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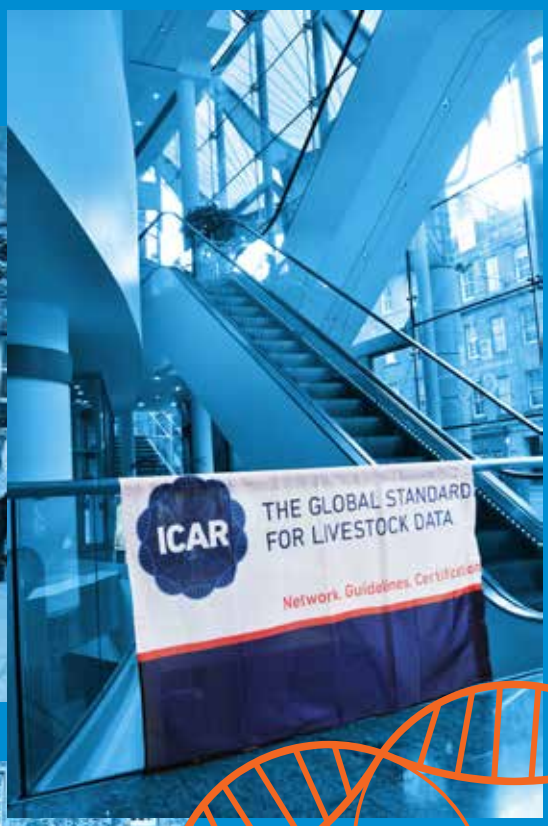
THE GLOBAL STANDARD FOR LIVESTOCK DATA

Network. Guidelines. Certification.

ICAR Technical Series no. 22

BIG IDEAS FOR BIG DATA

Proceedings of the 41st ICAR Conference
held in Edinburgh, UK,
14-16 June 2017



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Introduction

The 2017 ICAR Conference was held in Edinburgh Scotland (UK) and was expertly organised and hosted by AHDB Dairy, the not-for-profit organisation working on behalf of Britain's dairy farmers, and supported by SRUC (Scotland's Rural College). The title of the conference (Big Ideas for Big Data) provided a fitting description for the conference at which the various different aspects of data collection and analysis were considered.

The advanced Animal Production Sector (APS) is rapidly becoming a landscape with many new players with distinct, sometimes overlapping interests. In this arena a third party like ICAR has an important role to administer and facilitate the flow of information as a key element to maintaining the competitiveness and sustainability of the sector. Those involved into the game include; the farmers, industrial related companies, herd management organisations, international genetic evaluations centres and finally the retailers of the dairy and meat products.

The common theme that connected the three day ICAR Conference was the relevance of big data analysis in the APS, its beneficial repercussions over the sector and the ownership of such data. The most advanced tools developed for supporting the sector include automation and on-farm use of sensors, such as activity monitors, cameras, milking robots, pressure plates, milk analysers, etc. All these devices, coupled with an integration and interconnectivity among remote sensors and web data transfer, make these unprecedented volumes of data control, a relevant value for an industrial agriculture.

The integration and subsequent analysis of this data, produces information and knowledge which farmers request and use for beneficial effect in managing their business. The control and relevance of this data derived from different devices, are a source of debate concerning not only their accuracy, but also the access rights of the new information generated from integrating data and their statistical treatment.

Aspects which up-to-now have never been considered are beginning to arise on ownership of the raw data, access to unprocessed data from devices and ownership and access rights of information generated by integration of data. Questions such as "Who 'owns' the foreground IP?" and "who can use it?" are no more speculations nor rhetoric, but are questions in everyday life in the sector.

On the other side of the landscape are the companies whose main income is generated by taking data from the various on-farm devices, and integrate this new data with other sources of data to provide new solutions, and create a greater competitive advantage. The problem of how we assimilate or classify data is also an aspect that those involved in genetic and genomic evaluations face on a daily basis.

Access to livestock data has become a major issue in recent years, both for the breeders and for the organizations providing them with services. Breeder's control over this access requires prior consent towards the organization wishing to use them.

To assist better utilisation of big data, organisations must firstly strengthen breeders' confidence in the use of their data, which subsequently will make it easier to get their consent.

At the same time, relationships between organisations involved in genetic improvement are evolving in an increasingly competitive context. This is why data is becoming a matter of differentiation and its access an increasingly sensitive issue between organisations, but also with breeders.

To facilitate improved herd management, easier access and compatibility of various data sources on farm and from external databases is certainly a priority for ICAR and its member organisations.

It is true that extended services to farmers can generate added value by linking a variety of external data sources to design tailor-made answers beneficial to the profits of the farm enterprise. This includes extended health and treatment data, results from laboratories and milk quality composition from dairies, solutions to metabolic stresses, fertility predictions feeding needs, resource optimisation and early indications of animal health problems.

All these services based on in-line and on-line data, provided by herd management organisations, require the consent of the farmer, necessary standardisation of data exchange and data communication as well as due compliance with the legal aspects of data protection regulations.

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November 2017

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Data protection aspects by merging cattle data of various origins

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Abstract

To facilitate improved herd management, easier access and compatibility of various data sources on farm and from external databases are of high priority for Austrian farmers. Recent research projects have focused on extended services for farmers to generate added value by linking a variety of external data sources. This includes extended health and treatment data, findings from laboratories and milk quality information from dairies. These new online services will be provided by the cattle database (RDV) jointly operated by the Austrian and German performance recording organizations. The precondition for generating added value by merging data from various origins are beside standardization, data exchange and data communication, legal implications on data protection regulations. Within the project ADDA (Advancement of Dairying in Austria) the legal implications and requirements for merging data from different data sources have been elaborated. Due to the fact that there is no data ownership, the different roles like “person affected”, “contracting authority” and the “service provider” have to be defined and assigned to the data processed. The new General Data Protection Regulation (GDPR) and its impacts on the implementation related to provision of services based on cattle data of different origins and different circumstances and legal aspects for documentation and retention have been taken into account. The challenge is to set up a transparent system that guarantees the compliance of data protection regulations and minimize the administrative work for all parties involved when data from different data sources are integrated for routine applications as well as for research and development of advanced services. The presentation covers an outline of the basic legal data protection aspects and the example of implementation based on integrating data from farmers, veterinarians, performance and breeding organizations, labs and dairies in Austria.

Keywords: data protection, cattle data, legal implications, data integration.

Introduction

To facilitate improved herd management, easier access and compatibility of various data sources on farms and from external databases are of high priority for Austrian farmers. Recent research projects have focused on extended services for farmers to generate added value by linking a variety of external data sources. This includes extended health and treatment data, findings from laboratories and milk quality information from dairies. These new online services will be provided by the cattle database (RDV) jointly operated by the Austrian and German performance recording organizations. The precondition for generating added value by integrating data from various origins are beside standardization, data exchange and data communication, legal implications on data protection regulations. Within the project ADDA (Advancement of Dairying in Austria) the legal implications and requirements for integrating data from different data sources have been elaborated. This was done in collaboration with representatives from the different organizations involved representing different backgrounds and interests. The presented paper summarizes the outcome based on Austrian legal circumstances. The basic aspects will be also compatible with the new General Data Protection Regulation which will be directly applicable by 25th of May 2018 in all the EU member states.

Aspects of data protection

Legal background

To use data for various purposes different aspects need to be considered. Very often the questions asked are „Who is the owner of the data?“ or „Who may use the data for which purpose?“. The legal background is the constitutional law on data protection, where there are differences between the countries. The General Data Protection Regulation will be directly applicable by 25th of May 2018 in all the EU member states. There is a fundamental right for „personal data“, where “Everybody shall have the right to secrecy for the personal data concerning him”. Such data must be processed fairly for specified purposes and on the basis of a statutory obligation or authorization, a consent of the person concerned or other legitimate basis laid down by law. Everyone has the right to access data, which has been collected concerning him or her, and the right to have it rectified.

Basic principles of data processing

Each data processing has to fulfill the following preconditions: to act in good faith and according to purpose, transparency, principle of data minimization, correctness and limitation of data storage. Data processing is only legitimate if at least one of the following conditions is fulfilled: use in existential interest of affected person, legal authorization or legal obligation, consent of the affected person, predominantly entitled e.g. ensure compliance, data are permissibly published or indirectly specific to the individual.

Types of data

There are different types of data. Personal data are any information to an identified or identifiable person. If based on the animal-ID also the owner of the animal can be traced, the animal-ID is regarded as personal data. Sensitive data are data of persons about their racial and ethnic origin, political opinion, religious or philosophical beliefs, health or their sexual life. Indirect personal data („pseudo-anonymised data“): Data for a controller, service provider or recipient of a transmission, if the data relate to the

person in such a manner that its identity cannot be determined with legally permissible means. „Anonymised data“: Are not traceable to individual affected person by anyone. The measures on data protection depend on the type of the data.

Definitions of roles

For data processing there are different roles which have to be defined and assigned. Roles do change depending on the legal base which is applicable.

Contracting authority/controller: natural persons and corporate bodies, associations of persons or bodies of a local authority or business entities of such bodies if, on their own or jointly with others, they have taken the decision to use data, regardless of whether they use the data themselves or commission a service provider to do so. As to corporate bodies, associations of persons or bodies of a local authority or business entities of such bodies, this only applies in Austria under the current as well as the future Austrian Data Protection Act applicable after May 25, 2018 - the General Data Protection Regulation does not include such protection on an EU level.

Data subject: Any natural or legal person or consortium whose data are used (RDV: “affected” = cattle – holder of cattle only indirectly affected). In case of the diagnostic data, these are the farmers and veterinarians, if the ID of the veterinarian is documented and information about the animal with linkage to the farm is available.

Service provider/processor: Natural persons and corporate bodies, associations of persons or bodies of a local authority or commercial entities if they use data only for the production of a work applied to them.

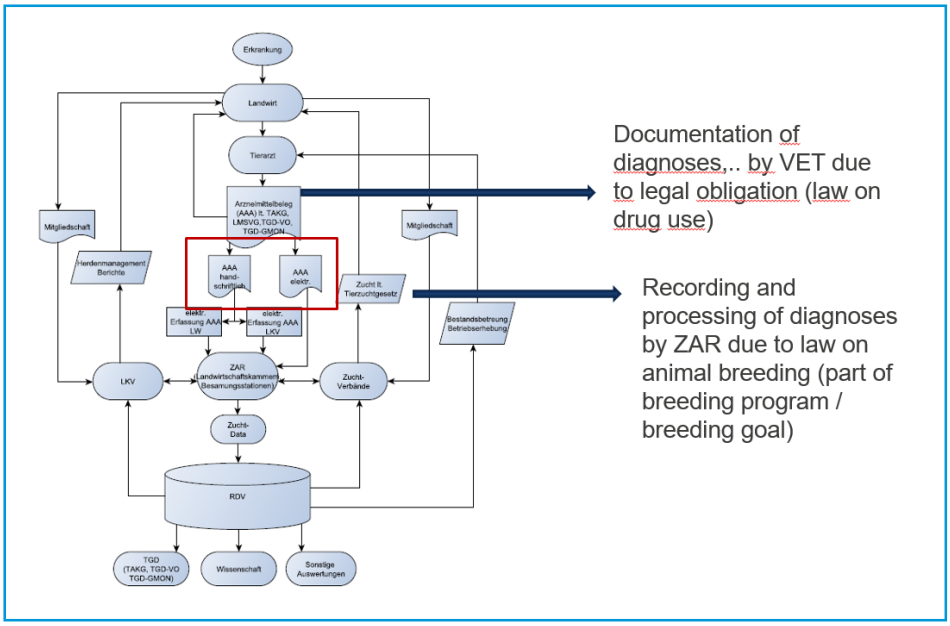

Figure 1. Overview of the process for documentation and recording of veterinarian diagnoses into the central cattle database with roles and legal background.

Ownership/usage of data/purpose of data collection

Concerning the discussion on data ownership it has to be stated that there is no data ownership as there is no civil law on ownership of data.

Entitled to disposal/ entitled to usage

Who is entitled to disposal? For which use?

Entitled to disposals is at first the data subject, whose data are used and who has a legitimate interest in the confidentiality of these data.

Who is entitled to usage? For which use?

Every data contracting authority/controller is entitled to use the data on the basis of an admissible legal basis, statutory obligation or authorization, contract, consent of the persons concerned, etc. - for predefined purposes.

To use the data, the contracting authority can engage a service provider. The service provider himself is within his contract not entitled to use the data for its own purposes, but only according the instructions of the controller (holding rights of use). Information on formal legitimacy is found under: §§ 6-9 DSG 2000, § 13 DSG 2000, §§ 17ff, § 50 DSG 2000, §§ 10f DSG 2000. If data are collected, there has to be a purpose/reason for collecting data (e.g. laid down in the bylaw of an organization). Examples can be that e.g. the breeding organization has the aim to improve animal health by genetics. The membership arrangement includes the collection of this data for this purpose.

Implementation of data protection aspects

If personal data are used, the data subject has to give its consent. '**Consent**' of the data subject means any freely given, specific, informed and unambiguous indication of the data subject's wishes by which he or she, by a statement or by a clear affirmative action, signifies agreement to the processing of personal data relating to him or her. If data from different sources are integrated, the challenge is that many different agreements are needed to administer. Additionally the consent need to be updated if new data are added. For implantation of the consent different possibilities do exist. It can be within the by law of the organization, but it has to be separate from other texts and needs an active confirmation. It can be within the membership agreement if it is within the purpose of the membership. Separate agreements on consent are another possibility (written, email, internet platform,..). If online agreements are possible for all members, updates can be implemented easily. Detailed information is found under Knyrim and Dolamic (2016).

Example of Legitimacy of data processing: veterinarian diagnoses

The presented example is according Austrian legal circumstances. Detailed information on data recording is found under Austrian Ministry of Health (2010), Egger-Danner *et al.* 2012, Obritzhauser *et al.* 2016 and Knyrim and Dolamic (2016).

Purpose of data processing: The purpose of data processing is laid down in the following regulations:

- Law of animal breeding / Animal breeding regulation: data within performance recording, genetic evaluation, breeding program.
  - Chamber of Agriculture: contracting authority
  - ZAR: service provider, ZuchtData: sub service provider
  - Data subjects: farmers and veterinarians
- Law on drug control / Residue Control Regulation / Veterinary Antibiotic Volume Flow Regulation:
  - Receipt for drug use has to be issued by the veterinarian. Information including animal, farm, diagnoses, treatment and date of treatment, Vet-ID,... has to be documented and issued by the veterinarian.
  - Contracting person for documentation: veterinarians
  - Data subjects: farmers

Right to collect and process data - example veterinarian diagnoses

Formal legitimacy (§§ 6-9 DSG 2000, § 13 DSG 2000, §§ 17ff, § 50 DSG 2000, § 10f DSG 2000).

There has to be a purpose/reason for collecting data (e.g. by law of an organisation,...)

- Aim of the organisation includes improvement of animal health by genetics
- Membership arrangement includes the collection of this data for this purpose
- ....

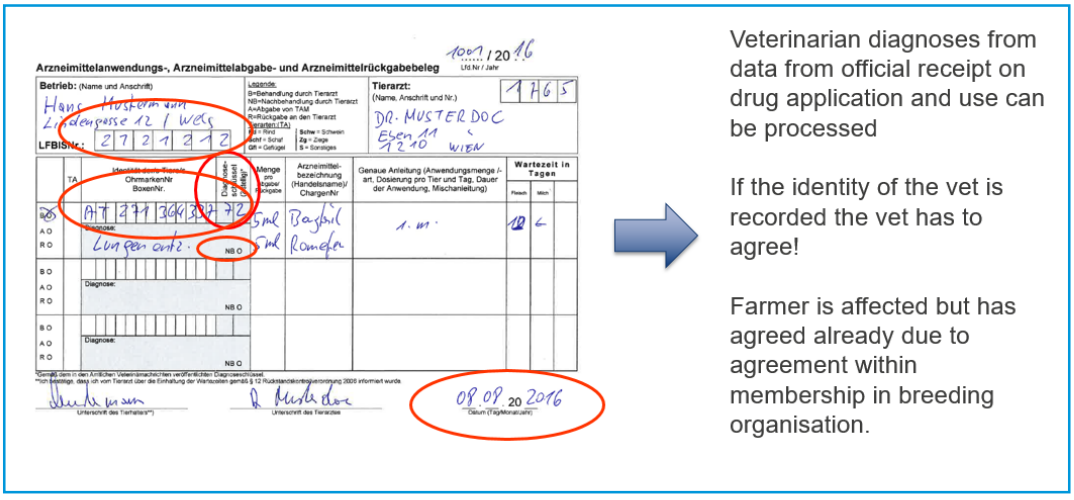

Figure 2. Example of recording veterinarian diagnoses from receipt for drug use

Conclusions

Integrating data from various origins can add value in different ways. New possibilities for benchmarking and elaboration of tools for improvement of herd management as well as genetics are coming up continuously. Data integration is a sensitive issue. Data protection aspects need to be safeguarded. For each data set the different roles (contracting authority, data subject/affected person, service provider/processor) have to be assigned. Roles do change based on the legal bases. If personal data are involved, the data subject needs to give his or her consent. If data are shared, it has to be defined: who is sharing the data, with whom, who is benefiting from sharing data. Clear structures, agreements on use of personal data, transparency in use of data e.g. are important to build up trust of the stakeholders and affected persons (data subject).

Acknowledgements

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A computerized consent management tool for breeders: why, how?

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Abstract

Access to livestock data has become a major issue in recent years, both for the breeders and for the organizations providing them with services. Breeder's control over these accesses requires his prior consent towards the organization wishing to use them.

Professional organization "France Génétique Elevage" (FGE) manages a database gathering zootechnical data collected for the purposes of genetic improvement. In order to perpetuate recording of these data and allow their better valorization, this organization must consolidate breeders' confidence in particular on the respect of their consent.

Regulatory texts concerning access to livestock data are numerous and fall into different legal fields, which makes concrete rules complex to be defined and implemented: whether or not the consent of the farmer is mandatory depends on data type, use made of data and person who wants to use it. They also evolve over time and a new 2015 text on genetic information systems brings new obligations whose impact is yet to be measured.

At the same time, relationships between organizations involved in genetic improvement are evolving in an increasingly competitive context. This is why data are becoming a matter of differentiation and their access an increasingly sensitive issue between organizations but also with breeders.

Since 2009, FGE has been providing a data exchange service between its database and breeders or, more recently, a body designated by them. This service has recently been enriched with a consents management tool with 2 features:

- Registration procedures adapted to various organizations in the field,
- Consultation of all consents granted (in order to be able to terminate them if necessary).

This tool has several innovative features to address consents management needs:

- Choice of web service with a standardized interface that allows a smooth use by all information systems (breeder, company, mutualized ...),

- Functional wealth with a detailed description that not only contains the "basic" consent data (holder's exploitation, consent beneficiary) but also clarifies its scope by indicating: the species concerned, Access to data is granted and, where appropriate, the breed and the family of data (eg dairy control, animal insemination ...).

Presentation outlines legal context, challenges and features of this new consent management tool and refers to its possible positioning to address wider use than in the field of genetic data alone.

Keywords: data management, access, consent, livestock

Introduction

In France, genetic improvement of ruminants has involved many (around 200) professional and public organizations for several decades. Professional bodies are organized by activity (Performance recording organizations, Insemination agencies, Identification and pedigree recorders, Breeding societies, Technical institute, Meat interbranch organization, Computer regional centers), and mostly by geographical area. Public stakeholders are in charge of regulation (Ministry of agriculture) and of official genetic evaluation (National Agronomic Research Institute, INRA). Since 2006, most of them are clustered in an interbranch organization: "France Génétique Elevage" (FGE).

To optimize efficiency of the dispositive, organizations have built a collective information system which has been legally entrusted to France Génétique Elevage in October 2016 by extension of an Interbranch agreement “on recording and management of National Genetic Information System data”. Organized on regional databases exchanging with a national one, this system manages data about Breeders (holding identification number, name and address) and animals: identity and movements, reproductive events and certified filiations, milk and meat performances, morphological scores and qualifications, genetic values and public insemination males’ data.

Initially collected and used on genetic improvement purpose, these data have been more and more used for technical advice and, on this scope, have been completed with numerous technical information.

Consequently, FGE is responsible of a huge database containing many data completely concerned by the access issue which has become very pregnant in last years particularly with the development of concurrency between different organizations sending advice.

Data access is subject to complex and evolving regulations. To fulfill its responsibilities, FGE must analyze its obligations about management of breeders’ consent and propose an effective solution for its collection and centralized management.

Regulatory context of breeders’ consent

Regulation on data access at the conception of the system

National Genetic Information System (SNIG) was built at the end of the nineties to improve reliability of data used in genetic evaluation. At that time, the issue was technical more than regulatory, the need was to consolidate collection with two types of checking:

- Make sure that organization which collected data on the field is agreed for this kind of data. Indeed, agreement supposes engagement of the organization to respect a national collect protocol.

- Apply consistency computerized management rules at three levels: database integrity, zootechnical likelihood and regulatory conformity.

Consequently, write access to the database has been completely locked by allowing such access exclusively towards collective updating modules guaranteeing the respect of above rules.

Regulation about data was very simple at that period. The main regulatory framework was the 1978 Law on "Informatics and Freedom" (still effective nowadays) but the only concrete interpretation at that time was mandatory declaration of every database constituting the system. These declarations were made conscientiously.

Concerning genetic data, a decree published in 1973 said: "*Have access to all data, for their genetic improvement missions: INRA, Livestock Institute, Breeding Societies, Selection Agencies*". This list covered all national organizations.

But above all, system's stakeholders, both public and professional did not feel particularly concerned. Indeed, their activity was by law (Livestock Act of 1966) organized in functional and geographic monopolistic areas so that there could not be any competition to sell service to breeders. So that data access didn't interest anyone.

On the contrary the collective aim was to facilitate data valorization at the motive that using data is the best way to detect and correct errors.

Consequently, read access to the database has been left completely open from the collective computer tool's point of view: Every computer center had the responsibility of developing data access checking tools to enforce regulation and access rights decided between local organizations.

Evolution of regulation in the early 2000

In 2006, "Agricultural Guidance Act" put an end to the geographical monopoly zones for animal insemination, opening concurrency among artificial insemination centers: recruiting new breeders becomes crucial!

Among the texts implementing this law, a decree on genetic information systems was published on 12 September 2007. This decree contains complex specifications defining several categories of data and, for each, which organizations have access to them and for what uses.

In a context of local organizations restructuration, and as data became a tool for prospecting new clients, the rules specified in the decree were gradually implemented. Interpretation of the specifications proved to be difficult on this occasion, since its redaction was sometimes ambiguous. Another difficulty revealed when it came to implementing the rules directly in computer tools: locking read access a posteriori on an extremely rich application patrimony has proved impossible because requiring to modify all the programs.

These difficulties have had consequences on the perception of the system, by the stakeholders first and then by the breeders. Data security in the collective system has been questioned, leading to a centrifugal movement of privatization of data in business systems or complementary databases.

In 2014, a new decree opened also animal performance recording to competition: new organizations, which had not participated to collective information system building, arrived on the market. At the same time, breeders are massively equipping themselves

with new equipment collecting data (milking robots, sensors, etc.) and also providing technical consulting tools: manufacturers of such equipment become competitors for MRO.

Actual regulation: obligation of breeders' consent management

Sensitized to the question of data access by the evolution of general environment (development of digital economy, prospect of a new European regulation on processing of personal data…) and by those of agricultural development dispositive (see above), Ministry of Agriculture issued a new decree on genetic information systems in April 2015.

Indeed, they made the analysis that zootechnical data, although characterizing animals, meet the definition of a personal data since they can be attached to a holding and its holder. This same analysis leads the organizations involved in animal data's management to check impact on the collective scheme of the European Regulation 2016-079, which will apply in May 2018.

In consequence, the decree which defines the data to be managed in the collective information system mostly refers to the Computer and Freedom Act of 1978 and requires breeder's consent for almost all access and use of data collected on their animals. Local organizations most of the time anticipated this obligation by collecting these consents in their membership contracts but without recording them in the collective information system.

Latest regulatory development, following the decree, is the extension of the interbranch agreement on recording and management of SNIG data (October 2016), giving it a legal scope. Through this agreement, France Génétique Elevage takes responsibility for the management of the collective system and undertakes to ensure compliance with the decree, in particular obligation to collect and respect breeders' consent.

This commitment assumes the visibility of actually received consents by national team of interbranch: recording into the system becomes mandatory.

French collective computerized consent management tool

Generalization of consent's collect and recording into collective system represents a new and heavy task for system's stakeholders. They consider it a new constraint that should not entail investment on their part nor complicate their profession. Interbranch France Génétique Elevage had therefore obligation to provide a tool adapted to the different field operating procedures or computer organizations (private or shared systems).

Terms of reference for the collective consent management tool

To provide this flexibility, the tool must allow organizations to register their own consents. But this possibility makes possible drift by the improper recording of consents that have not actually been collected from the breeder. To guard against this, breeders must be given permanent visibility on consents that have been registered on their behalf.

Thus, the tool must offer both functions of recording and consultation.

Functional characteristics

Consents are defined with numerous parameters allowing breeders to specify finely the scope of the authorization they grant. These parameters are: data type (see figure), breed of the animals concerned, duration of consent (start and end dates) and use that can be made of the data.

Consent recording operation is accessible to all organizations already providing data to the system (empowered organizations) and also breeders. It allows organizations to record consents they're granted and consent to a third-party organization, to breeders to record consents they grant and to both of them, to close consents.

Consents and regulatory access rights consultation allows organizations to list farms from which they can access data and breeders to list organizations having access to their data.

Technical characteristics

The tool must allow automatic recording of consents that can be deducted from contracts: it must be possible to add corresponding step the overall processing of contracts recording. For this purpose, the tool contains batch database updating module.

It must also facilitate recording by all external information systems (breeder software, enterprise system ...). This is why the module has been encapsulated in a web service easily integrated into a client application.

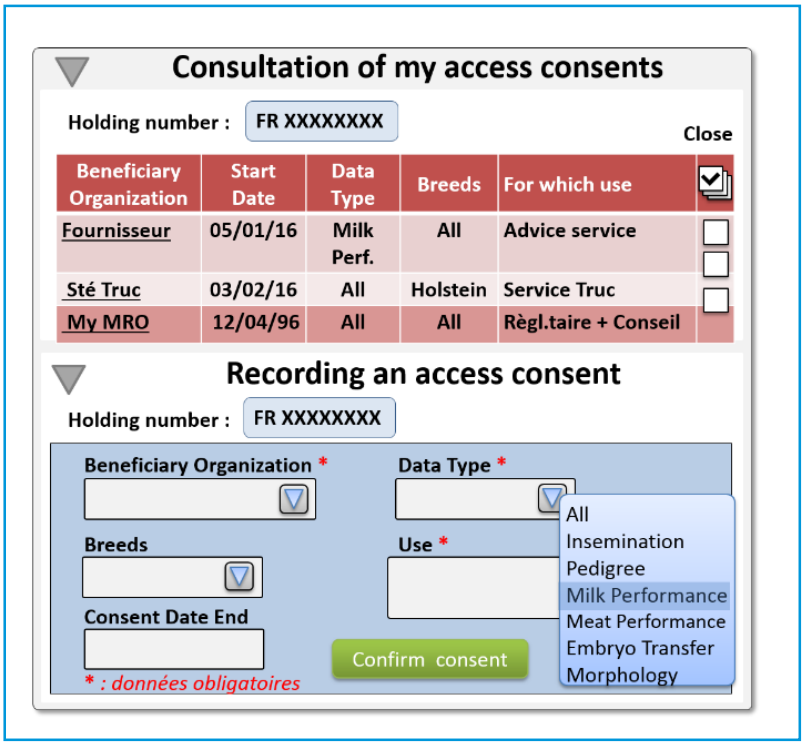

Figure 1. Mock-up of screen using « Consent management » Web Service

Conclusions

With the adoption of new European zootechnical regulation, interbranch wondered about durability of the consents' management tool in the new dispositive that will be built. The main change is the assignment of genetic improvement responsibility to breeding societies but the regulation does not deal with information systems. Without prejudging reorganizations, it can be affirmed that data recording and management will remain necessary. And since the analysis leading to the personal status of animal data will not be called into question, obligation to consents' collect can only be strengthened in the future.

Thus, the need for a recording modern, adaptive and efficient tool will remain.

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Use of daily robotic progesterone data for improving fertility traits in Finnish Ayrshire

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Abstract

Currently, cow's ability to return to cyclicity after calving is mostly evaluated using the first insemination measurements, which are highly influenced by management decisions. However, if consecutive progesterone measurements are used the first heat can be identified accurately even if the cow does not show the clear signs of heat. The data from 14 Finnish dairy herds using DeLaval Herd Navigator™ (HN) system were used to study cow's ability of returning to cyclicity after calving. 1230 Ayrshire cows from parities 1-3 were included in the analysis. The HN system takes milk progesterone samples automatically during milking and apply biological models to calculate the time of oestrus and probability for pregnancy if the cow is inseminated. In this study, the data of the first heat identified by the HN system (CFH) based on progesterone concentrations between 1-100d after calving was used. Commencement of luteal activity (C-LA) was also studied. For first parity cows the mean number of days were 49.9, 38.1, 78.9 and 30.5 for CFH, C-LA, interval from calving to the first insemination (CFI) and interval from first to last insemination (IFL), respectively. Most of the cows in the data had been inseminated for the second heat identified by the HN system. When phenotypic estimates were compared with those from previous studies CFI was 4.5d shorter and IFL 10.3d shorter in HN herds for the first parity Ayrshire cows. Heritability estimates for first parity cows were calculated using DMU software and the linear animal model being 0.27±0.13, 0.23±0.12, 0.07±0.07 and 0.03±0.06 for CFH, C-LA, CFI and IFL, respectively. Genetic correlation between CFH and C-LA for the first parity cows was high, being 0.95±0.06. Because of the small number of animals in the data most of the estimates had high standard errors. However, the magnitudes of the estimates are in line with previous studies where higher heritability estimates have been found for endocrine fertility traits than traditional fertility traits. Results suggest that using milk progesterone information to detect heats shortened CFI in first parity cows and IFL in parity 1-3 cows.

Keywords: progesterone, heat detection, dairy, ayrshire.

Introduction

Fertility is one of the major factors affecting the efficiency of dairy farming. In dairy breeding schemes a large emphasis has been put to selection on high milk yield in past years and many studies have revealed a negative genetic correlation between milk production and fertility traits (e.g. Berry *et al.* 2014). Failure in heat detection also reduces fertility. Poor fertility is associated with high production costs and is one

of the most common reasons for culling. The efficient heat detection program and correct timing of service are crucial to achieve high conception rates. Currently, cow's ability to return to cyclicity after calving is mostly evaluated using the first insemination measurements (CFI), which are highly influenced by management decisions and have low heritabilities (e.g. Berry *et al.,* 2014). There can be large differences between herds on the length of the voluntary waiting period and the visual checks of heats.

Progesterone (P4) is a hormone which is produced by the corpus luteum and the reproduction status of the cow can be determined from P4 concentration. DeLaval Herd Navigator™ (HN, DeLaval International, Tumba, Sweden) management program samples and analyses milk P4 concentration automatically during milking. If consecutive P4 measurements are used, heats can be identified accurately even if cows are not showing the clear signs of heat. Several studies have also revealed that endocrine fertility traits have higher heritabilities than traditional fertility traits (Royal *et al.*, 2002, Berry *et al.,* 2012).

The objective of this study was to estimate genetic parameters of endocrine (P4) fertility traits measured by HN system and compare those traits with the traditional fertility traits in Finnish Ayrshire cows.

Materials and methods

The data from 14 Finnish dairy herds using HN system were used to study cows' ability of returning to cyclicity after calving. Progesterone data were provided by Lattec I/S (Hillerød, Denmark). Data from a period of 2014-2017 were available although some herds had joined later (6 in 2015 and 3 in 2016). 1230 Ayrshire cows from parities 1-3 were included in the analysis. Herd Navigator starts to sample and analyze P4 concentrations 20 d after calving. Raw P4 measurements are smoothed using an extended Kalman filter and a biological model is used to predict the reproductive status of the cow (Friggens & Chagunda 2005, Friggens *et al.,* 2008). The model classifies cows to three different reproductive categories (0 = postpartum anestrus, 1 = oestrus cycling and 2 = potentially pregnant) and calculates the time (d) to the next sample (DNS) (Friggens *et al.,* 2008). Two P4 traits, days from calving to the first heat identified by HN system (CFH) and days from calving to luteal activity (C-LA), were studied. C-LA was calculated as a reproduction status change from 0 to 1 or 2.

CFH is defined as a second heat after calving. Cows tend to have constant low P4 concentrations after calving, therefore first heat is difficult to detect by the P4 curve. In addition, cows are rarely inseminated to the first heat. The model detects when P4 concentration changes from high to low, issue a heat alarm to the user, record that a heat has occurred and will be searching for new heat from around 17 - 18 days later.

Insemination, test day and pedigree data were provided by Faba Coop (Vantaa, Finland) for all cows in those 14 HN farms described above. Four traits were studied, days from calving to the first insemination (CFI), days from calving to the last insemination (CLI), days from first to last insemination (IFL) and the number of inseminations (NI). Two different datasets were created, data 1 had observations for CFH and traditional fertility traits (restricted by CFH = 100 d and CFI = 230 d) and data 2 had observations for CFH and C-LA (restricted by CFH = 100 d).

For statistical analysis DMU software (Madsen & Jensen 2013) and linear animal model were used. Genetic analysis were performed for parity 1 except for C-LA where parities 1-3 were also analyzed together. Herd, calving year, calving month and calving age were included as fixed effects and an animal effect as a random factor. Interactions were not included because of the small data size.

Results and discussion

Descriptive statistics for parity 1 for datasets 1 and 2 are shown in Tables 1 and 2. The mean number of days in univariate analysis were 49.3 (n=763), 50.9 (n=715) and 52.9 (n=465) for CFH and 39.8 (n=752), 37.7 (n=689) and 40.5 (n=460) for C-LA for parities 1, 2 and 3, respectively. Most of the cows in the data were inseminated to the second heat identified by the HN system (First 17.3%, Second 31.2%, Third 18.5%). The mean number of days from calving to the first insemination (CFI) varied between 78.9-86.5 and interval from first to last insemination (IFL) between 30.5-38.7d depending on the parity. Phenotypic estimates from HN herds in parity 1 were 4.5d shorter for CFI and 10.3d shorter for IFL compared to those from previous studies (Kargo *et al.,* 2014, Muuttoranta *et al.,* 2015). CFI was 1d and 5.7d longer and IFL was 6.6d and 4.9d shorter in HN herds for parities 2 and 3, respectively. The mean number of inseminations in HN herds was around 2 for all parities, which are similar with the estimates from previous studies. According to Kargo *et al.* (2014) the average cost of CFI is 0.51 Euros/day and IFL is 2.56 Euros/day for the red dairy breed in Finland. The improvement in herd economic results after HN system is installed could therefore depend on the herd size and herd age structure. HN also reduces farmer's working time in visual checks of heats.

Table 1. Descriptive statistics for CFH and traditional fertility traits for first parity cows (dataset 1).

Trait (days)	n	Mean	SD	Min	Max
CFI	676	78.9	15.8	46.0	184.0
CLI	676	109.4	43.0	52.0	296.0
IFL	676	30.5	40.4	0.0	234.0
CFH	676	49.9	17.7	22.0	100.0

CFI= calving to first insemination, CLI=calving to last insemination
IFL= interval from first to last insemination
CFH= first heat identified by Herd Navigator

Table 2. Descriptive statistics for CFH and C-LA for first parity cows (dataset 2).

Trait (days)	n	Mean	SD	Min	Max
CFH	723	48.4	17.1	22.0	100.0
C-LA	723	38.1	15.7	20.6	89.6

CFH= first heat identified by Herd Navigator, C-LA= commencement of luteal activity

Table 3. Heritabilities (±SE) for commencement of luteal activity (dataset 2).

	C-LA	lnC-LA[1]
Parity 1, n=723	0.23 (0.12)	0.17 (0.10)
Parities 1-3, n=1933	0.22 (0.04)	0.23 (0.04)

[1]natural logarithm of commencement of luteal activity

Heritability estimates for first parity cows in data 1 were 0.27±0.13, 0.23±0.12, 0.07±0.07 and 0.03±0.06 for CFH, C-LA, CFI and IFL, respectively. Correlation between CFH and C-LA from data 2 for first parity cows was high as excepted since traits are quite similar, genetic correlation being 0.95±0.06 and phenotypic 0.90. In bivariate analysis (data 2), heritabilities were lower than in univariate analysis, being 0.20±0.12 for CFH and 0.14±0.11 for C-LA. Heritabilities for C-LA traits are shown in Table 3. These estimates are close to those in previous studies, e.g. Tenghe *et al.* (2015) reported heritabilities of 0.11±0.06 and 0.12±0.05 for CFI and lnC-LA, respectively. Because of the small number of animals in the data, most of the estimates had high standard errors. However, the magnitudes of the estimates are in line with previous studies where CFH and C-LA have found to have higher heritabilities compared to traditional fertility traits (Royal *et al.,* 2002, Berry *et al.,* 2012).

Conclusions

Results suggest that using milk progesterone information to detect heats shortens CFI in first parity cows and IFL in parity 1-3 cows. Progesterone traits (CFH, C-LA) had higher heritabilities than traditional fertility traits and the correlation between these traits were high. Some of the standard errors were high because of the small data size. However, these results suggest the data on endocrine fertility traits measured by automatic systems is a promising tool for improving fertility, specifically when more data is available. It is important that this kind of data from automatic devices is made available to recording and breeding organizations in the future.

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Collecting milking speed data as part of official milk recording

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Abstract

Due to the growing use of robotic milking systems, the interest in optimizing the milk output of the robotic milking unit has added a new dimension to breeding and managing dairy cows. Milking speed, milking unit attachment speed and time required for cows to enter the robotic milking unit are three major factors in determining which cows are more suitable for robotic milking systems and maximize returns on investment. Milking speed also has application in conventional parlors, and can have a direct factor on operational expenses associated with milking the herd. High producing cows with consistent milking speed will optimize parlor throughput and increase the amount of milk collected on a daily basis. Dairy producers have had the opportunity to purchase in-parlor milk meters and collect data that would help in the optimization of parlor performance, however costs and maintenance concerns have limited the adoption in the United States. The data that is produced from existing systems varies in format and archive history and is rarely transmitted as part of milk recording services, thus no national genetic evaluation of milking speed currently exists in the United States.

AgSource has been a long-time user of Tru-Test (Tru-Test Inc, Mineral Wells, TX) Electronic Milk Meters (EMMs). EMMs are used to collect monthly DHI milk weights, milking durations and milk samples. Due to the growing interest in parlor efficiency, in 2015, AgSource started collecting the milking duration times using its EMMs. Milking speed records in the form of milk weight and milking duration data are collected on approximately 100 large farms totaling over 100,000 cows. Beneficial to analysis and utilization, data is measured as a continuous variable (kg/minute) versus a standard categorical measurement. AgSource milking speed data proved to be a consistent measure based on stage of lactation and parity.

Milking speed values averaged 2.6 kg/minute and ranged from 1.4 to 4.5 kg/minute. Further analysis showed that milking speed data was positively correlated to DHI Mature Equivalent (ME) 305-day milk production and negatively correlated to somatic cell score at low and high milking speeds. Using genotypes supplied by the USA A.I. cooperative, Genex, resulting breeding values were calculated on over 60,000 cows and bulls.

Employing new technologies in regular DHI recording result in new reliable and consistent phenotypic measures that can be combined with genotype data to identify new markers, new genetic traits of economic importance and be incorporated in DHI value-added management reports.

Keywords: milking, speed, parlor, efficiency.

Introduction

The United States continues to see increased adoption of robotic milking systems. Maximizing the amount of milk collected from a robotic milking system is a key element in being more profitable. There are three components that have a significant impact on robot efficiency: amount of milk collected per minute, time required to attach the milking unit and time required to move the cow in and out of the robotic milking system. Although not a new concept, analysis of milking speed data on individual cows has gained more interest in recent years. Cows that milk faster while maintaining good udder health will be more efficient and profitable than slow milking cows. Although the interest in milking speed data has increased due to increased use of robotic milking systems, the same principle applies to conventional parlor systems as well. Farms that milk cows 24 hours a day can also optimize milk output by analyzing parlor flow and grouping slow milking cows or potentially even remove them from the herd.

Dairy producers using conventional parlors have had the option to purchase in-parlor electronic milk meters and utilize data collected by the meters to manage individual cows. Adoption in the United States has been slow due to costs and maintenance concerns. Dairy Herd Improvement (DHI) programs allow for the use of milk weights from in-parlor based milk meters, however there is a wide variety in how data is formatted and transmitted between systems. In addition, producers are required to make sure meters are calibrated and always functional. Milking speed or milking duration data from in-parlor systems is typically not transmitted to DHI and therefore not utilized in any national genetic evaluations.

AgSource has been a long-time user of Tru-Test (Tru-Test Inc, Mineral Wells, TX) Electronic Milk Meters (EMMs). EMMs provide additional data over conventional DHI milk meters. In addition to the milk weight, the system also provides start time, milking duration and stall number. Due to the growing interest in parlor efficiency, in 2015, AgSource started collecting the milking duration times using its EMMs. Over 900,000 individual milking speed records have been collected on approximately 100 large farms totaling over 100,000 cows as of May 2017. Data are transmitted as part of the monthly test day data flow to the AgSource Dairy Record Processing Center. Beneficial to analysis and utilization, data is measured as a continuous variable (kg/minute) versus the current standard categorical measurement.

Materials and methods

The goal of the research was to utilize the raw data provided by the EMMs, by first calculating milking speed values on individual milking observations and analyzing the results for data quality and consistency within lactation and across lactations. After analysis, data filters were defined to remove observations that were considered in error. Utilizing the filtered milking speed values, further data analysis was conducted looking at the overall dataset to develop a management report that incorporates the milking speed data and to develop genetic evaluations for milking speed.

Overall data set

Using Microsoft SQL Server 2012© individual cow data was obtained from the AgSource Dairy Records Processing Center database. The overall data set includes individual test day information (days in milk, milk weight, milking speed, fat and protein percent, and somatic cell score), and was combined with 3-generation pedigree information, calving date, parity, 305-day mature equivalent milk production, and lactation linear somatic cell score. The resulting data set was further analyzed using Microsoft Excel©.

Genetic evaluations

Test day records (n=681,029) were extracted from the AgSource Dairy Records Processing Center database. Data was used from cows with complete individual and sire IDs, and at least five records existed where milk duration was less than 20 minutes, and milking speed less than 9 kg/min). A cow had to have either first or second lactation data to be included in the analysis. After quality control, there were 351,341 records on a total of 35,693 cows, from 3,216 sires. The pedigree consisted of 93,664 animals. A population of 109,732 animals with 50K genotypes were used to estimate genomic breeding values. Breeding values were estimated for all individuals in the pedigree using BLUPF90, and variance components were calculated using the AIREML procedure within the BLUPF90 suite of programs (Misztal *et al.*, 2015).

Results and discussion

Data quality

Prior research related to milking speed has generally used categorical data. Since the EMM data is continuous data, it was key to ensure we have good quality data. Cows with extreme milking speeds both positive or negative could point at problems related to milking equipment attachment. The milking speed value is not a measurement made by the EMM, milking speed is calculated by using the EMM milk weight and milk duration. One of the concerns regarding the milking speed calculation was related to what value the EMM returned for milking duration if the milking unit suddenly disconnects and then is reconnected. Based on the data, any observations where milking speed was less than 0.45 kg/min or greater than 6.8 kg/min or milking duration was greater than fifteen minutes could be considered suspect. The number of observations outside the criteria only accounted for 1.4% of the total dataset. When removing these outliers, the average milking speed value remained unchanged at 2.6 kg/min.

Data variability

DHI milk recording typically collects a single milk sample and milk weight per month. Not knowing if milking speed data varies per milking or within lactation, it was important to find out if there are other factors such as days in milk or lactation that need to be considered. If milking speed data changed based on days in milk or lactation, its use in a management report grouping cows would be considerably more complex. Based on the data collected, it was decided to require a minimum of five milking speed observations per cow. After excluding cows with less than 5 observations, 790,294 observations on 72,614 cows remained. Results are shown in Table 1, and provide various statistics on the distribution of milking speed values and corresponding standard deviations.

Table 1. Milking speed distribution.

	Milking Speed (kg/min)	Standard Deviation (kg/min)
1st Quartile	1.9	0.4
2nd Quartile	2.4	0.5
3rd Quartile	3.1	0.6
4th Quartile	3.4	0.6

Table 2. Variance components and heritability estimates for milking speed.

	Variance est.	Var SE
Additive (animal)	0.3630	0.0199
PE	0.4349	0.0161
Residual	1.2204	0.0031
Total	**2.0183**	
Heritability	17.99%	
Repeatability	39.53%	

Based on the results in Table 1, the spread in milking speed between cows is quite large. The 4th quartile cows (fast) produce on average 1.5 kg more milk per minute than the 1st quartile cows (slow). In addition, the average standard deviation for each cow is only 0.2 kg/min larger for the 4th quartile cows versus 1st quartile cows. Statistical analysis showed that a 95% confidence interval variation between lactations was 0.003 kg/min and within lactation was 0.57 kg/min. Based on these results, the variation per cow within lactation is relatively small and across lactation is negligible.

Milking speed analysis

To understand more about the value of milking speed data and how it relates to overall lactation, milk production, and udder health, cows were grouped in 9 categories. The first category includes cows milking less than 1.4 kg/min. Subsequent groups were generated at 0.45 kg/min increments. The last group were cows milking 4.5 kg/min or higher. Figure 1 shows the distribution of cows across the 9 groups. The distribution is a typical normal distribution. Figure 2 shows the actual lactation ME 305 day milk production and the LSSCC score for the same 9 groups. Initial expectation were that the lactation average LSSCC would be lowest for the slowest milking cows and highest for the fastest cows, however the distribution in Figure 2 shows that both slow and fast milking cows had a slightly higher LSSCC. ME 305 day milk production had a strong relationship with milking speed where by the fastest cows also tended to produce the most milk in the lactation.

Producer opportunities

As indicated prior, milking speed data can provide a valuable tool to optimize parlor performance. U.S. herds typically house and manage cows in groups. Milking schedules are based on bringing a single group of cows through the parlor. Grouping strategies are typically based on nutritional needs, reproductive status and sometimes health status. Adding milking duration and milking speed to the decision criteria can further optimize parlor throughput. Table 3 shows an example of a large herd group report

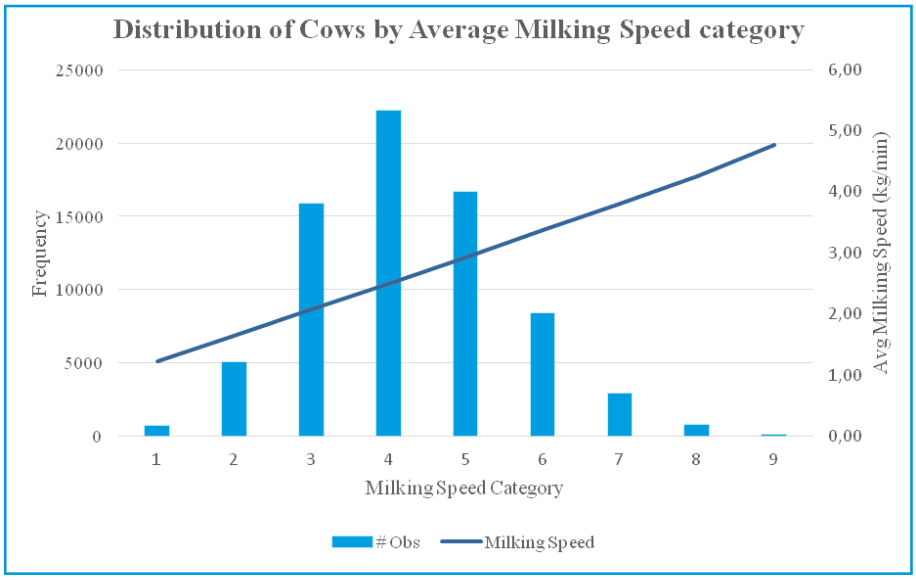

Figure 1. Cow distribution by milking speed category

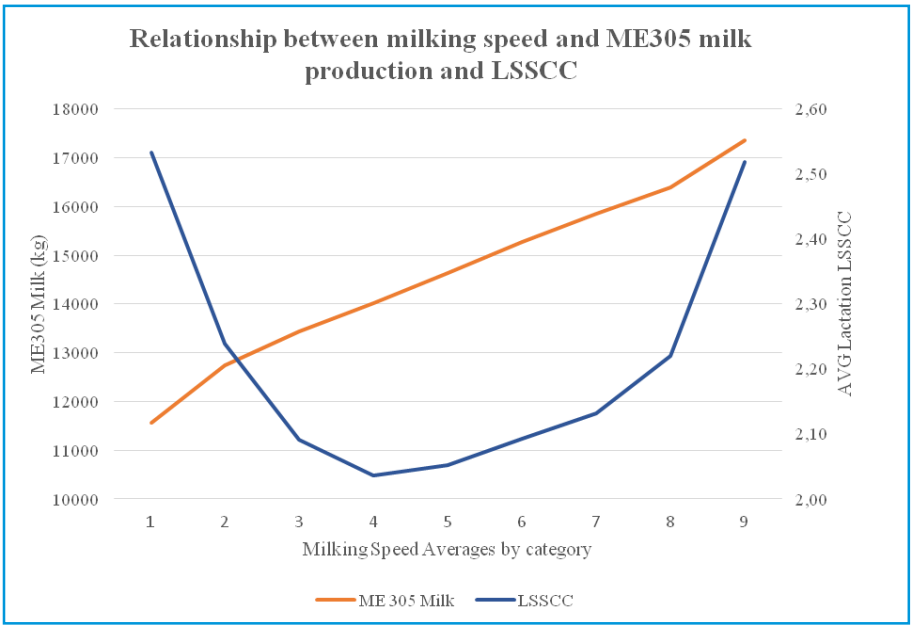

Figure 2. Relationship between milking speed and ME 305 Milk and Lactation Average LSSCC

Table 3. Sample milking speed grouping report.

Control #	Lact #	Number of milking times collected	Avg milk (kg/min)	Avg milk duration (min)	Avg milk (kg/min)	Days in milk	Milk (kg)	LSCC	Avg Milk/Min	Milking Duration (Min)
5	2	3	2.58	5.07	2.37	454	54.9	2.7	2.55	**7.3**
8	2	2	2.58	5.07	4.11	239	37.2	2.9	4.23	3
10	3	1	2.58	5.07	3.96	40	54.9	4.6	3.96	4.7
33	2	1	2.58	5.07	2.57	92	50.8	0	2.57	6.7
37	1	3	2.58	5.07	3.01	199	29.5	0.1	3.33	3
50	1	2	2.58	5.07	2.29	148	39.9	0.7	2.62	5.2
51	1	3	2.58	5.07	2.51	198	32.2	0	2.47	4.4
77	4	2	2.58	5.07	1.90	278	20.0	2.2	2.06	3.3
84	2	3	2.58	5.07	2.89	199	41.3	2.9	2.70	5.2
102	4	4	2.58	5.07	1.58	163	38.6	2.8	1.60	**8.2**
118	2	1	2.58	5.07	2.65	29	56.2	0	2.65	**7.2**
119	3	1	2.58	5.07	2.38	100	42.6	2	2.38	6.1
127	2	1	2.58	5.07	2.32	325	30.8	6.7	2.32	4.5
130	3	4	2.58	5.07	1.76	395	37.2	5.9	1.76	**7.2**
131	1	3	2.58	5.07	2.29	172	28.1	0	2.38	4
132	1	3	2.58	5.07	1.96	103	33.6	0	2.10	5.4

utilizing individual cow milking speed and milking duration data, and compares against the group average milking speed and milking duration. Cows with red highlights indicate milking speed values that are 0.45 kg/min less than the group average. Cows with yellow highlights indicate milking durations that exceed the group average by 2 minutes.

When reviewing the results in Table 3, cow control # 102, for example, had 4 individual milking speed records collected, and averaged 1.58 kg/min milking speed for her lactation. On her last test date she milked 1.6 kg/min and took 8.2 minutes to milk. Based on her milking speed and production level, she would be a good candidate to place in a separate group of slow milking cows.

Milking speed genetic evaluations

One of the project goals was to utilize the milking speed information and establish breeding values for cows and bulls. Various linear mixed models were tested, the final model used was:

$$Y_{ijklmno} = m + MM_i + LS_j + HYM_k + L_l + DIM_m + 1\%Cow_m + 1\%PE + e_{ijklmno}$$

Where $y_{ijklmno}$ is the milking speed observation for a particular cow, μ is the population mean, MM_i is the fixed effect of meter milk (kgs of milk produced at the current milking), LS_j is the fixed effect of linear somatic cell score, HYM_k is the fixed effect of herd-year of calving-month of calving, L_l is the fixed effect of lactation (1 to 4), DIM_m is the fixed effect of days in milk, $1|Cow_n$ is the random effect of cow, distributed as $N(0, I\sigma^2_{Cow})$, and $1|PE$ is the random permanent environmental (PE) effect, distributed as $N(0, I\sigma^2_{PE})$, which is the non-genetic effect assumed to be common to all observations on the same cow, and eijklmno is the random residual, distributed as $N(0, I\sigma^2_e)$. Variance components and heritability are shown in Table 2.

Genomic estimated breeding values (GEBVs) were standardized by dividing one-fifth of the additive genetic standard deviation ($\frac{\sqrt{0.3630}}{5} = 0.1205$) and deviating from a base of 100. Therefore, a one-unit change on the 100-scale indicates 0.1205 change in

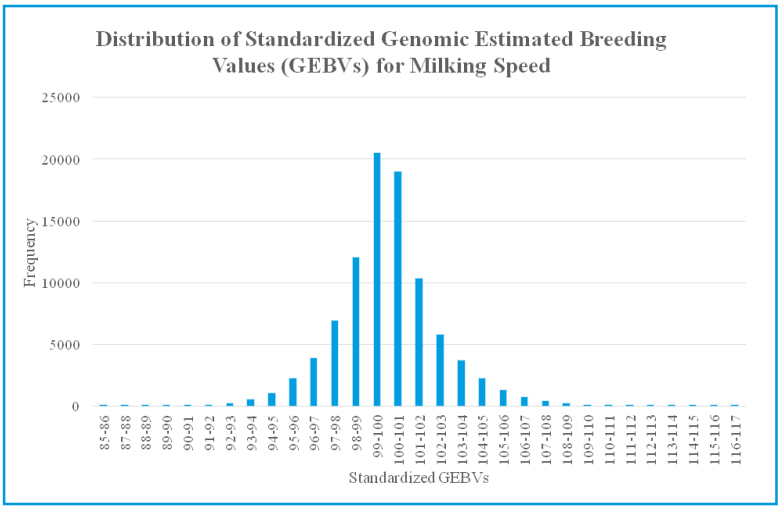

Figure 3. Distribution of GEBVs for parents and offspring.

milking speed from the population average. Figure 3 shows the spread of standardized GEBVs for both males and females. Reliability of estimation for breeding values was calculated for both males and females.

Conclusions

Milking speed data, combined with milk production and milk duration data, can provide a valuable tool to dairy producers for grouping cows or as a consideration for culling. Milking speed data collected through the use of EMMs provides consistent and high quality information and can be turned into an added-value service by DHI milk recording organizations. The use of continuous data recorded through EMMs also provides a valuable tool to estimate genomic breeding values on cows and bulls.

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Towards a robust protocol for enteric methane measurements using a hand held Laser Methane Detector® in Ruminants

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Abstract

Direct measuring of enteric methane in breath of ruminants is becoming popular. Since the first peer-reviewed publication (Chagunda et al., 2009) showed the potential application of the proprietary Laser Methane Detector® (LMD) in ruminants, it has been shown to have strong relationship with traditional techniques such as respiration calorimetric chambers. For example, Chagunda et al, (2013) reported sensitivity and specificity for cows of 95.4% and 96.5%, and for sheep, sensitivity was 93.8% and specificity was 78.7%. However, there is no joined-up protocol covering all aspects, including, data collection, data extraction, data handling, and estimating methane volume from the measured concentration.

Using data from two studies this paper presents results from tests and analysis to develop a method for data extraction, determine optimal recording duration, differentiating breath from eructation; and conversion of methane concentration to volume. The first study used a group of 71 dairy cows with repeated measurements over a 5 week period. Methane was measured by pointing the LMD at the nostril of the cow from a distance estimated to be 1m in the feed-face after midday milking. Measurements lasted 4 to 5 minutes. For each individual time-series measurement, time of recording and cow's tag number were recorded. In the second study measurements were taken from 18 Holstein Friesian heifers simultaneously by the LMD and the metabolic chamber.

In differentiating eructation from breath, one standard deviation for the individual measurement-window, was used as a threshold. This proved to be a biologically meaningful and statistically effective way of distinguishing methane coming from the rumen through eructation and that from the normal breath. An example is the mean of 395.8 (with a standard deviation of 182.7) ppm. To determine the optimum recording duration, five levels of 60s, 120s, 180s, 240s and 300s were created. Gross average of methane emissions was calculated for each recording window. Significant difference was tested using analysis of variance (ANOVA). In this test the only group that resulted in significantly low measurements ($p<0.001$) was the 60s. Given that eructation episodes in cow breath cycles are estimated to be one to three per minute, measurement windows of less than 3 minutes would risk missing out on some eructation episodes. When methane was measured when animals were standing

the relationship between LMD methane and Chamber methane was highest (r = 0.65) while daily averages had the weakest relationship (r = 0.48). This strong and positive correlation allowed us to build regression equations for estimating methane volume (g/day) from methane concentration (ppm) measured by the LMD.

Key words: enteric methane, measuring protocol, breath cycles.

Introduction

Agriculture faces considerable challenges to limit global warming. Livestock play an important role in greenhouse gases emissions, especially in methane. If livestock farming represents 14.5% of the total GHG of human origin (FAO 2010), cattle is the main emitter with 65% of the sector's total output (FAO 2010). Enteric methane produced during digestion is the largest source as 80 to 85% is exhaled. Methane emissions can be reduced by modifying feed intake, feed ration, and through animal genetics. However, collecting enough measurements on a sufficient number of animals to test different reduction strategies is challenging especially with standard techniques such as respiration calorimetric chambers and tracer gas method (SF6). These techniques, although effective and reliable, are however expensive and time consuming. New approaches and proxies will allow measurement to be taken at farm level, in large numbers and without disturbing the animals.

The LMD is a proprietary hand-held methane detector that measures instantly and specifically methane. It is made by Tokyo Gas Engineering Company. It is generally used in detecting methane leaks in such places like gas transportation networks, old mine pits, and landfill. Methane measurements from the LMD are based on infrared absorption spectroscopy, and measures methane concentration while accounting for the plume thickness in ppm-m. The use of Laser Methane Detector (LMD or LMm), suggested for the first time by Chagunda et al, (2009) seems to be a promising and practical tool. Since the first peer-reviewed publication (Chagunda et al., 2009) showed the potential application of the LMD in ruminants, it has been shown to have strong relationship with traditional techniques such as respiration calorimetric chambers. For example, Chagunda et al, (2013) reported sensitivity and specificity for cows of 95.4% and 96.5%, and for sheep, sensitivity was 93.8% and specificity was 78.7%. However, there is no joined-up protocol covering all aspects, including, data collection, data extraction, data handling, and estimating methane volume from the measured concentration. Using data from two studies this paper presents results from tests and analysis to develop a method for data extraction, differentiating breath from eructation; determine optimal recording duration, and conversion of methane concentration to volume.

Materials and methods

LMD data extraction and data agreement with metabolic calorimetric chamber

Metabolic calorimetric chambers are the gold standard for measuring enteric methane emissions in ruminants. For both the validation of the LMD and developing a robust data extraction protocol, there ought to be a strong agreement between data from the LMD and the metabolic chamber. In the current study, eighteen heifers were used at AFBI (Agri-Food and Biosciences Institute) in Hillsborough, Northern Ireland. Methane was measured simultaneously by the Chamber and the LMD from the same animals. The chamber took a measure every 4 minutes meaning that the dataset from the chamber had one measurement in ppm at every 4 min interval. The emissions per day were calculated in g/day. Data from the Chambers and those from the LMD were aligned in a single file using the unique timestamp. The closest measurements in time from the Chamber were associated to the ones from the LMD. In contrast to the chamber, the LMD takes measurement every 0.5s so there is no direct match as

intervals are different. There were 93,184 LMD individual measurement and 85,270 measurements from the chamber, representing a total of 128 recording windows. Heifer activity and behaviour at the time of LMD measurement were recorded. These activities were lying, lying and ruminating, standing and eating, standing, standing and restless, standing and ruminating, drinking and eating. The normality of the distribution was tested using mean (μ), standard deviation (σ), and quantiles. On the high end of the distribution, 99%, 95% and 90% quantile while 1% and 5% quantiles, on the low end, were used to test normality. On the low end, standard deviation was also used to separate methane measurements from normal breath from those culminating from eructation. In this regard, the standard deviation for each measurement window for each cow was calculated. Only individual measurements above one standard deviation were used to calculate the average for each measurement window (Ricci *et al.*, 2012). In order to determine the agreement and best fitted equation between the LMD enteric measurement and the Chamber daily emissions, Pearson correlation and regression analysis were used.

Measuring duration

In order to examine the optimal recording duration, data from a group of 71 dairy cows measured over a five-week period were used. In each week, methane measurements were carried out on 3 consecutive days. Fifteen cows had methane measured every week from the feed-fence after midday milking. The distance between the LMD and the cow was maintained at an estimated 1 m. Measurements were taken for up to 5 minutes per measurement window from each cow. The cow id as well as time of recording was recorded to allow joining the LMD data to the individual-cow specific data. From the original data set, 5 new dataset are created in order to calculate a gross average of methane emissions relative to 60s, 120s, 180s, 240s and 300s. The first one contains all the measurements taken between 0 and 60s,; the second one on the same pattern but for measurements up to 120s, and so on until 300s. The following mixed model was used to test the difference in the methane measurements for the different duration windows:

$$Y_{ijkl} = \mu + \alpha_i + \tau_j + \beta_{jk} + \varepsilon_{ijkl}$$

where,

Y_{ijkl} = average value of the α_i measurement time, the τ_j cow and the l^{th} sample.
μ = the grand mean.
α_i = the effect of the ith measurement time.
τ_j = the effect of the j^{th} cow. τ_j effects are independent and follow a Normal distribution with a variance σ^2CowID and represent the variation due to individuals.
β_{jk} = nested factor with "CowID" i. β_{jk} effects follow a Normal Distribution with a variance σ^2.
ε_{ijkl} = random residual N(0, σ^2).

Results and discussion

LMD data extraction and LMD data agreement with chamber

The descriptive statistics for the enteric methane concentration measured by the LMD and the metabolic chamber are presented in Table 1. Although the averages for the methane measured using the different methods were not massively different, the raw LMD data indicated very high variation. When the LMD measurements were processed as described in the methodology section, both the distribution and the variance normalized.

In general, the measurements of enteric methane concentration from the LMD were higher than those measured using the metabolic chamber. Enteric methane emissions measured by the chamber displayed a normal distribution (Figure 1).

Initial inspection of the raw data indicated a highly skewed distribution. Although the value at 99% quartile was 562.3 ppm, the maximum value was 49287 ppm. As a results two tests were carried out, one by keeping 99% of the dataset and another one by keeping only 95%. For the 99% dataset, measurements above 562 ppm were removed while for the 95% dataset, the threshold of 238 ppm was used. This procedure normalized the distribution without need to transform the data (Figure 2).

Another of the important factors to take into account during enteric methane measurement is the animal activity. Animals always exhibit different behavioral activities. The concentration of methane measured during these activities is also shown to differ

Table 1. Descriptive Statistics for enteric methane measured by the LMD and the metabolic chamber

	Raw LMD data (ppm)	Processed LMD data (ppm)	Chamber methane (ppm)	Chamber methane (g/day)
Minimum	0	24	12	85
Maximum	49287	237	177	170
Mean	125.3	114	84.7	127.8
Variance	294656.9	2020.0	519.3	240.2
SD	542.8	45	22.8	15.5

Number of observations 44208 for LMD and 44208 for the indirect open-circuit respiration calorimetric chamber.

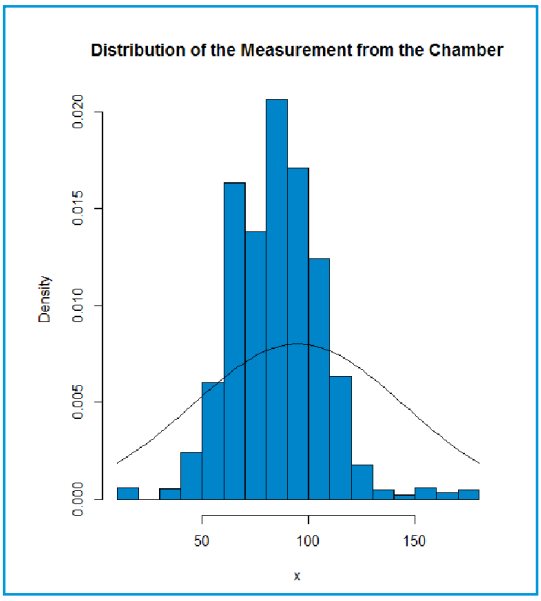

Figure 1. Gaussian distribution curve for enteric methane measured using an indirect open-circuit respiration calorimetric chamber

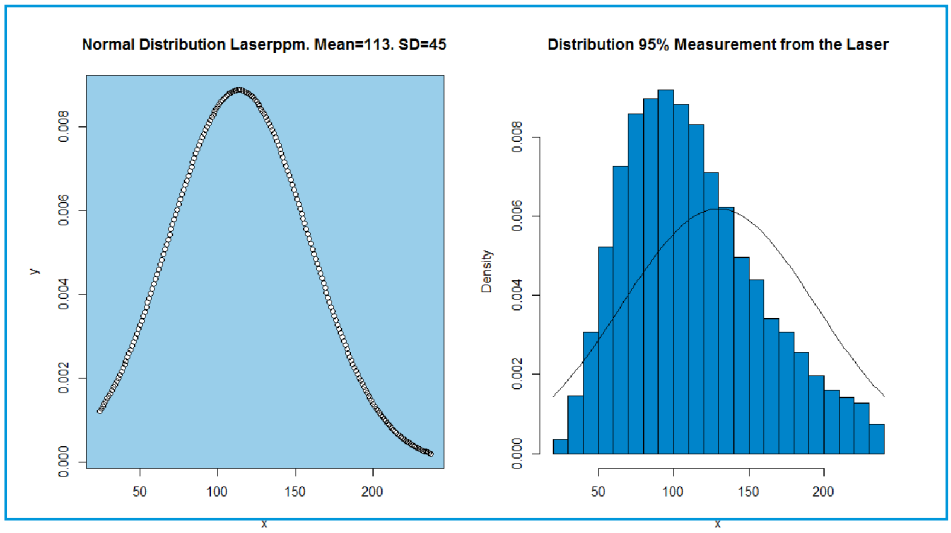

Figure 2. Gaussian distribution curve for enteric methane measured using a Laser Methane Detector.

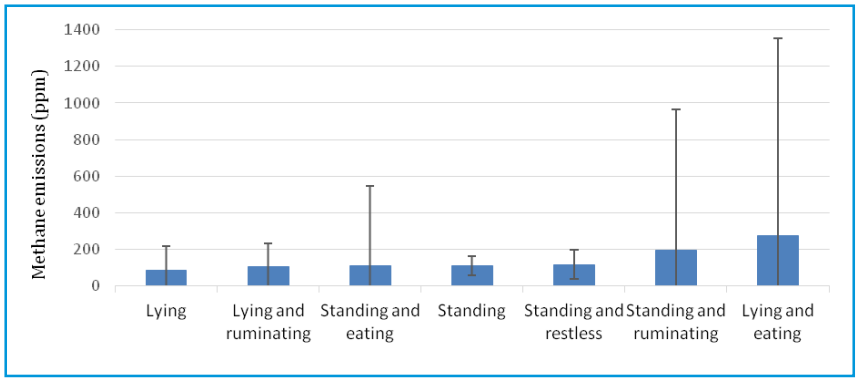

Figure 3. Enteric Methane Emissions (ppm) measured with the LMD depending on the activity.

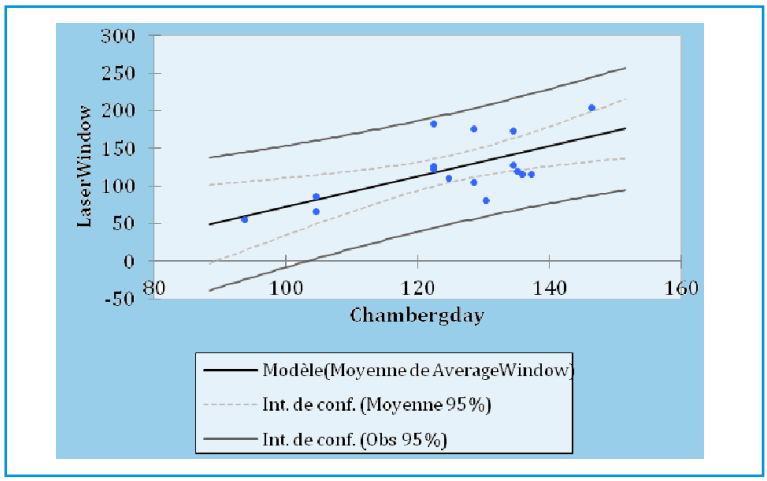

Figure 4. Regression between Laser methane Detector and indirect open-circuit respiration calorimetric chamber.

(Figure 3). When the heifers were standing and eating, standing and ruminating, and lying and eating, the standard error associated with these measurements were very high.

Agreement with the indirect open-circuit respiration calorimetric chamber

For all data, the highest Pearson correlation coefficient was between the Average Laser measurements per day (ppm) and chamber measurements expressed as g/day (r = 0.47). Although this value may not seem very high, the correlation is good. This is because it is a fact the Chamber measures a total methane emission whereas the LMD focuses on enteric methane as it targets the nostrils. The relative strong and positive correlation allowed us to build regression between the LMD and the Chamber data. Inverse regression was used as a calibration method: the value from the LMD is used to estimate the value in g/day that would have been obtained from the Chamber, the gold standard. The LMD measurements were therefore regressed on the Chamber measurements. For prediction, equations were inverted. Two models were built to predict methane emissions in g/day: the first one used an average calculated on one individual-measurement and the second one used the average of the four measurements realized on the day for each heifer. As heifers were involved in different activities while measurements were taken, activities were reported and compared. The activity that showed the best coefficient of determination was the Standing, R^2 = 0.42 and r = 0.65 (Figure 4).

The equation of the model is: LMD (ppm) = -127.21 + 2.00*Chamber (g/day). Therefore, the predictive g/day from a LMD (ppm) from a standing activity is:

$$\mathbf{Chambergday} = \frac{\mathbf{LaserWindow} - \mathbf{127.21}}{\mathbf{2}}\mathbf{.00}$$

Measuring duration

Results indicated that the measurement duration had a significant effect (P<0.01) on the concentration of methane measured by LMD. The results from the ANOVA demonstrate acceptance of the homoscedasticity hypothesis. Pair-wise analysis showed that the only group that resulted in significantly low measurements (P<0.001) was the 60s. This meant that all measurement duration equal to or more than 120s would give results that are not significantly different from each other. However, as eructation happens every minute in cows (Garnsworthy *et al.*, 2012) we suggest that LMD measurement window should be at least 3 minutes long.

Conclusions

The current study was one in a series aimed at generating enough evidence to contribute to developing a robust protocol for enteric methane measurements using a hand held Laser Methane Detector® in Ruminants. Methane measurements from the LMD have shown strong agree with those from the gold standard, the indirect open-circuit respiration calorimetric chamber. Results have also demonstrated the importance of testing and normalizing the distribution of the data before further analysis. Measurement windows longer than 3 minutes are recommended in order to get robust data which capture the required number of eructation.

Acknowledgements

We are grateful to Institut de l'Elevage, Service Productions Laitières (IDELE) for funding Thiphanie;s internship and staff and colleagues at Agri-Food & Biosciences Institute, Hillsborough and at SRUC Dairy Research and Innovation Centre for assistance in data collection. SRUC receives financial support from Scottish Government.

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Sharing data through an API platform - API AGRO

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Abstract

Sharing data is becoming a hot topic in agriculture and for livestock in particular. This paper outlines the main features of the organization which has been recently established in France to facilitate data sharing through Application Programming Interface (API) for agriculture and breeding industry. The different issues which have been addressed to operate the services are described in detail: the need analysis, the implementation strategy, the establishment of an API service provider, the description of the first set of services which are already available, the development plan for the future and the IT architecture. The conclusion underlines the interest of that technology to share data for an industry which needs a lot of update reference data and sophisticated calculation which may not be performed locally because of the complexity of the calculation or because of the size of the data bases and for privacy reason.

Keywords: API, livestock, breeding, application, cloud, web services.

Introduction

Remote Process Call (RPC) is an Information Technology (IT) which is existing for more than twenty years. The lack of standards and the lack of widely used and standardized network have limited the uptake of that technology for many years.

Now, the extensive use of connected applications through the internet protocols and Hyper Text Transfer Protocol (http) pave the way to opportunities to create new services which may enhance the value delivered by connected applications in a transparent way for their end users at a reasonable price.

This paper deals with the case of the implementation of Application Programming Interface (API) for breeding industry starting from the business requirements to the IT architecture including implementation strategy and service description.

Goal

For animal breeding, a majority of farmers and almost all the technicians are using connected applications to optimize their activities.

The uptake of update reference data and of sophisticated calculation requiring large data bases remains complicated.

The driving idea is to meet the needs of the breeding industry, by providing the missing resources by remote services through the cloud using API.

The target is the players of the French breeding industry: farmers, breeding companies, breed societies…

Implementation strategy

Operating API services implies to consider several stakeholders:

- The end users whose applications are using API services. These applications may operate either on line or off line as long as to be connected permanently with the cloud of the company which has developed the software. The purpose of this last provision which mainly addresses farm management applications is to avoid too many customers and the problems resulting in poor network performance. Two main types of end users are considered, the farmers who are using farm management applications, more than the half of the French dairy farmers, and the technicians who are providing farmers with advice for mating plan with artificial insemination sires.
- The technology providers which are providing the end users with applications integrating the API services in their software. These companies play a critical role to channel API services to the end users. In case of off line farm management applications, the company should also reroute the requests and the responses between the end user applications and the API service provider through its cloud. In France, it means approximatively ten companies.
- The API service provider which is operating API services based on data provided by data owners. The API service provider do not need to be the data owner, it should only have got the authorization to use data from the owner. The value of the services should not be linked to data ownership but based on the service availability, the data reliability, the neutrality of the calculations and the seriousness of the methodology.
- The data owners which are providing the API service provider with data either to be distributed or for calculation.

Figure 1 provides the value chain for API services.

The critical issue is sharing the value with the stakeholders through appropriate contracts with the additional problem when data ownership is not clearly defined.

The API services should be developed step by step, starting with a Minimum Viable Product (MVP) which consists in as set of services starting by those having the highest value for the end users. This first step is critical, since, in addition to MVP, it needs to address simultaneously organization and IT arrangements which will be used for the other steps.

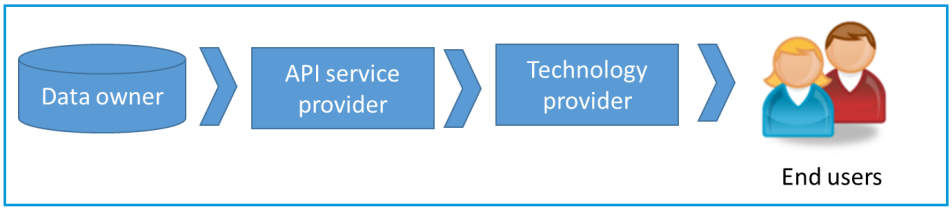

Figure 1. API services value chain.

Establishing the API service provider

Considering the potential of API for agriculture, a consortium that includes IDELE - Institut de l'Elevage, and the French key players of research and development and of technology providers established and invested in 2016 in a common subsidiary, API AGRO® (api-agro.fr) to promote API services for all agriculture: crops, livestock, poultry, vegetable…

Currently, about 40 API are already available dealing with different topics such as localizations, weather, soil, phytosanitary products, economics, livestock…

API services for breeding industry are available through that company whose mission is to provide its users with resources to operate API services under satisfactory economic conditions:

- A central repository to register the API with standardized tags to make them findable through a search engine.
- Monitoring the uptake of each API.
- Tools to allow the data owners to make by themselves their data available through API.
- Control of authorizations.
- License management.
- Data for automatic invoicing.
- Basic data visualization.
- API version management.
- …

Most of the above services are delivered through the cloud by an API platform which is operated by a company which has contracted with API AGRO®: Open data soft®.

Description of the services

Business requirement specifications

For the first step, the below needs have been considered:

- All user applications need at any time a unique update list of breed code.
- All user applications need at any time a unique update list of sires which are available through artificial insemination.
- To optimize mating plans, farmer and technician applications need at any time to test different options through the on line calculation of inbreeding coefficients for a limited set of parents. These coefficients should be calculated with a unique method, accurately described and widely used with all the data, the end user of the application is authorized to use.
- When network is missing or when network performance is too poor, the application of the technicians needs to calculate in advance, the inbreeding coefficient for the farms which will be visited.
- The application developers need streamlined services, easy to implement, with working principles which must be easily understood.

Service description

The first release includes four services:

1. "Breed code": that service is free. It can be used through a simple request by anybody according an open data license which provides that commercial use is possible but that no derivative is allowed in compliance with the "Creative common" framework.
2. "Sire list": the service is free. It can be used by anybody through a simple request according an open data license which provides that commercial use is possible but that no derivative is allowed in compliance with the "Creative common" framework.
3. "On line inbreeding coefficient": a paid service which requires a contract. It is available every hour, every day through requests which allow to submit a set of a maximum of 5 males and 150 females.
4. "Off line inbreeding coefficient": a paid service which requires a contract. It is available on working days through requests which allow to submit a set of a maximum of 80 males and 100 000 females with the guarantee to get the results in less than eight hours.

Table 1 below reported gives the distribution of the service and of their users.

Table 1. Services and users.

	Name of the service			
End user	Breed code	Sire list	On line inbreeding coefficient	Offline inbreeding coefficient
Farmers	X	X	X	
Technicians / mating advice	X	X	X	X

Development plan

For 2017, we have planned to sell services to at least three major breeding organizations representing several hundred of technicians who are providing farmers with mating advice.

By the end of 2018, it is expected to sell services to technology providers which are developing farm management software in order to address several thousands of farmers.

IT architecture

The API services should be designed in order to facilitate their uptake by people who are developing the applications. It implies at least:

- Fine grained services whose working principle may be easily understood.
- Few data to be exchanged.
- Using a widely spread language.
- Clear documentation.
- A test environment to test the integration of the API services in the software.

Because it is widely used, easy to implement and relevant for simple data structure, it was decided that the API services will operate as REST FUL web services.

Figure 2, provided below, gives the general architecture.

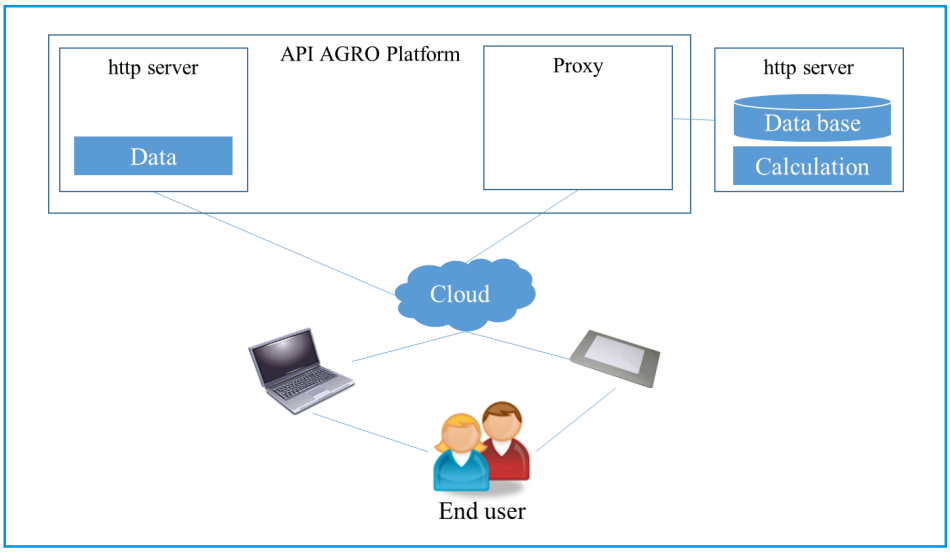

Figure 2. General architecture.

Two "http" servers are hosting the services: one for data, breed code and sire list, one for inbreeding coefficient calculation.

The data server is provided by the API AGRO platform which is only a proxy the calculation server which is located on an other platform.

End user PC or smartphones are connected to the servers through the cloud using internet protocols.

The communication between end user application and API services is performed by http protocol:

- Each service which has a specific URL (Uniform Resource Locator), for instance /api/consang/syncDemande for the service "On line inbreeding coefficient".
- The service is invoked by the client application through a specified "htpp" method. For the service 'Online inbreeding coefficient' the method 'POST' should be used in conjunction with the transmission of parameters. The request looks like "POST /api/consang/syncDemande PARAMETERS"
- PARAMETERS includes two lists of animal identification codes, on for the males and the other for the females.

" The format used for exchanged data is J son. PARAMETERS looks like {population1": ["string"] , "population 2:" ["string"]} where "population1" is the list of males and "population2" the list of females.

- The response is transmitted by a J son file which contains for each couple of male and female the inbreeding coefficient.
- Because of the size of the files, for the service "Offline inbreeding coefficient", FTP (File Transfer Protocol) is used in combination with http.

Upcoming developments

For breeding industry we have planned to develop an improved release including some new services which would be :

- High precision inbreeding calculation for technicians who are in charge to prepare mating for the next generation of sire.
- Inbreeding calculation for sheep and goats.
- Inbreeding calculation including foreign pedigrees.
- Risk assessment of genetic abnormalities and mortality.

Conclusion

API have a huge interest for agriculture where a lot of applications for farmers and for technicians need update reference data and sophisticated calculation from large data bases. Both, may be delivered through the cloud by remote API services.

However, operating professional API requires several pre requisites to make the users confident in the services: availability of the service, quality of the service, result neutrality and privacy.

Operating API at a reasonable cost requires also resources which should be easily provided by one of the numerous marketed API platform.

The impact of research and development should strengthened when the results and the methods will be available through API.

The new CombiFoss 7 DC. Differential somatic cell count and other advancements in milk testing

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Abstract

FOSS has launched the 7th generation of CombiFoss milk analysers in October 2016. The new CombiFoss™ 7 DC seamlessly integrates MilkoScan™ 7 RM and Fossomatic™ 7 DC and allows to test raw milk for up to 19 parameters, including the brand new Differential Somatic Cell Count (DSCC) parameter, simultaneously in just 6 seconds. The objective of this work is to provide an overview on the key advances of the instrument and an update on the latest developments in terms of working with new parameters for milk testing, particularly DSCC, from around the world.

The MilkoScan™ 7 RM can be used to test for up to 17 different milk component parameters. The latest generation technology includes improvements of the optics and flow systems that result in better statistics, in particular for minor components such as urea and BHB (beta-hydroxybutyrate). Apart from that standardisation of spectra is still done using FTIR equalizer (FTIR - Fourier transform infrared spectroscopy), which is particularly important nowadays where full spectra information is utilised for various purposes.

The Fossomatic™ 7 DC allows to measure 2 parameters, SCC and DSCC, simultaneously at a speed of up to 600 samples per hour. The key elements of the new milk analyser are a new chemistry, a new incubation unit, and a new measuring module. Besides, the design of the instrument allows easy accessibility of the different modules inside the instrument.

DSCC is a new biomarker for mastitis management. Mastitis remains to be a significant challenge on dairy farms and still causes tremendous economic losses to the dairy industry. DSCC provides more information on the actual inflammatory status in the cow's udder by revealing the percentage of individual immune cells (i.e., DSCC represents the combined proportion of neutrophils and lymphocytes). Several research projects on the practical application of DSCC in the frame of dairy herd improvement (DHI) testing are currently running around the world.

A first research study, where the DSCC parameter was investigated before, during, and after artificially induced mastitis under controlled conditions was recently completed. The results showed that DSCC values changed significantly during the course of the experiment (i.e. <60%, >90%, and <70% before, during, and after infection, respectively). Hence, first indications on where to set a threshold for DSCC to distinguish between normal and active (e.g., mastitis) inflammatory response are available.

In conclusion, the new CombiFoss™ 7 DC allows highly accurate, fast, reliable, repeatable, and robust determination of up to 19 parameters from raw milk samples at low cost. DSCC is a new parameter providing more detailed information on the actual inflammatory response of the mammary gland and thus opens up the possibility to develop new tools for improved mastitis management that can be offered through DHI testing programmes.

Keywords: mastitis, ketosis, SCC, DSCC, dairy herd improvement testing, milk quality.

Introduction

The analysis of milk samples for payment and dairy herd improvement (DHI) purposes has evolved evidently since the 1970s where just milk fat, protein, lactose, and somatic cell count (SCC) were tested. Numerous new parameters were developed since serving optimisation of both milk quality and the management of dairy herds. Various new milk testing services based on new or newer parameters are currently in development are in the phase of implementation around the world. The overall aim of offering new parameters and milk testing services is to provide dairy farmers with more information for improved decision making.

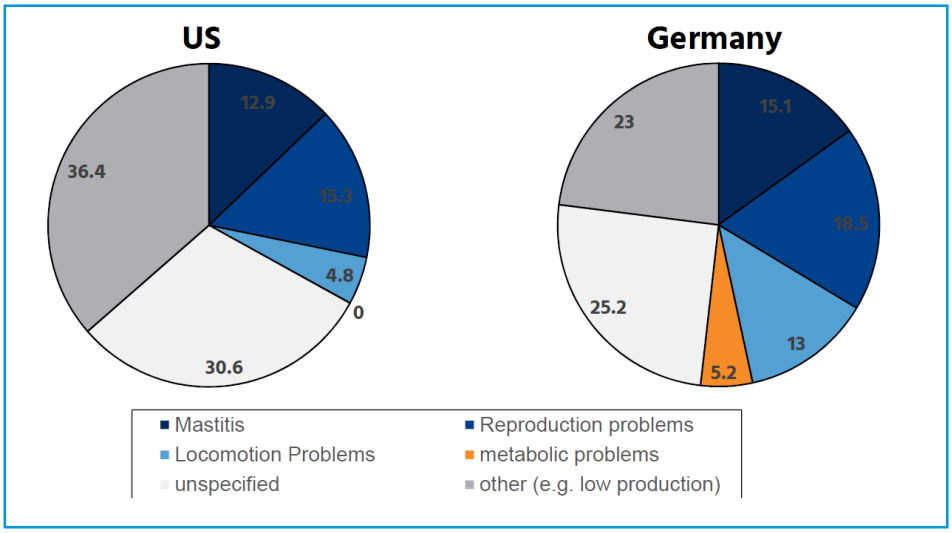

Figure 1. Overview on reasons for cows exiting dairy herds in the US (left) and Germany (right). Sources: CDCB, 2015; VIT 2016.

Mastitis, the inflammation of a cow's udder, is still causing tremendous losses of 32 billion Euros to the dairy industry worldwide (Seegers *et al.*, 2003). It is still one of the most common reason for cows to exit dairy herds in countries such as the US (9 million dairy cows) and Germany (4 million dairy cows) as illustrated in Figure 1. SCC is a well-accepted and broadly used indicator for mastitis and became a standard tool for mastitis management. However, SCC represents the total number of cells per ml of milk and does not harbour information about proportions of individual immune cells occurring in milk (i.e., macrophages, polymorphonuclear neutrophils (PMN), lymphocytes). Hence, a new parameter, Differential Somatic Cell Count (DSCC), indicating the combined proportion of PMN and lymphocytes in percent was recently developed (Damm *et al.*, 2017; Schwarz, 2017a). The percentage of macrophages is 100 - DSCC. It is well documented that both the total SCC and composition of the

immune cells change evidently during mastitis. Milk from healthy mammary glands is low in SCC that consist mainly of macrophages and lymphocytes (Lee *et al.*, 1980; Schwarz *et al.*, 2011a, b; Pilla *et al.*, 2012). However, SCC increases significantly and PMN are the predominant milk cell population in the presence of infection (Paape *et al.*, 2002). While SCC indicates the change in the total number of cells, DSCC reveals the change in the composition of the immune cells.

Ketosis, a metabolic disorder in high yielding dairy cows, where energy demands exceed energy intake is another issue causing significant economic losses on dairy farms nowadays. The incidence of ketosis has been estimated to be 25-60% in dairy herds with costs of 260 Euros per case (Mc Art *et al.*, 2013, 2015; Mahrt *et al.*, 2015). The possibility of using DHI milk samples and FTIR technology for herd level screening with good values for sensitivity and specificity has been demonstrated (de Roos et al., 2007; Denis-Robichaud *et al.*, 2014).

FOSS has recently launch the 7th generation of the CombiFoss milk analyser, which allows testing for up to 19 parameters including the brand new DSCC. The objective of this work is to provide an overview on the key advances of the instrument and an update on the latest developments in terms of working with new parameters for milk testing, particularly DSCC, from around the world.

The new CombiFoss 7 DC

The new CombiFoss™ 7 DC seamlessly integrates MilkoScan™ 7 RM and Fossomatic™ 7 DC. It offers the possibility to test for up to 19 parameters, including the brand new DSCC parameter, simultaneously in just 6 seconds (at a speed of 600 samples per hour).

The MilkoScan™ 7 RM employs Fourier Transform InfraRed (FTIR) technology for measuring a full range of milk compositional parameters. Two types of material, diamond and calcium fluoride, of the cuvette are offered. Furthermore, the latest generation technology includes improvements of the optics and flow systems that result in better statistics, in particular for minor components such as urea and BHB (beta-hydroxybutyrate), due to an improved signal to noise ratio. Apart from that standardisation of spectra is still done using FTIR equalizer (FTIR - Fourier transform infrared spectroscopy), which is particularly important nowadays where full spectra information is utilised for various purposes.

The Fossomatic™ 7 DC allows to measure 2 parameters, SCC and DSCC, simultaneously at a speed of up to 600 samples per hour. The key elements of the new milk analyser are a new chemistry, a new incubation unit, and a new measuring unit and were described in detail elsewhere (Schwarz, 2017a). Besides, the new modular design of the instrument allows easy accessibility of the different modules inside the instrument.

The new Differential Somatic Cell Count (DSCC) Parameter

DSCC is FOSS's new parameter for mastitis management. The concept and method behind the parameter have been described previously (Damm *et al.*, 2017; Schwarz, 2017a). DSCC represents the combined proportion of PMN and lymphocytes in percent and thus provides more detailed information on the actual inflammatory response of the mammary gland. This, in turn, opens up the possibility of developing new tools for improved mastitis management.

The development of the two parameters SCC and DSCC before, during, and after artificially induced mastitis under controlled conditions was recently studied in detail (Wall *et al.*, 2017). Briefly, both SCC and DSCC increased evidently after mastitis was induced. Interestingly, DSCC increased significantly even when the observed SCC increase was moderate only. SCC and DSCC returned to normal levels within a couple of days after mastitis had been artificially induced.

In general, the combination of SCC and DSCC allow a more detailed description of the udder health status of dairy cows compared to SCC alone. The International Dairy Federation (2013) recommended a SCC threshold of 200,000 cells/ml for differentiation between normal/healhty and (unspecific) mastitis. The novelty coming with the availability of DSCC information is the possibility of distinguishing between active or inactive inflammatory response as well (Figure 2). In this context, a threshold for DSCC might be at a level of 75%, however, it requires further research to determine that threshold precisely. The following 4 groups could be described working with SCC and DSCC:

- Low SCC and low DSCC: *normal/healthy*.
- Low SCC and high DSCC: *onset/early stage of mastitis*, elevated proportions of PMN have been described in udder quarters with SCC <100,000 cells/ml and were interpreted as early inflammatory reactions that must be triggered by bacteria (Schwarz *et al.*, 2011 a, b; Pilla *et al.*, 2012).
- High SCC and high DSCC: A condition where the cow's immune system actively *combats mastitis pathogens*.
- High SCC but low DSCC: A condition where fairly high proportions of macrophages instead of PMNs occur. Scientific literature suggests that this happens in *chronically-infected cows* (Leitner *et al.*, 2000).

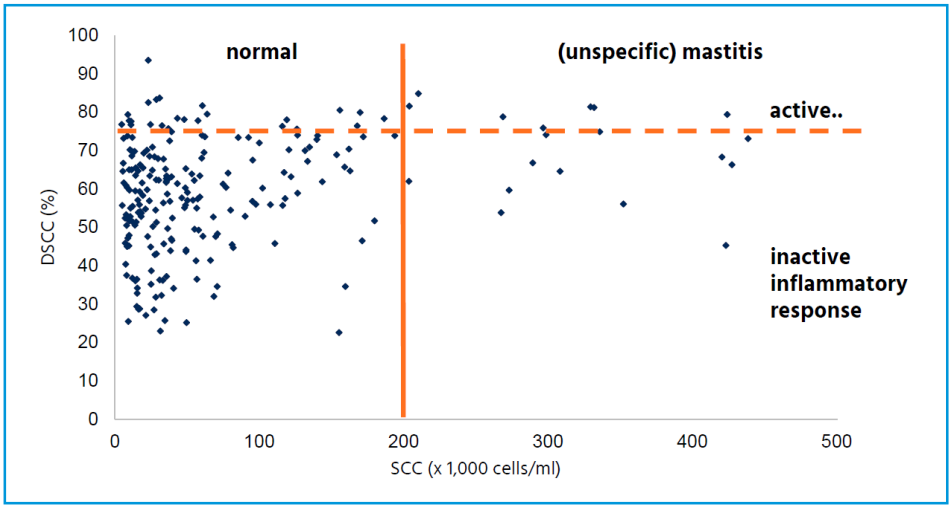

Figure 2. Example for SCC and DSCC results from a monthly DHI testing in a Danish dairy herd with 200 cows. Besides differentiation of normal and (unspecific) mastitis based on SCC, differentiation of active and inactive inflammatory response based on DSCC is possible. Each symbol represents the test result for one cow, overlapping is possible.

The 4 groups described and their interpretation is currently under investigation in various research projects around the world. Besides, specific applications for DSCC such as selective dry cow therapy, enhanced analysis of udder health in fresh lactating cows, and selection of milk samples for bacteriological testing (i.e., PCR) are currently under validation/in development.

Ketosis screening

Numerous applications for FOSS's ketosis screening calibrations were developed and are widely utilised by dairy farmers, e.g. Ketodetect, CLASEL, France; Ketolab, Valacta, Canada; Ketomonitor, AgSource, US; Ketoscreen, CanWest DHI, Canada; ketosis screening by CRV and Qlip, the Netherlands, today. The service has been described as simple, practical, rapid, and inexpensive as well as highly valuable to milk recording clients as it elevates awareness of an otherwise undetected problem (Schwarz *et al.*, 2015). The service has actually helped to reduce the incidence of ketosis by 10% in Canada and France, as presented previously (Schwarz *et al.*, 2015). It was further seen that the keys to success in establishing ketosis screening as a service were the use of a quality assurance programme as well as proper and clear communication of test results to dairy farmers (Schwarz, 2017b).

Other applications

Two of the more recent other applications utilising FTIR spectra are adulteration screening and fatty acid profiling. Briefly, adulteration screening allows to screen for either intentional or unintentional adulteration of milk (e.g., in connection with payment testing) using targeted or untargeted models.

Fatty acids can be categorised according to chain length and/or degree of saturation as well as the major fatty acids can be determined using FTIR technology. Fatty acid information are used for different purposes such as, e.g., optimisation of feeding of dairy cows or production of value-added dairy products (i.e. products containing enhanced concentrations of unsaturated fatty acids).

Conclusions

The dairy industry demands new parameters that further help in terms of optimising milk quality and dairy herd management. The recently launched CombiFoss 7 DC allows laboratories to measure up to 19 parameters in milk samples at low cost and at high accuracy, speed, reliability, repeatability, and robustness. Ketosis screening, which is well-accepted and valuable service in many countries, is one example for new, value-added services that can be offered to dairy farmers today. New services/ applications in terms of mastitis management based on FOSS's new DSCC parameter, which provides more detailed information on the actual inflammatory status of a cow's udder, are currently under validation in several countries.

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Evaluation of a new qPCR test to specify reasons behind total bacterial count in bulk tank milk

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Abstract

Milk quality in Bulk Tank Milk (BTM) is measured by flow cytometry technology as Total Bacterial Count (TBC) and Somatic Cell Count (SCC). To investigate SCC problems, culture or PCR can be used to identify mastitis causing bacteria e.g. Mastit 4, a commercially available qPCR test. TBC in BTM can be investigated further using culture-based methods such as standard plate count, laboratory pasteurization count, coliform count, and spore counts. To our knowledge, no qPCR addressing the bacteria involved in TBC has been commercially introduced.

The aim of this study is to evaluate a recently introduced three-hour qPCR test, TBC 4. The TBC 4 qPCR detects four target groups, *Pseudomonas, Streptococci, Enterobacteriacea/Enterococcus*, and *Bacillus/Clostridia*. These target groups relates to problems on the farm such as cooling, mastitis, environment, and silage. We will continue with new research to compare the TBC 4 qPCR test with traditional culture. For this study BTM samples from different TBC intervals were selected based on BactoCount results found at routine payment investigation at Eurofins laboratory (Vejen, Denmark). These samples were analyzed using TBC4 qPCR assay within 24 hours.

In total 346 BTM samples were divided into 6 different intervals of colony forming units (CFU). For all four targets in each of the different intervals of CFU, the average Ct-value, percent positive samples with Ct<30 and Ct<25 were calculated.

For *Pseudomonas, Streptococci*, and *Enterobacteriacea/Enterococcus* the number of positive samples with lower Ct-values (high bacteria content) correlated with the CFU/mL. We found *Enterobacteriacea/Enterococcus*, *Pseudomonas*, and *Streptococci* in high number of bacteria (Ct <25 figure d) in 25%, 19% and 56% of samples with CFU/mL between 50,001-100,000 and 53%, 44%, and 39% in samples with CFU/mL>100,000. The TBC 4 qPCR test showed to be a strong and fast tool for farmers, advisors and service technicians to address problems with high TBC and ensuring the delivery of good quality milk to the dairy.

Keywords: tbc, btm, quality, qpcr.

Introduction

Milk quality in Bulk Tank Milk (BTM) is measured by flow cytometry technology as Total Bacterial Count (TBC) and Somatic Cell Count (SCC). There has been a long tradition for using cultivation of BTM samples to identify different bacteria causing high SCC in the milk. Also qPCR tests e.g. Mastit 4 a commercially available qPCR test (DNA Diagnostic, Denmark) can be used to detect mastitis bacteria in BTM (Rattenborg *et al.* 2015).

Tests for milk quality and bacteria in BTM includes standard plate count (SPC), coliform count (CC), and laboratory pasteurization count (LPC) (Murphy 1997).

Milking machine wash failures is strongly associated with in-line CC, which suggests that proper and consistent washes play a fundamental role in minimizing BTM contamination with coliforms (Pantoja *et al.*, 2011). The study of Lucali *et al.* (2015) underlined the correlation between forage quality, dairy farm management practices and the presence of milk and cheese anaerobic spore-forming bacteria.

It is well known that *Streptococci* from mastitis cows can cause high TBC. Zadoks *et al*. (2004) found that *Streptococci, Staphylococci*, and Gram-negative bacteria accounted for 69%, 3%, and 3% of TBC variability, in 48 BTM samples from New Your State. Keefe *et al*. (1997) found that herds infected with Strep. agalactiae were 5.48 times more likely to be penalized for a high SPC.

Detection of bacterial DNA can be used for analyses of bacterial content in BTM. Katholm *et al.* (2012) tested Danish BTM samples with qPCR and found the highest correlation to TBC for, *Enterococcus*, *Strep. uberis* and *Strep. agalactiae* of the bacteria investigated.

To our knowledge, thus far no qPCR addressing the bacteria involved in TBC has been commercially introduced. The aim of this study is to evaluate a recently introduced three-hour qPCR test, TBC 4 (DNA Diagnostic, Risskov, Denmark). The TBC 4 qPCR gives a Ct-value for four targets, *Pseudomonas, Streptococci, Enterobacteriacea/ Enterococcus*, and *Bacillus/Clostridia*. These four targets correlates to problems on the farm related to cooling, mastitis, environment, or silage.

Material and methods

In the period between 7th March and 5th April 2017 BTM samples obtained from Eurofins laboratory (Vejen, Denmark) were measured for TBC by routine flow cytrometry with Bactocount. For this study we selected 346 milk samples from different TBC intervals for qPCR test with TBC 4. The samples were selected among all Danish dairy herds.

After the result from the flow cytometry TBC test was obtained, the samples were immediately transported on ice to the laboratory of DNA Diagnostic A/S, Risskov, Denmark and tested by the TBC 4 qPCR test within 24 hours.

Results and discussion

The results from the TBC 4 test of the 346 BTM samples in different groups of CFU/mL is shown in Table 1.

In total 158 (46%) samples were positive for *Pseudomonas*, 157 (45%) for *Streptococci*, 128 (37%) for *Enterobacteriacea/Enterococcus*, and 122 (35%) for *Bacillus/Clostridia*.

In each of the different intervals of TBC, the percent of positive samples, average Ct-value of positive samples, percent samples with Ct. < 30 and percent samples with Ct. < 25 were calculated for all four targets of the test (Figure a,b,c, and d).

Table 1. Number of bulk tank milk samples tested in each group of CFU/mL.

CFU / mL	N
≤5,000	53
5,001 – 15,000	67
15,001 – 30,000	73
30,001 – 50,000	65
50,001 – 100,000	52
>100,000	36
Total	346

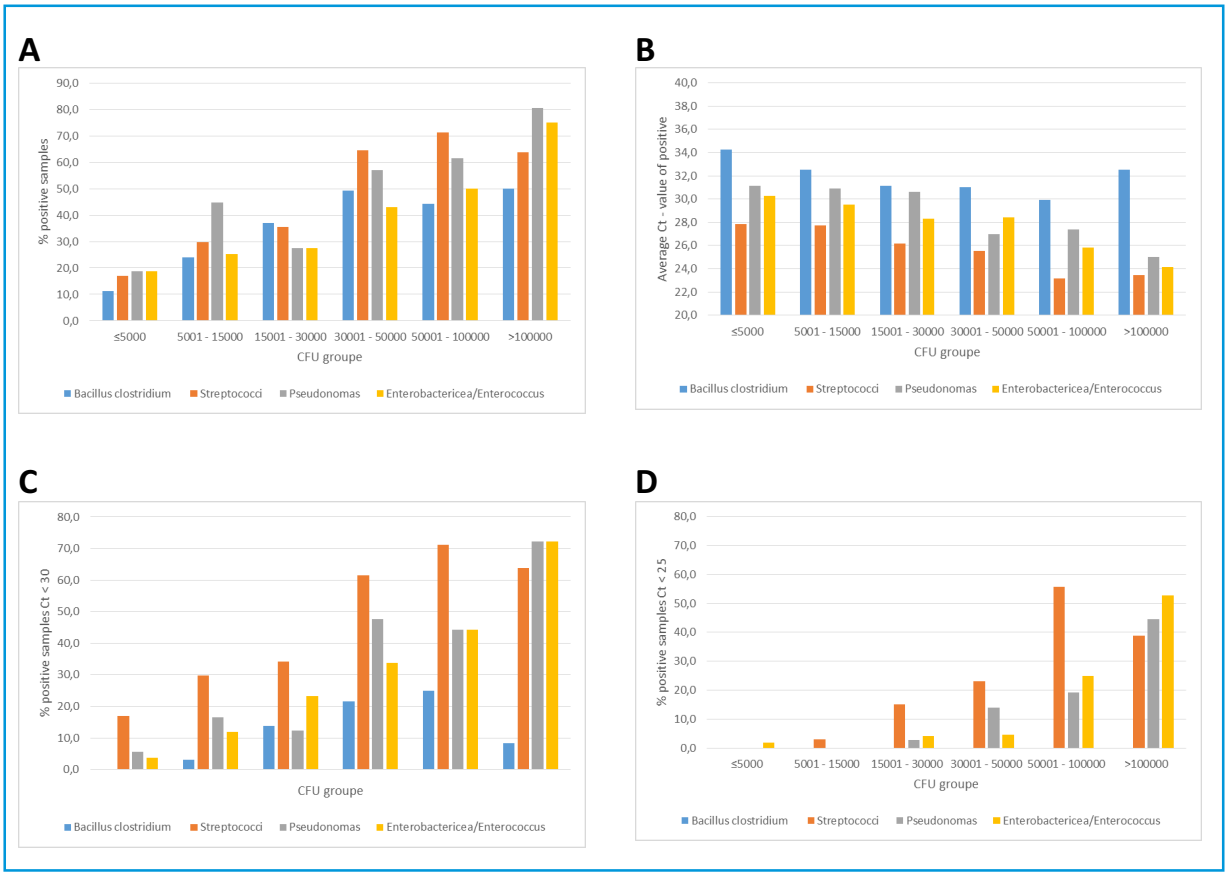

Figure a,b,c, and d: a) percent of positive samples, b) average Ct-value for positive samples, c) percent Ct-values under 30 and d) Percent Ct-values under 25 for the different groups of CFU for each of the four different targets in the qPCR test the TBC 4.

The *Pseudomonas, Streptococci and the Enterobacteriacea/Enterococcus* target showed increasing percent positive samples with higher CFU and also reduced Ct-value at higher CFU, indicating more of these bacteria is present at higher CFU. For *Bacillus/ Clostridia* the increase in positive samples stopped at 30,000 CFU/mL and the average Ct-value were above 30 in all groups of CFU. (Figure a and b). The percent positive samples with Ct-value below 30 and 25 is shown in figure c and d. As it can be seen, we did not find many *Bacillus/Clostridia* positive samples with really low Ct-values. For the *Streptococci* they have the highest percent of samples with low Ct-values in the samples up to 100,000 CFU/mL, whereas both the *Pseudomonas* and the *Enterobacteriacea/Enterococcus* target have the highest percent of samples with low Ct-values in the samples above 100,000 CFU/mL.

The new qPCR test TBC 4 enables the user to classify high TBC in BTM to four different groups of problems related to cooling, mastitis, environment, or silage. Not all problems with high TBC are solved by optimizing cooling and the washing procedures, as we found 46% of samples positive for *Pseudomonas* and 37% for *Enterobacteriacea/Enterococcus*.

Of the four targets investigated by the TBC 4 qPCR test the *Pseudomonas* the *Streptococci* and the *Enterobacteriacea/Enterococcus* seems to have the highest influence on the CFU in BTM collected during March and April 2017 in Denmark. This is seen in the Figure 1 b where the low Ct-values for these targets in samples with CFU/mL >30,000 indicates higher number of bacteria. We found *Enterobacteriacea/ Enterococcus, Pseudomonas*, and *Streptococci* in high number of bacteria (Ct <25 Figure d) in 25%, 19% and 56% of samples with CFU/mL between 50,001 - 10,0000 and 53%, 44%, and 39% in samples with CFU/mL > 100,000. Holm *et al*. (2004) found, in Danish BTM samples with > 30,000 CFU/mL, microorganisms primarily associated with poor hygiene dominated the microflora in 64% of the samples; bacteria also related to poor hygiene, but in addition associated with growth at low temperatures (psychrotrophic bacteria) dominated the microflora in 28% of the samples; and bacteria mainly associated with mastitis dominated the microflora in 8% of the samples. Their findings for microorganisms, primarily associated with poor hygiene and psychrotropic bacteria, corresponds with our findings for *Enterobacteriacea/Enterococcus*, and *Pseudomonas*, whereas our data indicates much more problems related to mastitis bacteria. In contrary to the data from Holm *et al*. (2004) our mastitis primer only detects *Streptococci*, but the *Streptococci* primer can also detect *Streptococci* not so often related to mastitis e.g. *Strep. bovis*.

Our findings, that *Streptococci* is an important factor in high TBC, is in accordance Gillespie *et al*. (2012) that found strong correlation between SPC and *Streptococcus* spp. counts. Katholm *et al*., 2012 found the best correlation between TBC in bulk tank milk and Ct-values from real time PCR assays specific for *Enterococcus, Strep. uberis* and *Strep. agalactiae*, less correlation to Ct-values for *Strep. dysgalactiae*, *E.coli* and *Klebsiella*, and no correlation to *Staph. aureus*. Our findings, that the *Enterobacteriacea/ Enterococcus* is an important finding in milk samples with high CFU is in accordance with Pyz-Lukasik *et al*. (2015), they tested the microbiological quality of milk sold directly from producers to consumers in Poland. They found *Enterobacteriaceae* ranging from 6.4×10^1 to 1.7×10^6 CFU/mL.

Conclusion

The new TBC 4 qPCR test proved to be useful in indicating the major causes of high TBC in Danish BTM samples. We expect the test to be a strong and fast tool for farmers, advisors and service technicians to address problems with high TBC and ensuring the delivery of good quality milk to the dairy.

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Genetic evaluation for claw health traits as part of the integrated system for health monitoring in German Holstein dairy cattle

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Abstract

The important role of claw health and its management has motivated installation of monitoring and improvement programs for dairy cattle worldwide. Significant genetic variation implies that breeding measures can valuably contribute to keeping prevalences and incidences of lameness and claw disorders low. However, new concepts are required for ensuring sufficient amount and quality of phenotypic data as basis of reliable genetic and genomic evaluations. The aim of this study was to use data and results from the genetic evaluation prototype for claw health traits from the German R&D project GKUHplus for illustrating the potential of integrated use of trimming and treatment data.

Health data collected in dairy farms from 2009 to 2016 were available for this study. Considering only health records for German Holsteins, approximately 269,000 lactations of 134,917 cows were informative for claw health traits and provided the basis of the genetic evaluation. Standardized recording that included the affected claw or limb was safeguarded across documentation systems used on the farms and by the claw trimmers. Direct electronic transfer of information from hoof trimming was enabled for approximately 30% of the lactation records. Treatment data and manually entered claw health data from trimming completed the data pool for the genetic analyses. Dates when animals entered and left the herd were available for all participating farms and allowed, in combination with the integrated claw health data, definition of comparison groups. For maximum differentiation between individuals, the number of distinct claw health events per lactation was analyzed using linear animal repeatability models. Genetic parameters and breeding values (EBV) were estimated univariately for six individual claw health traits: interdigital hyperplasia, IH; laminitis, LA; white line disease, WL; claw ulcers, UL; digital phlegmona, PH; digital dermatitis, DD. Weight of traits for the derived Claw health index were 30% for DD, 10% for IH, and 15% each for LA, WL, UL and PH. With heritability estimates ranging between 0.06 and 0.11, results were consistent with literature and routine applications most of which referred to trimming records as exclusive data basis. Full integration of treatment and trimming data was therefore seen as feasible approach to increase coverage and avoid bias of available information on claw health from commercial dairy herds. In total, 5,955 Holstein AI bulls were represented with on average 19 daughters in the genetic evaluation for claw health

traits, but the proportion of bulls with up to10 daughters was high (73%) and only 412 bulls had 50 or more daughters with claw health information. Analyses of distributions of individual EBV and Claw health index showed significant phenotypic differentiation between progeny groups of sires, implying substantial opportunities to reduce frequencies of claw disorders in dairy cattle through routine genetic evaluation which integrates treatment and trimming data and that way makes optimal use of available claw health information.

Keywords: standardized claw data recording, heritability, estimated breeding values, genetic evaluation for claw health traits

Introduction

Undisturbed locomotion is a major criterion of animal welfare, and for a dairy cow it is also prerequisite to function as part of her herd. Impaired locomotory health and in particular claw conditions which are clearly dominating among the locomotory disorders have accordingly substantial impact on the efficiency and sustainability of dairy farming (Cha *et al.,* 2010, Charfeddine & Pérez-Cabal, 2017). Furthermore, alterations in the claws are often very painful and therefore causing lameness, high frequencies of which in modern livestock keeping are seen as significant animal welfare issue.

Great differences between farms regarding the prevalences of lame cows and underlying causes of lameness indicate the potential of measures to improve the health of feet and legs in dairy cattle (e.g. Cramer *et al.,* 2008, Foditsch *et al.,* 2016). Claw health is accordingly an important, though complex component of health monitoring projects and programs. Besides strong impact of management, studies have shown the relevant genetic background of claw conditions in dairy cows (e.g., König & Swalve 2006, Malchiodi *et al.,* 2015), implying that breeding can valuably contribute to reducing the proportions of affected animals in the population. However, different potential data sources and related technical and logistical challenges, lacking standardization and harmonization as well as concerns regarding overall data quality have hampered the increase of the number of routine genetic and genomic applications for claw health in dairy cattle worldwide (Heringstad *et al.,* 2017).

Through records from routine hoof trimming, highly valuable information on the claw health status of all cows trimmed becomes available. However, information on the more severe cases of foot and leg disorders may originate from veterinary medical treatment data, and observations of farmers may supplement to both of the aforementioned data sources. Accordingly, data integration concepts should be most appropriate for ensuring sufficient amount and quality of phenotypic data as basis of reliable genetic and genomic evaluations. The comprehensive and integrated system for health monitoring in dairy cattle in Germany is including veterinary diagnoses, observations of farmers, screening records (e.g. for reproduction disorders) and documentation from routine hoof trimming. This is enabled by ensured standardizing coding of health events across data sources and documentation systems as supported by the internationally agreed recording standard (Stock *et al.,* 2012). The aim of this study was to use data and results from the genetic evaluation prototype for claw health traits from the German R&D project GKUHplus for illustrating the potential of integrated use of trimming and treatment data.

Material and methods

Major tasks of the German Innovation Partnership GKUHplus, supported by funds of the German Government's Special Purpose Fund held at Landwirtschaftliche Rentenbank, were extending the collection and use of health data and strengthening routine applications for direct health traits in dairy cattle. Strong regional partners and close interdisciplinary collaboration have contributed to the success of the project, and since 2016 health records for German Holstein dairy cattle from all federal states and Austria are considered in the prototype genetic evaluation for direct health traits.

For this study, health data collected in dairy farms from 2009 to 2016 were available. Claw health traits were defined in line with the internationally harmonized standard for claw data recording (ICAR 2015) and based on the hierarchical codes of the central key (ICAR 2016). Standardized recording that included the affected claw or limb was safeguarded across documentation systems used on the farms and by the claw trimmers. Direct electronic transfer of information from hoof trimming was enabled for approximately 30% of the lactation records. Treatment data and manually entered claw health data from trimming completed the pool of phenotypic information for the genetic analyses. Dates when animals entered and left the herd were available for all participating farms and allowed, in combination with the integrated claw health data, definition of comparison groups.

Considering only health records for German Holsteins, 269,439 lactations of 134,917 cows were informative for claw health traits and provided the basis of the genetic evaluation. For maximum differentiation between individuals, the number of distinct claw health events per lactation was analyzed using linear animal repeatability models. Genetic parameters and breeding values (EBV) were estimated univariately for six individual claw health traits: interdigital hyperplasia, IH; laminitis, LA; white line disease, WL; claw ulcers, UL; digital phlegmon, PH; digital dermatitis, DD. Weight of traits for the derived Claw health index were 30% for DD, 10% for IH, and 15% each for LA, WL, UL and PH.

Pearson correlation coefficients and Spearman rank correlations were determined between EBV of Holstein AI bulls from the prototype genetic evaluation for claw health and the official routine genetic evaluation for dairy cattle (vit 2017). Statistical analyses were performed using the SAS software package (Statistical Analysis System, SAS version 9.3; SAS Institute Inc., Cary, NC, USA, 2017). PEST software (Prediction Estimation; Groeneveld & Kovac 1990) was used for the genetic evaluation.

Results and discussion

Descriptive statistics and heritability estimates of the six claw health traits considered are given in Table 1. With restrictive definition of control animals (presence in the herd, i.e. under health monitoring, without respective diagnosis records for at least 75% of 305 days standard lactation), lactation incidences of 5 to 20 percent were calculated, illustrating the quantitative importance of claw conditions of dairy cows. However, additional information on locomotion (lameness) was not available for the cows and severity of alterations were not considered, so no direct conclusions can be drawn on the clinical relevance of these findings.

With estimates of between 0.06 and 0.11, heritabilities were consistent with literature and routine applications most of which referred to trimming records as exclusive data basis. Full integration of treatment and trimming data was therefore seen as feasible approach to increase coverage and avoid bias of available information on claw health from commercial dairy herds. However, thorough data processing is crucial when linking different sources of data, and demands increase the more heterogeneous recording intervals and overall data structure are.

Table 1. Claw health traits in the genetic evaluation with frequencies (lactation incidences, LI) and heritabilities (h^2), with additional information on the composition and heritability of the claw health index.

Trait	Number of lactations	LI	h^2	Index weight	Index h^2
Interdigital hyperplasia, IH	240,312	5.0 %	0.11	10 %	0.08
Laminitis, LA	242,160	8.7 %	0.06	15 %	
White line disease, WL	241,257	7.6 %	0.06	15 %	
Claw ulcers, UL	203,344	14.5 %	0.09	15 %	
Digital phlegmon, PH	199,342	12.8 %	0.07	15 %	
Digital dermatitis, DD	217,817	20.2 %	0.07	30 %	

Standard error of $SE_{h^2} < 0.01$

Table 2: Correlations (Pearson correlation coefficients) between breeding values for claw health and results of routine genetic evaluation for dairy cattle (April 2017) referring to conformation of feet and legs in 436 Holstein AI bulls with at least 50% reliability of the claw health index.

Trait	RZ Spr	RZ KWi	RZ HBs	RZ HBw	RZ Bew	RZ Fun
Claw health index	0.07	0.04	0.08	-0.16	0.36	0.27
Interdigital hyperplasia, IH	0.09	0.06	0.16	-0.11	0.31	0.27
Laminitis, LA	0.05	0.02	0.01	-0.07	0.22	0.16
White line disease, WL	0.13	-0.03	-0.02	-0.03	0.22	0.17
Claw ulcers, UL	0.06	0.06	0.07	-0.17	0.34	0.26
Digital phlegmon, PH	0.12	-0.06	0.06	-0.12	0.27	0.21
Digital dermatitis, DD	0.00	0.05	0.09	-0.16	0.29	0.21

Spr = Sprunggelenk / hock quality, KWi = Klauenwinkel / foot angle,
HBs = Hinterbeinstellung / rear leg set rear view, HBw = Hinterbeinwinkelung / rear leg set side view, Bew = Bewegung / locomotion,
Fun = Fundament / feet

Table 3. Correlations (Pearson correlation coefficients) between breeding values for claw health and results of routine genetic evaluation for dairy cattle (April 2017) for the total merit index and major trait complexes in N=436 Holstein AI bulls with at least 50% reliability of the claw health index.

Trait	RZG	RZM	RZS	RZR	RZN	RZE
Claw health index	0.36	0.21	0.17	0.17	0.38	0.03
Interdigital hyperplasia, IH	0.20	0.07	0.11	0.05	0.26	0.11
Laminitis, LA	0.29	0.20	0.11	0.10	0.27	-0.01
White line disease, WL	0.37	0.18	0.19	0.23	0.40	0.13
Claw ulcers, UL	0.42	0.23	0.23	0.20	0.43	0.10
Digital phlegmon, PH	0.19	0.02	0.16	0.08	0.32	0.02
Digital dermatitis, DD	0.24	0.18	0.08	0.11	0.21	-0.07

RZG = total merit index, RZM = production, RZS = somatic cell score, RZR = fertility,
RZN = longevity, RZE = conformation

In the genetic evaluation for claw health traits performed in the GKUHplus project in January 2017 and considering health data from January 2009 to December 2016, 5,955 Holstein AI bulls were represented with on average 19 daughters (range 1 to 2,052). However, 73 percent of these bulls had between one and ten daughters and only 412 bulls had 50 or more daughters with claw health information. Average reliabilities of EBV were therefore low, and further extension of the phenotypic data basis will be needed to increase the number of bulls with reliably estimated conventional breeding values for claw health traits.

Nevertheless, analyses of distributions of individual EBV and Claw health index showed significant phenotypic differentiation between progeny groups of sires, implying substantial opportunities to reduce the frequencies of claw disorders in dairy cattle through routine genetic evaluation. Correlation analyses with the currently available genetic proofs clearly showed the limitations of using conformation related indicator traits (Table 2). At the same time, selection for improved claw health should not interfere with genetic progress in other trait complexes (Table 3).

Conclusions

Claw health requires particular attention in dairy production and should be seen as essential part in initiatives for monitoring and improving health of dairy cows. Challenges related to routine access and use of claw data do exist, but comprehensive concepts with integrative approaches make it possible to efficiently increase information density and by this strengthen routine applications. However, awareness of remaining challenges related to phenotyping (harmonization and standardization of data recording), logistics, data quality management and definition of traits may be crucial to ensure long-term success of the engagement for improving the health of feet and legs in dairy cattle.

Results from the German R&D project GKUHplus demonstrate feasibility of integrated use of claw data for genetic evaluation for claw health traits in Holstein dairy cattle. Furthermore, they also indicate the potential of using cow phenotypes on claw health collected broadly in the field as basis for developing genomic applications for new traits, as it is done in the new R&D project KuhVision which is a joint initiative of the German Holstein breeding organizations and aims at setting up a female reference population.

Acknowledge-ments

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Cow's Own Worth - synergising data to provide a new tool to aid in culling decisions in seasonal dairy herds

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Abstract

The ability to identify cows with the highest future profit potential will have a substantial impact on herd profitability and efficiency. The Cow's Own Worth (**COW**) is a decision support tool that was developed to aid producers in making informed decisions on dairy females for culling and retention. The COW ranks dairy females on expected profit for the remainder of their lifetime, taking cognisance of both additive and non-additive genetic merit, permanent environmental effects, and current states of the animal including the most recent calving date and cow parity. The objective of this study was to pilot the COW on commercial dairy herds and to conduct a survey to gauge farmer's impression and interest in this potential added value service from the Irish Cattle Breeding Federation (ICBF).

The framework of the COW consisted of the profit accruing from:

1. the current lactation;
2. future lactations; and
3. net replacement cost differential.

The COW was generated from estimated performance values (**EPV**; sum of additive genetic merit, non-additive genetic merit and permanent environmental effects) of traits, their respective net margin values, and transition probability matrices for month of calving, survival, and somatic cell count; the transition matrices were to account for predicted change in a cow's state in the future. Transition matrices were generated from 3,156,109 lactation records from the national database between the years 2010 and 2013. Phenotypic performance records for 162,981 cows in the year 2012 were used to validate the COW. A pilot group of 83 commercial herds were recruited in 2016 to trial the COW and to conduct a survey on the potential delivery of an added service to data recording herds.

The Pearson correlation between individual animal COW value and national breeding index (EBI) value was 0.65. Month of calving in the current lactation explained 18% of the variation in the COW with parity explaining an additional 3 percentage units of the variance in the COW. Females ranking higher on the COW yielded more milk and milk solids and calved earlier in the calving season than their lower ranking contemporaries. The difference in phenotypic performance between the best and worst quartiles was larger for cows ranked on COW than cows ranked on EBI.

The response rate to a survey of randomly selected pilot users of COW was 52%. The results indicated that 91% of respondents would use the COW to help inform culling decision if it were to become a routine service from the ICBF. Furthermore, 93% of participants felt that their milk recording information had more value because the COW was available to them. Overall, 95% would recommend the national extension of the COW to all dairy milk recording herds in 2017.

The COW is a useful management tool to rank dairy females for culling decisions. COW integrates multiple sources of available data, and critically, is complementary to the EBI which identifies the most suitable females for breeding replacements. The COW offers future prospects to improve herd profitability by adding value to existing services such as milk recording and genotyping of dairy females. In order to maximise the efficiency of the COW, farmers need to fully engage in on-farm data recording for example inseminations, pregnancy diagnosis, and health (e.g. mastitis and lameness) events.

Keywords: culling, milk recording, genetic, permanent environment.

Introduction

The ability to identify cows with the greatest predicted future profit potential will have a substantial impact on herd profitability and efficiency. Dairy producers make significant investments in data recording (e.g. milk recording, pregnancy diagnosis and genotyping) but collating all these data sources into one value per animal is key to aid decision making. A decision support tool was developed to aid producers in making informed decisions on dairy females for culling and retention. The Cow's Own Worth (**COW**) combines multiple sources of information to identify the expected profit potential for the remainder of every dairy female's life. The COW generates a value for every cow within a herd and ranks cows using additive genetic merit (estimated breeding values), non-additive genetic merit, permanent environment effects and current states of the cow (i.e., lactation number, calving date, and predicted calving date from available inseminations or pregnancy diagnosis). Farmers can quickly identify under-performing females to cull, thereby retaining only the most profitable females. Other benefits of this management tool are the reductions in time, effort and resources farmers spend on culling and retention decisions while getting more value from their data recording strategies.

The Irish Cattle Breeding Federation (ICBF) operates a single shared database to meet the needs of the Irish cattle breeding industry and has the potential to integrate data to provide the COW as an added value service to dairy farmers. Information from multiple sources (e.g. calf registrations, milk recordings, inseminations, health events) can be collated and are readily available for each dairy female. The COW can be calculated for spring-calving milk recording herds. The COW was developed and validated by Teagasc Moorepark (Irish dairy research centre) and results indicated the validity and usefulness of this management tool (Kelleher *et al.*, 2015). The objective of this study was to trial the new management tool on commercial herds using ICBF's database. Results from this trial will determine the commercialisation of this service to the wider industry.

Materials and methods

Model

The framework of the COW consisted of the profit accruing from:

1. the current lactation;
2. future lactations, and
3. net replacement cost differential.

Full details of the formulation of the COW have been previously described by Kelleher *et al.* (2015). The COW was generated from estimated performance values (**EPV**; sum of additive genetic merit, non-additive genetic merit and permanent environmental effects) of traits, their respective net margin values (obtained from the Moorepark Dairy Systems Model (**MDSM**; Shalloo *et al.*, 2004), and transition probability matrices for month of calving, survival, and somatic cell count; the transition matrices were to account for predicted change in a cow's state in the future. Transition matrices were generated from 3,156,109 lactation records from the national database between the years 2010 and 2013.

Validation

Individual cow EBI values (national breeding index) and COW values were generated using the information from the April 2011 national genetic evaluations. Cows were categorised, within herd, into 4 groups based on their value for either the COW or EBI index. Only cows that had phenotypic performance data for the calendar year 2012 were retained. After editing, phenotypic performance records for 162,981 cows in the year 2012 were used to validate the COW.

A fixed effects linear model was also used to quantify the association between each quartile of the COW and EBI index separately (independent variable) with milk, fat and protein yield, as well as somatic cell score (dependent variable) using PROC GLM (SAS Institute, 2011). Quartiles for the COW or EBI index as well as parity were included as fixed effects in the model.

Commercial herd pilot study

A pilot group of 83 commercial herds were recruited in 2016 to trial the COW. A random sample of herds were selected from farm holdings operating spring-calving systems, routine milk recording, as well as recording fertility events (i.e. inseminations and pregnancy diagnosis). Herd owners were contacted via email and invited to participate in the pilot study. The email included key pieces of information:

- A COW information leaflet.
- A COW report.
- On-farm performance results (milk records, fertility records, etc.).

A survey was conducted of these pilot users to gauge farmer impressions on the usefulness of the COW as an aid in decision making.

Results and discussion

Validation

The Pearson correlation between individual animal COW value and national breeding index (EBI) value was 0.65. Month of calving in the current lactation explained 18% of the variation in the COW with parity explaining an additional 3 percentage units of the variance in the COW. Females ranking higher on the COW yielded more milk and milk solids and calved earlier in the calving season than their lower ranking contemporaries. The difference in phenotypic performance between the best and worst quartiles was larger for cows ranked on COW than cows ranked on EBI.

Commercial herd pilot study

The response rate to the survey was 52% from a total of 83 herds recruited for the study. Results were overwhelmingly positive, with 95% of farmers recommending a national rollout of the COW (Figure 1). Furthermore, 91% of respondents would use the COW to help inform culling decisions if it was to become a routine service from the Irish Cattle Breeding Federation and 98% would like the COW to be generated for their herd from now on. A high proportion (93%) of participants felt that their milk recording information had more value because the COW was available to them. Overall, 98% would recommend the national extension of the COW to all dairy milk recording herds in 2017.

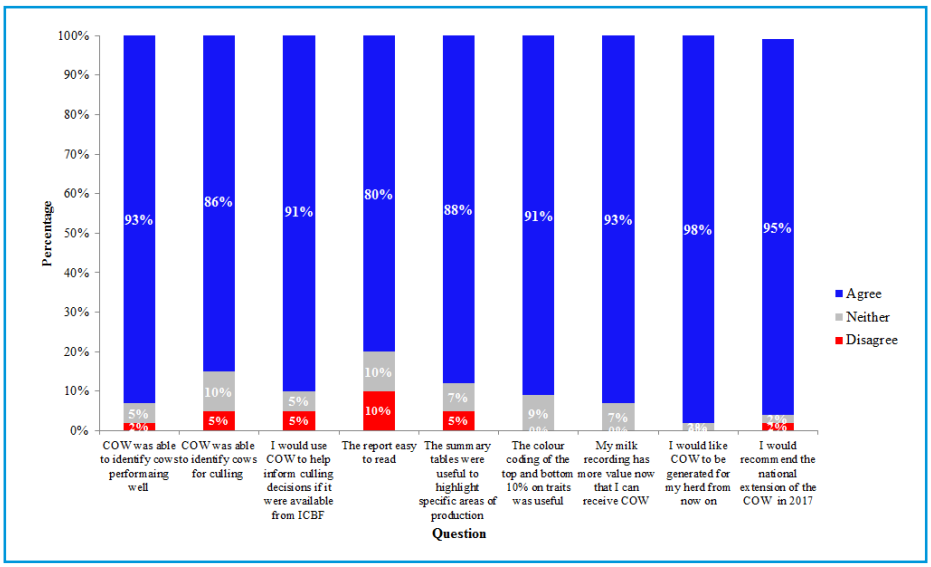

Figure 1. Responses to survey questions from commercial herd pilot study conducted by ICBF in 2016.

Commercial roll out

Overall, the impression of the effectiveness of the COW from the piloted commercial herds was exceptionally positive. The demand for the service justified the investment of resources to develop an on-line profile page for the COW for farmers with adequate levels of herd recording. To this end, farmers who have invested in recording services such as milk recording, inseminations, pregnancy diagnosis services, genotyping for example, will be offered the opportunity to generate an on-line live COW report for their herd. Using this service, the farmer can quickly identify under-performing females to cull thereby retaining only the most profitable females while getting more value from their data recording strategies.

The COW tool provides an excellent incentive for dairy producers to record traits that currently lack routine collection. Farmers who wish to generate a live COW reports using the ICBF Herdplus website can be prompted to update cow information such as inseminations, pregnancy diagnosis and health traits (e.g. mastitis and lameness events) prior to generating the COW report so that the most up-to-date information is used to rank dairy females within the herd. This will improve the accuracy of the COW rank of each cow in the herd for the farmer as well as provide an extra enticement to farmers to record more data (and potentially more accurate data). These additional data can be subsequently used for genetic evaluations, and will be of particular value for genetic evaluation of traits that are not routinely recorded currently.

Conclusions

The COW is a useful management tool to rank dairy females for culling decisions. COW integrates multiple sources of available data, and critically, is complementary to the EBI (Ireland's national breeding index) which identifies the most suitable females for breeding replacements. The COW offers future prospects to improve herd profitability by adding value to existing services such as milk recording and genotyping of dairy females. In order to maximise the efficiency of the COW, farmers need to fully engage in on-farm data recording for example inseminations, pregnancy diagnosis, and health (e.g. mastitis and lameness) events. The COW is currently under development as a profile page on the ICBF website. An on-line pilot scheme for the profile is underway. Commercial launch of COW are contingent on the results of the on-line profile pilot scheme.

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Possible principles for breed association models in the genomics era, with reference to beef cattle and sheep breeds

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Abstract

Beef cattle and sheep breeding in some countries is characterised by important roles for breed associations or societies, including delivery of multi-trait genetic evaluations. In parallel, research and development is typically predominantly funded by the public sector and/or the whole of industry. The breeding sector is therefore providing a genetic improvement service to the rest of industry, while engaging in competition for market share both between and within breeds.

The basis on which inputs to genetic improvement are funded can vary, but typically involves some investment by breeders themselves, usually to cover costs of providing database and data analysis services. In such situations, there is considerable scope for very low relationship between investment and return, at the individual breeder, the breed or the industry level.

This potential misalignment can be exacerbated in the genomics era, in which it is possible to completely decouple investment in performance recording from obtaining estimated breeding values (EBVs) and other genetic information, and from genetic improvement. At the same time, "genomics" offers scope for almost unlimited increase in scale in multiplication and hence harvesting of value.

These developments create conditions in which it is appropriate to consider carefully the nature of breeds and how they self-organise, with issues including:

- Should all input services (such as access to database and evaluation) be provided on a cost-recovery or cost-plus basis, or
- Should value-creation models be considered, where the value of data contributed, and the use to which EBVs are put, be recognised and in some way rewarded
- If it is possible to apply some form of value-creation model, what governance would be needed, and who across an industry and community could or should contribute?

The perspective of this paper is that genetic improvement, and contribution to generating and delivering it, are - at least in multi-enterprise industries - quite particular economic goods, and further, that current models of organisation and of technology delivery are poorly aligned with the overall goal of maximising genetic progress. In

very general terms, this is usually described as market failure, but this avoids the mental effort of diagnosing accurately what contributes to value and examining whether value-creation is prioritised.

Increasingly, genetic improvement in multi-agent organisations and industries will need to accommodate more nuanced thinking about externalities both within the breeding sector, and through the value chain, and whether and how to apply learnings from the literature on club or merit goods. Failure to do so will almost certainly lead to under-performance in terms of rate of genetic progress, likely coupled with hollowing-out of breed associations and loss of potentially valuable variation in decision-making.

There is real scope to evolve to new models of organisation and collaboration in this space, but very real changes in the "rules of engagement" in breed associations will be essential. This paper identifies some of the key challenges, and offers possible principles and approaches to addressing them.

Keywords: breeds, organisational models, genomics.

Introduction

Genetic evaluation systems in beef cattle and sheep are typically delivered via or with breed associations, and to date have usually been on a within-breed basis. Submission of animals to the genetic evaluation is usually governed by some minimum criteria for data: for example, a date of birth, some pedigree data and at least one weight, might be required. There will usually be some charge for submission of animal records to the evaluation, although what such charges cover and how they are designed can vary. There will usually also be some cost for data collection on-farm (in the bull- or ram-breeding herd or flock), which may attract some support from the breed and/or government, and there may be some breed-level investment in special data collection herds, such as the Beef Information Nucleus herds developed in Australia (Banks, 2009).

Countries and breeds vary in their approaches to rules regarding what animals can be included in evaluation, and what traits can or must be recorded, but at least in Anglo-Saxon countries, access to genetic evaluation is relatively open, provided the animals meet some level of breed "purity", as defined on the basis of recorded pedigree. Extending this point, there is no automatic or necessarily close linkage between governance of the breed association and development and application of genetic evaluation.

A central economic fact of these systems is that data collection is tightly linked, or coupled, to evaluation: the breeder has to supply some performance and pedigree data in order to obtain estimates of genetic merit on his/her animals. This implies that the breeder anticipates receiving sufficient income from sales of genetic material (animals and/or semen, ova) to cover the cost of production of the animals, the cost of whatever recording is done, and any costs imposed for genetic evaluation.

As livestock evaluation makes increasing use of genomic methods, this tight coupling of data collection and genetic evaluation can be completely broken. Provided that a sufficiently large reference population is in place, animals can be evaluated on the basis of a genotype alone.

This decoupling generates additional complexity for breed associations, with the risk that they may not have the financial, managerial or technical resources to manage this complexity. Banks (2016) proposed a future role for breed associations, as R&D organisations, aiming to:

- maximise r.δ$ per funds invested for some defined gene pool.
- maximise ir/L.

Achieving this will require new forms of association, likely new pricing and return models, and almost certainly include long-term partnerships with others in the value chain (either private and/or public). Van Eeenannam and Drake (2012) expressed this similarly:

"*Breeds/groups that can organize themselves and technologically and structurally to seamlessly obtain and marry entire supply chain phenotypes and genotypes and take advantage of the rapidly-declining cost of genotyping to capture the cumulative value derived from using genomic information for multiple purposes (selection, parentage, genetic defects, marker-assisted management, product differentiation, traceability) will be ideally positioned to fully realize the nascent potential of genomic information*."

An additional dimension of challenge and opportunity arises from the fact that many breeds have populations in several countries. The opportunity arises from the potential to share reference data - genotypes and phenotypes - across countries, and thereby potentially increase the accuracy of genomic selection within each collaborating country (Berry, 20??).

The challenges include:

- Simply achieving collaboration.
- Ensuring that rules and procedures for including data (genotypes, phenotypes, pedigree) within- and across-countries are consistent, and ideally are equitable and efficient (in the sense of providing transparency in relation to incentives to collect phenotypic data), and minimise free-riding.
- Determining whether shared or coordinated design adds value and can be achieved, including options such as coordinated young sire sampling, designed phenotyping and genotyping .
- Managing collaborative R&D, which is essential to create the opportunities and overcome at least some of the challenges.

An obvious question that arises from these considerations is whether "breeds" need to work as global partnerships or networks to survive? The answer seems obvious in that there will almost certainly be advantage in doing so.

This paper explores some of the challenges that breed associations will face and have to overcome in order to survive and prosper in the genomics era, and suggests some principles that will be fundamental to success.

Breed associations and genomics

The decoupling of phenotyping and evaluation that is enabled with genomics generates major challenges and opportunities for groups of breeders working with a defined gene pool - a breed association. Assuming that they engage with genetic evaluation, such associations usually have some core costs associated with genetic evaluation, including database, staff, and analysis, but costs of phenotyping are dispersed across the members of the association. The members are usually diverse:

- They vary behaviours (recording, selection, marketing).
- They vary in contribution, measured as amount of genetic progress times number of animals generated.

Incentives for member breeders include stud and herd bull sales. The system of data collection and evaluation generates externalities (Banks, 2014) only a small proportion of which are captured by the breeders (Banks, 2017). The scale of such externalities can be considerably greater with genomics, through the capacity to evaluate essentially infinite numbers of animals or animal-derived products from any point in the value chain.

To a large degree, breed associations have only very limited procedures and regulations relating to genetic evaluation and improvement technologies, and have restricted their regulatory systems to issues of breed purity. Accordingly, unless closely and strongly supported by technical resources, such associations face considerable organisational challenges in adopting and exploiting genomic technologies. These will include those around variation in the quality of phenotypic data, which animals are genotyped and phenotyped and so constitute the reference population, and the effectiveness of selection decisions. These 3 dimensions of investment and decision-making jointly determine the potential and actual value created and maintained by a breed.

In relation to breed associations and the breeds themselves, it is reasonable to ask "is there a reason to care?" How this question is addressed depends on the perspective of the questioner, will vary between countries, and involves consideration of both a technical and economic efficiency dimension, and a risk dimension (which could of course be included in economic efficiency) - is there any benefit from spreading investment and decision-making risk amongst multiple decision-makers, as opposed to some more corporate approach.

A simple model

One aspect of the economic dimension of the challenge can be explored through a simple model. If we assume a breed that has arranged its affairs such that it has:

- A reference population (n = 1,000 cows), where all recording takes place.
- A breeding nucleus (n = 10,000 cows) which produces bulls, which breed commercial progeny (n = 360,000 per year).

If the reference population costs $1mAUD per year, a simple approach to recouping that investment is impose a surcharge on the costs of genotyping nucleus bulls and heifers, and commercial progeny. It seems reasonable to charge more for tests on bulls and heifers because they have more expressions: approximately 45 expressions per nucleus bull or heifer, and 1 expression per commercial animal. Under the assumption of the reference population cost, and the numbers of animals in each category, this means surcharges of $54 per nucleus animal and $1 per commercial animal, on top of the cost of genotyping.

If this approach has merit, it will be essential to ensure transparency, and a satisfactory return on investment at both levels (nucleus and commercial): charging too much or too little will cause distortions in investment.

In real life, things will be more complicated: the reference population will likely include some defined collective investment in HTM traits, and some variable investment by individuals in other traits. It will be important to consider how to deal with the variable investment made by nucleus breeders, and how to return some share of the surcharge collected to those breeders.

Two "easy" solutions seem available for managing this coordination problem:

- Completely rule-defined, allowing no variation. This potentially more expensive, simply because of the imposition and monitoring of rules, and that additional cost must be met by someone. It also requires a very strong belief in the rules, and the ultimate success achieved by applying them. It also requires agreement on who sets the rules
- Completely market-based. Superficially this is very easy to implement ("the market decides"), and hence implementation risk and cost is minimised. At the same time, outcome risk is maximised

Neither is ideal.

Principles

Breed associations that survive and prosper in the genomics era will have to manage the following issues:

- Phenotypes vary in quality, or value - this needs to be recognised, ideally at the point or time of the recording (investment) decision.
- Variation in selection (direction, rate) affect both the individual and the breed, and ideally needs to be minimised.
- A mechanism for "payment" is needed - the individuals investing in reference phenotyping and genotyping must have confidence that their investment will be recouped. This will be challenging for most breed associations, in that financial payments are likely to be impossible for most organisations, and rewards or incentives must have limits (otherwise there is a redemption risk ie "payment" for phenotypes and genotypes could bankrupt the association). Any such incentives or rewards also have to be finely judged, since they are likely to reinforce any existing market rewards, and/or the risk of breeders leaving the association or ceasing to collect phenotypes. To avoid the problems of financial mechanisms, waiving genotyping surcharges, and/or providing technical advice may be more feasible options.
- Consideration should be given to developing point of decision apps help shift all decisions towards optima.

Breed associations that can devise and manage simple, transparent and equitable mechanisms for these issues, and hence solve what in economic terms are referred to as coordination problems, will prosper. Those that cannot will disappear.

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Data collection methods used in the Beef Data and Genomics Programme (BDGP) and the development of restful API's for recording herd data

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Abstract

The Beef Data and Genomics Programme is a scheme approved by the EU to reduce greenhouse gases caused by cattle in Ireland by breeding more sustainable and profitable animals.

The BDGP requires participants to complete various surveys on animals in their herd, such the docility of the animals, calf birth size, calf vigour, dam milk-ability, and the departure reasons of the sires and dams that have left the herd.

Various recording mechanisms have been made available to record this data by ICBF which includes scannable paper forms, data recording screens for mobile and desktop devices, and a simple API system to allow data to be submitted from 3rd party software applications.

ICBF are also developing a Restful API system that will allow JSON formatted data to be transferred between the ICBF database and other systems over the internet. Authentication is provided via the transfer of tokens using the oAuth 2.0 protocol.

This system will allow for real-time read and write access to the farmers' data stored in the ICBF database and will be made available to 3rd party software providers for the benefit of the Irish farmer.

Keywords: data recording, bdgp, api.

Introduction

There is an established need to collect farmer recorded data on animals in large volumes which can then be used in genetic evaluations. A scheme such as the Beef Data and Genomics Programme has various requirements where the farmer must record this data on his herd in order to be compliant with the terms of the scheme.

Also required is the need to provide the IT systems that will be capable to take advantage of the many advances in technology that has taken place in recent years, and to make it easier to collect accurate data from various sources and make it available to the farmers when they need it.

Over the last few years, ICBF has provided various data recording paper on online forms to collect information from farmers for the Beef Data and Genomics Programme, and most recently an API system has been developed that will allow third party devices used by the farmer to read and write animal data to the ICBF database.

Beef Data and Genomics Programme (BDGP)

The Beef Data and Genomics Programme is a six year scheme approved by the European Commission and launched by the Minister of the Department of Agriculture, Food and Marine, Simon Coveney TD in 2015.

The programme provides up 52 million per annum to the suckler beef sector to deliver accelerated genetic improvement in the National herd and improve its environmental and economic sustainability ("Coveney launches 300 Million Euros Beef Data and Genomics Programme", 2015).

In 2017, the scheme was expanded to make it available to new applicants.. ("Creed Announces Re-Opening", 2017).

There are six requirements to the scheme:

1. Calving details - In addition to the statutory requirements for tagging and registration; for each calf, a calving ease survey must be provided along with the tag number or the AI code of the sire.
2. Surveys - Applicants will be required to complete survey forms on cows, calves, and stock bulls on the holding. Survey forms are supplied by ICBF. See Table 1 for information on the data collected.
3. Genotyping - Applicants will be required to take a tissue sample from animals selected for genotyping. The amount of animals that are to be sampled will be at least equivalent to 60% of number of calved suckler cows on the farm in 2014.

Table 1. Information on the data collected as part of BDGP requirements 1 and 2.

Trait	Description	Data format
Sire	The tag number or AI code of the calf	
Calving ease	The calving ease score of the calf	4pt scale
Calf birth Size	The size of the calf at birth	5pt scale
Calf vigour	The vigour of the calf at birth	5pt scale
Calf docility	The docility of the calf at 5 months	5pt scale
Calf quality	The quality of the calf at 5 months	5pt scale
Calf scour	The number of occurrences of scour at 5 months	0, 1 or 2+ occurrences
Calf pneumonia	The number of occurrences of pneumonia at 5 months	0, 1 or 2+ occurrences
Dam docility	The docility of the dam	5pt scale
Dam milk-ability	The milk-ability of the dam	5pt scale
Dam departure reason	The reason for the dam leaving the herd	List of departure reasons
Stock bull docility	The docility of the stock bull	5pt scale
Stock bull functionality	The functionality (feet and legs) of the stock bull	5pt scale
Stock bull departure	The reason for the stock bull leaving the herd.	List of departure reasons

4. Replacement Strategy - For applicants using a stock bull, there must be at least one stock bull on the farm on a particular date that is genotyped 4 or 5 stars on the Terminal or Replacement index. The applicant must ensure that a percentage of heifers or suckler cows are genotyped and are four or five stars on the replacement index on particular dates detailed in the scheme's terms and conditions.
5. Carbon Navigator - All applicants must complete the Carbon Navigator in the first year of the scheme. The Carbon Navigator is an online farm management package produced by Bord Bia and Teagasc. In subsequent years of the scheme, applicants must update this information using forms provided by ICBF.
6. Training - Applicants must attend a training course in the first year of the scheme.

The source of the above requirements is the Department of Agriculture, Food and Marine, Terms and Conditions, 2015. There are currently 23,500 herds participating in the scheme.

BDGP Data Recording

Requirement 1 and 2 of the BDGP scheme requires the farmer to complete various surveys on the animals in their herd that are eligible for the scheme. Paper forms and a web application have been made available by ICBF to record this information.

Paper forms

There are potentially 550000 eligible calves born to BDGP participating herds each year. Due to the high volumes of animals, and the number of traits that are recorded against each animal, the forms have been produced so that the information can be extracted via a scanning process.

To ensure that the scanning process is as accurate as possible, each form developed requires the farmer to simply circle or mark a specific value for each trait on each animal. Also, each animal listed on the form has its tag number rendered as a 2D barcode. This helps to avoid data being lost due to a tag number being read by the scanning process incorrectly. Overall, this approach has allowed for very high accuracy rates of around 99.7% across all traits collected.

The exception to this is with the sire recording, it was not possible to take this same approach with the other traits as the farmer needs to write in the tag number or AI code of the calf's sire. This handwriting reduced the scanning rate by about 20%, which greatly increased the number of forms being presented for validation to the keying personnel. As a result, sire tag numbers and AI codes are manually keyed into a web interface. Fortunately, only a relatively small number of sire recording forms are issued as this information is typically recorded at calf registration.

There are five different forms issued as part of the BDGP. All forms have a unique form number, presented as a 2D barcode to improve readability, so each form can be tracked throughout the process. Each form is issued with an addressed freepost envelope for returning the forms. When the forms are returned, they need to be sorted into batches of the same type and processed together. To aid this, each form is printed on different coloured paper.

ICBF works with the company Capita Customer Solutions (*www.capitacustomersolutions.ie*) to process the forms. Capita uses scanning software and equipment provided and developed by SoftCo (*www.softco.com*). The scanning

software extracts the recorded data from the form, and makes it available to ICBF in a data file which is loaded to the ICBF database nightly. A scanned image of the form is then archived so that it is easily accessible if required.

Paper forms are used by around 60% of the herd-owners participating in the BDGP as the primary method of recording the required information for requirement 1 and 2.

Online data recording facilities

ICBF provides an online web application for recording all information for requirement 1 and 2 of the scheme. All herd-owners participating in the scheme can log on to *www.icbf.com* using their username and password and access the Beef Data and Genomics Programme application.

As well as providing the various data recording web pages, this application provides summary and detailed information on the status of the herd in relation to the scheme requirements, as well as the information that has already been recorded.

The ICBF web application is also mobile compatible to allow the farmer to record or review their data on a mobile or tablet device. In order to make the application as accessible as possible, it has also been made available via the Android and Apple stores, by wrapping the application in an App.

Herd-owners can also record their BDGP data via other Department of Agriculture approved software providers as well as on the Department of Agriculture's own web application, www.agfood.ie. All data recorded on these other web sites are transferred to ICBF daily using various web services.

There are several options available to herd-owners to record this information online, but the majority of herds continue to prefer the paper-based option.

Herd Application Programming Interfaces (API)

There have been many changes in technologies in recent years which have increased the sources of data available. Examples of this would include the smart phone, robotics, artificial intelligence, Internet of Things (IoT) devices and sensors. ICBF also has an increasing need to communicate with other companies in real-time. For example, with genomics, ICBF transfers data to and from the Weatherby's laboratory when processing returned samples.

As a result, ICBF has been actively developing a series of APIs to exchange data with third party devices and applications, and in particular, an API is being developed to make it easy for the farmer to access and record data on his animals through devices like those listed above.

The ICBF Herd APIs are a set of web services available to software and sensor providers to provide data services to farmers. They are built using Representational state transfer (REST), the alternative that was considered was SOAP (Simple Open Access Protocol), but REST was chosen as the data transfer was not restricted to XML, and JSON (JavaScript Object Notation) could be used.

JSON was preferable over XML as it is shorter, which reduces the size of the data transfer, and it is quicker to read and write.

ICBF uses an API builder call Apigility (*https://apigility.org*) which simplifies the creation and maintenance of useful, easy to consume and well-structured APIs. Apigility structures the services according to the Hypertext Application Language (M Kelly, 2011)

specification which readily achieves the Richardson Maturity Model Level 3 (Fowler, 2010). This ensures that each resource contains relational links, and that a standard, identifiable structure for embedding other resources is used.

Authorisation and Authentication is handled using oAuth 2.0 which is an industry standard protocol for authorization. OAuth 2.0 focuses on client developer simplicity while providing specific authorization flows for web applications, desktop applications, mobile phones, and other devices (oauth.net/2).

A particularly important advantage of using oAuth 2.0 is that is keeps the farmer's authorisation details away from the client devices which are typically considered insecure. It does this with a series of unique token exchanges. This ensures that if the client device becomes compromised, the farmer's authorisation details are still safe.

The Herd APIs currently available from ICBF are listed in Table 2.

Table 2. List of Herd APIs currently available from ICBF.

Scope	Service	Methods available	Description
Herd Details	Animal Details	Read	The animals currently in the herd and their details such as birth date, sex, breed, arrival date etc.
Herd Fertility	Heat	Read|Write|Update|Delete	The heat data recorded on animals in the herd
	Inseminations	Read|Write|Update|Delete	The insemination data recorded on animals in the herd
	Pregnancy Diagnosis	Read|Write|Update|Delete	The pregnancy diagnosis data recorded on animals in the herd
Herd Evaluations	Beef	Read	The beef evaluations of animals in the herd, e.g. Maternal and Terminal Indexes etc.
	Dairy	Read	The Dairy evaluations of animals in the herd, e.g. EBI, Milk and Fertility Indexes
Herd Weight	Live Weight	Read|Write|Update|Delete	The weights data recorded on the animals in the herd
Herd Health	General Health	Read|Write|Update|Delete	The general heath data recorded on the animals in the herd, e.g. mastitis, lameness etc.
Herd Lactation	Period	Read|Write|Update|Delete	Lactation data recorded on the animals in the herd, including milk recording information. Dry off dates can be recorded and updated

Conclusion

ICBF continues to receive high volumes of quality data from farmers through paper forms, regardless of the continued investment made to provide alternative electronic methods. The number of herds using the paper forms to record data is gradually decreasing over time, but the pace of decline is slow and the issuing for forms will continue for the foreseeable future.

ICBF is currently developing a suite of API's that will allow for the sharing and recording of farmer recorded data across many third party software and devices. These APIs have many wide-ranging advantages for the agricultural industry, but the software, devices and sensors need to be put in place to interact with them. The adoption rate of these technologies remains to be seen.

Acknowledge-ments

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Implementation of genomic selection in small populations - Croatian case

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Abstract

Dual purpose Simmental breed represents dominant part of Croatian cattle population which is mainly raised in a limited number of countries (Germany, Austria, Czech Republic, north Italy, Slovenia, and Croatia). Holstein is the second largest breed population in Croatia. In order to maintain and improve production of young Simmental bulls based on a genomic breeding value of young calves, Croatia joined German-Austrian system of genomic evaluation in July 2013. The inclusion was justified since the breeding of Croatian Simmental is closely related to Austrian and Bavarian breeding. Bull's sires and bull's dams are coming from these populations and there is a long-standing import of breeding heifers and bull's semen for artificial insemination. In contrast to Simmental, the main goal of genomic improvement in Holstein population is based on female calves in order to identify potential dams at a young age. Croatia does not have a sufficiently large reference population. Therefore the potential female candidates were included in German Holstein genomic evaluation system, starting from 2016.

Young male and female candidates were chosen based on parent average, interesting bull lines, as well as dam exterior. Based on these criteria, 254 young Simmental and 96 Holstein calves were selected, genotyped and genomic breeding values were estimated for them. Additional benefits of genomics, beside genomic evaluation, are parentage verification and information about major gene/disease defects specific for Simmental and Holstein populations. The recommended criterion for entry of potential young Simmental bull in the centres for AI is total merit index over 130. Furthermore, candidates should not be carriers of known genetic defects or recessive for them. On the basis of agreed criteria, seven young bulls were selected as potential bulls for AI. The recommended criteria for selection of Holstein female candidates are a total merit index of 150, without gene defects and so far none of them reached these standards.

Croatian Agricultural Agency as milk recording organization is deeply included in genomic services through collecting recording data, breeding value estimation and consequently parent average calculations, processing and publishing of the genomic evaluation results. At the farm level, genomics for females becomes an attractive option to capitalise on the benefits of using this technology. At the national level, Croatia has gone from a country that imported most of its genetics to a country which now uses own semen. The usage of genomic bulls has increased from 8% of all used bulls in 2012 to 23% in 2016. In addition, Croatian AI companies are now marketing semen of two young bulls internationally.

Key words: genomic selection, Simmental and Holstein breed, male and female calves,

Introduction

Dairy cattle population in Croatia (CAA, 2017) is composed of Simmental (62.8%), Holstein (24.3%), and Brown Swiss (2.8%) breeds. The remaining proportion includes crossbreeds (5.6%), and other minor breeds (4.3%) including indigenous breeds. Although the number of cows decreased in the past ten years (from 234,671 to 167,628), the number of cows in milk recording was constant. Dual-purpose traits, adaptability and long breeding tradition of Simmental (SIM) breed have a great relevance to the Croatian cattle production. SIM cows represent around 57.5% of all cows in milk recording. Holstein (HOL) cows are the second most important cattle population in Croatia. This breed is used mainly on enterprises specialized in milk production. The enlargement of existing farms, establishment of new farms, as well as the transition of medium sized and dual-purpose farms has led to a constant increase of specialized milk producing facilities. The proportion of HOL cows in milk recording was nearly 40% in 2016.

Phenotypic data collected through various recording schemes (milk and fertility recording, type classification, etc.), together with pedigree information, provide a basis for breeding value estimation (EBV). In the past decades, genetic progress in Croatian SIM and HOL cattle population has been low. Breeding organizations were not sufficiently powerful during the transition period to define rules of conducting the breeding program. At that time massive and, in most of the cases, unnecessary imports of heifers have occurred. Beside the justified use of bulls with a high BV, a lot of bulls used in artificial insemination could not provide expected genetic gain due to low BV. At that time, production of young bulls from the national breeding program was reduced to a minimum.

During the past five years, breeding organizations started to grow and recognized the importance of genomic selection program, which opens the possibility of revitalization through the production of competitive young bulls. The most important breed for Croatia is dual-purpose SIM, which is also raised in a limited number of countries (Germany, Austria, Czech Republic, northern Italy and Slovenia). Due to generally small population, the inclusion to joined German-Austrian genomic evaluation system in July 2013 was a reasonable solution. The participation was justified since bull's sires and bull's dams are coming from this population and there is a long-standing import of heifers and bull's semen. In contrast to SIM, the main goal of genomic improvement in HOL population is based on female calves in order to identify potential dams at a young age. These dams will be further inseminated via ET and usage of sexed semen to produce replacement heifers and to insure the market of female breeding material. For that purpose, selected Croatian female calves were included in the German Holstein genomic evaluation starting from March 2016. The inclusion was reasonable due to pedigree connection with German population through the long-standing import of breeding heifers.

The objectives of this study were to describe the steps in an implementation of genomic selection in a small population of Croatian SIM and HOL breed and to show the results of its implementation for Croatian candidates.

Material and methods

Agreement for Implementation of genomic selection is the main act which defines the rules and obligations of all participants involved in the implementation of genomic selection for Simmental and Holstein breed. The participants are: Simmental and Holstein breeding associations (BA's), Croatian Agricultural Agency (CAA), artificial insemination centres (AIC's), and scientific institutions (SI's). BAs are involved in the selection of potential candidates (male and female calves) and for using of semen of selected young bulls. CAA participates in the selection of potential candidates, updating

the herdbook and preparing the pedigree of candidates, performs analysis of genomic BV and is responsible for the publication of results. AIC's are also involved in the selection of potential candidates, they collect and send biological samples (blood or tissue) to the official laboratory, as well as purchase and hold the genomically tested young bulls. SI's have advisory and educational function in the implementation of genetic-population parameters. The main step in the implementation of genomic selection is a selection of potential candidates and all participants are involved in this step. Young male and female candidates are selected based on following criteria: a) they are progenies of the most interesting genomically and progeny tested sires; b) pedigree is important since the interesting sire and dam lines are considered; c) parent average is calculated in the case of Croatian sires; d) dam exterior has to be scored.

Altogether 260 SIM and 109 HOL calves were selected, genotyped and included in the genomic evaluation system. Genotyping is carried out using standard IlluminaBovine50K chip. Genotypes are bases for further genomic evaluation of candidates. For SIM breed, genomic evaluation is conducted monthly in German-Austrian genomic evaluation system for a total of 44 traits. A two-step approach using G-BLUP (VanRaden, 2008) is used for genomic evaluation of all traits. Direct genomic values (DGV) are estimated for all genotyped animals. These DGV are further blended with the conventional breeding values (EBV) or parent averages (PA) in combined genomic breeding values (GEBV) as described by VanRaden et al. (2009) including modifications (Edel et al., 2010). Genomic evaluation has been routinely conducted for German Holstein breed since 2010 for a total of 44 traits. The evaluation is based on a BLUP SNP model with a trait-specific residual polygenic variance as described by Liu et al. (2011). DGV and PA were combined based on selection index method (Liu et al., 2011) to obtain GEBV for all traits. GEBV are the officially published breeding values of a genotyped animal, either of SIM or HOL breed.

Results and discussion

For the Croatian SIM population, GEBV and DGV were estimated for 254 calves which are progenies of 60 bulls mostly of German or Austrian origin. In the case of HOL breed, 96 females with estimated GEBV and DGV were progenies of 51 bulls. The distribution of sires by year of birth in SIM and HOL breed is shown in figure 1.

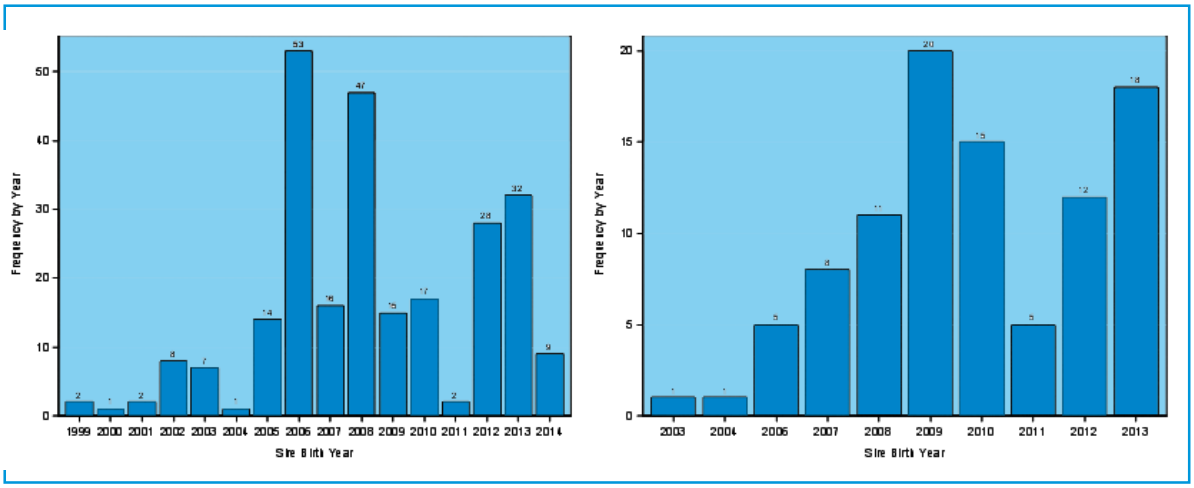

Figure 1. Number of progenies per bull in SIM and HOL breed

Distribution of GEBV (Figure 2a) showed a similar proportion of animals by classes of the standard deviation of GEBV by the trait group. The highest proportion of animals has GEBV which is one standard deviation from the average. The recommended criterion for entry of young SIM bulls in the centre for AI is total merit index over 130. On the basis of agreed criteria, seven young bulls were selected as bulls for AI. The figure 2a represents GEBV from the last monthly evaluation where only three animals have passed criterion. However, since the GEBV changes over time, the selected animals had met the criteria set in the given monthly evaluation. As a result of higher selection intensity on genomic bulls, the 1:35 ratio of selected and genotyped male candidates was observed which is similar to the ratio in other countries. At the national level, Croatia moved from a country that imported most of its genetics to a country which now uses own semen. The usage of genomic bulls has increased from 8% of all used bulls in 2012 to 23% in 2016. In addition, Croatian AI companies are now marketing semen of two young bulls internationally.

When calves were ranked based on GEBV, around 10% of them were incorrectly assigned to the top of the list compared to the rank based on PI evaluated in the genomic system. However, it is hard to compare PI between the national genetic evaluation and genomic evaluation since some bulls selected as sires are not progeny tested in our population. Furthermore, GEBV were not transformed to the Croatian scale due to the lack of transformation formula for many of traits. Another criterion for selection of candidates as bulls for AI is that they should not be carriers of known genetic defects or be recessive for them. In the German-Austrian genomic evaluation system, nine genetic defects specific for SIM breed were discovered. However, there

Figure 2a

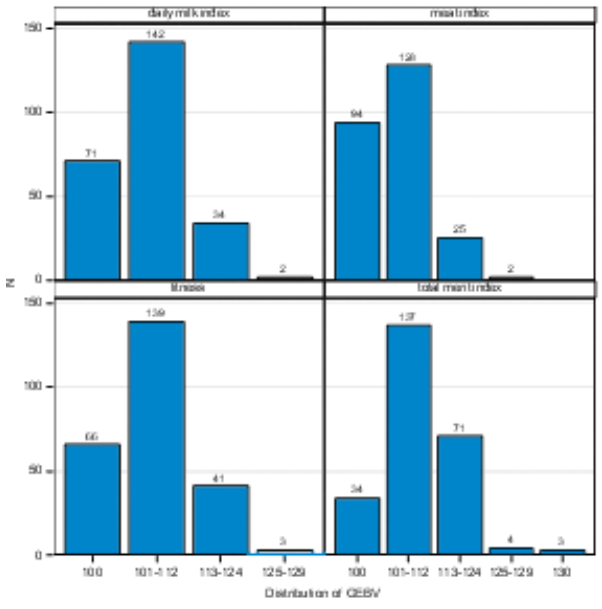

Figure 2b

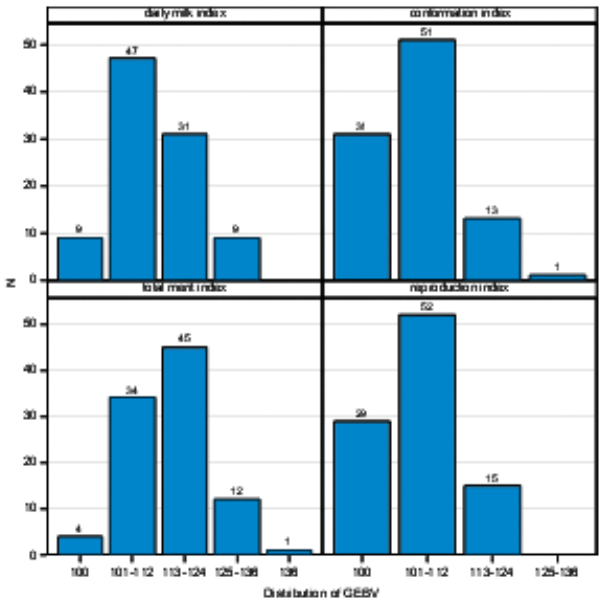

Figure 2a Distribution of GEBV for main group of traits in SIM breed .
Figure 2b Distribution of GEBV for main group of traits in HOL breed

are also data on traits like polled and kappa casein, which should be expanded over populations. The proportion of animals that carry one or more of genetic defects or is recessive for them decreased in the genotyped population since sires having defects are no longer used on genotyped animals or should not be in the dam's pedigree.

The recommended criteria for selection of HOL female candidates are a total merit index of 150, without gene defects and so far none of them reached these standards. Distribution of GEBV for the main group of traits (Figure 2b) was similar to SIM breed: the highest proportion of animals belonged to the group within one standard deviation from the average. However, there are selected HOL with a high genetic potential since animals having GEBV with two or three standard deviations better than average existed. Eight of genetic defects specific for HOL breed, were also detected using genomic information. The proportion of animals that are carriers of a specific defect was low.

An additional benefit of genomics, beside genomic evaluation and information about gene/disease defects, is parentage verification. The proportion of animals with pedigree conflict was low in SIM breed (0.04%). However, the proportion is higher (1%) in HOL breed which is coming from large farms. In the most of the cases pedigree was updated based on genomic data and offered potential sire which exists in German base.

Despite all benefits, some obstacles exist in the implementation of genomic selection in Croatia. Although genomics brings back to the breeders confidence in the national breeding program, the number of active breeders is small. There is still insufficient use of the bulls with a respectable either EBV or GEBV as bull sires. The price of implementation of genomic selection in SIM breed is still high. Furthermore, GEBV, DGV, and PI are given on German scale and one of the future steps will be an adaption of German system to the national. Since the past year, our population is dealing with lumpy skin disease threat and obligatory vaccination. Breeding Associations are in negotiations with a Ministry of Agriculture to exclude genomic calves from vaccination.

Conclusions

Croatian Agricultural Agency as milk recording organization is deeply included in genomic services through recording data, breeding value estimation and consequently parent average calculations, processing and publishing of the genomic evaluation results. At the farm level, genomics for females becomes an attractive option to capitalise benefits of using this technology. At the national level, Croatia has gone from a country that imported most of its genetics to a country which now uses own semen. The usage of genomic bulls has increased from 8% of all used bulls in 2012 to 23% in 2016. In addition, Croatian AI companies are now marketing semen of two young bulls internationally.

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Designing a reference population to accelerate genetic gains for novel traits in Canadian Holstein

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Abstract

Genomic selection has played a major role in Canadian dairy cattle breeding programs and has substantially increased the industry competitiveness worldwide. The development of the national health-recording program and various ongoing research projects funded by several Canadian and International organizations have led to the collection of a large number of phenotypes for novel traits. In order to remain a world leader in the competitive international market, it is key to include those traits in future breeding programs. Some novel traits (e.g., clinical mastitis and metabolic diseases) have been recently included in the Canadian national genetic evaluation, while other traits such as digital dermatitis, feed efficiency, immune response, methane emission, and fertility disorders are expected to be included in the near future. The size of the reference population (both phenotyped and genotyped animals) for these traits has a major impact on the accuracies of genomic estimated breeding values (GEBVs), and is presently the greatest limitation. Our current potential female reference population amounts to 20,000 cows for health traits, with an increase of approximately 4,000 cows per year. The number of genotyped cows with hoof health records is much smaller (below 5,500 cows). Therefore, the main goal of this project is to advance the rate of genetic progress for novel traits by enlarging the size of the female reference population for a variety of novel traits. The most cost effective strategy is to select cows that already have phenotypic records for novel traits (as well as the traditional traits), have not been preferentially treated based on their genetic merit, and are from herds that do not have any genotyped animals or are only partially genotyped. Thus, in addition to increasing the size of the reference population, it is key to design it in an efficient way by genotyping non-preferentially treated cows and individuals from herds that do not routinely genotype their animals but do collect phenotypes for traits of interest. A new genotyping strategy will be developed to maximize the imputation accuracy from low to medium density SNP panels, by integrating the right balance of low density and medium density genotyping within a given herd. The newly genotyped cows, in addition to the current reference population based on proven bulls, will allow more accurate estimation of genomic evaluations. A single step genomic evaluation is expected to be more useful for novel traits with limited

recorded populations. By improving the accuracy of GEBVs, the rates of genetic progress will be accelerated, thereby reducing the economic concerns and improving health, production efficiency, and welfare of Canadian dairy herds.

Keywords: Genotyping strategies, novel traits, female reference population, production efficiency.

Introduction

Which breeding goals should be prioritized to design the cow of the future? The answers to this question have changed substantially over time and across countries (e.g., Miglior *et al.*, 2005; Egger-Danner *et al.*, 2014; Miglior *et al.*, 2017). In a rapid growing society, with changing habits, and environmental conditions challenged by the consequences of industrial and technological advancements, efficient food production with reduced footprints is a top priority in the third millennium. The dairy cattle industry is expected to play a major role in this scenario. Fortunately, the majority of traits related to production efficiency in dairy cattle are under genetic control (Egger-Danner *et al.*, 2014) and in the past decades, sophisticated selection methods (e.g., genomic selection; Meuwissen *et al.*, 2001) and advanced reproductive technologies (Thomasen *et al.*, 2016) have enabled accurate assessment of genetic variability to advance genetic progress in various livestock species. The worldwide dairy cattle industry has excelled in the implementation of these novel technologies. However, key advancements are still needed to efficiently face new challenges and remain sustainable and competitive in the long term.

Genomic selection (GS) has been successfully implemented in Canadian dairy cattle and the rates of genetic gain have doubled for various economically important traits (Canadian Dairy Network, 2017), such as production, conformation, longevity and fertility traits (Figure 1). A key factor for this success was the development over the last decade of a well-designed and large size reference population (i.e., animals genotyped and measured for the traits of interest) for various traits that are routinely measured in Canada and other countries within the Intercontinental Consortium. This consortium includes Canada, USA, UK, Italy, Switzerland and Japan. All genotypes are routinely shared among all those countries, thus allowing each country to add foreign bulls to their local bull reference population.

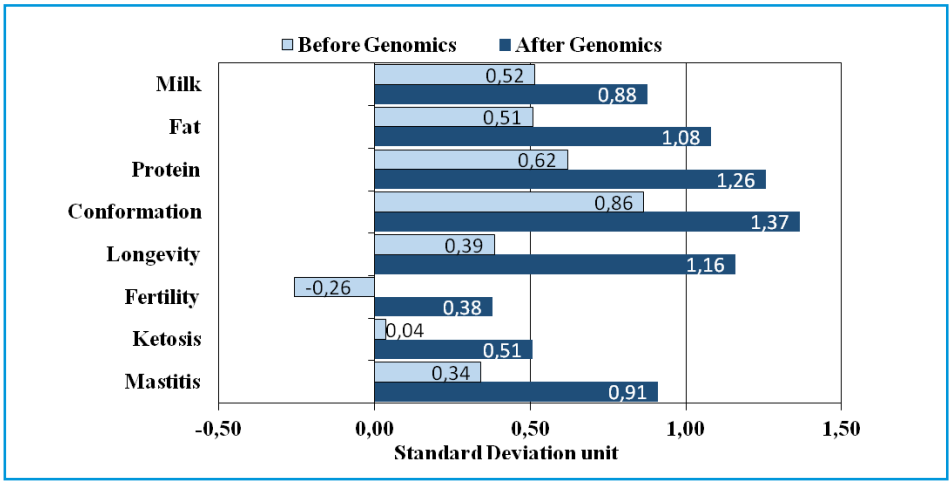

Figure 1. Impact of genomics on genetic progress for selected traits in Canadian Holstein cattle.

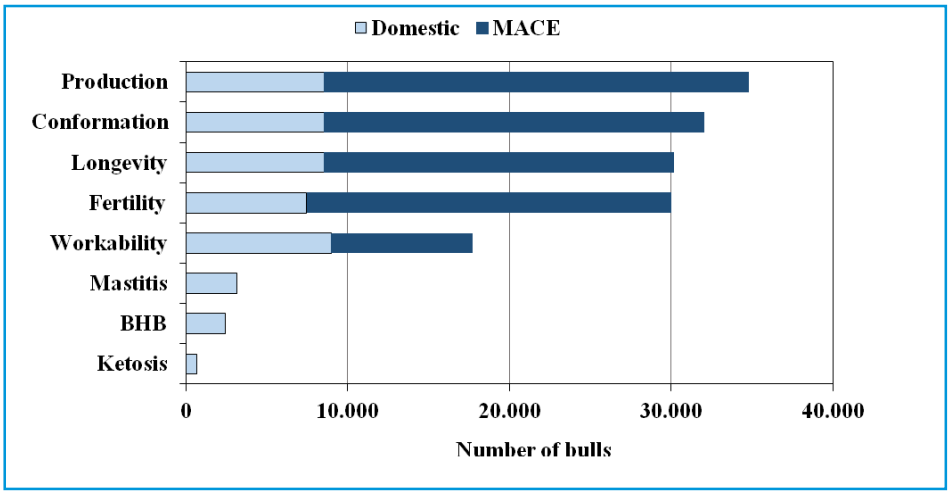

Figure 2. Size of male reference population by selected trait for Canadian Holstein cattle (April 2017 run).

In the April 2017 official genetic evaluation run, CDN (Canadian Dairy Network, www.cdn.ca) used the following reference bull populations for various group of traits in Holstein (Figure 2): 35,000 for production; 32,000 for conformation; 30,000 for longevity and fertility; 18,000 for workability; 3,000 for mastitis resistance; 2,400 for Beta HydroxyButyrate (BHB); and 600 for ketosis (the last three traits included only Canadian proven bulls while the remaining used international MACE evaluations as pseudo-phenotypes). For health traits and other novel traits, genomic selection (GS) is still limited, given that a) so far Canada and UK are the only countries evaluating those phenotypes within the Intercontinental consortium, and b) data collection has started relatively recently in Canada, thus a much smaller group of bulls have been evaluated for those traits. Such a limited reference population has a direct effect on the accuracy of genomic evaluations. Therefore, the objective of this paper is to present and discuss the work-in-progress and the near future plans of the Canadian dairy cattle industry to implement GS for a variety of novel traits aiming to address new challenges for sustainable production, and to address societal demands.

Novel challenges, novel breeding goals

As shown in Figure 3 with some traits taken as examples, genetic trends for various traits in Canadian Holstein cattle have substantially increased over time, highlighting the success of the adopted selection and breeding methods. However, livestock industries, including dairy cattle, are currently facing new challenges, which need to be addressed in order to remain competitive and sustainable in the long term. Little genetic improvement has likely been achieved for various traits known to significantly affect the economic efficiency of dairy cattle production such as feed efficiency. This is mainly due to the difficulty and cost to accurately measure this trait (or indicator traits) in a large number of animals. Furthermore, small or negative genetic response has been observed for some low heritability traits such as fertility, reproduction and disease resistance. This might be due to: a) the lack of accurate phenotypes for these traits; b) non-inclusion (or insufficient weighting in the national selection indexes) of these traits in the breeding objectives. Additionally, the effects of climate change have become more evident, highlighting the need to genetically select for adaptation to

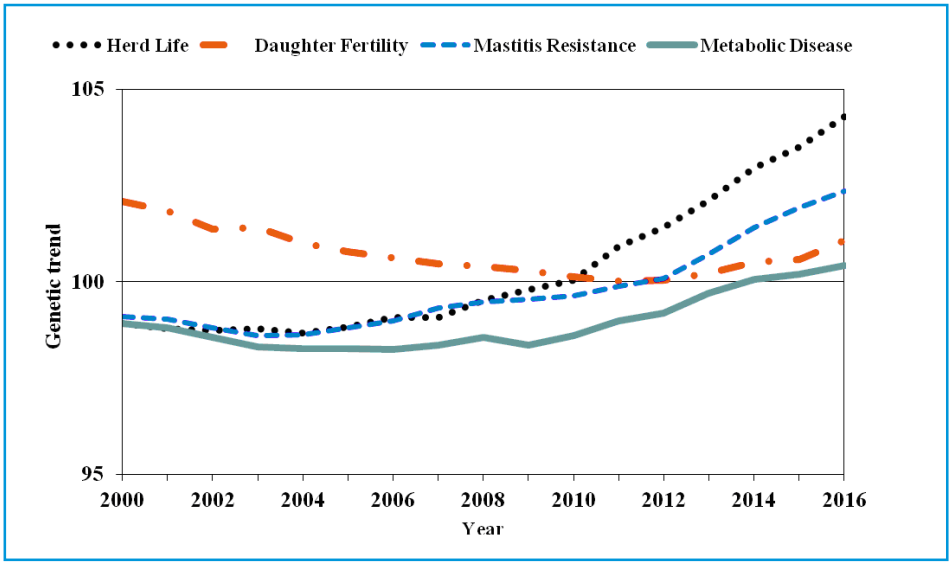

Figure 3. Genetic trend for selected traits in Canadian Holstein cattle (SD =5 for included traits).

extremer temperatures and harsher environments (Misztal, 2017). There is an opportunity to use novel strategies to advance genetic progress more rapidly for traits related to animal health, fertility, welfare, nutritional properties of milk and reduced environmental footprints.

The development of the Canadian national health-recording program in 2007 and various undergoing research projects funded by several Canadian and international organizations have led to the collection of a sizeable number of phenotypes for novel traits. These traits include feed efficiency, methane emission, clinical mastitis, metabolic diseases (ketosis, displaced abomasum, and indicator of disease, i.e., milk BHB), fertility disorders (metritis, cystic ovaries, and retained placenta), and hoof health (digital dermatitis and other hoof lesions). It has been estimated that the inclusion of genomic selection for novel economically important traits will generate an additional $200 million/ year in annual net benefits to the industry due to increase in genetic progress for new relevant traits (Chesnais, 2016).

How to implement or increase the efficiency of genomic selection for novel traits?

A large reference population is essential for a precise and accurate estimation of marker effects, which leads to reliable genomic estimated breeding values (GEBVs) (Meuwissen *et al.*, 2001; Goddard, 2009; Hayes *et al.*, 2009). Despite the large size of the Canadian reference population for routinely measured traits (i.e., performance, reproduction and conformation), there is still a great need to increase the size of the reference population for novel traits of relevance to the industry, as already described.

Various alternatives to increase the size of reference populations for GS have been sought worldwide. One is to enlarge the reference population by including individuals from the same breed but from different countries (Cooper *et al.*, 2016). However, there are limitations to the implementation of this strategy for novel traits in Canada. Due to great advancements in the Canadian dairy breeding programs, the novel traits of interest here are also novel traits elsewhere, which means that there are not many phenotypes available in other countries to allow a shared reference population yet,

even though there are important initiatives in progress. Another option is to combine the breed-specific reference population with other breeds (Hayes *et al.*, 2009; Olson *et al.*, 2012; Hozé *et al.*, 2014). However, the great majority of dairy cattle in Canada are Holstein, which limits the feasibility of multi-breed reference populations. A third option is to include cows in the reference population (Pryce *et al.*, 2012; Calus *et al.*, 2013; Cooper *et al.*, 2015), which is considered the best alternative at the moment.

It has also been reported that when only a small part of the population has both phenotypes and genotypes and other related animals are also phenotyped, single-step genomic evaluation methodology gives more accurate results than other methods. Currently, there are around 50,000 Holstein cows with production records genotyped in the CDN database, with a yearly increase of around 10,000 cows. Given that 40% of milk recorded herds collect health data, we can assume that we currently have a potential female reference population of 20,000 cows for health traits, with a yearly increase of 4,000 cows. The number of cows with hoof health records is currently much smaller (total of ~ 6,500 cows genotyped and phenotyped).

Female reference populations

Cows that are usually genotyped by breeders used to be elite cows, which could cause a preferential treatment bias. Because of concerns about biased elite cow traditional evaluations, females have not been included in the reference populations in Canada (Schenkel *et al.*, 2009), Germany (Reinhardt *et al.*, 2009), and New Zealand (Spelman *et al.*, 2010). A feasible solution is to genotype non-elite cows and also animals from herds that record phenotypes but have not yet started genotyping their animals.

The importance of developing a large and well-designed reference population for novel traits based on females' data can be further justified, as with the wide use of genomics bull reference populations are expected to become less informative (i.e., on average smaller breeding value reliabilities of bulls and cows). This is due, among other factors, to the random progeny testing programs that have stopped or reduced drastically since the adoption of genomics and the smaller number (on average) of daughters per proven bulls. In addition, it is important not only to increase the size of the reference populations for novel traits, but also to design them effectively in order to maximize the benefits of genomic selection. This can be achieved by creating a random and least-selected reference population covering the whole genetic variability of the population. A quick start in genomic evaluations for these new traits is only possible using genotyped animals with own performance, which includes the development of a female reference population.

Some studies have investigated alternatives to the inclusion of cow information in genomic programs. As discussed by Chesnais *et al.* (2016), for traits that are expensive or difficult to record (e.g., feed efficiency, methane emission, immune response), genotyping all animals with phenotypes is more efficient than using, for example, only the genotypes of their sires, even if those are already available. The use of a cow reference population is, therefore, the most cost-effective way to generate genomic evaluations for such traits (Van Grevenhof *et al.*, 2012; Calus *et al.*, 2013).

The development of these reference populations for novel traits will become more feasible as technological advancements make it easier to collect phenotypes for many of these traits (Chesnais *et al.*, 2016). For instance, some new traits/measurements are derived from sensors on farm (e.g., locomotion, heat detection, rumination), derived from additional data analyzed by labs (e.g., spectral data, hormones' status), collected by veterinarians, producers and technicians (e.g., disease incidence or claw health collected by hoof trimmers and health traits recorded by farmers). For such traits, the

main challenges are ensuring national standardization of data collection and the development of data pipelines and expansion of a national database (Chesnais *et al.*, 2016; Miglior *et al.*, 2016). There are many herds in Canada that have measurements for various traits mentioned above; however, some of those herds are still not genotyping their cows. Therefore, genotyping thousands of non-elite cows originating from these herds with known history of excellent quality of recording for (some) novel traits, in addition to other routinely recorded traits, is a priority for the Canadian dairy industry.

Strategies to incorporate cows into reference populations have been reported. For instance, using simulated data, Montero *et al.* (2012) studied optimal genotyping designs that includes females in the reference population and suggested that two-tailed strategies (i.e. genotyping based on extreme phenotypes for the traits of interest) are preferable to increase the reliability of genomic selection (Jenko *et al.*, 2017). Another possible approach is to select a group of genotyped cows in the same breed that mimics the population structure in which selection for the novel trait will be applied. This should be done for both reference and candidate animals. It would not matter that these animals do not have a novel phenotype, as long as the structure of the population resembles what will eventually occur in practice (Chesnais, 2016).

Thomasen *et al.* (2014) reported that the inclusion of cows in the reference population increased monetary genetic gain and decreased the rate of inbreeding. In addition, they showed that genotyping cows is a profitable investment. Buch *et al.* (2012) showed that a reference population consisting of cows with a specific phenotype resulted in higher reliability compared with a reference population only including the sires of these cows. Similarly, to maximize the accuracy of GEBV, Van Grevenhof *et al.* (2012) found that the same individuals should be genotyped and phenotyped instead of genotyping parents and phenotyping their progeny. The inclusion of cows in the reference population will also decrease the generation interval in the dam-bull pathway and significantly contribute to genetic gain within the population as a whole. Moreover, validation studies based on random samples of genotyped Holstein cows in North America showed that the accuracy of genomic prediction using a cow reference population is even larger than that predicted by the Daetwyler formula (Chesnais *et al.*, 2016).

What else is needed for successful breeding schemes incorporating genomics?

Other than enlarging the reference populations for novel traits, there are other methodologies that need to be applied to increase the accuracy of GEBVs. Firstly, all cows that are genotyped using a lower-density panel can be successfully imputed to 50K and up to whole-genome sequence (Larmer *et al.*, 2012, 2016; VanRaden *et al.*, 2012). This imputed genotype data can be used for genome-wide association analysis (GWAS) and further fine mapping aiming to identify causal mutations affecting the traits of interest. The inclusion of more informative SNP markers and/or more trait phenotypes to train the SNP effects can be incorporated into the Canadian dairy cattle breeding programs to further increase the accuracy of GEBVs. A functional analysis of the identified gene will improve the biological understanding of the genetic control of the traits. There is indeed a growing interest in examining interactions among genes and networks of genes that underlie traits of interest (Fortes *et al.*, 2011).

Other sources of information that can be incorporated into genomic evaluations need to be investigated and the recent developments and availability of "omics" technologies provide new opportunities for generation of relevant additional information. This information could characterize either the animal itself, or its microbial environment involved in nutrition as the rumen flora or in infectious diseases such as mastitis or

metritis. Some applications have already been investigated. For instance, to predict meat quality (Guillemin *et al.*, 2011), as well as different kinds of diagnostic tests for infectious diseases (e.g., Koskinen *et al.*, 2009).

Single-step genomic BLUP (ssGBLUP) is a method that combines the pedigree relationship matrix (A) with the genomic relationship matrix (G). By including genotyped and non-genotyped animals simultaneously in the evaluation, ssGBLUP method has the potential to yield more accurate and less biased genomic evaluations (Aguilar *et al.*, 2010; Christensen and Lund, 2010). In addition, other benefits of ssGBLUP include simplicity of application (another BLUP), avoidance of double counting, and (at least partially) accounting for pre-selection on Mendelian sampling (Legarra *et al.*, 2014).

Building the future

Research projects and initiatives led by Canadian institutions are aiming to generate tools to accelerate the rate of genetic progress for novel traits by designing an enlarged female reference population for genomic prediction of novel traits via ssGBLUP and to investigate the incorporation of additional "omics" data in Canadian dairy cattle breeding programs. The most cost effective strategy seems to be to select cows that already have phenotypic records for the novel traits, have not been preferentially treated based on their genetic merit, and are from herds which do not have any genotyped animals or are already partially genotyped. The majority of the animals will be genotyped with lower-density SNP chip panels and accurately imputed to 50K and then up to the whole-genome sequence genotypes (Larmer *et al.*, 2014, 2016). In addition, various other ongoing research projects have been generating other "-omics" data for a variety of important traits (e.g., fertility, feed efficiency and methane emission) that can potentially be incorporated to genomic evaluations in order to increase the accuracy of genomic breeding values.

Conclusions

A major constrain in the application of genomic selection for novel traits is assembling large enough reference populations to enable accurate predictions. Alternatives to enlarge reference populations for novel traits in Canadian Holstein have been investigated. By improving the accuracy of GEBVs, the rates of genetic progress will be accelerated, which is expected to generate an additional $200 million/year in annual net benefits to the industry and bring more health, production efficiency, and welfare into Canadian dairy herds.

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(Edmonton, Canada), Victoria Agriculture (Australia), Scotland's Rural College (Edinburgh, UK), USDA Agricultural Research Service (United States), Qualitas AG (Switzerland), Aarhus University (Denmark).

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Body weight prediction in Italian Holstein cows

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Abstract

Body weight (BW) is an important trait used in order to control maintenance cost within herds. It is unfeasible to get routine data collection on BW, but BW can be estimated from routine type classification scores. Body weight for Italian Holstein cows was estimated based on actual BW and linear scores for different type traits of 890 first parity cows collected in 30 different herds over a 3-yr period (2013-2015). Actual BW was collected thanks to availability of automatic weighting systems in milking robots. The selected type traits used to predict BW, included stature, chest width, body depth, rump width and body condition score. The predictive ability of models was tested with 2-fold cross-validation. Correlation between predicted BW in training and validation data-sets ranged from 0.62 to 0.70. The model used for actual BW genetic parameter estimation included herd-year-season of weighted cows, month of calving, age at scoring and interval in days (±30 days) between the weighing and the scoring days. Heritability for actual BW was 0.51±0.06. The BW prediction equation was applied to the national routine type classification data. Average actual BW was equal to 598.24±73.00 kg and average predicted BW was equal to 597.21±40.94. Genetic relationships of predicted BW with type traits included in the prediction equation have been estimated. Heritability for predicted BW was equal to 0.21±0.01. At this stage the derived BW prediction equation has been used in the new economic functional index (IES) for the Italian Holstein population. Next steps will be to make use of this trait in order to develop a proxy for feed efficiency breeding values to include in the national evaluation system.

Keywords: Body weight, automatic milking system, genetic parameter, feed efficiency.

Introduction

Body weight (BW) is an important trait used in order to control maintenance cost within herds. This trait can be also involved in the calculation of energy balance (Coffey *et al.*, 2001).

The costs of milk production are mainly related to feed costs, and lately there is a growing interest in improving feed efficiency in dairy cattle. This is defined as the ratio between milk production and dry matter intake. Dry matter intake is a very interesting trait for management and would be interesting to include in a breeding goal in order to select individuals who produce more but simultaneously ingest less dry matter.

Unfortunately, it is not easy to collect this trait at population level. In the past, several models and different formulas have been developed to estimate feed efficiency from other traits. Animal body weight is an important factor in managing the cost of managing livestock and in order to derive animal efficiency, not only at farm level, but above all at the individual level. Body weight is not easily routinely recorded but it can be derived by other traits routinely recorded by the national system. Aim of this paper was to set up an algorithm to predict body weight (pBW) in Italian Holstein cows, using type traits officially recorded, and to estimate heritability values for actual and predicted body weight.

Materials and methods

Initial data-set consisted of 6,895 individual weights belonging to 3,256 Italian Holstein cows distributed in 36 farms. Actual BW was collected, over a 3-yr period (2013-2015), thanks to availability of automatic weighting systems in milking robots. Data have been merged with routine linear score data-set. Only fist parity records with a maximum interval of 30 days between weighting and linear scoring dates have been retained. Final data-set consisted of 890 first parity cows belonging to 30 different herds. The following final model was used to derive a phenotypic prediction equation for body-weight:

Y= HYM + MC +SL + predictors + e.

where
Y = actual body-weight;
HYM = herd-year-months of weighting;
MC = month of calving;
SL = stage-of-lactation.

Other predictors: age of cow at scoring and stature, chest-width, body-depth, rump-width and body condition score (if available). The fixed effect were determined in a series of preliminary analysis in which the effect of various factors on body-weight were assessed. Factors included in the model were those with the highest significant effect on body-weight. Based on stepwise regressions estimators have been identified. The data-set has been splitted in training and validation sets. Algorithms have been developed in the training data-set (70% of total data-set) and tested on the validation set (30% of total data-set). Solutions were applied to the validation set using the following formula:

$Y = \text{constant} + b * \text{age-at-scoring} + \Sigma\beta * x$

where
Y = predicted body-weight phenotype of cow;
constant = sum of solution of the overall mean effect and average solutions of HYM + MC + SL effects;
b = estimate of slope of regression on age of cow at scoring and
β = estimate of slope of regression on conformation trait (x) summed over all conformation traits.

Predicted body weight was compared with the actual body weight in the testing data-sets. The final model has been chosen based on higher R^2, lower root MSE, and correlation between real and predicted body-weight. Subsequently the algorithm developed has been applied to the national data-set. A model similar to the official national evaluation for conformation traits has been applied and genetic parameters for the traits have been estimated.

Table 1. Descriptive statistics and genetic parameter estimation for real and predicted body weight in the validation set.

Trait	Mean±SD	Range	h^2±SE
Actual body weight (kg)	598.24 ± 73.00	427 – 821	0.50±0.06
Predicted body weight (kg)	598.29 ± 46.45	453 – 742	

Results and discussion

In Table 1 are reported statistical descriptions of actual and predicted BW, in the group of validation animals. As expected, predicted BW (pBW) showed similar average and lower standard deviation compared to actual BW (aBW). Once the algorithm was tested on the validation data set was tested we applied the prediction formula on the whole conformation database. At population level, pBW for primiparous and multiparous cows were 567.26±44.00 and 680.00±55.57 kg, respectively. Heritability for actual BW was equal to 0.50 (±0.06), while at population level, pBW showed a lower heritability and equal to 0.21±0.01. Results of this study are comparable to what has already been published by other authors (Haile-Mariam *et al.*, 2014) .

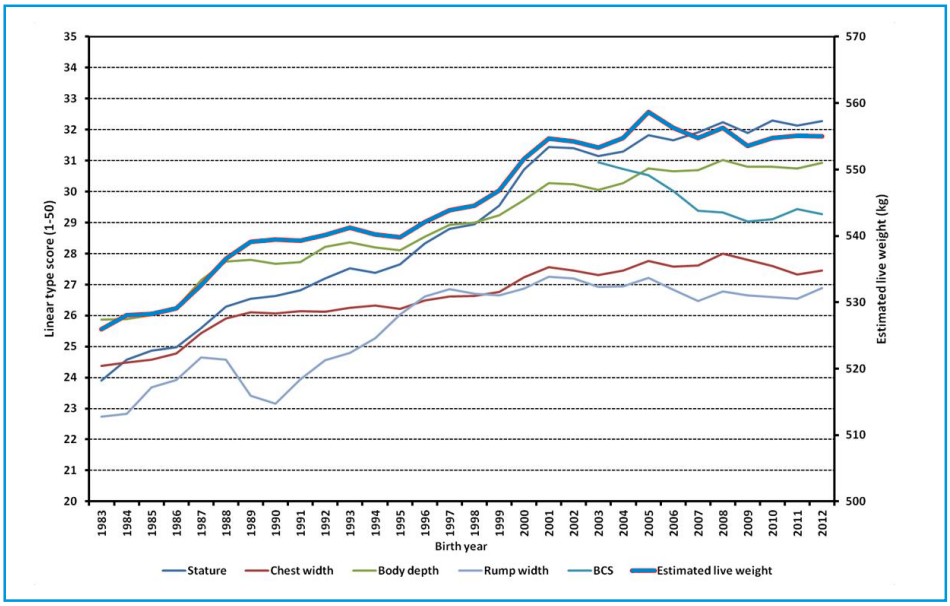

Figure 1. Trend of phenotypic type traits and live weight across years for Italian Holstein.

Figure 1 shows the trend for cow's year of birth for type traits included in the prediction formula for pBW. It is evident that until 2005 they animals gained weight, and in more recent years the weight trend remains stable and equal to all type traits included in the formula, with an evident reduction for body condition score. Knowing the increment of milk yield in the last years, this result is an evident result of the production improvement of the whole Italian Holstein population.

Conclusions

An algorithm was set up in order to predict body weight in Italian Holstein cows, using type traits. Heritability value of predicted body weight was estimated and a moderate value was obtained. Therefore, a tool for herd management and monitoring animals is now available for calculating animal maintenance costs, and moreover to estimate

feed efficiency and methane emission by rumen. An indirect way is now available for Italian Holstein for implementing new traits to improve profit for farmers and, moreover, to mitigate greenhouse gasses emission. At this stage the derived BW prediction equation has been used in the new economic functional index (IES) for the Italian Holstein population.

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Lactose in milk - How can lactose concentration data be beneficial in management and breeding?

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Abstract

Lactose is a major component of milk dry matter, but it has by tradition not been highly valued. More recently, dairy processors have invented methods to refine lactose and found markets that pay well for refined lactose. However, in Denmark, milk payments are based on kilo fat and kilo protein and a negative price on volume, but without adjustment for lactose content. For herd management, the requirement of individual cows depends on all components in the milk, often summarized as "energy corrected milk, ECM" where the lactose accounts for around 750 kJ of the 3140 kJ/Kg ECM, or 24% of the energy in Holstein milk and 18% in Jersey milk. The 24% and 18% are average fractions that varies between cows and within cow with lactation stage and parity number. Also, results from controlled studies have shown how feeding can affect lactose concentrations in milk. These effects are often hidden because lactose is not measured in milk from test days, despite that the results can be obtained by simply switching on this option on the infrared analyzer instruments.

Feeding rations with higher energy concentration, either with higher concentrate proportion or with forages with higher digestibility, resulted in increases in milk lactose concentrations between 0.05 and 0.10 % units.

There are systematic effects of parity so that older cows with higher yield have less lactose in their milk than first parity cows. During lactation, lactose percentage follow the shape of the yield volume curve, so that peak concentrations are found at 50 to 70 DIM, followed by a steady decline, in parallel between first and later parities. Systematic breed differences are small between Red Danish Cattle and Holstein but Jersey have somewhat lower lactose concentrations than the larger sized cows.

Lactose concentrations are much less variable that fat or protein concentrations, but individual differences were clearly detected with repeatability estimates in the range of 0.70 up to 0.90, within lactation. Estimates of heritability are scarce in literature and results from experimental herds show estimates in a range similar to that of protein concentrations. There is clearly a lack of estimates for heritability, but more importantly estimates of genetic correlations to other production traits or health traits are very few.

In conclusion, there is a need to investigate how lactose from test day samples can benefit management and breeding, so large volumes of data to support this should be obtained from simple expansion of the range of milk components determined in the test day schemes.

Keywords:Lactose, ECM, test day samples, feeding, genetics.

Introduction and background

Lactose is a major component of milk dry matter, but has hitherto not been highly valued. More recently, dairy processors have invented methods to refine lactose and found markets that pay well for refined lactose. This prompted us to revisit the feasibility of analyzing cow test-day samples for lactose content, with a view to utilize the information in feeding, management and genetic selection. Moreover, this should be an easy step as the base data is readily available from already running MIR based analyzers.

Lactose in milk constitutes 4.5 to 5.0% and is less variable that protein and fat content, and constitutes between 18 and 25% of the energy content in milk. Lactose is a disaccharide composed of one glucose and one galactose that can be enzymatically split by lactase. In-vivo lactase is found in the digestive tract of young mammals, but lactase disappears with advancing age in some individuals who then become lactose intolerant. A similar lactase based process is used industrially to make "lactose-free" milk, which is well tolerated.

There is an increasing world market for lactose as a component in pharmaceutical products, in baby milk and in a range of specialty foods. Dry milk powder, especially "infant formula" is required to hold a certain percentage of lactose, which is not met directly if based on Jersey milk. Lately some milk processing inventions has led to factories able at separating and purifying lactose from milk and especially from whey. Purified lactose is sold on the world market, and some European dairy processing companies are now adjusting payments according to lactose content or rather to delivered amounts of lactose, whereas others have not implemented this practice.

Test-day milk samples are collected and analyzed using MIR spectral data which are turned into concentrations of fat, protein, lactose, citric acid, urea, and a range of fatty acids, all depending on which calibration algorithm is used on the given instrument. All calibrations need regular maintenance from operators, and often license agreements add cost for every new analyte requested. In the next step, herd managers must have an idea on how to utilize the information returned, and in a final step genetic evaluations and selection index procedures need to be revised according to genetic parameter estimates. In this study, we aimed at collecting data from a range of published results and some unpublished studies, in order to evaluate the feasibility of adding lactose to the panel of components included in the base panel at milk recording laboratories. To do so we investigated normal biological variation, effects of feeding regimes, and genetic variation, and co-variation with related traits. Hence, the approach is a literature review supplemented with some minor investigations on own data.

Biological variation in milk lactose content

Holstein cows kept at the Danish Cattle Research Centre (DCRC, AU-Foulum, Denmark) milked in AMS are considered representative for high yielding TMR fed cows Denmark and in northern Europe. In their first parity we have observed the yield characteristics shown in table 1, with an average lactose percentage close to 5.0 ranging between 4.49 and 5.44. Lactose is here expressed as the mono-hydrate form, where

the corresponding values for the anhydrous form would be smaller (mean = 4.86%; molar weights 360.3 and 342.3, respectively, see Table 1).

The experimental herd at DCRC also comprise Jersey cows, and cows are kept for the first 3 parities. Milk samples were collected at weekly test sessions covering 48 hours with all samples assayed. This allowed insights to the development over lactation as shown in Figure 1.

Table 1. Yield characteristics of first parity Holstein cows at DCRC, mean and percentile ranges.

	Mean	P_05%	P_95%
Lactose %	4.97	4.49	5.44
Protein %	3.54	2.97	4.19
Fat %	4.20	3.17	5.49
Milk Kg/d	28.3	17.3	39.0

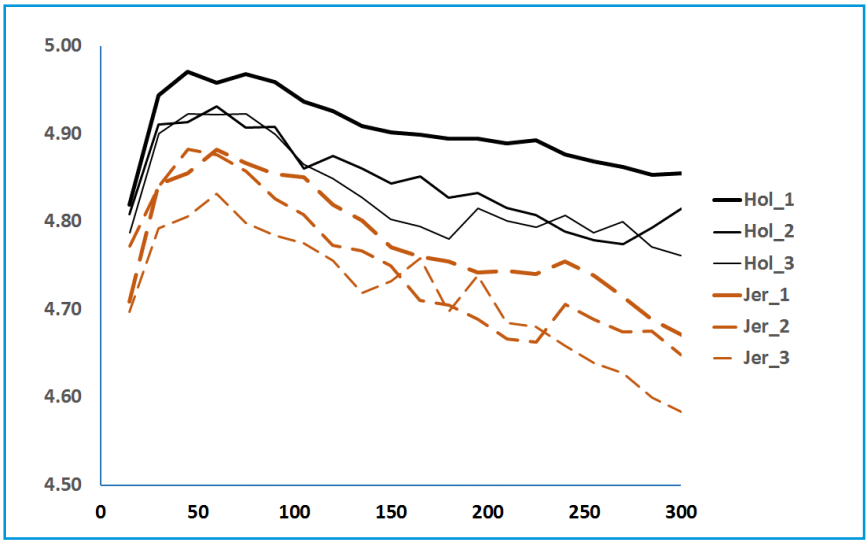


Figure 1. Lactose concentration (%) in Holstein and Jersey milk during 300 days of lactation in the first 3 parities.

The "lactation curves" for lactose percentage clearly follow the shape of those for milk yield, but the changes in level between parities are opposite, so that older cows, although having higher yield also have lower lactose concentration in their milk.

Energy content of milk

Lactose is energy rich and for calculation of Energy Corrected Milk (ECM) Sjaunja *et al* (1990) used the following formula:

1. ECM = Milk(Kg)*(383*Fat% + 242*Protein% + 157*Lactose% + 20.7) / 3140,

   where 3140 is the energy content in KJ, and the other coefficients are energy contents of each component. The 20.7 is covering energy in citric acid and other minor components outside the standard panel of milk components. In case lactose is not available the alternative is Fat and Protein Corrected Milk given by a very similar formula (Sjaunja *et al.*, 1990):

2. FPCM = Milk(Kg)*(383*Fat% + 242*Protein% + 783.2) / 3140,

   where the lactose content is considered constant at 4.86%. Although FPCM is a useful proxy for ECM there will obviously be some deviation between the two calculations, and given the changes in yield and lactose% over lactation these differences will show a systematic pattern (Figure 2) as illustrated with Holstein data from DCRC.

Although the deviations may seem small using only fat and protein corrected milk would systematically underestimate the energy produced by young cows and more so in early than in late lactation.

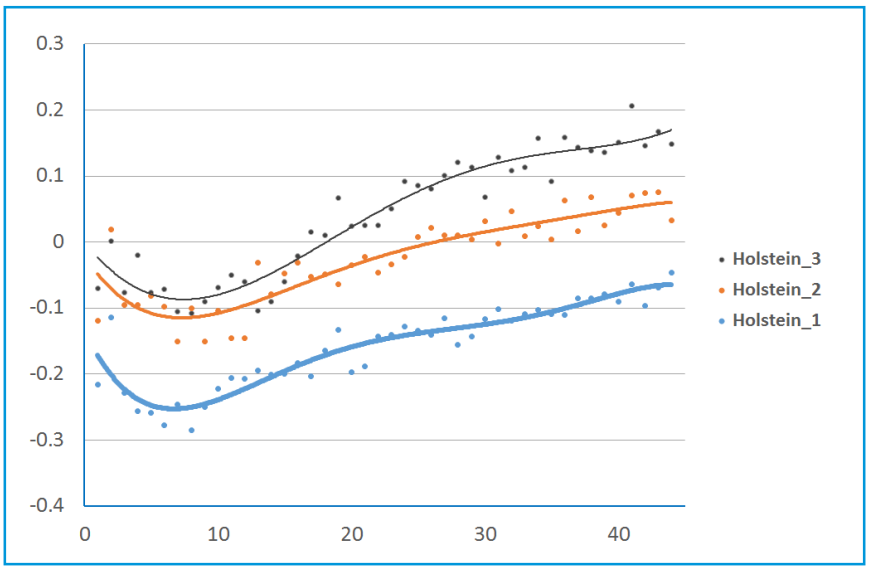


Figure 2. Deviations between FPCM and ECM (FPCM - ECM in Kg/d) yield in Holstein cows during their first 3 lactations at DCRC. X-axis is week of lactation.

Feeding effects

The composition of the feed ration can impact on lactose% as shown by Andersen *et al.* (2003). In the first 16 weeks after parturition a group fed high (75%) concentrates had higher lactose (+0.13% units) than a low (25%) concentrate group. In the same experiment, cows were milked either 2 or 3 times per day, but that had no effect on lactose percentage. Cows on high concentrates were also having larger energy intake and yielding more ECM.

Genetic effects

Genetic variation in lactose% was recently reported for pasture fed Holstein cows in Australia (Haile-Meriam & Pryce, 2017), together with lactose yield and other yield traits. While the heritability for lactose percentage was moderate to high, around 0.30 in mid lactation, the heritability for lactose yield per day was lower, around 0.10 to 0.20. With data from an older experiment, Løvendahl *et al.* (2003) found somewhat higher heritability for lactose%, and found that it changed over lactation, and was slightly higher in second than in first lactation (Figure 3). These parameters were estimated using a random regression model, and it should be noted that changes in heritability followed a similar pattern in first and second parity.

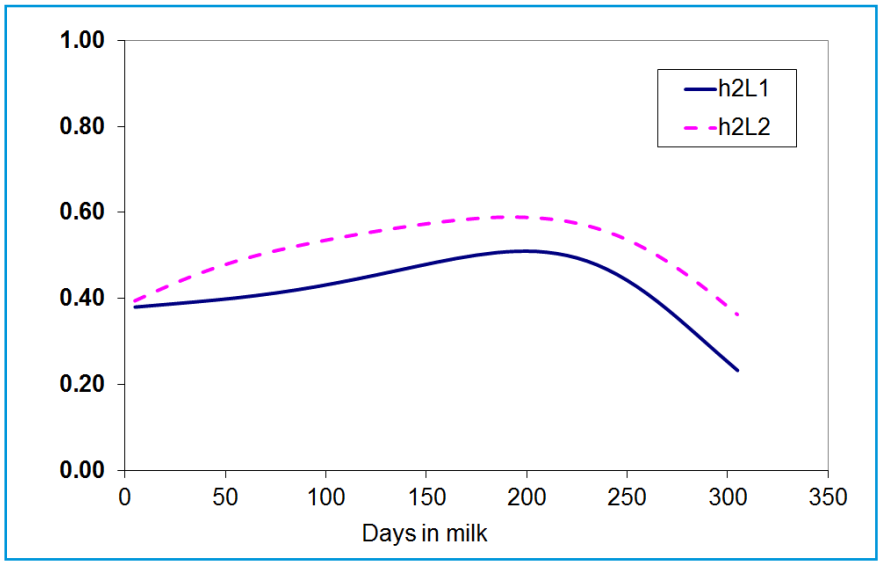
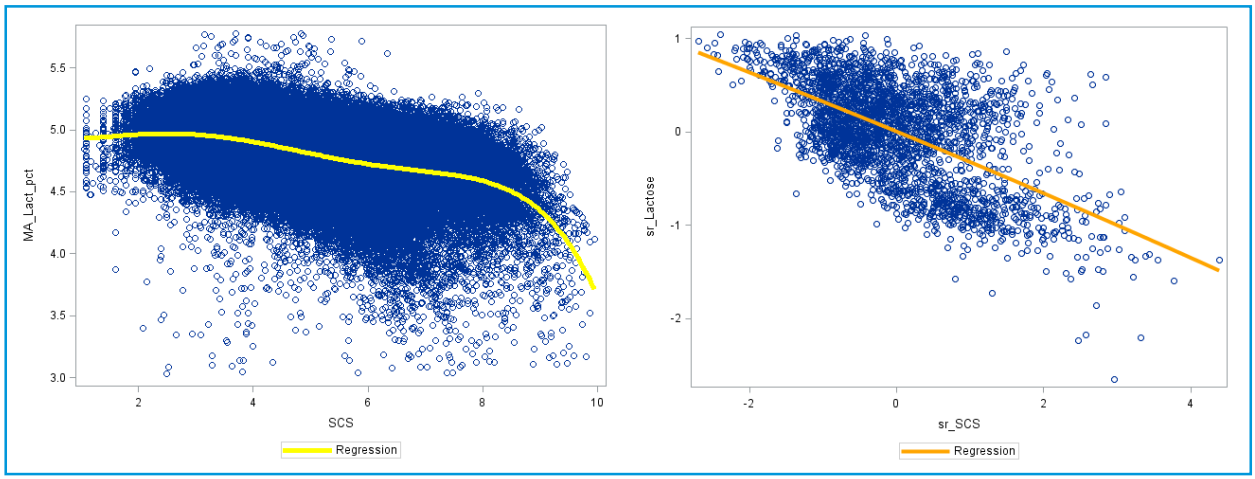


Figure 3. Heritability estimates for lactose percentage in first and second parity cows (from Løvendahl et al*. 2003).*

Correlations between traits

Out of curiosity, we have further investigated the relationships between lactose% and somatic cell score in samples for our experimental herd (DCRC). What we found was a negative correlation (r = -0.44) between lactose% and SCS (Figure 4a), when considering single samples slightly smoothed using a moving average. In a next step extracted random animal solution from linear mixed models, centered around zero, and obtained a stronger and still negative correlation (r = -0.59; Figure 4b).

The relationships between lactose and somatic cell count may be caused by biological events or alternatively by bias in lactose calibration when milk samples contain high amounts of cells, as it is well known that samples with high cell count (i.e. mastitis) also have deviating fat and protein percentage, and often yield is affected too. Thus, the presented relationships need to be further investigated to validate and qualify the findings.



Figures 4a, 4b. Relationship between Somatic Cell Score and lactose% in single milk samples (4a, left) and between random cow-solutions (centered around zero) from a linear mixed model for the same traits.

Conclusion

This study has shown that lactose content of milk varies with age of cow, stage of lactation, breed, feeding level, and that it has sufficient heritability so that genetic selection could be used to change lactose content. The findings of a negative correlation between SCS and lactose percentage indicate that selection for higher lactose content would not harm udder health, or rather it would be somewhat beneficial. This is fortunate because the market for lactose is increasing so that larger production of lactose should be encouraged. A required instrument to this is routine assaying of test-day milk samples for lactose. This is easy to establish in most milk labs if not already running.

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Genetic analyses of ketosis and a newly developed risk indicator in Fleckvieh, Braunvieh and German Holstein

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Abstract

Data related with health traits of cattle can be used to improve and to optimize the management of dairy herds in a short term. Using these data in a breeding context will improve the health status in herds and in the whole population in the long term. In Baden-Württemberg data for direct heath traits were collected in a health monitoring project since 2012 (GMON) and used in an across-country evaluation of breeding values for the breeds Fleckvieh (dual purpose Simmental) and Braunvieh (German Braun Swiss). Four different diseases or disorders are evaluated at the moment. But due to the data collecting scheme only the more severe cases are usually recorded and used in the breeding value evaluation. The frequency of recorded cases for metabolic disorders is generally very low. This and the binary character of the traits lead to very low estimates for the heritabilities. Therefore the utilization of other data sources which also can detect subclinical cases especially for metabolic disorders would be very interesting. In 2015 a model for the prediction of ketosis risk has been developed at the German milk recording organization LKV BW. The model is based on routinely registered ketosis diagnoses by veterinarians. Data from 396 farms with a total of 112.545 milk samples linked to healthy cows and 194 samples linked to ketosis were available for model calibration and validation. The samples were collected on Fleckvieh, Braunvieh and German Holstein cows during the first 120 days in milk. Ketosis risk probability was modelled by using a Lasso regularized generalized logistic regression model on a combination of standard milk recording parameters and milk components calculated from standardized milk mid infrared spectra (MIR). The final model showed robust prediction results and has been applied since October 2015 on the LKV BW dairy population in order to provide the farmer with ketosis risk indicators in the early lactation stage. Genetic analyses for ketosis and one of the ketosis risk indicators (KetoMIR-index) were conducted. Via the GMON project direct observed cases of ketosis were analyzed as a binary trait, while the KetoMIR-index has quantitative characteristics. Next to these two traits data from the standard milk recording scheme are used to estimate genetic correlations between the ketosis traits and the performance traits in the three breeds. Heritabilities for the KetoMIR-index are considerable higher than for ketosis itself. It looks promising that the estimators for the heritabilities and the genetic correlations might be used in the routine breeding value evaluation in order to lower the impact of a metabolic disorder like ketosis.

Keywords: Ketosis, risk indicator, heritabilities, genetic correlations

Introduction

Ketosis is a metabolic disorder in ruminants. Indigestion, decreasing food consumption as well as very high milk fat percentages and a rapid decrease in total milk yield are some symptoms of this disorder. As a result, infection risk and the susceptibility for other diseases increase. Also, fertility declines. Ketosis is boosted by various factors: for example, this can be feeding mistakes but also genetic factors. Different authors showed low heritabilities for metabolic diseases or problems (Stock *et al.*, 2014). Vosman *et al.* (2015) found heritabilities for ketosis within a range of 0.13 to 0.18, depending on stage of lactation. Their analysis was based on 1.23 million cows in the Netherlands. They used a combination of a sire- with a multi-trait-model. In field studies, subclinical ketosis is seldom detected. As a result, data on subclinical ketosis are mostly not available as phenotype information. Therefore it is difficult to analyse the genetic background of ketosis risk. Based on the mid-infrared spectral analysis of milk samples within the routine milk performance testing a risk indicator for ketosis (KetoMIR-index) was developed (Grelet *et al.*, 2016). The risk indicator was originally intended to be a herd management tool but the study at hand analysed if KetoMIR-index could also be used for breeding purposes.

Materials and methods

Ketosis risk in dairy cows is highest if the energy supply from the fodder does not match the high energy needs after birth. The resulting energy deficit leads to a mobilization of body fat and finally to an increase in free fatty acids (FFAs) in the blood. Some of these fatty acids are rebuilt to ketone-bodies (acetoacetic acid, hydroxibutyric acid, and acetone) through metabolic processes. An increased number of ketone-bodies finally cause ketosis. Two progressive forms of ketosis are defined, subclinical and clinical ketosis. Clinical ketosis can be clearly seen by definite expression of ketosis symptoms. Animals with subclinical ketosis do not show clear symptoms. Therefore, it is difficult to detect them. The frequency of clinical ketosis within early lactating cows is 3-5%, the frequency of subclinical ketosis 20-30% (LKV Baden-Wuerttemberg 2016). The biggest losses in dairy production are caused by subclinical ketosis.

The KetoMIR-index was derived by combining direct recorded health data from the health monitoring system (GMON) with the routinely assessed MIR-spectra of test-day milk samples (Grelet *et al.*, 2016). Cases of acute ketosis from the health monitoring data were used as calibration basis for the calculation of KetoMIR-index. Besides the usual milk ingredients other information like the amount of ketone-bodies are part of the KetoMIR-index. Additionally, breed effect and calving number were used as factors when standardizing the KetoMIR-equation. The final index results in continuous values between 0 and 1. Figure 1 shows a hypothetical probability distribution of the KetoMIR-index and the classification in three hazard classes ("healthy", low and high ketosis risk).

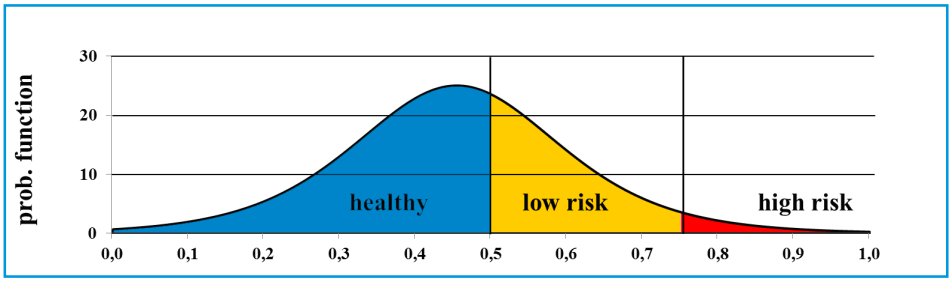

Figure 1. Probability function of KetoMIR-index and ketosis hazard classes.

The equation derived from health monitoring and milk testing data was used retroactively for interpreting the test day samples from the last years. The genetic analysis was carried out for the main dairy cattle breeds in Baden-Wuerttemberg, Fleckvieh (FV), German Holstein (DH) and Braunvieh (BV). In a first step, performance and pedigree data files were compiled. For FV 37.846 lactation were analysed, for DH 31.425 lactations and for BV 15.771 lactations. For each lactation, the first three test-day milk samples were used for analysis. Prerequisite was that somatic cell score and KetoMIR-index were available for these test-day milk samples additionally to the milk ingredients. Also, the direct ketosis-diagnoses from the GMON data were assigned as 0/1-trait to the corresponding lactations. Variance components were estimated with the software program VCE 6.0 (Groeneveld *et al.*, 2010). A within breed repeatability model was used. The model compiled the factors herd-year-season, lactation number, days in milk, permanent environmental effect and additive animal effect. The results of the first three milk samples were analyzed either as single traits or as mean of the three samples (variant "I"). The KetoMIR-index was analyzed as continuous trait (variant "I") and as categorical hazard classes (variant "C3"). Furthermore, the hazard classes were merged into binary traits in two different ways. Once the class "healthy" was compared with the group "at risk" (compiling low and high risk class) (variant "B050") and once again the compiled class "healthy and low risk" was compared with the group "high risk" (variant "B075").

The overall question is to check if the KetoMIR-index could be used as auxiliary trait in a breeding program. Within the current study it is analyzed if the KetoMIR-index or the hazard classes are heritable and how the KetoMIR-index is genetically related to ketosis.

Results and discussion

Table 1 shows the heritabilites of the KetoMIR-index and the categorical and binary analyzed hazard classes for the three different breeds. There are similar trends for all breeds. The heritabilities for the KetoMIR-index are considerable higher than for the hazard classes (categorical and binary). Looking at the variant "I", heritability ranges between 0.22 and 0.24 for the first test-day milk sample and increase with increasing test day. The increase is higher for the dairy breeds DH and BV than for the dual purpose FV. The results for the test day mean reflect these similarities resp. differences. The standard errors for the estimated heritabilities range between 0.01 and 0.05. All heritabilities estimated for the hazard classes (categorical and binary) are very low. Assigning continuous data to classes leads to a loss of information. Therefore, using the continuous index trait seems to be the most promising approach.

Table 1. Heritabilities for the KetoMIR-index, categorical and binary classes.

	FV				DH				BV			
TD	I	C3	B050	B075	I	C3	B050	B075	I	C3	B050	B075
1	**0.22**	0.09	0.09	0.02	**0.23**	0.11	0.09	0.02	**0.24**	0.13	0.12	0.04
2	**0.22**	0.04	0.05	0.01	**0.28**	0.08	0.09	0.01	**0.28**	0.12	0.12	0.02
3	**0.30**	0.04	0.05	0.01	**0.34**	0.11	0.11	0.01	**0.39**	0.13	0.13	0.01
Ø	**0.30**	0.08	0.08	0.01	**0.33**	0.11	0.10	0.00	**0.34**	0.15	0.14	0.03

FV = Fleckvieh; DH = German Holstein; BV = Braunvieh; TD = test day; I = KetoMIR-index; C3 = hazard classes; B050 = comparing hazard class health with classes at risk; B075 = comparing hazard classes healthy and low risk with high risk class.

Table 2 shows the genetic correlations between KetoMIR-index and the observed ketosis diagnoses. Correlations for FV are not shown because due to the far less ketosis diagnoses in FV than in DH and BV the equation system converged but the estimate for all correlations was equal to 1.00.

The highest genetic correlations to the acute ketosis-diagnoses were estimated for the KetoMIR-index values of the first test day. This relation is consistent with the temporal occurrence of ketosis within early lactation and shortly after calving.

Table 2. Genetic correlations between ketosis (clinical) and the KetoMIR-index and categorical classes.

TD	DH		BV	
1	0.44	(0.20)	0.75	(0.29)
2	0.05	(0.18)	0.38	(0.22)
3	0.05	(0.18)	0.07	(0.27)
Ø	0.32	(0.17)	0.24	(0.29)

TD = test day; FV = Fleckvieh; DH = German Holstein; BV = Braunvieh.

Conclusions

With relatively high heritabilities combined with low to medium genetic correlations the KetoMIR-index could be an additional tool in breeding to reduce the susceptibility of dairy cows to ketosis in the long term.

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