81 (displaced abomasum, ketosis). Only three traits (displaced abomasum, mastitis, metritis) had 300 or more bulls with traditional reliabilities of at least 0.50. A multiple-trait sire threshold model was used to compute genomic PTA for 2,649 genotyped bulls. The increase in reliability from including the genomic data ranged from 0.38 (displaced abomasum) to 0.48 (lameness). These results suggest that enough data may exist in on-farm computer systems to enable the routine calculation of genetic and genomic evaluations for the most common health disorders in US Holstein cattle.

Keywords: dairy cattle, genetic evaluation, genomic selection, health traits.

Introduction

A negative relationship of production with fitness traits, possibly in response to selection for increased dairy cattle production over the last 50 years, has become apparent (Rauw *et al.*, 1998). Declining health of cows can impact the profitability of a herd in several way, including increased culling rates, decreased and withheld milk, veterinary expenses, and additional labor. Kelton *et al.* (1998) estimated the cost of several common health events, which ranged from $39 per lactation with an incidence of cystic ovaries to $340 per case of left displaced abomasum. Over the past fifteen years, however, these economic costs may have drastically changed.

Improvement of health traits by genetic selection is appealing because the approach is well understood and gains are cumulative. The potential for genetic improvement in health-related traits has been demonstrated in Scandinavian cattle breeds (Abdel-Azim *et al*., 2005), and mastitis incidence has been successfully improved in Norwegian cattle (Heringstad *et al*., 2003). However, there is no mandated or consistent data recording system for health traits in the United States.

Several previous studies have addressed the use of producer-recorded health information for genetic improvement. Zwald *et al*. (2004a) used producer-recorded health event records from 2001 through 2003 and concluded that those data are useable for genetic selection. Parker Gaddis *et al*. (2012) recently showed that similar data accurately reflected the true incidence of health events, and confirmed that phenotypic relationships among common health events were consistent with results from epidemiological studies. The amount of producer-recorded data stored in on-farm computer systems in the US is increasing, and may provide the records needed to implement routine genetic evaluations for health traits.

The objective of this study was to use genetic and genomic analyses and producer-recorded health event data to estimate variance components and heritability for common health traits in US dairy cattle. A multiple-trait genetic analysis was used to identify genetic relationships between health events. Single-step methodology was used to incorporate genomic information in a multiple-trait analysis of those traits.

Material and methods

Producer-recorded health event data from US farms between 1996 and 2012 were available from Dairy Records Management Systems (Raleigh, NC) (Table 1). The health events used for analysis were mastitis (**MAST**), metritis (**METR**), cystic ovaries (**CYST**), digestive disorders (**DIGE**), displaced abomasum (**DSAB**), ketosis (**KETO**), lameness (**LAME**), reproductive problems (**REPR**), and retained placenta (**RETP**) from cows of parities one through five. Previous editing was applied to the data for common health events as described in Parker Gaddis *et al*. (2012).

Table 1. Summary statistics for each health event of interest.

Health event	Number of records	Number of cows	Number of herd-years
Cystic ovaries	222 937	131 194	3 369
Digestive disorders	156 520	97 430	1 780
Displaced abomasum	213 897	125 594	2 370
Ketosis	132 066	82 406	1 358
Lameness	233 392	144 382	3 191
Mastitis	274 890	164 630	3 859
Metritis	236 786	139 818	3 029
Reproductive disorders	253 272	151 315	3 360
Retained placenta	231 317	138 457	2 930

Univariate analysis

A logistic sire model was used in ASReml (Gilmour *et al*., 2009) due to the binary nature of the data. The model is given as follows:

$$\eta = X\beta + Z_h h + Z_s s$$

where η is the logit of observing the health event of interest, β is a vector of fixed effects including parity as first versus later parities and year-season, ***X*** is the corresponding incidence matrix of fixed effects, ***h*** represents the random herd-year effect, ***s*** represents the random sire effect where $s \sim N\left(0,\ A\sigma_s^2\right)$ with ***A*** representing the additive relationship matrix, and Z_h and Z_s represent the corresponding incidence matrices for the appropriate random effect. Variance components and heritabilities were estimated for each common health event individually. Accuracies and reliabilities of each sire's estimated breeding value (EBV) were calculated as:

$$rel = \frac{SE^2}{(1+f)\sigma_2^s}$$

where *rel* is the reliability, SE^2 is the squared standard error of the sire's EBV, *f* is the sire's inbreeding coefficient, and σ_s^2 is the estimated sire variance. Accuracy was calculated as the square root of reliability. The variance component estimates were then used as starting values of variance components in the multivariate analysis.

Multivariate analyses

A multiple trait threshold sire model was used to fit a seven-trait model for the following most common health events: MAST, METR, LAME, RETP, CYST, KETO, and DSAB. The model is given below:

$$\lambda = \mathbf{X}\beta + \mathbf{Z}_{\mathbf{h}} h + \mathbf{Z}_{\mathbf{s}} s$$

where λ represents a vector of unobserved liabilities to the given diseases, β is a vector of fixed effects including parity as first versus later parities and year-season, **X** is the corresponding incidence matrix of fixed effects, ***h*** represents the random herd-year effect, ***s*** represents the random sire effect where $s \sim N\left(0,\ \mathbf{A}\sigma_s^2\right)$ with **A** representing the additive relationship matrix, and $\mathbf{Z}_{\mathbf{h}}$ and $\mathbf{Z}_{\mathbf{s}}$ represent the corresponding incidence matrices for the appropriate random effect. Variance components and heritability were determined from parameter estimates calculated using THRGIBBS1F90 (Tsuruta and Misztal, 2006). A total of 100,000 iterations were completed with the first 10,000 discarded as burn-in, saving every 25 samples. Post-Gibbs analyses were completed using POSTGIBBSF90 (Misztal *et al*., 2002). Posterior means of sire predicted transmitting abilities (**PTA**) were estimated on the liability scale as well as converted to probabilities of disease as described by Zwald (2006). Highest posterior densities for the 95% interval were calculated for each parameter. Reliabilities of estimated sire PTAs were calculated as shown above using the posterior mean of additive variance of each health event, standard deviation of each estimate distribution, and inbreeding coefficients of the sires.

Genomic data was incorporated through the use of a blended **H** matrix following single step methodology implemented with preGSf90 software (Aguilar *et al*., 2011). The software has a maximum number of genotyped animals that can be used, which was met by restricting the genotype data to only include sires with at least five daughters. Default editing conditions were applied as set by the software resulting in genomic data being included for 2,649 sires with 37,525 markers. The blended **H** matrix was incorporated into the same multiple trait threshold sire model as previously described using THRGIBBS1F90 (Tsuruta and Misztal, 2006). Difficulties were initially encountered with convergence using all seven traits. To obtain better starting values, 2 preliminary analyses were performed. One analysis contained four traits (MAST, METR, LAME, and KETO) and the second analysis contained the remaining three traits (RETP, CYST, and DSAB). The posterior means of these analyses were then used as starting values in the full, seven-trait analysis. Post-Gibbs analyses were completed with POSTGIBBSF90. Convergence was assessed using the Coda library (Plummer *et al*., 2006) of R (R Core Team, 2012). Reliability of genomic estimated breeding values (GEBV) was estimated following Misztal *et al*. (2013). The reliabilities from the pedigree-based multiple trait analysis were used as reliabilities calculated without genomic information. These reliabilities were then converted to the effective number of records for genotyped animals following the formula given below:

$$d_i = \alpha\left[1/\left(1-rel_i\right)-1\right]$$

where α is the ratio of residual variance to genetic variance calculated from the pedigree-based multiple trait analysis. The inverse matrix **Q** was calculated as:

$$\mathbf{Q_i} = \left[\mathbf{D} + \left(\mathbf{I} + \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1}\right)\alpha\right]^{-1}$$

where $\mathbf{G}^{-1}$ is the genomic relationship matrix and $\mathbf{A}_{22}^{-1}$ is the inverse of the pedigree-based relationship matrix for genotyped animals only. The genomic reliabilities were then approximated as shown below:

$$rel_i = 1 - \alpha q^{ii}$$

where q^{ii} is the diagonal element of $\mathbf{Q}^{-1}$ corresponding to the i^{th} animal.

Results and discussion

Heritabilities and standard errors estimated from the single trait analyses are shown in Table 2. All traits exhibited a genetic component, but most were lowly heritable. The highest heritability was found for DSAB at 0.20. This heritability is very close to that estimated with a similar but smaller dataset (Zwald *et al*., 2004a). The high heritability for DSAB may be at least partially explained by the severity of the event, often requiring veterinary intervention. Zwald *et al*. (2004b) found DSAB to be the most consistently recorded health event among producer recorded data. Lower heritabilities were found for traits such as CYST, LAME, REPR, and RESP. These are events that are generally much less likely to be recorded in a consistent manner. For example, producers may have differing opinions regarding what constitutes an incidence of lameness that needs to be recorded.

Table 2. Heritability estimates and standard errors from single-trait analyses using pedigree-based relationship matrix, $\boldsymbol{A}$.

Health Event	Heritability	Standard Error
Cystic ovaries	0.03	0.006
Digestive disorders	0.06	0.02
Displaced abomasum	0.20	0.02
Ketosis	0.07	0.01
Lameness	0.03	0.005
Mastitis	0.05	0.006
Metritis	0.06	0.007
Respiratory disorders	0.04	0.01
Reproductive disorders	0.03	0.006
Retained placenta	0.07	0.01

Sire posterior mean of daughters' probability to each disease are shown in Figure 1. The mean probability of displaced abomasum was the highest equal to 0.53, though again, it is likely to be one of the diseases that are reported most consistently. The probability of daughters experiencing displaced abomasum ranged from 0.33 to 0.73. The mean probability of MAST was 0.515 and ranged from 0.29 to 0.66. These estimates are higher than those previously reported by Zwald (2004a). Probability of mastitis is more similar to those reported by Harder *et al.* (2006) when analyzing udder disorders as a group. Probabilities of experiencing a reproductive disorder are also similar to those reported by Harder *et al.* (2006).

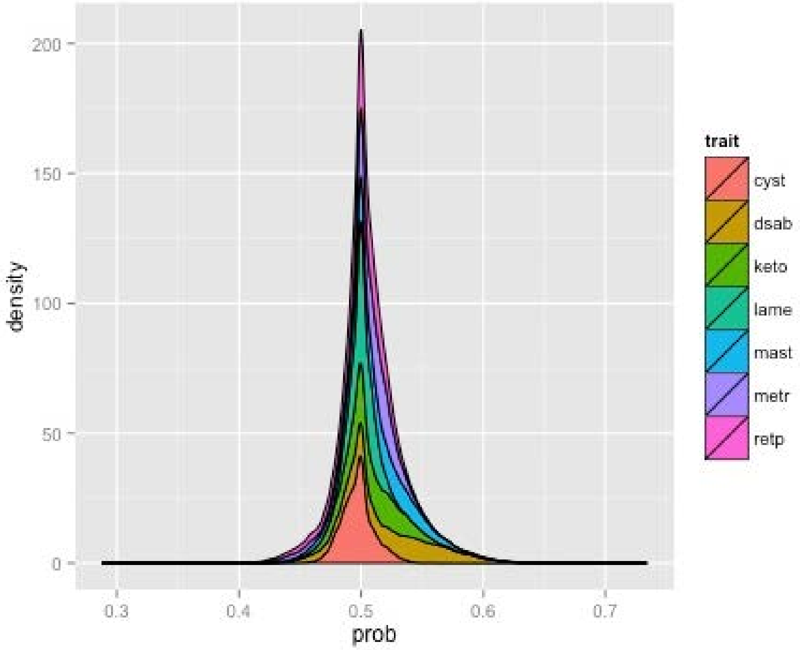

Figure 1. Sire posterior mean of daughters' probability to each disease (CYST = cystic ovaries; DSAB = displaced abomasum; KETO = ketosis; LAME = lameness; MAST = mastitis; METR = metritis; RETP = retained placenta).

Heritability estimates and 95% HPD from the multiple-trait threshold model are shown in Table 3. Genetic correlations between health events are included on the off-diagonals. Some traits with very low heritability estimates from the single-trait analyses were not included in the multiple-trait analysis. All heritability estimates were significantly different from zero. Heritability estimates of MAST and KETO increased in the multiple-trait model. Heritability estimates for METR, LAME, RETP, and DSAB decreased, whereas the estimate for CYST remained relatively constant. The heritability estimate for DSAB is similar to what has been reported previously (Zwald *et al.*, 2004b). Health events that were lowly heritable in the single trait analyses did not increase greatly through the use of a multiple-trait model. Several significant genetic correlations were found between health events. A genetic correlation of 0.81 [95% HPD = (0.70, 0.92)] was estimated between DSAB and KETO. Zwald *et al.* (2004b) estimated a genetic correlation between these two events equal to 0.14 (0.03) whereas a higher genetic correlation of 0.64 (0.10) was estimated by Koeck *et al*. (2012). This correlation also is consistent with previous analyses of these data using an informal path analysis that found an animal to have odds 15.5 times higher to have an incident of DSAB given that they previously had KETO (Parker Gaddis *et al.*, 2012). A high genetic correlation was also estimated between RETP and METR. This correlation is higher than a previous estimate found equal to 0.62 (0.11) (Koeck *et al.*, 2012). Significant, positive genetic correlations were also found between METR and KETO and METR and DSAB.

Table 3. Estimated heritabilities (95% HPD1) on the diagonal with estimated genetic correlations below the diagonal from multiple-trait analysis.

	Mastitis	**Metritis**	**Lameness**	**Retained placenta**	**Cystic ovaries**	**Ketosis**	**Displaced abomasum**
Mastitis	0.1 (0.09, 0.12)						
Metritis	-0.30 (-0.45,-0.15)	0.04 (0.03, 0.05)					
Lameness	-0.29 (-0.46,-0.11)	0.21 (0, 0.45)	0.019 (0.01, 0.03)				
Retained placenta	0.01 (-0.14, 0.16)	0.78 (0.68, 0.88)	-0.14 (-0.36, 0.07)	0.05 (0.03, 0.06)			
Cystic ovaries	-0.09 (-0.29, 0.13)	-0.17 (-0.37, 0.06)	-0.19 (-0.40, 0.06)	-0.12 (-0.34, 0.12)	0.026 (0.02, 0.03)		
Ketosis	-0.28 (-0.47,-0.07)	0.45 (0.26, 0.64)	0.08 (-0.17, 0.34)	0.10 (-0.17, 0.35)	-0.15 (-0.37, 0.13)	0.08 (0.05, 0.11)	
Displaced abomasum	0.001 (-0.15, 0.17)	0.44 (0.28, 0.60)	-0.10 (-0.29, 0.09)	0.06 (-0.12, 0.25)	-0.10 (-0.31, 0.10)	0.81 (0.70, 0.92)	0.13 (0.11, 0.16)

Heritability estimates from the multiple-trait analysis using single-step genomic BLUP (Table 4) were very similar to what was estimated using pedigree information, but the reliability of sire PTAs were improved. The addition of genomic information improved the reliabilities of sire PTAs for all health events as shown in Table 5. The reliabilities for these traits are low in comparison to production traits, however, the percent improvement that is obtained from the addition of genomic information is substantial. Percent improvement over reliabilities from single-trait analyses with pedigree information ranged from a 25% improvement in KETO to a 37% improvement in both MAST and METR.

Table 4. Estimated heritabilities (95% HPD1) on the diagonal with estimated genomic correlations below the diagonal from multiple-trait single-step analysis.

	Mastitis	**Metritis**	**Lameness**	**Retained placenta**	**Cystic ovaries**	**Ketosis**	**Displaced abomasum**
Mastitis	0.12 (0.10, 0.14)						
Metritis	-0.36 (-0.53, -0.19)	0.04 (0.027, 0.043)					
Lameness		0.13 (-0.1, 0.34)	0.026 (0.015, 0.034)				
Retained placenta				0.04 (0.03, 0.05)			
Cystic ovaries				-0.02 (-0.22, 0.16)	0.03 (0.01, 0.04)		
Ketosis	-0.16 (-0.31, 0.01)	0.44 (0.26, 0.64)				0.08 (0.05, 0.10)	
Displaced abomasum				0.01 (-0.21, 0.16)	-0.11 (-0.29, 0.13)		0.12 (0.09, 0.14)

Table 5. Mean reliabilities of sire PTA computed with pedigree information and genomic information.

Health event	**Pedigree information**	**Blended pedigree & genomic infomation**
Mastitis	0.30	0.41
Metritis	0.30	0.41
Lameness	0.28	0.37
Retained placenta	0.29	0.38
Ketosis	0.28	0.35
Displaced abomasum	0.30	0.40

Conclusions

These results suggest that enough data may exist in on-farm computer systems to enable the routine calculation of genetic and genomic evaluations for the most common health disorders in US Holstein cattle. Multiple-trait analysis is challenging because of demanding computational requirements, but the gain in information from correlated traits may be worth the additional time required for analysis.

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Session 6

Challenges for health data recording - Roundtable with representatives from the different stakeholders and open discussion

Challenges and Benefits of Health Data Recording in the Context of Food Chain Quality, Management, and Breeding - Perspectives of different stakeholders

A veterinary perspective

Perspective by a veterinary: by Rolf Mansfeld[1] and Siegfried Moder[2]

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[2]Federal Chamber of Veterinary Surgeons, Germany

Given the global current and future trends of shrinking agricultural areas from 5.000 m2 per resident in 1950 to 2.000 m2 in 2050 (Pallauf, 2002) there is a requirement for research in improving farm efficiency through technologically advances. The world human population is projected to be around 9 billion people in 2050. It has become more than clear that feeding the growing population is the "Major Challenge" into the future. Of course, providing sufficient drinking water is another big issue that needs to be solved. The key to feeding a growing population without harming wildlife habitats is research into high yielding farm automation and biotechnology (Avery 1996); that means further sustainable improvements are still required for already high yielding aspects of agriculture. The consequences are not only more complex production processes such as the use of more modern technologies, the implementation of quality assurance programs, but also breeds of high yielding animals managed and controlled by high yielding well educated and specialized humans.

There have been tremendous increases in milk yield over many decades. We have to face the risks associated with high performance, such as the analogy that modern cows are like high performance athletes requiring very high levels of management, housing, and feeding. But not only the cows themselves are demanding; the basic conditions such as consumer demands, legal requirements, reduction of the use of antibiotics and last, but not least the financial situation of milk producers has changed. Everyone involved in the process of milk production, such as process quality, product quality, animal health and animal welfare, abatement of epizootic diseases, consumer protection and - again last not least - economic affairs has to adapt to all these requirements and challenges and therefore has to be well informed at any time

Concepts of data processing systems including the integration of all people involved as farmers and veterinarians, consultants and public authorities, dairy industries, breeding organizations, and veterinary scientists were already published in the early 90's of the last century (Mansfeld and Grunert 1990). All the data processing and transmitting technologies they would have needed to become realized are available and affordable today. Therefore there is an obvious need for standardization and some kind of centralization to make all the data useful for every person involved in the whole process. There also is a need for legal rules concerning the ownership and utilization of data.

For "Food Chain Quality" we have to know that product quality at the farm level is a result of process quality, and process quality itself is a result of -using all relevant information. Successful data processing needs a row of key indicators of animal health and performance, hygiene, biosecurity, and economic aspects. Those indicators must be provided by research; they should be evidence based as far as possible; they must be available for all partners involved in the production process. That means that farm data must be available for researchers and for the veterinarians engaged in production medicine practice.

The main challenges for researchers are:

- to perform epidemiological studies to get evidence based and practicable indicators for risk of disease (to develop early warning systems and health monitoring systems)
- to perform clinical studies to get evidence based and practicable indicators for animal welfare (housing, environment, feeding a.s.f.).
- to perform studies to get further knowledge of genetic disposition of diseases (genomic selection, breeding programs).
- to develop new management and therapy procedures based on data processing (total or selective drying off procedures for example).

For all the challenges mentioned above the availability of current and consistent data is a must. For that a superior cooperation of all partners and a clear allocation of responsibilities are necessary.

A farmer perspective

Perspective of a farmer: by Morten Hansen

(Dairy farmer in Denmark, near Hjorring, Northern Jutland. Vice president of the Red Breed Committee of Viking Genetics)

240 cows and 160 ha; educated as Agronomist and in animal breeding; has been working with research and advisory service of dairy cattle before becoming a farmer.

A well-functioning, fertile cow just producing milk without health problems is very important for me and other farmers. To achieve this goal we know that we need data from as many farms as possible. Today the farmers are willing to extensively record disease, both because of legislation and also because health data is needed for monitoring and benchmarking on the farms. Farmers are also aware of the importance of collecting health data for a national monitoring and national breeding program. On Danish dairy farms a new health program started some years ago that allowed farmers to treat animals for ordinary production diseases, such as foot rot, mastitis, metritis, retained placenta, and milk fever. More and more farmers have willingly enrolled in this program. In this program farmers must do the registration (of health traits) on their own. Before, it was the vet who did all registrations.

The day of a dairy farmer is very busy, so registrations must be easy and simple to do for both farmers and his employees. So far, registrations have been done on paper, and then the farmers entered the data on a PC later, or he submitted the paper to others who entered the data.

But of course there is a big need for other electronic applications for disease registrations. From my point of view it must be simple (e.g., you cannot have 100 different disease categories) and easy to use. Also, the application should be used for monitoring the disease records and, for example, it could be used with all other data of the cow to find unprofitable cows that should be culled. But again, I would like to stress for the people developing these applications: do not be too ambitious!!! It is better to have a simple program that works well and farmers use that instead of a full package with a lot possibilities and details. A detailed app would be rarely used because we do not put energy into learning all the possibilities. As an example, I still have and love my five-year-old cellular phone. First of all, I have learned all the menus and possibilities so it is easy to use. Secondly, it has a very good antenna, good sound, long-lasting battery, and if I drop it, it still works. All this is much poorer on the new smartphones. Things that we must also consider!

A performance recording organisation perspective

Perspective by a performance recording organisation: by Daniel Lefebvre

Director of Valacta, Canada

Challenges and opportunities mentioned:

- Case definition.
- Maintenance of producer interest.
- Producer and vet focus on "pain points".
- Frequency of reporting to producer.
- Significance of rates in small herds for some diseases.
- Canadian Quality Milk program.
- Test- and sensor-based methods.

An AI industry perspective

Perspective by an AI industry: by Xavier David

Director of Unceia, France and Coordinator of EuroGenomics

The context of breeding has changed a lot:

For about 10 years, the context of animal breeding has been evolving a lot, especially in the developed countries. In the past, animal breeding was focused on technical performance to afford enough productivity for the farmers and enough food for the consumer. Beside these goals that are more and more relevant because of the perspective of the increase of the world population, the society expresses new needs: such as consumers pay attention on health and life conditions of the animals in (at) the farms, on the impact of agriculture, and also animal production on environmental impact, and stress more and more the link between food and human health. Farmers want also to minimize the use of antibiotics to have healthy animals, which is also very much in line with consumers' concerns about antibiotics used on farms.

These trends are now so important, and the lobbying of NGO's so effective, that governments on the national levels, and on the European level, propose to legislate in this way: 2 new European laws, i.e., the Animal Health Law and the Animal Welfare Law, are currently discussed.

New era for animal breeding

Since 2008, animal breeding is able to use innovative tools such as genomic selection. The dramatic decrease of sequencing costs opens new ways of selection: now some area of SNPs, and later some genes responsible of trait performances. The goal is still to keep smart breeding, which means selecting the best animals without modification of the genome.

On parallel: farmers who run larger herds with less human labor look for new breeding goals with emphasis on easy-going cows with high economic performance.

Challenges of health traits

Selecting health traits is certainly a big challenge for various reasons.

Firstly, the low heritability level (<0,2) makes the impact of environment important which emphases the need for larger number of reliable data.

Secondly, health traits are complex due to the status of immunity coming either from birth or from treatment, and from the interactions with other functions, such as reproduction, or nutrition.

Thirdly, the recording of health data is difficult: which is the opposite of production or type traits, health traits are collected by different players, sometimes for different purposes. Farmer's organization collect health traits to keep the health status of farms as safe as possible. Vets work with them to provide the best service to their customers in terms of preventive actions and advices, while the AI industry requires such data to match new phenotypic data with genomic information for better selection.

And lastly, there are also other difficulties related to health data records: there are variable clinical signs for the same disease, and collecting the information of healthy animals is relevant data, too.

Recommendations of AI industry

Even if the prior target of collecting health data is to help the management of the herd, AI industry, especially within EuroGenomics, sets up some new and modern breeding goals including health traits.

The success of these breeding goals is based on reliable registration tools making the recording for the farmer simple. Such tools are also developed to be reliable by optimization of the new technologies of information and communication.

Finally, the priority should be put on traits with an economic impact on profitability of the herd, such as udder health in dairy farming.

As examples of traits selected in the population within EuroGenomics, there are clinical mastitis (DFS, Austria and France), quality of hoof (The Netherlands and DFS), and paratuberculosis (France).

To conclude

The AI industry helped t in the 1950s to dramatically improve the health status of the herds in Europe, and at present the new challenge is to focus breeding on healthy, easy-going and sustainable animals for dairy and beef farms.