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A model for the genetic evaluation of number of clinical mastitis cases per lactation in Czech Holstein cows

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ABSTRACT

Cases of mastitis from 9,550 lactations of 6,242 cows were recorded on 5 farms in the Czech Republic from 1996 to 2008. The number of clinical mastitis (CM) cases per cow adjusted to a lactation length of 305 d was analyzed with 4 linear single-trait animal models and one 3-trait model, which also included lactation mean somatic cell score (SCS) and 305-d milk yield. Factors included in the model of choice were parity, combined effect of herd and a 2-yr calving period, calving season, permanent environmental effect of the cow, and additive genetic effect of the cow. From both the single-trait and multiple-trait models, estimated heritability of number of CM cases was 0.11 (±0.015 for the multiple-trait model). Permanent environmental effects accounted for approximately one-third of the phenotypic variance. Heritability estimates for lactation mean SCS and 305-d milk yield were 0.17 ± 0.019 and 0.25 ± 0.011, respectively, and genetic correlations of these traits with number of CM cases were 0.80 ± 0.059 and 0.34 ± 0.079, respectively. Genetic evaluation of the number of CM cases in Czech Holsteins could be carried out including data from all parities using a 3-trait animal model with SCS and milk yield as additional traits.
Key words: dairy cow, clinical mastitis, genetic evaluation

INTRODUCTION

Mastitis is the most common and costly disease in dairy cattle (Halasa et al., 2007). Despite improved methods of prevention and treatment, mastitis incidence has not declined substantially in recent years. Extensive recording of health traits in the Scandinavian countries showed that genetic improvement of mastitis resistance is possible through genetic selection (Heringstad et al., 2000). In other countries, recording of clinical mastitis (**CM**) is not yet widely established, but several countries use udder-related type traits and SCC to select against mastitis. Although the correlation of SCC to CM is relatively high (0.65–0.70 in most populations; Rogers, 2002), the inclusion of CM in a selection program can substantially increase the genetic response in resistance to mastitis. Philipsson et al. (1995) reported a 20% increase in selection efficiency for CM when both CM and SCC were included in a selection index. Bloemhof et al. (2009) calculated that the increase in the accuracy of the current Dutch udder health index for bulls with 100 daughters would be 3 to 8% if parity-specific CM and SCS during the first 150 d of lactation were included. For well-proven sires with 10,000 daughters, a 15% increase in accuracy was predicted. Heringstad et al. (2000) reported a reduction in CM incidence of 0.19%/yr for cows born later than 1990 following the implementation of CM recording and selection against CM in Norway in 1978.

In initial studies in the Scandinavian countries, CM was considered as a binary trait and analyzed using a linear sire model (Heringstad et al., 1999). Further developments aimed at taking the binary nature of CM incidence into account resulted in threshold models of various kinds (univariate, multivariate, longitudinal; Heringstad et al., 2003; Chang et al. 2006). Other genetic analyses were conducted using number of CM cases or the number of quarters with CM during certain periods of lactation (Nash et al., 2000; Heringstad et al., 2006; Motta et al., 2006) as information sources. Day of lactation at first CM incidence was a further possible indicator trait for CM resistance (Sæbo et al., 2005; Carlén et al., 2006).

In the Czech Republic, SCS has been mainly used as an indicator trait for udder health. Furthermore, breeding values have been calculated for linear type traits including udder conformation since 1999. Registration of every CM occurrence has been obligatory on all dairy farms since 1997, but resultant records have not yet been transferred to the central database. Each treatment with antibiotics and affected quarters must be recorded on farm.

The objective of the present study was to analyze data on CM and other traits recorded on Czech dairy

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Table 1. Distribution of cows and lactations over herds

Herd	Data collection period	Cows (n)	Lactations (n)	Average herd size[1] (cows)
1	Jan. 1, 2000 to Mar. 26, 2008	2,741	4,410	1,000
2	Dec. 23, 1998 to Aug. 23, 2007	1,578	2,225	800
3	Jan. 13, 1999 to Feb. 14, 2008	535	775	200
4	Jan. 31, 1996 to Feb. 23, 2008	485	819	200
5	Dec. 30, 2003 to Feb. 29, 2008	903	1,321	1,000
Total		6,242	9,550	

[1]Approximate average number of cows per herd per year.

farms to determine their suitability for breeding value estimation for mastitis resistance.

MATERIALS AND METHODS

Animals and Trait Definition

Data on mastitis incidence were collected from 5 Holstein herds between 1996 and 2008. The observation length on these farms is given in Table 1. The farms were not randomly chosen from the national population, but rather were those willing to participate in the study. They were of different sizes and from distinct regions but used management, feeding, and housing systems commonly applied to dairy herds in the Czech Republic. On all farms, straw was used for bedding and cows were fed a balanced TMR and milked twice per day. All cows were treated with antibiotics at the time of drying off on farms 2 to 5, whereas only cows with CM at some time during lactation plus all high-producing cows received such treatment on farm 1. No other special mastitis control program was applied on the farms.

Records collected on farms included cow identification, date of beginning CM treatment, date of the end of CM (i.e., the last day that milk from a treated cow was discarded), and identification of infected quarters. Detection of CM was done by farmers on the basis of visual or perceptible signs of the udder or milk. However, a detected mastitis case was recorded only if it was treated with antibiotics prescribed by the veterinarian. Thus, CM was defined as a veterinary-treated udder disease.

The remaining data required for genetic evaluation of CM (birth date, calving date, parity, length of lactation, culling date, test-day milk yield, cumulative milk yield for lactation, and test-day SCC) together with a pedigree file were made available from the national database for progeny testing.

Only cows that started their lactation after the initiation of data collection and had a lactation length between 200 and 450 d were included in the analysis. Furthermore, it was required that cumulative milk yield (the calculation of which was based on at least 5 test-day records) for the lactation was known. The number of cows and lactations in the analyzed dataset after data editing are shown in Table 1. The approximate herd size was between 200 and 1,000 cows. Cows were daughters of 987 sires; the number of daughters per sire was between 1 and 114, with a median of 2.

The trait of interest was number of CM cases per lactation. A new case of CM for the same cow was indicated when the period between the end of the previous case and the next occurrence was at least 5 d. The frequency of cows with CM as a function of the day of lactation is shown for all parity classes in Figure 1. The distribution of cows over the number of CM cases per lactation is shown in Table 2. Of all cows having CM, 52% had only 1 case per lactation, 23% were ill twice, 12% had 3 cases, and 13% had more than 3 cases per lactation.

To make the number of CM cases comparable between cows and lactations, the number was preadjusted to a lactation length of 305 d [**NCMC(305)**; for details see equation [3] below]. For comparison purposes, the actual (unadjusted) number of CM cases [$\mathbf{NCMC(}t_{lac}\mathbf{)}$] for the given lactation length t_{lac} was analyzed as well. Furthermore, a second preadjusted trait was calculated [$\mathbf{NCMC(305}c\mathbf{)}$] that was identical to NCMC(305) for lactations shorter than 305 d and the actual number of CM cases in the first 305 d for lactations with a length greater than 305 d. In addition to these 3 trait definitions, CM was also considered as an all-or-none trait with values of 0 (no CM case) or 1 (at least 1 CM case).

Somatic cell count was not analyzed directly but was first transformed to SCS according to the following equation:

$$\mathrm{SCS} = \log_2\left(\frac{\mathrm{SCC}}{100,000}\right) + 3. \qquad [1]$$

The profile of average SCS across lactations is shown in Figure 2.

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