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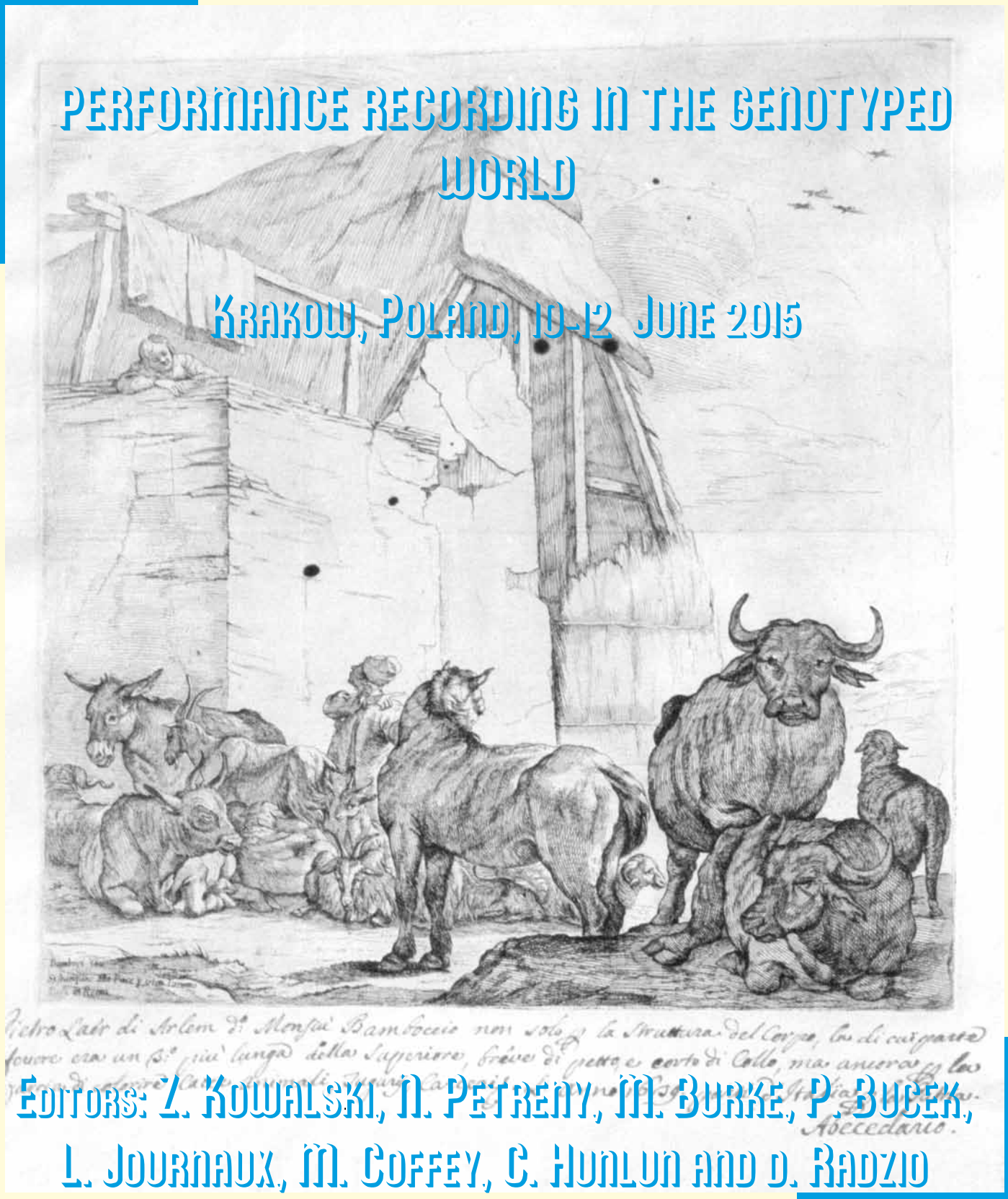
Performance recording in the genotyped world

Krakow, Poland, 10-12 June 2015



Editors: Z. Kowalski, N. Petreny, M. Burke, P. Bucek, L. Journaux, M. Coffey, C. Hunlun and D. Radzio

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

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Proceedings of the ICAR Technical Meeting
held in Krakow, Poland, 10-12 June 2015

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November 2015

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Preface

This publication contains the Proceedings of the ICAR Technical Workshop held in Kraków, Poland in 2015. Nearly 350 participants from 41 countries of all 5 continents attended the workshop which main topics were the role of nowadays performance recording in the genotyped world.

There are always questions for the dairy world that affect all the organisations being active in this branch. We hope that these days in Krakow strengthened the good cooperation between all ICAR members.

Nowadays reality changes and evolves faster and faster. The technological revolution is being played in front of our eyes. Therefore, the organisations responsible for animal performance recording have to keep improving their services.

The ICAR Technical Workshop is the most appropriate and important forum to exchange experience and even create new ideas and solutions. The intention of our Technical Workshop is to have presentations on available applied technologies, which have in practical scale proven their adequate functionality. And this practical aspect has to be highlighted this time because even genomics achievements can not function without a basis that performance recording creates.

This publication contains full manuscripts describing topics presented during open sessions with extended version of survey made among ICAR and non ICAR members on nowadays worldwide trends in performance recording. The range of covered topics is quire wide including:

- milk analysis for detection of pregnancy;
- metabolic disorders and mastitis;
- advisory services built on recorded data;
- manufacturers showcase;
- milk, meat and fibre recording in sheep, goats and beef cattle;
- genomics at farm and phenotyping strategies;
- as well as a workshop presented by the team of auditors for ICAR's Certificate of Quality.

All these points were debated during open sessions and parallel satellite meeting either by means of technical approaches or as a introductory elements for a wider discussion occurred among the participating experts.

The idea of creating of this paper is to gather all papers in one document available for all interested users on the ICAR website. This publication shows the crucial points which are field of interest of ICAR Members.

The success of the conference was not in first place a result of the organisers´ work. It was also a result of the engagement of all participants, speakers and experts at the meetings as well as the contributions of the sponsors and exhibitors who all played a crucial role to make this event a successful. Therefore once again thank you very much for your engagement and support and we hope you will enjoy with the content of this publication.

The Polish Organising Committee

Session 1

What else can we learn from milk samples?

Global experience on ketosis screening by FTIR technology

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Abstract

The purpose of this study is to summarise the latest global experience on the application of a fairly new service that dairy herd improvement organisations can offer their customers - ketosis screening.

Ketosis is a metabolic disorder which usually occurs in dairy cattle during the early lactation period when energy demands for milk production exceed energy intake. This negative energy balance results in the cow using her body fat as an energy source, leading to an excessive accumulation of ketone bodies (i.e. acetone (Ac), β-hydroxybutyrate (BHB)) in blood as the fat is broken down faster than the liver can process it.

The Fourier Transform InfraRed (FTIR) spectrometry method developed for measuring ketone bodies in milk indicated adequate correlations with chemical method results and was proven to be valuable for screening dairy herds for the occurrence of ketosis.

In Quebec, Canada, Valacta has started offering the Ketolab ketosis screening service based on the measurement of BHB in milk as an option to farmers since April 2011. The service is optional and subject to an extra fee. Approximately 71% of farms have used the service in 2014 and over 54% of cows are now screened for ketosis. In 2011, prevalence of ketosis was 26% and has been declining steadily to 15% in 2014. Compared with negative (BHB <0.15 mM/l), cows with elevated (≥0.20 mM/l) BHB produced 2.4 kg less milk on test day, had higher fat and somatic cell count (SCC) and lower protein and urea content in milk. Reproductive performance was also severely affected by ketosis: cows with elevated BHB in early lactation had 24 more days open than negative cows. Furthermore, hyperketotic cows were 41% more likely to leave the herd before the next lactation.

In France, CLASEL offers the FOSS Ac and BHB calibration consolidated in a bio-model called CetoDetect® to predict the risk of ketosis based on the analysis of regular milk recording samples. The scale ranges from 0 to 5, where 0 = healthy animals; 1 and 2 = subclinical ketosis; 3 to 5 = clinical ketosis. Overall, the prevalence of ketosis varied between 10 and 30% according to the season and thus the feeding. Lower values were associated with high quality of grass for grazing during the spring months, whereas the prevalence increased when low quality silage was fed over the winter. Evidently higher values for milk yield and fertility parameters but lowest for SCC values were observed in cows with a score of 0 compared to those with a score of 5. The ketosis testing service is offered for 3 • per cow and year and utilised by approximately 50% of all farmers.

In the Netherlands and Flanders, Belgium, ketone bodies are routinely measured with milk recording analysis at Qlip. FTIR predictions for Ac and BHBA are combined with a few cow-related parameters into a binary (yes / no) score for ketosis developed by CRV. Ketosis scores for cows in the first 60 days of lactation are provided to dairy farmers through the milk recording report and are also used by the feed companies for evaluation of the transition period and the ration. The prevalence of ketosis in the Netherlands is 16%. Ketosis is a moderate heritable trait (heritability of 20%). Breeding values for ketosis are published since December 2014 and are part of the CRV breeding index "Better Life Health". This new service to provide routinely ketosis scores for fresh cows is well valued by the dairy farmers and feed companies.

In conclusion, screening for ketosis using milk Ac and BHB levels clearly indicates metabolic challenges in early lactation that have profound negative effects on subsequent performance. The service is profitable with a return on investment of about 10 to 1 and has also an added value in terms of breeding purposes. Ketosis screening offers high value to milk recording clients and elevates awareness of an otherwise undetected problem. This in turn can help reduce the incidence of the problem.

Keywords: ketosis, Fourier Transform InfraRed (FTIR), early lactating cows, screening tool.

Introduction

Ketosis or hyperketonemia is one of the most frequent metabolic disorders in high-producing dairy cattle, occurring typically in the first two month after calving. It is caused by a severe negative energy balance, where energy demands for milk production and body maintenance exceed energy intake. To compensate, cattle mobilise their body fat. Free fatty acids thus released from adipose tissue can then be used as an energy source or incorporated into milk fat. Hyperketonemia arises when the rate of release of fatty acids exceeds the ability of the liver to process intermediates of fatty acid oxidation, resulting in an accumulation of ketone bodies (i.e. acetone (Ac), β-hydroxybutyrate (BHB) and acetoacetate (AcAc)). Hyperketo-nemia negatively affects milk yield, reproductive performance, and increases the risk of subsequent diseases such as clinical ketosis, displaced abomasum, metritis, and lameness (e.g., Opsina *et al.*, 2010; Duffield *et al.*, 2009). The costs per case of ketosis has been estimated to be 289 US$ (McArt *et al.*, 2015).

In the absence of clinical signs in cases of subclinical ketosis (Andersson, 1988), diagnosis of this common type of hyperketonemia depends solely on the measurement of ketone body concentrations in blood, milk, or urine. The gold-standard test is measurement of the blood BHB concentration by laboratory methods (Oetzel, 2004). For on-farm testing, electronic hand-held blood BHB meters with high accuracy and time-related benefits have been evaluated (Iwersen *et al.*, 2009). However, one of the drawbacks of such hand-held blood BHB meters is the additional farm labour resources required to systematically test all animals at risk for hyperketonemia.

Implementing a ketosis surveillance programme using monthly available milk recording samples in the frame of Dairy Herd Improvement (DHI) offers a more practical and less labour-intensive approach. Fourier Transform InfraRed (FTIR) spectrometry (Hansen, 1999; de Roos *et al.*, 2007) is nowadays a common applied technique for analysis of milk recording samples on fat, protein, and lactose in milk and more recently other minor components such as urea, BHB, and Ac. For milk Ac and milk BHB, the correlation coefficients between the FTIR predictions and the results obtained with segmented flow analysis (Skalar, the Netherlands) were around 0.80 (de Roos *et al.*, 2007) for log-transformed values. Studies from Canada and the Netherlands showed that using milk BHB and Ac measured in regular DHI samples, ketosis could be detected with a good sensitivity (69 and 87%) and a very high specificity of 95% (de Roos *et al.*, 2007; Denis-Robichaud *et al.*, 2014). Hence, milk Ac and milk BHB are valuable parameters for screening herds on the occurrence of subclinical ketosis (de Roos *et al.*, 2007; Denis-Robichaud *et al.*, 2014)

The objective of this study is to compile an overview on the latest global experience on the application of ketosis screening as a new tool offered by DHI organisations.

Material and methods

Determination of milk BHB and acetone values

The observations are based on routinely performed DHI testing in Canada (region Quebec), Belgium (region Flanders), France (regions Pays de la Loire and Centre) and the Netherlands from January 1, 2012 to December 31, 2014.

Milkoscan FT+ (FTIR) instruments (FOSS Analytical A/S, Denmark) with a FOSS calibration for Ac and BHB measurements were used for analysis of regular DHI samples.

The protocol was established and validated according to FOSS recommendations. Briefly, 2,000 milk samples were analysed by a segmented flow analyser and FTIR to build the calibration. For further validation another set of 1,500 samples was analysed. All raw data was processed in collaboration with FOSS.

At Valacta, Canada, 100 samples submitted for routine analysis of BHB are randomly selected to be analysed for BHB by reference method (Skalar continuous flow analyser, Skalar, the Netherlands) every month to validate FTIR predictions against reference values. Furthermore, BHB content of routine pilot samples is analysed by reference method. This allows to monitor predictions on each instrument every 20 minutes.

At CLASEL, France, determination of Ac and BHB in milk was established in 2012 as described elsewhere (Johan and Davière, 2014). A monthly validation of the FTIR calibration against the Skalar chemistry reference method on the basis of 100 pilot samples is performed.

Qlip, the Netherlands and Flanders, Belgium, still applies the original basic calibration established in 2006 (de Roos *et al.*, 2007). No slope adjustment and no bias setting based on outcome of repeated tests of pilot milk with a more or less constant average concentration of Ac and BHB was performed.

Classification and application of results

The predicted milk BHB concentration is expressed as mM/l.

At Valacta, results are reported as risk for ketosis: milk BHB <0.15 mM/l = low risk; milk BHB ?0.15-<0.20 mM/l = medium risk; milk BHB ?0.2 mM/l = high risk.

At CLASEL, results from a decision tree including milk Ac and milk BHB are reported in a scale ranging from 0 to 5, where 0 = healthy animals; 1 and 2 = subclinical ketosis; 3 to 5 = clinical ketosis.

At Qlip and CRV, FTIR predictions for milk Ac and milk BHB are combined with the ratio between fat and protein percentage, parity of the cow and month of milk recording into a binary (yes/no) score for ketosis.

Results and discussion

Ketosis screening on herd level is widely used in Canada, France, Belgium and the Netherlands where Valacta, CLASEL, and Qlip operate (Table 1). Between 48% (Canada) and 85% (Belgium and the Netherlands) of farms are enrolled for the ketosis screening service, thus leading to 51 to 90% of cows that were screened for hyperketonemia. The proportion of farms enrolled for ketosis screening has increased during the observed period.

Valacta and CLASEL indicate the risk for ketosis (low, medium, high) in the DHI report provided to their customers enrolled for ketosis screening. CRV processes the data generated at Qlip and indicates ketosis 'yes' or 'no' for individual cows in the DHI report. The occurrence of high risk cows decreased slightly from 5 to 4% in Canada and France, respectively, between 2012 and 2014 (Figure 1). Medium risk cows occurred evidently less frequently in Canada (2012: 19%; 2014: 11%) and France (2012: 22%; 2014: 13%).

Table 1. Overview on the proportion of samples, farms and cows under ketosis screening from January 1, 2012 to December 31, 2014.

Laboratory	Total number of DHI samples analysed	Proportion of samples with milk BHB analysis (%)	Proportion of farms using ketosis screening (%)	Proportion of cows under ketosis screening (%)
Canada	7,600,000	54	71[1]	54
France	9,600,000	100[2]	48	51
BE and NL[4]	35,000,000	100[3]	85	90

[1] Proportion of farms that used the service for at least one test-day.
[2] Ac and BHB values were predicted for all samples, but reported back to farms enrolled for CetoDetect® only.
[3] All milk recording samples; however, just reported back for cows with days in milk<60.
[4] Belgium and The Netherlands.

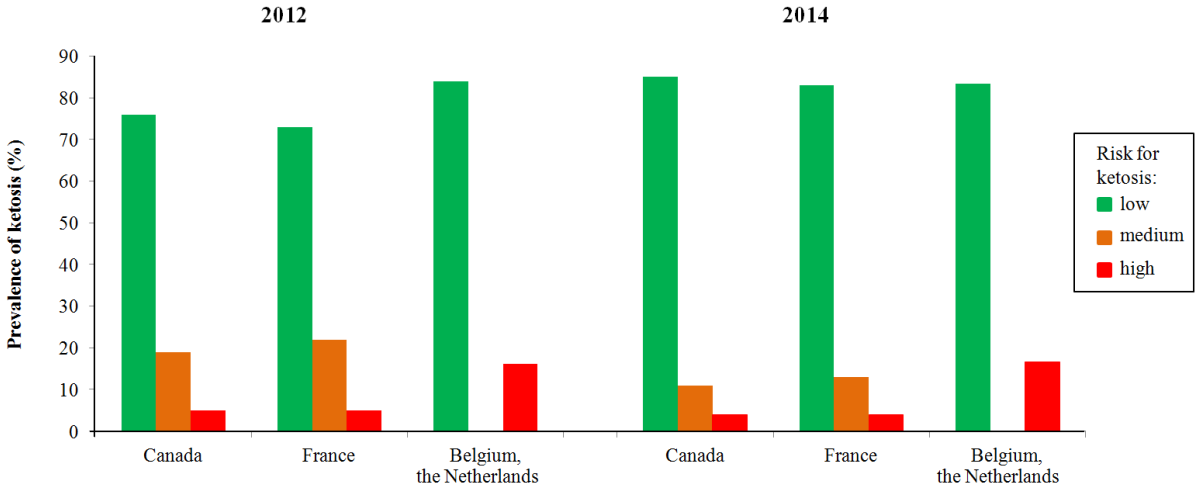

Figure 1. Prevalence of ketosis (low, medium, high risk) in Canada (Valacta), France (CLASEL) and Belgium (region Flanders) and the Netherlands (Qlip) in 2012 and 2014, respectively. Data for Belgium and the Netherlands are expressed as ketosis yes (high risk) or no (low risk).

The increased awareness and associated interventions due to ketosis screening might be an explanation for lower prevalences seen in 2014 (Figure 1). Nonetheless, experience from France shows that the quality of feed also contributed to this positive development. While the quality of corn silage harvested in 2011 was exceptionally poor, it was fairly high in 2013. The occurrence of cows classified as 'ketosis yes' in the Netherlands and Belgium, however, was steady at a level of 16.1% and 16.7% in 2012 and 2014, respectively (Figure 1). Ketosis screening was implemented in DHI programmes in the Netherland and Belgium already early 2011 and thus these countries have had a head start compared to Canada and France, where the service has been offered since late 2011 and early 2012, respectively.

The prevalence of ketosis varied among herds between 5 and 80%. It was generally higher in multiparous (26%) than in primiparous (20%) cows. The prevalence of ketosis further varied between 10 and 30% depending on the month of calving and thus the associated feeding during early lactation. Lower values could be found when cows were fed with high quality grass during the spring months compared to when low quality silage was fed over the winter.

Negative implications of ketosis in the early stage of the lactation on the subsequent performance of dairy cows were observed in all countries analysed. Cows with a high risk for ketosis produced between 2 and 6 kg and those with a medium risk between 1 to 3 kg less milk per day compared to the low risk group. Somatic cell count values were evidently high in the groups of high (>360,000 cells / ml) and medium (>318,000 cells / ml) risk cows (low risk group: 230,000 cells / ml). The risk of subsequent diseases such as clinical ketosis and displaced abomasums was also clearly increased in medium and high risk cows. Moreover, reproductive performance (e.g., calving to first service, non-return rate) of high and medium risk cows was clearly worse than of low risk cows. These observations are in accordance with the literature (e.g., Opsina *et al.*, 2010; Duffield *et al.*, 2009).

The presentation and interpretation of results from ketosis screening are exemplified based on experience from Valacta, where Ketolab is offered as a herd-level screening tool. Individual results are presented to farmers graphically in the form of a scatter graph of test-day BHB values by date of calving with an indication of the proportion of positive cows through time. In this way, trends over time can be visualized. A second scatter graph shows the current test day results by DIM at test-day, allowing to get a sense of when problems arise. A high frequency of positive cows in the first 2-3 weeks post partum points to metabolic issues related to nutritional status during the dry period (type II of ketosis, excess energy supply, over-conditioning, 'fat cow syndrome', insulin resistance, etc.) whereas hyper-ketonemia occurring further into lactation would relate to a large energy deficit in early lactation (type I of ketosis). Suggested corrective actions focus ration formulation, feeding management and environmental conditions (feed bunk access, overcrowding, cow comfort) during the relevant period. Individual results are also presented to farmers and they may elect to initiate preventative treatment on hyperketotic cows, but given the normal frequency of DHI testing and the window risk this is not the focus of the service.

At CRV, the information from ketosis screening is utilized for both animal health management and breeding. Lately, a breeding value for ketosis was introduced in the frame of the "Better Life Health" indicator. This value is available for all CRV bulls today and enables dairy farmers to breed for cows that are healthier. Hence, a decreasing prevalence of ketosis is expected in the long run.

Conclusions

The experience from 3 years of ketosis screening in Canada, France, Belgium and the Netherlands using FTIR technology on regular DHI milk samples clearly shows that this is a valuable service for farmers. Metabolic challenges of early lactating cows that have significant negative effects on their subsequent performance can be uncovered at low costs in a very practical way and subsequently addressed in a new way (i.e. critical evaluation of dry cow nutrition). The service is profitable with a return on investment of about 10 to 1 and has also an added value in terms of breeding purposes. Ketosis screening offers high value to milk recording clients and elevates awareness of an otherwise undetected problem. This in turn can help reduce the incidence of the problem.

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New milk mid-FTIR metrics for dairy cattle management

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Abstract

The key FA parameter that was positively correlated with bulk tank milk fat and true protein concentration was *DeNovo* FA (g / 100 g milk). Structural parameters of FA chain length (carbon number) and total unsaturation (double bonds / FA) were negatively correlated with fat and protein (g / 100 g milk). This was true for both Jersey and Holstein. When *DeNovo* FA (relative % of FA) were higher, fat test was higher for both Jersey and Holstein. As *DeNovo* FA (g / 100 g milk) increased, fat (g / 100 g milk) increased ($P < 0.001$) at a much faster rate (i.e., higher slope) than when preformed FA (g / 100 g milk) increased (slope 2.28 vs. 1.29) for Jersey and for Holstein (slope 2.16 vs. 1.22), for *DeNovo* vs. preformed, respectively. As the proportion of *DeNovo* FA increased (and fat percent increased), the measured FA chain length and double bonds per FA decreased ($P < 0.001$). True protein (g / 100 g milk) increased as *DeNovo* FA (g / 100 g milk) increased. The gross difference in farm income from milk between the low *DeNovo* and high *DeNovo* fatty acid farms was approximately $30,000 per year per 100 cows with income higher for the high *DeNovo* fatty acid farms. Both groups of farms averaged over 23 kilograms of milk per cow per day. High *DeNovo* fatty acid farms bulk tank milk was 0.43% (m / m) and 95 grams per cow higher in fat yield ($0.46 / cow / day) on average. High *DeNovo* fatty acid farms bulk tank milk was 0.31% (m / m) and 59 grams per cow higher in protein yield ($0.51 / cow / day). Milk price caluculations were based on values of $8.59 / kg milk protein and $4.85 / kilogram milkfat (USA milk price in the Northeast US in November 2014).

Introduction

Classically, information from the mid-infrared (mid-IR) spectra is used to measure fat, protein, and lactose content of milk for payment and DHIA testing. The first generation of instruments used optical filters to select for specific wavelengths of infrared light absorbed by key chemical bonds in fat, protein, and lactose in milk. In the mid to late 1990's, the first commecial Fourier Transform Infrared (FTIR) milk analyzers were marketed. FTIR instruments used a different approach to collect information by producing a full infrared spectra of each sample. The information at the classical wavelengths for measurement of fat, protein and lactose could be extracted from that spectra and allowed the speed (samples per hour) of analysis to be increased.

There are many secrets hidden within the mid-IR spectra and only recently have we started to understand how to reveal them using advanced statistical methods. The first secret is the wealth of information about milk fatty acid composition that could be useful for nutrition and feeding managment. We have just scratched the surface of other predicitive information that can be extracted from the spectra that may allow a more proactive management of indivdual cow health and reproduction. Today, I will focus on

the use of milk fatty acid (FA) information for feeding management of dairy cows and report the status of a major on-going research project. Our objectives were: 1) measure FA composition of individual producer milks using new chemometric models for FTIR milk analysis and 2) determine if there are correlations between milk FA composition and bulk tank milk fat and protein tests

Materials and methods: 430 farm survey

Prior to the current study a group of partiail least squares (PLS) chemometric prediction models were developed from mid-IR spectra. The spectra of modified milk calibration samples (Kalylegian *et al*., 2006a,b), bulk tank milks, and individual cow milks were used in combination with chemical reference chemistry for fat (AOAC, 2000; method 989.05; 33.2.26), total protein (AOAC, 2000; method 991.20; 33.2.11 and nonprotein nitrogen (AOAC, 2000; method 991.21; 33.2.12) with true protein calculated by difference, anhydrous lactose (Lynch *et al*., 2007) and gas liquid chromatography (Barbano and Sherbon, 1980; Lynch *et al*., 1992) for FA analysis using a Varian CP-SIL88 capillary column [(100m x 0.25 mm x 0.2 µm film thickness), ID code # CP7489; Varian, Inc., Lake Forest, CA], installed in a Hewlett Packard 6890 GC System equipped with an automatic liquid sampler and a flame ionization detector (Hewlett Packard Co., Wilmington, DE). A library of chemometric prediction models for the major components in milk and milk FA composition for use on a Lactoscope FTA (Delta Instruments, Drachten, The Netherlands) has been developed. A variety of individual FA and groups of FA were measured. The following individual FA were measured by mid-IR: C16:0; C18:0; C18:1 *cis*9, *cis*12; C18:1 *trans* 10; andC18:1 *trans* 11. The following groups of FA were measured: total FA; *DeNovo* (C4:0 to C14:0), mixed origin (C16:0, C16:1, C17:0), preformed (C18:0 and longer); total unsaturated FA, total *cis* FA; total *trans* FA; mono unsaturated FA; and poly unsaturated FA. All FA measures produce results from the IR in grams of FA per 100 grams of milk. Some researchers have used the grouping of FA as short, medium, and long chain FA but the exact definition of those groups varies among researchers. The group definitions of *DeNovo*, mixed origin, and preformed FA is much more clear and consistent because they are based on the biochemical pathways for FA synthesis and have better potential to be correlated with the biology, metabolism, and feeding of dairy cows.

In addition to the measures of FA concentrations, two fat concentration independent measures of FA structure were also done on each sample: mean FA chain length (expessed as mean carbon number per FA) and mean FA unsaturation (expressed as double bonds per FA). The measure of total FA (not fat) in g / 100 g of milk is used as a new basis for a more accurate measurement of total fat content in the milk. This approach eliminates most of the weakness of traditional measurses of fat by IR using the Fat A (C=O stretch) and Fat B (C-H stretch) because it compenstates sample by sample for differences in FA composition when trying to estimate the total fat content of the milk in comparison to ether extraction (Kaylegian *et al*., 2009a,b). The relative proportion of the total FA in milk that are represented by an individual or group of FA can be expressed on a relative basis as a precent of total FA in the sample. Thus, it is possible to produce a simulated gas chromatograph FA analysis of milk fat directly from the same (IR spectra) of milk tested on the IR for fat, protein, and lactose concentration. Validation of IR FA results was done split sample anaysis to compare IR and GLC FA estimates on samples through out the study. The manual model Delta Instruments Lactoscope FTA used in this study provided measurements of milk components and FA composition at a rate of about 100 milks per hour. A larger automated FTIR instrument can operate at about 6 times this speed. Reference testing for FA composition by GLC takes approximately 3 days to analyze 18 milks.

The calibration adjustment of the fat, true protein, anydrous lactose and all FA measures on the IR milk analyzer is done once per month using a set of 14 modified milks described by Kaylegian *et al*. (2006a,b) that has reference values in (g FA per 100 g of milk) for each of the individual or groups of FA measured. The set of calibration samples is produced monthly at Cornell and was used to check the calibrations during the month. Bulk tank

milks from 430 farms located in Northern Vermont and Northeastern New York State were sampled and tested 3 to 20 times per month per farm for 15 months during the period from June 2012 to August 2013 using mid-FTIR (Lactoscope FTA, Delta Instruments, The Netherlands) for fat, protein, lactose and FA composition. FA data were organized and analyzed by breed: Jersey and Holstein.

Results

The data from this survey of milk FA composition represents a wide range of farm managements practices and a wide range of herd sizes (herds that deliver about 10,000 pounds of milk per month to herds that deliver over 3 million pounds of milk per month). The present study is an observational survey that was intended to provide a view of milk FA composition of milk fat and and detect correlations between milk fat and protein concentration in bulk tank milk and milk FA composition on a large population of farms over a period of at least one year. The study produced a large amount of data and it cannot all be shown here. Therefore, the most interesting observations have been selected for presentation. In general, FA composition within farm from day-to-day was fairly consistent. When there was a major change in FA composition within a farm, it was usually due to a major change in feeding that shifted the FA composition. There was an overall breed (Holstein vs. Jersey) difference in FA composition, but there was a large amount of variation within each breed. Overall, the level of *trans* FA was not high in this population, particularly the C18:1 *trans* 10. Indicating that for the most part, classical milk fat depression was not a common problem in this population of farms, but there were some exceptions. The most interesting parameters in the FA data that were correlated with the concentration of fat and true protein in the bulk milk were the groups of FA (*DeNovo*, mixed origin, and preformed FA) and that is the primary focus of the results presented in this paper.

Milk fat

The relationship between g / 100 g of milk of *DeNovo* FA and bulk tank milk fat content is shown (Figure 1). There is a positive correlation of increasing bulk tank fat test with increasing *DeNovo* FA concentration in milk for both Holstein and Jersey milks. These FA are synthesized from the betahydroxy butryrate (BHB), acetate, and proprionate produced in the rumen by forage fermentation and are transported via the blood, taken up by the mammary cells and used to synthesize the *DeNovo* FA and about half of the C16:0. The linear regression equation is located in the lower left hand corner of the graphs and the slope is about 2.2 to 2.3.

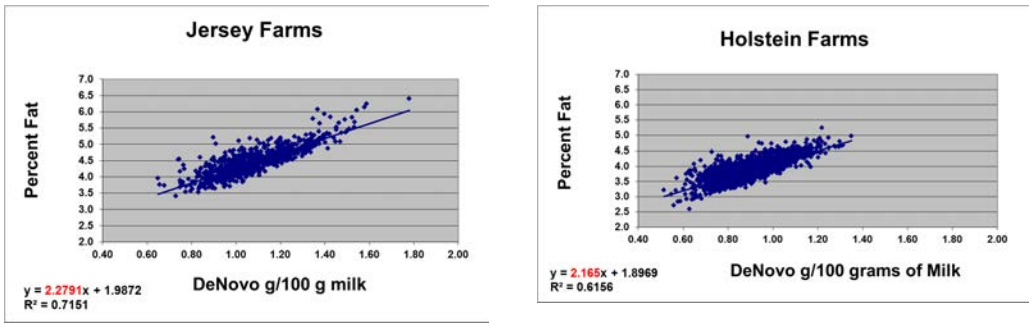

Figure 1. Bulk tank fat test (%) for Jersey and Holstein herds plotted as a function of milk DeNovo fatty acid content.

The relationship between the g / 100 g of milk of mixed origin FA and bulk tank fat milk fat content is shown in Figure 2. There is a positive correlation of increasing bulk tank fat test with increasing mixed origin FA concentration in milk in both Holstein and Jersey milks. Palmitic acid (C16:0) is the major FA in this group. It can come preformed from the diet, or it can be synthesized in mammary cells *DeNovo* from acetate. The relative contribution of these two orgins of C16:0 changes systematically with stage of lactation. In early lactation the C16:0 is primarily from mobilized body fat (i.e., preformed), but after a cow achieves positive energy balance, more of the C16:0 in the milk should be produced within the mammary cells from acetate (i.e., *DeNovo*). The linear regression is located in the lower left hand corner of the graphs and the slope is about 1.8 to 1.9, which is lower than the slope for the *DeNovo* FA.

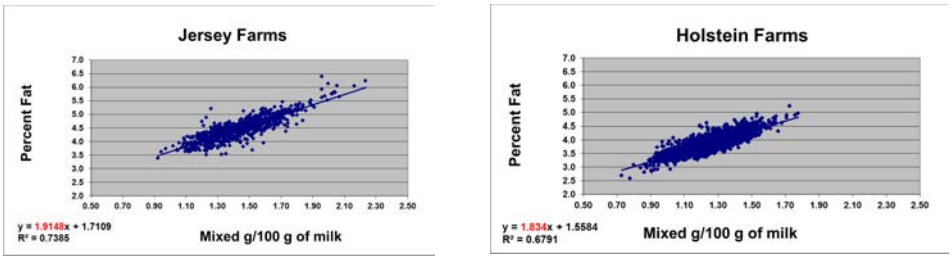

Figure 2. Bulk tank fat test (%) for Jersey and Holstein herds plotted as a function of milk mixed origin fatty acid content.

The relationship between the g / 100 g of milk of performed FA and bulk tank fat milk fat content is shown in Figure 3. There is a positive correlation of increasng bulk tank fat test with increasing mixed origin FA concentration in milk for both Holstein and Jersey milks. The linear regression is located in the lower left had corner of the graphs and the slope is about 1.2 to 1.3, which is much lower than the slope for the *DeNovo* and mixed origin FA.

The much lower slope for the preformed (Figure 3) than then *DeNovo* FA (Figure 1) would seem to indicate that increasing the concentration of *DeNovo* FA in milk will produce a more rapid increase in total fat in the milk than inceasing preformed FA (dietary origin). Enhancing production of *DeNovo* FA and increasing fat test in the bulk tank should be related to forage quality and efficiency of forage fermentation and digestion in the rumen.

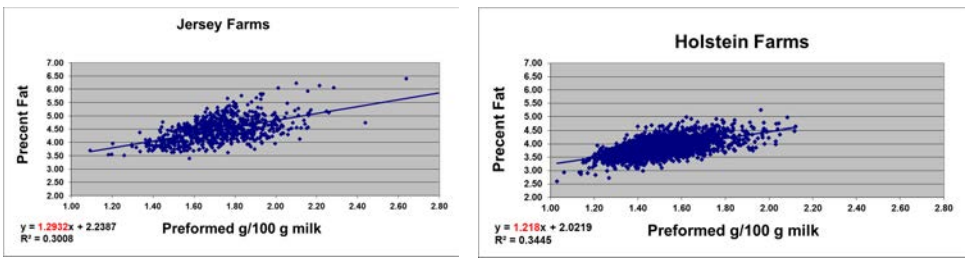

Figure 3. Bulk tank fat test (%) for Jersey and Holstein herds plotted as a function of milk preformed fatty acid content.

Another independent measure of the characteristics of milk fat is the measurement of the average chain length and degree of unsaturation of the milk FA. These measures of fat structure by FTIR are independent of fat concentration in the milk. The relationships between mean FA carbon number and double bonds per fatty FA and bulk tank fat milk fat content are shown in Figures 4 and 5.

As the proportion of preformed FA in milk fat increases, it would be expected that the average FA chain length would increase. Thus, from the relationships shown in Figures 1, 2, and 3, it would be expected that milk fat concentration in bulk milk would decrease as FA chain length increased and this is what is shown in Figure 4. In general in milk fat, increased FA chain length is positively correlated with increased unsaturation (i.e., double bonds per FA. Therefore, as the observed amount of unsaturation in the milk increased in the population of 430 farms, the percent fat in the bulk tank decreased (Figure 5). The higher level of preformed FA in the milk fat could reflect higher levels of supplemental and by-pass feeding. From a biosynthesis perspective high levels of preformed fat entering the mammary cells will have a tendency to inhibit the enzyme acetyl COA-carboxylase that is a critical first step in *DeNovo* systhesis of FA from acetate in the mammary tissue.

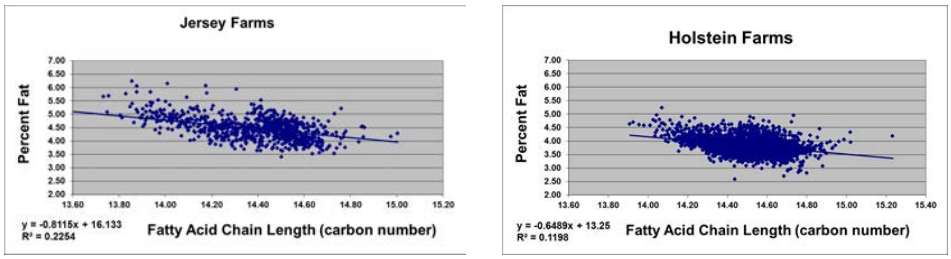

Figure 4. Bulk tank fat test (%) for Jersey and Holstein herds plotted as a function of milk FA carbon number per FA.

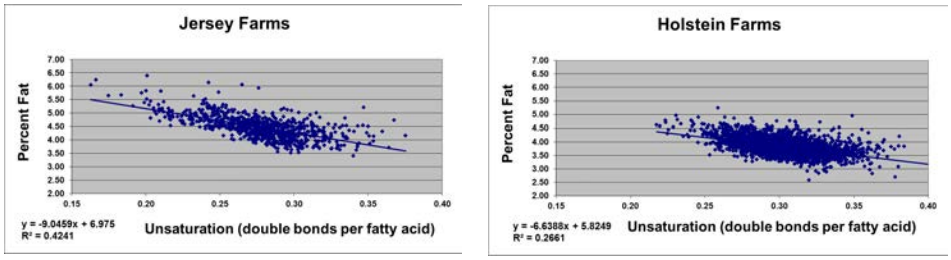

Figure 5. Bulk tank fat test (%) for Jersey and Holstein herds plotted as a function of milk fatty acid double bonds per fatty acid.

Milk protein

At the beginning of the survey we had not focused on bulk tank milk protein content, but we were collecting the data. Upon analysis of the data we were surprised by the high positive correlation between milk FA composition and bulk tank true protein concentration. The relationship between the g / 100 g of *DeNovo* FA in milk and bulk tank milk protein content is shown in Figure 6. There is a positive correlation of increasng bulk tank true protein test with increasing *DeNovo* FA concentration in milk in both Holstein and Jersey milks. This was not expected. The range from high to low in bulk tank true protein concentration was large within both the Jersey and Holstein breeds and would have a significant impact on cheese producton and composition of dried milk protein ingredient products.

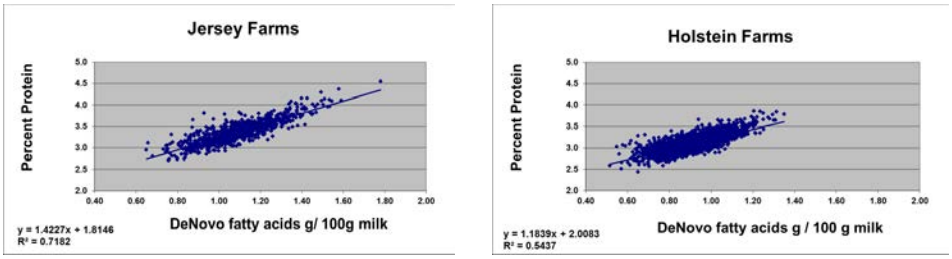

Figure 6. Bulk tank true protein test (%) for Jersey and Holstein herds plotted as a function of milk DeNovo fatty acid content.

Why did we observe a strong positive correlation between *DeNovo* FA concentration in milk and milk protein concentration? Protein is synthesized with the mammary tissue from amino acids. Preformed milk proteins do not enter the mammary tissue from the blood. There are 2 groups of amino acids used to synthesize milk proteins: essential amino acids and nonessential amino acids. The nonessential amino acids can be produced throughout the cow's body and in the mammary tissue. The essential amino acids have to come from the diet. Generally, free amino acids in the rumen are rapidly metabolized by the rumen microflora. There are 3 sources of rumen undegradable (or by-pass) protein: proteins in the diet that do not degrade in the rumen at neutral pH, proteins containing essential amino acids that are part of the cellular biomass produced during rumen fermentation, and protected amino acids fed in the diet. When rumen function and fermentation of digestible carbohydrates is working well then the rumen microflora biomass (i.e., essential amino acids) and rumen volatile FA (i.e., butyrate, acetate, and proprionate) should be maximized. Therefore, *DeNovo* FA output in g / 100 g milk may be an indicator of both excellent production of volatile FA and microbial biomass providing a rich source of essential amino acids in support of milk protein synthesis.

Conclusion: 430 farm survey

The key FA parameter that was positively correlated with bulk tank milk fat and true protein concentration was *DeNovo* FA (g / 100 g milk). Structural parameters of FA chain length (carbon number) and total unsaturation (double bonds / FA) were negatively correlated with fat and protein (g / 100 g milk). This was true for both Jersey and Holstein. When *DeNovo* FA (relative % of FA) were higher, fat test was higher for both Jersey and Holstein. As *DeNovo* FA (g / 100 g milk) increased, fat (g / 100 g milk) increased ($P < 0.001$) at a much faster rate (i.e., higher slope) than when preformed FA (g / 100 g milk) increased (slope 2.28 vs. 1.29) for Jersey and for Holstein (slope 2.16 vs. 1.22), for *DeNovo* vs. preformed, respectively. As the proportion of *DeNovo* FA increased (and fat percent increased), the measured FA chain length and double bonds per FA decreased ($P < 0.001$). True protein (g / 100 g milk) increased as *DeNovo* FA (g / 100 g milk) increased. What we do not know from this work is if the production of milk components per cow per day are higher when *DeNovo* FA as a proportion of total FA is higher. This will be critical in determining if feeding and management strategies to increase *DeNovo* FA production per day will also increase output of fat and true protein per cow per day. That will be the focus of a follow-up farm management field study.

Farm management study: 40 farms

We hypothesize that feeding and farm management practices influenced *DeNovo* FA production and milk fat and protein (g / 100 g milk) by influencing the volatile FA production in the rumen and microbial biomass. A group of 20 Jersey and 20 Holstein farms of interest that had a wide range of *DeNovo* FA (g / 100 g fat) and grams of *DeNovo* FA per 100 g of milk fat were selected for a more in-depth field study, that began in April 2014, to determine if there are cost effective feeding and management practices that can be used to increase fat and protein tests based on monitoring milk FA composition. During the 14 month period of our study, the 10 Holstein and 10 Jersey low *DeNovo* herds averaged 3.62 and 3.97% fat and 2.99 and 3.15% true protein, while the 10 high *DeNovo* Holstein and Jersey herds averaged 3.92 and 4.80% fat and 3.09 and 3.62% true protein, respectively. A field study was conducted to identify feeding and management practices that produce differences in milk FA composition and milk component concentrations at the bulk tank level. Farms that had low *DeNovo* fatty acids had lower fat and lower protein concentrations and had higher stocking density (i.e., more cows per space at feeding and more cows per resting space) and fed a higher fat content in the ration. The farms with higher milk *DeNovo* fatty acid content produced more milk per cow. The gross difference in farm income from milk between the low *DeNovo* and high *DeNovo* fatty acid farms was approximately $30,000 per year per 100 cows with income higher for the high *DeNovo* fatty acid farms. Both groups of farms averaged over 23 kilograms of milk per cow per day. High *DeNovo* fatty acid farms bulk tank milk was 0.43% (m / m) and 95 grams per cow higher in fat yield ($0.46 / cow / day) on average. High *DeNovo* fatty acid farms bulk tank milk was 0.31% (m / m) and 59 grams per cow higher in protein yield ($0.51 / cow / day). Milk price caluculations were based on values of $8.59 / kg milk protein and $4.85 / kilogram milkfat (USA milk price in the Northeast US in November 2014).

Future work: Milk testing for individual cows

Going forward, this work is leading to individual cow milk testing direclty on large farms within the US to provide real-time farm management data. Concepts for integration of mid-IR milk analysis directly into the milking systems on large farms are being considered. The combination of milk weight and the component concentrations (i.e., fat, protein, lactose, and milk NPN / Urea content) will allow calculation of enegy output in the milk and in combination with feed input data will allow an estimate of energy and protein balance of individuals or groups of cows within the herd.

Some other measures that we have developed for use in individual cow milk testing that are blood BHB and blood nonesterfied fatty acids (NEFA) for ketosis and metobolic disorder prediction, in addition to milk BHB and milk acetone concentrations. The measurement and rate of change of blood NEFA estimated from every milking analysis of milk will provide a view of the metabolic status and when combined with energy balance estimates will provide indices of potential first insemination success rate in breeding and the potential to identify individual cows where a delay in breeding might be the most economically correct management decision. Indirect measurement of rumen pH through milk analysis might provide insight into how a cow is interacting the complex mixture of nutrients in the rumen (i.e., subacute ruminal acidosis and displaced abomasum), as it impacts the chemistry of the milk.

Measurements of milk *trans* FA that predict classical milk fat depression using a ratio of C18:1 *trans* 10 to C18:1 *trans* 11 isomers could be very useful in identification of those cows that are predisposed to milk fat depression on certain types of feeding strategies. It may be possible to develop a milk analysis model to provide an index of rumen pH that could be useful when making changes in rations. It could be that realtionships with animal genetics will become apparent when large data sets are available. Combinations of individual parameters that provide more predictive indices of feed efficicency, ketosis, and probability of successful breeding may be derived from the current PLS models for milk analysis. In the future, development of models to determine pregnancy status and loss of pregnancy will bring further benefit in the applications of mid-IR milk testing for real-time farm management milk testing.

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Predicting the risk of ketosis using mid infrared spectrometry

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Abstract

Mid infrared (MIR) spectrometry is used in all milk analysis laboratories to estimate fat and protein contents. For over a decade MIR spectrometry has been used to estimate new milk components such as fatty acids, proteins and minerals. Currently, the European OptiMIR project aims to use this method to predict the physiological status of a cow, directly from its MIR spectrum. The purpose of this study was to consider the possibility of preventing ketosis by using MIR spectrometry. Ketosis is a metabolic disease caused by a disturbance of energy metabolism which affects highly productive dairy cows in high negative energy balance in early lactation. Beta-hydroxybutyrate (BHB) and non-esterified fatty acids (NEFA) contents in blood are the gold-standard for ketosis monitoring. Indeed blood BHB and NEFA are respectively the biomarkers of energy metabolism deviation and the use of fatty reserves. A data collection took place in four experimental farms in France and Germany on 214 Holstein, Montbeliarde and Abundance cows in early lactation. Once a week from calving to 50 days in milk one blood sample and one milk sample from every cow were collected. The blood sample was analysed to measure BHB and NEFA contents and the milk sample was analysed by MIR spectrometry. Blood BHB and NEFA contents were used to classify the samples according to the risk level. 798 samples were identified as "low risk" and 421 as "high risk". The samples identified as "high risk" were then classified into three states according to the type of risk: "risk of type I ketosis", "risk of type II ketosis" and "suspected ketosis". An 81% sensitive and 69% specific prediction equation of the risk level was developed by logistic Partial Least Square (PLS) regression. In order to distinguish the type of ketosis risk a second prediction equation was developed using canonical powered PLS regression and discriminant analysis. Applied on the samples predicted as "high risk" a well classified rate of 85% could be achieved.

Keywords: mid infrared spectrometry, milk analysis, ketosis.

Introduction

The transition period after calving and the beginning of the lactation is a very critical period on which the success of the lactation is based. During this period, every cow is in negative energy balance because of the increase in the energy demand for milk production and in parallel the low intake capacity that does not allow them to cover those requirements. The more the dry matter intake decreases, the more energy the cow will

draw from the breakdown of her own body reserves. As a consequence, non-esterified fatty acids reach the liver where they are oxidised into glucose which will feed the organs (Duffield *et al.*, 1997; Goldhawk *et al.*, 2009).

When the mobilisation of body reserves becomes too intense the liver is exposed to excess non-esterified fatty acids which the cow cannot oxidise completely because of a lack of energy. This partial oxidation provides ketone bodies (acetone, acetoacetate and beta-hydroxybutyrate) that accumulate in blood, leading to a metabolic trouble called ketosis. This is particularly true in the case of high-yielding dairy cows because their demand for milk production is very high and their energy intake is often lower than required. This ailment has a lot of consequences on animal welfare and farms competitiveness because it leads to an increase in veterinarian costs and a loss of milk yield (Enjalbert *et al.*, 2001). It also modifies milk composition, especially the fat to protein ratio (Duffield *et al.*, 1997; de Roos *et al.*, 2006). We can distinguish 2 types of ketosis: the first is caused by a non-sufficient energetic density of the diet; and the second is caused by a too important body condition at calving. Two biomarkers can be taken into account to diagnose ketosis: the non-esterified fatty acids content (NEFA) in blood which relates to energy balance, and the beta-hydroxybutyrate content (BHB) in blood which is considered the gold-standard for ketosis detection (Duffield *et al.*, 1997; Oetzel, 2006). Most often the lack of symptoms leads to a poor detection of the disease. However, if you cannot diagnose it accurately, you cannot manage it well (Oetzel, 2006; Goldhawk *et al.*, 2009).

The OptiMIR project aims to develop innovative tools for milk production management through the use of mid infrared (MIR) spectral analysis of milk recording samples, which is a fast and cheap alternative method used in every lab to analyze milk composition. The purpose of this work is to determine if MIR spectroscopy could be a reliable method to monitor ketosis. The aim of the present study was two-fold. Firstly, to use both BHB and NEFA contents to classify the cows according to their risk situation for ketosis. Secondly, to predict this risk situation by using MIR spectroscopy.

Material & methods

Herds and animals

Four French and German research farms were involved in the data collection with the objective to cover a large diversity of breeds and feeding systems.

The French farm of Les Trinottières belongs to the agriculture chamber of Maine-et-Loire and is located in an oceanic lowland area of the western part of France. The cows of this farm are all Holstein cows calving in autumn and fed with a maize silage diet all year long.

The experimental farm of Marcenat belongs to INRA and is located in Auvergne Mounts, in the central part of France. In this area the climate is cold and rainy and the altitude can reach 1,000 meters. The Holstein and Montbeliarde cows calve in spring, are fed with hay and concentrate in winter and are grazing from the month of May.

The breeding center of Poisy, located in the French Savoy Mountains, belongs to the agriculture chamber of the departments of Ain, Isère, Savoie and Haute-Savoie. The Abundance, Montbeliarde and Holstein cows are calving from August to December and are fed with hay, maize and concentrates in winter and fresh grass in summer.

The Hofgüt Neumühle is located in Rhineland-Palatinate, Germany. The Holstein cows calve mainly in summer and receive a maize silage based diet all year long.

Measurements and observations

The data collection was performed on the cows from 1 to 7 weeks in milk in each herd, in the same way. In total the results of six test-days per cow (one test-day per cow per week) were stored in a common database. Samples and measurements were collected each test-day. One blood sample was collected on each cow. After centrifugation, plasma was frozen in heparinised tubes. Tubes were sent to the LDHVet laboratory where BHB and NEFA contents were determined by enzymatic method. One milk sample was collected on each cow the same day as the blood sample, for the measure of fat and protein contents and extraction of the spectrum. Each cow was weighted and body condition scored on a 5 notes scale (from 1 to 5) and their feed intake was measured. Sanitary events and overall data concerning the cows were also collected. In total 1,219 records combine a spectrum and a blood analysis (Table 1).

Table 1. Overall information on data collected per farm.

	Observations			Breed			Parity	
	Cows	Cow* test-day	Test period	HO[1]	MO[2]	AB[3]	Range	Percentage of primiparous
Marcenat	39	232	Mar-Aug 2013	49%	51%		1-8	44
Neumühle	60	358	Jul 13-Jan 14	100%			1-9	32
Poisy	49	274	Aug 13-Jan 14	6%	49%	44%	1-8	20
Trinottières	61	355	Sept 13 Jan 14	100%			1-8	43

[1] Holstein
[2] Montbeliarde
[3] Abundance

MIR spectra

In order to decrease the root mean square error and the bias due to apparatus deviation, the spectral data were standardized as described by Grelet *et al.* 2015.

Definition of ketosis status

Phenotypic correlations between the biomarkers were calculated using SAS® software. Both BHB and NEFA content values were combined into a classification in order to define the ketosis status of each observation. Thresholds used to discriminate the classes were defined on from the literature. These classes are our reference data. First, the samples were split-up into 2 classes defining the risk level: "low risk of ketosis" (LRK) versus "high risk of ketosis" (HRK). Secondly, HRK observations were split-up into 3 groups according to the type of risk: "risk of type I ketosis" (RK1), "risk of type II ketosis" (RK2) and "suspected ketosis" (SK).

Statistical models

Mathematic models were developed to assess the link between MIR spectra and ketosis status. The detection limit of the enzymatic method to measure BHB and NEFA content are respectively [0.10; 3.20] and [0.10; 3.00]. As a consequence BHB contents equal to 0.10 or 3.20 and NEFA contents equal to 0.10 or 3.00 were removed from the calibration dataset. Finally, 958 data constitute the calibration set.

The prediction equation of the risk level (LRK versus HRK) was processed by logistic partial least square regression using R software. The two thirds of the data were used for calibration and the last third was used to validate the model. The number of observations in each group was balanced in calibration dataset to avoid a distortion of the model. Sensitivity, specificity, positive predictive value and negative predictive value were calculated to assess the precision of this first model.

The prediction model of the type of risk (RK1, RK2, and SK) was developed by canonical powered partial least square regression and discriminant analysis using R software. Once again the two thirds of the dataset were used to calibrate and the last third to validate the model. Accuracy of the model was calculated to assess its precision.

Results and discussion

Phenotypic correlation between biomarkers and classification of the samples

The correlation between BHB and NEFA contents in blood is very low (0.03) as Figure 1 shows. This demonstrates the physiological difference between type I and type II ketosis risks. That is why both biomarkers were combined in order to classify the samples.

Table 2 shows the distribution of the observations across the different classes. About two thirds of the population is in the LRK group, which is consistent with the prevalence quoted in the literature (Hubbard *et al* 2010). Within the HRK group, about a half of the observations are classified as risk of type I ketosis, about 40% are classified as risk of type II ketosis and about 7% are in a situation of suspected ketosis. A third of the RK1 situations occur in the first three weeks in milk whereas only a half of the RK2 situations and two thirds of the SK situations occur in this same three-week period.

Milk yield is higher in HRK situations than in LRK situations which is consistent with the fact that ketosis is more prevalent in high-yielding dairy cows. Fat content is higher in HRK situations, especially in SK cases (49.2 g/kg in average versus 37.9 g/kg in LRK group). On the contrary, protein content is lower in SK cases, which is consistent with the lack of energy in this group. As a consequence, the average fat to protein content ratio is higher in HRK situations than in LRK situations and much higher in SK situations.

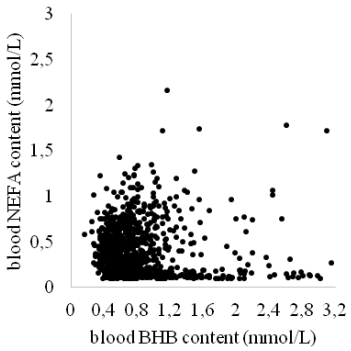

Figure 1. Phenotypic correlation between BHB and NEFA contents in blood (n=958).

Table 2. Distribution of the observations into the different classes.

	Ketosis risk level		Type of ketosis risk		
Class	LRK[1]	HRK[1]	RK1[2]	RK2[2]	SK[2]
Frequency	798	421	216	176	29
Percentage	66	35	51	42	7
MY	29.6 ± 8.3	32.9 ± 8.4	32.6 ± 7.0	33.5 ± 9.4	31.2 ± 11.3
FC	37.9 ± 6.5	41.6 ± 7.0	40.9 ± 6.9	41.1 ± 6.2	49.2 ± 8.3
PC	30.4 ± 2.9	30.2 ± 2.8	30.4 ± 2.8	30.2 ± 3.0	29.4 ± 2.7
FC / PC	1.25 ± 0.20	1.38 ± 0.24	1.35 ± 0.23	1.37 ± 0.22	1.68 ± 0.30

[1] LRK: Low Risk of Ketosis; HRK: High Risk of Ketosis
[2] RK1: Risk of type I Ketosis; RK2: Risk of type II Ketosis; SK: Suspected Ketosis
[3] MY: Milk Yield; FC: Fat Content; PC: Protein Content

367 samples were used to validate the model. Table 3 shows the results obtained on this validation dataset. The sensitivity, which is the probability of predicting HRK observations correctly, reaches 81% (78 out of 96 observations). The specificity, which is the probability of predicting LRK observations correctly, reaches 69% (188 out of 271 observations). The negative predictive value (NPV), which is the probability to be effectively observed as LRK when predicted LKR, reaches 91% (188 out of 206 predictions). However, the positive predictive value (PPV), which is the probability to be effectively observed as HRK when predicted HRK, is quite low: it reaches 48% (78 out of 161 predictions).

This model is efficient to detect HRK situations but its low PPV leads to an important proportion of false-positives. A first potential solution to explore this will be to better balance the calibration dataset.

Table 3. Accuracy of the ketosis risk level model – results on validation dataset.

	Prediction		
Observation	LRK[1]	HRK[2]	Total
LRK[1]	188	83	271
HRK[2]	18	78	96
Total	206	161	367

[1] Low Risk of Ketosis
[2] High Risk of Ketosis

Table 4. Accuracy of the type of ketosis risk model – results on validation dataset.

	Prediction			
Observation	RK1[1]	RK2[2]	SK[3]	Total
RK1[1]	65	4	2	71
RK2[2]	4	15	2	21
SK[3]	1	1	2	4
Total	70	20	6	96

[1] High Risk of type I Ketosis
[2] High Risk of type II Ketosis
[3] Suspected Ketosis

96 samples were used to validate the second model which was applied only on HRK observations. The overall accuracy of this model reaches 85%. With more details, 65 out of 71 RK1 observations (92%), 15 out of 21 RK2 observations (71%) and 2 out of 4 SK observations (50%) are well-classified, as Table 4 shows.

The model has a very good ability to detect RK1 situations. RK2 situations are also quite well detected but there are only 21 RK2 observations in the validation dataset. There are only 4 SK observations in the validation dataset so we have to be careful when interpreting the results. To improve this model, an increase in the number of records is necessary. Secondly, the calibration dataset should be balanced.

Conclusions

This study shows that predicting ketosis risk level and type using MIR spectroscopy is possible and reliable. The high sensitivity of the ketosis risk level prediction model allows us to consider the possibility to give information on animals to the farmers, to monitor and / or to treat them. What's more, the good accuracy of the type of ketosis risk

prediction model could highlight the breeding practices to check and change (e.g. energy density of the diet in early lactation, dry period management etc.). However these models have to be tested on farm to validate their accuracy on more data. To finish, the models give some alerts but do not replace clinical observation of the animals and veterinarian diagnosis.

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Novel model of monitoring of subclinical ketosis in dairy herds in Poland based on monthly milk recording and estimation of ketone bodies in milk by FTIR spectroscopy technology

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Abstract

The aim of this paper is to present the new system of monitoring of subclinical ketosis (SCK) in Poland, based on monthly milk recording. The preliminary results of such a monitoring are presented as well as the main risk factors for SCK in Poland. To our best knowledge, the system presented here is the only one all over the world, by which the whole nationally recorded population of cows is being systematically monitored for SCK.

SCK is an excess of circulating ketone bodies in the blood without clinical signs of ketosis, such as decreased appetite and weight loss. The lack of clinical signs makes SCK difficult to detect. However, using blood β-hydroxybutyrate acid (BHBA) testing to measure the incidence or prevalence of SCK in a herd is a powerful and useful tool. In Poland we use milk content of BHBA (BHBAM) and acetone (ACEM) to detect cows and herds in risk of SCK. BHBAM and ACEM are determined by MilkoScans with FTIR, placed in four labs of Polish Federation of Cattle Breeders and Dairy Farmers. The system was introduced into the practice in April 1, 2013 and about 720 000 cows are being monitored annually. The cows between 6 and 60 days in milk (DIM) are not diagnosed but identified as "in risk". These cows are pointed as "K!" A special statistical method was implemented to calculate the probable frequency of SCK (so called PFSK). If it is higher than 10 or 20%, the herd is recognized as "in risk" or "in high risk", respectively. The results of such a monitoring are presented to the farmers in monthly reports delivered by the internet.

A preliminary survey (after 24 months) of the results shows that about 10% of cows at 6-60 DIM are in a risk of SCK. Surprisingly, more ketotic cows have been found in lower productive herds than in higher productive ones. So, the high milk yield is not a risk factor for SCK in Poland. Other factors are shown and discussed in the paper.

Keywords: subclinical ketosis, monitoring, Fourier Transform InfraRed (FTIR).

Introduction

Excessive negative energy balance in the early lactation of dairy cows results in metabolic disorders, such as ketosis, fatty liver and displaced abomasum (LeBlanc, 2010). They are highly responsible for substantial financial losses due to decreased milk yield, poor reproduction, increased susceptibility to immunosupression and culling rate (Ingvartsen, 2006; McArt *et al*., 2012).

Ketosis, defined as clinical (CK; blood β-hydroxybutyrate acid (BHBA) > 3 mmol/L) or subclinical (SCK; blood BHBA > 1.2 mmol/L) (Oetzel, 2007), is considered the most frequent metabolic disorder of dairy cows. In the study of Suthar *et al.* (2013) the average prevalence of SCK in 528 dairy herds in 10 European countries (5 884 cows) was 21.8%, ranging from 11.2 to 36.6%. For each ketotic cow the total costs of SCK have been calculated to be $960 (Esslemont, 2012) or $340 (Gohary, 2013). The lack of clinical signs makes SCK difficult to detect, especially on the herd basis.

Since the prevalence of SCK is so high, and economic losses so obvious, there is an unquestionable need for monitoring of SCK in dairy herds. Cow-side tests, using glucometers, strips, or nitroprusside powder to detect ketone bodies are commonly available but their sensitivity and specificity are highly variable (Oetzel, 2007). Moreover, a routine monitoring of SCK by these means is costly and difficult organizationally, especially in such countries like Poland where the average herd size is less than 10.

The method of milk chemical composition analysis based on Fourier Transform Infrared (FTIR) spectroscopy allows for the determination of ketone bodies (BHBA and acetone (ACE) in milk (Hansen, 1999), using calibrations proposed by de Ross *et al.* (2007). The first diagnostic model for detection of hyperketonemia in early lactation dairy cows at test days, using FTIR technique and test-day information, was published by Dutch group of van der Drift *et al.* (2012).

In Poland we use milk content of BHBA (BHBAM) and acetone (ACEM) to detect cows and herds in risk of SCK. BHBAM and ACEM are determined by MilkoScans with FTIR, placed in four labs of Polish Federation of Cattle Breeders and Dairy Farmers (PFCBDF). The system (Kowalski *et al.*, 2015) of SCK monitoring was introduced into the practice in April 1, 2013. To our best knowledge, the system presented here is the only one all over the world, by which **the whole nationally recorded population of cows is being systematically monitored for SCK**.

The objectives of this paper are to overview the model and system of SCK monitoring used in Poland by PFCBDF as well as to present the main statistical data on prevalence of SCK in Poland, based on the two-year monitoring.

A model of SCK monitoring in Poland

In the developing of the model our aim was to create a cheap, easy and massive monitoring method of dairy herds for SCK, based on monthly milk recording, to give the information on risks of individual cow and herd.

A model was developed based on the dataset which contained data collected in January - March 2012, from about 1100 dairy cows, from randomly selected Polish farms enrolled in the system of milk recording provided by PFCBDF. The cows were between 6 and 60 days in milk (DIM). A sample of milk from each cow was taken during the morning milking, and analyzed for chemical composition, including BHBAM and ACEM. Milk composition was determined in the laboratory of PFCBDF, using MilkoScan FT6000 (Foss Analytical A/S, Hillerød, Denmark). The FTIR instrument was calibrated for BHBAM and ACEM (de Roos *et al.*, 2007)

At the same test-day, between 1100 and 1400 h the blood samples were drown from the jugular or coccygal veins, and the concentration of blood BHBA (BHBABG) was determined using the Optium Xido glucometer (Abbott Laboratories Poland). The BHBABG was transformed to the laboratory value (BHBAB) using our own linear regression equation.

The model was developed using above dataset and logistic regression method. It was assumed that a cow was ketotic (depended variable) when BHBAB was 1.4 mmol/l The logistic regression equations were determined using stepwise and manual backward selection procedures (P-value for retention <=0.15). The factors (potentially predictive variables) tested were milk components, such as milk fat, protein, lactose, urea, BHBAM

and ACEM contents, and milk fat-to-protein ratio (F / P). Sensitivity and specificity of the model was tested using receiver operator characteristic (ROC) analysis. The optimal cutoff value for each test variable or variables was defined as that cut point where sensitivity plus specificity were at a maximum (van der Drift *et al*., 2012).

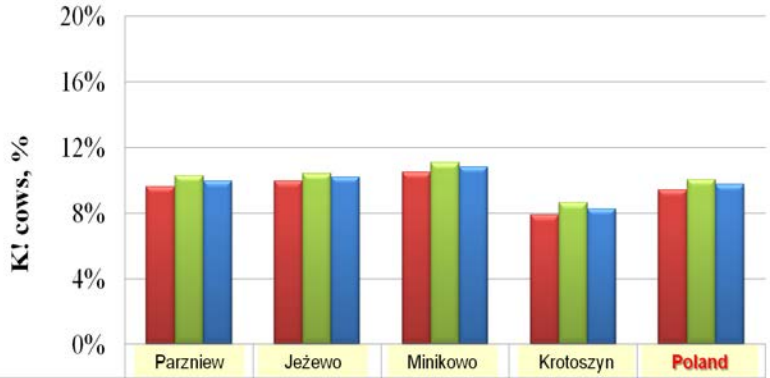
Finally, a logistic regression model which was introduced into the practice, consists of 3 independent variables: BHBAM (P<0.001), ACEM (P<0.001) and F / P (P<0.035). According to this model a cow is marked by the "K!" if she is considered as being in th e SCK risk. By indexing the cow as K! the farmer is informed that there is a considerable (> 70%) probability, that on the test-day this cow suffered from SCK. The estimation of K! is not equal with the diagnosis of SCK.

Since in Poland still a substantial part of recorded cows are located in small herds (less than 50 cows), a simply calculation of herd risk of SCK based on the percentage of K! cows is not valid. Instead, we developed the system in which the degree of SCK risk in the herd is determined by the statistical model. It considers the frequency of K! cows in the group of cows at 5-60 DIM, number of cows and sensitivity and specificity of the method. Finally, the farmers are informed about the risk of herd by so-called "estimated frequency of subclinical ketosis" (PFSK). The herd is considered with 90% probability as being "at risk" or "at high risk" if PFSK is higher than 10 or 20%, respectively.

Both parameters, i.e. K! (defining risk of individual cow) and PFSK (risk of herd) are provided to the farmer by PFCBDF either in the electronic (internet) or printed form.

What have we learnt about ketosis in Poland ?

As mentioned above, the system was introduced into the practice on April 1st, 2015. Since it, a huge number of data, exceeding 1.8 million, has been collected. A preliminary survey of the results shows that 9.73% of cows are in a risk of SCK (Figure 1). Moreover, the prevalence varies due to the area of Poland. The highest is found in area of Minikowo laboratory, where small farms are in majority, whereas the lowest prevalence is observed in the area of Krotoszyn, where bigger farms are much common.



	Parzniew	Jeżewo	Minikowo	Krotoszyn	Poland
2013/2014	9,60%	9,95%	10,50%	7,88%	9,42%
2014/2015	10,29%	10,40%	11,07%	8,61%	10,03%
2 years	9,94%	10,19%	10,80%	8,26%	9,73%
N of milk samples	548283	343228	448171	507194	1846876

Figure 1. Prevalence of SCK in Poland (2 year monitoring - 2013/2014 and 2014/2015), and in the areas of four laboratories of PFCBDF.

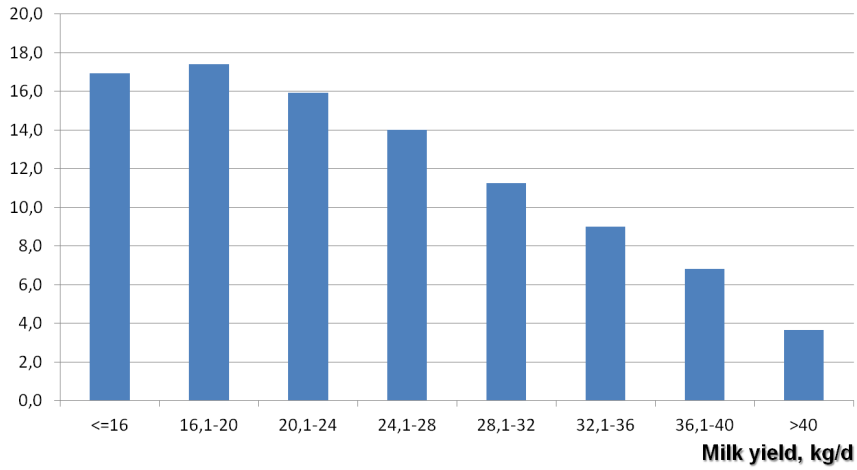


Figure 2. Prevalence of SCK in Poland depending on daily milk yield of monitored cows on the test-day.

Surprisingly, more ketotic cows were found in lower productive herds than in higher productive ones (Figure 2). Among cows producing daily more than 36 litres of milk only less than 6.5% were considered as ketotic, whereas the cows producing 16.1-20.0 litres of milk more than 17.5% were at risk of SCK. Similar tendency was found when the prevalence was analyzed in relation to the average daily milk yield of the herd. So, the high milk yield seems not to be a risk factor for SCK in Poland.

According to Oetzel (2007), there are two types of ketosis in the early lactation period of dairy cows. The "type 1" ketosis is defined as spontaneous and it is related to underfeeding, especially in the peak of lactation. In our system of monitoring we assume that this type of ketosis occurs from 22 till 60 DIM. On the other hand, a cow is in the "type 2" ketosis when she is in a negative energy balance and begins mobilizing body fat prior to or at calving (Oetzel, 2007). Fat cows are at the highest risk for this problem because they are

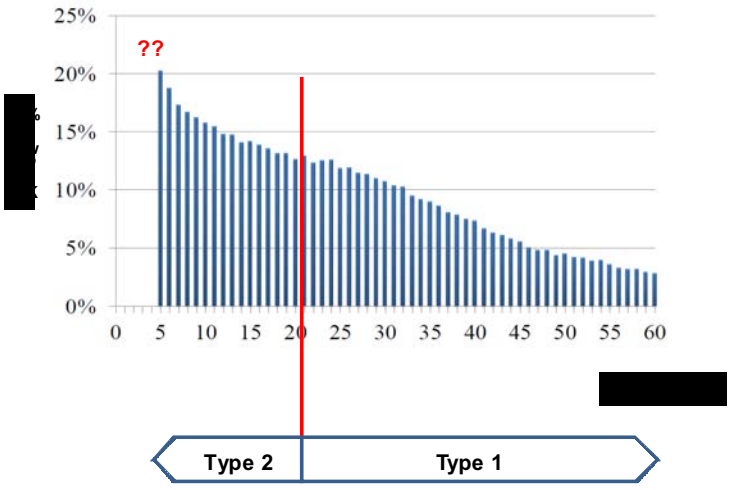


Figure 3. Prevalence of two types of ketosis in Poland depending on days in milk (DIM): type 1 (22-60 DIM) and type 2 (5-21 DIM).

prone to dry matter intake depression around calving, but thinner cows are also at risk if nutritional management during the pre-fresh and/or maternity period is poor. In our system of monitoring we assume that this type of ketosis occurs from 5 till 21 DIM. The prevalence of SCK in Poland based on such a categorization of ketosis types is presented in Figure 3. The average prevalence of type 2 ketosis was much higher than type 1 (15.2 vs. 7.2%, respectively). Unfortunately, the system of monitoring cannot consider the cows being in 2-4 DIM, but we assume that on these days the prevalence might be even higher.

The prevalence of above types of ketosis depends not only on the DIM, but also on the parity (Figure 4). The primiparous cows in Poland are much more prone to the type 2 ketosis than the older cows. In our opinion, among factors responsible for higher risk of type 2 ketosis the overfeeding (excessive body condition) is the most important. On the other hand, older cows are more than primiparous ones suspected to the type 1 ketosis, due to the higher requirements for energy which is related to the higher milk yield in the peak of lactation period. The differences among parities should be considered in the educational programme provided by the PFCBDF, including feeding and welfare.

Based on the results of one year (2014/2014) monitoring, among 20 371 dairy farms in the system, 7.3% of them have been classified as "in risk" and 11.4% as "in high risk", which means that almost 18.7% farms are considered "with ketosis". They should be included in the educational programme provided by the PFCBDF.

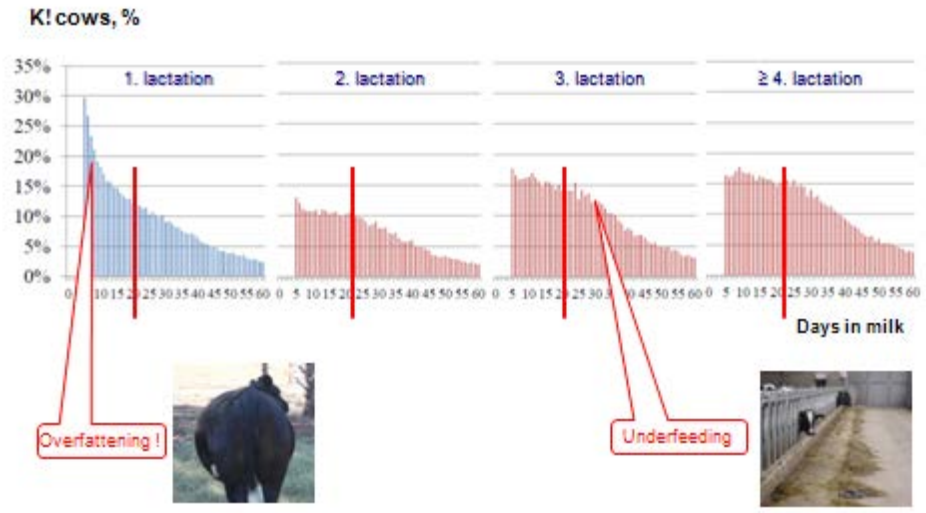


Figure 4. Prevalence of two types of ketosis in Poland depending on days in milk (DIM) and parity: type 1 (22-60 DIM) and type 2 (5-21 DIM).

Conclusions

The experience from two years of ketosis monitoring in Poland based on milk recording and milk analysis for ketone bodies using FTIR technology clearly shows that a system has been well accepted by the farmers. The prevalence of subclinical ketosis in Poland is lower than in other countries due to the differences in methodology of monitoring. However, it is still too high both on the cow and herd level for a profit of farmers. From the two year monitoring we have found that milk yield is not a risk factor of SCK in Poland. We have also found that in the categorization of types of ketosis the parity should be considered.

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Experience of milk based farm monitoring of Livestock Performance Testing (LTP) Ltd.

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Abstract

The one page summary report was developed by LPT Ltd. The report not only provides easy to use information about the urea content of the milk samples, but also informs about subclinical acidosis. It is easy to point out if any changes occur in protein or energy supply by lactation numbers and stages. High urea level has negative effect on reproduction due to excess of protein (degradable, soluble protein).

High milk urea (higher than 32 mg / dl) or increasing value (higher than 4 mg / dl) is caused by the following feeding situations:

- Feeding too much total crude protein.
- Feeding too much rumen degradable (RDP) or soluble (SP) protein.
- Amino acid imbalance.
- Ration low in fermentable carbohydrate or non-fiber carbohydrate (NFC).
- RDP and fermentable carbohydrate are note synchronized in time.
- Inefficient rumen fermentation due to subacute ruminal acidosis (SARA).
- Heat stress.

High urea level (> 36 mg / dl) can be connected to the failure of conception rate by 15-20%. A high MUN value suggests that energy is being utilized to convert ammonia to urea and is being diverted from milk production. Hutjens (1996) suggests, using the Cornell model, that cows with MUN values over 42 mg / dl will produce 3,5 kg less milk.

Low milk urea (less than 18 mg / dl) or decreasing value (higher than 4 mg / dl) is caused by the following feeding situations:

- Low feed intake.
- Too low total crude protein or low in RDP or SP in the diet.
- Feeding too much NFC.
- Inefficient rumen fermentation.

Milk fat content depends on many factors, like milking interval, season, number of rumination, heat stress etc. However, milk fat depression reaching the point of 2,5% milk fat content is most likely related to acidosis, as agreed by most of the authors. If the relative frequency is over 10% of the cows producing less than 2,5% milk fat in any herd, they most likely suffer from subacute ruminal acidosis (SARA).

Our experience with farm monitoring reflects that milk urea and the occurrence of SARA are independent of quantity and contents of milk. Optimal values can be obtained by good feeding and sound management at any milk production level.

Keywords: milk urea, protein supply, SARA

Introduction

Milk urea is the fraction of milk protein that is derived from blood urea. Milk urea in Holstein normally represents about 0.19 percentage of the normal 3.2% total milk protein. The milk urea content is mainly determined by the feeding program. Following the changes of milk urea can effectively support the controlling and fine tuning of the feeding program. The synchrony of protein and energy balance can be evaluated. The values show the consequence of the feeding program. Do not forget, there are at least 3 diets at the farm:

1. the formulated diet.
2. what can be scaled and mixed in the TMR wagon.
3. the consumed diet and what sorted out.

How to use urea value

Urea dates differ from farm to farm and are specific of them. Having determined the farm specific urea value, the raising and decreasing tendency informs about any challenge in the diet and feeding management as well. It is essential to analyze feed ingredient in order to make accurate formula. Beside the row material analysis, do not forget to examine the TMR time to time. The key factor is providing available carbohydrate to provide the energy for rumen microbes to convert ammonia into microbial protein. The desired milk urea level varies from 20 to 30 mg / dl.

High milk urea (higher than 32 mg / dl) or increasing value (higher than 4 mg / dl) is caused by the following feeding situations:

- Feeding too much total crude protein.
- Feeding too much rumen degradable (RDP) or soluble (SP) protein.
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- RDP and fermentable carbohydrate are note synchronized in time.
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- Low feed intake.
- Too low total crude protein or low in RDP or SP in the diet.
- Feeding too much NFC.
- Inefficient rumen fermentation.

SARA: Sub Acute Ruminal Acidosis

Oetzel G. R. (2013.) determined the three major causes to consider -over-feeding unsaturated fats, monensin feeding, and ruminal acidosis. Since monensin only can be used by individual treatment by bolus, it has no significance under Hungarian conditions. Excessive intake of dietary unsaturated fats is the most predictable and repeatable of all the causes of milk fat

depression. Unsaturated fats cause milk fat depression when they are transformed and then incompletely biohydrogenated in the rumen. Some of the intermediate forms of these fatty acids (particularly trans 10 18:1 fatty acids) are then absorbed at the small intestine and taken up by the mammary gland. There they strongly inhibit milk fat synthesis, even at very low doses (5 grams or less per day). High rates of passage also contribute to more escape of these fatty acids to the rumen. These fatty acids do not have detrimental health effects themselves; thus, it is possible for a herd to have milk fat depression without cow health problems (Oetzel G.R., 2013.)

Ruminal acidosis is the third major cause for milk fat depression. It apparently causes milk fat depression by inhibiting bacteria responsible for fatty acid biohydrogenation in the rumen. Experimentally induced SARA for only one day does not apparently cause milk fat depression, even when the ruminal pH depression is severe. This suggests that microbial responses to ruminal acidosis may be slow, and/or that multiple acidotic insults are necessary before ruminal biohydrogenation is inhibited enough to cause milk fat depression (Oetzel G.R. 2013.).

Table 1. The one page summary report.

Farm: Example Farm ENAR: No Date of controlling: xxxxxxxxxx

	Cows		Milk yield and composition			Fat less than 2.5%		Fat/prot< 1	Urea (mg/dl)					
Days in milking	Total head	Sample head	Milk kg	Fat %	Cr. Prot %	head	%	%	< 14	15 - 25	26 - 31	31 <	Avg.	W. avg last 6 mont
									Head					
1. lactation														
1 - 40	36	36	31,7	3,72	2,91	3	8,3	19,4	22	12	2	24,8	24,9	24,2
41 - 100	89	89	38,4	3,18	2,98	10	11,2	36,0	8	32	49	32,2	32,3	29,3
101 -199	184	184	36,3	3,29	3,16	9	4,9	34,8	3	26	155	35,8	35,8	29,5
200 -305	80	79	31,3	3,48	3,27	3	3,8	30,4	1	28	50	33,1	33,1	29,8
305+	131	131	26,9	3,88	3,54	1	0,8	28,2	5	34	92	34,1	34,2	28,3
Tot avg.	520	519	33,2	3,45	3,20	26	5,0	31,6	39	132	348	23,6	33,7	28,8
2. lactation														
1 - 40	32	32	41,6	3,91	2,99	0	0,0	9,4	5	18	9	29,3	29,5	25,3
41 - 100	72	70	46,8	3,09	3,00	11	15,7	44,3	3	15	52	33,6	33,5	27,9
101 -199	136	136	40,6	3,30	3,21	12	8,8	41,2	3	31	102	34,8	34,8	28,3
200 -305	108	108	32,4	3,46	3,45	9	8,3	41,7	2	19	87	35,3	35,5	27,8
305+	88	88	24,6	3,81	3,64	5	5,7	37,5	3	26	59	33,3	33,7	26,5
Tot avg.	436	434	36,4	3,41	3,26	37	8,5	38,7	16	109	309	34	34,1	27,5
3.+ lactation														
1 - 40	16	16	42,2	3,93	3,06	1	6,3	6,3	4	6	6	28,5	29,0	24,6
41 - 100	71	71	48,6	3,16	2,97	9	12,7	35,2		26	45	33,5	33,6	27,8
101 -199	137	137	40	3,27	3,18	15	10,9	47,4	5	39	93	34,9	35,1	28,6
200 -305	119	119	33,7	3,42	3,35	5	4,2	41,2	4	23	92	34,8	35,1	27,9
305+	66	66	23,4	3,76	3,59	2	3,0	33,3	4	27	35	32,1	32,6	26,5
Tot avg.	409	409	37,1	3,36	3,22	32	7,8	39,6	17	121	271	33,9	34,2	27,4
Total lactation														
1 - 40	84	84	37,4	3,85	2,98	4	4,8	13,1	31	36	17	27,2	27,8	24,7
41 - 100	232	230	44,1	3,14	2,99	30	13,0	38,3	11	73	146	33,0	33,1	28,3
101 -199	457	457	38,7	3,29	3,18	38	7,9	40,5	11	96	350	35,2	35,3	28,8
200 -305	307	306	32,6	3,45	3,37	17	5,6	38,6	7	70	229	34,5	34,7	28,6
305+	285	285	25,4	3,83	3,58	8	2,8	32,3	12	87	186	33,4	33,7	27,4
Tot avg.	1365	1362	35,4	3,41	3,23	95	7,0	36,3	72	362	928	33,8	34,0	27,9
Productiong roups														
01	142	142	37,3	3,28	3,10	9	6,3	31,7		10	132	36,8	36,8	31,0
02	139	138	34,4	3,29	3,17	7	5,1	36,2	4	44	90	33,3	33,4	27,7
03	47	47	33,7	4,16	3,00	1	2,1	6,4	23	19	5	25,8	26,0	22,3
04	97	97	30,3	3,69	3,47	1	1,0	33,0	3	23	71	34,5	34,6	3,1
05	68	68	37,4	3,24	2,98	8	11,8	35,3	17	35	16	28,3	28,3	28,8
06	96	96	40,6	3,21	3,19	13	13,5	49,0	2	32	62	33,9	34,0	28,0
07	95	95	33,3	3,50	3,50	8	8,4	48,4		14	81	36,1	36,3	28,3
08	93	93	37,4	3,24	3,28	8	8,6	49,5		19	74	35,4	35,5	26,6
09	94	94	33,8	3,62	3,45	3	3,2	29,8	1	14	79	35,3	35,4	27,7
10	83	82	42,3	3,37	3,06	5	6,1	37,8	1	27	54	33,5	33,5	29,6
11	91	90	47,9	3,01	2,98	19	21,1	40,0	2	28	60	33,1	33,1	27,3
12	93	93	42,8	3,46	3,18	3	3,2	32,3	2	16	75	36,2	36,2	28,0
13	105	105	20,7	4,15	3,61	0	0,0	18,1	11	34	60	32,1	32,2	23,8
14	80	80	33,7	3,32	3,31	9	11,3	52,5	4	29	47	33,1	33,2	28,8
15	42	42	17,2	3,83	3,63	1	2,4	35,7	2	18	22	31,7	32,1	24,1
Tot/avg	1365	1362	35,2	3,41	3,23	95	7,0	36,3	72	362	928	33,8	34,0	27,9

Milk fat content depends on many factors, like milking interval, season, number of rumination, heat stress, etc.. However, milk fat depression reaching the point of 2,5% milk fat content is most likely related to acidosis, as agreed by most of the authors. If the relative frequency is over 10% of the cows producing less than 2,5% milk fat in any herd, they most likely suffer from subacute ruminal acidosis (SARA).

Our practical report is applicable to show changes in protein and energy supply and to monitor the prevalence of SARA. Our experience with farm monitoring reflects that milk urea and the occurrence of SARA are independent of quantity and contents of milk. Optimal values can be obtained by good feeding and sound management at any milk production level.

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A screening method using Milk Amyloid A measurement in cow milk to significantly reduce the use of intramammary antibiotics at drying off

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Abstract

Milk Amyloid A (MAA) has been suggested in several studies as a biomarker of both clinical and subclinical mastitis. We conducted a study to evaluate the efficiency of the measurement of MAA by ELISA when used to make selective antimicrobial treatment decisions at mammary quarter level on cows at drying off. Mammary quarter milk samples from 112 cows, originating from low bulk tank somatic cell count (SCC) (<250,000 cells / mL) dairy herds and registered for drying off, were collected between two to seven days prior to drying off and once a week after calving, starting from two weeks until six weeks. All milk samples were cultured for bacterial detection and were analyzed for MAA concentration and for somatic cell count (SCC). Cow data and health events history were recorded. We performed a selective dry cow therapy at quarter level based on MAA results. The mammary quarters from cows with an MAA concentration ≥ 1 µg / mL (n=257) were treated with an intramammary antibiotic therapy and were infused with a teat sealant. The other quarters (MAA < 1 µg / mL) were only infused with a teat sealant and were not treated with an antibiotic therapy (n=94) or they were treated by antibiotic therapy and infused with a teat sealant (n=92). We developed an algorithm to identify an intramammary infection (IMI) at mammary quarter level at the end of lactation based on MAA and SCC results. The test characteristics of our screening method, called the MAA-Biotecklait method, were calculated and its negative (NPV) and positive (PPV) predictive values were estimated using bacterial culture as a gold standard. Our method was compared with the somatic cell count recording prior to drying off. The sensitivity and specificity of the MAA-Biotecklait method were both high, respectively 94.5% and 93.0% and the PPV and NPV when estimated in our study population were respectively 96.3% and 89.9%. The predictive values were both above 90% in populations where the proportion of udder quarters with an IMI at drying off ranged from 40% to 65%. By contrast, the sensitivity and the NPV of the SCC were low, respectively 68.7% and 62.8%. We concluded that the use of the MAA-Biotecklait screening method in a selective dry cow therapy programme at the quarter level would allow a significant reduction in the use of intramammary antibiotics at drying off with a low risk of missing infected udder quarters. In our study, its application would have reduced the use of antibiotic treatments by 29% and also would achieve the quantitative objectives of reducing antibiotic use in veterinary medicine by 25%, advocated by the French "ecoantibio 2017 plan". Moreover, we didn't observe a clinical mastitis six weeks after calving for quarters with a negative MAA-Biotecklait test that were not treated with antibiotics and were only infused with a teat sealant. These quarters have achieved success in the treatment and prevention of IMI over the dry period.

Keywords: Milk Amyloid A; Selective dry cow therapy; Reduction of antibiotic use; Algorithm; Intramammary infection.

Introduction

Worldwide, mastitis remains the most common disease of dairy cattle and the most economically important disease in bovine dairy production, with subclinical mastitis accounting for almost two-thirds of the economic loss (Seegers *et al*., 2003; Halasa *et al*., 2007). As part of mastitis control, most dairy producers in North America (USDA, 2008; Dufour *et al*., 2012) and in many European countries (Smith, 2014) treat all quarters of all cows with an intramammary antibiotic therapy at the end of lactation. This practice aims at reducing the prevalence of IMI, both by clearing up any existing IMI already present at drying off and by preventing new IMI from occurring during the dry period (Bradley and Green, 2001).

Antibiotic use creates a selective pressure on bacterial populations and contributes to the development of antimicrobial resistance (Tacconelli, 2009; Landers *et al*., 2012). In this context, organizations such as The Food and Drug Administration, recommend reduction in the use of antibiotics. In France, the "ecoantibio 2017 plan" advocates a cautious and rational antibiotic use. This plan is hinged around quantitative objectives of reducing antibiotic use in veterinary medicine by 25% in 5 years. To meet these recommendations and to achieve these quantitative objectives in dairy production, an alternative approach to treatment of all mammary quarters would be to target antimicrobial treatment only at infected mammary quarters at drying off. Therefore, udder quarters that are not suspected of having an IMI at drying off would enter the dry period without having received intramammary antibiotics. Only an internal teat sealant is administered to them.

In order to be successful, a selective dry cow therapy requires an easy, cost-effective and rapid method to identify cows with an IMI at the time of drying off (Sanford *et al*., 2006). The measurement of MAA by ELISA seems to be adapted for this purpose. MAA is suggested as a reliable biomarker of both clinical (Molenaar *et al*. 2009; Kovác *et al*., 2011; Pyörälä *et al*., 2011) and subclinical (Eckersall *et al*., 2006; Gerardi *et al*., 2009; Safi *et al*., 2009; Pyörälä *et al*., 2011) bovine mastitis. A specific ELISA kit for the measurement of MAA is commercially available. Its reliability when used in the diagnosis of subclinical mastitis in dairy cows was tested and was proved (Gerardi *et al*., 2009).

The objective of the study was to evaluate the efficiency of the measurement of MAA by ELISA when used to make selective antimicrobial treatment decisions at drying off at quarter level on cows originating from low bulk tank SCC. We developed a screening test (MAA-Biotecklait method) based on an algorithm to identify an IMI at quarter level at the end of lactation. Our algorithm has been developed based on MAA and SCC assay results carried out prior to drying off. The test characteristics and predictive values were determined using bacteriological culture as a reference method. Our method was compared with the SCC recorded just prior to drying off.

Materials and methods

Cows

Cows were selected from low bulk tank SCC (<250,000 cells / mL) dairy herds in the year prior to the trial. They were required to present with an apparent good health status, with no evidence of clinical mastitis, no intramammary anti-biotherapy and no systemic anti-inflammatory treatment within the last three weeks prior to drying off. Cows were also required to be pregnant in order to calve once again. A total of 112 Prim 'Holstein cows from 6 herds in 4 different locations in France were selected for the testing and were enrolled at drying off. All cow data and health events history of each cow were recorded.

Milk analysis and selective antibiotic treatment at drying off

Individual quarter milk samples of each cow selected for the testing were collected between two to seven days prior to drying off and once a week after calving, starting from two weeks until six weeks. The milk samples were collected aseptically in duplicate according to the procedures recommended by the Laboratory Handbook on Bovine Mastitis (National Mastitis Council, 1999). Immediately after sampling, one replicate of

each quarter milk sample was frozen to -20°C before submission to the laboratory for standard bacteriological culture and species identification. The other quarter milk sample replicates were stored at 4°C and were sent to a lab for SCC and MAA analyses. Milk analysis for MAA and for SCC was performed by a dairy laboratory that contributes to a French DHI programme (Oxygen Laboratoires d'Analyses, Maroeuil, France). The concentration of MAA was determined using a commercial ELISA kit (Milk Amyloid A-MAA Assay Kit, cat. no. TP-807; Tridelta Development Ltd, Maynooth, Ireland) in accordance with the manufacturer's recommendations. SCC was assessed by fluoro-opto-electronic cell counting (Somacount FCM; Bentley Instruments, Maroeuil, France). The mammary quarters were treated at drying off according to their MAA concentration results. A MAA cut-off value of 1 µg / mL was used. This value is in agreement with the study of Åkerstedt *et al*. 2011 in which MAA was measured below 1 µg / mL in the clinically healthy quarters. Earlier studies suggested cut-off values between 0·8 and 1·4 µg / mL to indicate an inflammatory response in quarters and in cow composite milk samples (Grönlund *et al*. 2003; Jacobsen *et al*. 2005; O´Mahony *et al*. 2006). The quarters with an MAA concentration ≥ 1 µg / mL (n=257) were treated with an antibiotic therapy and were infused with a teat sealant. The other quarters (MAA < 1 µg / mL) were only infused with a teat sealant and were not treated with an antibiotic therapy (n=94) or they were treated with an antibiotic therapy and infused with a teat sealant (n=92).

Bacteriological culture and IMI definitions

Bacteriological culture and species identification were performed by a COFRAC accredited laboratory (LABÉO Manche, Saint-Lô, France). The milk samples were cultured using standardized protocols based on the NMC guidelines (Hogan *et al*., 1999). A mammary quarter was defined as having an IMI if ≥ 100 cfu / mL of milk of any pathogen was cultured as either pure or mixed growth, except coagulase negative staphylococci (CNS). For CNS, a definition ≥ 200 cfu / mL was used. These definitions are in accordance with the recent publication of characterization of IMI based on single sample bacteriological testing (Dohoo *et al*., 2011). A sample from which three or more different species were cultured was classified as contaminated.

Statistical analysis

An algorithm has been developed to identify an IMI at quarter level at the end of lactation. It is based on MAA and SCC assay results of the quarter milk samples collected from the 112 cows selected in this study (MAA-Biotecklait Method). Further details are not given for reasons of commercial sensitivity. The characteristics of the MAA-Biotecklait method and of the SCC method were calculated using 2 × 2 contingency tables and by using bacteriological culture as a reference method. Sensitivity was defined as the proportion of quarters with an IMI that were classified as positive with a screening method. Conversely, specificity was defined as the proportion of mammary quarters without an IMI that were classified as negative with a screening test. The PPV was the proportion of udder quarters with positive screening test results that truly had an IMI. The NPV was the proportion of quarters with negative screening test results that did not have an IMI. A threshold of 100,000 cells / mL for primiparous cows or of 150,000 cells / mL for multiparous cows was used for the calculation of sensitivity and specificity of the SCC method. The performance of the MAA-Biotecklait method in different cow populations with varying degrees of infected mammary quarters was examined. The predictive values were calculated for prevalence estimated ranging from 1 to 100% and using the formulas based on Bayes' theorem.

Results

Bacteriological culture

The distribution of pathogens isolated in quarter milk samples is presented in table 1. The environmental streptococci were grouped together and encompassed *Aerococcus viridans* (n=10), *Enterococcus faecalis* (n=3), *Lactococcus gravieae* (n=4), *Micrococcus* sp. (n=1), *Streptococcus dysgalactiae* (n=2) and *Streptococcus uberis* (n=3). Gram-negative bacteria were also amalgamated into a grouping, and included *Acinetobacter* sp. and *Acinetobacter baumannii*. The most frequently isolated pathogens at the end of lactation were minor pathogens, in descending order, CNS, followed by environmental Gram-positive pathogens *Corynebacterium* spp. and environmental streptococci, predominantly *Aerococcus viridans*. Two bacteria species were isolated in some udder quarter samples (12%), with CNS constantly present. The percentage of contaminated samples and of samples lost was respectively 29.3% and 14.5%. According to our extrapolated bacteriological culture results, the prevalence of an infected quarter prior to drying off in our cow population was 65.5%.

Table 1. Distribution of pathogens isolated in quarter milk samples collected between two to seven days prior to drying off. Results are presented as the number quarter and as a percentage of total quarter infected or not with an organism. The number of analyzed bacteriological culture results was n=249.

Pathogens	Number of quarters	Percentage of total quarters
No growth	86	34.5
Coagulase negative staphylococci (CNS)	78	31.4
Corynebacterium spp. (C. spp.)	27	10.9
Streptococci[a] (Strep.)	23	9.2
CNS + C. spp.	20	8.0
CNS + Strep[b]	10	4.0
Coliform	0	0
Gram-negatives[c]	2	0.8
Strep. agalactiae	3	1.2
Contaminated	130	-
No sample	64	-

[a]Streptococci include: *Aerococcus viridans, Enterococcus faecalis, Lactococcus gravieae, Micrococcus sp., Streptococcus dysgalactiae and Streptococcus uberis.*
[b]Strep. encompass *Aerococcus viridans, Streptococcus uberis and Lactococcus gravieae.*
[c]*Acinetobacter sp.* and *Acinetobacter baumannii*

Test characteristics and predictive values of the screening methods

The characteristics of the MAA-Biotecklait and SCC screening methods to identify an IMI at mammary quarter level were calculated by using bacteriological culture as a reference method. The predictive values of the methods were estimated considering only prevalence of IMI in our studied population (65.5%) (Figure 1).

The sensitivity and the specificity of the MAA-Biotecklait method were both high respectively 94.5% and 93.0%. The estimation of the PPV was 96.3% and that of the NPV was 89.9%. By contrast, a high specificity (97.7%) was obtained using SCC method whereas the sensitivity was low (68.7%). The calculated PPV and NPV for this method were respectively 98.2% and 62.8%.

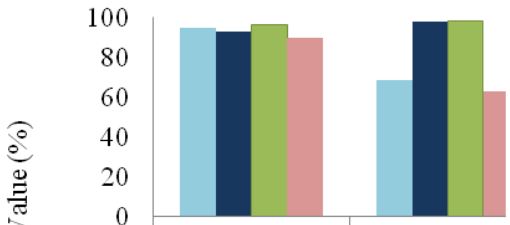
The performance of the MAA-Biotecklait method in different cow populations, with varying degrees of infected quarters, was more specifically examined. The predictive values were calculated for prevalence estimation ranging from 1 to 100% (Figure 2).

The PPV and NPV were both high, above 90%, in populations where the proportion of udder quarters with an IMI at drying off ranged from 40% to 65%. These were also maintained at high enough levels (> 85%) in populations where the prevalence at a quarter level of an IMI ranged from 30% to 75%.

Discussion

The aim of a selective treatment at a mammary quarter level is to reserve intramammary antibiotic therapy for quarters that are suspected of having an IMI at drying off. No antibiotic is administrated to quarters presumed not to have a subclinical mastitis at the end of lactation. An internal teat sealant (ITS) is only applied to protect them against an infection during the non-lactating period. This practice would contribute to reduce antibiotic use in dairy production. Therefore, such a treatment programme requires a screening method to identify the health status of udder quarters at drying off. An ideal method would have maximum sensitivity and specificity to minimize the proportion of false-negative and of false positive results (Dingwell *et al.*, 2003; Midleton *et al.*, 2004; Sanford *et al.*, 2006). Therefore, the treatment of infected quarters and reduction of antibiotic use for healthy quarters would be magnified. Our results indicate that the screening test to detect an IMI at drying off using SCC at a threshold value of 100,000 cells / mL for primiparous cows or of 150,000 cells / mL has low sensitivity. The use of this method as part of a selective programme at a mammary quarter level at the end of lactation thus seems unsuitable. In our cow population, more than 30% of infected quarters would be missed and not treated. In contrast, our results show that when used to detect an infected quarter at drying off, the MAA-Biotecklait screening method had high sensitivity (94.5%) and high specificity (93.0%). As a result, this method could be used to make selective dry cow treatment decisions with the confidence that very few infected udder quarters would be missed and that high proportion of the healthy mammary quarters would be not treated with antibiotic therapy. They would be only infused with a teat sealant.

In our study, the most frequently isolated pathogens in mammary quarters were coagulase negative staphylococci. The prevalence of this group of species in our total mammary quarter population was 43.4%. Similar results of prevalence were reported in earlier studies. In a German study, 35% of quarters with subclinical mastitis harbored CNS (Tenhagen *et al.*, 2006). The highest prevalence of intramammary infections with CNS was reported in Finland, where CNS were isolated from 50% of the quarters positive for bacterial growth in a nationwide survey (Pitkälä *et al.*, 2004). The effect on somatic cell



	MAA-Biotecklait Test	SCC Test
Sensitivity	94,5	68,7
Specificity	93,0	97,7
PPV	96,3	98,2
NPV	89,9	62,8

Figure 1. Test characteristics, positive (PPV) and negative (NPV) predictive values of MAA-Biotecklait and SCC methods to identify an IMI at mammary quarter level at the end of lactation in cow population originated from herds with a low bulk tank SCC (<250,000 cells/mL). A threshold of 100,000 cells/mL for primiparous cows or of 150,000 cells/mL for multiparous cows was used for SCC method.

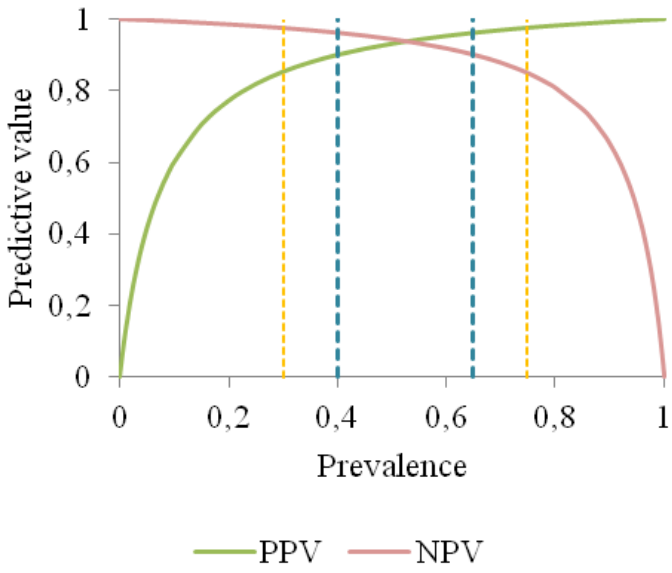


Figure 2. Positive predictive values (PPV) and negative predictive values (NPV) of the MAA-Biotecklait screening method when used to diagnose an IMI at mammary quarter level at drying off in cows from herds with low bulk tank SCC (<250,000 cells/mL) and for prevalence of IMI ranging from 0 to 100%. The vertical blue dashed lines indicate the prevalence range (40-65%) for which the PPV and the NPV both are above 90%. The yellow lines indicate the prevalence range (30-75%) for which the PPV and the NPV both are above 85%.

count is accepted to be generally limited or nonexistent for CNS as a group (Vanderhaeghen *et al.*, 2014). This nonexistent effect would explain the low sensitivity obtained in our study for the SCC method. In contrast, our results indicate that the sensitivity of the MAA-Biotecklait method was high. This method is based on an algorithm developed from SCC level and from the MAA concentration in milk. Therefore, taking into account the MAA concentration in milk seems to enable us to detect mammary quarters infected by CNS at the end of lactation. The possible use of MAA concentration levels in milk samples to detect mammary quarters infected by coagulase-negative staphylococci has been previously described (Pyörälä *et al.*, 2011).

The predictive values of a positive or negative MAA-Biotecklait test across cow populations with varying levels of infected udder quarters at drying off were calculated from the test characteristics of the MAA-Biotecklait method. As illustrated in Figure 2, for a prevalence of infected quarters ranging from 40% to 65%, the PPV and the NPV were both high, above 90%. Then, the proportion of udder quarters truly infected with a negative test (1 - NPV < 10%) that would not receive an intramammary antibiotic treatment would be small in herds where the prevalence is ranged from 40% to 65%. Moreover, in herds with this prevalence range, few of udder quarters truly healthy with a positive test sentence (1 - PPV < 10%) would be treated with an antibiotic therapy. Similar but more moderated results were obtained for a prevalence ranging from 30% to 75%. Consequently, the use of the MAA-Biotecklait method to make selective treatment decisions at udder quarter level at drying off would allow the significant reduction of antibiotic use on dairy farms, with a low risk of missing infected udder quarters. In our study, its application would have reduced the use of antibiotic treatments by 29%. The use of the MAA-Biotecklait method at drying off will allow us to achieve the quantitative objectives of reducing antibiotics in veterinary medicine by 25% advocated by the French "ecoantibio 2017 plan". In parallel, the dairy producer will obtain cost savings regarding the management of herds.

Conclusions and perspectives

The MAA-Biotecklait screening method, based on an algorithm developed from SCC and MAA assay results of quarter milk samples has high sensitivity and specificity, high positive and negative predictive values, when used to diagnose an infected cow mammary quarter at drying off. Its application in a selective dry cow therapy programme at the mammary quarter level would allow a significant reduction in the use of intramammary antibiotics at drying off with a low risk of missing infected udder quarters. Moreover, our first results at calving show no clinical mastitis six weeks after calving for quarters with a negative MAA-Biotecklait test that were not treated with antibiotics and were only infused with a teat sealant. These quarters have achieved success in the treatment and prevention of IMI over the dry period.

We plan to reinforce our algorithm by the addition of thousands of MAA and SCC assays to the database that is used to support it. We are launching a cost-effective service at drying off for dairy farmers based on our MAA-Biotecklait method from September 2015. We use a simple and high throughput laboratory ELISA assay. The MAA assay and the access to our algorithm are available in France from our group Biotecklait and worldwide from Tridelta Development Ltd. We also intend to launch other services for the dairy farmers based on our algorithm.

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Pregnancy detection from milk samples obtained for routine milk yield measurements - results and evaluation

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Abstract

The side effect of increasing milk production compromises the reproductive result in many high producing dairy herd in Hungary. The challenge is how to decrease the calving interval which has a detrimental effect on profitability of the dairy farm. The sooner detection of pregnancy shortens the calving intervals by identifying open cows earlier. Chemical tests for early pregnancy diagnosis that use qualitative measures of pregnancy-associated glycoproteins (PAGs) originating from the placenta have been developed and commercialized. PAGs are produced specifically by the placenta, the presence of PAGs in blood can be used to accurately determine pregnancy status. Recognizing the emerging importance of early detection of pregnancy, our company has introduced a PAG based bovine pregnancy testing from milk by IDEXX Milk Pregnancy ELISA test in April of 2013. The same sample which is routinely analyzed under milk recording procedure also can be appropriate for PAG test. The test can be applied since 35 days of pregnancy (nowdays 28 days). Up to now, a large number of samples has been examined and the results are continuously evaluated on the basis of reported number of calving. Inclusive January 2015, 29 440 tests were performed. By the end of April 2015, 92 stocks numbering 27 823 cows were involved in the service. The efficiency of the method was verified by taking reported number of calving as "golden standard" assuming 285 days pregnancy time +/- 14 days tolerance threshold. On the basis of our rationale the test fulfills the specificity and sensitivity criteria expected from a bovine pregnancy test and might be a reliable new method in detecting bovine pregnancy.

Key words: Milk, pregnancy test, PAG, milk-recording

Introduction

The profitability and the competitive position of a dairy farm depends on many factors. Recently the profitability of a dairy farm is fundamentally influenced by its reproductivity. As the milk production is increasing, the reproductive problems occur more frequently, the calving interval dramatically becomes longer (437 days), the average conception rate is above 3. To maintain profitability a 400-day calving interval is preferable. Regarding the conception rate 2 or less than 2 is acceptable, in any dairy herd 80% of the cows should produce calves.

The key factor to decrease calving interval is the sooner detection of pregnancy. The average economic loss due to the reproductive problems is about 40.000-80.000 HUF (155-315 Euros) per cow per year in Hungary (Ózsvári 2012). One "empty day" in a dairy herd means a loss of 500-900 HUF (an average of 700 HUF = 2.7 Euros). This means 60.000 HUF reproductive loss per cow. In a dairy herd of 1000 cows this represents 60 million HUF (233.000 Euros) loss that can be 9-11% of the revenues of a dairy herd. Probably the reproductive problem represents the largest economic damage in Hungary.

An appropriate pregnancy test should be sensitive and specific. Sensitivity means the safe and correct identification of the pregnant cows (avoiding iatrogenic abortion), the specificity means the accurate detection of empty cows. The consequences of false negative results (pregnant cows diagnosed empty) which come from the low sensitivity of the test is more serious. False positive results (open cows diagnosed pregnant) coming from the low specificity of the test, can cause the later detection of the empty cows. The early and the late embryonic loss may influence the accuracy of the pregnancy test, the earlier the pregnancy test is done the more significant is this distortion. However the cow is defined empty by the test it must be examined by palpation and ultrasound methods (avoiding iatrogenic abortion), but due to the infertility testing it is also proposed. To use these two additional above mentioned examinations, we can evaluate the early embryo and fetus loss. The table chart below helps us to evaluate the losses well (Szelényi, 2014):

Table 1. Evaulation of losses (Szelényi, 2014)

Early embryonic death	Late embrionic death	Early fetal death	Late fetal death	Abortion
0 – 16 day	16 – 42 day	42 – 90 day	90 – 150 day	150 – day

PAG ELISA pregnancy Test

The milk pregnancy test is an enzyme-linked immunosorbent assay kit (ELISA) that is suitable for the detection of the placenta produced pregnancy related glycoproteins (PAGs) from milk sample. It makes possible to detect pregnancy from the 35th day after the insemination so it has a very important role in early identification of empty cows. The test can be used from 60th days after the preceding calving due to the persistency of the PAGs produced during the previous pregnancy. The pregnancy proteins (Pregnancy Associated Glycoproteins - PAGs) are the family of almost 100 different identified protein molecules produced by the placenta both the fetal and mother part. PAG can be detected from milk samples from the 35-40th days after the insemination till 60 days after calving accurately. The quantity and the contents of the PAGs measured in the milk samples are variable. The variance between individual cows is bigger. The threshold of the method (cut off line) considers the quantitative variations. The level of the PAGs decreases gradually after calving. Their half-life period is long. However they completely empty from the body by the 60-90 days after calving.

Integration of pregnancy testing into the milk-recording system

The milk pregnancy test can be easily integrated in the activities made by the Livestock Performance Testing Ltd. The calving interval may be reduced by the early detection of the empty cows. The advantages of including milk pregnancy test into the routine animal recording programme as follow:

- Milk sampling connected to animal recording made by sample technicians (certainly it can be made more frequently).
- Not necessary to hold and tie the animals.
- Not invasive intervention.
- No extra delivery and sampling cost.
- No extra labour needed.
- Fast and reliable results (within 48 hours).

The summary of the test criteria:

- The test can be performed from the 35th day of the conception.
- The test can be performed from the 60th day of the preceding calving.
- The test is not reliable in mastitis infection.

The milk samples are currently being received by two ways. With samples arriving through animal recording we know all the breeding data, so we can analyse them as "gold standard" taking the date of calving declared as a basis. In case of samples sent separately we can state the result.

1. Data preparation for the sampling

The PAG samples are originated from test day milk samples (it can be defined of the same sample, the result is not influenced by preservatives). The first step - as usual during the animal recording - is data capture. The first data is being uploaded according to the general system. The cows are assorted with a data handler called WinTell Prior to the milking

2. Sampling

The laboratory use violet-coloured sampling vials for pregnancy test. These vials are the same as the other ones used for general milk recording, only their colours are different.

During the test day when the cow is identified in the milk stand, the program warn the sample technicians (M-first sample, E-control sample) that PAG sample must be taken as well. In case of these cows the samples are taken into violet-coloured vial instead of white one. Using TruTest the white vial must be changed to violet one in the marked milk stands. In case of installed sampling equipment the vials must be changed in the sample collecting track (stand positioned vials) and the samples must be poured into these vials. The further procedure of the milk recording does not change.

3. Laboratory

Pregnancy test is based on a kind of sandwich ELISA method. The test takes 4-4 ½ hours. The milk test laboratory provides the results to further data with IDs (barcodes) of the vial.

4. Evaluation, data providing

In the data processing department we assign the test results to the cows and we send the reports to the farms. We provide the test results within two days after the arrival of the samples. We can provide the test results also in e-mail in data file, on demand. The report contains the number of the tested samples and the test results in a table chart.

Table 2. PAG measurements between 04/2013 – 03/2014 (1 year).

Month	Number of samples	Pregnant	Open	To repeat
		All measurement		
04/2013 – 03/2014	14315	8288	5383	640 (4,47 %)
		Through the Milk laboratory		
	6383	3174	2992	220
		Through the Data processing		
	7932	5114	2391	420
		Days of gestation		
0-34 days	394 (NE)	166 (NE)	199 (NE)	29 (NE)
35-45 days	2661	1368	1035 (38,89 %)	168
46-60 days	1901	1028	724	149
Over 60th days	3066	2555	435	76

NE= not evacuate.

Table 3. Detailed review of the PAG samples (04/2013 – 03/2014)

Based on gestation days (passed time since AI in days). Pregnancy: 285 +-/14 days		Results of pregnancy examination				
		Results according to the reported calvings				
Days passed since AI	PAG	Cows	Notification	Cows	Remark
36 - 45 days	1268 pregnant	916	In time		
		143	False notified date of AI		Calving of earlier AI
		304	No calving		Late embryonic death ~ 16,32 %
				97	Waste or out of measurement
	1035 open	1028	Open		99,32%
		7	Pregnant		
	168 to repeat	6	Pregnant		
		162	Open		
46 - 60 days	1028 pregnant	728	In time		
		102	False notified date of AI		Calving of earlier AI
		148	No calving		Early fetal death ~ 8,85 %
				57	Waste or out of measurement
	724 open	720	Open		99,44%
		4	Pregnant		
	149 to repeat	40	Pregnant		
		109	Open		
More than 60 days	2555 pregnant	2172	In time		
		239	False notified date of AI		Calving of earlier AI
		144	No calving		Early fetal death ~ 2,66 %
				76	Waste or out of measurement
	435 open	430	Open		98,85%
		11	Pregnant		
	76 to repeat	26	Pregnant		
		50	Open		

Results

Until the end of April this year 92 herds with 27 823 cows have used our service. We have already made 29 440 tests until the end of April 2015.

We can evaluate only the pregnancies running through our data processing because we only have breeding data of those cows. The cows detected pregnant are also distinguished according to the days passed after the conception. The selected day for sampling meet the criteria of the early pregnancy detection. As you can see, more sample arrived in the laboratory that could not meet the requirements of the test. Of course these samples were not evaluated. The most frequent mistake: the minimum 35 days have not passed after the insemination.

The data processing of the LPT Ltd. considers an insemination successful, if the recorded calving is around 285 +/- 14 days after the announced insemination!!! The results below are evaluated concerning this fact.

In the second table chart we can closely define the rate of fetus and embryo loss.

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Estimation of the prevalence of subacute ruminal acidosis in dairy herds

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Abstract

Subacute ruminal acidosis (SARA) is a nutritional disorder encountered in the high-producing dairy cows. This disease appears in cases of high nutrient density diets including an increase in the proportion of concentrates and a decrease of the forage particle size. The consequences of SARA include a reduction of milk production (milk yield, milk fat, milk protein) and an increase of associated pathologies (laminitis, rumenitis, diarrhea, liver abscesses…). French milk recording organizations set up a study in order to: - developed knowledge on SARA on field conditions based on farms located in the west of France - to validate risk factors described in the literature - and to assess the sensitivity of milk fat and protein contents as an indicator of SARA. The experimental plan was articulated in two parts. In the first part, prevalence of SARA has been estimated on commercial farms. 144 dairy cows from 12 dairy herds were investigated in the West of France. In each herds, pH measurements were made on 12 selected cows using a ruminal fluid sample collected with an oro-ruminal probe. Additional measurements were: rumen fill, body condition score (BCS), faeces consistency, counting undigested maize grain and the composition of the diet. Individual milk records associated to these measurements were also collected (milk yield, milk fat and protein contents, somatic cell count). In the second part, assessment of the reliability of milk fat and protein contents as predictor of SARA was conducted using a population database with more than 350,000 dairy cows. In the surveyed farms, the prevalence of SARA is 2.1% with a pH threshold of 6.2 to define SARA. Symptoms associated with SARA in the literature were not significantly related to ruminal pH in our study. Calculated prevalence on the population database according to indicators [fat / protein<1], [0<fat-protein<3] and [fat<35] are respectively 4.60%, 8.70% and 27.10%. Indicators derived from milk fat and protein contents are not sensible and specific enough to detect low pH values.

Keywords: subacute ruminal acidosis, SARA, dairy cow, oro-ruminal probe, pH, milk fat, milk protein.

Introduction

Subacute ruminal acidosis (SARA) is currently considered as a major nutritional disease for high-producing dairy cows (Plaizier *et al.*, 2009). SARA is associated with high nutrient density diets, most of the time made of a larger proportion of concentrates and a reduced forage particle size compared to regular diets (Peyraud *et al.*, 2006). Other risk factors of SARA according to the literature are: high quantity of concentrate per meals, high-producing cows (big capacity of ingestion), first lactation heifers (competition for feed) and difficulty for getting access to feedbunk (Garrett *et al.*, 2007). SARA has no specific clinical sign but is associated with a decrease of dry mater intake (DMI), milk yield and milk fat content

(Krause *et al.*, 2005). Worldwide, 8 to 28% of cows could be affected by SARA (Kleen *et al.*, 2012). In France, few studies have estimated the prevalence of SARA in commercial dairy farms, about 1.8% according to Mannessiez (2009). Current definitions of SARA are based on the pH of rumen fluid. The various technique used to measure rumen pH (rumenocentesis / oro-ruminal probe / indwelling electrode / ruminal cannulation) can affect the pH values and make difficult a scientist consensus for a pH threshold significant of SARA (Tajik *et al.*, 2011; Plaizier *et al.*, 2009). These difficulties to diagnostic SARA induce a lack of knowledge on the disease. The objectives of this study are 1) developed new knowledge on this disease on field conditions based on farms located in the west of France, 2) to validate risk factors described in the literature, 3) to assess the sensitivity of fat to protein ratio as an indicator of SARA.

Material and methods

The experimental plan was articulated in two parts.

Part 1: Prevalence of SARA has been estimated on commercial farms deriving the methodology from Garrett *et al.* (1999). Farms were selected according to 3 conditions: the existence or suspicion of SARA risk factors (according to the farm nutritionist), the presence of head-lockers in the farm and the agreement of the farmer. In each herd, pH measurements were made on 12 selected cows. Samples of ruminal fluid have been collected with an oro-ruminal probe (LPG). Cows were selected according to the risk they were affected by SARA. If the farm used a total mixed ration (TMR), cows between 100 and 150 days in milk (DIM) were selected because they have a high intake capacity. If the farm made an individual distribution of concentrates, cows between 5 and 50 DIM were selected because some of them receive high quantity of concentrates. Ruminal fluid was collected when pH values were suspected to be the lowest: between 5 to 8 hours after feeding if the diet is a TMR or 2 to 5 hours after individual concentrate feeding. About 0.5 L of rumen fluid was thrown before performing pH determination using an electronic pH meter (Hanna HI 8424 model). Additional measurements were: rumen fill, body condition score (BCS), faeces consistency, counting undigested maize grains and the composition of the diet. Individual milk records associated to these measurements were collected and consisted of milk yield, fat and protein contents and somatic cell count.

Part 2: Assessment of the reliability of fat and protein contents as predictor of SARA was conducted. A population database with more than 350,000 dairy cows from 8 to 120 DIM was built. This database contains results of individual milk records: milk yield, milk fat and protein contents, somatic cell count, days in milk and rank of lactation. Using the population database, three indicators were tested to diagnose cows affected by SARA: 1) a fat to protein ratio below 1 [fat / protein<1], 2) a difference between fat content and protein content are between 0 and 3 [0<fat-protein<3], and 3) a fat content below 35 g / kg of milk [fat<35] (Sauvant *et al.*, 1999; Sauvant *et al.*, 2010; Herman, 2012).

Statistical analysis: Descriptive analysis and ANOVA (lm procedure) were performed using the R 3.0.0 statistical package. Difference were considered significant at $P<0.05$ (***<0.001; **<0.01; *<0.05).

Results and discussion

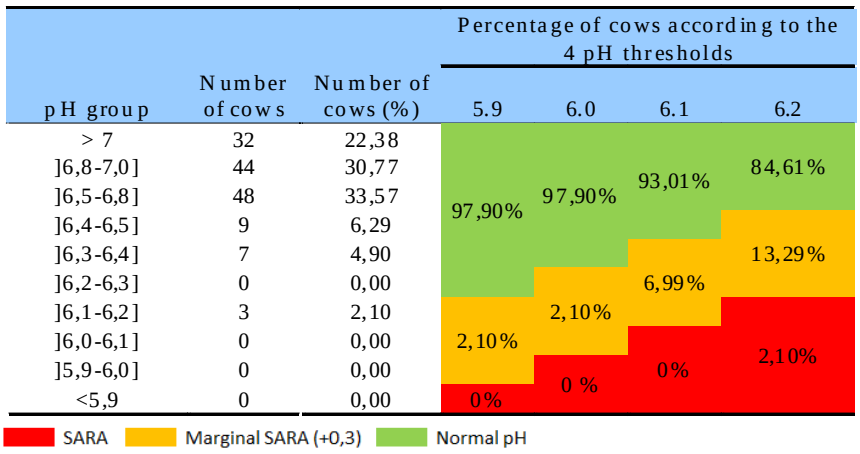
In total, 143 pH measurements were collected. The average ruminal pH was 6.81. No cow had a ruminal pH below the threshold of 5.9. Only 3 cows (2.1% of the studied population), had a ruminal pH below 6.2. Sixteen cows had a ruminal pH between 6.2 and 6.5, and 124 cows have a ruminal pH above 6.5. Values of ruminal pH were classified in 6 groups with a constant pH-interval [<6.2], [6.2-6.4], [6.4-6.6], [6.6-6.8], [6.8-7.0] and [>7]. Anova performed on milk parameters (milk yield, fat and protein contents, somatic cell count) and on farm measurements (rumen fill, BCS, faeces consistency, counting undigested maize grains and the composition of the diet) according to the 6 pH groups did not present significant

differences. However, significant correlations were found between ruminal pH and rumen fill (-0.24**), ruminal pH and herd milk yield (-0.17*) and ruminal pH and quantity of concentrate per day (-0.23**).

Rumen fluid pH thresholds, of samples collected by rumenocentesis, used to diagnose SARA are below 5.5 (Garrett *et al.*, 1999). However, there is no scientific consensus on a pH threshold for the rumen fluid samples obtained by the oro-ruminal probe method. The use of an oro-ruminal probe induces a contamination of ruminal fluid by saliva which can increase the pH. An adaptation of the interpretation thresholds is needed. Duffield *et al.* (2004) report a difference between oro-ruminal probe method and rumenocentesis of +0.35 pH points. Among the literature, the adjusted threshold to detect SARA in ruminal fluid sampled through oro-ruminal probe vary from 5.9 to 6.2 (Duffield *et al.*, 2004; Hofirek *et al.*, 2001).In this study, 4 different thresholds of pH were tested: 5.9, 6.0, 6.1 and 6.2 Depending on thresholds used, prevalence of SARA was ranged from 0 and 2.1% (table 1). This is a low prevalence in comparison to others studies conducted in different countries (Kleen *et al.*, 2012), however, this is in agreement with a French study conducted in 2008 which reports - with the rumenocentesis method - a prevalence of 1.8% in 52 Brittany dairy herds (Mannessiez, 2009).

Table 1. Distribution of cows according to the pH groups and percentage of cows with SARA, marginal SARA and normal pH according to the 4 pH thresholds: 5.9, 6.0, 6.1 and 6.2.

			Percentage of cows according to the 4 pH thresholds			
pH group	Number of cows	Number of cows (%)	5.9	6.0	6.1	6.2
> 7	32	22,38				
]6,8-7,0]	44	30,77				
]6,5-6,8]	48	33,57				
]6,4-6,5]	9	6,29				
]6,3-6,4]	7	4,90				
]6,2-6,3]	0	0,00				
]6,1-6,2]	3	2,10				
]6,0-6,1]	0	0,00				
]5,9-6,0]	0	0,00				
<5,9	0	0,00				



When using the methodology based on fat and protein contents, prevalence of SARA was 4.6% using the fat / protein ratio, 8.7% using fat-protein contents and 27.1% using a threshold for fat content (figure 1). These results are in accordance with the results of Herman (2012) who calculates an annual prevalence of 5.5%, 9.3% and 15.56% in France with the same indicators. However, the estimated prevalence really differs according to the indicator used. The comparison between pH values and milk fat and protein contents shows that milk fat and protein contents are not relevant to identify cows with lowest ruminal pH values. With the threshold of ruminal pH value of 6.2 + 0.3 pH points which corresponds to "marginal SARA" (cows which could develop SARA in the future - Duffield *et al.*, 2004; O'Grady *et al.*, 2008), the sensitivity (capacity to detect cows with lower pH values than 6.5) and specificity (capacity to detect cows with a pH value above 6.5) are presented in the table 2.

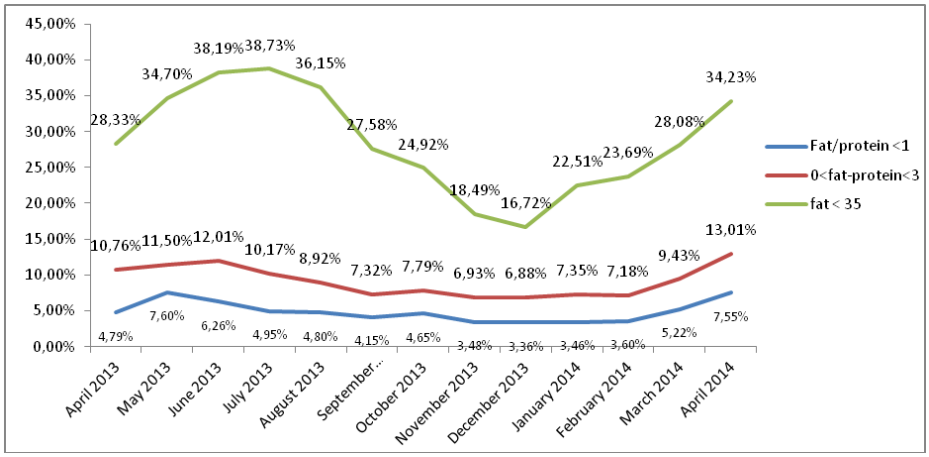


Figure 1. Monthly prevalence according to the three indicators tested (April 2013 - April 2014).

Table 2. Calculation of sensitivity and specificity of 3 indicators derived from milk fat and protein contents to detect low ruminal pH (pH threshold: 6.5).

		pH threshold (6.5) > = 6,5	Predictive quality < 6,5 = SARA	Sensitivity	Specificity
Indicator 1	Fat/protein ? 1	116	16		
	Fat/protein < 1	10	1	6%	92%
Indicator 2	0 ? fat – protein ? 3	106	13		
	0 < fat – protein < 3	20	4	24%	84%
Indicator 3	Fat ? 35	77	10		
	Fat < 35	49	7	41%	61%
	Total	126	17	143 cows	

Conclusions

Samples of ruminal fluid were collected with the oro-ruminal probe. Because of saliva contamination, the pH threshold of 6.2 was selected to define a SARA. In the surveyed farms, the prevalence of SARA is 2.1%. This prevalence of SARA is lower than the prevalence reported in other European countries. Symptoms associated with SARA described in the literature were not significantly related to ruminal pH in our study. Indicators derived from milk fat and protein contents are not sensible and specific enough to detect low pH values. Further studies are needed to determine a threshold for ruminal fluid collected through oro-ruminal probes in order to diagnose SARA.

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Session 2

Advisory services built on recording data

Organizing advice for dairy herds breeders: Example of a Milk Recording Organisation in the west of France

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Abstract

BCEL Ouest is a milk recording organization run by farmers for farmers. BCEL Ouest directs its action and innovates to support dairy farmers to develop their performance and competitiveness as part of their operating strategy.

Our approach is to help farmers to express the genetic potential of their livestock. For this purpose, our advisors and consultants assist farmers in efficient herd management based on data and predictive indicators.

Keywords: advice organization in dairy herds, herd management.

Introduction

BCEL Ouest is a milk recording organization that works with more than 6,000 dairy farms located in Brittany, in the west of France. The average farm in Brittany is on 85 hectares of crops and pastures, has a 63 dairy cows' herd that produces 8050 kg of milk per cow (2014).

We offer a wide range of services as: milk recording, herd management advice, agronomy advice, cattle housing design, trimming, testing of milking machine, etc. ….

The members of our non-profit organization represent 72% of the milk producers of our area for milk recording, and 65% for herd management advice.

The milk recording organization

The whole data collection organization relies on 300 operators totally dedicated to this activity. 6 data collecting protocols are offered. 85% of collections are realised by our operators and 15% by the breeders themselves. Since 5 years, the collection of data is realised during milking and totally digitalized through PDA. The traceability of collected samples is guarantee by the RFID technology. Information is immediately transferred to regional data bases. This data collection will be soon available on smart phones.

Since 2013 cattle disease data are also recorded by the operators at the end of milking. This allows us to establish a health data base.

The advisory approach

A network of 160 advisors

Over the years, the milk collection process allowed us to develop an activity of herd management advice. We have today a network of 160 advisors who propose their expertise to dairy farmers on our territory (divided into 8 areas). Most of our advisors have obtained a Master's degree, specializing in livestock production.

Each advisor works with 30 to 50 farms throughout the year. The advisor comes between 6 to 11 times per year in the farm, number based on the contract signed between BCEL Ouest and the dairy farmer. Each working session takes place during 3 hours. It usually occurs after a data collection sequence which provides the recent data on the dairy animal behavior and livestock performance.

As a result of his active listening from the dairy farmer at each meeting, and his knowledge of the herd and the area production conditions, the advisor establishes a diagnosis of main results and actions regarding the herd management. He gives breeders advices about:

- Herd performances analysis.
- Livestock feeding and forage production: ration proposal, monitoring the cost on food margin.
- Forage stocks management.
- Cattle disease prevention: reproduction, milk quality and udder health.
- Herd renewal and genetic selection: heifers breeding, mating choice.
- Forecasting of milk volumes to be delivered in the next year.

The advisor has a permanent access to the data of the livestock through a specific software at his disposal.

An annual technical report

Each year we establish a technical management annual report that allows an analysis of the strengths and issues for improvement in herd management. It is focused on different results such as milk quality, reproduction performances, levels of milk reference achievement and describes especially the feeding system.

This global diagnosis of dairy management helps us to plan for the future of the farm.

It is a common tool shared by the breeder and his advisor to identify the technical focus on improving, and to measure the financial impacts obtained.

The compilation of these data in the followed farms allows us to establish some technical and economic references adapted to different breeding systems. Thus, 15 different reference groups are identified according to the breed, the size, the feeding system of the herd, the yield per cow and the milking system.

A breeder extranet for perfect traceability

Breeders have a permanent access to their own dedicated extranet, where they can find all the information concerning the milk recording results of each cow and of the herd. They will also find all the technical reports about herd management and agronomy advices. Our aims trough this extranet are to make the data available as soon as possible, to guarantee the data's traceability and ensure the quality of our advisory approach.

50 Groups of farmers

Beyond the individual advisory approach, many farmers wish to share their experience in a collective process. We have 50 existing groups today, each one ruled by a specific advisor. They meet 4 times a year in the farms of the members; they choose the issues on which they wish to work, exchange experience and practices. Each session is an opportunity to highlight effective ways of innovation, to identify the successful practices of breeding and to compare regularly their technical and economic results.

Our approach within the company is to make this collective reflection enriching the process of the individual advice brought to them.

The collective support and sharing of experience are the keys to progress.

Conclusion

Our operators and advisors are daily present at the heart of dairy operations. Today, advice activity represents 45 000 professional meetings between our experts and dairy producers, and 25% of our business.

In addition to the milk recording activity, the advisory approach builds trust between BCEL Ouest and its 6 000 members and offers us the opportunity to develop solutions to help breeders to face the future.

Benchmarking in dairy production: "How to transform data to valuable decision support"

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Abstract

From raw data to operational daily management - examples from DMS (Danish Dairy Management System)

The Danish Cattle database system has a very long tradition for collecting data within the areas of first milk recording, later reproduction, breeding and feeding. The data sources are many; the farmers, different service people around the farm, milking and feeding equipment, dairies and slaughterhouses. Since nobody do the registration of data for fun it is important that there is a strong motivation for doing the registration. In Denmark the motivation is output in management tools, breeding evaluation and different law regulations.

This very enormous amount of raw data gives good and solid background for processing of data into valuable management tools in daily operational management and periodic Key Performance Indicators. Knowledge Center for Agriculture in Denmark - owned by the farmer's organizations - has a long tradition for developing decisions support tools for the farmer at his advisors. In the dairy cattle business a management package is offered and used by more than 80% of the dairy farms, either directly by the farm manager or through the Veterinarian or the Advisor. Today the package - Dairy Management System (DMS) - includes modules for animal registration and management, feed ration planning and optimization, for production and economic planning, for production follow up on the production operational (day to day) and tactic level (quarterly) and this prognosis tool for prediction of the production.

For the operational management DMS offers 3 different tools to present the KPI's from processed data:

- KPI tool.
- Benchmarking tool.
- Reporting system with different kind of analysis on the production.

With these tools the farmer can follow the daily production and benchmark against a comparable group of herds and analyses for reasons in problematic areas presented in pedagogical graphical presentations. The tools are still under development, but are released in its first version. So far the focus has been milk production, reproduction, health and feeding

Introduction

With more animals to manage pr. labor hour and a growing focus from the financial partner, there is an increasing need to have a precise overview of the dairy production on a daily operational level. The manager needs to know in real-time about the production efficiency within milk production, reproduction, health and feeding areas. The overview

can be found partly in different management system, but often the picture is insufficient, due to lack of data, and the manager has to look in different systems to get the total overview.

In Denmark Knowledge Center for Agriculture (today SEGES) - owned by the farmer's organizations - has a long tradition for developing decisions support tools for the farmer at his advisors. To meet the needs for Dairy farmer of today and tomorrow there has been focus on what kind of information are valuable to the farmer and his manager in the different decision situations. There is a need for a daily "Am I on the track" tool. For that purpose an operational KPI tool with daily updated Key figures has been developed

The decision maker also has a need to find areas for improvement, and for this purpose a Benchmarking system has been developed. The Benchmarking can be done against your own goals or a group of herds comparable with your own herd.

To complete the decision support there is a need for a system to analyze the different factors impact on the specific Key figure. To meet that need an analyzing system has been developed. The system has a few standard reports, and a setup, where you can build up your own user defined reports from a huge variety of analysis on the specific Key figure

The tool

The basic under the three described systems are the Danish Cattle Database. In the database we have a very solid data background. Data are delivered from very many sources around the dairy production:

- Mandatory recordings.
- Milk recordings.
- The farmer own voluntary recordings.
- Recordings from service suppliers.
- Veterinarians.
- A.I technicians.
- Breeding advisors.
- Nutritional advisors.
- Dairies.
- Slaughter houses.
- Etc. ...

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

The system includes 15 KPI's which are calculated each day on the newest data. The 15 KPI's shows the efficiency of the production in the above mentioned areas. In the system the single KPI is benchmarked against the goal set be the manager, and with a green or red dot indicate if the production is on target or not. This gives the manager a tool, where he very quickly can see where to act (Figure 3).

Benchmarking system

In the Benchmarking module there are a number of standard reports, telling about the performance of the herd within production, reproduction and udder health. The reports consist of a number of key figures, for each key figure the user can see the actual performance for the periods "last month", "last 3 months" or "last 12 months". The actual achieved result is benchmarked against the former period and the users own goal. It is

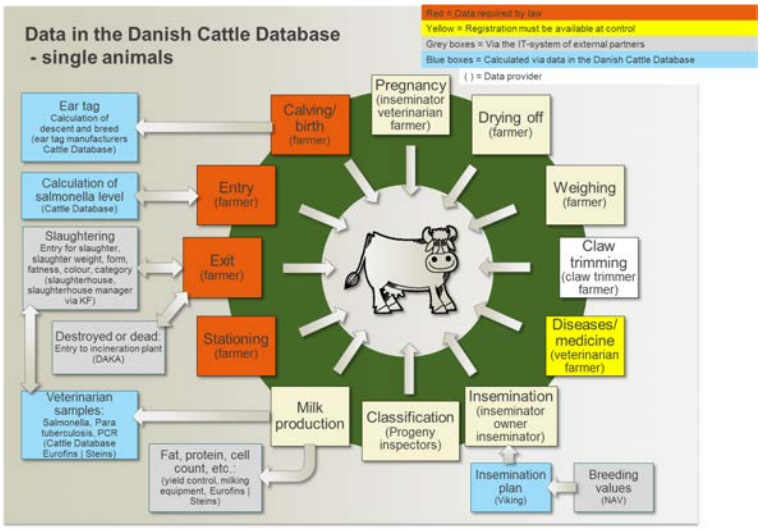


Figure 1. Data in the database at the single animal stage.

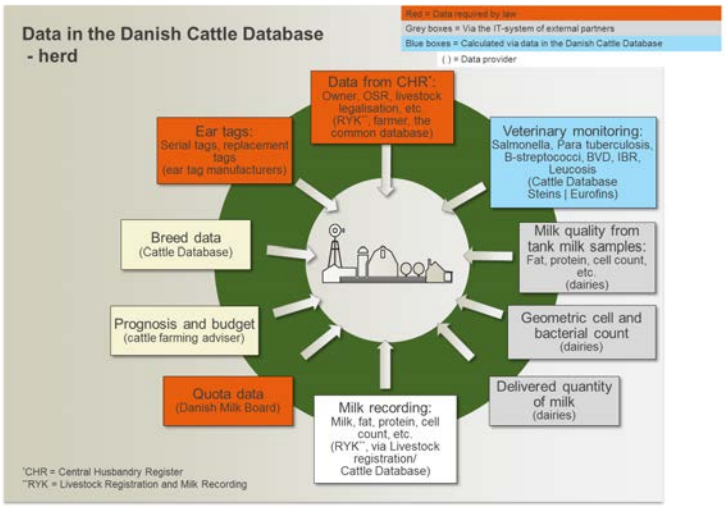


Figure 2. Data in the database at the herd stage.

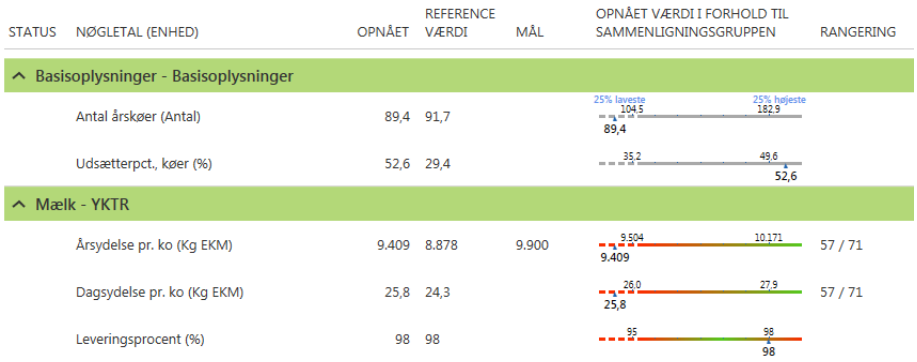
Topic	Status	Key figure (unit)	Achieved	Alarm limit	Reporting period
Milk	✓	Milk delivered (kg/day)	8.906	Min 7.835 \ Max 9.072	Latest delivery
	✓	Milk quality (number of deduc-tions)	0		Latest measure-ment
Reproduction	✓	Inseminations of cows (Numbers)	8	Min 3	Last 7 days
	●	Inseminations of heifers (Numbers)	1	Min 2	Last 7 days
	●	Not pregnancy examined cows (Numbers)	4	Max 0	Last day
	✓	Not pregnancy examined heifers (Numbers)	0	Max 0	Last day
Health	✓	Disease treatment, cows (Numbers)	0	Max 4	Last 7 days
	✓	New infection, lactation (%)	8	Max 15	Last milk recording
	✓	New infection, dry period (%)	14	Max 35	Last milk recording
	✓	Dead animals (Numbers)	0	Max 1	Last 7 days
Feeding	✓	Energy efficiency (%)	97	Min 93	Last feed control
	●	Milk minus feed cost (kr/kg ECM)	1,38	Min 1,50	Last feed control

Figure 3. KPI Example

also benchmarked against the comparison group, which is set from a number of characteristics. On a graphic display the achieved key figure is placed as shown below with yearly milk production per cow as example

In the Benchmarking module it is possible to set up your own report from a large number of key figures within the areas:

- Milk production.
- Reproduction.
- Health.
- Mortality.
- Meat production.



STATUS	NØGLETAL (ENHED)	OPNÅET	REFERENCE VÆRDI	MÅL	OPNÅET VÆRDI I FORHOLD TIL SAMMENLIGNINGSGRUPPEN	RANGERING
Basisoplysninger - Basisoplysninger						
	Antal årskøer (Antal)	89,4	91,7		25% laveste 104,5 / 25% højeste 182,9 / 89,4	
	Udsætterpct., køer (%)	52,6	29,4		35,2 / 49,6 / 52,6	
Mælk - YKTR						
	Årsydelse pr. ko (Kg EKM)	9.409	8.878	9.900	9.504 / 10.171 / 9.409	57 / 71
	Dagsydelse pr. ko (Kg EKM)	25,8	24,3		26,0 / 27,9 / 25,8	57 / 71
	Leveringsprocent (%)	98	98		95 / 98 / 98	

Figure 4. An example for the benchmarking report.

The analysing system

In the analyzing system the under can choose between a few dedicated reports On of the Standard reports is the output of the milk recording, where analyses of the milk production, BHB and Somatic Cell Count test are put together in one report.

In addition the user can put together his own report from a huge number of analysis bock on specific topics e.g. the history of a certain Key figure. Below there is examples of two Key figures, which can be relevant to put together in the same report.

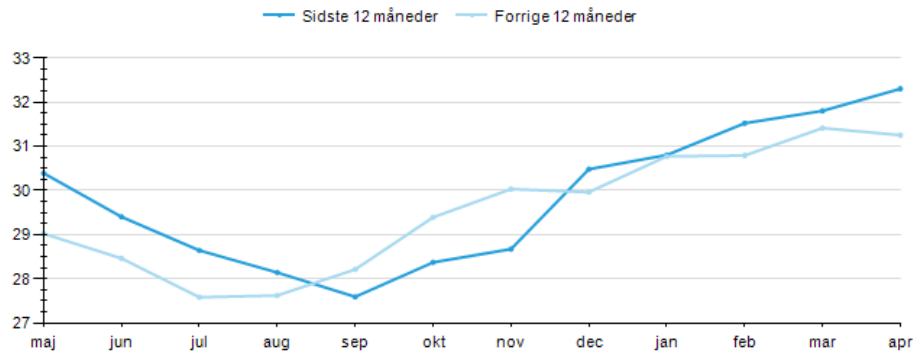


Figure 5. Daily yield per cow (Kg ECM).

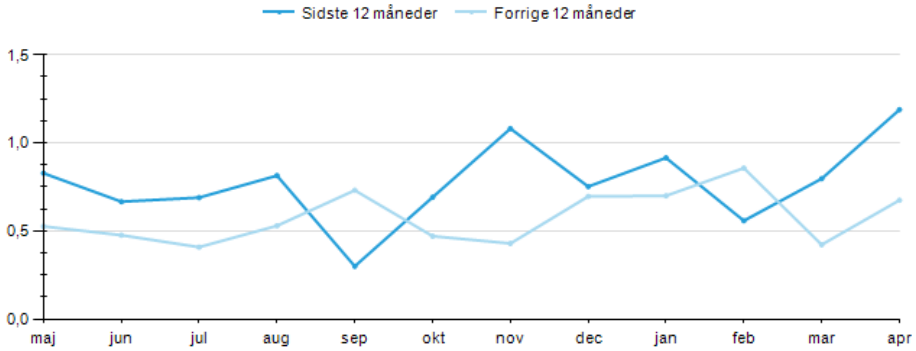


Figure 6. Incidence of recorded nutritional diseases.

Conclusion

The three described system are each included as modules in the total management system, DMS, which is a broadly used IT tool for the farmer and his advisors. In DMS the modules are integrated in each other so the user only has to enter the same data item once e.g. a goal for yield is entered under "goals" and is available in all modules

DMS is used for the mandatory and voluntary registration in the dairy (and beef) production. DMS is also used for feed management and economic management. 95% of the dairy farmer user of the Basic package of DMS.

With DMS the Farmer gets a "all in one" tool to manage his dairy production

Operative background of the Hungarian farm monitoring system based on milk and TMR analyses

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Abstract

The Milk Testing Laboratory (FTIR and FCM) and the Feed Laboratory (NIR) at the LPT Ltd. in Hungary are involved in a countrywide monitoring system based on TMR- and milk sample analyses. The new system was introduced in 2014 with contribution of 130 farms. The aim was to evaluate the actual nutritive value of the high milking dairy cow diet having potential effect on milk production, milk composition and animal health. Correlations between the milk and the TMR results are evaluated monthly. The farm TMR samples are taken 12 hours before the milk samples and analyzed for dry matter content, crude protein, crude fibre, crude fat, starch, crude ash, sugar, NDF, ADF, ADL, NFC, NSC, NEl, OMd, DOM, FOM, NDFd, and dNDF, pH, nitrate by NIR-technology.

The milk samples routinely analyzed for fat, protein, lactose, urea, and somatic cells. Reports of the high milking TMR samples are based on the measured nutrient concentration and the presumable dry matter intake. The reports contain a figure (diagram) showing the required dry matter intake to cover the actual nutrient demand according to the measured nutrient concentration in the TMR and the actual milk yield (milk data given by the milk test).

The difference among the optimal, the real and the required dry matter intake shows the inadequate / adequate nutrient concentration, the presumable effect on milk production and milk composition, animal health risk, moreover the management problem on the farm. Other important practical data about the farms are given to our experts from our technicians. Having analyzed the milk and the TMR samples a complex expert's report is being created to our customers.

Keywords: milk-recording, diet, monitoring system, coordination.

Introduction

The unified and regular milk recording of dairy cattle population was established in 1910 and actively serves dairy farmers during the last 105 years in Hungary. The system and methods of regular milk recoding are presently organized and made by the Livestock Performance Testing Ltd (LPT Ltd). The company established the Feed Laboratory in 2012. This is the first independent NIR laboratory in Hungary, which is specialized for forages. Our mission is to help farmers in Hungary and in Central Europe.

Approximately 178 thousand dairy cows (85% of the Hungarian population) were recorded in 2014. These cows were held in 461 farms, so the average number of recorded dairy cows per a farm was 387 in the last year.

At the beginning of 2014, with contribution of 130 farms, a countrywide monitoring system has started by the Milk Laboratory and the Feed Laboratory of LPT Ltd, based on TMR- and milk sample analyses. By now, 250 farms have contracts, and close to 49,5% of

the recorded cows are concerned in this monitoring system. The aim was to evaluate the actual nutritive value of the high milking dairy cow diet having potential effect on milk production, milk composition and animal health (SARA risk assessment - prognosis).

Material and methods

Sample making and receiving by the milk and feed laboratories

Since the milk-recording in Hungary is mainly supervised (more than 90% is performed by the method A), the sampling technicians and their managers have an important role in the coordination of this monitoring system. The demand of the sampling boxes is indicated by the managers of the sampling technicians to the head of the laboratories. According to a prepared integrated list, the sampling boxes (both for milking and for the forage) are posted to the farms. The TMR samples are taken and boxed by the farmers 12 hours before the milk sampling, then all samples (milk and TMR) are sent by the technician together, but in separate boxes to the LPT Ltd.

Sample analyses by the milk and feed laboratories

The arrived TMR samples are analyzed in our Feed Laboratory for dry matter content, crude protein, crude fibre, crude fat, starch, crude ash, sugar, NDF, ADF, ADL, NFC, NSC, NEl, OMd, DOM, FOM, NDFd, and dNDF, pH, nitrate by NIR-technology. The milk samples are routinely analyzed in our Milk Laboratory using FTIR method for fat, protein, lactose in the frame of the Milk-recording system. Milk urea (FTIR), and somatic cells (Flow cytometry method) are analyzed in the monitoring system automatically as well.

There is an oppurtunity to measure the minerals from the TMRs in severe packages. M4 package includes Ca, P, K, Na, Mg, S, and Cl, so DCAD can be calculated. M5 package includes the composition of M4, and moreover Cu, Zn, Mn as well. Farm reports based on analytical results prepared by advisors Reports of the high milking TMR samples are based on the measured nutrient concentration and the presumable dry matter intake. The reports contain a figure (diagram) showing the required dry matter intake to cover the actual nutrient requirement according to the measured nutrient concentration in the TMR and the actual milk yield (actual milk data are derived from the milk recording database). The difference among the optimal, the real and the required dry matter intake shows the inadequate/adequate nutrient concentration, the presumable effect on milk production and milk composition, animal health risk, moreover the management problem on the farm. The parameters are showed on a diagram, and values are indicated too. The blue color shows the adequate supply, the green-lineal column shows nutrient deficiency, the redspotted ones overfeeding in intensive Holstein herds.

Table 1. The measured parameters in the Milk Laboratory of LPT Ltd.

Parameter of measurement	Range of measurement	Unit
Fat	1,5-5,8 g/100g	g/100 g
Protein	2,0-5,0 g/100g	g/100 g
Lactose	4,0-5,5 g/100g	g/100 g
Somatic cells	100-900.000 cells/cm3	x103 cells/cm3
Urea	0,010-0,060	g/100 g

Measured data are sent within 48 hours on electronic way (pdf) to the farm, report with the figure is emailed within 72 hours since sample receiving. The results of milk samples are sent within 7 days from the time of sampling, by e-mail, or by the post.

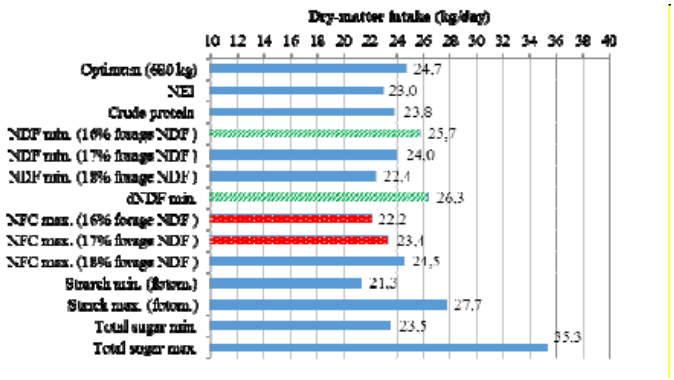

Figure 2. The nutrient supply based on the TMR measured nutrient concentration and presumable drymatter intake (NRC 2001 recommendation). The supposed milk-production of the group fed by the analysed TMR: 40 kg milk/day/cow.

Farm advisory

Several important practical data are delivered to our advisers by the technicians about the farms. Having analyzed the milk and the TMR samples a complex monitoring report is being created for our customers. This final report is sent within 10 days after the sample receiving. As participant of the farm monitoring system, customers can get a global view about their farms month by month- with details of the herds' performance level, management efficiency and health status changes - as a useful practical tool in their hand for decision making.

Web advisory tools to support dairy production in Slovenian herds

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Abstract

A good 80,000 or nearly 80% of dairy cows in Slovenia are included in the dairy recording scheme, with an average herd size of 21 dairy cows. Recording data are collected in the central database, which is the main unit of the Cattle Information System. In addition to recording and breeding data processing, a number of other tools to support farm management are included in this system. The aim of this article is to introduce advisory tools and services of the Web portal Cattle (WPC) ? which are available to farmers, professional advisers and other experts ? To help farmers manage their dairy farms. The gate to the farm advisory tools is the 'Farm Identity Card', a tool which provides summary data on the latest dairy recording of the farm. Brief information on the production, lactation and reproduction status of the herd is included, as well as information on the possible digestive disorders and excessive body reserve mobilization, based on the milk fat to protein ratio. Milk urea concentration and somatic cell count (SCC) distribution are presented in graphical form. Each section provides links to in-depth data. For example, by clicking the link for the latest milk production data, we access in-depth information on the recordings of a particular cow. The index of the SCC with values in a range from 1 to 5 was introduced to support animal health and good welfare information concerning the SCC in herds and in a particular cow. In the reproduction section of the portal Cattle, information on inseminations, expected calvings, heats and reproduction results is available. Reproduction reports for the farm can be prepared on the basis of farm management practice. To support herd-level feeding management, the system includes a tool for planning feed rations, which is based on the recording data, as well as data on the nutritional value of feed, feed analyses and feeding knowledge. With its extensive volume of available data and information, easy access and presentation, the WPC is the main advisory tool used by Slovenian breeders to manage their dairy herds.

Keywords: cattle, dairy herd, web advisory tool, Slovenia.

Introduction

Cattle breeding has an important role in animal husbandry branches in Slovenia. In the rather heterogeneous alpine agricultural regions, dairy production is characterised by farming on a limited arable farmland which is often divided into many small parcels. A good 80,000 or nearly 80% of dairy cows are currently included in the dairy recording scheme, with the average herd size of 21 cows per herd (Sadar *et al.*, 2014). In order to effectively process recording data and make it available to farmers and other clients, the Cattle Information System (CIS) based on Oracle's database platform has been introduced (Logar *et al.*, 2005). The CIS supports informational necessities of the cattle recording sector and caters for most information requirements in the cattle breeding scheme. Breeders, experts, veterinarians, advisers and other professionals can access the online central database in accordance with their needs and access rights and utilise user-specific applications. The web portal Cattle (WPC, www.cattle.si) provides applications which

support dairy herd management. The aim of this article is to introduce the WPC as an advisory tool and service for supporting management decisions in Slovenian dairy cattle breeding.

Recording Data Management

The CIS and its WPC. provide support with information for all herds in the recording scheme. Farms included in the recording scheme have the possibility to apply for electronic informing. In that system, a SMS and / or an e-mail message is sent after each processing of the recording data. The message contains summary information for the last milk recording and alerts for cows that exceed the critical value for somatic cell count (SCC) that is 200.000 SCC / ml. All further information, including recording reports, is available on the WPC. After entering the system as a farmer, different views are available and jointly named the Farm Identity Card (see Logar *et al.*, 2005).

The module provides the latest summary data on dairy recording at the farm. In the initial view, the summary data of the last milk recording are presented, i.e. data on milk yield with fat and protein contents, as well as the average SCC of the herd. On the basis of fat and protein contents, fat to protein ratio is calculated and presented in graphical form, which is useful as a tool to manage feeding on the farm. Together with the graphical presentation of milk urea concentration, it is possible to identify possible feeding disorders and nutritional deficiencies.

Lactation and reproduction statuses of the herd are also shown. In the section of feeding management and planning of cow groups, the lactation stage presents useful information. All of these views can be expanded to provide the more detailed views for deeper data inspection. In addition to the information which is instantly available via the 'Farm Identity Card' (see *www.cattle.si* - DEMO), the list of views and modules is disposed.

By selecting a particular service, the farmer can examine a great volume of information, among others a detailed pedigree data of active and culled animals. Several tools to manage and avoid inbreeding rate are available as well. We will present only some of those which are related to the SCC, reproduction and feeding management.

Somatic cells

Somatic cells count in milk is an indicator of cow health status, especially of the health status of mammary gland, the quality of milk and the suitability of farm management. The somatic cells are not problematic as long as their numbers are kept within the normal range. In order to present the issue of the SCC, we use the index of somatic cell count (ISC). The index is used to evaluate the measured SCC with regard to consecutive lactations, the quantity of milk at the recording as well as the lactation stage. With the same SCC, higher ISC has been observed with cows in early lactation, cows with higher milk yield and cows in mid lactation. Since other factors are taken into consideration along the SCC to calculate the ISC, the SCC and ISC are not truly linearly related. In practical terms this means that a cow with the highest SCC in the stable does not necessarily have the highest ISC as well. The ISC is presented with values from 1 to 5, wherein 1 means excellent health status of the mammary glands and 5 means very poor health status of the mammary glands.

The module 'Somatic cells' presents the situation at the last milk recording. On the top is a presentation of the calculated somatic cell count for the bulk tank on the recording day for the period of the last 12 months (Figure 1). When the 200,000 SCC / ml limit is exceeded, the colour of the value turns red. Below (Figure 2), there is a list of cows at the last milk recording, which includes the following data: consecutive lactation, the amount of milk on the recording day, the SCC, the bulk somatic cell count (BSCC), the ISC, the individual cow's contribution of the SCC to the bulk tank in SCC and percentages, the number of

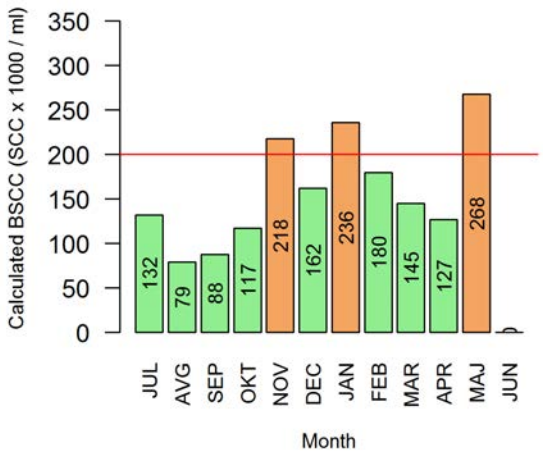


Figure 1. Bulk somatic cell count in the last 12 months.

				Milk	SCC	BSCC	ISC	PSC	Months after	Days after insem.
No.	Cow ID	Name	Lact.	kg	(x 1000)/ml			%	calving	insem.
1	SI 63632107	ANTA	4	29	1642	275	5	56,5	3	
3	SI 63267424	JASNA	6	14,5	927	132	4	16	8	82
7	SI 63825332	HANA	3	20,6	281	88	3	6,9	1	
4	SI 13541990	CULA	5	30,5	124	72	2	4,5	2	
2	SI 14034260	ANUK	1	19,4	150	64	3	3,5	10	66
11	SI 94034255	CENKA	1	14,3	178	56	2	3	13	214

Figure 2. Somatic cell count at the last milk recording per individual cow.

months after calving and the number of days after the last insemination. A review of this data shows the severity of the issue of high SCC within a herd, as well as critical cows with their contributions to the total SCC.

The scatter plot (Figure 3) presents the ISC dynamics. The presentation includes the last two milk recordings which show the transition of cows between individual ISC. The diagram consists of nine fields, wherein the desired fields are marked with green and the undesired with orange colour. The figure shows an example of the transition of a cow with a high index (ISC = 3-5) to the level of the desired index (ISC = 1-2). From a farmer's point of view, it is desirable that most of the dairy cows from the quadrant ISC = 1-2 do not transition at all. The diagram allows us to monitor whether the SCC management within the herd has been successful. If it has been unsuccessful (when compared to the previous milk recording), the cows will remain in the quadrant with high ISC. Simultaneously, we can assess the intensity and number of newly detected potential infections which result in the high ISC.

There is also module that shows the movement of ISC within the herd for the period of the last 12 months (Figure 4). The data is presented in the table, with the ISC figures shown on the coloured background. The colour of the indexes (e.g. orange and red colour represent poor indexes) help us to recognise the problematic cows, how many cows within the herd have been infected, as well as repetition and the pattern of repetition of increased SCC. Cows in which increased SCC (over 200,000) has been detected in the last three recordings are marked as problematic cows with a red triangle and an exclamation mark. The module also provides information on when the SCC has first increased above the value of 200,000, in which lactation and period after calving has this occurred and how

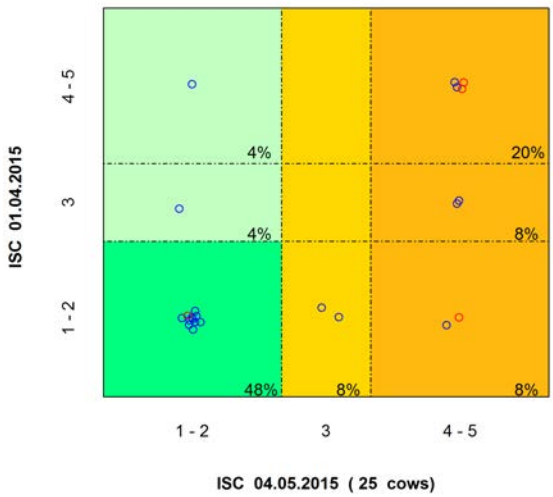


Figure 3. Index of somatic cell count (ISC) in the last two milk recordings.

		Date				SCI in last 12 months (month.year)												Curent TD			Inseminations		
No.	Cow ID	Dry-off	L	MD	L_P*	06.14	07.14	08.14	09.14	10.14	11.14	12.14	01.15	02.15	03.15	04.15	05.15	SCC	Milk	BSCC%	last	days	all
1.	SI 63632107	01.02.15	4	78	1 - 2x M1	1	1	1	2	1	1	1	1			3	5	1461	30,5	41,9	14.05.15	20	
2.	SI 14034260		1	292					1	2	1	2	1	2	2	2	2	70	20,7	1,4	27.03.15	68	9
3.	SI 63267424	31.08.14	6	238	1 - 7x M12	3	2	2			5	4	4	5	5	5	5	717	20,1	13,5	11.03.15	84	3
4.	SI 13541990	27.02.15	5	46	3 - 5x M12	2	2	2	2	3	3	2	1	3			3	193	30,1	5,5			
5.	SI 23632118	30.05.14	3	342	1 - 5x M2		2	1	1	1	1	1	2	1	1	1	1	104	16,5	1,6	11.11.14	204	2
6.	SI 53632115	01.07.13	2	661	2 - 5x M2	2	2	2	2	2	2	3	5	2	1	1	1	185	10,5	1,8	07.10.14	239	8
7.	SI 63825332	29.03.15	3	31	1 - 3x M2	2	3	2	3	4	2	4	3	3	3			876	28,1	23,1			

Figure 4. Index of somatic cell count (ISC) in the period of the last 12 months.

frequent has it been. Additional data includes the quantity of collected milk at the last test day (TD), the SCC and contribution of an individual cow to the bulk SCC, as well as data on the last insemination, days open and the number of inseminations after the last calving.

Reproduction

The 'Reproduction Calendar' module (Figure 5) enables monitoring and planning of the main reproduction events within the herd in the form of a calendar. Farmers can create calendars for the desired time period. Based on the previously entered reproduction events from various data sources, the system calculates and plans future activities (heat, insemination, checking cows for pregnancy) for the envisaged period. Entering data has been simplified - if the data is not yet in the database, the breeder enters only the date of the event in the corresponding field, except in the case of checking cows for pregnancy when the result of the check-up has to be entered as well.

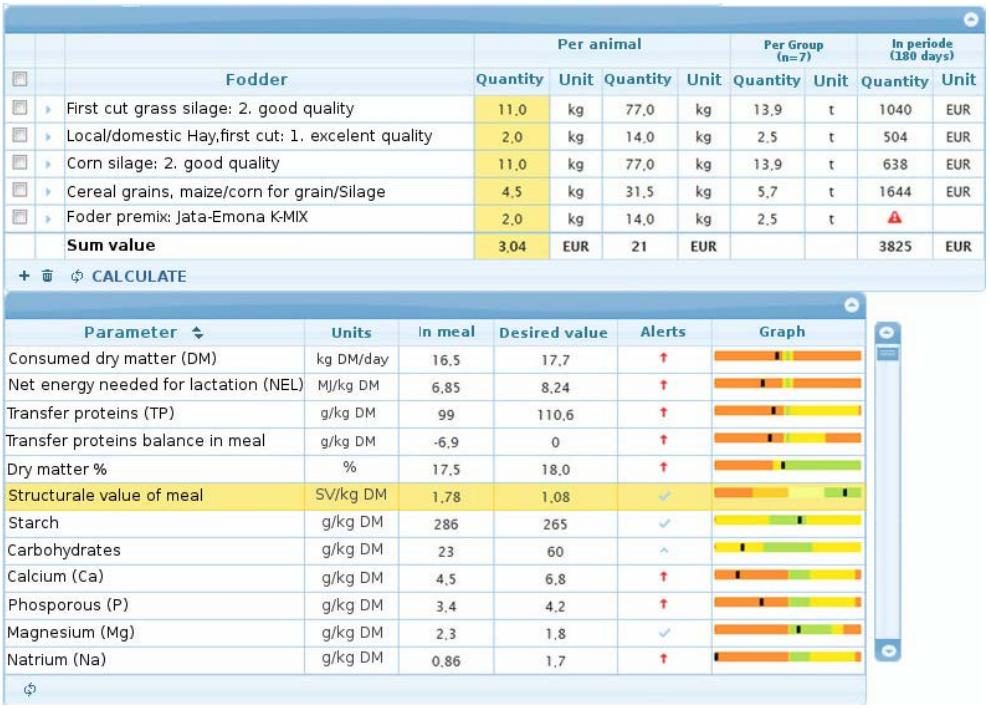
Feed Ration Planning

Dairy nutrition is essentially as simple as understanding the nutrient requirements of dairy cows at various stages of lactation and combining various feed ingredients to meet those needs in a cost-effective manner. However, many dynamic factors influence both nutrient requirements and nutrient availability from feeds. In addition, successful feeding

No.	Animal ID	Name	Calving date	Days after calving	No. of services	Last insem.	Insem. date	Pregnancy check	Remark	Heat check
1	SI62958484	STELA	17.05.15	8	0		27.05 - 01.06			
2	SI03199044	GINA	07.09.14	260	3	02.03.15	25.05 - 28.05	25.05		
3	SI53199049	RIŽA	13.09.14	254	2	03.03.15	25.05 - 29.05	25.05 - 26.05		
4	SI53390051	SAVA	03.10.14	234	1	08.12.14	25.05 - 28.05			
5	SI93390057	SONJA	09.11.14	197	0		27.05 - 01.06			
22	SI54043336	CIKA	25.04.15	30	0		26.05 - 01.06			
23	SI54230101				1	18.04.15	27.05 - 01.06			
24	SI44230102				1	17.04.15	26.05 - 01.06			

Save Back Insert Print

Figure 5. Reproduction calendar module.



Fodder	Per animal Quantity	Unit	Quantity	Unit	Per Group (n=7) Quantity	Unit	In periode (180 days) Quantity	Unit
First cut grass silage: 2. good quality	11,0	kg	77,0	kg	13,9	t	1040	EUR
Local/domestic Hay,first cut: 1. excelent quality	2,0	kg	14,0	kg	2,5	t	504	EUR
Corn silage: 2. good quality	11,0	kg	77,0	kg	13,9	t	638	EUR
Cereal grains, maize/corn for grain/Silage	4,5	kg	31,5	kg	5,7	t	1644	EUR
Foder premix: Jata-Emona K-MIX	2,0	kg	14,0	kg	2,5	t		
Sum value	3,04	EUR	21	EUR			3825	EUR

CALCULATE

Parameter	Units	In meal	Desired value	Alerts	Graph
Consumed dry matter (DM)	kg DM/day	16,5	17,7		
Net energy needed for lactation (NEL)	MJ/kg DM	6,85	8,24		
Transfer proteins (TP)	g/kg DM	99	110,6		
Transfer proteins balance in meal	g/kg DM	-6,9	0		
Dry matter %	%	17,5	18,0		
Structurale value of meal	SV/kg DM	1,78	1,08		
Starch	g/kg DM	286	265		
Carbohydrates	g/kg DM	23	60		
Calcium (Ca)	g/kg DM	4,5	6,8		
Phosporous (P)	g/kg DM	3,4	4,2		
Magnesium (Mg)	g/kg DM	2,3	1,8		
Natrium (Na)	g/kg DM	0,86	1,7		

Figure 6. Feed ration calculation tool.

of dairy cows requires accurate mixing and delivery of rations so that the diet fed is the same as the diet formulated. The tool named 'KOKRA' is aimed at calculating feed rations for different cow production groups within the herd (Figure 6). When feed rations are calculated, it is important to take into consideration the physiological characteristics of ruminant animals, as well as knowledge on their nutritional needs. The software enables integration of different sources of data, i.e. feed and analytical data of agrochemical laboratories, data on the composition of concentrates per individual producer and milk recording data. When it comes to feed ration planning, you have to firstly define the feed basis which is available at the farm, as well as the production price of feed. Secondly, choose and name the groups for which you want to calculate feed rations (Figure 6 - Category). The groups have been pre-set with regard to their lactation stages (1-3 months, 4-6 months, more than 6 months after calving, all cows) and the dry period (cows in the last 4-6 weeks and cows 3 weeks before calving). Having chosen the appropriate group,

the software provides a selection of cows (Figure 6 - List of animals). This can be changed according to your needs until you have created the desired list of cows within an individual group.

The segment "Information about the animals and feeding" (Figure 6) contains the average data for a selected group of animals. You can make certain changes to the proposed data. For example, you can change the target milk yield in standard lactation with regard to the predicted standard lactation curve for milk yield per individual group, the average mass of cows, the frequency of feedstuffs intake, as well as certain other parameters on which the feed ration calculations depends. In the segment below, you enter feedingstuffs and forage ("Fodder") with the envisaged daily feed rations per animal. When entering these quantities, you will get an approximate idea of the needed quantities of individual feedingstuffs, as well as information on the price of feed rations. Below the composition of nutritional value parameters is calculated in a timely manner. A graphical presentation shows how close the feed ration is to the optimal value. Until the parameter is within the appropriate range, you will get professional advice by clicking the "Alerts" button. Feed rations can be corrected by adding and reducing the amount of feedingstuffs until you get a balanced feed ration. Users can create several feed rations and save them in their archive for possible later use.

Conclusion

All farms in the Slovenian recording scheme have access to the WPC which offers a wide range of tools. In this article, we have presented only some of the tools which are closely related to management support. With its extensive volume of available data and information, easy access and presentation, the WPC is the main advisory tool for supporting dairy management in Slovenian herds. More and more farms regularly monitor recording results and other data. For example, in January 2015 a quarter of the farms with nearly 40% of Slovenian cows in the recording scheme visited WPC. This provides new challenges for future development of the WPC.

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SIEL web and an innovative software: MIL'KLIC

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Introduction

SIEL is an association of French MRO's which decided to develop a new software. This software is aimed to advisors and breeders for collecting datas and get a better collecting process.

Presentation of SIEL

SIEL is an association of French MRO's which represent :

- 32 MRO's
- 13 300 breeders
- 780 000 cows

These bodies developed a new application called MIL'KLIC.

The association is composed through its members of :

- 360 advisors
- 732 weighers
- 100 staff

The area of use of the application is shown in red on the map reprted in figure 1.

We use Mil'Klic through a web interface. Breeders and advisors have the same tools. Farmers use the application in online mode only and advisors use the application on connected and / or disconnected mode. It depends if they have an internet connection.

The data collection comes from :

- Paper : the persons who do the milk recording use at this moment a list of cows
- Smartphone : we are going to develop a new application on a smartphone support
- ORI-AUTOMATE and ORIGINAL robot
- Others sources of information from the French genetic information system (insemination, animal identification, ...)

Mil'Klic is an online application in line with the overall SIEL database and calculated based on known data. It allows alert, identify, analyze and compare data from one farm to groups. Mil'Klic also keeps track of its breeding events and lactating dairy herd.

Mil'Klic formats playful and interactive outcomes for members and advisors. The valuation was built around the various technical topics related to the dairy herd

" The control results

" Analysis stage of lactation

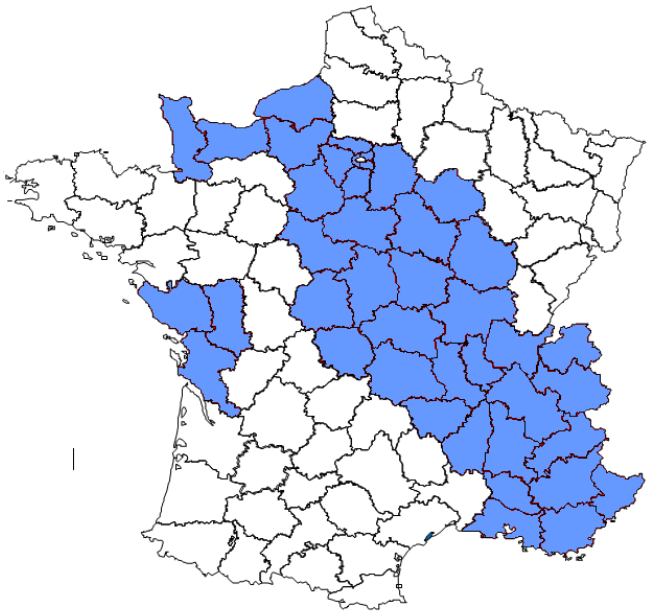

Figure 1. Geografic areas of action of SIEL.

- Food alerts
- Economic valuation of the ration techno
- Udder alerts
- Reproduction alerts

For each theme a complete history of the 13 last test results used to complete the analysis.

A complete "Dossier animal" classifying the events of the animal by category (Identity, Production, Repro / Calving, Health fattening state) provides a graphical view of events on the life of the animal.

A unique feature called "E-Conseil" allows the counselor to file specific alerts to visited pages to maintain a link between the advisor and the farmer visits between 2 boards.

Comparisons of groups are present on the screens results of control, distributed power and udder alerts. The groups are managed Mil'Klic. The group composition is from the farm and features an automatic recalculation of farms affected the comparison group to place 1 to week.

The data groups (averages) are, however, updated every night. The average of a group therefore is the average of the last inspection of the group's farms (moving average) as shown on figure 12

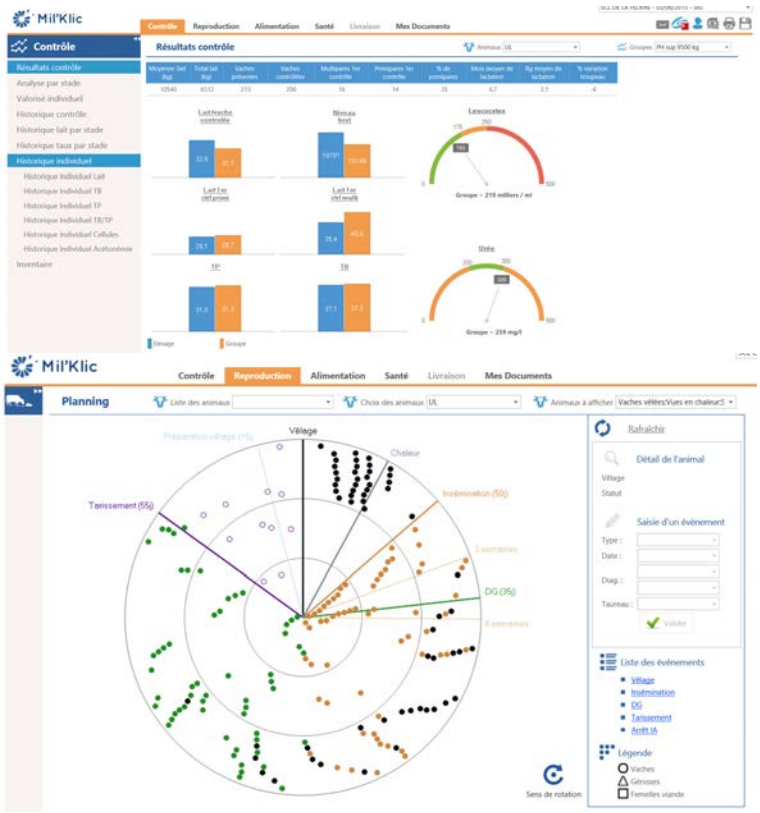

Figure 2. Example of Reports generated by Mil'Klic.

Next developmets for Mil'Klic

The next evolutions of Mil'Klic :

- Milk production forecast.
- Nutrition tool.
- Pregnancy diagnosis.
- Smartphone application for farmers to have warnings.

On farm recording of fertility and health data using mobile devices

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Abstract

Cow fertility and health traits are of continued interest to breeders due to their economic importance and slow genetic progress. Optimized herd management is important for financially successful farming, thus it should include functional traits. Genomic selection provides new opportunities in genetic improvement of these traits by use of cow reference populations with a limited number of observations compared to national systems. Both, genetic and environmental improvement, require information collected on farms. Several sources of this type of data exist: milk recording, AI organizations, veterinarians, on-farm computer software. Unfortunately, even if all sources are combined, they do not cover all areas of interest. Lack of completeness of insemination records, for example, limits their usefulness for both management and genetic evaluations. Moreover, for short term decisions (e.g. whether to continue to inseminate or not) on farm recording of fertility is regarded as probably the only practical solution as it provides fast access to information. Immediate use by the breeder of the data collected on farm could be, to a large extend, a guarantee of their quality and completeness. It is important for the farmers and veterinarians to have quick and easy access to herd fertility data. Only then can acute fertility problems, which may be related to management, be detected and addressed promptly. Hence an Internet-based tool was developed. A hybrid mobile / web application is proposed for online and offline collection of cow fertility data available for mobile devices. It can be run on different platforms (Android, iPhone, Windows Mobile) and PCs under various operating systems (Windows, Linux, iOS). Capabilities of modern web browsers are utilized to enable operation without Internet connection by using browser's local storage and offline web application mechanism. The central database is accessed through an HTTP API which provides possibilities for additional processing with simple tools. The system aims to collect broad range of female fertility and health data including: calving dates, insemination, fertility disorders, results of pregnancy tests and further hormone assays, heat observation, veterinary treatments, hoof trimming results and culling data. The system can be easily fed with milk production and composition data. By doing so we obtain a complete set of basic information required by veterinary and nutritional advisors. Collecting a complete set of information opens up opportunities for cooperation between veterinarians and nutritionists who aim to cooperate on the development of this system. The system can be used for making quick management decisions, can provide information on the current status of the herd and trends including recent years. By collecting adequate cow fertility and health data for complex analysis of the status of individuals and herds we hope to enable opportunities for genetic evaluation of new functional fertility and health-related traits with higher accuracy than offered by the current national system

Keywords: dairy cattle, health and fertility traits recording, genomic selection.

Introduction

Cow fertility and health traits are of continuous interest to breeders due to their economic importance and slow genetic progress. Optimized herd management is important for financially successful farming, thus it should include functional traits. Reproduction, mastitis, feet and legs problems are the main reasons for involuntary culling (CanWest DHI and Valacta, 2014). Direct information on health traits could increase the efficiency of breeding programs not only for mastitis resistance (Heringstad *et al.*, 2007) but also for claw health (Van der Linde *et al.*, 2010). The challenge is to develop a system for recording diagnoses nationwide. Genomic selection provides new opportunities for genetic improvement of these traits by use of cow reference populations with limited number of observations compared to national systems (Pszczola *et al.*, 2012). Both, genetic and environmental improvement, require information collected on farms. Several sources of this type of data exist: milk recording, AI organizations, veterinarians, on-farm computer software. Unfortunately, even if all sources are combined, they do not cover all areas of interest (Egger-Danner *et al.*, 2013). Lack of completeness of inseminations, for example, limits their usefulness for both management and genetic evaluations. Moreover, for short term decisions (e.g. whether to continue to inseminate or not) on farm recording of fertility is regarded as probably the only practical solution as it provides fast access to information. Immediate use by the breeder of the data collected on farm could be, to large extend, a guarantee of their quality and completeness. It is important for the farmers and veterinarians to have quick and easy access to herd fertility data. Only then can acute fertility problems, which may be related to management, be detected and addressed promptly.

Material and methods

Hence an Internet-based tool has been developed for online and offline collection of cow fertility data. It is accessible on different mobile platforms (Android, iPhone, Windows Mobile) and PCs under various operating systems (Windows, Linux, iOS). Hardware independency allows following technical progress and avoids vendor lock-in to ensure reasonable prices. Numerous capabilities of mobile devices and modern web browsers are utilized to enable operation in the field work, i.e. without Internet connection or constant power supply. Open source software is used for data processing and storage for limitless extensibility and code transparency. The central database can be accessed through an HTTP API which provides possibilities for additional processing with simple scripts and tools.

The profitability of dairy farms is limited by involuntary culling resulting from deterioration of fertility and health. Therefore, the system aims to collect broad range of female fertility and health data including:

- Basic reproduction data: calving dates, insemination.
- Novel fertility data: heat observation, ovarian activity, results of pregnancy tests.
- Fertility disorders: metritis, cystic ovaries.
- Veterinary treatments and hormone assays.
- Hoof trimming results and claw disorders.
- Culling data.

The system can be easily fed with milk production data. By doing so we obtain a complete set of basic information required by nutritional and veterinary advisors.

Results and discussion

Data was recorded in one of the big commercial dairy farms in the Wielkopolska region. Herd of about 330 Polish Holstein-Friesian cows was housed in a free-stall barn with automatic milking system. Information on pregnancy status and fertility related health records was collected from 309 cows between November 2014 and April 2015. Gynecological examination was carried out by a veterinarian using rectal palpation and ultrasound measurement. Pregnancy was checked 247 times and 66% of the tests were positive. Twin pregnancy were found in two cases. Date of heat was determined in 181 cases. Ovarian activity and state of the uterus was examined in 543 animals. The overall incidence of metritis, cystic ovaries and inactive ovaries were 5%, 5% and 2%, respectively. Disease frequencies are low and therefore the accuracy and completeness of the data is extremely important (Figure 1).

Collection of data on claw and leg disorders was implemented earlier and performed for 13 months. Data was entered by a hoof trimmer. Scored claw disorders were digital dermatitis (DD), interdigital dermatitis (ID), interdigital hyperplasia (IH), sole ulcer (SU), sole hemorrage (SH), white line disease (WLD), interdigital necrobacillosis (IN)

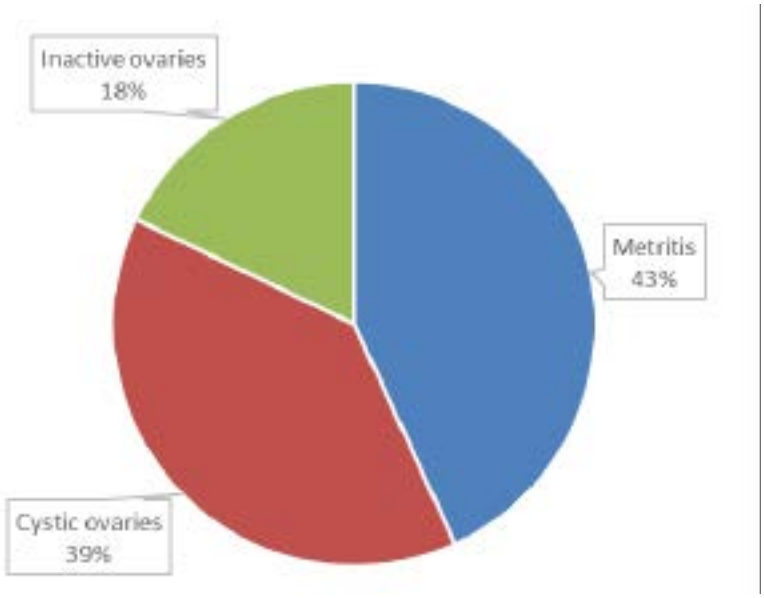

Figure 1. Percentage of cases of fertiliti disorders.

and heel erosion (HE). 1214 diagnoses were recorded, in 53% of the cases lesions were found. The highest percentages of disorders were found for SU and DD. The remaining disorders accounted for less than 10% of the cases (Figure 2).

The system can be used for making quick management decisions, can provide information for current status of the herd and trend including recent years. Simple access to the data on individual animals is a key, however large volumes of collected information requires better integration of data and creation of parameters which could be an indicator of overall management. Consultancy nowadays requires a comprehensive analysis of the causal factors in order to identify effective solutions for a problem. For example, low pregnancy rate in a herd can result from prolonged anestrus, disorders of ovarian activity, prevalence of silent heat, low effectiveness of artificial insemination or embryonic death. The data collected allow not only to diagnose problems in a herd, but also to identify the

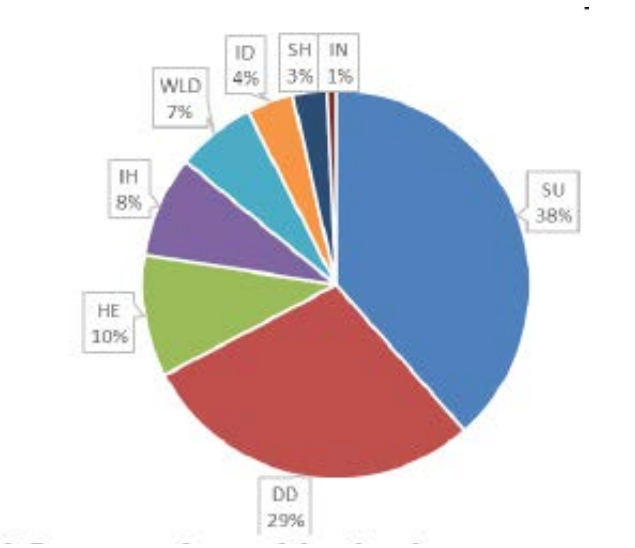

Figure 2. Percentage of cases of claw disorders.

causes of their occurrence. Furthermore access to information about the history of treatment supports making the right decisions on continuation of medical treatment. A number of indicators which measure herd reproductive performance are calculated and could be used to assess effectiveness of hormonal therapy. The system based on user-defined estrus synchronization programs calculates the date for subsequent drug applications and creates a list of tasks for a dairy farmer to complete each day. The system allows to enter information directly, right next to the cow, which should limit the number of errors. Collecting this kind of complete set of information opens opportunities for cooperation between veterinarians and nutritionists who aim to cooperate in the development of this system. By collecting adequate cow fertility and health data for complex analysis of the status of individuals and herds, we hope to be able to create opportunities for genetic evaluation of new functional fertility and health-related traits with higher accuracy than offered by the current national system. Pregnancy check enables early detection of insemination effectiveness and avoids limiting the data to cows with subsequent calving. At the same time interval between calving and first heat is a better indicator of ability to resume luteal activity in the postpartum period than the interval from calving to first insemination because it is independent from voluntary waiting period. Information about occurrence of diseases allows for direct selection for improved health. In order to obtain accurate and complete health data cooperation with veterinarians and farmers is necessary. User-friendly tool can replace on-farm documentation and become a source of data for management purposes not only for large farms. However in small herds veterinary care is not permanent and veterinary diagnoses occur only in sporadic cases. Therefore, the information especially concerning fertility, will be collected from large herds of high-quality management and probably performance above the national average (Figure 3).

Health and fertility traits are not easy to improve using genetic selection. Although genomic selection allows us to double the genetic progress in functional traits, collecting phenotypes for these traits is still a challenging task. Milk recording is run and insemination records are collected however completeness of the collected data is limited causing problems in genetic evaluations. The proposed system due to low investment costs and immediate use of collected records can solve these limitations.

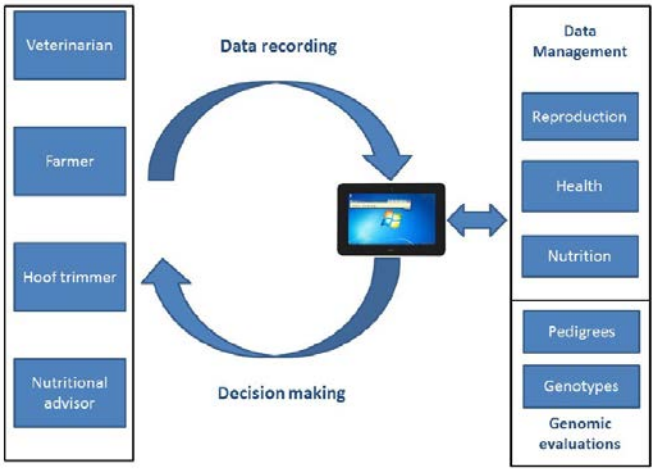

Figure 3. Diagram of the system.

Collection of a substantial number of records should allow, in the future, to make use of them in genetic evaluations. As genomic selection is becoming popular in Poland, running genomic evaluation should also be possible, with a possible female and male reference population. One of the limiting factors, which may arise is due to the fact, that the system will most probably be preferred by large herds with intense production. It may therefore introduce bias in the evaluations.

Conclusions

The new system for collection of reliable phenotypes without additional work of farmers was implemented on the first dairy farm. It allows for collection of complete data as the collected information is used immediately to support management decisions. By collecting a broad range of information on health and fertility status, current status and trends in herds can be presented and used by extension. Further development of the system includes a comprehensive analysis of data for management purposes. In the future the system will allow for comparisons between herds, support benchmarking and overall herd management evaluation. Through close cooperation with academia, research can easily continue. As more farms use the system, further collection of data for use in genomic evaluations should be feasible.

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Session 3

Manufacturers showcase

Routine check and installation of milk meters with ICAR approved calibration software module from DeLaval - experience from practice

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Abstract

Using software instead of time consuming bucket milking makes this new method efficient and data continuously available for monitoring. This is a completely new and fast way of working with milk meter accuracy in terms of calibration, installation test and routine check. It has the potential to long term revolutionize the organization of milk recording in many regions.

The method which was ICAR approved in December 2013 is based on a calculation in the Herd Management software of milk meter accuracy per milking point by using yield data statistics per cow and milking session as well as bulk tank receipt information. A minimum number of cow milk recordings should be registered in the software to get good statistical data before calibration. A well functioning ID system is also a prerequisite.

Every farm that wants to live up to any accuracy standard regarding official milk recording need methods for milk meter calibration, installation test and routine check which are all simplified by the new method.

This case study emphasizes on the evaluation of potential benefits of using this new method. In eight cases (farm studies) in four countries (Sweden, Netherlands, France, Germany) the following benefits were assessed: labor savings, increased profitability, positive effect on animal welfare, reduced impact on resources, environment and energy, positive impacts on work-facilitating and work safety. The methods used were analysis of registered calibration data as well as a survey with representatives in contact with the farmers as well as workers performing milk meter calibration, installation test and routine check.

The result shows that the new method gives real benefits in all areas. By all respondents the new method was regarded as a very positive development in the field of milk meter calibration and test. One comment from the survey was: Perfect combination of labor saving calibration and milk meter accuracy.

The experiences from this study can be used to improve future organization of milk meter calibration with ICAR approved calibration software module from DeLaval.

Introduction

DeLaval has developed a new calibration method for milk meters in conventional milking systems based on data present in the Herd Management system.

Briefly the method is based on that the system over a number of milking sessions compares the yield measured by the milk meter to the expected yield of the cows. The system also compares the total bulk tank volume according to the receipt with the total yield in the system. The BIAS of each milk meter is then calculated automatically and must be entered by the service technician into the milk meters (Olsson T, 2011)

The main advantage of using this calibration procedure instead of other traditional procedures is that it is much faster and saves labor as bucket milking is eliminated, or at least significantly reduced. Beyond the obvious labor savings there are potential benefits of increased profitability, positive effect on animal welfare, reduced impact on resources, environment and energy and positive impacts on work-facilitating and work safety.

ICAR approved this new method (Idensjö H, 2013) in December 2013 under the name Milk meter calibration software module, present in DeLaval Herd Management system ALPRO 7.2, to be used for initial calibration, installation test as well as routine test. The ICAR approval is at this time valid for the 'Free flow' based milk meters in the MM25- and MM27-series including MM27BC (ICAR, 2013).

The purpose of this study was to assess the real benefits of using this new calibration software about one year after the approval by studying some cases of farms in Europe where this method has been used.

Material and methods

A survey was sent out to DeLaval representatives experienced in milk meter calibration in SE, NL, DE and FR. The focus was to assess benefits of cases from specific farms however assessment of systematic benefits by using the new software calibration method was also desired (Table 1).

In total eight people responded to the survey of nine people asked. Additional contact was taken in cases of unclear data from the respondents. Eight farms were assessed and two assessments were made of systematic benefits. Quantitative calibration data from four of the farms were analyzed.

Results

Type of farms

For the eight farms number of milking cows ranged from 80 to 1100 and number of milk meters from 16 to 60 pieces. Systems represented were parallel parlour, rotaries and MidiLine with swing over arms. In addition one of the farms were an AMR (DeLaval Automatic Milking Rotary) with 24 milking points and 96 milk meters for which ICAR approval of the calibration method is pending.

Type of action

Most of the cases reported concerned initial calibration and installation test. In only one case the new method had been used for routine check. However in the descriptions of systematic benefits routine check was included. In two cases initial calibration was not possible due to low identification rate at the time and the traditional method was used instead. In the other cases the new calibration method was used and the result was good.

Table 1. Survey as sent out to respondents.

Milk Meter software calibration - benefits
I would like to know your experience from using MM software calibration instead of calibration with bucket milking.
I'm interested in your view of the benefits of using this new method.
Please think of an example and try to fill in data for as many of the below points as possible. Quantitative data is the best, however if you can't express that your qualitative judgment and comments are also welcome. Try not to be too short.
Survey
Farm name (this is only for reference and will not be published)
Type of parlour
Number of cows
Number of Milk Meters
Milking sessions / day
Type of action (initial milk meter calibration, installation test, routine check)
Benefits:
Labor savings
Farm profitability
Animal welfare
Work-facilitating
Work safety
Environment and energy
Resource need
Other
General comments

Labor savings

Overall the labour associated with the new software calibration method compared with traditional methods using bucket milking only is reduced from man days to one or a few man hours. The labor saving differs depending on how the new method has been utilized in the local protocols for approval for official milk recording. From the assessment the following figures were mentioned:

NL, saving of 4-8 bucket milkings per milk meter and saving one visit to the farm

FR, saving of 6 bucket milkings for every milk meter exceeding six of the milk meters in the parlour (for which bucket milking is still required as verification during installation test)

SE, for a double 12 parlour the labor cost over a five year period including initial calibration, installation test and routine checks is calculated to be reduced with over 90%

DE, for a 60 places rotary the labor saving for initial calibration and installation test was four man days.

Farm profitability

With the new method the parlour is not filled up with workers disturbing the milking routine during calibration and test, like with the traditional method, thus avoiding less milk out and less total milk during calibration. For rotaries reduced capacity and downtime was improved with the new method and less waste milk during calibration. Overall the cost for the farmer of initial calibration and installation test could be reduced.

The new method also gives better overview for the farmer of the performance of the milk meters making it possible to faster detection of a deviating milk meter.

Animal welfare

The disturbances during calibration and test could lead to stress for the cows. Less risk of over milking as faulty milk meters can easier be found.

Work-facilitating and safety

Several answers in the survey witnessed about the bad ergonomics of carrying buckets with milk weighing 15-25 kg to the scale and tank as is required with the traditional calibration method. In e.g. NL it is not even allowed with manual lifting above 23 kg. The menu for the new method in the Herd Management program was said to be easy to use. As bucket milking is reduced or eliminated the new method was regarded as safer.

Environment, energy and resource need

With the new method the following environmental savings during calibration and test were mentioned in the survey:

- Shorter milking session, gives shorter vacuum pump running time - energy saving
- Less buckets to clean - hot water and detergent saving
- Less people and fewer visits - less transportation

Other considerations

For AMR (Automatic Milking Rotary) the calibration is practically not possible to do according to manual ICAR guideline due to complexity, resource need and down time.

Discussion

One could question this survey to be limited in the number of cases studied. However the coverage of different countries, herd sizes as well as different milking systems was good. At the same time the only consideration expressed about using this new method was that ID performance must be good which is also valid for using Herd Management systems in general. By all respondents the new method was regarded as a very positive development in the field of milk meter calibration and test. One comment from the survey was: Perfect combination of labor saving calibration and milk meter accuracy.

There was very little evidence from the survey of how the new calibration method can benefit routine check of milk meters. This is not surprising considering the limited time this method has been ICAR approved and the fact that routine check is usually done once a year. We should expect to have more experience of routine check with this method in the years to come.

Conclusions

Every farm that wants to live up to any accuracy standard regarding official milk recording need methods for milk meter calibration, installation test and routine check which are all simplified by this new method from DeLaval.

Using software instead of time consuming bucket milking makes this new method efficient and data continuously available for monitoring. This is a completely new and fast way of working with milk meter accuracy in terms of calibration, installation test and routine check. As there are many benefits with the new method as shown by this study it has the potential to long term revolutionize the organization of milk recording in many regions.

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Detection of pregnancy associated glycoproteins in routine milk recording samples

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Abstract

Recently an ELISA for detection of pregnancy-associated glycoproteins (PAG) has been commercialized. This test can be used for early pregnancy testing using routine milk recording samples from cows or goats from 28 days post breeding. In order to assess potential carry over from one sample to the next when using milk testers the DHIA lab of LKV Weser-Ems, Germany has conducted a study on five farms. The average herd size was 116,4 cows. The average number of milking cows was 103,4. Samples were collected in fall 2014 on each farm. The milk samples were analyzed for the presence of PAGs within one day from collection. All cows that had questionable results were examined by ultrasonography. Results from 464 cows were analyzed. 4,7% of cows in conventional milking systems had a different result compared to ultrasonography. In the herd using the robot this value was 7,3%. A slight carry over at milk recording cannot be excluded. Carry over should be avoided when collecting milk recording samples.

Keywords: pregnancy diagnosis, pregnancy-associated glycoproteins in milk.

Introduction

Initial diagnosis of non-pregnancy is necessary so that cows can be re-inseminated if not pregnant to a previous artificial insemination (LeBlanc, 2013). And it is an important part of any effective reproductive management plan for modern dairy farms. On most farms, early diagnosis of pregnancy is done by a skilled veterinarian, either by trans-rectal palpation or ultrasonography of the uterus. Pregnancy diagnosis can be a problem for dairy farmers in areas where veterinary support is limited. An alternative approach is to use a pregnancy detection assay (Lawson et al., 2014). Recently an ELISA for detection of pregnancy-associated glycoproteins (PAG) has been commercialized. This test can be used for early pregnancy testing using routine milk recording samples from cows or goats from 28 days post breeding which facilitates the workflow on the farm as the samples can be collected during the milking process and cows do not need to be tied and prepared for palpation and ultrasound at any time during the day.

Material and methods

In order to assess potential carry over from one sample to the next when using milk testers the DHIA lab of LKV Weser-Ems, Germany has conducted a study on five farms. The average herd size was 116,4 cows (58 to 182). The average size of milking cows was 103,4 (51 to 161). In three herds milk samples were collected by TruTest milk testers (TruTest Group Ltd.). In one farm stationary Metatron milk tester (GEA Farm Technologies) was used and another farm used the milking robot AMV Lely A3. Samples were collected

in fall 2014 on each farm. Milk volume and animal identification numbers were recorded. The milk samples were analyzed for the presence of PAGs within one day from collection. All cows that had questionable results were examined by ultrasonography.

Results

Results from 464 cows in conventional milking systems were analyzed. 4,7% of cows classified as being ?28 days post insemination had a different result compared to ultrasonography. In the herd using the robot this value was 7,3%. Slight carry over at milk recording cannot be excluded. However, in this study the trend of deviation was from "open" to "recheck" or "pregnant". No pregnant cow was determined "open" by the milk pregnancy test when testing milk recording samples.

Table 1. Carry over study in five herds. Herds A-D had conventional milking systems. Herd E was using a robot.

	All cows			Cows >28 days post insemination		
Farms	Tested	Concordant	Discrepant	Tested	Concordant	Discrepant
A	106	100	6 (5.7%)	66	65	1 (1.5%)
B	123	112	11 (8.9%)	72	68	4 (5.6%)
C	160	151	9 (5.6%)	80	79	1 (1.3%)
D	75	64	11 (14.7%)	39	33	6 (15.4%)
A-D	464	427	37 (8.0%)	257	245	12 (4.7%)
E	100	88	12 (12.0%)	55	51	4 (7.3%)

Conclusions

A slight carry over at milk recording cannot be excluded. Carry over should be avoided when collecting milk recording samples.

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MooMonitor+ Smart Sensing Technology and Big Data - Resting time as an indicator for welfare status on farms

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Abstract

A healthy and happy cow will produce more milk and is more likely to live longer. The European animal welfare legislations acknowledges sentience in farm animals. Dairy cows are considered sentient creatures with the right to express natural behaviour and to have provision of the animal's basic needs. Included in this is an emphasis on the owner regards animal welfare and cow comfort. Resting time can be used as an indicator of welfare in different farming systems. Resting enhances blood flow through udder tissue and the gravid uterus. It improves overall claw health while reducing stress and increasing cow comfort. This is reflected in the animal's health status and her reproductive performance and productivity. On the other hand, long bouts of increased resting time can be an indicator of welfare problems. The MooMonitor+ (Dairymaster, Causeway, Co. Kerry, Ireland) system automatically identifies different behaviourisms of the cow and is used to detect estrus, health and welfare events in cows by means of monitoring activity, feeding, rumination and resting time. Using this commercially available device a trial was set up to determine welfare status on dairy farms. This paper interprets and discusses the trial in relation to the impact of season, house design, lameness, production system and overall health on resting time.

Keywords:MooMonitor+ Smart Sensing Technology, animal welfare, resting time, sustainability,

Introduction

Since 1 December 2009 the Lisbon Treaty incorporates the legal recognition of animal sentience. This means that full regards needs to be paid towards the welfare requirements of animals. Numerous studies in the past have shown that improved welfare increases milk output (Fourichon, *et al.*, 1999; Haley, *et al.*, 2001; Regula, *et al.*, 2004). With eye on the future of dairy farming - expanding herd sizes and ultimately space and environmental emission constraints - it seems the most logical step to start getting more milk from the same animals by improving their circumstances on farm. Accordingly longevity in dairy livestock should be a goal to strive for. Milk yield increases per parity up to the 4th and 5th lactation to decrease slowly afterwards (Vlaamse Overheid, 2008). But even in the 6th and 7th lactation significantly more milk is produced compared to production levels of heifers. With this in mind and the fact that adult animals use their energy more efficiently, farm managers can opt for a more sustainable herd profile with higher and longer life productions of the same animals.

In order to improve sustainability at farm level, attention must be paid to the overall health and comfort status of the animal. Animal welfare plays a big part in this. The American Veterinary Medical Association defines animal welfare as - an animal that is healthy, comfortable, well-nourished, safe, able to express innate behaviour, and that is not suffering from unpleasant states such as pain, fear, and distress (AVMA, 2013). One of the key indicators to identify animal welfare in cows is monitoring resting time. A dairy

cow rests on average between 10 and 14 hours per day (Drissler, *et al.*, 2005; Cook, *et al.*, 2005). Longer resting times are considered beneficial to both productivity and overall claw health (Metcalf, *et al.*, 1992; Cook, 2008). Too little or excessive resting however can both be an indicator of sickness, stress, pain, poor shed design, management defects or overall malaise of the animal.

Monitoring welfare by means of automated data recording has proven its value in the past already. Among others data loggers, videotaping material, automatically weighing feed troughs and activity monitors have successfully been used to record different indices that are correlated with a cow's welfare status on farm (Hussey, *et al.*, 2005; Ito, *et al.*, 2010; Mattachini, *et al.*, 2011). This shows great value for commercially available accelerometer technology that uses smart sensing software, such as the MooMonitor+. Different behaviourisms can be accurately identified and used in daily farm management. Although much is written about dairy cow welfare especially concerning lameness and mastitis, little is known about the impact of a generalised common health event on the average total daily resting time of the individual cow if monitored automatically. In this trial we focussed on this one aspect of cow welfare. The goal of this study was to investigate any existing correlation between automatically monitoring daily resting time in cows and the occurrence of health events and whether this feature can be used in cow welfare protocols in future.

Materials and methods

Data collection

In this trial resting time for cows affected with one or more health event - or other events that affects cow welfare - was recorded and by means of statistical analysis compared to daily resting time of healthy cows. To record resting time cows were fitted with a MooMonitor+ collar (Dairymaster, Causeway, Ireland). This is a commercially available device that measures the cow's neck movements using nanotechnology. The device is able to distinguish different types of behaviour and can aid in heat detection, health monitoring, feed conversion calculations and overall herd management. One of the behaviours it identifies is resting time. Every 15 minutes information is transferred back from the device to the cloud server and gives a measurement of how long the cow was resting for in that 15 minute period (alongside other behaviours).

Animals and health events.

For the data analysis resting time data of 172 cows from 1 commercial herd over a 4 month period were collected. A subset of data was observed for different types of health related events that were present during this time frame. Different types of disorders were included in this list such as mastitis, lameness, diarrhoea, displaced abomasum, retained foetal membranes, metritis and others. All these events were brought together under the common denominator 'health event'.

Statistical analysis

Health events were translated into "sick days". An animal was considered sick 4 days before and 4 days after the health event was given. A total of 391 "sick days" were found. Total daily resting time of sick days was then compared to total daily resting time for non-sick days. The contrast between resting time on "sick days" and "normal days" was calculated. This is the average difference between resting time on the days around a noted health event and other days for the same cow.

Results

The total length of the trial data set was 126 days. In total 14,087 records were used for the trial. For the 391 "sick" days, each cow rested on average 101 minutes (P<0.001) longer than that cow rested on other days. A 95% confidence interval (CI) for this contrast is 92-110 minutes. Also in the period around the health event (-4 to +4 days) cow's activity levels remained (sub) normal and a reduction of increased activity was observed (Table 1).

Table 1. Characteristics of resting time data in this trial.

Characteristic	Data
Number of animals	172
Length of trial[1]	126 d
Days sick[2,3]	391 d
Daily resting data cows on normal days	511.64 (508.03; 515.24) min/d
Daily resting data cows on sick days[2,3]	612.84 (593.29; 632.40) min/d
Surplus resting on sick days	101.20 min/d

[1]List of health events and real time resting data recorded in the period 01/01/2015 till 06/05/2015.
[2]Sick days includes health event +/-4 days.
[3]Health events included cases of abscess formation, bloat, diarrhoea, displaced abomasum, leg or hip injury, lameness, mastitis, metritis, retained foetal membranes, rumen pathology and indigestion.

Discussion

Cow welfare in the dairy industry is becoming increasingly more important these days. A dairy cow needs to be looked after in correlation with certain standards pointed out in European legislations. Moreover, contemporary consumers put more and more emphasis on the origin of their products. Milk should ideally come from well treated healthy cows with low cell counts, top diets and living in a stress free environment. Milk co-ops that want to distinguish themselves from their competitors can do so by listening to these consumer requirements. They present various obligatory health and welfare guidelines on top of the European legislations to be followed by their milk producers. If they conform to all legislations and guidelines producers gain status and better payment amongst their peers enabling themselves as well as the other producers to produce a product at a higher quality level. This benefits the competitive market strategy of Europe and at the same time enhances product quality.

A cow expresses both her physical and physiological well-being in her behaviour. When behaviour changes this can often be associated with a health event and this in turn will affect her well-being. Automatically monitoring resting time can accurately identify these changes and can be used in daily farm management routines (Vasseaur, *et al.*, 2012). This will aid the farm manager with making interventional decisions concerning welfare management. Welfare of cows can be improved by adjusting shed layout, flooring, cubicle design, ventilation, animal handling facilities, overall farm management, sick cow management, culling policies, milking technique, milking equipment and many others. Even small adjustments such as introducing a mastitis cow protocol or a more comfortable bedding material in the cubicles to increase resting time can have a massive influence on the cow's performance (Cook, 2008; Cook & Nordlund, 2009).

Hours spent resting per day varies among different shed layouts. In a study done by Haley *et al.* resting time was used as an indicator of well-being in cattle to evaluate stall floor design and quality (Haley, *et al.*, 2001). Resting time increased for animals when shed layout became more comfortable. Season also seems to play a role in average daily resting time. Animals appear to lie down more in the winter months than in summer. However, geographical location, behavioural thermoregulation and climate seem to have a major effect on these records (Steensels, *et al.*, 2012). When cows suffer from heat stress they tend to lie down less hours per day. This could be an explanation of greater resting time records in winter than in summer (Allen, *et al.*, 2013). This study however was performed over a 4 month period which is too short of a timeframe to take these kind of environmental differences into account.

In this trial welfare status of individual dairy cows in one herd were mutually compared by means of measuring resting time data. Cows with health events rested on average 101 more minutes per day than healthy cows (CI: 92 to 110 minutes). This is in agreement with findings of Dantzler that sketches the typical image of a sick animal by means of non-specific symptoms of sickness namely lethargy, anorexia and social withdrawal which includes fatigue and increased resting (Dantzler, 2001). Health issues included in the trial were among others: mastitis, diarrhoea, injuries, retained foetal membranes, displaced abomasum, various rumen pathologies and lameness events. Ito *et al.* found that resting time of individual cows increases with the incidence of lameness events. Severe lame animals were resting on average 12.8 hours per day (CI: 12.0 to 13.7) compared to 11.2 hours per day (CI: 10.7 to 11.8) and had longer duration of lying bouts. The study also points out that cows that on average rest > 14.5 hours per day are at greater risk of experiencing a severe lameness event (Ito, *et al.*, 2010). In contrast Siivonen *et al.* found that resting time of animals decreased in the case of an acute clinical mastitis event. A possible explanation for this is that in case of very swollen udder tissue the animal tries to cope with both swelling and pain and would do the exact opposite of what one would expect - by trying to avoid the swollen tissue to rest on the surface when lying down. With other words pain in udder tissue can override the motivational status of the animals and therefore affect daily resting time negatively. In accordance with their study results a higher level of restlessness was discovered in these cows (Siivonen, *et al.*, 2011). Restlessness is another feature that can be monitored by the MooMonitor+. However more research is necessary to value the impact on the daily measurements of the device concerning acute clinical mastitis cases.

In the period around health events (-4 to +4 days) it was observed that in many cases activity levels of the animals in this trial were below normal and animals experienced a reduction of activity intensity as well in this period. This phenomenon could be explained by the body's need for rest in the early stages of disease as a central motivational state to promote recovery (Kelley, *et al.*, 2003) where the non-specific symptoms such as fatigue and anorexia are preceding the more typical clinical symptoms. Recognising early stages of disease by measuring daily resting time can be helpful in detecting health events automatically.

Conclusions

Daily resting time plays an important part in expressing a cow's emotional and physical health status. It can be used as a key indicator for monitoring cow welfare on farm. In this study one aspect of animal welfare - namely health - was observed to find out the effect a health event has on the daily resting time of an individual animal. It is concluded that in this study animals experiencing a health event rest on average 101 minutes longer (CI: 92 to 110 minutes) than animals that are not experiencing a health event. Also, sick animals can be subjected to a period of reduced activity intensity compared to healthy cows. These stats express the ability of the MooMonitor+ system to detect changes in daily resting time caused by various health events. Likewise, analysis of daily resting time data offers great potential as a farm management tool and this feature could be incorporated in various cow welfare protocols on farm.

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Increasing the value and traceability of milk samples with NFC technology: SmartLY

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Abstract

Eilyps decided to create SmartLY in 2014 to devlop improved data collection on the farm. SmartLY is a mobile application which allows to take a milk sample identified with an RFID tag. This tag could be linked to animal electronic identification in farms. The enhancement of the electronic identification is an option which needs an LF / HF reader in milking parlours. The NFC technology secures data collecting, sorts milk samples and by consequence multiplexing the number of analyses in the same sample.

Keywords: milk sample, nfc, rfid.

Introduction

To continue development and to create differentiation in a competitive market, Eilyps decided to make a mobile application for data collecting in dairy farms. This application allowed to continue our historical profession while at the same time answering breeders' future needs and adapting to the new information technologies.

SmartLY is composed of different modules dedicated to precise parts of milk recording. Each module can be sold separately to breeders or milk recording companies.

This solution could be integrated in to different types of information systems and data bases.

Mobility

SmartLY offers a range of our Service Oriented Architecture ILYCO on mobile devices. That means this ILYCO server host rules management, norms, control and data treatment. SmartLY is dedicated only for data collection and its functioning is simplified.

In this way, we find four levels on the server and smartphone:

- Common tools
- Business controls
- Storage buffer
- Web services proxy

All data exchange between SmartLY and ILYCO is based on WebService

Electronic data collection and health module

The origin of the creation of SmartLY was data collection in dairy farms.

The first aim was to reduce to the maximum delay between milk recording operations and giving results to farmers. At same time, we wanted to decrease the amount of manipulation during data collection.

The second objective was to increase traceability and data reliability with using RFID technology.

In fact, with the emergence of new more precise analyses for some types of animal, it is necessary to reduce mistakes to the absolute minimum.

SmartLY collects all the information concerning the milk recording such as animal identification, farm identification, date and time, weight of milk for each cow.

The employee or the breeder using SmartLY transfers data immediately after milking to the database and receives in return all the validated data.

Health data for each animal can be collected with a specific module of SmartLY. These health events are archived to create some indicators for advisors. SmartLY is the software to keep animals' health profiles fully up to date.

Specific analyses

More and more specific analyses are appearing in the dairy cow industry. To answer the demand from breeders, SmartLY has developed a specialized module to manage distinctive analyses.

With the collaboration of laboratories, we can sort all samples with a specific identification during data collection at the dairy farm.

Some management rules in data base select the animal concerned by specific analyses and check in a list on the smartphone. It is possible to choose one or more analyses for the same sample. SmartLY flags a sample's tag to differentiate specific analyses during data collection.

After validation by breeders, the employee writes on the tag with the NFC technology.

In the laboratory, the vials identified by a specific code on the chip are sorted and can be directed to the particular analytical operations.

Animal electronic identification

To increase traceability from the animal to the sample, SmartLY comes with an option. With the LF / HF reader of Reyflex, it is possible to read the cow's anklet and write on a tag fixed on the milk meter.

Once cows are milked, SmartLY reads the milk meter. All information is recorded on SmartLY and written on the tag inside the sample.

This option increases traceability and efficiency during milk recording operations.

Further development

Eilyps and its milk recording companies partners want to develop a new module. The aim of this module is to make it easier to complete the activity report by using flash code technology to geolocate employees and timestamp the activity. With the smartphone camera, it is now possible to read all the information to create the report automatically.

This option could also be used in other farm activities.

Session 4

Milk recording in cattle, meat and fibre performance in sheep, goats and beef cattle

World-wide trends in milk-recording in cattle

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Abstract

It was decided that the Dairy Cattle Milk Recording Working Group would update ICAR Guidelines Section 2, which focuses on milk recording, and to organise a worldwide survey to cover all relevant dairy countries around the world, including ICAR members and non-members. The questionnaire included 106 questions focusing on milk-recording, management, methodology, organisation and new technology as applied to Section 2 of the ICAR Guidelines. This paper is one of three articles prepared on the basis of this survey for the ICAR Technical Workshop to be held in Krakow in June, 2015. The goals included the monitoring of the current situation in milk recording and the organisation of milk recording and trends in methodology and management in milk-recording organisations, improvement of the ICAR Guidelines and strengthening communication with ICAR members in order to obtain useful comparisons of methodologies, protocols and practices. This survey serves as a starting point for the continued work of milk-recording organisations. The survey was prepared by the Dairy Cattle Milk Recording Working Group together with invited milk recording organisations. Data were obtained from 46 organisations across the world. All participants completed a questionnaire. The respondents represented 287 organisations (some of the responding organisations are representing their member organisations on the national level), 169 laboratories and 21,486,116 cows.

Keywords: ICAR, Dairy Cattle Milk Recording Working Group, milk recording, survey, ICAR Guidelines, questionnaire, milk-recording organisations.

Introduction

In recent years we have seen many changes to milk recording in cattle along with rapid technological development. It was decided that the Dairy Cattle Milk Recording Working Group would update Section 2 of the ICAR Guidelines, which focuses on milk recording, and to prepare a worldwide survey to cover all relevant dairy countries around the world, including ICAR members and non-members. A thorough analysis of survey results will provide the basis for an enhanced version of Section 2 of the ICAR Guidelines. This survey is an official project of the ICAR Dairy Cattle Milk Recording Working Group and features a wide range of the most important ICAR members and non-members.

The survey

The survey included 106 questions covering the most important phases of milk recording, incorporating the collaboration and feedback of milk-recording organisations involved in the project. The main goal of this part of the survey is to analyse methodological aspects of milk recording, which are covered in Section 2 of the ICAR Guidelines and to analyse approaches used in data capture, milk-recording identification, sample transport, milk-recording methods, sampling, calculation of 24-hour milk production, lactation calculation and other relevant methodological milk-recording aspects.

Data capture was designed electronically using SurveyMonkey software and optionally for some participants using PDF formats. Obtained results were checked from a logical and methodological point of view and some of the points were clarified with participating organisations. Data were obtained from 46 organisations (Table 1). All participants completed a questionnaire of 106 questions. The respondents represented 287 organisations, (any one organisation may represent other organisations in its own country), 169 laboratories and 21,486,116 cows (Table 2). The Dairy Cattle Milk Recording Working Group acknowledges and thanks all participants in the survey for the feedback used in the project.

Most of the responses covered entire countries (74% organisations). Responses covering parts of countries only totaled 26%. If we take a look at the number of organisations, only 27% were umbrella organisations.

Results

This part of the survey covers areas relevant mainly for methodology and ICAR Guidelines.

Lactation calculation methods (calculation of accumulated milk yield)

The ICAR Guidelines cover the needs of milk-recording organisations. With that in mind, it seems likely that some of the methods listed under "other options" will be selected, which should extend the options open to ICAR members.

Data about lactation calculation methods were obtained from 43 countries; 3 countries skipped this question. The most common approach is to use only one method for lactation calculation (93%); only 7% of organisations use two methods for lactation calculation. No organisation uses more than two methods for lactation calculation, which means that organisations included in the survey mostly use a unique system of lactation calculation.

From the analysis (Table 3), it is evident that most organisations use the Test Interval Method and Interpolation using Standard Lactation Curves.

Table 1. Organisations (countries) which provide raw data along with relevant contacts and responsible persons (authors from milk-recording organisations).

Country	Organisation	Respondent
ARG	Asociación Criadores de Holando Argentino	Liliana Chazo
AUT	LKV Austria	Karl Zottl
BEL	Association wallone de l'élevage asbl	Carlo Bertozzi
BGR	Executive Agency on Selection and Reproduction in Animal Breeding	Vasil Nikolov
CAN	CanWest DHI	Neil Petreny and Richard Cantin
CHE	Association of Swiss Cattle Breeders	Eric Barras
CHL	Cooprinsem	Eduardo Winkler
CHN	Shanghai Dairy Cattle Breeding Center Co., Ltd.	Pengpeng An
COL	Asosimmental - Simbrah Colombia	Filippo Rapaioli
CZE	Czech Moravian Breeders´ Corporation	Pavel Bucek, Josef Kucera (CFBA) and Zdenka Vesela (IAS)
GER	German Association for Performance and Quality Testing	Folkert Onken
DNK	RYK	Uffe Lauritsen
EGY	Mansoura University, Faculty of Agriculture	Elsaid Z.M. Oudah
ESP	Asociacion Nacional De Raza Parda	Francisco Javier Castro Gutier
ESP	CONAFE	Sofia Alday
EST	Estonian Livestock Performance Recording Ltd.	Aire Pentjärv
FIN	ProAgria Group	Juho Kyntäjä
FRA	France Génétique Elevage	Gilles Thomas and Laurent Journaux
GBR	Quality Milk Management Services Ltd	Andrew Bradley
GBR	National Milk Records plc	Tony Craven
GBR	Cattle Information Services	Suzanne Harding
HRV	Croatian Agricultural Agency	Zdravko Barac
HUN	LPT LTD / Hungary	Julianna Kóti Seenger
IND	BAIF Development Research Foundation	Ramchandra Bhagat
IRL	Irish Cattle Breeding Federation	Brian Coughlan
ISL	The Icelandic Agricultural Advisory Centre	Gudmundur Johannesson
ISR	Israel Cattle Breeders Association	Yaniv Lavon
ITA	Associazione Italiana Allevatori	Mauro Fioretti and Riccardo Negrini
JEY	RJA&HS	David Hambrook
LTU	Animal Recording Control	Gintare Kisieliene
LUX	CONVIS s.c.	Armand Braun
MAR	Coopérative Mabrouka Des Eleveurs de Bovins	Nadia Mousili
NLD	CRV	Louwrens van Keulen and Hans Wilmink
NOR	TINE SA	Tone Roalkvam
NZL	LIC	Bevin Harris
POL	Polish Federation of Cattle Breeders and Dairy Farmers	Danuta Radzio
ROU	Innovative Agricultural Services	Cosmin Popa
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USA	Lancaster Dairy Herd Improvement Association	Jere High
USA	NorthStar Cooperative	Kevin Haase
ZAF	South African Stud Book and Animal Improvement Association	Japie van der Westhuizen

Table 2. General overview of the project and available data.

Indicator	Number
Dairy cows covered in the questionnaire	21,486,116
Number of recording organisations	287
Number of milk-analysis laboratories	169
Number of organisations that completed the questionnaire	46

Table 3 Lactation calculation methods used in milk-recording organisations.

Answer options	Number of organisations
Test Interval Method (TIM) (Sargent, 1968)	29
Interpolation using Standard Lactation Curves (ISLC) (Wilmink, 1987)	8
Multiple-Traits Procedure (MTP) (Schaffer and Jamrozik, 1996)	2
Best prediction (VanRaden, 1997)	5
Other methods	7

Table 4. Daily-yield calculation methods used in milk-recording organisations.

Answer options	Number of organisations
AM/PM milkings, Liu et al. (2000)	14
Delorenzo and Wiggans (1986)	10
Correction based on preceding intervals, ICAR Guidelines 2.1.7.1.	8
AMS (milking robots); Data used from more than one day (Lazenby et al., 2002)	16
AMS (milking robots); Data used from 1 day (Bouloc et al. 2002)	3
AMS (milking robots); Estimation of fat and protein yield (Galesloot and Peeters, 2000)	7
AMS (milking robots); Sampling period (Hand et al., 2004; Bouloc et al., 2004)	2
Electronic Milk Metre (EMM); Data used from more than one day (Hand et al., 2006)	3
Other methods (in brief)	12

Table 5. What is the minimum sampling duration on the test day (in hours)?

	Response	
Answer options	Percentage	Number of organisations
Less than 10 hours	36	11
11-15 hours	13	4
16-24 hours	48	15
More than 24 hours	3	1

Seven organisations used other methods and from these 7 organisations 2 did not describe the methods used. These 5 additional methods will be analysed if it is feasible to include them in the new version of the ICAR Guidelines. The future policy of the Dairy Cattle Milk Recording Working Group is to continuously monitor development and keep the ICAR Guidelines updated in this field.

Daily-yield calculation methods used in milk-recording organisations

A very important part of the Dairy Cattle Milk-Recording Working Group's operations is revision of daily yield calculation methods used in milk-recording organisations. The data must be obtained by direct measuring, so as to avoid any alterations. Computation of 24-hour yields are performed by the milk-recording organisation, not by the milking equipment software. This is done in order to guarantee the harmonisation of calculation methods between the different brands of equipment. The same recommendation is valid for lactation calculations.

42 organisations filled in this question and 4 skipped this question. The highest share of methods for daily-yield calculation (Table 4).

- AMS (milking robots); Data used from more than one day (Lazenby *et al.*, 2002).
- AM / PM milkings, Liu *et al.* (2000).

It is planned that other options will be analysed if some of these methods become valuable and feasible for the ICAR Guidelines.

Milk recording using milking robots (automatic milking systems)

From the answers in the survey it is evident that most of the organisations have less than 5% of milking robots (24% in interval 0-1% milking robots and 33% in interval 1.1-5% milking robots). The share of milking robots increased year by year and 14% of organisations were in interval 5.1-10% of milking robots, 10% organisations are in interval 10.1-20.0% of milking robots and 19% organisations in interval 20% and more of milking robots. Some organisations do not record this option separately.

Analyses showed that countries use different minimum sampling durations for milking robots (Table 5). This trend reduces sampling duration due to the high costs for milk recording in AMS. It is most common to employ a minimal sample duration lasting between 16-24 hours. Some countries use minimal sampling durations of less than 10 hours. Only one organisation has a minimal sampling duration of more than 24 hours. This question was answered by 31 organisations.

Results for the number of samples taken when using automatic milking robots were provided by 37 organisations. Most of the organisations use only one option for sampling when using milking robots (84%). 8% of organisations use two options for sampling and 8% of organisations offer 3 options for sampling.

Due to the high costs involved, organisations prefer only one sample (27 organisations) (Table 6).

In the case of more than one sample, organisations mostly analyse samples separately (11 of organisations). Some of the organisations use "Samples are mixed proportionally" (just one sample analysed) - 5 organisations and "Samples are mixed in a fixed amount" (just one sample analysed) - 3 organisations (Table 7). The most common approach is to have one sampling scheme in the case of more than one sample. Only one country marked 2 options from table 7.

Table 6. How many samples do you take during the sampling period?

Answer options	Number of organisations
Only one	27
From each milking	14
How many from a limited number of milkings?	5 (in all cases, 2 samples)

Table 7. In the case of more than one sample, how are these samples taken?

Answer options	Number of organisations
Separately (each sample is analysed)	11
Samples are mixed proportionally (just one sample analysed)	5
Samples are mixed in a fixed amount (just one sample analysed)	3
Other options	1

Table 8. Over how long a period is milk yield production recorded and calculated (e.g. 1, 5, 7 days, 1 month, etc.)?

	Response	
Answer options	Percentage	Number of organisations
Test day only	44	16
Multiple number of days - test day included	50	18
Multiple number of days - test day excluded	6	2

A total of 36 organisations provided data on the duration of milk-yield production, recording and calculation and 16 for the number of days (Table 8). Organisations mostly use options with multiple numbers of days including the test day (50%). In the case of multiple numbers of days - it is not common to exclude the test day. A large share of organisation use the test day only (44%). Almost all countries use only one option in the duration section and only one organisation uses 2 options. 25% of organisations specified 1-3 days; 19% - 4 days; 13% - 5 days; 0% - 6 days and 43% - more than 6 days. From the survey, the maximum period given was 10 days.

If milk-yield production is recorded from a period greater than one day, the approach on how to combine data of this multiple milk yield with fat and protein measurements is a very important issue. Milk-recording organisations currently use different approaches of combining these data. The most common method is to use milk production from multiple days with the milk content from the test day (8 organisations), to calculate percentage of fat, percentage of protein, etc. on the basis of the milk yield from the test day (7 organisations), and then to combine contents of solids from the test day with the milk production from the test day. Two types of milk production are recorded (one for protein and fat production calculation, and the other for officially published milk yield production for milk production from a multiple number of days). Five organisations used this method. Other approaches are less common.

Stationary parlour meters

Stationary parlour meters ensure easy access to data on milk yield production. This part was filled in by countries that use milk-yield production from more than one day (e.g. stationary parlour metres, data used from more than one day (Hand *et al.*, 2006). There are more stationary parlour meters than milking robots. 29 organisations filled in this question (Table 9). In this case test days from one day (69%) is mostly used. Results from more than one day are less common (31%).

46% organisations use 1-10% of stationary parlour meters, 15% organisations use 10.1-20% of stationary parlour meters and 39% organisations use more than 20% of stationary parlour meters.

The most common approach found in the survey was the period of milk yield from test day only. Using an approach with multiple numbers of days was less common (Table 10). This table was filled in by 21 organisations.

The length of the period from which milk yield production is recorded over multiple number of days is usually 7 days and for one organisation, 5 days.

There are different ways of combining content of fat and protein with milk-yield production. The most common options are: combine milk production from multiple days with the milk content from the test day; calculation of % of fat, % protein, etc. on the basis of the milk yield from the test day (weighted average); combine contents of solids from the test day with the milk production from the test day. Two types of milk production are recorded: one for protein and fat production calculation; the other for officially published milk yield production for milk production over a multiple number of days.

Table 9. Stationary parlour meters - do you use milk yields from more than one day?

	Response	
Answer options	Percentage	Number of organisations
Yes	31	9
No	69	20

Table 10. Over how long a period is milk yield recorded and calculated (e.g. 1, 5, 7 days, 1 month, etc.)?

Answer options	Number of organisations
The test day	16
Multiple number of days – test day included	5
Multiple number of days – test day excluded	1

Milk-recording methods

ICAR uses three milk-recording methods:

- A technician (supervised).
- B farmer (unsupervised).
- C combination of supervised and unsupervised.

43 organisations filled in and 3 skipped this question. According to ICAR nomenclature, method A is still the most common method (Table 11).

Most organisations use more than one milk-recording method in their herds. Only 1 method was used in 42% of organisations, 2 methods in 30% of organisations and 3 methods in 28% organisations.

13 organisations used method A only, while 5 organisations used only method B. Method C was used in combination with other methods.

The share of methods with respect to herds is in accordance with the distribution of milk recording methods with respect to the share of cows (Table 12).

Table 11. Milk-recording methods.

Answer options	Number of organisations
A (technician)	38
B (farmer)	30
C (combination of A and B)	12

Table 12. Milk-recording methods.

	Response	
Answer options	Cows (millions)	Number of organisations
A (technician)	14.9	38
B (farmer)	5.5	30
C (combination of A and B)	0.4	12

Sampling schemes

One of the most important tasks for the Dairy Cattle Milk-Recording Working Group is to revise sampling and to design an easy-to-use and understandable nomenclature. Some methods were not given, but this could benefit many ICAR members and add flexibility. Method Z is an important method, but the most common method of sampling is alternate one-milk-recording T. Information on sampling was obtained from 41 countries with 5 countries skipping this question.

Table 13. Sampling schemes.

	Response	
Answer options	Cows (millions)	Number of organisations
Proportional sampling (P)	4.6	15
Equal measure sampling (E)	5.3	17
One-milking sampling with milk weights from more than one milking (Z)	3.2	19
Multiple sampling (M)	0.6	6
Alternated one-milking recording (T)	7.0	31
Constant one-milking recording (C)	0.05	2

The most important method was alternated one-milking recording (T) with 7.0 millions cows in 31 organisations (Table 13). It seems a new nomenclature is needed in order to update the ICAR Guidelines and offer more flexibility. The discussion on sampling schemes seems yet to continue and improvements may well be made before the next issue of the ICAR Guidelines.

It is very usual to have more than one option for sampling. One scheme of sampling is used in 29% organisations, two in 32% of organisations, three in 34% of organisations and more than three in 5% of organisations.

Recording intervals in weeks

Information on recording intervals was obtained from 41 organisations, which offer very often more than one option for recording intervals. The 4-week interval (Table 14) is still the most common. Other commonly used options are five, eight and six weeks. Discussion on daily milk recording will be of particular importance to the Dairy Cattle Milk Recording Working Group in the future.

Table 14. Recording intervals in weeks.

Answer options	Response	
	Cows (millions)	Number of organisations
Daily	0.154	3
1	0.011	1
2	0.024	4
3	0.193	2
4	11.599	36
5	2.869	11
6	1.418	10
7	0.254	2
8	3.25	11
9	0.659	1

What system for identifying animals is approved for official milk-recording?

This question was filled in by 45 organisations and only 1 skipped it (Table 15). The key prerequisite for accurate milk recording and for ensuring data quality is to use a proper method of identification, preferably a unique national scheme.

Common practice among ICAR members is to use an official identification number (unique national scheme), implemented in 40 organisations (Table 15). In 9 organisations, herdbook numbers are used. Only 5 organisations use different schemes (e.g. official ID used as a herdbook number, management number or a combination of a herdbook and freeze number). Most organisations use 1 system for animal identification (80%), while 20% accept 2 systems.

Table 15. What system for identifying animals is approved for official milk-recording?

Answer options	Number of organisations
Official identification number (unique national scheme)	40
Herdbook number	9
Other option (please specify)	5

Which methods do you use to identify animals during milk recording?

Data for this question were obtained from 45 organisations and only 1 skipped this question. The most common methods for identifying animals are to use either permanent visual plastic eartags without barcodes or permanent visual plastic eartags with barcodes. RFID eartags are also very common. Other milk-recording identification methods include metal eartags, RFID boluses, tattoos and cuts. Some organisations use collars, freeze brands or a combination of freeze brands and eartags; all of which are included in "other options". Some organisations combine official identification methods (e.g. permanent visual plastic eartags without barcodes as well as RFID eartags, etc.).

Only 33% of organisations use only one option of identification. Most organisations offer 2 or more options for animal identification during milk recording.

Table 16. Which methods do you use to identify animals during milk recording?

Answer options	Number of organisations
Metal eartag	5
Permanent visual plastic eartags without barcode	29
Permanent visual plastic eartags with barcode	23
RFID eartags	19
RFID boluses	2
Tattoo	3
Cut	1
Other option or comment	10

Do you use any additional methods of identification (during milk recording)?

In the survey, additional animal identification methods were also analysed. 29 organisations specified that they use them. Most use one additional identification method (76%), while others use two (24%).

Aside from official identification methods, it is common for ICAR members to use other identification methods for cattle milk-recording. Most organisations use farm transponders and freeze numbers. In some cases, the names of the animals and tattoos are given. 29 organisations entered additional tools, but some did not enter any.

Table 17. Do you use any additional methods of identification (during milk recording)?

Answer options	Number of organisations
Farm transponder	22
Freeze number	12
Others	2

Are repeated tests for recording (supervisory control) implemented?

45 organisations completed the information for repeated tests, while 1 organisation skipped it. 62% of organisations use repeated milk-recording testing and 38 % do not (Table 18).

Table 18. Are repeated tests for recording (supervisory control) implemented?

	Response	
Answer options	Percentage	Number of organisations
Yes	62	28
No	38	17

Repeated testing is carried out using different options (Table 19). Data were obtained from 30 organisations. The most common is repeated testing applied in herds, where an extraordinary increase in production was recorded for leading herds/cows and herds outside confidence intervals (e.g. fat %). Most organisations combine different approaches and use more than one option when repeated testing is used.

How are the supervisory controls (repeated tests, repeated recordings) carried out in the field?

Table 19. How are the supervisory controls (repeated tests, repeated recordings) carried out in the field?

Answer options	Number of organisations
Random	13
Leading herds / cows	17
Producers of AI bulls	9
Herds outside confidence intervals (e.g. fat %)	16
Herds with an extraordinary increase in production	18
Other (please specify in brief)	7

Organisations often combine different methods for retesting animals. Some combine retests for all animals and selected animals in the herd (26 retest all animals and 8 retest selected animals). Some organisations use both options (Table 20).

Animals inspected in repeated recordings (supervisory control, repeated tests)?

Table 20. Animals inspected in repeated recordings (supervisory control, repeated tests)?

Answer options	Number of organisations
All	26
Selected animals in the herd	8

The three most important traits for retesting are: milk production, fat percentage and protein percentage. Protein and fat production are less often used (Table 21). Other possibilities include lactose, SCC and urea. 29 organisations filled in this question and most use a combination of different traits.

Which traits do you use for repeated tests (supervisory control) and who provides these tests?

Table 21. Which traits do you use for repeated tests (supervisory control)?

Answer options	Number of organisations
Milk production	27
Fat %	23
Fat kg	12
Protein %	21
Protein kg	12
Other (please specify these traits)	7

Table 22. Who performs the supervisory control?

Answer options	Number of organisations
Managers of milk recording organisations (not the usual sample taker)	10
Specialist supervisors from milk recording organisations (supervisors who are not your usual sample takers, and who are in some cases involved in other milk-recording inspections, i.e. identification)	18
Authorised personnel outside milk recording organisations (outsourced)	3
Other options	5

For which herds is a bulk tank comparison implemented?

Bulk tank comparison is a very useful tool for quality inspections, and 20 milk-recording organisations use this method (Table 23).

The most commons traits used for bulk tank comparisons are milk yield, fat % and protein % (Table 24). Other possible options include fat and protein production, but the shares of these two traits are very low.

Table 23 For which herds is a bulk tank comparison implemented?

Answer options	Number of organisations
All milk-recording herds	20
Only in specific cases, e.g. method B (farmer, owner sampling)	4
Not implemented	13
Other possibilities and specific approaches used (please specify)	7

Table 24 Which traits do you use to compare milk-recording with bulk tank

Answer options	Number of organisations
Milk yield	26
Fat %	24
Fat kg	2
Protein %	22
Protein kg	2
Other	7

Conclusion

The survey reviews the situation in milk-recording as it applies to Section 2 of the ICAR Guidelines. On the basis of the results, it might be possible to expand the guidelines with regards to the lactation calculation methods and daily-yield calculation methods used among milk-recording organisations. It is evident that the group's priority should be given over to automatic milking systems (dairy robots) and stationary parlour meters, since the current trend is for automatisation. Some organisations are interested in in-line analysers, which will be a very important issue during the group's discussions. The group is planning to extend sampling parameters as it applies to the ICAR Guidelines because some of the options which meet these criteria are in use, yet absent from the ICAR Guidelines, especially method Z. The most common milk-recording interval in use is still 4 weeks. Flexibility will need to be increased due to the decrease in milk-recording

subsidies. A major challenge is the improvement of quality management in the ICAR Guidelines, which is partly covered in this paper as per the request of milk-recording organisations. The Dairy Cattle Milk Recording Working Group is also preparing new parts for section 2 of the ICAR Guidelines to cover all processes (e.g. training, transport, etc.).

These results are important in order to monitor the situation in milk-recording organisations. They also serve as a basis for changes and improvements to the ICAR Guidelines and to identify new approaches. They are also useful for the ICAR Guidelines in defining new needs of milk-recording organisations, while also being valuable for participating countries, providing feedback and comparisons of the most common milk-recording practices among ICAR members and non-members. Results of this survey can offset changes in different milk-recording organisations. Another benefit of the project is the strengthening of collaboration and communication between the Dairy Cattle Milk Recording Working Group and milk-recording organisations. This survey could serve as an inspiring document for the work of milk-recording organisations in its catering for the different structures, environment, management, economic conditions and practical responses to the requirements and needs of milk-recording organisations.

New requirements from milk recording organisations arose from the survey (only selected comments are included):

- Absence of some "production systems", which are not necessarily Western. In particular India and other Asian countries.
- ICAR milk-recording training in Colombia.
- Lactation calculation methods.
- The calibration system.
- How to rework data in cases where milk-yield production is calculated over more than one day.
- We did find the guidelines to be very useful for DHI performance checks (checking sample limits, etc.).
- ICAR guidelines on missing results and / or abnormal 2.1.7 intervals.
- AMS daily milk recording
- There is information in the guidelines which states that MROs have to implement a supervision system but there is no more information on what it should look like. Some general frames might be useful.

The group is planning to incorporate some of these requirements and use them during the preparation of the new version of the ICAR Guidelines. All of the suggestions and generous support are greatly appreciated. A future survey will be conducted, targeted at addressing specific issues but restricted to a limited amount of questions.

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Worldwide trends in milk recording: milk recording and new technologies

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Abstract

Milk recording organisations are currently more interested in additional milk analyses from the recording sample than in extracting data from on-farm sensors. The most attractive additional analyses in the near future are pregnancy tests, milk ketones and mastitis pathogens. From automatic on-farm sensors, there is most interest for milking speed, activity monitoring, heat monitoring and body condition scores. The future is largely dependent on how the milk recording organisations will learn to extract and report the relevant figures in the information flood recorded on farms and also how to do that with minimal farmer effort..

Keywords: new technologies, milk recording, on-farm sensor, milk sample.

Introduction

Recent years have provided farmers and milk recording organisations with numerous new possibilities to gather data and measurements about their cows. In this study, we will look at how these possibilities are being utilised now by both farmers and milk

recording organisations, and how are the organisations planning to use them in the near future. We will consider automatic measurements on the farm but also new analytical services in the milk recording laboratory.

Materials and methods

This paper is part of the survey "World-wide trends in milk recording", initiated and carried out by the ICAR Working Group on Dairy Cattle Milk Recording. The survey was filled in by 46 organisations representing 287 milk recording providers who record data from a total of 21.5 million cows. The respondents and their respective organisations are listed in the main paper of this survey (Bucek *et al.*, 2015). The survey was conducted as an internet survey, with a possibility to answer the same questions on paper by request. This paper is limited to a couple of questions in the survey while the rest is covered by other presentations.

Farmers' use of automatic monitoring

Automatic monitoring is an important part of the new technologies relevant to milk recording organisations. Farmers' use of these technologies was studied by Borchers & Bewley (2014) in a study where 108 farmers from 10 countries listed what they are already monitoring automatically and also rated the potential usefulness of a number of data sets. Almost one third (31%) of respondents did not have any form of automatic monitoring. Milk yields and cow activity were monitored automatically much more often than any other features.

Table 1. Most common automatically monitored features by share of respondents (Borchers & Bewley, 2014).

Feature	Share of respondents, %
Daily milk yield	52
Cow activity	41
Mastitis	26
Milk components	25
Standing heat	21
Feeding behaviour	13
Body temperature	13
Body weight	11
Rumination	10

Table 2. Features considered by farmers to be most useful for automatic monitoring (Borchers & Bewley, 2014).

Feature	Average usefulness points[1]
Mastitis	4.77
Standing heat	4.75
Daily milk yield	4.72
Cow activity	4.60
Body temperature	4.31
Feeding behaviour	4.30
Milk components	4.28
Lameness	4.25
Rumination	4.08
Hoof health	4.05

[1]Scale 1 to 5 points (1= not useful, 5= very useful)

In the same study, farmers were also asked about how useful they would consider monitoring certain features automatically. Here we can see that most of these features concern daily and hourly management decisions: which cows to check, which cows to treat etc... . (Table 2).

Generally, one can say that robot and parlour data systems respond very well to farmer expectations: they are operating on cow and group level, helping to make daily and weekly management decisions. Milk recording data, on the other hand, extends from these to a more strategic management level (herd, farm) with a longer time span (Figure 1).

Not everything in on-farm data systems is interesting from milk recording, and some data that is relevant for milk recording, is not necessarily so for on-farm management systems. One important aspect in milk recording is to highlight differences between animals.

Table 3. Novel analyses from the milk recording sample by number of milk recording organisations (MRO= milk recording organisation).

Analysis	MRO's routinely analysing	MRO's planning to start analysing	MRO's total
Pregnancy	19	13	32
Ketones	11	13	24
Mastitis pathogens	15	5	20
Free fatty acids	9	9	18
Disease control	11	6	17
Infrared spectra	7	10	17
Unsaturated fatty acids	8	7	15
Casein fractions	7	6	13

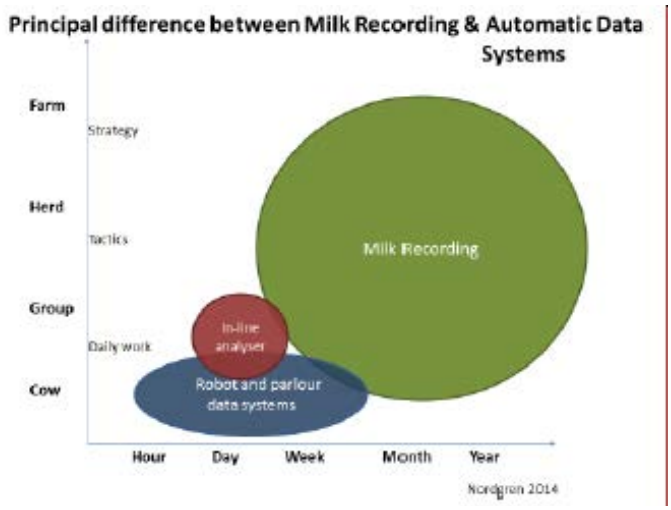

Figure 1. Relationship of milk recording and on-farm data systems to strategy levels and time spans (Nordgren, 2014).

Milk recording organisations and new technologies

In our study, milk recording organisations around the world were asked how they are utilising new technologies now and how they plan to utilise them in the near future. The new technologies were divided into two main groups: novel analyses from the milk recording sample, and data from on-line sensors on the farm (Table 3).

Additional analyses from the milk recording sample are generally seen as a convenient way of creating added value for milk recording without extra work on the farm. Some additional analyses were routinely done or planned in the near future by more than half of the respondent organisations.

Pregnancy diagnosis was by far the most common novel analysis routinely done in today's milk recording, followed by mastitis and certain other pathogens, and ketones. Biggest growth in the near future is expected in pregnancy diagnosis, ketones, milk infrared spectra, and free fatty acids. Pathogen arrays for mastitis, Johne's disease, salmonella etc. seem to already be in use in most of those organisations who have interest in them (Table 4).

Table 4. Data used from on-line sensors by number of milk recording organisations.

Feature	MRO's routinely using	MRO's planning to start using	MRO's total
Milking speed	11	11	22
Activity monitor (lameness)	3	11	14
Heat	4	8	12
Body condition score	2	10	12
Body weight	3	8	11
Teat placement	1	9	10
Milk conductivity	2	5	7
Milk yield by quarter	0	5	5
Rumen monitors	1	3	4
Body temperature	1	2	3

The number of organisations interested in data from on-line sensors is generally lower than with additional analyses. This is due to data being generally oriented towards day-to-day management than breeding and strategic planning, and the data only being available on those farms that have on-line monitoring systems in place. The interest will probably grow in the future as the on-line sensors become more common and the milk recording organisations find ways of utilising the data obtained from them.

Milking speed is by far the most commonly extracted on-line sensor data utilised in milk recording at the moment. Some organisations are also utilising heat, body weight and activity monitoring data. Many more milk recording organisations are planning to start using this data. The most popular traits to plan were, again, milking speed, followed by activity monitoring, body condition scores, and teat placement.

Milk recording organisations were also asked about their use of in-line analyser data. At the moment, only two MRO's are utilising them, while nine others are planning to. Most organisations are presently not interested.

Conclusions

There is great interest among the milk recording organisations to broaden the spectrum of recorded traits, especially towards novel analyses from the milk recording sample, but also towards traits and events recorded by on-line sensors on the farms. In the future, there will be more and more data available from a greater number of farms. The challenge is how to find the relevant figures and how to report them so that they will be interesting both for the farmer and the milk recording organisation. Another future trend certainly is that clients are less and less willing to put their own effort in data transfer. Therefore, automated data extraction is crucial, and where that is not possible, services to replace farmer effort should be offered.

Acknowledgements

The Dairy Cattle Milk Recording Working Group acknowledges and thanks all participants in the survey and for their feedback used in the project.

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World trends in milk-recording management and organization

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Abstract

A survey was prepared by the Dairy Cattle Milk Recording Working Group together with invited milk recording organisations. This paper is one part of this project and focuses on management and organisational questions. The management of recording organizations in the current climate of growing competition is more challenging than ever. The main part of this approach is how to develop a clear relationship with customers and how to provide value to farmers in regard to collected data and samples. New tools of analysis are already very common in some countries, while other participants are now focusing on maximizing increased efficiency in data capturing and processing. In those countries whose workflow is technician-based, training and certification are major components in improving human resources. The reporting of results back to farmers is also a very challenging area. The use of paper and pdf-reports is very common, but new online technologies and smartphone usage now provide new opportunities for farmers to manage information. Real value is created by additional analyses from identified milk samples.

Keywords: ICAR, milk recording management, customer care, technician training, human resource, data capturing, sample identification, reporting to the farmer.

Introduction

The milk recording business has changed a lot during the last decades. This paper as a part of the project "World Trends in Milk Recoding" of the ICAR Working Group on Dairy Cattle Milk Recording will focus on the results of this challenging change. Especially the organisational structure of the recording organisation themselves and the involvement with the laboratories is in question as well as the need to develop a clear image of the farmer as a customer for the recording services. Thinking about the customer again changes some core issues of recording. Data capturing has to be efficient and the reporting of the results must be convenient for management purposes. The process of recording, transporting the sample and analysing them in the laboratory must be organised in an efficient and transparent way, because the customer might expect a maximum guaranteed runtime from the recorded milking to the availability of the results on his report.

Material and methods

This paper is part of the survey "World-wide trends in milk recording", initiated and carried out by the ICAR Working Group on Dairy Cattle Milk Recording. The survey was participated by 46 organisations representing 287 milk recording providers who record data from a total of 21.5 million cows. The respondents and their respective organisations are listed in the main paper of this survey (Bucek *et al.*, 2015). The survey was conducted as an internet survey, with a possibility to answer the same questions on paper by request. In this paper questions about managing the recording from the organisation structure to the process of recording itself and reporting the results to the customer are in the focus.

Results

Changes in organisation structure and competition

The recording business faces very different situations in the 46 attending organisations, which range from close cooperation to competition. Therefore it is not surprising, that only 27% of the answers came from umbrella organisations. There is a maximum of 60 local or regional members in countries with umbrella organisations and a maximum of 84 organisations in countries without umbrella organisations.

Cooperation in data processing seems quite common, but 51% of the MRO's or members of the answering umbrellas compete within their country.

Due to strategic or political decisions the number of organisations changed during the last decade in different ways. In those countries with more than one organisation, 33% states that the number did not change, while 40% say that it has decreased. Only 27% answered that the number increased. For the future, the percentage of increase is stable, while more than 27% see a further decrease and 54% of the attendants have reached a situation where the count of organisations is stable.

As milk recording is very near to the farmer, it might not surprise, that cooperatives and associations are the vast majority of the MRO's, and even if they are limited companies, milk recording is mainly organised as a non-profit business. More than 60% of the represented MRO's are owned by breeders and dairy farmers. The AI companies influence about 14%. But even commercial companies are among the owners. This situation is not likely to change much, as 95% of the answers report that no change of ownership is expected by the organisations themselves. However, external influences such as changes in EU legislation might have quite a significant impact on the MRO's and integration with other organisations involved in genetic improvement will be discussed.

The necessary access to high quality milk analyses at competitive prices brought a strong involvement between MRO's and the laboratories. Only 31% of the attendees have the lab completely outsourced, while even a bit more (33%) run it of their own. As the result of the requirement, that analyses has to be independent and objectively. In 38% of the cases the lab is operated by the authorities. But still 32% of them are run by commercial companies and 26% by the dairy industry.

Milk recording as efficient service for customers

The organisation structure and the legal form is a necessary tool for providing efficient services to the farmers and other customers like the breeding and AI business.

To develop the service according to the needs of our customers means to know them. The MRO's in the survey use different approaches to get feedback from their customers as shown in figure 1.

The personal interview outweighs all other ways of getting feedback, but it tends to emphasise the subjective opinion and a single situation. A very important way to improve the service is to look at reclamations and react to the mentioned topics. Regular surveys are a way to get professional and unbiased information about the needs and wishes of the customer while feedback from meetings has to be interpreted carefully. Any opinion leader might get a strong impact by a question or comment on the whole mentioned topics. If some steps are taken to avoid such biases, feedback from group meetings and discussions is very useful and valuable.

A suggestion box on the website or as a phone line is surely a source for developing new services. The same comes up for feedback from the technicians and from breeders associations. But here again it is necessary to take care about possible subjective filtered information or on the other hand to invest especially in training and supervision of the staff.

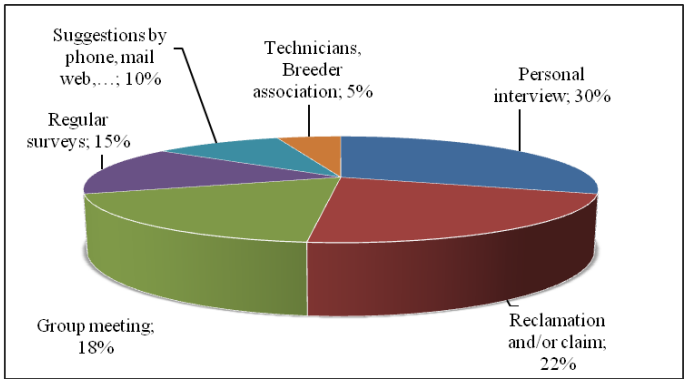

Figure 1. Feedback from the customer.

Human resources

To get reliable results from the milk recording, it is important to train the sample technicians. For providing reclamations for management decisions in the recording organisation itself, this is even more crucial. From the survey the clear picture arose, that many organisation work with employed technicians as well as with the farmer or farm staff in the method B. The sum in figure 2 is more than 100, due to this reason.

Although all organisations respect the core function of the technician as the "recording organisation" in situ and have some sort of training for new technicians, a certification protocol for them is in 45% of the attending organisations not in charge (Figure 3).

In order to ensure that recording is done consistently in each session and in any herd, a regular training is maybe more necessary than an initial certification. It will be the same, if anything in the recording process has to be added like new traits or to be changed, implementing a new data capturing procedure or identification scheme for the samples, just to mention some aspects from the core of recording.

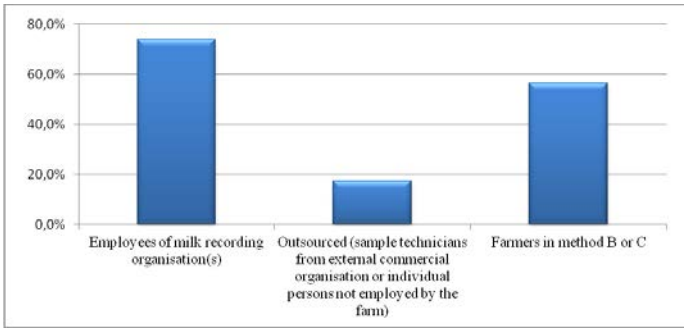

Figure 2. Who employs the sample technicians?

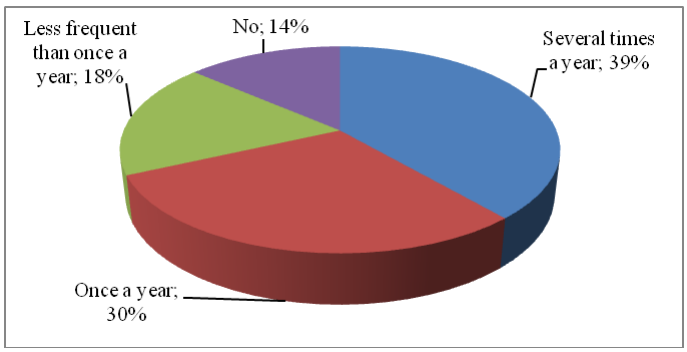

Figure 3. Technicians training and frequency.

The knowledge that was provided to the technicians in their training is still not the same as knowing that the information is really applied. This can be shown in exams, which are implemented by 28% of the organisations, yet.

Finally, the starting point of anyone's career in recording is influenced by the personal level of education. As in any service company the education level requirements differ depending on the technicians duties. An agricultural graduation is preferred but in at about 50% there are no defined requirements, because the skills and knowledge needed for recording can be learned in courses during the initial training scheme.

Inspecting the quality of recording and sampling

A tool to measure the quality of the service is auditing or inspecting the work of the technician e.g. the recording and sampling process on the farm. This is done at 44% of the attendants in this survey. Most inspectors are sent by the government (45%), but 20% are commercial auditors. In some countries an internal training and certification scheme for inspectors is approved by the national breeding and / or recording authorities. This provides specialised auditors and approves a high quality of the inspection itself.

Notifying the farmer about the recording

Milk recording must bring a representative result of the cattle performance and shall not be influenced, neither intentionally nor unintentionally. To achieve this aim in 25% of countries it is practice to notify the farmer only a very short period of time before the recoded milking. This means either no notification or just after the milking before the recorded milking.

On the other hand especially in countries with bigger farms or with the B method it is necessary to provide the labour force for the recording. Therefor at least some days before the recording or on the previous test day notification is given. Up to 40% of the organisations have a scheme, where the test days are scheduled over the long term, e.g. over a whole year.

Especially in growing herds with employed labourers a surprised recording is very difficult, so other reglementations, like bulk tank comparisons, have to be in charge to ensure a representative result of the recording.

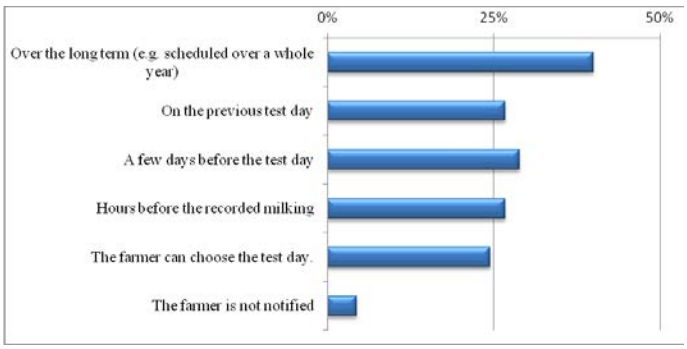

Figure 4. How much notice is given before the recording to the farmer?

Notifying the farmer by phone call happens in 70% of the cases. But as the availability of the people on the phone decreases other ways of communication have been established. So the second most common way of notification is now a short message to the mobile followed by an e-mail, maybe to be read on the mobile, too. Fax has lost importance very much. Other ways are short notices, left at the previous recording or even letters (Figure 4).

Data capturing

Quod scriptum est manet - the motto of ICAR is surly meant for data processing. But to provide reports, records or estimated breeding values to the farmer means to capture data on farm in an efficient and safe way. Even in 2015, paper is still the most common way to do it. But entering the data on farm directly to the database (via online access or by transmitting a data file) using a laptop or PC has reached a similar level. As a single method or hardware PDA's or data handlers have the same spreading as Laptops.

As a very favourable way of entering the data to the database of milk recoding automated data exchange will be the hot issue for the rest of the decade either with milking robots, stationary electronic meters in the milking parlour or farm management software (Figure 5).

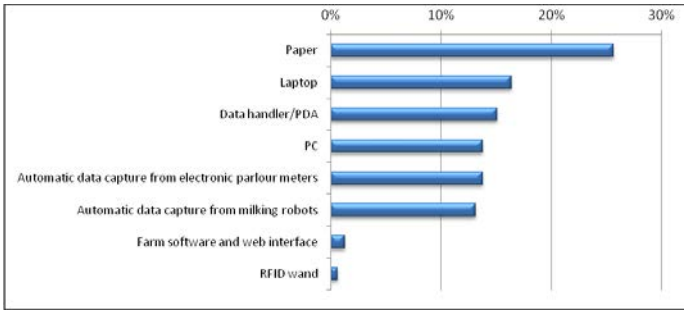

Figure 5. Tools for data capture on farm

The expectations for the future are, that with the increasing number of milking robots the direct data exchange will get more and more common. For the recording organisation it might be crucial to show the competence to do so and provide processed results to the management software on the farm.

In manual data capture a change is on the way. Paper will get a strong competition from the electronic devices like smartphone or tablets, which can in many cases be directly linked to the database and therefore provide a very favourable situation to do data checks almost in real time while entering the data or at least before leaving the farm.

In the same growth rate as internet services are provided by the recording business to the farmer there will be web applications running, which offer the possibility to enter not only information for management proposes but records for breeding or performance calculation in real time either from mobile devices or from any PC or laptop.

Sample identification and transport

A clear and safe identification of the sample, which is never lost during the whole process is one key to success in milk recording. Therefore due to general industrial standards the bar code system is actually the most spreaded ID scheme in milk recording. A very simple and still safe system is manual marking of the vial with the ID. A very common and cheap system is the position in the racket. This system requires a high level of exercise to be sure, that no mistakes happen, but it is a very quick and powerful system then.

A technically more sophisticated way of sample identification is the RFID tag. If implemented in the recoding system it allows additional information to be directly connected to the sample. To get the whole benefit of the system, this way of identification and smart information has to be implemented in the recording process and in the laboratory. There RFID allows a high level of automation, too. The full dataset and requests for analyses can be stored on the RFID device. In this case, the box must be marked only with the address of the lab.

The additional information on or in the box with the vials for analyses is mainly to provide basics for plausibility checks in the lab like the number of samples and maybe some hints to sour samples, if the day of sampling is gone too long.

A change in the way of identifying the samples is in milk recoding connected to the installation of new meters in recording, which need an identified vial or new equipment in the laboratory, which allows a direct link between sample taking and recording result. Currently, 70% of the organisations are not planning to change their sample ID-system. Those organisations, which are to change the sample ID have decided for bar codes or RFID (Figure 6).

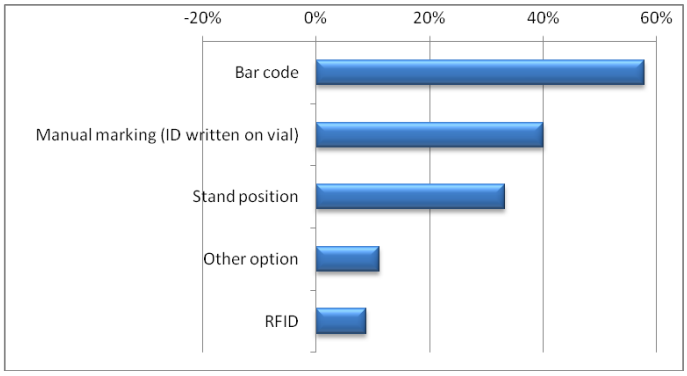

Figure 6. Implemented identification systems for the milk sample (multiple answers).

In order to minimize the number of sour milk samples, the vast majority of the organisations (90%) preserve the milk sample, mainly with Bronopol or similar chemical products. As a result, in many countries the rate of sour samples is less than 1%. A monitoring for the sample quality is done by each organisation and enables the possibility to react if the share of bad samples is rising.

The transport of the samples to the laboratory is the next step. It has to be done quite quick in order to get the results for proper herd management but especially in countries with smaller herds it would be too expensive to send the samples from each recoding directly to the lab. So they are gathered by technicians and the transport takes place at regularly intervals.

In order to keep the sample quality as good as possible, 25% of the organisations have temperature requirements and loggers for the transport. Those requirements are between 4°C and 8°C. In addition, 13% use isolated transport boxes to prevent the samples from freezing in winter or to avoid the warming during transport in summer. Almost two-thirds of the organizations do not have any temperature requirements for the sample transport and have still a very low figure of bad samples.

The transport of the samples themselves is in 17 cases outsourced to mail or courier service. Even in 22 cases a lorry or van with a refrigerator does this, which is maybe a reason for not defining a temperature requirement for the sample itself. About half of the samples are sent directly to the laboratory or transported via a fixed route with collecting points.

As the sample is together with the collected data the core of the recording business in two-thirds of the cases the transport is duty of the technicians of the milk recording organisation. This might add up if you consider that in method "B" the farmer is responsible for the transport (13%). The remaining 20% are managed by the dairy companies, again a business very strongly related to the milk farmer and depending on correct sample analyses.

Milk analyses and reporting the results to the customer

In the laboratory infrared analyses as a powerful, reliable and efficient method is nowadays the standard. While fat and protein is anywhere part of the milk recording and paid by the recoding fee, urea (19 cases), somatic cell count (7 cases) and lactose (2 cases) are analysed at an additional charge. In addition to the standard analyses mentioned the labs

offer a big range of additional services like fatty acid analyses, total solids, ketone, citric acid and even a lot disease control checks out of the recording sample to add value to the sampling process and provide benefit to the farmer out of the correct identified sample.

The reporting process brings the results of the recorded milking and of course the analyses from the laboratory back to the farm. Taking into consideration, that the captured data have to be available in the database and the sample must be transported and analysed this takes some time. But on the other hand the farmer has to decide within a very short time about milk quality, health questions and of course feeding. Therefore a quick response is asked.

Due to the transporting and the workflow in the lab in best cases the reports are after 48 hours available in the database. The average runtime for this is a bit above 5 days and 90% of the reports are delivered at an average just below 6.7 days. As a clear sign of customer care 2/3rd of the attending organisations have already a guaranteed reporting time, which on average is about 7.1 working days.

Of course this is influenced by speed and way the data are provided, which might especially in method B add some time if you have to ask the farmer to forward the dataset and the analyses result is already available (Figure 7).

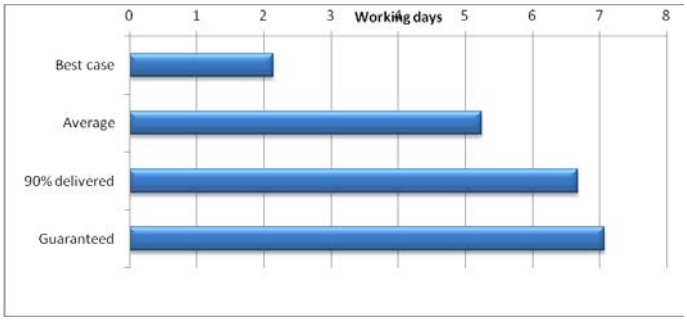

Figure 7. Runtime from recording to reporting the result to the farmer.

The most powerful data capture combined with the quickest transport and sample analyses will lose all advantages if the report itself has to be printed and sent to the farm per surface mail. Although this is still the most common way of reporting, the farmer's demand for a quick response and the organisations are seeking ways to fulfil this. During the last decade web based services became very important. Almost 75% of the reporting is done via web applications and data files and e-mail reports are provided to the customer in 2/3rd of the answers. More than half of the attendants provide their own farm management software, where the new results are added in a very convenient way.

Mobile communication has of course reached the herds over the last years. Actually 16 organisations provide the possibility of an SMS - alert for available results. In combination with an application for mobiles this allows the responsible person to get the information very quick for management decisions. 13 organisations use this service in early 2015 (Figure 8).

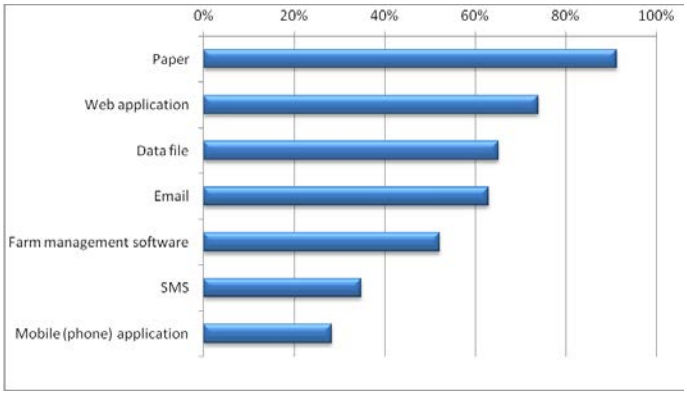

Figure 8. Reporting the results to the farmer.

Conclusion and outlook

The milk recording business has always been in strong relationship with data processing and providing results for management decisions, first on a more strategic level for selecting the herd and providing data to breeding value estimation for the breeding programs. In addition, the ready availability of reliable recorded data is now a daily part of management decisions on farms, which has in turn strengthened the relationship between customer and MRO.

Currently, customer (farmer) care is one of the core issues as in any other service related business. So modern reliable tools like surveys and reclamation reviews provide input to develop the recording business that will fit to the needs and expectations of the customers, who have to pay for it.

The employed technicians bring additional feedback from the herds. Training and certification of the staff is another issue to ensure that the processes are running in a proper way. Especially if changes in any steps of the recording or reporting have to be done, it is necessary to provide the information to the employees and farmers in training sessions. But even in doing the recording in the usual way, regular training is very useful to keep experienced technicians on a high level of skill. Witness audits like in the ICAR certificate of quality are a simple tool to check those skills and identify ideas for the business or the need for training.

In sample identification the clear message is accuracy first. The bar code system is dominant and will stay so for some more time. Manual systems like stand and position or marking the vial with the written ID are common, too. Those few organisations, which are planning to change their system, are heading towards bar codes or maybe more convenient RFID systems.

Transporting and analysing the samples has to be handled in a very efficient way. The correct identified sample in the lab brings even in the near future some very interesting possibilities for additional analyses as the broad field of available analyses tools provided by the manufactures of infrared devices show. Necessary disease checks and parameters for advisory services like ketones are today very common. Additional benefit is added by new services like the pregnancy test, which seems to be already part of routine today. This test is a very simple proof, how customer oriented and innovative recording organisations and laboratories are.

Data capturing and reporting is still very paper based. But in both situations mobile devices have entered the parlour. In data capturing the possibility to enter the records on farm directly into the database provides a high degree of plausibility and completeness

checks. Therefore data handlers, PDA's or mobiles and tablets will in the near future be the backbone of data capturing. On the other hand, automatic data exchange between the recording database and the systems on the farm will increase, too. Especially when considering milking robots this brings safety to the data and convenience to the farmer.

In reporting back to the farmer, the printed report, even if sent by e-mail, is some kind of a backup system, which will stay. But modern communication has found its way to the herds. After about 15 years of developing web based services and management software to be run on the PC, no matter if on or offline, the next step is asked by farmers. They want available information in shed and parlour. The mobile gadgets can be bought in each store around the corner and the recording organisations already provide SMS - alerts for new results and mobile applications.

So the identified trends out of this survey are

- The clear statement about customer care,.
- The way to electronic data capture by using mobile devices and automatic data exchange.
- Innovative laboratory analyses are quickly implemented.
- Reporting to the farmer has reached the mobile world in apps and SMS.

Acknowledgements

The ICAR Dairy Cattle Milk Recording Working Group acknowledges and thanks all participants in the survey and for their feedback used in the project.

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Innovations in sheep performance recording in new zealand

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Abstract

Sheep performance recording in New Zealand commenced in the late 1950s and early 1960s with a sole focus of producing genetic improvement in the national flock. The first selection index was produced in 1961. Since that time, New Zealand has operated a number of national sheep recording schemes with the current "Sheep Improvement Limited" (SIL) service operating since 1998. This service is now incorporated into B+LNZ Genetics, a subsidiary of the farmers' levy-funded organisation, Beef + Lamb New Zealand.

In 2014 B+LNZ Genetics commenced a substantial programme to upgrade the SIL system, to improve accuracy of data collection through electronic identification and in-field recording tools, to increase size of the genetic evaluation, and to integrate the use of SNP data into a single-step breeding value calculation.

New web and mobile tools are being developed to encourage better use of genetic information by commercial farmers and livestock agents, supported by an extension programme. New mobile and in-field data collection tools are being developed to streamline the process of performance recording by breeders. Research work is being undertaken to improve the prediction of lean meat yield and to include ewe longevity (stayability) and maternal body condition score (BCS) in the traits evaluated.

Background

The first release of sheep into New Zealand was in 1773 by the explorer James Cook. Released to run wild in the forest, it is likely these animals died within days. Ruminant livestock farming started in 1814 with the importation of sheep and cattle from Australia to support missionary endeavours. Performance recording for genetic improvement started in the 1960s, with the first selection index calculated in 1961 (Dalton, 2014) and the first national sheep scheme in 1968 (Clarke and Rae, 1977).

Performance recording and selection for genetic improvement has made a substantial contribution to the performance of the New Zealand flock. Genetic trends from 1995 to 2014 show improvement in average genetic merit for number of lambs born (NLB) of 0.13 lambs, for weaning weight (WWT) of 2.7kg, and for carcass weight (CW) of 1.6kg. Figure 1 illustrates the trends for NLB and WWT.

A key measure is the delivery of the genetic improvement to the national flock. Sheep numbers in New Zealand have declined markedly from a high of 70 million wintered in the early 1980s to 29 million in 2014, as shown in Figure 2. During that time, meat and wool production have remained close to static, reflecting the productivity benefits of improved livestock genetics, nutrition and pasture genetics, and animal health.

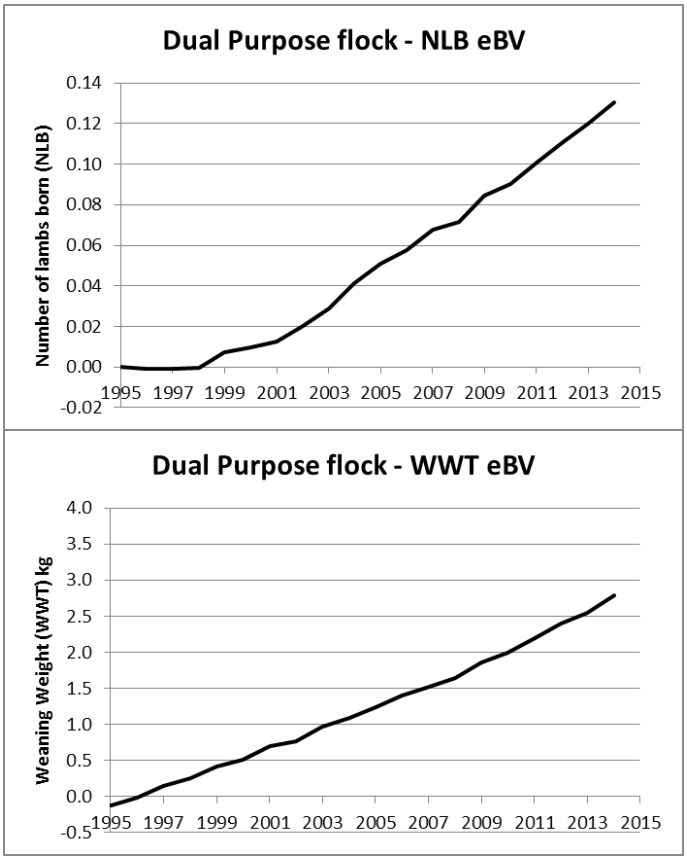

Figure 1. SIL ACE Dual Purpose Genetic Trends for NLB and WWT.

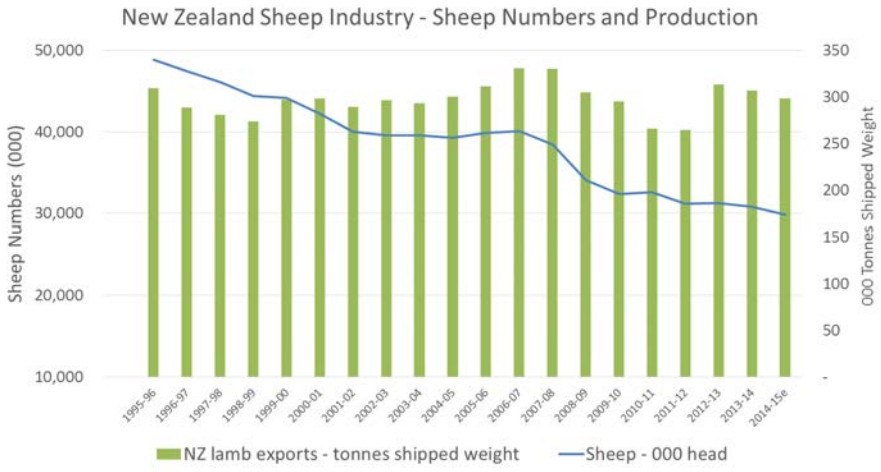

Figure 2. New Zealand Sheep Numbers (wintered) and lamb production (source: Beef + Lamb New Zealand).

In 2014 B+LNZ Genetics, a wholly-owned subsidiary of Beef+Lamb New Zealand was formed, bringing together the genomic research and development performed by Ovita, the SIL sheep performance recording system, and the B+LNZ Central Progeny Test.

B+LNZ Genetics is commencing a five-year programme to improve the rate of genetic gain in New Zealand performance recorded flocks and to increase the effective adoption of improved genetics by the wider sheep industry. It will do this by a number of means, but one of the key mechanisms is a set of improvements to the SIL performance recording system, focusing on:

- Improved accuracy of recording through better data collection and increased use of DNA parentage;
- Improving the accuracy of breeding value estimation by using a single-step genetic analysis incorporating increasing quantities of genotype data;
- Delivering better tools to breeders and commercial farmers enabling them to understand and make selection decisions and informed ram purchases.

Existing workflows and outputs

The existing Sheep Improvement Limited (SIL) performance recording system and database was developed in 1999 based on system designs from the early- and mid-1990s. It is a traditional performance recording system based on animal identification and phenotype observations collected by breeders. These observations were manually recorded on paper forms, and sent to a regional bureau operator to be entered into the computer system. These bureau operators would also produce selection index reports and pre-lists for breeders "on demand", sending these out in paper form (and more recently, as PDF documents that breeders could print). Figure 3 demonstrates the flow of information in this system.

Some interesting characteristics of the current New Zealand SIL system are:

- Animals are identified by a "Birth ID" which consists of the flock registration code, year of birth, and a unique number assigned within that flock and year of birth. If animals are transferred to another flock they may be re-tagged for convenience, but the official identifier from the flock of birth remains. An ICAR identifier is not used. Radio-frequency identification (RFID or EID) tags have been adopted only recently and are not yet used by all breeders. New Zealand does not currently operate a national individual animal identification and traceability system for sheep, although it does for cattle and deer.

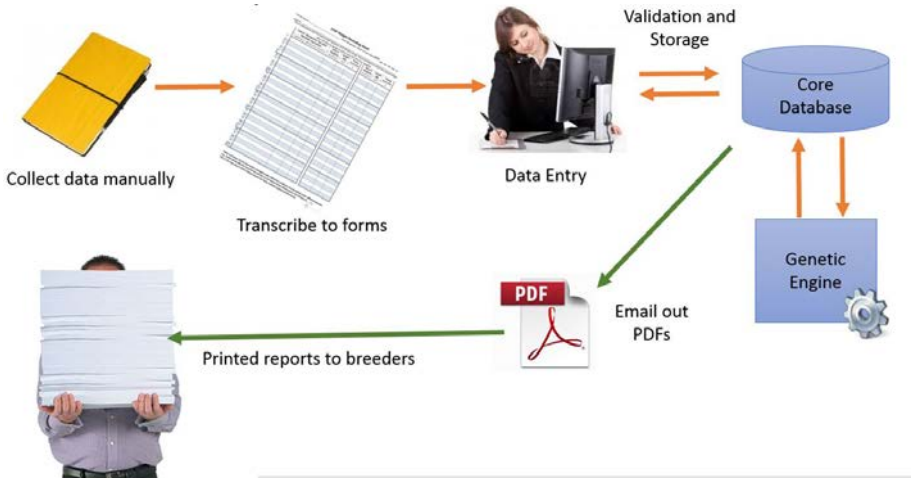

Figure 3. Data flows through the current SIL system.

- Genetic evaluation was carried out primarily using separate "within-flock analyses", with some collaborative breeding groups carrying out across flock-evaluations, until the SIL-ACE across-flock evaluation was instituted in 2004 (Young and Newman, 2009). SIL-ACE is still an "opt-in" analysis in which over 300 flocks now participate (representing 55% of SIL flocks and 78% of new animals born). However, not all flocks record all traits, and some are not well connected.

A feature of the original within-flock analysis model that appealed to breeders was that they could request an updated analysis at any point in time, and so did not have to return their data by a specific deadline. A weakness of this flexibility was that bureau operators and the SIL system were expected to respond to at-times unreasonable demands where a breeder submitted their data and then expected a new within-flock analysis and report the next day.

- Genotype data has been managed entirely separately, being delivered from the laboratory to a research provider to generate breeding values, which are then combined with the SIL breeding values for reporting.

- The SIL database system was built using a unique object-oriented database system called JADE (www.jadeworld.com). The JADE database system allows animals and their relationships to be modelled as entities using object-oriented design principles and then stores these directly without attempting to map them to a relational database. This is a strength when collecting, editing, and manipulating records of individual animals, but object-based systems tend to be slower when attempting to carry out set-oriented update or processing operations on thousands or millions of records.

Next generation workflow and analysis

As part of the B+LNZ Genetics development programme, new information technology tools and processes are being implemented in the core SIL system and extended to the wider set of tools used by industry to support adoption of improved genetics. The resulting system model is illustrated in Figure 4, and includes:

- Changes to the core SIL database, including migration from JADE to a SQL database and new software tools will facilitate more rapid development of new services.

- Genotype data will be moved into the core database, storing processed allele data from the laboratory as well as its FImpute (Sargolzaei *et al.*, 2014) format to enable rapid extraction for analysis. Genotype service providers (retailer and laboratory) are separate organisations that will connect to deliver data (and retrieve lists of animals) through an integration interface (Application Programming Interface or API).

- A single-step across-flock analysis (Aguilar *et al.*, 2010) will replace the current within-flock and across-flock analyses. This analysis could be run as frequently as weekly to maintain much of the flexibility from which breeders currently benefit. Pedigree, phenotype trait observations, and genotype data will be delivered from the SIL database to the genetic analysis system using automated routines.

- In-field data collection tools utilising smartphone and wireless technology, and connecting to weigh-scales, tag readers, and auto-drafters will encourage adoption of electronic animal identification, streamline the process of capturing data, and remove transcription errors. Our analysis of farmer demographics suggests that a number of breeders will continue to use traditional data entry services, particularly in smaller flocks, and breeders will be able to separately contract organisations to provide this data entry on their behalf.

  As well as providing a set of in-field data collection tools, the SIL system will provide a full integration interface (API) that allows third-party developers to create and provide other tools which breeders may elect to use.

- A new web-based user-interface will allow breeders to directly review their own data to see validation errors or warnings and approve its submission into the core database. Alternatively they may prefer to delegate this task to an expert or advisor who can undertake this process on their behalf. Breeders and advisors will be able to interactively request reports utilising standard templates with support for flexibility in the columns of data shown and the filtering that can be applied. These reports will be able to be downloaded in a range of formats for printing or use by other tools.

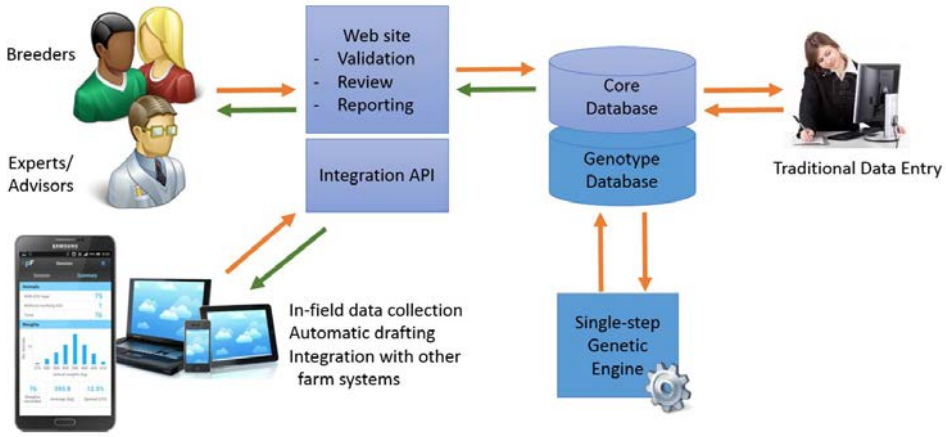

Figure 4. Data flows in the next-generation SIL system.

Next generation tools

B+LNZ Genetics is also investing in the creating of a range of tools that will support commercial farmers in their application of improved sheep genetics.

The first of these tools, the B+LNZ Genetics FlockFinder is a mobile application intended for primary use by commercial farmers, livestock agents, and others who assist farmers with ram selection or purchasing. Illustrated in Figure 5, the application works on Android and iOS smartphones and can be downloaded from the Apple store or Google Play. It allows farmers to choose a breed of animals, region, and the goal traits that the breeder is recording for. The application returns a list of registered SIL breeders and provides contact details as well as showing these on a map.

Other tools planned will allow breeders to understand how their flock compares to its peers in average flock index merit and rate of genetic gain, and to present SIL information to commercial farmers in a way that supports ram buying with more emphasis on using a relevant index and eBVs.

Tools for commercial farmers will allow them to assess the performance of their current or intended ram team in the light of their farm goals. This sort of tool will link to other industry benchmarking tools currently being developed by Beef + Lamb New Zealand.

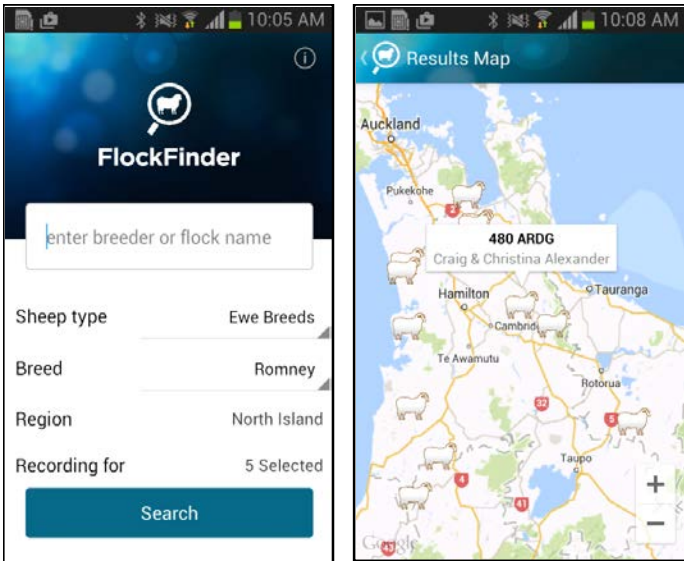

Figure 5. B+LNZ Genetics FlockFinder application.

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Organization of milk recording in goats in France: Looking for new recording schemes

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Abstract

In France, milk recording for goats began in the 1960s, with the same method as for cows (the A scheme) but by measuring nitrogen content instead of fat content, in order to adapt breeding goals to the economical context of this species (cheese production exclusively). Since the 1980s, both fat and protein contents have been measured, and somatic cell count since the 1990s.

Since 1992, farmers have choice among several methods other than the A scheme, at first AT, and 10 years ago AZ and CZ have been introduced. Moreover, farmers who are not interested in getting genetic evaluations for their goats can choose another simplified and less expensive method.

However, for few years, MROs, helped by Institut de l'Elevage, have been looking for new schemes, that would simplify their work and that would be more flexible, if possible without any loss of accuracy.

The main issue of the AT procedure is the obligation to get records morning and evening alternately, which is sometimes difficult to implement. Therefore the present work aims at estimating daily milk, fat and protein yields and contents by using Liu's approach, from results obtained during one milking only and from estimated coefficients, according to period between two milkings, stage of lactation and parity.

Regression coefficients were obtained from a training dataset of 28,700 daily results of 5,500 goats, for which morning and evening performances were both available. Then, on an independent validation dataset of 1,700 goats, two approaches were used to estimate performances of each lactation: i) the current AT scheme (which assumes that each milking represents 50% of the daily yield); ii) a new recording scheme (called AC), in which all the records are those obtained either mornings, or evenings, and in which daily performances are estimated by using Liu's coefficients computed with the training dataset. Results show that protein yields and contents are accurate and unbiased in all the situations. The accuracy is lower for fat and the bias is larger, but AT and AC results are comparable. This is why the Liu's approach, applied in recording schemes where only one milking is measured will be proposed for an agreement by ICAR and it will be used by the French MROs in a near future.

A second issue is the acceptable period between two records: until now, severe bounds have been required in France with A4 and A5 schemes. In the near future, these constraints will probably be replaced by a requirement on the average period between records, computed within the first 250 days or within two periods (until the lactation pick and after).

With these changes, the French renewed organization of goat milk recording will be more flexible and thus better fitted to the demand. But performances estimated with the various proposed schemes being not at the same level of accuracy, a study is engaged by MROs and Institut de l'Elevage in order to find the most appropriate way to publish the results and to help farmers to interpret the performances according to their accuracy.

Keywords: Milk recording, goats, alternate testing scheme, Liu's method.

Introduction

The first recording scheme used for goats in France required monthly visits, with measure of both daily milk yields, and a single sample half part for both milkings. The development of the goats' cheese production, and the implementation of a breeding scheme for Alpine and Saanen breeds in the 1980s contributed to increase the demand for goat milk recording: the number of recorded goats trebled within 20 years, and reached 300,000 goats in the 2000s.

Obviously milk recording schemes had to be adapted to the various technical needs of the farmers and to the logistic constraints of the Milk Recording Organizations ("MROs"), due to the large heterogeneity of herd densities and sizes. New procedures were implemented in 1992, with larger accepted periods between two records. The recording scheme was also simplified by measuring one milking only, alternatively mornings or evenings, as it is recommended for AT. In 2006 the AZ method was recognized. With AZ, milk yield of both milkings are measured, but only one sample is taken, alternatively mornings and evenings. The implementation of this new method was motivated by the use of the new milk recording device Lactocorder®. Indeed, MROs have adapted their organization in order to reduce their staff, sometimes with the breeder's involvement (in this case, the scheme is called CZ according to ICAR terminology, Leclerc *et al*., 2004).

The main issue of the AT and AZ procedures is the obligation to get records in the morning and in the evening alternately, which is sometimes difficult to organize: about 3% of

recorded lactations are nullified for this reason. Therefore the present work aims at estimating daily milk, fat and protein yields and contents by using Liu's approach (Liu *et al*., 2000), from results obtained during one milking only and from estimated coefficients. The final objective was first to try to improve the quality (accuracy and reduced bias) of estimated performances with alternate schemes (AT or AZ), but also to look for new schemes in which the performances could be obtained with a non-alternated way (called "AC" in the paper).

Material and methods

Data used were collected on Saanen goats by several MROs, from November 2007 to November 2010, according to an A method with two separate samples for morning and evening milkings. Milk recording was implemented with Lactocorder®, which allowed to collect milking times for each goat.

The data set was split in two parts: a training population of 28,700 test-days records and a validation data set of 11,370 test-day records. Both data sets are described in table 1.

Table 1. Description of the data sets.

	Training population	Validation population
Nb of test-day records	28,700	11,370
Nb of lactations	5,500	1,700
Mean of test-day per lactation	5,2	6,9
Percent of 1st parity	35	33

For each performance (daily yields and contents) and for each combination of parity x lactation stage x milking interval, regression coefficients b0 and b1 were estimated with the training data set by using either morning or evening data, according to the model used in Liu *et al*. (2000):

$$yA4^{[ijkl]} = b_0^{[ijk]} + + b_1^{[ijk]} y_{AT}^{[ijk]} + e^{[ijkl]}$$

where yA4 represents the daily performance of the lth goat (being in parity i, lactation stage j, and the milking's interval k) and $e^{[ijkl]}$ is the residual.

Each of these effects was divided in classes presented in table 2.

Coefficients obtained with the training data set were used to estimate daily production of the validation set, either from morning or from evening data. Coefficients were estimated for milk, fat and protein yields, and fat and protein contents. For contents, an alternative could be to derive the daily contents from the ratio between both estimated daily matter (Fat or Protein) yield and Milk yield. This option has been tested (not presented here), but the results were close to those obtained by using directly the content measured during the AM or PM milking.

Table 2. Definition of classes used in the model.

Effects	Nb of classes	Class definition
Parity	2	1st lactation, 2nd and later lactations
Lactation stage (in months)	10	1, 2, 3, 4, 5, 6, 7, 8, 9, 10 +
Milking interval	5	AM : <12.5h;12.5h-13h;13h-13.5h;13.5h-14h;>14h PM : >11.5h; 11h-11.5h; 10.5h-11h; 10h-10.5h; <10h

Results

Table 3 presents daily production calculated with both milkings (reference) or estimated from data of only one milking (AM or PM). The results obtained without corrective factor for contents are first presented, then results obtained with correction according to Liu's approach.

Liu's approach leads to a reduction of all the biases, especially for fat content, and thus it improves significantly the test-day results delivered to the farmer. The loss of accuracy compared to "A" method ($1-R^2$) are similar when using Liu's coefficients or not. Loss of accuracy is ranged between 5 and 7% for protein content and it is much larger for fat content (17 to 26%, better with the evening data than with the morning ones). However, slopes obtained from the regression between true and estimated performances are much closer to the unit by using Liu's approach than without any correction, which is a very interesting result: it indicates that error does not depend on the performance level of the animal, which is very important for genetic evaluations.

Table 3. Results for daily performances for the validation set.

		Estimated performances		Bias			
		Mean	Std	Mean	Std	Slope	(1-R2)%
Milk yield (kg)	Reference	3.52	1.19				
	AM *2	3.68	1.29	+0.15	0.39	0.88	8.9
	PM *2	3.38	1.21	-0.15	0.39	0.93	10.1
	AM Liu	3.49	1.16	-0.04	0.35	0.98	8.5
	PM Liu	3.53	1.15	0	0.39	0.97	10.4
Fat content (g/kg)	Reference	39.6	7.3				
	AM sample	35.7	8.0	-3.9	3.6	0.81	26.2
	PM sample	43.9	8.2	+4.3	3.8	0.78	17.3
	AM Liu	38.6	6.8	-1.0	3.5	0.94	22.6
	PM Liu	39.0	6.3	0.6	3.3	1.03	17.3
Protein content (g/kg)	Reference	33.6	3.8				
	AM sample	33.2	3.9	-0.4	0.8	0.96	5.6
	PM sample	34.0	3.9	+0.4	0.9	0.94	5.4
	AM Liu	33.4	3.7	-0.2	0.8	1.00	7.4
	PM Liu	33.6	3.7	0.0	0.9	1.00	7.7

Table 4 presents the results obtained at the lactation level; performances were computed for a standard lactation length of 250 days according to Fleischmann method. For AT method we used alternatively mornings or evenings data, and for AC method, the data from the same milking for each test day were used, either morning or evening.

Liu's approach allows to get a similar bias for all methods. Losses of accuracy are always around 1% for milk, 5% for protein contents. For fat contents, the loss of accuracy is important in all the cases: 25 % using "AT" method or "AC" with the morning data, 18% when using "AC" with evening data. However, as for estimated daily performances, slopes are close to 1 (all of them are ranged between 0.90 and 1.12) and they are comparable with both recording schemes.

Table 4. Results for lactation performances (250 days) for the validation set.

		Estimated performances		Bias				
		Mean	Std	Mean	Std	Slope	Correlations	(1-R2)%
Milk yield (kg)	Reference	639.9	389.2					
	AT AM/PM	650.7	394.5	10.8	36.7	0.98	0.996	0.86
	AC AM Liu	629.9	381.3	-10.0	33.6	1.02	0.996	0.72
	AC PM Liu	633.1	377.8	-6.7	41.9	1.02	0.994	1.10
Fat content (g/kg)	Reference	40.1	6.0					
	AT AM/PM	39.3	6.0	-0.8	2.5	0.91	0.911	24.8
	AC AM Liu	39.5	6.0	-0.7	2.6	0.90	0.908	25.7
	AC PM Liu	39.3	5.1	-0.8	2.4	1.07	0.914	18.3
Protein content (g/kg)	Reference	33.0	2.9					
	AT AM/PM	32.9	2.7	-0.1	0.9	0.99	0.950	3.6
	AC AM Liu	32.7	2.6	-0.3	1.0	1.04	0.946	4.1
	PM Liu	33.0	2.4	0	1.0	1.12	0.947	5.1

Discussion and conclusion

These results are different from those obtained with cows performances by Bourrigan *et al.* (2011): in this case, higher accuracies were found for fat and protein contents when using Liu's approach.

The study needs to be completed with additional data before implementation. It is also planned to estimate daily performance for somatic cell count and to adapt the model to AZ method in fitting the milk yield of the other milking as a covariate (Bünger *et al.*, 2010).

However, this work shows that Liu's method leads to a better estimation of daily performances, which are important for herd management. The loss of accuracy on lactation performances is about the same with all simplified methods of dairy recording (with alternate as with non alternate records), and it does not depend on the performance level. Therefore a new recording scheme based on non alternate records and using correction factors estimated with Liu's approach will be proposed in France in a near future. This new recording scheme, which is as accurate as AT (recognized by ICAR), is also proposed for an agreement by ICAR.

Acknowledgements

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Implementation of new milk recording practises in Finland

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Abstract

For the last two years, the Finnish milk recording provider ProAgria has been running a development project on milk recording. The aim of the project is to improve data capture, data quality and data utilisation in order to give added value to the farmers. In the beginning of 2015, many developments have been implemented. They concern yield calculations as well as reporting and customer services. As an example, more variety in recording intervals was introduced, data capture from AMS farms changed from monthly sum to 24-hour milk yield, data quality points were introduced as a motivating data quality supervision tool, and technical staff was trained to offer services in milk recording. We are still in the process of improving milk recording reports and customer services. A wide range of stakeholders has been involved in the project. ProAgria and many of the stakeholders have made large investments in order to achieve the project aims. Such a major reform of milk recording requires a vast amount of training to the staff and farmers. The project has been challenging in terms of communication, since many in the business had to implement new procedures. A lot of attention has been paid to continuous monitoring and quick response to customer feedback. The effect of the developments on customer satisfaction can be assessed more fully at the end of the milk recording year.

Keywords: development, milk recording, data capture, data quality, customer services.

Introduction

ProAgria is a Finnish agricultural advisory organisation providing services in milk recording. Services are provided by 15 independent organisations around Finland, which employ around 600 farm advisors. The central organisation is taking care of strategic planning, marketing and development work.

Since 2013, ProAgria has been running a development program on milk recording with aim to enhance the services and give added value to the farmers. One of the goals is to increase the share of cows in milk recording to 90% (4/2015: 84%). Improvement of data quality and utilisation of data on farms are the key tasks in the project.

Many developments related to milk yield calculations, reporting and customer services were implemented in the beginning of this year. We are also changing milk recording vials and starting to offer additional analyses from milk samples. Such major reform requires a vast amount of training, communication and monitoring in order to be successful. The project is based on customer feedback, and therefore communication with farmers and stakeholders has played an important role in the whole project.

Milk yield calculations

Milk recording intervals have been rather fixed over the past 50 years and customers have not been able to change the interval actively. Most of the customers, 97%, have had a B48 recording. The aim of the change in recording intervals was to give more benefit to customers, by giving them more options and possibility to utilise milk recording more efficiently in farm management.

New milk recording and sampling intervals offered in Finland are 2, 6 and 8 weeks. A milk recording vacation is now possible with 2 and 4 week intervals. Table 1 shows that some changes have happened already in the first four months. Those with a 2-week recording interval are mainly AMS customers and those with an 8-week interval are small herds.

During the years 2003 to 2014, the AMS customers used a monthly milk sum method for milk yield calculations. It was substituted by 24-hour milk yields (Table 2). The new method allows the customers to utilise all new intervals, choose freely their recording day and send all the data to database at once. In the old system, they had to wait for the end of the calendar month until milk recording was ready and could be reported. AMS customers will further benefit from the new method and shorter intervals, when the pregnancy testing from milk samples will start later this year.

Feedback from AMS customers was devastating in the beginning of the year. Despite of a large amount of education, proper information did not reach customers on time. This has led to many misunderstandings and large amount of feedback claiming that the recording results were not correct compared to AMS averages. Eventually most customers have come to see the benefits and no movement away from milk recording has been observed.

Reporting

Data quality points (DQP) is a novel tool for supervision of recording data quality, introduced in the beginning of this year. They take into account e.g. recording intervals, deviations from dairy deliveries and milk meter testing (Wahlroos et al., 2014). Better quality of data gives added value to the customer, to advisory services and to breeding evaluations. DQP is now reported to the customer and advisor after each recording,

Table 1. The number of herd by milk recording and sampling interval in May 2015.

	Milk recording interval	Sampling interval
Intervals	Number of farms	Number of farms
2 weeks	68	7
4 weeks	5605	382
6 weeks	23	25
8 weeks	310	5626

Table 2. Milk yield calculation for AMS farms, 24-hour yield

	Milking at AMS		
	Time at milking	Yield, kg milk	Recorded milk yield
At sampling	10:00	10	20 kg milk in 20 hours
Previous	0:00	10	= 20 kg * (24 / 20) =
Previous to previous	14:00		= 24 kg milk yield on recording day

making immediate action possible. In earlier years, data quality was first assessed after the recording year was finished. DQP have gained a notable amount of attention among customers. Most of the feedback is positive and plenty of actions have been taken to improve data quality on farms.

Periodic reports have been reformed, according to customer needs and because of the additional information we will be receiving from milk samples. Most wanted figures, lifetime production per day and breed averages, were added to the summary report. On the periodic report milk yield target of the herd is reported on group level and can be easily compared to the milk yield on recording day. Earlier it has been possible to set the target, but no simple monitoring tools were available. Also, possibilities to divide the periodic reports between different groups within the herd have been designed and will be introduced later this year. Those will be helpful on farm as management tools.

Internal reporting on milk recording practises and results is done on weekly basis. Weekly statistics are delivered to local centres, where they can be utilised for better supervision of the milk recording services and for better customer service. Statistics include e.g. detailed information about unanalysable samples with reason, vial type and milk meter type. Customers with milk sample problems can thus receive more specific advice.

Customer services

Traditionally all dairy advisors have been performing milk recording related services. This has been a challenge for the quality and cost-efficiency of the services. Customer services were re-organised during the project so that each local center now has a few specialised milk recording advisors and technicians.

Milk recording advisors monitor the milk recording data and advice the customers. They also provide milk yield data capture services, e.g. they can extract the necessary data from AMS system via remote access if the client so wishes. Technicians use milk sampling devices for AMS, TruTest electronic milk meters, EziScanners and mechanical milk meters. Variety of equipment differ between the centers. The share of pre-coded vials used with on-farm barcode readers has reached 25% of all samples.

A major challenge for the technical services is to make them cost effective. Distances between the farms are great and number of customers is still low due to our long history of B recording.

Communication

Customers have been informed about the new possibilities through several media such as articles in special journals, telephone campaigns, social media, on-line meetings, electronic newsletters and SMS services. Local centers have also organised a lot of seminars and "morning porridges". Communication with stakeholders has also been continuous since the start of the project.

One aim of the project was to decrease the delay from milk recording to the day when milk yields are in database. Around 70% of the milk yields in Finland are reported by the farmer. A milk recording reminder service was started to remind customers about milk recording day, missing milk yields from data base and available new reports. The service was offered to all customers as part of milk recording (Table 3). Messages seem to be useful, since only less than 20% have resigned from the service. With this service we have been able to catch many customers who have reported milk yields to data base. Most probably this service has had a significant effect on decrease of the reporting delay.

Table 3. The use of milk recording reminder –services in April 2015

	No of messages	
	SMS	Email
Recording date	4946	58
Missing yields	969	7
Reports available	4633	51

Results

The number of samples analysed has increased somewhat compared to previous years, which is due to the available shorter sampling intervals and reminders to prevent farmers forgetting to sample. More frequent sampling creates customer value to milk recording. The old monthly sum method for AMS farms has caused problems at milk laboratories and technical services on AMS companies, since most of the samplings were done during the last week of the month. Samples are seen to arrive more evenly nowadays.

The DQP system has been in use only few months now, thus real development will be seen first in the end of recording year. The trend is promising. DQP average was 3.7 in August 2014 and 5.0 in April 2015. We have had approximately 25% of unofficial farms last recording years and the goal of the project was less than 10%. In April 2015 we had 14.5% farms which were under critical DQP level (=0 points). This is a clear evidence that quality matters to customers and DQP has an impact on data quality (Figure 1).

It seems that the actions have also had a significant effect on reporting delays. The most effective actions have been frequent contacts with customers using several media and continuous communication about the meaning of reporting delay to customer value. Typical average for reporting delay has been for years at 28 days. As shown in figure 1 the delay is decreasing rapidly. Customers are using the services of milk recording advisors in similar manner than before, but on average they have paid much more attention to reporting data immediately after milk recording. There is still work to do, since we aim at <5 days delay.

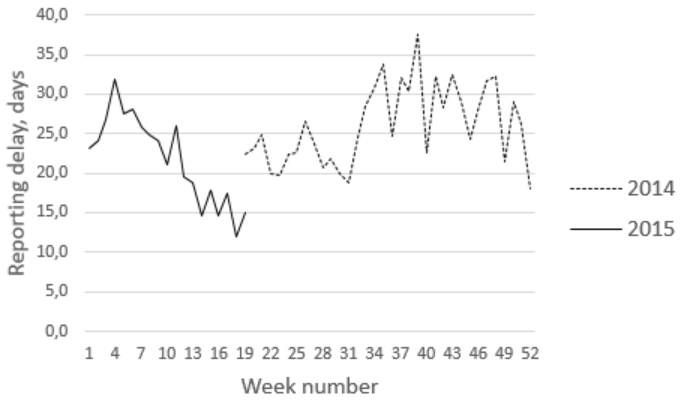

Figure 1. Development of milk yield reporting delay.

Further developments

Changes in customer services are still under development. Services provided by milk recording advisors are not the same in all local centers, which causes a challenge in customer satisfaction. However, feedback from customers has been mainly positive, since somebody is now actively and regularly keeping track of their records.

Technical services need to be further developed to make it more interesting for the customers and more cost-effective for ProAgria centers. Route optimization has been considered as a solution. It requires unification of the services throughout the country, investments on equipment and borderless services, which again would make the services more cost-effective. Testing of milk meters should also be included in technical services and turned into products.

Milk recording reports should be further improved, so that they are easy to use, contain information in useful form and can be customised to meet different needs. New tools and reports are under construction and will be introduced to customers in 2016.

There cannot be enough communication with customers, advisors and stakeholders in such a development project. Lot of effort has been made last year, but surely it was not enough. Improved communication methods and quantity has been in use this spring, when informing customers about the milk sample vial change and additional analyses. Most of the customers appreciate contacts by phone, SMS and email. After receiving the information many have called and asked more details from the advisors. Thus, education of the staff is very crucial in introducing changes.

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Session 5

Genomics at farm and phenotyping strategies

Recording of claw and foot disorders in dairy cattle: current role and prospects of the international harmonization initiative of ICAR

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Abstract

Claw and foot disorders causing lameness are among the major culling reasons in dairy cattle around the world and play a significant role in farm profitability and compromised animal welfare. In recent years, several countries have started routine recording of claw health data. Documentation of claw health status during regular claw trimming has been identified as a valuable source of information on feet and legs conditions in individual cows and can also provide an important insight into the health status of the entire herd or population. However, heterogeneous documentation practices complicate the routine collection of claw health data and consequently the use of the data. To document the current situation of recording and the use of claw health data among ICAR member countries, the ICAR Working Group for Functional Traits (ICAR WGFT) carried out an online-survey during August and September 2014. Responses from 18 countries showed that around half of them have a single national key for recording claw and foot disorders.

Information is collected on 6 to 20 different disorders, in many cases including severity grades using numeric or descriptive recording and affected sites. Professional claw trimmers were found to be the main source of data collection, often using hand-held electronic recording devises and customized software. Digital dermatitis, white line disease, sole ulcer, interdigital phlegmon (foot rot);interdigital hyperplasia (corns), and sole hemorrhage are among the most commonly recorded disorders. Routine genetic evaluation for claw health has been implemented in the Nordic countries in 2010 (Denmark, Sweden and Finland) and Norway (2014). Since 2010, the Netherlands has published breeding values for claw health. Other countries including Canada, Spain, and France have successfully set up recording schemes for claw health information. Other countries also have plans to initiate projects. To be able to make comparisons of claw health between countries and for breeding purposes, the harmonization of the terminology of claw disorders is advantageous. Since May 2014, ICAR WGFT has been engaged in a collective effort involving international claw health experts and interdisciplinary collaborators to develop harmonized definitions for claw disorders along with representative photographs of each disorder. The focus is on descriptive findings. The objective is to establish an international claw health atlas which can guide future developments towards better claw health data that can be used to improve management and breeding of dairy cattle.

This paper provides an overview of the recording of claw and foot disorders in dairy cattle with a focus on aspects of breeding and presents the results and prospects of the work of the ICAR WGFT and international claw health experts on harmonization of terminology and definitions of claw disorders.

Key words: claw health, harmonization, claw disorders, genetic evaluation.

Introduction

Along with reproductive- and udder health problems, foot and claw disorders are major reasons for involuntary culling in dairy cattle. Culling caused by lameness problems accounts for 10-15% of all culls and shows the economic importance of this trait complex (Green *et al.*, 2002; ADR, 2009; Bruijnis *et al.*, 2010; Cha *et al.*, 2010). In general, there are negative genetic correlations between milk yield and functional traits and because of this, an increase in incidences of lameness may be expected worldwide (Veerkamp *et al.*, 2003; Gernand *et al.*, 2012). German figures have shown this unfavorable trend in lameness and involuntary culling over the last decades (ADR, 1980-2009).

According to Van der Waaij *et al.* (2005) more than 70% of cows in The Netherlands have at least one claw disorder. The study is based on data from routine claw trimming over a period of 1.5 years. Rouha-Mülleder *et al.* (2009) found an incidence rate of lameness of 36% in the average of 80 dairy herds in Austria reported variation of 0 to 77% between herds during two consecutive visits. Hoof lesions compromise the welfare of animals (Whay *et al.*, 2003) and coincide with reduced milk yield (Warnick *et al.*, 2001; Amory *et al.*, 2008), reduced fertility (Hernández *et al.*, 2001; Meléndez *et al.*, 2003) and an increased risk of premature culling (Rajala-Schultz and Gröhn, 1999; Booth *et al.*, 2004). Studies estimate a loss of up to 450 Euro per lame cow per year. According to Cha *et al.* (2010), 38% of the loss of $216 (US) due to sole ulcer is because of lower milk yield; 42% of the $120 (US) costs for digital dermatitis are due to labor costs and 50% of the costs of interdigital phlegmon are due to reduced reproductive performance.

Foot and claw disorders are often accompanied by pain and are therefore a major animal welfare issue. According to EFSA (2012) a maximum of 10% lame cows with a lameness score of 2 or higher is tolerable. Weber *et al.* (2013) suggested that lameness might be a useful indicator for claw and leg health. The conformation of feet and legs are recorded routinely by linear type classification systems that are often part of the services offered by breeding societies and some traits may be useful indicator traits for claw health. Although they cannot replace direct measures of claw health, because of low genetic

correlations with claw disorders, routinely collected conformation data can be used to increase the reliabilities of estimated breeding values (EBVs) (Häggmann and Juga, 2012; Chapinal *et al.*, 2012).

In addition to the information from claw trimming, veterinary diagnoses are potentially valuable sources of information, particularly for more severe cases. Genetic studies on foot and claw disorders have shown the advantage of using direct claw health data when breeding for improved claw health (Linde *et al.*, 2010; Koenig and Swalve, 2006), and heritability estimates were generally higher when data from claw trimming were used (Koenig *et al.*, 2005; Boelling *et al.*, 2008; Laursen *et al.*, 2009; Linde *et al.*, 2010). Boelling *et al.* (2008) suggested an index where the different relevant data sources are combined. For effective improvement of the feet and legs complex by breeding, it is important to establish systems that allow the collection of comparable data from claw trimmers.

Standardization of the terminology of foot and claw disorders within and across countries supports activities including genetic evaluation. International cooperation is an important way to support the development of genetic evaluations for novel traits with limited numbers of phenotypes. For example, there has recently been success in pooling dry matter intake data from 9 countries for genomic prediction purposes (de Haas *et al.*, 2015). A survey on the needs of ICAR member countries regarding functional traits showed that there is substantial interest in the feet and legs trait complex and claw health traits (Stock *et al.*, 2012). Establishing a working group with international experts on claw health and assessing the situation in the different countries was an obvious first step towards global harmonization. A meeting was held in May 2014 in conjunction with the ICAR annual meeting in Berlin, Germany to lay the groundwork for such an initiative. Subsequently, a survey on the status of recording of claw health data in the different ICAR member countries was conducted. Based on the needs of international harmonization of foot and claw disorders, the ICAR WGFT and international claw health experts began working on the harmonization of descriptions of foot and claw disorders in October 2014 and this global collaboration concluded with the publication of the ICAR Claw Health Atlas in June 2015.

Survey on recording of foot and claw disorders

To better understand the current situation on claw health and feet and legs disorders in the different member countries of ICAR, a survey using a questionnaire was conducted from mid-August to the end of September 2014. The overall response rate among the 53 ICAR member countries was 60 percent, with answers to all questions from 18 countries and partial information from further 14 countries.

Harmonized key of claw disorders by country

Using the information from these questionnaires about harmonized key of claw disorders, 10 countries (Denmark, Finland, France, Germany, Israel, Norway, Spain, Sweden, The Netherlands, United Kingdom) reported that they each have a single key on claw disorders and leg conditions used throughout the country. Countries using a single key collect information on 6 to 20 different disorders. The level of information collected on foot and legs conditions varies widely from cow level information (2 countries) to single claw information (4 countries); others gathering information at the cow leg level (9 countries).

In addition to claw lesion information, several countries also record information on severity grades using numeric (1 = mild, 2 = moderate, 3 = severe) or descriptive codes (mild, moderate, severe) of the lesions observed.

Eight countries (Australia, Austria, Canada, Czech Republic, Italy, Poland, Slovenia, United States) have no key for data recording. The absence of a key does not mean that there is no effort to collect information; for example, electronic devices are used by trimmers in Austria, Canada and the United States to collect information that stays at the farm level.

Which disorders are recorded?

For the 18 countries that use a single key for recording claw disorders, Figure 1 shows the frequency of different claw disorders White Line Disease (WL), Sole Ulcer (SU), Interdigital Phlegmon (IP), Interdigital Hyperplasia (IH) and Digital Dermatitis (DD) are the most frequently recorded lesions (12 countries). Sole Haemorrhage (SH) is recorded in 10 countries, followed by Heel Horn Erosion (HHE) and Double Sole (DS) in 9 countries.

Other disorders recorded in several countries are horn fissures (horizontal, vertical, axial), Digital Dermatitis associated with White Line Disease, and Digital Dermatitis associated with Sole Ulcer. In most cases the most frequently recorded lesions across countries are also those claw disorders ranking with the highest priorities. However, regional differences were observed. For example, in Australia wall cracks (Axial Horn Fissure (HFA)) are the 2nd most important lesion, whereas wall cracks are not mentioned in any other country under the most frequent lesions. A similar observation is Corkscrew Claws (CC), which is of high relevance in Norway and Finland.

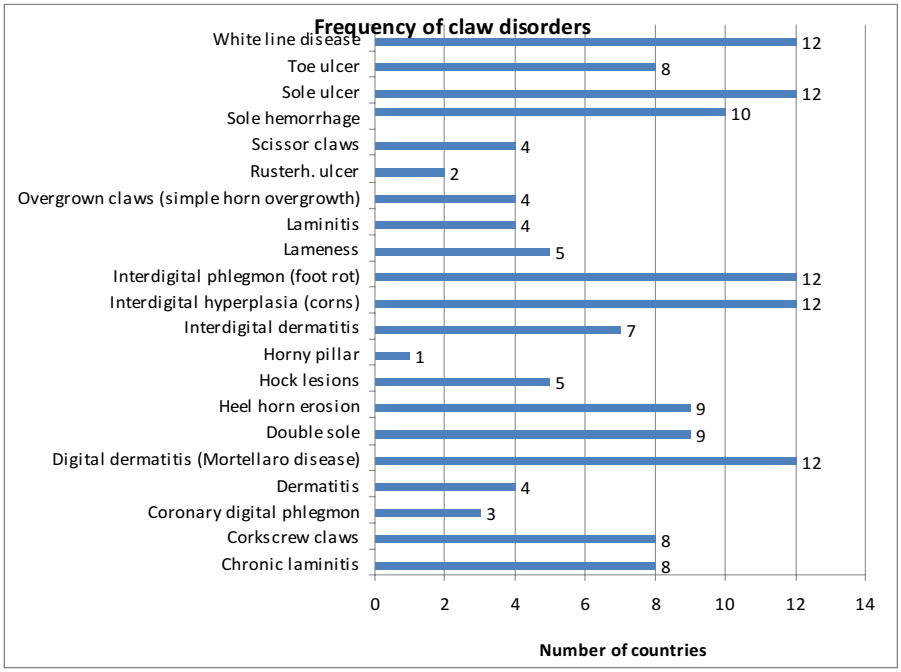

Figure 1. Frequency of the claw disorders most often recorded.

Education and training of claw trimmers

The survey revealed that claw trimmers are the main source for the collection of information and events on these specific dairy cattle disorders in most countries. As veterinarians mainly intervene at the farm when cases are severe, they represent an incomplete source of information for claw health. It is estimated that 40-60 % of claw trimming is done by professional claw trimmers in most of the countries (Austria, Canada, Germany, Italy, Netherland, Norway, Sweden, United Kingdom).

In countries including Finland, and France, 60-80% of the trimming is by professional claw trimmers. In Denmark, Israel, and Spain 80-100% of claw trimming is done by professionals. In countries including New Zealand and Australia, where cows are on pasture most of the year, claw trimming is not a standard practice on most farms.

Trimming also is done by people who have not received special, such as dairy farmers. In some countries (Austria, France, Germany, Italy, Sweden, Finland and Norway, trimmers are licensed and / or certified. In other countries (Canada, Denmark, Finland, Israel, Spain, The Netherlands or United Kingdom) claw trimmers are provided with either special education programs or training by experts. Most of the trimmers use an illustrated guide for the identification of lesions which includes pictures and definitions. As most countries do not have a national scheme to collect information about the people doing this work, it is often difficult to figure out the exact proportion of professional trimmers that are involved.

Some countries with established infrastructures to collect and store data from claw trimming centrally for breeding purposes also organize regular training sessions, or undertake other measures to ensure comparability of the results between the different claw trimmers (e.g. Charfeddine, 2014; Van Pelt, 2015).

Recording practices

The conditions and circumstances of claw care differ widely across countries. The percentage of trimmings recorded by professional trimmers varies. For large farms, claw care is generally carried out by farm staff, professional claw trimmers, or the farmers themselves. It is interesting to note that there are many different tools used to record information on claw disorders and foot and leg conditions, including individual free-text notes (no standardized form), standard forms with reference to the key for claw health on paper sheet reports, free-text or standard forms on mobile electronic devices, and herd management software. The tools most widely used among countries are electronic devices and either mobile or herd management software (11 countries), followed by formatted paper sheet reports (5 countries). In most cases a mixture of recording practices coexist. Despite the different tools available for data recording, it is assumed that many claw trimmings are not documented at all. No exact figures about the documented and centrally recorded claw health information relative to the percentage of dairy cows under milk recording agencies are available. In countries with routine genetic evaluations for claw health, data from claw trimming are stored in a central database and also are used for herd management recommendations. A key aspect of the successful initiatives to build routine genetic evaluations for claw and leg health is the development of an infrastructure for electronic documentation and recording of claw trimming data (Kofler *et al.*, 2011, 2013; Nielsen, 2014; Van Pelt, 2015). Kofler (2013) published an overview of computerised claw trimming database programs which were currently available worldwide.

Status of genetic evaluation for claw health

The current status of the collection and use of claw trimming data from different countries was presented at the 2014 ICAR annual meeting in Berlin *(www.icar.org/Documents/ Berlin_2014/ functional_traits_meeting.htm)*. The status of such system varies widely internationally. Routine genetic evaluations for claw health have been implemented in Denmark, Sweden, and Finland since 2010, and since 2014 they have published genomic breeding value for claw health. 10,000 genotyped cows with phenotypes were included in the genomic reference population (Johansson et al, 2011; NAV, 2014). Norway has published breeding values for claw health since 2014 (Odegard et al, 2013). The Netherlands have published breeding values for claw health since 2010 and Spain and France have successfully managed to set up an infrastructure to capture claw trimming data (25-30% of cows) (Charfeddine, 2014; Thomas and Leclerc, 2014). In other countries claw trimming information have been collected from commercial dairy farms for research projects purpose (e.g. Canada, Germany). In summary, the survey indicated that many activities and projects are under way.

International harmonization of foot and claw disorders

The survey and presentations at the ICAR WGFT meeting in Berlin showed that several countries have recently introduced electronic systems to routinely record foot and claw, and many more are planning or have committed to begin recording in the near future. The broad range of recording practices and documentation schemes with mixture of descriptive and etiological codes has suggested a need for a standardized, practice-oriented approach that accommodates most common circumstances in the field. This motivated the ICAR WGFT to prioritize foot and claw health and to invite internationally recognized claw experts to collaborate in the development of best practices for data recording. This collaboration was intended to complement existing research on specific aspects of the claws and feet of dairy cattle, focusing solely on the standardization and harmonization of data recording. This fruitful interdisciplinary collaboration among experts from different backgrounds (claw health experts, claw trimmers, bovine practitioners, geneticists) resulted in harmonized descriptions of 27 different lesions, providing comprehensive coverage of theoretical and applied needs. It is designed to provide a universal tool for claw trimmers and practitioners and presents guidelines for the recording of important conditions affecting the claw health of cattle. Descriptive trait definitions are used to ensure that accurate classifications are made, which will support the collection of comparable and high-quality data within and across countries to support many activities (e.g., genetic evaluation purposes).

ICAR Claw Health Atlas

After the harmonized descriptions of foot and claw disorders were agreed upon by the international experts and members of the ICAR WGFT, the next step was the collection of representative photographs of each lesion in the key. Claw experts, trimmers, veterinarians, and other contributors submitted photographs, and the most representative examples were selected by voting. The results were discussed and the final selections made by the working group. Harmonized descriptions, photographs, and other descriptive information were assembled to create the first ICAR Claw Health Atlas (Egger-Danner *et al.*, 2015). This Atlas, published in the official ICAR language (English), will be available for translation by any country that would like to distribute it to its professionals and / or farmers. Information about translation and access to a print-quality version will be provided by ICAR. An on-line English-language version will be available on the ICAR website once it is approval by the ICAR member countries: *ww.icar.org/Documents/ ICAR_Claw_Health_Atlas.pdf*.

Conclusion

The ICAR Functional Traits Working Group has focused on a range of very important traits in dairy cattle including: fertility, udder health, and feet and legs. This work is part of ICAR's strategy for helping its members to provide better services to farmers and to facilitate the genetic improvement of farmed livestock, particularly dairy cattle.

For the first time there is an international atlas and coding system available for claw traits in dairy cattle. This represents a major step forward in ensuring that the incidence of claw defects affecting animal health, welfare, and productivity can be reduced in the future.

Acknowledgements

The ICAR Working Group on Functional Traits acknowledges the excellent cooperation with international experts on claw health, and expresses its gratitude for their support and ideas for the development of new standards for recording claw health information. Without their expertise and their great support it would have been impossible to succeed with the ambitious plans of making available this new ICAR Claw Health Atlas.

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Efficient cow: Strategies for on-farm collecting of phenotypes for efficiency traits

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Abstract

Under the condition of limited resources production systems have to adopt their strategies for producing milk and beef. Especially the competition on farmland and the resulting higher prices for concentrated feed causes a higher interest in increasing efficiency.

The Federation of Austrian Cattle Breeders (ZAR) started the project "Efficient Cow" in 2013. The aim of the project is to evaluate the possibilities for genetic improvement of efficiency in cattle breeding under Austrian circumstances. Efficiency is seen as a combination of already existing traits: milk, beef and functional traits and traits aiming at feeding efficiency and health. In the year 2014 a one-year data collection was conducted. Data of approximately 5,400 cows, i.e. 3,100 Fleckvieh (dual purpose Simmental), 1,300 Brown Swiss, 1,000 Holstein, kept on 167 farms were recorded. In addition to routine performance recording, new traits like body weight, body measures (body condition score, chest circumference, ...) and data about feed quality, feed intake and health (lameness score, ketosis milk test, claw health, ...) were collected all year round. Further, 3,000 cows with complete data recording are being genotyped.

The next steps are to estimate genetic parameters for newly defined efficiency traits and genetic correlations to other traits within the total merit index. The main focus is on the evaluation of body weight and feed efficiency. A further project aim is modelling the effect of different milk production systems on greenhouse gas emission based on individual animals under Austrian circumstances. Possibilities to increase efficiency in cattle breeding as well as to reduce emissions indirectly will be analysed.

By collecting this wide range of different information on the project farms, the approach is to find auxiliary traits that are easier and cheaper to measure than the direct traits. Especially automatically collected data from milking and feeding systems could be a new data source for routine phenotypes. But also a structured recording of different management tools like body condition or lameness scoring on a limited number of cows would be a good starting point for further developments of Austrian dairy cattle breeding programs.

Keywords: efficiency, phenotypes, dairy cows, functional traits.

Introduction

In the next decades the world human population will further increase, and therefore the demand for dairy products will expand rapidly. Due to limited agricultural area, dairy production will compete with production of other food and bio-energy. Against this background improving resource efficiency is of increasing international interest. Additionally, because feed costs represent more than 50% of total costs in dairy production, improving of feed efficiency is a viable approach to increase herd profitability (de Haas *et al.*, 2014). Under these conditions of production, a focus has to be put on how to get more milk from each unit of feed rather than on the annual milk yield per cow. In several countries efforts are therefore being made to establish genomic breeding values for feed efficiency. Efficiency is not only described by feed efficiency. Also other aspects as health, good reproduction and longevity are of economic importance. Efficiency needs to consider input and output. Output can be defined in means of progeny, dairy and beef production, but also reduced production costs due to a higher feed efficiency or little losses due to involuntary culling or low health associated costs. A survey among Austrian farmers in 2012 (Steininger *et al.*, 2012) showed their increasing awareness and interest in efficiency and health traits as higher costs for concentrates are expected. The ongoing discussion about greenhouse gas pollution has been another reason that the project "Efficient Cow" was started in Austria. As the facilities to record such data in research herds are limited in Austria, the focus of this project is to explore data from on-farm recording. As the major interest is genetic improvement of these traits a reasonable number of animals needs to be available for the estimation of genetic parameters for newly defined efficiency traits and genetic correlations to other traits within the total merit index. Aspects are to evaluate the context of body weight and feed efficiency or to explore the relationship of efficiency and health. A further project aim is modelling the effect of different milk production systems on greenhouse gas emission based on individual animals under Austrian circumstances. Possibilities to increase efficiency in cattle breeding as well as to reduce emissions by using auxiliary traits will be analysed.

Recording of phenotypes

The Federation of Austrian Cattle Breeders (ZAR) started the project "Efficient Cow" at the end of the year 2012. The aim of the project is to evaluate the possibilities for genetic improvement of efficiency in cattle breeding under Austrian circumstances. Efficiency is seen as a combination of already existing traits: milk, beef and functional traits and traits aiming at feed efficiency and health. In the year 2014 a one-year data collection was conducted. Data of approximately 5,400 cows, i.e. 3,100 Fleckvieh (dual purpose Simmental, 1,300 Brown Swiss, 1,000 Holstein) kept on 167 farms were recorded. In addition to routine performance recording, new traits like body weight, body measures (body condition score, chest circumference, ...) and data about feed quality, feed intake and health (veterinarian diagnoses, lameness score, ketosis milk test, claw health, ...) were collected all year round. In total, 3,000 cows with complete data recording are being genotyped within the project Gene2Farm. The mid-infrared (MIR)-spectra have been standardized and stored as well. The farms were selected in a way that different production circumstances in Austria are covered. This means that included farms cover low input farms located in the very mountainous regions but also intensive farms in climatically favourable regions. The average herd size with 32.6 cows is almost double of the Austrian average.

Efficiency traits

Feed efficiency in lactating cows is a complex trait consisting of and influenced by several parameters. For lactating animals, many feed efficiency definitions exist in the literature (Hurley *et al.*, 2014). Berry and Crowly (2013) describe two types of traits, ratio and residual traits of efficiency. Ratio traits include milk production per unit intake, called feed conversion efficiency (FCE) or milk production per kg body mass or intake per kg body mass. FCE is commonly used to describe feed efficiency, but this definition does not take note of the contribution of mobilisation of body reserves to the energy supply of the

animal (Roche *et al.*, 2009). Berry and Crowly (2013) suggest the definition for FCEadj, which includes body tissue change. Also the partial efficiency of milk production (PEMP) is used to express feed efficiency. Therefore the energy corrected output is divided by feed intake after accounting for energy required for maintenance. Currently residual feed intake (RFI) replaces ratio traits for calculating food efficiency. RFI is defined as the difference between energy intake and demand and is usually estimated as the residuals from a least squares regression model regressing feed intake on the various energy sinks. Improving RFI is a costly and complex challenge due to the difficulties to measure the individual animal feed intake. Genomic selection has allowed renewed interest in breeding for feed efficiency, because genomic predictions for DMI and RFI derived from research projects in several countries, where many data are collected from reference animals in experimental herds (Weigel *et al.*, 2014).

Data of this project are collected on farms and there is no possibility for measuring daily individual feed intake in general. From some feeding systems the amount of concentrates fed per animal and day is available. Nevertheless many details of feeding are collected and feed intake is estimated using the evaluation formula of Gruber *et al.*, (2004). Due to a lack of data of on individual feed intake, feed efficiency will be calculated with FCE, FCEadj and PEMP. For calculating these traits the data basis seems to be appropriate, because data of live weight and BCS are collected several times over the entire project duration.

The individual feed intake estimation by the Austrian Agricultural Research and Education Centre Raumberg is scheduled for summer 2015. Therefore only simple efficiency traits, like milk yield by metabolic weight (ECM / weight0.75) can be calculated in the meantime.

Further research topics are to develop parameters to measure production efficiency where also other information concerning beef traits, reproduction, mobilisation and different health aspects are considered.

Observed data

Within the scope of the routine performance recording all dairy cows were weighed, chest circumference and waist circumference were measured as well as body condition score (1 to 5), muscularity (1 to 9) and lameness score (1 to 5) were recorded (Table 1).

Beside these traits also data about feed quality, fodder and health (ketosis milk test, claw health, ...) were collected. On the 7th and 14th day after calving a ketosis milk test was done. Table 2 shows the distribution of results in percent.

Feedback for farmers

For the motivation of the participating farmers a benefit for their farm is important. Therefore an individual feedback based on the data of their farm is in elaboration. A first analysis including density plots for traits collected at every routine performance recording (body weight, BCS, ..) and raw data were provided in August 2014, a midterm report in May 2015 and a final more extensive report is expected in November 2015.

Table 1. Means and standard deviations for weight, waist circumference (WAIST), chest circumference (CHEST), muscularity (MUSC), body condition score (BCS) and lameness score (LAME) by lactation group (LACT) and breed (FL = Fleckvieh / Simmental, BS = Brown Swiss, HF = Holstein Frisian).

	Breed	Cows	N	Lact 1	Lact 2	Lact >=3
Weight	FL	3984	29763	685 (±79)	734 (±83)	776 (±84)
	BS	1605	12788	618 (±77)	665 (±79)	691 (±78)
	HF	1215	8836	624 (±77)	677 (±79)	709 (±76)
Waist	FL	3981	30031	251 (±14)	259 (±14)	265 (±13)
	BS	1604	12497	243 (±14)	251 (±13)	256 (±13)
	HF	1215	8890	249 (±14)	258 (±13)	262 (±13)
Chest	FL	3982	30039	208 (±10)	212 (±10)	217 (±10)
	BS	1604	12498	200 (±9)	205 (±9)	209 (±9)
	HF	1214	8888	207 (±10)	212 (±10)	215 (±10)
Musc (1-9)	FL	3977	29866	5.58 (±1.21)	5.72 (±1.33)	5.89 (±1.4)
	BS	1604	12501	4.75 (±1.3)	4.76 (±1.34)	4.6 (±1.42)
	HF	1215	8897	4.08 (±1.51)	4.13 (±1.56)	4.15 (±1.51)
Bcs (1-5)	FL	3981	30044	3.32 (±0.52)	3.33 (±0.55)	3.37 (±0.62)
	BS	1604	12500	3.21 (±0.46)	3.17 (±0.53)	3.08 (±0.59)
	HF	1215	8903	2.99 (±0.68)	2.93 (±0.67)	2.9 (±0.71)
Lame (1-5)	FL	3981	29768	1.13 (±0.43)	1.2 (±0.52)	1.42 (±0.77)
	BS	1603	12754	1.11 (±0.44)	1.18 (±0.5)	1.36 (±0.73)
	HF	1214	8778	1.18 (±0.5)	1.33 (±0.63)	1.56 (±0.81)

Table 2: Distribution of ketosis milk test results in percent by lactation group (L. 1 – L. ?3) and breed (result groups: <100 µmol/l ... negative (-), 100-200 µmol/l ... weakly positive (~), 200-750 µmol/l ... positive (+), >= 750 ... strongly positive (++).

	Fleckvieh / Simmental			Brown Swiss			Holstein		
	L. 1	L. 2	L. ?3	L. 1	L. 2	L. ?3	L. 1	L. 2	L. ?3
Negative (-)	71.7	69.1	58.1	62.0	50.6	50.4	68.1	58.7	54.6
Weakly positive (~)	23.4	24.0	31.8	30.3	39.0	38.4	25.5	33.8	33.6
Positive (+)	4.9	6.7	9.8	6.1	9.5	9.8	5.7	7.1	9.9
Strongly positive (++)	0.1	0.1	0.3	1.6	0.9	1.4	0.7	0.4	1.9

First results and discussion

As the first efficiency trait energy corrected milk yield by metabolic weight (ECM / weight0.75) has been calculated. About 45.400 weighings were included in the analysis. The parameter was calculated for each observation by the formula:

$$ECM / weight^{0.75} = \frac{(0.38 * fat\% + 0.24 * protein\% + 0.816) * milk\ yield}{3.14 * weight0.75}$$

Because the impact of ECM / weight 0.75 is very hard to explain, for comparing the results between animals and herds plots showing only ECM against weight but with trend lines for efficiency were generated. All plotted elements were standardized for

lactation day 100 and no pregnancy. In the first step a model for estimating the predicted weight on lactation day 100 was set up. The model for estimating weight includes following effects:

$$weight = lactday + pregday + pregday^2 + lactgroup + calving\ age + farm + farm:cow \quad (1)$$

where lactation day (lactday), day of pregnancy (pregday), lactation group (lactgroup - levels: 1, 2 and ?3) and the age at first calving (calving age) are used as fixed effects. Farm and cow nested within farm (farm:cow) were used as random effect.

In a second step for the three lactation groups separate linear models were set up to derive the relationship between the weights of animals and ECM in this lactation group. These three models were used to plot this relationship. Following effects are included:

$$ECM = weight + weight^2 + lactday + lactday^2 + pregday + calving\ age + fodder + \\ + fodder:farm + fodder:farm:cow \quad (2)$$

where ECM is the observed energy corrected milk and weight, lactation day (lactday), day of pregnancy (pregday) and fodder (levels: with or without silage maize in the diet) are fixed effects. As nested random effects fodder:farm and fodder:farm:cow are used.

For each cow the estimated random effects for ECM and weight were added to the expected value of a standard cow in this lactation group on lactation day 100 and no pregnancy. Figure 1 and 2 are showing for two example farms these generated values together with the fitted curves of model 2. For comparison between farms similar plots were also generated with the mean values of farms within a specific district or group of related farms.

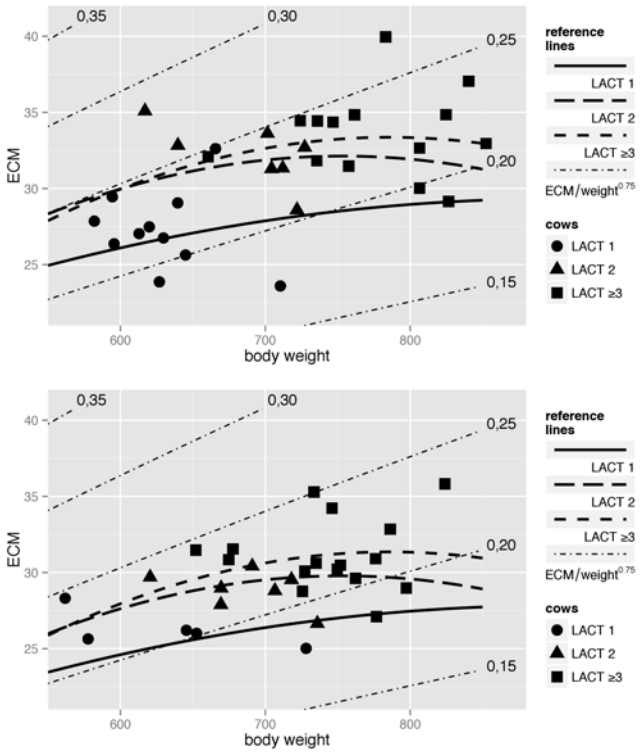

Figure 1 and 2. Estimated random effects for ECM and body weight of all cows from two farms and reference curves for the three lactation groups considering the fodder group of the farm.

All analysis was done for each breed separately. So no breed effect was taken into account in any of the models used.

Conclusions

The extensive recording of novel phenotypes from about 5,300 cows under on-farm-conditions has been a big challenge. Recording of body weight was easier to handle than taking different body measures which were intended as auxiliary traits for body weight. Positive feedback was given regarding recording of management tools like lameness or body condition scoring. The biggest difficulty is to record the feeding information per individual across the different feeding systems and ration compositions on-farm. The amount of concentrates can be recorded more or less accurately when concentrates are distributed by automation. If total mixed ration (TMR) or partial mixed rations (PMR) is fed, no detailed information about the amount of concentrates eaten is however available per animal. The quality of the feed stuff was analysed continuously and a formula to calculate the feed intake (Gruber *et al.*, 2004) is used. Comparison with data from station may help to estimate the bias associated with this calculation. The advantage of this on-farm-trial is the availability of data from a large number of animals. The genetic parameters will give insight into the value of auxiliary traits describing efficiency. For the ongoing discussion concerning genotyping of cows with extensive recording of phenotypes the expected results might help to define reliable, repeatable traits that can be recorded with limited amount of work. The experience shows that the more data can be used from automation the better it is. The limitation of these data is quite often the standardization and the availability of interfaces for data exchange.

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SNP selection for nationwide parentage verification and identification in beef and dairy cattle

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Abstract

As parental verification in livestock species moves from microsatellite- to single nucleotide polymorphism (SNP)-based methods, the accuracy of pedigree verification will increase if robust methods and high quality SNP are used. In beef and dairy cattle, the international standard for SNP-based verification has been to use the ISAG100 or ISAG200 SNP set for Bos taurus breeds. We show that while these SNP sets do provide a higher level of accuracy than microsatellites, more SNP should be used for parentage verification and prediction, and some SNP should not be used due to genotyping quality. The Irish Cattle Breeding Federation (ICBF) is in the unique position of having access to both beef and dairy genotypes on Irish cattle, and through recent government schemes a large portion of ICBF genotypes come from commercial herds which have both purebred and crossbred animals. By analysing different SNP levels across beef and dairy cattle, we were able to determine that at a minimum >500 SNP are needed to consistently predict only one set of parents. If only the ISAG200 SNP are used for parentage prediction, then >1 sire or dam can be predicted at <1% misconcordance rate levels. Since if >1 parent can be predicted using the ISAG200 SNP set, then in theory it is also possible to validate the wrong parent for an animal. Recent analysis of SNP clustering patterns in Illumina BeadStudio software indicated that some SNP, including 3 from the ISAG200 panel, have clustering issues which only become apparent when thousands of samples from multiple breeds are analysed together. Minor allele frequency (MAF) and call rates (CR) were calculated for the Illumina LD base SNP across >180,000 genotyped animals that represent >20 breeds, from this 2 ISAG200 SNP with MAF <0.01 were identified. ICBF currently uses 800 SNP for parentage validation and prediction, which is comprised of 195 SNP from the ISAG200 panel and 605 SNP based on their minor allele frequency (>0.47) and SNP genotyping quality in >160,000 Irish beef and dairy animals. The use of a larger set of high quality SNP has resulted in a highly accurate pedigree validation and prediction regardless of the animals breed composition or pedigree status.

Introduction

Pedigree verification has been performed with DNA makers for almost 50 years in cattle. It was initially performed with the analysis of blood groups (Stormont, 1967), then microsatellite markers (MS) (Davis and DeNise, 1998), and is currently in a transition phase to single nucleotide polymorphisms (SNP). While the cost and availability of each new technology has hindered its initial use, the benefit of reducing pedigree errors cannot be ignored. A 10% pedigree error rate has been estimated to have a 6-13% effect on the inbreeding coefficient, 11-18% reduction on genetic trends in estimated breeding values (EBV), and a 2-3% loss in the response to selection (Visscher *et al.*, 2002, Banos *et al.*, 2001), and causes a downward basis in heritability estimates (Israel and Weller, 2000). While sire error rates have been estimated at 3-23% in different national Holstein-Friesian

populations missing sire rates (10-40%) can also be substantial, especially when using pedigree data from commercial herds (Sanders *et al.*, 2006, Harder *et al.*, 2005). Missing sire data can have a large effect on the response to genomic selection and the variance of breeding value (Harder *et al.*, 2005). While sire errors have a larger effect than missing sire information on genomic progress, their effect on genetic gain is additive (Sanders *et al.*, 2006).

As with all technology there is a need to balance the cost with its performance. For parentage validation the question has often been how many markers are needed to obtain a high probability that the parents, usually just the sire, are correct. For MS markers the international standard is the International Society of Animal Genetic (ISAG) panel of 12 markers (http://www.isag.us/Docs/CattleMMPTest_CT.pdf) although additional or different MS marker sets are used at times for higher parentage accuracy and in research settings (Van Eenennaam *et al.*, 2007, Fernández *et al.*, 2013, Sanders *et al.*, 2006). Given their limited variability (i.e. biallelic nature) and therefore inherent lower resolving power, more SNP are needed to provide the same parentage discriminating power of a MS panel. The current ISAG recommended panel of 100 SNP (ISAG100) has a parental exclusion probability (PE) of >0.999 and the ISAG200 panel of 200 SNP has a PE >0.9999999 (*www.isag.us/docs/Workshop report CMMPT 2014.pdf*). The ISAG100 panel is used by many groups world-wide for initial parentage validation and until recently by the Irish Cattle Breeding Federation (ICBF).

The ICBF had routinely been using 120 SNP for initial parentage validation which consisted of the ISAG100 and a subset of the additional SNP from the ISAG200 panel. For parentage prediction the ICBF had been using the set of 2,000 SNP which are common across all commercial Illumina SNP panels (3K, LD, 50K, and HD) (Illumina Inc., 2010, Illumina Inc., 2011b, Illumina Inc., 2011a, Matukumalli *et al.*, 2009). For parentage validation only 1 misconcordance was allowed (which is where for a SNP the sire is AA and the offspring is BB) to account for potential genotyping errors. For parentage prediction up to 10 misconcordances were allowed. This equates to a 1% and 0.5% misconcordance rate for the validation and prediction processes. Occasionally an animal would be presented for parentage validation and its listed sire would fail due to 2-3 misconcordances from the 120 SNP panel but then would be predicted as the sire from the 2,000 SNP panel. Upon investigation ICBF staff would find evidence that the sire had a genotype error for those 2-3 SNP where he was called homozygous but he should have been heterozygous based upon his other SNP validated progeny. The genotype errors did not prevent the sire being predicted due to the large number of SNP used. While 2,000 SNP used for parentage prediction was very accurate the computational time needed was a concern, especially as the number of animals being genotyped began to sharply rise in 2014. Given the issues generated with low SNP numbers and large SNP numbers being used for parentage validation and prediction a more optimal number of SNP for both validation and prediction was needed.

At the ICAR meeting in Berlin, Germany (May, 2014), the question was raised on how many SNP are used by various groups for parentage prediction. As no consensus was given, the ICAR- Parentage working group asked for work to be done in determining a minimum SNP panel needed for parentage prediction. ICBF agreed to take up this task as their database contains genotypes from multiple SNP panels, beef and dairy breeds, both commercial and purebred animals, and it dovetailed nicely with already initiated projects.

Material, methods, and results

Minimum SNP needed to generate 1 predicted sire

The ICBF database contains animals genotyped on the Illumina 3K, LD, 50K, and HD SNP chips along with those genotyped on the custom International Beef and Dairy (IDB) chip (Mullen *et al.*, 2013), with 56,147 genotyped animals being present in June, 2014. The animals genotyped represent a mixture of Irish beef, dairy, purebred, crossbred, pedigree, and commercial male and females from >20 Bos taurus breeds. As the Illumina 3K has not been commercially available since September, 2011 (personal communication, André Eggen, 23 Feb. 2015), and given its higher variability in genotyping accuracy (Wiggans *et al.*, 2012) 3K genotypes were not used for this study. Across multiple commercial and custom bovine SNP chips the 6,909 SNP from the LD beadchip are a common core of SNP. Minor allele frequencies (MAF) on the core LD SNP were calculated across all genotyped animals in the ICBF database and SNP were ranked on their MAF. Panels of SNP (200, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1100, and 1250) were designed that contained the ISAG200 SNP and increasing numbers of top MAF ranked SNP.

To test how many sires are predicted at different SNP densities at the standard accepted 0.5-1% misconcordance rate 7,092 animals, which had previously had their listed sire SNP validated (420 also had the dam SNP validated), were run through sire prediction with 56,147 animals being in the reference population. The prediction program will return all sires and dams that had less than the set number of SNP misconcordances (<1.0% for <500 SNP, <0.5% for >600 SNP), and were >18 months older than the animal. The breed, pedigree status, herd, farm location, and AI status of the animal and predicted parents were not considered, only age difference to the animal and misconcordance counts (Table 1).

Table 1. Major breed percent in reference populations.

Breed	Jun-14	Mar-15
HOL	68.65	30.08
LIM	7.94	22.34
CHA	9.09	19.2
AAN	4.42	7.22
SIM	2.35	6.77
HER	3.23	4.73
BBL	1.01	2.75
MSH	0.06	1.57
SAL	0.04	0.92
JER	0.17	0.67
PAR	0.17	0.64
LMS	1.91	0.59
BAQ	0.04	0.59
AUB	1	0.53
PIE	0.55	0.17
MON	0.14	0.05
IRM	0	0.03
NWR	0.09	0.03
RED	0.01	0.03

The result from this analysis showed that using the ISAG200 SNP for sire prediction would result in >1 sire being predicted at <1.0% misconcordance levels for 4.2% of the animals (Figure 1). Only when >500 SNP were used would only 1 sire be predicted at <1.0% misconcordance level. To provide an extra 'buffer' the 800 SNP set was chosen for parentage validation and prediction, with the intention of revaluating this later on. This was carried out because a large portion of the animals were dairy or dairy crossbreds (68%) in the 52,909 data set and ICBF was preparing to genotype >120,000 commercial and purebred beef animals from ~35,000 herds via the 2014 Beef Genomics Scheme (*http://www.icbf.com/?p=1725*). Going forward at ICBF the same 800 SNP set will be used for sire

prediction and validation as in theory if one can predict >1 parent then one could also accidently validate the wrong sire if <500 SNP are used for initial validations (Figure 1 and Table 2).

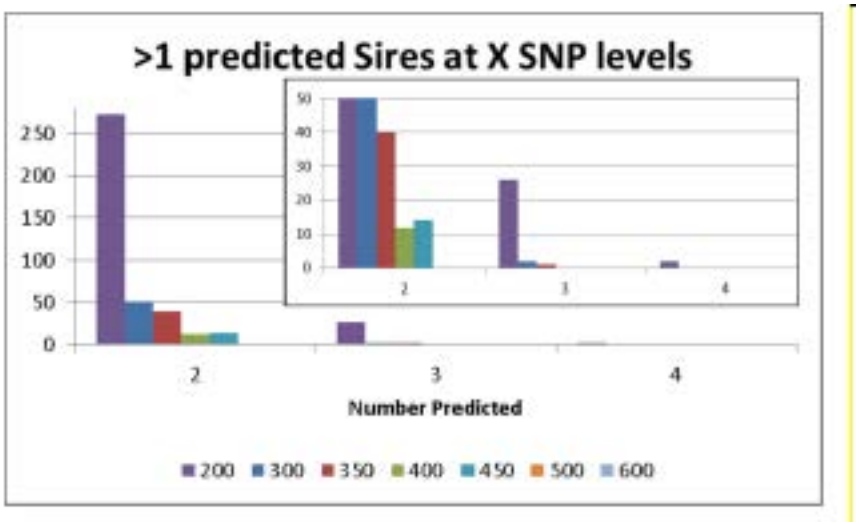

Figure 1. Count of predicted sires with <0.5-1% misconcordances at varying SNP density levels.

*Table 2. SNP excluded from Parentage analysis due to call rate (CR), Minor Allele Frequency (MAF), or Probe Clustering issues (**BOLD**).*

SNPID	Rs#	ISAG100	ISAG200	CR	MAF	Cluster
ARS-BFGL-NGS-103099	rs110896475	0	0	0.952	0.496	**1**
ARS-BFGL-NGS-112652	rs109504357	0	0	0.994	0.499	**1**
ARS-BFGL-NGS-11469	rs111032185	0	0	0.955	0.496	**1**
ARS-BFGL-NGS-118188	rs42156449	0	0	0.993	0.485	**1**
ARS-BFGL-NGS-3547	rs110206613	0	0	1	0.493	**1**
ARS-BFGL-NGS-43361	rs109934313	0	0	0.998	0.494	**1**
ARS-BFGL-NGS-53975	rs109456438	0	0	0.988	0.484	**1**
ARS-BFGL-NGS-62906	rs110146023	0	0	0.998	0.484	**1**
ARS-BFGL-NGS-66558	rs109817790	0	0	0.991	0.495	**1**
ARS-BFGL-NGS-76191	rs110846944	0	1	0.998	0.385	**1**
ARS-USMARC-PARENT-DQ786764-NO-RS	rs109943112	1	1	0.952	**<0.001**	-
ARS-USMARC-PARENT-DQ837645-RS29015870	rs29015870	1	1	**0.276**	0.389	**1**
ARS-USMARC-PARENT-EF034087-NO-RS	rs110665639	1	1	0.984	**0.005**	-
BTA-100621-NO-RS	rs41611675	0	1	0.928	0.452	**1**
BTB-00147175	rs43356919	0	0	0.99	0.491	**1**
BTB-01834338	rs42942345	0	0	0.999	0.498	**1**
HAPMAP47324-BTA-55159	rs41586638	0	0	0.984	0.496	**1**
UA-IFASA-9571	rs41659357	0	0	0.985	0.485	**1**

SNP quality control and MAF revaluation

By March 2015, >180,000 genotyped animals were in the ICBF database, and MAF for the core LD SNP were rechecked and an updated 800 SNP list was produced. This updated list allowed for the identification of SNP that were highly informative (MAF >0.45) across multiple breeds (Table 2). Theee ISAG100 SNP were noted to have either very low MAF (<0.001) or very low call rates (CR<0.3). Analysis of the Illumina BeadStudio files for the low CR SNP (ARS-USMARC-PARENT-DQ837645-RS29015870) revealed that it had clustering issues which were only apparent at high genotyping throughput rates, such as 4,000 samples a week. Analysis of all the ISAG200 and the next top 1000 MAF SNP revealed 15 SNP that have clustering issues. The clustering issues were not breed dependent.

A new set of 800 SNP for parentage validation and prediction was built using the ISAG200 SNP set as a base, minus the 5 listed in Table 1, and the next top 605 SNP based on MAF that did not have clustering issues (h*www.icbf.com/wp/wp-content/uploads/2013/07/ICBF_Parentage_SNP_Selection.csv*). All animals in the ICBF database had their parentage validation reanalysed with the new 800 SNP set to provide a consistent parentage analysis for all animals.

Misconcordance count distance between validated and failed sires

While most sire validated animals (>99%) in the ICBF database have only 0 or 1 misconcordance when using the 800 SNP set, <1% have 3 and 4 misconcordances. For failed animals >99% have >20 misconcordances, but a handful (N=10) have 13-20 misconcordances. LD core SNP analysis validated that all animals with 13-20 misconcordances from 800 SNP were true fails with >2% misconcordance rates.

To assess if <800 SNP could be used for parentage validation and prediction we analysed 8,626 animals that had >1 misconcordance count on their initial listed sire from the new 800 SNP set. SNP sets of 100, 200, 300, 400, 500, 600, and 700 were developed by using the ISAG 200 core set and then the top MAF SNP, the 100 SNP set was develop using the ISAG100 SNP set (*www.icbf.com/wp/wp-content/uploads/2013/07/ICBF_Parentage_SNP_Selection.csv*). Any SNP listed in Table 1 was not used.

While there is clear separation between validated and failed sires at 800 SNP the gap between these two outcomes rapidly narrows or disappears for smaller SNP sets (Figure 2). At the edges of the misconcordance count curves the gap between the number of counts

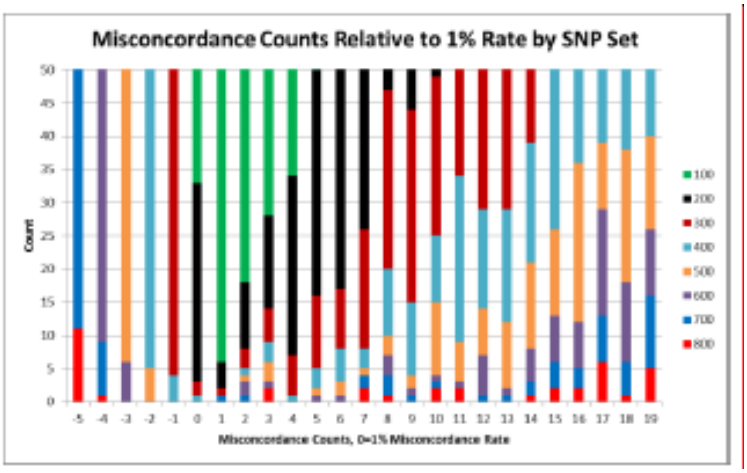

Figure 2. Misconcordance counts above and below the 1% misconcordance rate by SNP set on 8,626 animals with >1 misconcordance when their sire validation was analysed for 800 SNP. Image has been limited to focus on the counts around the 1% rate.

for failed and validated animals widens as more SNP are used. For 800 SNP there is a gap of 6 counts, for700 and 600 SNP its 4, 500 SNP is 3, and <400 it is <1. When you look at the number of SNP counts above the 1% misconcordance rate its only at 800 SNP that one reaches >2 SNP. For animals that passed sire validation at 800 SNP, 14 of them would have failed (>1% misconcordances) if only 100 SNP was used. More importantly for animals that failed sire validation at 800 SNP, 17 would have been validated at 100 SNP, 2 at 200 SNP, and 1 with the 400 SNP set.

Discussion and conclusion

While the ISAG100 and ISAG200 SNP panels do provide a good base for parentage validation via SNP they are not without their limitations. As shown here some of the ISAG SNP have genotyping problems due to their clustering patterns and some have very low MAF. More than 500 SNP are needed to predict only 1 sire when using all animals in your reference group as done at ICBF. If you restrict the prediction to only herd level fewer SNP could be used, but one will be hindered as this does not take into account potential errors from fence jumping breeding stock or mis-recorded semen straws. In Ireland the 800 SNP have proven very effective for initial validation and prediction. To date the only time >1 sire or dam has been predicted was due to a set of identical twin cows. While identical twins will have unique DNA methylation patterns (Kaminsky *et al.*, 2009) to date a method to use this for parentage validation in livestock has not been developed.

This study suggests that >500 SNP be used for parentage validation and that the SNP set described here works well for validation and prediction. ICBF has found that using the 800 SNP set for validation and prediction works well across multiple Bos taurus breeds and removes the possibility of accidently validating or failing a pedigree incorrectly. The number of SNP used by each laboratory, breed society, or national valuation centre will depend on cost and level of acceptable risk for a parentage error. As the cost of SNP genotyping decreases the value of having a near perfect pedigree will soon outweigh the cost of genotyping an animal with additional SNP.

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Phenotypic associations and genetic correlations between claw health disorders and, milk production, fertility, somatic cell score and type traits in Holstein Spanish dairy cattle

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Abstract

The objective of this study is to estimate phenotypic and genetic associations between claw health and feet and legs traits, production, somatic cell score and fertility performance in Spanish dairy cattle. Information of 6 claw disorders: dermatitis (DE), sole ulcer (SU), white line separation disease (WL), interdigital hyperplasia (IH), interdigital phlegmon (IP), and chronic laminitis (CL), and also a combined trait called overall claw disorder (OCD), defined as the absence or the presence of at least one of the six claw lesions, was used. Trimmers score up each disorder as mild or severe lesion for each claw. Claw trimming data including 108,468 records, collected from 2012 to 2014 in 804 Holstein dairy herds by 25 trimmers, and were merged with dairy milk recording and type classification data to estimate phenotypic associations between claw disorders, energy corrected daily milk production, somatic cell score, calving first service, calving conception service, services per conception and feet and legs traits score. A total of 49,963 claw health records corresponding to 35,337 cows with conformation data on feet and leg traits, yield data (305-d first lactation milk, fat and protein), somatic cell score, and days open between the first and the second calving in first lactation were used to estimate genetic correlations with claw disorders. The presence of claw disorders was associated with a significant decrease in milk production and an increase in SCS, especially for SU, WL and OCD. The presence of SU and WL during early lactation period was associated with an increase in the calving first service interval and calving service conception interval, mainly for severe lesions. Genetic correlations between feet and legs and claw disorders were low to moderate, although some of them seemed to be more negatively correlated to specific lesions, such as locomotion, and rear legs rear view. Cows with a good locomotion score are less likely to claw disorders. However, feet and legs conformation traits are not efficient as indicator traits for claw health selection. As expected, genetic correlation between claw disorders and production traits were positive, supporting that high yielding cows were more prone to claw disorders, especially to CL and IP. Our results showed a positive genetic relationship between claw health problems and poor fertility, as well as higher somatic cell score in animals affected by sole ulcer.

Key words: phenotypic and genetic association, claw disorders, feet and legs traits, production, somatic cell, fertility.

Introduction

The intensive selection for yield production during the last decades, jointly with the intensification of modern cattle husbandry and keeping larger herds of cows in loose-housing systems have led to higher risk of claw disorders. Claw disorders reduce profitability in dairy industry and involve an overuse of antibiotics. Then, nowadays

claw disorders are becoming a big source of economic loss and a big concern for the dairy farmer. These losses were mainly due to a reduced milk production (Green *et al.*, 2002) and poor fertility performance of lame cows (Barkema *et al.*, 1994).

In 2012, a centralized electronic recording system called I-SAP for 6 claw disorders was implemented in Spain and genetic parameters for claw disorders were estimated in order to perform the genetic evaluation for claw health traits (Charfeddine and Pérez-Cabal, 2014b). To include claw health traits in our breeding goal, economic values of claw disorders require the estimation of the associated decrease in the milk production, the increase in somatic cell score and the deterioration in the fertility performance. At the same time, genetic relationship with other traits evaluated in Spanish dairy cattle and included in Spanish merit index are needed. Then the main purpose of the present study is to estimate the phenotypic associated effect of claw disorders on milk production, test day somatic cell score, and reproductive performance, such as calving to first service interval and calving to conception interval and number of services per conception. Another aim of this study is to estimate the genetic correlations of claw disorders with feet and legs traits, production traits, and other functional traits, as lactation somatic cell score and days open.

Material and methods

Data

Claw health disorders

Claw trimming data included 108,468 records, collected from 2012 to 2014 in 804 Holstein dairy herds by 25 trimmers, involved in I-SAP program (Charfeddine and Pérez-Cabal, 2014a). This information was merged with dairy milk recording and type classification database to generate the data set for each analysis. Six claw diseases are recorded: Interdigital and digital dermatitis (DE), sole ulcer (SU), white line disease (WL), interdigital hyperplasia (IH), interdigital phlegmon (IP), and chronic laminitis (CL). Claw health data were scored as categorical trait (0: absence of disorder, 1: mild lesion and 2: Severe lesion) for each claw. A combined claw disorder trait which included all disorders was created. The new combined trait was called Overall Claw disorder (OCD), indicating the absence, or the presence as mild or severe lesion of at least one of the six claw disorders. In the case there is more than one disorder, the highest score is kept for OCD. A detailed description of each claw disorder recorded within I-SAP was given by Charfeddine and Pérez-Cabal (2014a).

Phenotypic association

The test-day milk recording data within 48,895 lactations obtained from the official milk recording system provided by CONAFE were used to perform phenotypic association analysis between milk production, somatic cell count and claw disorders. Daily milk yield, fat and protein content, were used to calculate daily energy corrected milk (ECM), which determines the amount of milk produced and adjusted to 3.5% fat and 3.2% protein. ECM was used as outcome variable in milk production analysis. The test day somatic cell count was transformed to somatic cell score (SCS). After a preliminary analysis in order to test the significance level, claw health diagnosis date corresponding to each milk test-day were limited to diagnosis within 4 weeks before and after test-day milk date. For each specific claw disorder a disease index variable was created for each test day date in order to estimate the effect on daily ECM and SCS. Claw health index variable was defined as follows: 1= test day collected between 15 d and 28 d before the claw diagnosis, 2= test day collected within14 d before claw diagnosis, 3 test day collected within 14 d after claw diagnosis, 4: test day collected between 15 d and 28 d after claw diagnosis, and 5= cow had not been diagnosed with any disease during the interval 28 d before and 28 d after the test day (used as the reference level).

To avoid the confounding effect of different claw disorders present at the same time, only records of healthy cows and records of cows with only a specific disorder at a time were included in the analysis. Due to the low frequencies of IP, CL and IH, the phenotypic associations were performed only for DE, SU, WL and the overall claw disorder OCD.

Days from calving to first service (CFS), days from calving to conception (CSC), and number of services per conception (SPC) of 15,159 lactations with claw disorder diagnosis data within the first 100 days of lactation (CD100) were used to estimate the effect of claw disorders on fertility performance. As the same as with production and SCS only cows with only one claw disorder at a time and cows without any disorder within 100-d of lactation were used in each analysis.

Conformation traits were routinely recorded by professional classifiers from CONAFE. Six feet and leg traits were considered to analyse phenotypic association and genetic correlations with claw disorders: feet and legs composite (F&L), foot angle (FA), bonne quality (BQ), rear leg side view (RLSV), rear leg rear view (RLRV) and locomotion (LOC).

Genetic analyses

For the genetic analyses, 49 963 claw health records, corresponding to 35 337 cows were used. Far visits with less than 5 cows trimmed were excluded. The data set has repeated records for a given cow because a trimmer visits the farm more than once a year and lesion status could change from one observation date to the next. The average number of trim per cow in the final data set was 1.4. Trimmers who scored hind and fore claw may be different, therefore for genetic parameters estimation, only rear leg claw disorders were included. Conformation data on feet and leg traits and yield data in first lactation were merged with claw health data. Yield traits were 305-d first lactation milk, fat and protein. Somatic cell count per test day was transformed to somatic cell score, then adjusted and averaged per lactation and considered as lactation somatic cell score (LSCS). Days open was calculated as the interval between the first to the second calving minus the pregnancy period. Pedigree of cows with records was the traced back for all the generations available. A total of 116 298 animals were included in pedigree file.

Models

Phenotypic association analysis

The phenotypic associations between the outcomes and potential predictor variables were evaluated using repeated measures analyses of variance using PROC MIXED of SAS Ver. 9.2 (SAS Institute Inc., Cary, NC). Initially, the predictor variables and their respective interactions were screened using a univariate approach, where variables with $P<0.20$ were retained in the general full model.

For ECM and SCS, the model included cow and herd as random effects, and as systematic effects season of calving, lactation number grouped as first and second or later lactations, age at calving, stage of lactation and the claw disorder diagnosis index.

For CFS, CSC and SPC, the model included the random effect of cow, and herd, and the systematic effects season of calving, lactation number grouped as first and second or later lactations, the production level (categorized as low and high level), and the claw disorder diagnosis within the first 100 days of lactation.

Genetic parameters estimation

Genetic correlations between claw health traits and type, production and functional traits were estimated by REML fitting a multi-trait linear animal model using the VCE 6.0 software (Groeneveld *et al.*, 2008). The models used were (levels are indicated between brackets):

- Claw health traits: The systematic effect considered were: lactation-calving age (31), days in milk at the moment of the trimming (grouped in 6 levels as follow: 0-60, 61-120, 121-180, 181-240, 241-305 and >305). The random effects considered were the comparison group herd-visit-trimmer (1679), the permanent environmental effect of the cow (35,337), and the random additive genetic effect (116,298).
- 305d production traits and days open: The systematic effects were age at calving (9), and the calving moth (12) .The random effects were the comparison group herd-year of calving (2852), and the animal additive genetic effect (116,298).
- LRCS: As systematic effect were included the age at calving (11), and calving moth (12), and as random effect were considered the effect of herd-year of calving (5062), and the animal additive genetic effect (116,298).
- Type traits: The model included the systematic effects age at calving (23), stage of lactation in the moment of type classification (11), and random effects herd-year of calving (5062), and animal additive genetic effect (116,298).

Results and discussion

Claw health disorders prevalence

Claw disease prevalence at cow level is shown in Table 1. Sole ulcer had the highest prevalence, whereas hyperplasia had the lowest. At least one disorder was shown in nearly 40% of cows in this study. Furthermore, the incidence of a severe lesion is very low in comparison with mild lesion. Incidences of claw disorders observed in our population were in a wide range, as it is reported in the literature (Van Der Waaij *et al.* 2005; Uggla *et al.* 2008).

Phenotypic effect of claw disorders on milk production and somatic cell score

The associated effects of DE, SU, WL and OCD on ECM and SCS at different intervals diagnosis date-control test-day, revealed from the mixed models, are shown in Table 2. The presence of claw disorders is associated with a significant decrease in milk production and an increase in SCS, especially SU, WL and OCD. The production loss caused by DE was low and statistically not significant. However, cows with SU and WL produce significantly less milk than the non-affected cows during 28 days before and after the diagnosis date. The production loss is larger before the trimming and the corresponding treatment, ranging from 0.94 to 1.27 kg / d for SU, from 0.94 to 0.88 kg / d for WL, and from

Table 1. Cow-level prevalence (%) of the claw disorders.

Claw disorders[1]	Total	Mild lesion	Severe lesion
DE	10.21	9.61	0.60
SU	14.71	13.09	1.62
WL	11.87	10.58	1.29
CL	2.96	2.68	0.28
IH	0.44	0.38	0.06
IP	1.00	0.74	0.26
OCD	37.6	33.77	3.83

[1]DE: Dermatitis, SU: Sole ulcer, WL: White line disease, CL: Chronic laminitis, IH: Interdigital hyperplasia, IP: Interdigital phlegmon, OCD: Overall claw disorder

Table 2. Phenotypic effect of claw disorders on the energy corrected daily milk production (ECM) and Somatic cell score (SCS).

	DE1		SU		WL		OCD	
Records affected cows	9582		14626		11138		33526	
Records non-affected cows	88473		83429		86917		61561	
Claw health level	β	SE	β	SE	β	SE	β	SE
ECM (Kg / d)								
Non-affected	0	…	0	…	0	…	0	…
-28 to -15 days	-0.06ns	0.16	-0.94***	0.12	-0.94***	0.13	-0.61***	0.08
-14 to test-day	-0.29ns	0.15	-1.27***	0.12	-0.88***	0.13	-0.81***	0.06
1 to 14 days	-0.35**	0.16	-0.88***	0.12	-0.53***	0.13	-0.49***	0.07
15 to 28 days	0.01ns	0.17	-0.76***	0.13	-0.03***	0.15	-0.38***	0.09
SCS								
Non-affected	0	…	0	…	0	…	0	…
-28 to -15 days	0.006ns	0.014	0.021ns	0.012	0.024ns	0.013	0.004ns	0.008
-14 to test-day	0.010ns	0.013	0.066***	0.011	0.038***	0.013	0.025**	0.006
1 to 14 days	0.026ns	0.016	0.016ns	0.012	0.038**	0.013	0.021**	0.007
15 to 28 days	0.009ns	0.015	0.024n	0.013	0.034*	0.015	0.019*	0.009

[1]DE: Dermatitis, SU: Sole ulcer, WL: White line disease, OCD: Overall claw disorder

ns: Not significant *$P<0.05$ **$P<0.01$ ***$P<0.0001$

0.61 to 0.81 kg / d for OCD. ECM yield began to decline 4 weeks before the diagnosis, and just after the trimmer visit showed a recovery until 4 weeks after. The SCS increase was more significant during the 14- d interval before and after the diagnosis date. Rajala-Schultz *et al.* (1999) reported more milk loss in Finnish Ayrshire dairy cows, whereas our results were more similar to estimates obtained by Warnick *et al.* (2001) in USA Holstein cows.

Phenotypic effect of claw disorders on fertility performance

The effect of claw disorders diagnosed within the first 100 days of lactation on calving-first service interval, calving-service conception interval, and number of services per conception are presented in Table 3. The presence of DE was associated with low and not significant effect on fertility performance. However, the presence of SU and WL was associated with an increase in the CFS and CSC intervals, mainly for severe lesions, varying from 4.83 to 17.43 days more than non-affected cows during the first 100 days of lactation. WL was associated with the highest deterioration of reproductive performance.

Claw disorders during the first 100 days postpartum showed negative effect but not highly significant on the number of services per conception. However, cows showing claw disorders during early postpartum period tended to have larger CFS and CSC intervals. It seems that cows were likely to become pregnant with fewer services per conception but to make this happen they need more time. Olechnowicz and Ja?kowski (2015) observed similar results in Polish Holstein-Friesian dairy cows, and Garbarino *et al.* (2004) reported that claw disorders have a detrimental effect on ovarian activity during the early lactation period, which support that claw disorders mask estrus expressions.

Table 3. Phenotypic effect of a claw disorders diagnosed within the first 100 days of lactation on fertility performance.

	DE[1]		SU		WL		OCD	
Cows with a mild lesion	985		848		842		2842	
Cow with a severe lesion	19		70		53		188	
Non-affected cows	12,129		12,129		12,129		12,129	
Claw health level	β	SE	β	SE	β	SE	β	SE
Calving-first service								
Non-affected	0	…	0	…	0	…	0	…
Mild lesion	1.97*	0.91	4.83***	0.99	4.94***	0.98	3.46***	0.58
Severe lesion	5.58^{ns}	7.16	8.00*	3.34	17.43***	3.94	10.24***	2.09
Calving-service conception								
No-affected	0	…	0	…	0	…	0	…
Mild lesion	0.48^{ns}	1.06	4.84**	1.08	3.51**	1.38	2.98**	0.72
Severe lesion	6.97^{ns}	6.82	8.96**	3.53	10.48**	5.51	8.05***	2.27
Services per conception								
No-affected	0	…	0	…	0	…	0	
Mild lesion	-0.047^{ns}	0.02	-0.058*	0.03	-0.032*	0.03	-0.054**	0.02
Severe lesion	0.187^{ns}	0.17	-0.025^{ns}	0.09	-0.172^{ns}	0.10	-0.112*	0.06

[1]DE: Dermatitis, SU: Sole ulcer, WL: White line disease, OCD: Overall claw disorder

^{ns}:Not significant $^{*}P<0.05$ $^{**}P<0.01$ $^{***}P<0.0001$

Genetic correlations

Genetic correlations for claw disorders and feet and legs, production, LRCS and days open in first lactation cows are shown in Table 4. The genetic correlation between claw disorders and feet and legs traits were, mostly negative, low to moderate, ranging from 0.25 to -0.64. The highest negative genetic correlations were found between F&L composite, RLRV, LOC and OCD, IH and IP. Our results are in accordance with other studies (Haggman and Juga, 2013; Larsen *et al.* 2009), reported that feet and legs conformation traits are not efficient as indicator traits for claw health selection.

The genetic correlations between claw disorders and 305-d first lactation production traits were positive, except between DE and fat yield, and low to moderate, ranged from -0.08 to 0.59. Koenig et al (2005) reported similar results. Positive genetic correlations between production traits and claw disorders indicate that intensive selection on production can have unfavorable increase of claw disorders incidence.

The genetic correlations obtained in our study between claw disorders and functional traits (LSCS and days open) were mainly positive, and ranged from -0.77 to 0.42. The highest unfavorable correlations were obtained for SU and OCD. Despite of the fact that correlations are low to moderate, it seems that there are genetic associations, as reported by Buch *et al.* (2011), between high SCS, and poor fertility with high incidence of claw disorders.

Conclusions

Claw disorders affected milk production and SCS during the 4 weeks before and after diagnosis date. SU and WL were the biggest cause of production loss and somatic cell increase. Mild and severe SU and WL lesions during the early period of lactation were associated with largest CFS and CSC intervals. Some feet and legs traits seemed to be more genetically correlated to specific disorders, such as LOC, RLRV and F&L composite with DE, SU, IH and IP. In general, cows with a good locomotion score are less likely to

Table 4. Genetic correlations between claw health disorders and feet and legs, yield, and functional traits for first lactation cows.

	DE[1]	SU	WL	CL	IH	IP	OCD
F&L	-0.26	-0.24	-0.01	-0.08	-0.46	-0.62	-0.29
FA	0.05	0.03	0.25	0.25	-0.17	-0.42	0.16
BQ	-0.06	-0.03	-0.27	-0.10	-0.35	-0.40	-0.21
RLSV	0.12	0.20	-0.01	0.12	-0.01	0.38	0.18
RLRV	-0.28	-0.04	0.24	0.15	-0.38	-0.64	-0.07
LOC	-0.38	-0.27	-0.02	-0.15	-0.43	-0.53	-0.35
F&L	-0.26	-0.24	-0.01	-0.08	-0.46	-0.62	-0.29
305-d yield							
Milk	0.05	0.13	0.19	0.32	0.12	0.41	0.20
Fat	-0.08	0.11	0.02	0.16	0.02	0.59	0.10
Protein	0.02	0.07	0.11	0.23	0.12	0.59	0.14
Functional traits							
LSCS	0.08	0.21	-0.07	0.09	0.09	-0.01	0.14
Days open	0.13	0.42	0.18	0.38	-0.07	-0.77	0.40

[1]DE: Dermatitis, SU: Sole ulcer, WL: White line disease, CL: Chronic laminitis, IH: Interdigital hyperplasia, IP: Interdigital phlegmon, OCD: Overall claw disorder.

F&L: Feet and leg composite, FA: Foot angle, BQ: Bone quality, RLSV: Rear leg side view, RLRV: Rear leg rear view, LOC: Locomotion, LSCS: Lactation somatic cell score

claw lesions. As expected, high yielding cows were more prone to claw disorders, especially to CL. Our results showed a positive relationship between claw health problems and poor fertility, as well as with higher SCS in animals affected by SU.

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Guidelines to measure individual feed intake of dairy cows for genomic and genetic evaluations

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Abstract

The widespread use of genomic information in dairy cattle breeding programs has presented the opportunity to select for feed intake and feed efficiency. This is because animals from research herds can be used as a reference population to calibrate a genomic prediction equation, which is then used to predict the breeding value for selection candidates based on their own genotype. To implement genomic prediction and perform genetic analysis for feed intake, several partners have brought together their expertise and existing feed intake records. Based on this experience we aim to provide some guidelines on the recording and handling of feed intake records. The consortium used a mixture of standardised experimental data coming from larger genetic experiments or several smaller nutritional studies. The latter has provided some statistical challenges. Also, data was combined across countries, experimental herds and feeding systems. Despite the perceived roughness of such data, it has proven to be very successful for genomic prediction, with proper statistical modelling. Ideally the whole lifetime of all cows should be measured, but this is unrealistic. Often, animals are recorded for part of one (or more) lactation(s) only. Guidelines on the proper statistical modelling and usefulness of existing data are needed. Selection index theory can help to establish the optimal recording period across and within lactation. It is also critical to identify how many records are required and what are the most informative animals for measuring feed intake. Genetic relationships with the selection candidates are an important criterion. Finally, since (residual) feed intake is only part of the breeding goal, it is important to consider recording of other traits as well, and the genetic parameters are needed to define the breeding goals properly.

Keywords: Feed intake, genomic selection, DMI, genetic evaluation

Introduction

The widespread use of genomic information in dairy cattle breeding programs has presented the opportunity to select for feed intake and feed efficiency. This is because animals from research herds can be used as a reference population to calibrate a genomic prediction equation, which is then used to predict the breeding values for selection candidates based on their own genotype. In the Netherlands (Veerkamp *et al.*, 2014) and Australia (Gonzalez- Recio *et al.*, 2014) the first breeding values for (residual) feed intake have been made available to the industry, but still phenotypes for feed intake are an important limiting factor to obtain high accuracy breeding values and perform genetic analysis for feed intake. To overcome this limitation, several initiatives have been taken, and partners have brought together their expertise and existing feed intake records. Based on these experiences, we aim to provide some guidelines on the recording and handling of feed intake records for genomic and genetic evaluations.

Utilising existing feed intake data

Designed experiments for genetic studies

Worldwide, there are relatively few designed experiments specifically suited for investigating genetics of feed intake (and related traits). Examples are, the long term experiment at the Scottish Agricultural College (now SRUC) Dairy Research Centre based at Langhill herd, Edinburgh (Pryce *et al.*, 1999, Veerkamp, 1996), the experiment at the Dutch farm 't Gen (Lelystad, the Netherlands) (Veerkamp *et al.*, 2000), the data collection at the dairy research farm Karkendamm of the Christian-Albrechts-University Kiel in northern Germany (Buttchereit *et al.*, 2011), or more recently data collected on young heifers in Australia (Williams *et al.*, 2011) and New Zealand (Waghorn *et al.*, 2012). The common denominator across these studies is that approximately a 1000 animals were recorded, that were fed ad libitum a total mixed ratio (TMR) diet, and the dairy cows were recorded from the start of the lactation up to a fixed point in lactation (10, 26 or 38 weeks).

Merging and sharing data

The designed studies are too small for a reference population using genomic prediction, and therefore in many countries additional sources of feed intake records have been added. For example, from nutritional experiments (Tempelman *et al.*, 2015 Veerkamp *et al.*, 2014), consortia have been formed that combined data across countries (Banos *et al.*, 2012 Berry *et al.*, 2014; de Haas *et al.*, 2012; Pryce *et al.*, 2012, Tempelman *et al.*, 2015), or utilising genomic information from beef breeds for dairy cattle (Khansefid *et al.*, 2014). Combining all these types of data is attractive and a cost effective way of increasing the reference population, but at the same time the data becomes more heterogeneous in many aspects. For example recording period during lactation might be different, repeated records within and across lactation might be available or not, and feeding systems might be different, especially across the nutritional experiments. This heterogeneous data collection directed attention to a statistical "use what we have"-approach rather than attention to design of the most optimal recording of feed intake.

One element of the statistical approaches is dealing with the different recording periods within and across parity. Nutritional experiments are often on second or later parity, and data collection might focus on the transition period (early lactation) or mid to late lactation. Experiments might be short (a month) or several months. Hence, a solution is required to standardize the data. One solution attempts to standardise the records to one DMI record for each cow, and that one record is utilised in sub sequential genetic analysis. The one trait could be standardised based on a random regression model prediction for a cow, based on the (repeated) records collected during different parties and the covariance structure found in the population (Banos *et al.*, 2012, Berry *et al.*, 2014), or the one trait could be based on the phenotypic records available for a cow in a standardised time, e.g. first 28-d period between 50 and 205 days (Tempelman *et al.*, 2015). An alternative to standardising to one trait is to utilise all available feed intake records in the genetic analyses accounting for no genetic permanent cow effects by using a fixed regressions test-day model (Veerkamp *et al.*, 2014).

A second important element of the statistical approaches is to account for differences in the mean and variance of DMI. The most common method to account for mean differences in genetic analysis is to perform the analysis within contemporary group: comparing daughters of different sires within a group of herd mates that receive the same treatment. Well established REML techniques are common practices for this. Traditionally, contemporary groups are based on treatment and season of calving, however, feeding treatments within studies change over time, and also rations might change over time (i.e., all cows on that day get silage out of the same silage pit, independent of calving date). Therefore it is often wise to adjust for time-dependent contemporary groups. Also, differences between animals might be larger due to experimental treatment, herd, diet or lactation stage of recording. For this reason often heterogeneous residual variances across treatments, or herds were fitted. Tempelman *et al.* (2015) demonstrated also that nevertheless, care should be taken to allow for different relationships between DMI and for example, yield or live weight across environments.

A third important element of the statistical approaches is to assume that trait definitions vary across countries, and therefore fitting a multitrait model allowing for non- unity genetic correlations between countries. Although this might appear obvious, this is only possible when each country has enough data to estimate the genetic correlation with reasonable precision. Ideally this requires common sires between the environments, but using genomic relationships assists in establishing genetic links between the countries (Pryce *et al.*).

Altogether, a reasonable amount of statistics is required to merge DMI data and perform subsequent genetic analysis; however, the common experience is generally positive. Genetic correlations between countries are relatively large and genomic predictions across countries have higher reliabilities than using a smaller within country dataset (de Haas *et al.*, 2012 de Haas *et al.*, 2015; Tempelman *et al.*, 2015).

Recommendations when setting up data collection

Merging and sharing datasets will be part of the future reference population, but also new data might be collected. Based on the experiences with setting up the experiments, but also with analysing the existing data, we make the following recommendations.

What and how to record?

The minimal requirement for recording individual feed intake is the amount of fresh feed offered and refused per cow per day, with the associated dry matter percentage. Direct measurement of stalled cows is straightforward but contamination of refused feed by drinking water must be prevented. Automated systems have been developed by Calan Broadbent (American Calan Inc. Northwood, NH), Gallagher Animal Management Systems (Hamilton, New Zealand), GrowSafe 4000 System (GrowSafe Systems, Ltd., Airdrie, AB, Canada), and the RIC-system (Insentec B.V., Marknesse, The Netherlands). Each system has unique challenges. In each case, consideration must be given to minimize the amount of feed wasted or stolen. Sorting of feeds should also be minimized, especially in systems that use multiple cows per feeding station. All animals must have adequate space and time to eat an intake that is truly ad libitum and does not cause alterations in feeding behaviour. Measuring DMI for grazing cows is obviously even more difficult; however, there has been some success, notably in Ireland with the n-alkane technique (Dillon *et al.*, 1993, Mayes *et al.*, 1986).

In addition to recording feed intake, it seems obvious that the cow identification and pedigree must be recorded for genetic analysis. However, nutritional experiments often use their own anonymous local identification number for cows, which makes it hard to trace the cow back to a national pedigree register. Ideally a DNA, or a hair or blood sample, should be collected from each cow to allow subsequent genotyping.

Other traits that should be considered for weekly recording are: milk yield and composition, liveweight, and body condition score. These energy sink traits can be especially useful for feed intake records that are of short duration and might be related to temporary production records that are not representative of the whole lactation. The utilisation of feed intake records determines which traits to record. For example, for national breeding values for AI bulls, there is little extra information in recording milk yield on this limited number of cows. However, to establish the genetic correlation between yield and feed intake, it might be very useful to collect these extra records, or when a genomic prediction is to be developed for RFI. For RFI recording the energy sink traits are essential. Health and fertility traits should also be considered for examining relationships with both intake and production. Ration composition might be useful for understanding Genotype x Diet interactions or calculating energy or protein efficiency. As mentioned, the choice depends on the purpose of recording. However, sometimes extra records are recorded as insurance: records might be important in the future, and compared with recording feed intake, the costs are relatively small.

Bulls, cows or youngstock?

Recording on milking cows might be difficult, and practically it might be easier to record feed intake on young stock or bulls, and genetic correlations of these non-lactating animals with lactating animals were above 0.74 (Nieuwhof *et al.*, 1992) indicating that more than 50% of the genetic variation among lactating animals can be observed in the non-lactating animals. In Australia and New Zealand, RFI was calculated for growing heifers. The extremes (top and bottom 10%) were retained for a lactating cow experiment, where it was shown that divergence for RFI was maintained ($P<0.01$) (Macdonald *et al.*).

When feed intake records are available on bulls and cows, these can be combined in one reference population (Calus *et al.*, 2013). Hence, there is potential in recording the number of records combining cow and bull reference populations. There is still little information on the optimal design for recording feed intake, and probably genetic parameters are not accurate enough yet, to do precise index calculations.

Which and how many cows?

When starting to collect feed intake records, an important question is how to optimize the "number of gate-days per year" by "number of cows x recording period per cow"? The number of cows can be established by the theoretical prediction from Deatwyler *et al.* (2008). The actual accuracy obtained with cross validation when records were used within country follows this pattern closely (Figure 1). In this example, actual accuracies were slightly higher than theoretical, likely because validation and training animals were closely related. Overall it is clear that thousands of cows need to be recorded to obtain accurate prediction equations.

To increase the accuracy, it is important that feed intake records should be collected on animals as closely related to the selection candidates as possible. The large genetic distance between historical data and current selection candidates is therefore a disadvantage.

Also, is the genetic connectedness between contemporary groups, through common sires, is important to separate the permanent environmental and genetic effects in the data. With many small nutritional experiments this could be a problem.

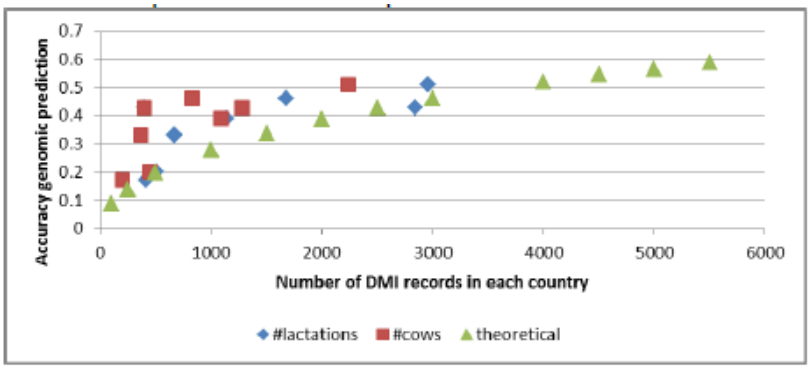

Figure 1 Accuracy of genomic prediction based on theoretical prediction (Daetwyler et al.*, 2008), and obtained by the gDMI analysis (De Haas et al., 2015), using information in each country alone. Using either #lactations or #cows available in each country as reference.*

When to record feed intake during lactation?

Ideally feed intake should be measured across the lifetime of an animal. This is not realistic and often only short periods of recording are available. In lactating animals it might be of particular importance to consider the period that feed intake is measured. Cows might compensate a more negative energy balance in early lactation by a higher intake during late lactation. Hence, biological feed intake might be a different trait during different parts of the lactation, which is supported by the relatively low genetic correlation between DMI during early and late lactation (Berry *et al.*, 2007; Buttchereit *et al.*, 2011; Coffey *et al.*, 2001; Koenen and Veerkamp, 1998; Li *et al.*, 2014; Manzanilla Pech *et al.*, 2014b; Spurlock *et al.*, 2012, Veerkamp and Thompson, 1999). One way to overcome this bias due to tissue mobilisation might be to use RFI, which is adjusted for energy sinks. Hence, in terms of improving feed efficiency across the whole lactation, it seems necessary to have feed intake records available during all stages of lactation, rather than focus collection on the first part of the lactation alone, as most designed experiment have done.

The question on when to record feed intake can also be approached from the quantitative genetics perspective using selection index methodology. Genetic parameters can be used to estimate the accuracy of DMI breeding values across the whole lactation, when only part lactation is recorded (Manzanilla Pech *et al.*, 2014a). These authors concluded that recording DMI for 15 weeks gave an accuracy of 0.58, which was on average 0.25 more accurate than recording DMI for 5 weeks, and 0.11 more accurate than recording DMI for 10 weeks. Also, starting to record DMI in mid or late lactation gave more accurate estimates for predicting lactation DMI than starting recording in early lactation (Manzanilla Pech *et al.*, 2014a). Still, more reliable estimates for genetic correlations between feed intake measurements across lactation are required to define more precisely when to record DMI.

If feed intake is measured as part of a comprehensive analysis of feed efficiency examining all energy sinks and calculating RFI, then the time and duration to record feed intake can be shortened and conducted earlier in lactation. Connor *et al.* (2013) found that correlations for weekly RFI across weeks, even as early as 4 wk, were high (r=0.8) and that the heritability of RFI was similar (h2=0.45) whether only the first 50 DIM or the first 100 DIM were considered; heritability for earlier assessments of RFI were lower.

What feeding system to apply?

The diet fed to the cows should be balanced to meet requirements for protein, minerals, and vitamins, and feeding a well-mixed TMR using silages or other wet feeds is likely to minimize sorting. If the feed is dry, such as a dry cubed feed, it can be important to measure the %DM in the refused feed separately.

Common practise is that the diet is fed ad libitum, but there is little known about the effects of not doing so. The diet should be comparable to that fed to commercial herds, representative of the average for a country. This is not always easy for a diverse country like the USA, where diets may differ markedly by region. RFI might then be useful, as this can be calculated within contemporary group (Tempelman *et al.*, 2015) which makes the composition of the diet less important. A high correlation of RFI was obtained when a cow was fed a high starch or low starch diet (Burczynski *et al.*, 2015, in press). However, it is clear that feeding a diet formulated according to level of production leads to bias; this would unfairly result in feeding a more digestible diet to the high producers and also might increase the correlation between DMI and milk yield. Perhaps the most important criterion is that diet must be the same for all cows that are in the same contemporary group, and contemporary groups should be sufficiently large (> 5 animals) and genetically connected through common (grand-)sires.

Genotyping and imputation?

One of the issues with combining data from research herds for genomic analysis is that different SNP chips may be used for each experiment. Fortunately, most of the commercially available SNP chips have many SNP in common, so a set of common SNPs can generally be identified. Another option is to impute genotypes from 50K to high density (HD), which may be advantageous for some (Bayesian) approaches to genomic prediction. This relies on a reference dataset of bulls or cows that are genotyped at high density and that have some genetic ties (i.e. haplotypes in common) with the animals in the dataset that is to be imputed from low density to HD. Pryce *et al.* (2014) showed that it was possible to impute the genotypes of research herd animals from 50K to HD using two independent reference datasets with high concordance. For animals with historical feed intake records, but no DNA information, imputation of the genotypes might be considered (Bouwman *et al.*, 2014; Pimentel *et al.*, 2013), when offspring were genotyped.

Conclusion

To implement genomic prediction and perform genetic analysis for feed intake, the "use what we have"-approach will be important for the foreseeable future. Based on this experience we were able to provide some initial guidelines on the recording of feed intake records.

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Maximizing genetic progress in the new age of genomics

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Abstract

Genetics have historically played a minor role in day-to-day herd management when compared to nutrition, udder health and reproduction. Genetic progress for most US dairies consisted of selecting AI sires that might improve the herd's main deficiencies, like production, feet and legs or udder composite. Culling low genetic merit cows was not an option because most dairies had insufficient heifer inventories to replace the low genetic value animals while maintaining herd size.

Modern technology offers a growing list of options when it comes to genetics decision making. With the introduction of genomic testing and sexed semen, managing herd genetics is no longer a minor part of the day-to-day herd management. With the variety of tools available, producers have to ask the question; am I maximizing genetic progress while managing inbreeding? AgSource provides four tools to assist producers with their genetic program decisions.

Keywords: decision aid, herd analysis, benchmarking, genetic progress, inbreeding.

Introduction

Introduced in 2014, the Genetic Summary Report (GSR) is a four-page analytical tool that features 13 different analyses focused on maximizing genetic performance while minimizing inbreeding. Among the many features, the report provides a comparison of the current herd genetics against AgSource's 80th percentile active cows and heifers, a genetic progress trend graph by year of birth, herd average genetic values by testday for cows and service sires, youngstock genetic analysis, and a performance analysis of the herd's top 12 bulls based on number of daughters. The GSR highlights many benchmarks, allowing the producer to measure how well the herd is doing compared to other herds.

The AgSource Genetic Selection Guide (GSG) reports provide producers with the power to maximize the future genetics in the herd using both genotypic and phenotypic information to make replacement, breeding and genomic testing decisions. The Genetic Selection Guide uses Net Merit$ (NM$), which is the most widely accepted US measure of a cow or heifer's genotypic ability to produce milk over a lifetime.

Materials and methods

To make the most informed decisions, producers have turned to genomic testing of newborn animals and are making more use of genetic information on cows and sires today to assist in the selection of animals for sale and breeding purposes. Decision support tools provided by DHI, AI companies and providers of genomic testing are geared toward helping producers

make the most profitable decisions, however to ensure the best decisions are being made, one should closely monitor the results and determine if the desired results are actually accomplished. Below, we will take a look at how the AgSource Genetic Summary Report and Genetic Selection Guide can provide dairy producers with an analysis and decision making tool to maximize genetic progress in the herd.

Results

Although we cannot cover all the analyses provided in the Genetic Summary Report, there are six major areas to consider:

- Summary of genetic traits for the current herd
- Trends of genetics by year of birth
- Trends of genetic traits for the herd by test date
- Analysis of phenotypic data as it relates to genetic information
- Inbreeding analysis and predominant genetics in the herd
- Trends of future genetics by evaluating genetic traits for service sires and young stock

Summary of genetic traits for the current herd

When reviewing the genetics in the herd, the first step is to review if the genetics of the cows and heifers currently in the herd are in line with other cows and heifers in the breed. To accomplish this, the GSR provides an overall snapshot of the cows and heifers in the herd and benchmarks the genetics and inbreeding values against animals of the same breed. Figure 1 shows an example of a Holstein herd with good genetics and shows that for most traits, the herd ranks between the 50th and 80th percentile compared to all other Holstein cows. For example, the NM$ average for cows is 127 NM$, which ranks them mid-way between the 50th and the 80th percentile cows, which is 170 NM$. Although the herd is doing well, there still is great potential for improvement. The average NM$ value of the top 80th percentile is 246 NM$, indicating there is significant room for improvement. Producers can review various traits and compare how they rank. In addition to the genetic

A Genetic Summary - Active Cows & Youngstock

	Cows					Youngstock				
		Percentile					Percentile			
	Your Herd	20th	50th	80th	Avg 80th	Your Herd	20th	50th	80th	Avg 80th
Number	2595		398010			2187		364170		
NM$	127	-67	54	170	246	273	48	175	294	370
CM$	128	-70	56	177	257	281	50	181	305	384
FM$	124	-65	49	159	231	255	40	160	272	344
PTA Milk	246	-372	34	444	722	472	-121	246	600	842
PTA Fat	12	-14	2	18	29	26	-1	14	28	38
PTA Fat %	0.01	-0.06	0.00	0.07	0.12	0.03	-0.04	0.02	0.08	0.11
PTA Pro	7	-9	2	12	20	17	0	10	20	26
PTA Pro %	0.00	-0.02	0.00	0.03	0.05	0.01	-0.02	0.01	0.04	0.05
PTA SCS	2.96	3.07	2.96	2.87	2.81	2.90	3.02	2.93	2.84	2.78
PTA PL	1.2	-0.9	0.5	2.0	2.9	2.3	-0.1	1.5	3.0	3.9
PTA DPR	0.2	-0.8	0.4	1.5	2.3	0.5	-0.4	0.6	1.7	2.5
Avg Inbred %	6.0		5.6			6.5		5.9		
Avg Fut Inbred %	6.2		6.0			6.5		6.3		

Figure 1. Current herd inventory genetic summary.

values, the inbreeding percentage is listed and, in the case of this herd, the herd inbreeding percentage has been higher than the average Holstein cows and heifers (6.0% cows and 6.5% for heifers) compared to all other cows and heifers (5.5% for cows and 5.8% for heifers) The genomic inbreeding percent is close to the inbreeding percent, based on pedigree.

Trend of genetics by year of birth

In addition to the current snapshot of the cows and heifers, the GSR provides a graphical breakdown of animals currently in the herd by year of birth. Annual averages are compared against AgSource averages by year of birth. These graphs allow the producer to look at trends for certain traits within the herd and compare these with other herds of the same breed. Figure 2 shows an example of the inbreeding trend (based on pedigree and genomic testing) within the herd compared to the inbreeding trend in US Holsteins.

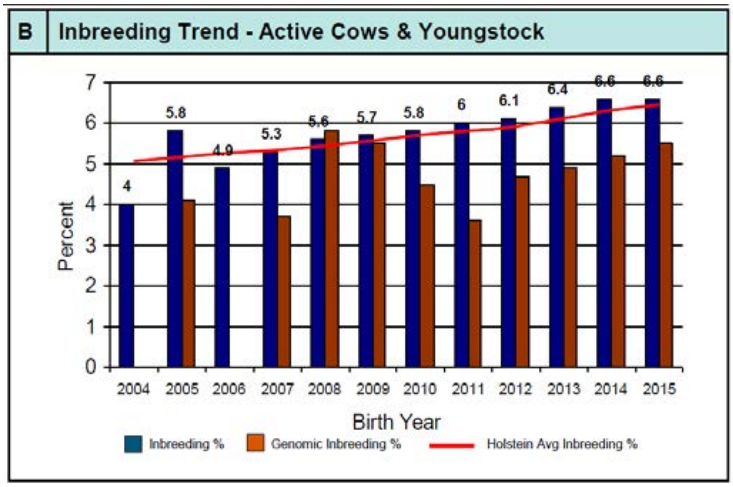


Figure 2. Inbreeding trend graph.

Trends of genetic traits for the herd by test date

As herd inventories continually change, reviewing how the genetics of the herd compare to prior months, the GSR provides graphs showing individual traits for the cows in the milking herd over a two year period. These graphs display the herd's and the 80th percentile herds' trend. Figure 3 shows an example of the NM$ trend. The drop in the graph was due to the US base change that took place in December of 2014. The genetics of

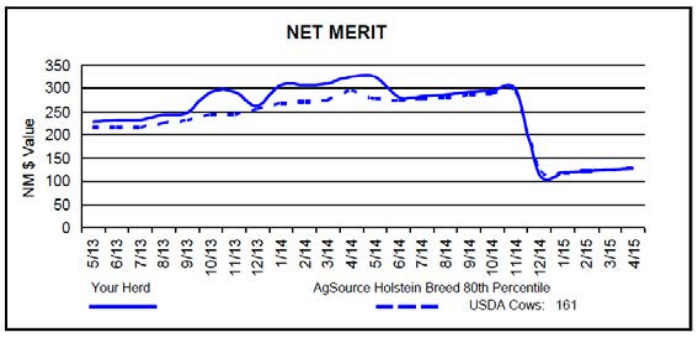


Figure 3. Net merit $ historic trend diagram.

the current herd, coupled with the history on some of the traits, will describe the current situation, plus it will tell you if the herd has been making progress at at a rate comparable to the top 80th percentile herds.

Analysis of phenotypic data as it relates to genetic information

Genetics play an important role in achieving higher production levels, but also in reducing the number of cows with udder health and fertility problems. Commercial producers question how much value genetics truly bring to the table relative to other management practices in which they can invest. Taking a look at how cows of different genetic levels perform in the herd can shine a light on what the opportunities are within the herd. Figure 4 provides a GSR analysis showing a breakdown of the milking herd in four NM$ quartiles. For each quartile we take a look at the phenotypic data. For the example herd, investing money in better genetics is showing a significant payoff in terms of higher production and healthier cows.

Based on both the genetic and phenotypic data, producers can make decisions as to what type of genetics they wish to invest in and monitor the payback.

H Genetic and Phenotypic Trend by NM$ Quartile - Active Cows

Quartile	Num Cows	NM $	CM $	PTA Milk	PTA Fat	PTA Pro	PTA SCS	PTA DPR	ME Milk	ME Fat	ME Pro	LSSCC	Days Open	TCI©
1	627	308	313	604	30	19	2.91	0.6	33631	1321	1008	1.8	135	187
2	626	173	177	305	16	10	2.94	0.4	32974	1277	994	2.0	135	228
3	626	84	85	173	8	5	2.98	0.1	32527	1225	976	2.1	133	142
4	626	-34	-38	-40	-4	-3	3.01	-0.2	31760	1175	944	2.4	146	-12

Figure 4. Genetic and phenotypic trend.

Evaluate how well your inbreeding management program is working

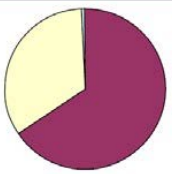
An area that is becoming of greater concern is inbreeding. As dairy cows within each breed have become more related, inbreeding has been steadily increasing. Most US dairy producers rely on mating software provided through an AI company to manage their inbreeding levels. Inbreeding levels are generally taken into account as part of the mating recommendation. The one thing to consider is that a mating recommendation is just that; a "recommendation".

The key is that the recommended sires are actually the ones that are used. Mistakes can happen during the breeding process, but also when semen inventories are running low other bulls may get used. To make sure producers have a handle on how well the mating program and the actual breeding process is working, it is key to evaluate on a regular

I Most Prevalent Genes - Top Sires based on Cows and Youngstock

Sire Name	Sire NAAB	Total Genes	# Daughters	# PG Daughters	# MG Daughters
PLANET	007HO08081	155.25	80	314	147
SHOTTLE	029HO12209	96.75	5	368	9
O MAN	007HO06417	92.25	3	338	25
GOLDWYN	200HO03205	89.25	1	350	5
SHAMROCK	007HO10849	69.75	93	66	27
SUPER	001HO08778	69.25	25	198	29
CROWN	007HO09321	62.50	93	0	64
ROBUST	007HO10524	60.25	22	191	6
MAYFIELD	007HO11283	59.75	112	0	15
MAN-O-MAN	014HO04929	58.25	6	213	8
BOLTON	029HO11111	58.25	9	172	43
SHOT	007HO09222	49.25	80	0	37

J Inbreeding Distribution - Active Cows and Youngstock



Top Inbreed %

Name	Inb %
9704	29.8
15495	28.8
14090	28.5
14632	18.7
15832	17.5
15893	17.3
15892	17.3
13997	17.3
13916	17.1
15057	14.4

Holstein Distribution	<3.12%	3.12 - 6.25%	6.25 - 12.4%	≥12.5%
Your Herd		65.3	34.3	0.4
AgSource	2.1	71.4	26.1	0.4

Figure 5, Most prevalent genes and inbreeding distribution.

basis how well the program is truly working. The GSR provides an analysis that looks at the current herd's distribution of percent cows inbred by different categories. Figure 5 shows the inbreeding distribution and predominant sire genes of the example herd.

In the example, there are no cows with an inbreeding percent below 3.12% (low inbreeding). However, there are 34.3% of animals with medium-high inbreeding levels (6.25-12.4%). Other AgSource herds have a lower percentage (26.1%) of cows with similar inbreeding levels. Closer attention should be paid to avoid the medium-high inbreeding levels in the herd. This can be as simple as making certain mating recommendations are followed, or making a change in the mating program settings to ensure higher inbreeding levels are avoided. One other possibility is to look for the predominant lines of genetics in the herd and find some AI sires that are of equal genetic merit, but less related to the animals in the herd.

Trends of future genetics by evaluating genetic traits for service sires and young stock

While the genetics of the cows and heifers in the herd cannot be changed, new genetics that are being brought into the herd should be selected based on their ability to improve the herd. The GSR provides graphs comparing the genetics of the service sires used against AgSource 80th percentile herds of the same breed. Figure 6 shows an example representing PTA DPR (Daughter Pregnancy Rate) and PTA PL (Productive Life) for service sires used and the comparison against 80th percentile Holstein herds for the same trait. The key for the producer is to look for those traits he considers important and make sure acceptable levels of progress are being made against each.

Evaluating the genetics of the calves and heifers in the herd is an important aspect for those producers who have low involuntary culling rates and can cull more heavily based on production or other management areas they wish to improve upon. Knowing how many heifers and what genetics are available, compared to the cows currently in the milking herd, will point at the amount of genetic progress that can be made replacing a milking cow with a heifer.

Genetic selection guide

To aid in the decision making process of which cows and heifers to breed to sexed semen, conventional semen, or possibly beef semen, the AgSource Genetic Selection Guide provides a tool that allows producers to find the animals in the cow and heifer population based on their overall genetic merit. The Genetic Selection Guide is generated for cows, young stock and unborn progeny. Animals are ranked by Net Merit $ value and broken up into four NM$ quartile groups. Producers can quickly identify the animals in the herd

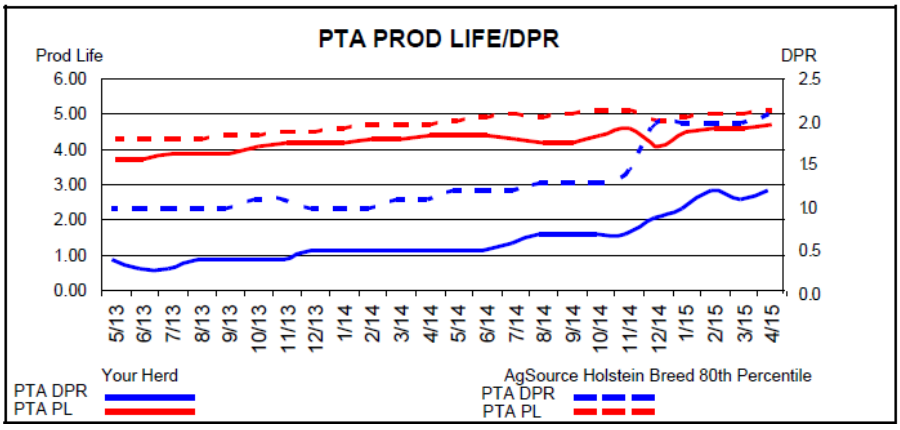
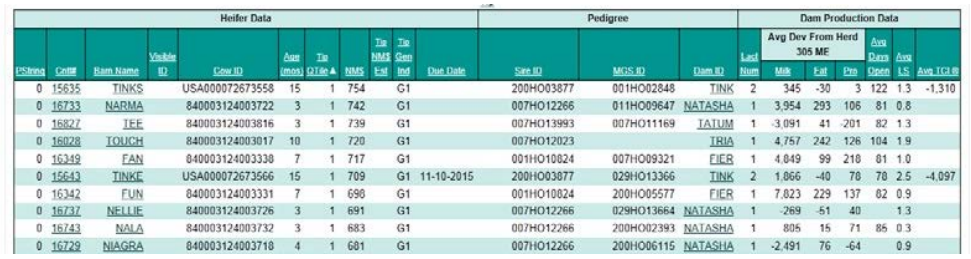


Figure 6. Future genetics in the herd.

with the highest and lowest genetic values. Animals that were genomically tested are marked on the report. Figure 7 shows an example of a Genetic Selection Guide for cows listing top quartile animals.

The Genetic Selection Guide for progeny provides a tool that will allow producers to determine the genetic merit of calves prior to birth. Knowing a calf's genetic merit at birth aids in the decision making process of which calves to keep and which to sell.



Heifer Data											Pedigree			Dam Production Data					
PString	Cntl#	Barn Name	Visible ID	Cow ID	Age (mos)	Tip QTile ▲	NMS	Tip NMS Est	Tip Gen Ind	Due Date	Sire ID	MGS ID	Dam ID	Lact Num	Avg Dev From Herd 305 ME Milk	Fat	Pro	Avg Days Open	Avg LS	Avg TCI ®
0	15635	TINKS		USA000072673558	15	1	754		G1		200HO03877	001HO02848	TINK	2	345	-30	3	122	1.3	-1,310
0	16733	NARMA		840003124003722	3	1	742		G1		007HO12266	011HO09647	NATASHA	1	3,954	293	106	81	0.8	
0	16827	TEE		840003124003816	3	1	739		G1		007HO13993	007HO11169	TATUM	1	-3,091	41	-201	82	1.3	
0	16028	TOUCH		840003124003017	10	1	720		G1		007HO12023		TRIA	1	4,757	242	126	104	1.9	
0	16349	FAN		840003124003338	7	1	717		G1		001HO10824	007HO09321	FIER	1	4,849	99	218	81	1.0	
0	15643	TINKE		USA000072673566	15	1	709		G1	11-10-2015	200HO03877	029HO13366	TINK	2	1,866	-40	78	78	2.5	-4,097
0	16342	FUN		840003124003331	7	1	698		G1		001HO10824	200HO05577	FIER	1	7,823	229	137	82	0.9	
0	16737	NELLIE		840003124003726	3	1	691		G1		007HO12266	029HO13664	NATASHA	1	-269	-51	40		1.3	
0	16743	NALA		840003124003732	3	1	683		G1		007HO12266	200HO02393	NATASHA	1	805	15	71	86	0.3	
0	16729	NIAGRA		840003124003718	4	1	681		G1		007HO12266	200HO06115	NATASHA	1	-2,491	76	-64		0.9	

Figure 7. Genetic selection guide for cows.

Conclusion

Evaluating sire selection criteria and breeding decisions should be an annual task. The Genetic Summary Report and Genetic Selection Guide provide two tools that provide a full picture of past, current and estimation of future genetics in the herd. A successful genetic management program is based on having good analysis information available and it all starts with accurate identification of the animal itself as well as the sire and dam of the animal. Evaluating the overall genetic program allows producers to make informed decisions about the criteria by which AI sires are selected, mating decision are made, sexed and / or beef semen is used, and finally how culling decisions are made.

Session 6

Certificate of Quality Auditors' Workshop

Data quality for management purposes and genetic evaluation

F. Reinhardt

The session consisted of only one presentation that was followed by an interactive questions, answers and comments session.

During the presentation a good overview was provided of the current purpose and situation in the animal data recording industry, and also a perspective was given of the possible future needs in terms of recorded data and the application of such data. It was postulated that the industry will probably move from a situation where 'the phenotype is king' to a scenario where 'he who owns and knows the data (phenotypes) is the real king'.

The future needs of a significant section of the role players in the industry are for higher quality data that will inevitably cost more and will have to be used more purposefully. A likely scenario could be that:

- 'Big data' with indifferent / undefined quality would probably only be used for on-farm management purposes; and
- 'Focused data' of high quality will be used in special ways for the genetic improvement of animal populations.

These circumstances will require special attention from ICAR, as an organisation, and from each individual member of ICAR, in many respects.

It was concluded that fully integrated data systems and applicable / modern communication technologies are essential components of successful animal recording in the future. Both phenotypes and genotypes will be important, for both management and breeding purposes, and new traits and unquestionable data quality will be critical components of a successful future scenario.

The presented material was discussed lively by the attendees, who mostly supported the ideas propagated in the presentation.