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Udder Health Shows Inbreeding Depression in Danish Holsteins

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ABSTRACT

The purpose of this study was to estimate inbreeding depression for udder health using records on mastitis incidence and somatic cell count (SCC). Data were selected based on a pedigree completeness index so that inbreeding coefficients were reliable. Average inbreeding was 3.3%. The presence or absence of mastitis was considered in first (CM1), second (CM2), and third (CM3) lactations, and was recorded as a binary trait. Somatic cell count was also included and analyzed on the log scale. A minimum of 140,000 cows with records were included per trait. Linear sire models were used and (co)variance components were estimated. Linear and curvilinear effects of the coefficient of inbreeding were included. Inbreeding significantly affected all traits investigated. Three traits, CM1, CM3, and SCC, showed a nonlinear relationship between phenotype and inbreeding coefficient. A cow with 5% inbreeding compared with a cow with 2% inbreeding had a higher SCC and a higher incidence of mastitis. The SCC increased by 1,500 cells/mL in first lactation and the incidence of mastitis increased by 1.08, 0.55, and 0.98% in first, second, and third lactation, respectively. The corresponding reduction in net return from these traits over 3 lactations amounted to US$11.00 under Danish production circumstances. These results are a step on the way to estimating the total cost of inbreeding depression to determine an acceptable rate of inbreeding.

Key words: inbreeding depression, udder health, mastitis, somatic cell count

INTRODUCTION

The focus of dairy cattle breeding has shifted during the last few decades from almost exclusive attention on production traits to the incorporation of cost-reducing functional traits in the breeding goal. Besides having low heritabilities, these functional traits are also expected to be prone to inbreeding depression. Significant inbreeding depression for milk, fat, and protein production has been found in a number of populations including North American Holsteins (e.g., Miglior et al., 1995b), North American Jerseys (e.g., Miglior et al., 1992), and Swiss Braunvieh (Casanova et al., 1992). Inbreeding depression has been estimated for some functional traits in dairy cattle (Smith et al., 1998; Thompson et al., 2000a,b; Adamec et al., 2006). Inbred animals tend to be older at first calving, have longer calving intervals, have fewer days of productive life, and have a higher risk of giving birth to stillborn calves.

DeRose and Roff (1999) reviewed studies on inbreeding depression in 54 species of wild and laboratory populations. They concluded that life history traits, such as fertility, fecundity, and survival, exhibited approximately 6 times as much inbreeding depression as conformation traits, such as adult body size. Inbreeding has been shown to reduce resistance to infectious diseases in other species in the laboratory (e.g., Spielman et al., 2004) and in the wild (e.g., Acevedo-Whitehouse et al., 2003). Inbreeding depression comparisons of livestock and wild or laboratory populations are not straightforward because selection pressure and rates of inbreeding can and will be different. However, it does not compromise the general conclusion of DeRose and Roff (1999) that life history traits are more prone to inbreeding depression than conformation traits. Milk production traits can be considered life history traits in the evolution of cattle because they contribute to offspring survival and therefore would be expected to show significant inbreeding depression, as has been seen.

To date, no studies have been published on inbreeding depression for mastitis incidence in dairy cows. However, some studies have estimated inbreeding depression for SCC. Miglior et al. (1995a) estimated a linear inbreeding depression in SCS to be 10.5% of a phenotypic standard deviation for a change of 0.1 in the inbreeding coefficient. Smith et al. (1998) and Thompson et al. (2000a,b) also estimated inbreeding depression for SCS but found no significant results. The Nordic countries, including Denmark, have a thorough system for gathering registrations on veterinary treatments, including mastitis treatments (Bundgaard and Høj, 2000). Therefore, these data can be used to test for the presence of inbreeding depression for udder health.

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Table 1. Phenotypic means and number of records, herds, herd-year-season (HYS) groups, sires, and animals in the pedigree file for the 4 traits

Trait[1]	Mean	No. records	No. herds	No. HYS	No. sires	Size of pedigree file
CM1	26.1%	376,363	8,256	38,305	3,271	19,156
CM2	28.0%	340,044	11,012	65,963	4,672	19,156
CM3	32.4%	144,222	9,452	43,723	2,805	19,156
SCS	11.26	529,377	9,703	53,060	4,068	15,654

[1] Incidence of mastitis in first (CM1), second (CM2), or third (CM3) lactation. Average SCC in first lactation was transformed to SCS using the natural logarithm prior to analysis. The mean SCC was 77,700 cells/mL, with 67% of the observations being between 36,600 and 164,900 and 95% of the observations being between 17,200 and 350,100.

A recent investigation has shown that inbreeding has accumulated rapidly (approximately 1% per generation) in Danish Holsteins over the last decade (Sørensen et al., 2005). Therefore, this breed is expected to show inbreeding depression for functional traits such as mastitis incidence and SCC. This paper tests the hypothesis that inbreeding increases the incidence of mastitis in the first 3 lactations and the SCS in the first lactation of dairy cows.

MATERIALS AND METHODS

Data

The Danish Cattle Database (Bundgaard and Høj, 2000) provided records of mastitis treatments and SCC for this study. Incidence of mastitis in first (**CM1**), second (**CM2**), and third (**CM3**) lactation and the average SCC in first lactation were analyzed. The traits considered in this study are used in the routine genetic evaluation and are therefore stored as described below. The period from 10 d preceding calving to 305 d after calving in first lactation was covered by CM1, whereas CM2 and CM3 covered the period from 10 d preceding calving to 100 d after calving in the second and third lactations, respectively. Mastitis incidence was recorded as a binary trait; either the cow was treated for mastitis (one or more times) during the period (in which case it was coded as 1) or it was not treated (in which case it was coded as 0). Somatic cell count was transformed to SCS using the natural logarithm prior to analysis. Table 1 summarizes the data used in this study.

We used the data set from the routine genetic evaluation, with additional editing according to the pedigree completeness. The degree of completeness of pedigrees was assessed for each cow individually by the index proposed by MacCluer et al. (1983). The coefficient for pedigree completeness (PEC), to quantify the possibility for detecting inbreeding in the pedigree, was

$$PEC_{animal} = \frac{2C_{sire}C_{dam}}{C_{sire} + C_{dam}},$$

where C_{sire} and C_{dam} are contributions from the paternal and maternal lines respectively, and

$$C = \frac{1}{d}\sum_{i=1}^{d} a_i,$$

where a_i is the proportion of known ancestors in generation i, and d is the number of generations taken into account. In this study, 5 generations are considered when calculating this index for each animal (d = 5). Records were included only if the cow had a pedigree completeness index of at least 0.9. This is comparable to the situation when one great-grandparent is unknown or when 2 great-great-grandparents are unknown. Individual inbreeding coefficients were calculated using the algorithm by Meuwissen and Luo (1992) and all available pedigree information. The average inbreeding was 3.3%, and the distribution of inbreeding coefficients of animals born in 2002 with a pedigree completeness of at least 0.9 shown in Figure 1 illustrates the overall distribution of inbreeding.

After having selected the animals with adequate pedigree completeness, additional editing was performed to have a minimum of 5 records per herd-year-season group and at least 20 daughters per sire for traits CM1 and SCS. For CM2 and CM3 a minimum of 3 records per herd-year-season group and at least 10 daughters per sire were required. This editing was done to use the most informative observations, given computational constraints. After the editing for pedigree completeness and size of herd-year-season groups and daughter groups, approximately one-third of the total records were left in the data set.

Models

The sire models used in the Danish routine genetic evaluation (Danish Agricultural Advisory Centre, 2003)