Breeding for health using producer recorded data in Canadian Holsteins

A. Koeck[1], F. Miglior[2,3], D. F. Kelton[4], and F. S. Schenkel[1]
[1]CGIL, Department of Animal and Poultry Science, University of Guelph, Guelph, ON
[2]Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, ON
[3]Canadian Dairy Network, Guelph, ON
[4]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON

INTRODUCTION

Health traits are of increasing importance to dairy producers. In the Scandinavian countries, direct selection for improved disease resistance has been carried out for more than 30 years (Philipsson and Lindhé, 2003). In these countries, veterinary treatments are recorded, as all treatments involving antibiotics and hormones have to be made primarily by a veterinarian. As veterinarians have extensive knowledge in disease diagnoses, a large number of different health disorders are recorded, e.g. the Norwegian disease code includes 67 different diagnoses (Østerås et al., 2007). Recently a similar disease recording system has been established in Austria (Egger-Danner et al., 2011).
In Canada, a national dairy cattle health and disease data management system was started in 2007. In contrast to the Scandinavian approach, recording is done by producers, as producers are allowed to initiate treatments using antibiotics or hormones. Eight specific diseases that are known to affect herd profitability are recorded by producers on a voluntary basis: mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovarian disease and lameness. Producers were provided with disease definitions, adapted from work by Kelton et al. (1998), as a guide for identification and recording of the eight disorders. Health data is recorded by producers using on-farm herd management software (e.g. Dairy Comp, Agri-Lacta) or record books. Data are collected by milk recording technicians at each test day herd visit and forwarded to the Canadian Dairy Herd Improvement (**DHI**) database. Besides, health data from producers participating in the "Dossier Santé Animale/Animal Health Record" (**DS@HR**) program is collected and forwarded to the DHI database by their veterinarians. In 2010, about 30% of all recorded health events originated from on-farm herd management software, 30% from record books and 40% from the DS@HR program.
The objective of this study was to investigate if health data recorded by Canadian dairy producer can be used for genetic evaluations. The specific objectives were to 1) analyze data quality, 2) calculate disease frequencies and, 3) estimate heritabilities and genetic correlations among health disorders.

MATERIALS AND METHODS

Data

Database. Health data from April 1, 2007 to April 20, 2011 were obtained from the Canadian Dairy Network (Guelph, Ontario). An overview about the entire database available is given in Table 1. The database consisted of 384,524 health events from 187,592 cows, of which 95.4% were from Holstein, 2.4% from Ayrshire and 1.7% from Jersey. A total of 5,723 herds were represented. Recording of mastitis was done in the majority of herds (89%), followed by

displaced abomasum (63%) and retained placenta (58%). Only 16% of herds had records for all eight health categories.
The number of reported health events per year and month increased constantly (Figure 1). Currently, participating herds are submitting an average of 11,000 health events per month. The decrease in the number of records at the end of the period is caused by a delay in data delivery. In contrast, the total number of herds recording health data remained almost unchanged over the years (Figure 2). In 2010, a total of 4,071 herds recorded health data, which represents about 40 % of all herds enrolled on DHI in Canada.

Data Validation and Editing. In order to ensure that all cows were from herds with reliable health recording several measures were applied separately for each disease. Only herds having at least two records of the disease being analyzed were considered. The first and last record had to be at least 180 d distant to remove herds which had done recording just for a short time period. In addition, minimum disease frequencies were applied to ensure continuous data recording within individual herds. Minimum frequencies (reported cases per herd and year) were 5% for mastitis and 1% for the other diseases. Between 40 to 60% of all herds had to be excluded by editing procedures for each trait.
Holstein is the most common dairy cattle breed in Canada (constituting up to 90 % of the dairy cows) and therefore, almost all health records were from Holstein cows. For this reason, genetic analyses were carried out for this breed only. Only records from first lactation cows with an age between 19 and 43 months were considered.

Trait Definition. Health disorders were defined as binary traits (0 = no treatment, 1 = treatment) based on whether or not the cow had at least one treatment recorded within the first 14 d after calving for retained placenta, within 100 d after calving for ketosis, within 150 d after calving for metritis, acute metritis, purulent discharge, endometritis, chronic metritis, and within 305 d after calving for mastitis, displaced abomasum, cystic ovaries and lameness. The trait metritis included all cases for acute metritis, purulent discharge, endometritis and chronic metritis. The trait lameness also included cases for foot rot, laminitis, sole ulcer etc., as these disorders are causes of lameness. The traits foot rot, laminitis, sole ulcer etc. were not analyzed separately because they were only recorded in a limited number of herds. Milk fever had a very low incidence in first lactation cows (0.20 %), and was therefore not considered in the analyses. Summary statistics of the analyzed data is given in Table 2.

Pedigree. The animal pedigree file was generated by tracing the pedigrees of cows with data 7 generations back and contained the relationship of 566,088 animals.

Model

For genetic analyses, bivariate linear animal models were fit using the AI-REML procedure in the DMU package (Madsen and Jensen, 2008). Bivariate analyses were performed among 1) acute metritis, purulent discharge, endometritis and chronic metritis, and 2) mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries and lameness. The model used was as follows:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Z_h h} + \mathbf{Z_a a} + \mathbf{e}$$

where $\mathbf{y}$ is a vector of observations for the two disease traits considered ; $\boldsymbol{\beta}$ is a vector of systematic effects, including fixed effects of age at calving and year-season of calving; $\mathbf{h}$ is a

vector of random herd-year of calving effects; **a** is a vector of random animal effects; **e** is a vector of random residuals; and $\mathbf{X}$, $\mathbf{Z_h}$, and $\mathbf{Z_a}$ are the corresponding incidence matrices. Random effects were assumed to be normally distributed with zero means and the covariance structure was:

$$\mathbf{Var}\begin{bmatrix}\mathbf{h}\\ \mathbf{a}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{H}_0 \otimes \mathbf{I} & 0 & 0\\ & \mathbf{G}_0 \otimes \mathbf{A} & 0\\ \mathbf{symm.} & & \mathbf{R}_0 \otimes \mathbf{I}\end{bmatrix},$$

where $\mathbf{H}_0 = \begin{bmatrix}\sigma^2_{\mathrm{h1}} & \sigma_{\mathrm{h1h2}}\\ \sigma_{\mathrm{h1h2}} & \sigma^2_{\mathrm{h2}}\end{bmatrix}$ is the (co)variance matrix between traits due to herd-year of calving effects; $\mathbf{I}$ is an identity matrix; $\mathbf{G}_0 = \begin{bmatrix}\sigma^2_{\mathbf{a1}} & \sigma_{\mathbf{a1a2}}\\ \sigma_{\mathbf{a1a2}} & \sigma^2_{\mathbf{a2}}\end{bmatrix}$ is the (co)variance matrix between traits due to animal additive genetic effects; $\mathbf{A}$ is the additive genetic relationship matrix; and $\mathbf{R}_0 = \begin{bmatrix}\sigma^2_{\mathbf{e1}} & \sigma_{\mathbf{e1e2}}\\ \sigma_{\mathbf{e1e2}} & \sigma^2_{\mathbf{e2}}\end{bmatrix}$ is the (co)variance matrix between traits due to residual effects.

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

Heritability estimates were calculated as the mean estimate from all bivariate analyses for each trait.

RESULTS AND DISCUSSION

Participation and Data Quality

In 2010, about 4,000 herds recorded health data, which accounts for 40 % of all herds under milk recording in Canada. A similar participation has been achieved in the newly established health monitoring system in Austria (Egger-Danner et al., 2011). By February 2011, 64% of all dairy herds participated in the Austrian health monitoring system, however only 62% of these herds recorded health data (Egger-Danner et al., 2011). This means that in 40% of all Austrian dairy herds health data is actually recorded.

In the present study between 40 to 60% of all herds had to be omitted by editing procedures for each trait. This was expected as the recording system is relatively new. Similar values were reported in previous studies. Pryce et al. (1997) discarded 42% of all herds during editing procedures based on health data from the UK. Using producer recorded health data from the US, Zwald et al. (2004a) excluded 17 % (for displaced abomasum) to 64 % (for lameness) of all herds, assuming unreliable documentation and recording. A better data quality was reported by Egger-Danner et al. (2011) based on Austrian health data, where presently about 27% of all farms recording health data do not meet the validation requirements.

Disease Occurrence

Figure 3 shows the distribution of first occurrence of each disorder according to days after calving in first lactation Holstein cows. A high proportion (35%) of mastitis cases occurred in the first month of lactation, whereas the remaining cases were equally distributed across lactation. Almost all cases of ketosis (99%) and displaced abomasum (91%) occurred during the first 100 d of lactation. Cases of retained placenta, acute metritis, purulent discharge, endometritis and chronic metritis were concentrated around calving, whereas cases of cystic ovaries were reported mainly during the breeding period. Cases of lameness were more evenly distributed throughout the lactation, with slightly more cases in early lactation.

Disease Frequencies

Mean disease frequencies after editing were 12.6, 3.7, 4.5, 4.6, 10.8, 8.2, and 9.2% for mastitis, displaced abomasum, ketosis, retained placenta, metritis (including acute metritis, purulent discharge, endometritis and chronic metritis), cystic ovaries and lameness (including foot rot, laminitis, sole ulcer etc.), respectively (Table 2). Kelton et al. (1998) conducted a literature review and found similar disease frequencies across studies: 14.2% for mastitis, 1.7% for displaced abomasum, 4.8% for ketosis, 8.6% for retained placenta, 10.1% for metritis, 8.0% for cystic ovaries, and 7.0% for lameness. In a more recent study in US Holstein cows, Zwald et al. (2004a) reported higher frequencies for mastitis (20%), ketosis (10%) and metritis (including retained placenta, 21%), whereas frequencies for displaced abomasum (3%), cystic ovaries (8%) and lameness (10%) were in agreement with our study.

Genetic Parameters

Heritability estimates for acute metritis, purulent discharge, endometritis and chronic metritis were 0.01, 0.03, 0.02 and 0.01, respectively (Table 3). Genetic correlations among these traits were almost one, except between acute metritis and endometritis that showed a lower genetic correlation of 0.76. The result may imply that dairy producers partly did not distinguish precisely between these traits. Therefore, in the subsequent analyses acute metritis, purulent discharge, endometritis and chronic metritis were considered as one trait (metritis).

Heritabilities for mastitis, displaced abomasum, ketosis, retained placenta, metritis, cystic ovaries and lameness were 0.02, 0.06, 0.03, 0.03, 0.02, 0.03 and 0.01, respectively (Table 4). These estimates are in the range of previous studies using linear models. In UK Holstein cows, Kadarmideen et al. (2000) obtained heritabilities of 0.04, 0.02, 0.004, 0.01 and 0.01 for mastitis, lameness, tetany, ketosis and milk fever, respectively. Dechow et al. (2004) reported heritability estimates in the range of 0.005 for reproductive disorders to 0.08 for displaced abomasum.

Genetic correlations among health disorders are given in Table 4. The strongest genetic correlations were found between displaced abomasum and ketosis (0.64) and retained placenta and metritis (0.62). Noticeable estimates were also found between mastitis and ketosis (0.36), mastitis and retained placenta (0.29), mastitis and lameness (0.49), displaced abomasum and metritis (0.44), displaced abomasum and lameness (0.31), and ketosis and metritis (0.32). Zwald et al. (2004b) obtained genetic correlations in the range of -0.01 (between mastitis and metritis) to 0.45 (between displaced abomasum and ketosis) among various health disorders. Low to moderate genetic correlations from -0.10 to 0.40 among mastitis, ketosis, milk fever and retained placenta were reported by Heringstad et al. (2005). Analyzing fertility disorders in first lactation Norwegian Red cows, Heringstad (2010) found

also a high positive genetic correlation of 0.64 between metritis and retained placenta. However, in contrast to our results, a significant negative genetic correlation of -0.26 was estimated between retained placenta and cystic ovaries.
In the present study, all genetic correlations between diseases that could be considered different from zero were positive. This is also consistent with the results from a selection experiment with Norwegian Red cows, where it was shown that selection against mastitis leads to favorable correlated selection responses in other diseases, like ketosis and retained placenta (Heringstad et al. 2007). These results indicate the existence of a general immune response. In a recent study by DeLaPaz (2008) it was found that cows with both high antibody and cell-mediated immune response have a decreased risk of disease occurrence for several diseases, including mastitis, ketosis, metritis and retained placenta, compared to cows identified as low responders.

Implementation in Routine Genetic Evaluation

Mastitis is the main recorded disease and thus the most promising trait to be included in routine genetic evaluation. The other diseases are not as widely recorded. Besides, the frequencies of some other diseases are rather low, as, for example, for displaced abomasum and ketosis. Therefore, combing them into a single trait (metabolic disorders) in genetic evaluations could be an option. The reasonable high genetic association between these traits would also justify this approach. In the Scandinavian countries the routine genetic evaluation of health traits is based on composite traits rather than on single traits (Interbull, 2011). A more general disease definition leads to higher frequencies and possibly to more accurately estimated breeding values. However, as not all herds that record displaced abomasum also record ketosis and vice versa, this approach might be difficult to implement.

CONCLUSIONS

The present study showed the potential use of producer-recorded health data from Canada for genetic evaluations. Although, about 40 % of all Canadian dairy producers participate in the health recording system, a lot of data is lost during data validation. Thus, dairy producers should be encouraged to keep accurate and complete health data. Mastitis, one of the most frequent and costly diseases of dairy cattle, is the most promising trait to be included in routine genetic evaluation.

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REFERENCES

Dechow, C. D., G. W. Rogers, U. Sander-Nielsen, L. Kiel, T. J. Lawlor, J. S. Clay, A. E. Freeman, G. Abdel-Azim, A. Kuck, and S. Schnell. 2004. Correlations among body

conditions scores from various sources, dairy form, and cow health from the United States and Denmark. J. Dairy Sci. 87:3526-3533.
DeLaPaz, J. M. 2008. Using humoral and cellular response to novel antigens in periparturient dairy cows as a measure of genetic disease resistance in dairy cows. MSc Thesis. University of Florida, Gainesville.
Egger-Danner C., et al. 2011. Registration of direct health traits in Austria – Experience review with emphasis on aspects of availability for breeding purposes. Manuscript in preparation.
Heringstad, B., Y. M. Chang, D. Gianola, and G. Klemetsdal. 2005. Genetic analysis of clinical mastitis, milk fever, ketosis, and retained placenta in three lactations of Norwegian Red cows. J. Dairy Sci. 88:3273-3281.
Heringstad, B., G. Klemetsdal, and T. Steine. 2007. Selection responses for disease resistance in two selection experiments with Norwegian Red cows. J. Dairy Sci. 90:2419-2426.
Heringstad, B. 2010. Genetic analysis of fertility-related diseases and disorders in Norwegian Red cows. J. Dairy Sci. 93:2751-2756.
Interbull 2011. Description of national genetic evaluation systems for dairy cattle traits as practiced in different Interbull member countries. http://www-interbull.slu.se/national_ges_info2/framesida-ges.htm. Accessed August 8, 2011.
Kadarmideen, H. N., R. Thompson, and G. Simm. 2000. Linear and threshold model genetic parameters for disease, fertility and milk production in dairy cattle. Anim. Sci. 71:411-419.
Kelton, D. F., K. D. Lissemore, and R. E. Martin. 1998. Recommendations for recording and calculating the incidence of selected clinical diseases of dairy cattle. J. Dairy Sci. 81:2502-2509.
Madsen, P., and J. Jensen. 2008. An User's Guide to DMU. A package for analyzing multivariate mixed models. Version 6, release 4.7. Danish Institute of Agricultural Sciences, Tjele, Denmark.
Østerås, O., H. Solbu, A. O Refsdal, T. Roalkvam, O. Filseth, and A. Minsaas. 2007. Results and evaluation of thirty years of health recordings in the Norwegian dairy cattle population. J. Dairy Sci. 90:4483-4497.
Philipsson, J., and B. Lindhé. 2003. Experiences of including reproduction and health traits in Scandinavian dairy cattle breeding programmes. Livest. Prod. Sci. 83:99-112.
Pryce, J. E., R. F. Veerkamp, R. Thompson, W. G. Hill, and G. Simm. 1997. Genetic aspects of common health disorders and measures of fertility in Holstein Friesian dairy cattle. Anim. Sci. 65:353-360.
Zwald, N. R., K. A. Weigel, Y. M. Chang, R. D. Welper, and J. S. Clay. 2004a. Genetic selection for health traits using producer-recorded data. I. Incidence rates, heritability estimates, and sire breeding values. J. Dairy Sci. 87:4287-4294.
Zwald, N. R., K. A. Weigel, Y. M. Chang, R. D. Welper, and J. S. Clay. 2004b. Genetic selection for health traits using producer-recorded data. II. Genetic correlations, disease probabilities, and relationships with existing traits. J. Dairy Sci. 87:4295-4302.

Table 1. Summary statistics of the health traits database.

Health category	Health event	Number of health events	% of health events	Number of herds	% of herds
Mastitis	Mastitis	154,292	40.3	4,927	86
Displaced abomasum	Displaced abomasum	20,509	5.3	3,594	63
Ketosis	Ketosis	12,642	3.3	2,049	36
Milk fever	Milk fever	15,157	3.9	2,704	47
Retained placenta	Retained placenta	33,747	8.8	3,336	58
Metritis	Acute metritis	22,686	5.9	2,043	36
	Purulent discharge	13,823	3.6	1,093	19
	Endometritis	5,452	1.4	538	9
	Chronic metritis	9,792	2.5	1,215	21
Cystic ovaries	Cystic ovaries	47,805	12.4	2,538	44
Lameness	Lameness	46,542	12.1	2,923	51
	Foot rot, laminitis, sole ulcer, etc.	2,077	0.5	410	7
Total		384,524	100	5,723	

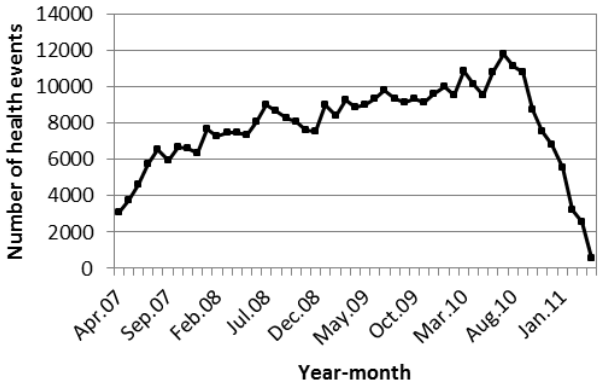

Figure 1. Number of reported health events per year and month.

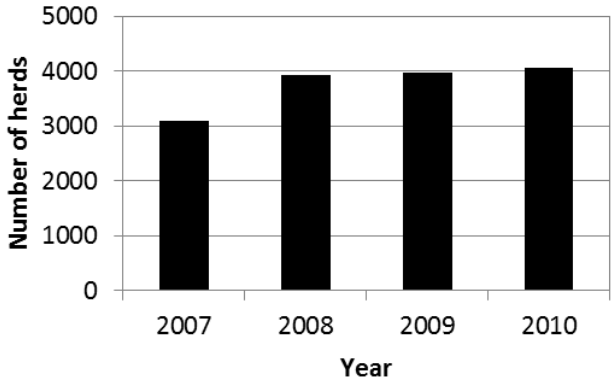

Figure 2. Number of herds recording health data per year.

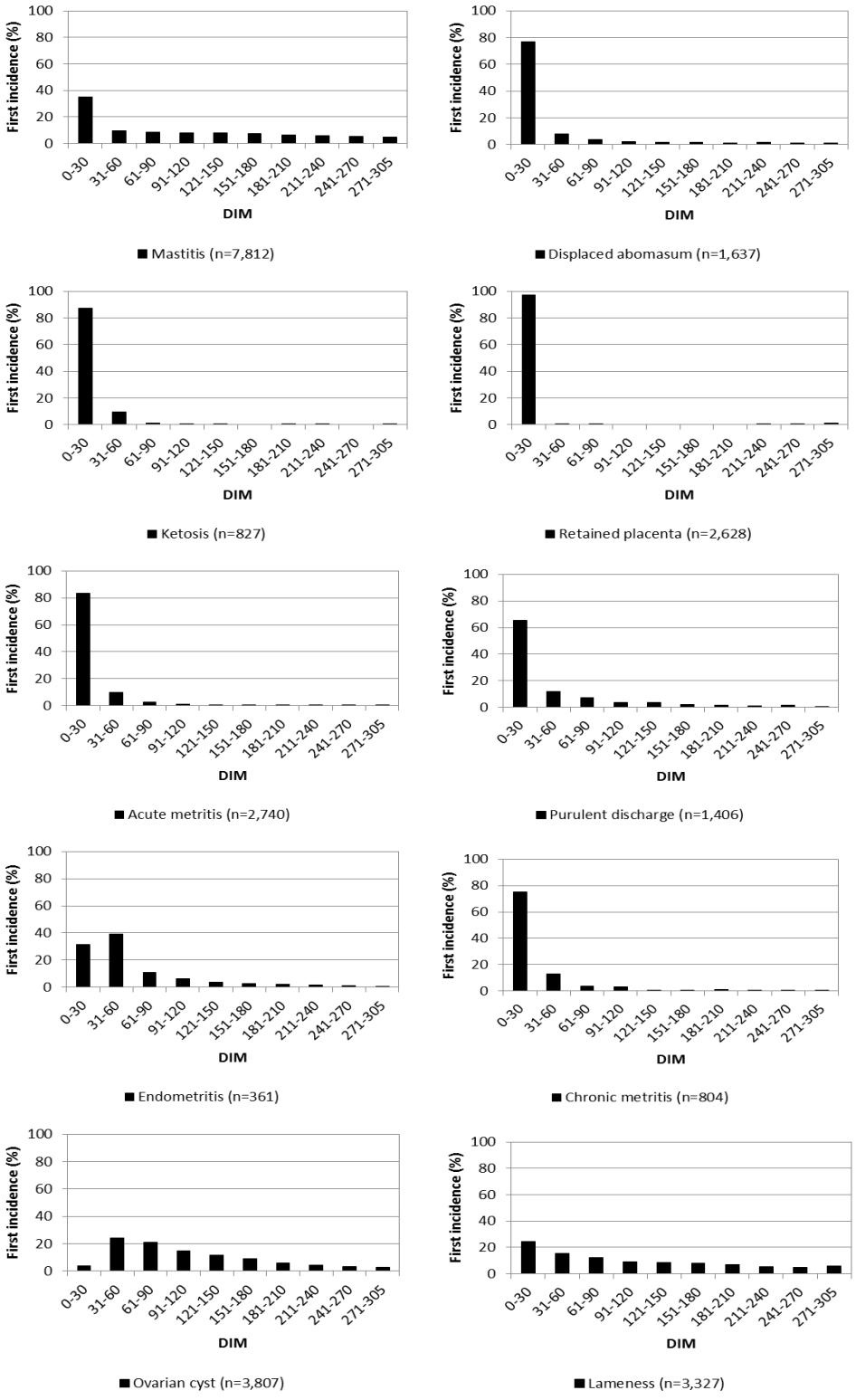

Figure 3. Occurrence of first incidence of each health disorder by stage of lactation, % of health events in each interval

Table 2. Summary statistics of analyzed data.

	Days from calving	No. of records	No. of herds	Frequency (%)
Mastitis	0 to 305 d	61,800	1,864	12.6
Displaced abomasum	0 to 305 d	43,833	1,293	3.7
Ketosis	0 to 100 d	26,802	776	4.5
Retained placenta	0 to 14 d	86,005	1,684	4.6
Metritis	0 to 150 d	59,575	1,464	10.8
Acute metritis	0 to 150 d	33,522	763	10.3
Purulent discharge	0 to 150 d	19,392	636	8.3
Endometritis	0 to 150 d	6,733	222	6.5
Chronic metritis	0 to 150 d	16,701	593	5.8
Cystic ovaries	0 to 305 d	46,341	1,248	8.2
Lameness	0 to 305 d	36,353	1,123	9.2

Table 3. Heritabilities and genetic correlations among acute metritis, purulent discharge, endometritis, and chronic metritis with standard errors in parentheses.

	Acute metritis	Purulent discharge	Endometritis	Chronic metritis
Acute metritis	0.009 (0.004)	0.99 (0.12)	0.76 (0.35)	1.00 (0.26)
Purulent discharge		0.025 (0.008)	0.99 (0.18)	0.94 (0.26)
Endometritis			0.023 (0.013)	0.99 (0.36)
Chronic metritis				0.007 (0.005)

Table 4. Heritabilities and genetic correlations among mastitis, displaced abomasum, ketosis, retained placenta, metritis, cystic ovaries and lameness with standard errors in parentheses.

	Mastitis	Displaced abomasum	Ketosis	Retained placenta	Metritis	Cystic ovaries	Lameness
Mastitis	0.022 (0.004)	0.20 (0.12)	0.36 (0.15)	0.29 (0.13)	0.20 (0.15)	0.19 (0.15)	0.49 (0.16)
Displaced abomasum		0.060 (0.008)	0.64 (0.10)	-0.07 (0.12)	0.44 (0.12)	-0.11 (0.13)	0.31 (0.16)
Ketosis			0.032 (0.008)	-0.07 (0.16)	0.32 (0.16)	0.12 (0.18)	-0.10 (0.21)
Retained placenta				0.027 (0.005)	0.62 (0.11)	0.23 (0.14)	0.11 (0.19)
Metritis					0.018 (0.004)	0.04 (0.16)	-0.22 (0.19)
Cystic ovaries						0.025 (0.005)	0.08 (0.20)
Lameness							0.012 (0.004)