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GENETIC PARAMETERS OF CLINICAL MASTITIS FOR DUTCH HOLSTEIN CATTLE BASED ON FARM MANAGEMENT SOFTWARE DATA

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INTRODUCTION

Clinical mastitis (CM) is one of the most common and costly diseases in dairy cattle. Economic losses from mastitis and increasing requirements regarding food safety and animal welfare are strong arguments to reduce CM frequency. Mastitis resistance has become an important part of many dairy cattle breeding objectives over the past years (e.g. VanRaden 1998). Improved resistance can be achieved by direct selection using CM records, by indirect selection using traits genetically correlated to mastitis or by a combination of both (Rupp and Boichard 2003). The current Dutch Udder Health index is based on breeding values of traits that correlate to CM, i.e. somatic cell count, udder depth, fore udder attachment, teat length and milking speed (De Jong and Lansbergen 1996; NRS 2004). As no direct information on CM is included the maximum reliability of this index is only 56% (Van Pelt 2004). Numerous Scandinavian studies have reported that CM data routinely recorded by veterinarians can effectively be used for selection purposes (e.g. Heringstad et al. 2000). Such a large-scale recording system of CM is unavailable the Netherlands. Recent developments in information and computer technology have facilitated the use of farm management software by dairy farmers. Disease data recorded using farm management software is a potential information source to select for improved CM resistance. With the increasing number of farmers that routinely record CM data, an analysis of the quality of these data is appealing. The aim of this study is therefore to estimate the genetic parameters for CM observations recorded in farm management software.

MATERIAL AND METHODS

Data.

A group of 202 Dutch dairy farmers recorded all treatments of CM using antibiotics in their farm management system between October 1999 and April 2005. Not all farmers participated during the complete period; for each farm the starting data was defined as the first date of CM recording and the end date was defined as the last date of recording. Only observations on herdbook registered Holstein cows (≥75% Holstein Friesian genes) during the first three lactations were considered. To be included in the analyses, cows had to have calved at least 15 days before the first recording and 210 days before the last day of recording at that herd. The final data included 30,202 lactations of 18,578 cows. In each lactation CM210 was defined as an all-or-none trait: either a cow had CM from 15 days before to 210 days in lactation or not. Cows with no CM treatments were assigned "0" and cows with at least one CM treatment were assigned "1".

Statistical analyses.

Initial analyses of CM210 included unadjusted means of parities, herds and sires. Genetic parameters were estimated using the following linear animal model:

$CM210_{ijkl}$ = $(\text{herd x year})_i + (\text{year x season})_j + age_k + animal_l + e_{ijkl}$,

where

$CM210_{ijkl}$ = observation of CM (0/1) in parity 1, 2 or 3;
$(\text{herd x year})_i$ = random interaction between herd and year of calving;
$(\text{year x season})_j$ = interaction between year and season of calving;
age_k = effect of age at calving (first parity only);
$animal_l$ = random additive genetic effect of animal;
e_{ijkl} = random residual.

Age at calving was divided into 10 monthly classes (≤23, …, >31) and 4 seasons of calving were defined. The pedigree file included all cows with observations and four generations of pedigree (n = 65,899 animals). Variance components were estimated in univariate and bivariate analyses using ASREML software (Gilmour *et al*. 2002). Heritabilities were defined as: $h^2 = \sigma^2_a/(\sigma^2_a+\sigma^2_{hy}+\sigma^2_e)$, where σ^2_a = additive genetic variance, σ^2_{hy} = herd-year variance, and σ^2_e = residual variance

RESULTS AND DISCUSSION

Incidences.

Incidences of CM210 in first, second and third parity were 12.1%, 14.7% and 18.6%, respectively. These incidences agreed well with an earlier analysis including only 13 experimental herds by Van Pelt (2004). Scandinavian studies generally reported lower incidences (Pösö and Mäntysaari 1996; Heringstad *et al.* 2003; Carlén *et al.* 2004). The main differences with the Dutch studies are that the Scandinavian studies usually analysed data recorded by verterinarians during the first 150 days of lactation. Figure 1 shows the cumulative frequencies of all first cases of CM as a function of lactation stage. In first parity, approximately 50% of all CM treatments occured already before day 5 after calving, whereas in higher parities it took almost 55 days before 50% of the first CM treatments occurred. Also Heringstad *et al.* (1999) and Carlén *et al.* (2004) observed most CM cases in early lactation.

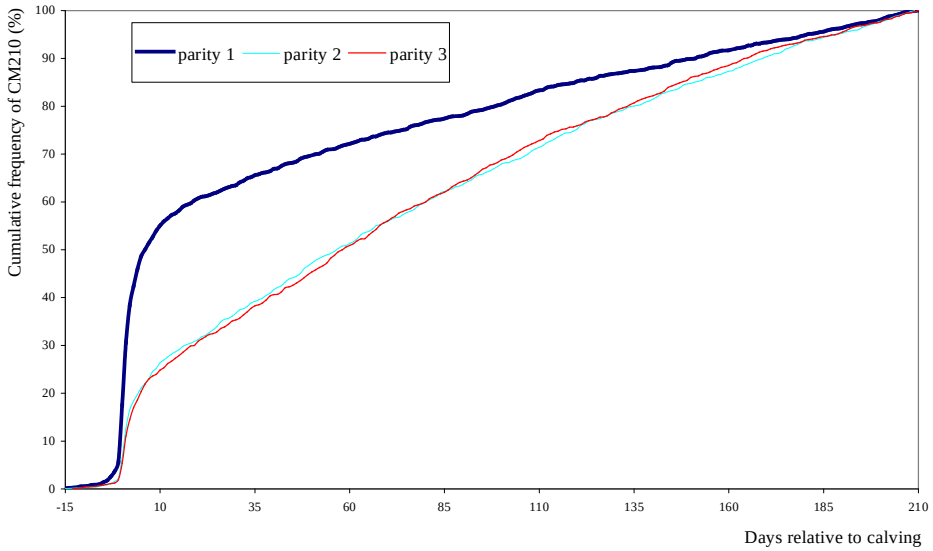

Figure 1. Cumulative frequency of first CM treatments in the first three parities between -15 and 210 days of lactation during the first 150 days in lactation.

Unadjusted herd means for CM210 varied largely: approximately 7% of the herds had a mean <5% whereas 1% of the herds had a mean >30%. Also daughter means for CM210 had a large variation. For example, mean CM210 incidence of the 8 bulls with at least 160 daughters in first lactation varied from 7.5% to 14.8%.

Genetic parameters. The additive genetic standard deviation ranged from 6% to 9% (Table 1). Estimated heritabilities for CM210 were 0.03 in parity 1 and 0.05 in parity 2 and 3. Genetic correlations across parities were high (0.81-0.92), but were clearly lower than unity. Although parameters estimates for CM are hard to compare across studies because of variation in frequency levels, trait definitions and statistical models, these estimates corresponded well to other studies (Pösö and Mäntysaari 1996; Nielsen *et al*. 1997; Carlén *et al*. 2004).

Table 1. Genetic parameters for CM210 in first, second and third parity

			Parity		
Parity	σ_A [A]	σ_{HY}	1	2	3
1	0.057	0.062	**0.03** [B]	0.90	0.81
2	0.077	0.076	0.03	**0.05**	0.92
3	0.085	0.099	0.03	0.05	**0.05**

[A] σ_A = additive genetic standard deviation; σ_{HY} = standard deviation of herd-year effect.

[B] Heritabilities on the diagonal, genetic and phenotypic correlations above and below the diagonal, respectively. Standard errors of heritabilities were 0.01.

IMPLICATIONS

The genetic parameters estimated in this study imply that CM data recorded by farmers in their herd management system can potentially be used for selection purposes. The practical advantage of CM data over the current selection

index in commercial breeding programmes largely depends on the number of daughters with CM records and on the relation between CM data and the traits in the index. Although the number of farmers that routinely records CM is currently too low to justify selection on only CM data, these data may already be used to increase selection accuracy of the current Udder Health Index.

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