Genetic Analysis of Somatic Cell Score in Danish Holsteins Using a Liability-Normal Mixture Model

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ABSTRACT

Mixture models are appealing for identifying hidden structures affecting somatic cell score (SCS) data, such as unrecorded cases of subclinical mastitis. Thus, liability-normal mixture (LNM) models were used for genetic analysis of SCS data, with the aim of predicting breeding values for such cases of mastitis. Here, putative mastitis statuses and breeding values for liability to putative mastitis were inferred solely from SCS observations. In total, there were 395,906 test-day records for SCS from 50,607 Danish Holstein cows. Four different statistical models were fitted: A) a classical (nonmixture) random regression model for test-day SCS; B1) an LNM test-day model assuming homogeneous (co)variance components for SCS from healthy (IMI−) and infected (IMI+) udders; B2) an LNM model identical to B1, but assuming heterogeneous residual variances for SCS from IMI− and IMI+ udders; and C) an LNM model assuming fully heterogeneous (co)variance components of SCS from IMI− and IMI+ udders. For the LNM models, parameters were estimated with Gibbs sampling. For model C, variance components for SCS were lower, and the corresponding heritabilities and repeatabilities were substantially greater for SCS from IMI− udders relative to SCS from IMI+ udders. Further, the genetic correlation between SCS from IMI− and SCS of IMI+ was 0.61, and heritability for liability to putative mastitis was 0.07. Models B2 and C allocated approximately 30% of SCS records to IMI+, but for model B1 this fraction was only 10%. The correlation between estimated breeding values for liability to putative mastitis based on the model (SCS for model A) and estimated breeding values for liability to clinical mastitis from the national evaluation was greatest for model B1, followed by models A, C, and B2. This may be explained by model B1 categorizing only the most extreme SCS observations as mastitic, and such cases of subclinical infections may be the most closely related to clinical (treated) mastitis.

Key words: Bayesian method, mastitis, mixture model, somatic cell score

INTRODUCTION

Breeding programs using SCC records in genetic selection for improved udder health to date have been based on either cross-sectional models (e.g., lactation mean SCS) or test-day models (e.g., repeatability models, random regression models) for genetic evaluations. These models are typically focused on selecting animals with the lowest average SCS. Several studies have found a positive genetic correlation between SCS level and risk of clinical mastitis (Mrode and Swanson, 1996). However, simply selecting for lower average SCS might not be the most optimal way of utilizing SCC data in selection for improved udder health. To illustrate this, Green et al. (2004) found that the within-lactation variation of test-day SCS and the maximum test-day SCS were the best indicators of clinical mastitis, rather than mean SCS. Lactation average and standard test-day models for SCS do not discriminate between SCS from healthy and diseased animals (because health status is usually unknown), and will thus assume identical location and dispersion parameters for SCS irrespective of infection status. Further, selection for lower SCS might favor not only cows having lower incidence of IMI, but also cows having lower levels of SCC when healthy (“baseline” SCC). Detilleux and Leroy (2000) have argued that high “baseline” SCC may increase resistance to IMI, and they have therefore suggested the use of mixture models for analysis of SCC test-day data.

Previous studies (Detilleux et al., 1997; de Haas et al., 2004) have found that SCC and the proportion of different somatic cell types differ dramatically with respect to IMI status. Generally, the proportion of poly-