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Does persistency of lactation influence the disease liability in German Holstein dairy cattle?

B. Harder, J. Bennewitz, D. Hinrichs, E. Kalm*

Institute of Animal Breeding and Husbandry, University of Kiel, D-24098 Kiel, Germany,
*email: bharder@tierzucht.uni-kiel.de

1. Introduction

Persistency is defined as the ability of a cow to maintain producing milk at a high level after the peak yield (Jamrozik et al., 1998). Dekkers et al. (1998) pointed out that a cow with a high persistency incurs less feed, health, and reproduction costs, and therefore is more profitable. The thesis that a good persistency leads to less health problems can be explained as follows. A cow with a flatter lactation curve is more persistent than a cow with the same total milk yield but with a curve that decreases rapidly after peak yield (Grossman et al., 1999). The lower peak yield at the beginning of the lactation causes less energy imbalance, and consequently the cows need to mobilise less body reserves to meet the increased nutrient demand for milk production (Tamminga, 2000), and thus have less metabolic stress. Due to this metabolic stress most health problems occur at the beginning of the lactation, i.e. between calving and peak yield. Following this, cows with a good persistency may have less reproductive and health problems than cows with the same total milk yield that are less persistent.

The aim of this study was to estimate variance components and breeding values for four health traits. In addition, genetic correlations between persistency of milk yield (PMY), fat yield (PFY), protein yield (PPY), milk energy yield (PEY), and liability to udder diseases (UD), metabolic diseases (MD), fertility diseases (FD), and claw and leg diseases (CLD) were estimated. Analyses were carried out for Holstein-Friesian dairy cattle using data from the first lactation and from all lactations, respectively.

2. Material and Methods

Data originated from three commercial milk farms with an overall of 3200 cows. 92.722 medical treatments were recorded from 1998 to 2003. From the above data, two data sets were formed. The first included only cows from the first lactation, and the second one included all lactations. The treatments were divided into five different disease classes, i.e. UD, FD, MD, CLD, and other diseases. Threshold sire models using Gibbs sampling were fitted for the estimation of heritabilities and subsequently for the estimation of breeding values (EBV) for the four disease categories. The EBVs were multiplied with the factor (-1) in order to assure that sires with daughters with less UD, FD, MD, and CLD than the average, respectively, receive higher breeding values. Breeding values for persistency traits were calculated from random regression coefficients obtained from routine sire evaluation. Pearson correlations were calculated between the respective EBV for the persistency traits and the disease traits. The estimated correlation coefficient were used to approximate genetic correlations with the approach proposed by Calo et al. (1973).

3. Results

Heritabilities for the health traits ranged between 0.04 – 0.12 depending on trait and model. For the first lactation MD showed the highest (0.12) and FD and CLD (0.07) the lowest h^2 estimates. The h^2 estimate for UD was intermediate (0.08). For all lactations h^2 for UD was identical to the one estimated only for the first lactation, whereas the h^2 of MD (0.08), FD (0.04), and CLD (0.04) were lower compared to the results of the first lactation.

As expected mean breeding values for the different disease categories, models, and data sets were close to zero. Standard deviations of EBV were lower for FD and CLD than for UD and MD. Mean reliabilities of EBV ranged between 0.23 and 0.56 depending on the disease category, the model and the data set. In general, mean reliabilities were highest for UD, followed by MD, FD, and CLD.

For the first lactation a high significant ($P_{comparisonwise} = 0.006$) Pearson correlation (genetic correlation) between PMY and CLD of 0.27 (0.46) was estimated, while significant ($P_{comparisonwise} = 0.05$) correlations of 0.19 (0.32) were found for PFY and CLD. In addition, a significant ($P_{comparisonwise} = 0.02$) correlation between PEY and CLD of 0.23 (0.38) was estimated. For the all lactation data set significant ($P_{comparisonwise} = 0.01$ to 0.07) correlations were estimated for PMY and FD, MD, and CLD in the range of -0.15 to 0.21, respectively. Correlations between PFY and CLD amounted to 0.13 (0.10), whereas correlations between PEY and MD were -0.14 (0.10), and correlations between PEY and CLD amounted to 0.16 (0.05).

4. Discussion

Strongest genetic correlations were found between PMY and CLD for first lactation (0.46). Even the stringent experimentwise error probability appeared to be significant ($P_{experimentwise}$ = 0.09). In addition, all persistency traits except PPY had positive, significant correlations with CLD in both data sets. The positive genetic correlations indicate that a persistent cow has a lower liability for claw and leg diseases. In contrast to this, the estimated negative genetic correlations between MD and different persistency traits indicate that cows which had metabolic diseases tended to have more persistent lactations. The majority of MD occurred during the first 50 days of lactation. Therefore, diseased cows had lower peak yields on day 60, possibly causing the antagonistic relationship between MD and persistency of lactation. The genetic correlations between FD and the different persistency traits were not always significant for both models and data sets, indicating a loose relationship between them in the present analysis.

5. Conclusion

The introductory thesis was that a good persistency leads to less health problems, based on less metabolic stress at the beginning of lactation. This thesis was partly affirmed by the significant positive correlations between PMY, PFY, and PEY and CLD. In contrast to this, the negative genetic correlations between persistency measures and MD as well as the loose relationships between UD, FD and the different persistency traits confute the thesis. Based on the results of the present study, it seems doubtful to include persistency in the breeding goal in order to improve the disease traits. This is even more as the genetic correlation between persistency and the different disease traits showed different signs.

6. References

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