



J. Dairy Sci. 100:1–15  
<https://doi.org/10.3168/jds.2016-11894>

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## Bivariate threshold models for genetic evaluation of susceptibility to and ability to recover from mastitis in Danish Holstein cows

B. G. Welderufael,\*†<sup>1</sup> L. L. G. Janss,† D. J. de Koning,\* L. P. Sørensen,† P. Løvendahl,† and W. F. Fikse\*

\*Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Box 7023, SE-750 07 Uppsala, Sweden

†Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Blichers Allé 20, PO Box 50, DK-8830 Tjele, Denmark

### ABSTRACT

Mastitis in dairy cows is an unavoidable problem and genetic variation in recovery from mastitis, in addition to susceptibility, is therefore of interest. Genetic parameters for susceptibility to and recovery from mastitis were estimated for Danish Holstein-Friesian cows using data from automatic milking systems equipped with online somatic cell count measuring units. The somatic cell count measurements were converted to elevated mastitis risk, a continuous variable [on a (0–1) scale] indicating the risk of mastitis. Risk values >0.6 were assumed to indicate that a cow had mastitis. For each cow and lactation, the sequence of health states (mastitic or healthy) was converted to a weekly transition: 0 if the cow stayed within the same state and 1 if the cow changed state. The result was 2 series of transitions: one for healthy to diseased (HD, to model mastitis susceptibility) and the other for diseased to healthy (DH, to model recovery ability). The 2 series of transitions were analyzed with bivariate threshold models, including several systematic effects and a function of time. The model included effects of herd, parity, herd-test-week, permanent environment (to account for the repetitive nature of transition records from a cow) plus two time-varying effects (lactation stage and time within episode). In early lactation, there was an increased risk of getting mastitis but the risk remained stable afterwards. Mean recovery rate was 45% per lactation. Heritabilities were 0.07 [posterior mean of standard deviations (PSD) = 0.03] for HD and 0.08 (PSD = 0.03) for DH. The genetic correlation between HD and DH has a posterior mean of –0.83 (PSD = 0.13). Although susceptibility and recovery from mastitis are strongly negatively correlated, recovery can be considered as a new trait for selection.

**Key words:** bivariate model, dairy cow, recovery ability, susceptibility to mastitis

### INTRODUCTION

Dairy cow mastitis is a typical and frequent disease causing large economic losses and problems in milk quality and dairy products worldwide (Halasa et al., 2007; Hogeveen et al., 2011). Most genetic evaluations of mastitis are performed based on either the analyses of recorded treatments of clinical mastitis (CM) or measurements of SCC. Recent studies show that off-farm CM records can be used in routine genetic evaluations (Jamrozik et al., 2013; Govignon-Gion et al., 2016). The assumption is that selection would be more efficient if genetic evaluations were performed on occurrences of mastitis. However, such routine recording of occurrences of CM at the farm or cow level is not easily available in many countries because of difficulties in detection of CM (Carlén et al., 2006). On the other hand, the technological advances in farming and especially automatic milking systems (AMS) have made SCC records easily accessible on a large scale and at almost no cost (e.g., through the online cell counter fitted in the AMS). At present, SCC or log-transformed SCC (SCS) values are therefore used as the major phenotypic measure in genetic evaluations to improve udder health (Sørensen et al., 2009). The use of SCC in genetic evaluations of dairy cattle has a long history. In the United States during the late 1970s and early 1980s, dairy herd breeding programs began to implement SCC measurements for assessment of mastitis cases (Shook and Schutz, 1994). Such historical and wide acceptance of SCC as a proxy for mastitis is due to its ease of recording and high genetic correlation with mastitis (Emanuelson et al., 1988; Gernand and König, 2014).

Often, mastitis is seen as a categorical or binary trait, reflecting the presence or absence of mastitis within a defined time interval (Vazquez et al., 2012). In genetic evaluations, this all-or-none trait definition may not fully utilize all information available in the data; for instance, the time that it takes to recover or different levels of infection (Carlén et al., 2005; Vazquez et al., 2009). Højsgaard and Friggens (2010) introduced the

Received August 19, 2016.

Accepted March 1, 2017.

<sup>1</sup>Corresponding author: [berihu.welderufael@slu.se](mailto:berihu.welderufael@slu.se)

concept of “degree of infection” to define a cow’s health status on a continuous scale where low values indicate healthy cows and high values indicate mastitic cows. A more recent concept, elevated mastitis risk, was introduced by Sørensen et al. (2016). Elevated mastitis risk (**EMR**) evaluates a cow for the risk of having contracted mastitis based on online SCC (**OCC**) recorded with an AMS. Online and inline sensor systems installed in the AMS (DeLaval International AB, Tumba, Sweden) are equipped with a cell counter from which OCC measures can easily be read and automatically recorded on a regular basis.

In current genetic evaluations, only susceptibility to mastitis is taken into account. In this study, we wanted to include the recovery process in the analysis. A method developed by Franzén et al. (2012) included both the disease susceptibility and the recovery process by modeling transitions to and from states of infection in a univariate analyses. More recently, Welderufael et al. (2017) developed a bivariate threshold sire model for joint estimation of breeding values for susceptibility to and recovery from mastitis based on changes in SCC. These methods and models enable us to include both directions of a disease—susceptibility to and recovery from mastitis—in the analysis. This enhances the genetic evaluation of mastitis by the ability to capture genetic variation not only for susceptibility to, but also for recovery from, mastitis. However, those studies (Franzén et al., 2012; Welderufael et al., 2017) were based on simulated data. In this study, we applied these models for the first time to real data. We analyzed real data obtained from Danish research and commercial dairy herds of Holstein-Friesian cows, each using AMS fitted with OCC measuring units. The objectives were, therefore, (1) to evaluate whether the model developed by Franzén et al. (2012) and Welderufael et al. (2017) is identifiable and can be fitted to real data, and (2) to estimate genetic parameters of mastitis susceptibility and recovery ability for Danish Holstein cows using bivariate threshold models.

## MATERIALS AND METHODS

### Data

Data were extracted from a database connected to VMS milking robots (Voluntary Milking System, DeLaval International AB) fitted with OCC measuring units. The data contained 2,903,447 milking records for milk yield, OCC, and electrical conductivity of milk from 3,193 cows, from April 1, 2008, to October 31, 2012, from one research herd (Danish Cattle Research Center, Tjele, Denmark) and 6 commercial dairy herds. The data were composed of different breeds (Danish

Holstein, Danish Red Holstein, Danish Jersey, Red dairy cattle, and a few cows of unknown breed). Part of the data from the Research Center (387 cows from 2 groups of Danish Holstein and 1 group of Danish Jersey), consisting of 150,468 milking records, were used by Sørensen et al. (2016) to develop a mastitis detection model.

Because individuals with an unknown sire are not very informative (especially in a sire model), they were filtered out. Only cows from sires with 5 or more daughters were kept. Because the data included relatively few Danish Jersey and Red dairy cattle, cows belonging to these breeds and cows of unknown breed were excluded, and 1,791 Danish Holstein cows were used for the final analyses. The data were further restricted to include only parities 1 to 3, and only the first 365 d of lactation. Table 1 shows the number of records, sires, and cows by herd for the edited data used in the final analyses. For cows changing herds during the lactation, only the records from the first herd were kept.

### Converting OCC to EMR

The OCC were converted to EMR values according to the procedure outlined by Sørensen et al. (2016). In brief, raw OCC values were checked for validity and then log-transformed to reduce the skewness of the distribution, followed by a single exponential smoothing at sensor level performed to minimize errors caused by instruments. Next, the level and trend in OCC values were determined by fitting a time-series model at cow level, using a double exponential smoothing. The level and trend were combined into a latent using factor analysis, followed by a sigmoid transformation to convert the latent indicator variable to a continuous [0; 1] scale. This indicator, referred to as EMR, predicts the risk of a cow having mastitis: values close to 0 indicate

**Table 1.** Number of transition records, sires, and cows by herd

Herd <sup>1</sup>	Sires	Cows	Records <sup>2</sup>
1	45	134	9,848
2	68	388	13,039
3	68	270	11,102
4	45	233	7,006
5	61	346	14,896
6	52	224	15,569
7	43	302	17,772
Total	382	1,897	89,232

<sup>1</sup>The first 6 herds were commercial farms; herd 7 was a research herd.

<sup>2</sup>Records were made for weekly transitions between assumed states of mastitis and non-mastitis: 0 if the cow stayed within the same state during the whole week, and 1 if the cow changed state. For cows changing herds during the lactation, only the records from the first herd were kept.

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