Udder Health Data in Dairy Cattle Breeding: An Alternative Approach for Genetic Evaluation

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Introduction

Improvements of health traits in dairy cows can be achieved by environmental means as well as through genetic improvement. In general, however, health traits like udder health or resistance against mastitis exhibit only moderate to low heritabilities. Estimates of the heritability of the auxiliary trait somatic cell count (SCC) usually are somewhat higher than those for mastitis resistance (Heringstad 2000) and genetic correlations with mastitis resistance or mastitis incidence often reach values between 0.50 and 0.80. This correlation clearly differs from unity and hence the use of the trait somatic cell score (SCS) is subject to controversial discussions. Firstly, some mastitis agents may not cause increases in SCS, and secondly, very low cell counts may be indicators for an insufficient immune system rather than indicate good health (Coffey *et al*., 1986). In Scandinavian countries, health recording schemes have been developed. Mastitis cases are routinely reported to a central data base and can be evaluated jointly with milk recording data. Genetic evaluations for udder health thus are based on recorded cases of mastitis as well as on SCC (Philipsson and Lindhé, 2003). However, it is a demanding investment to collect this data.

According to European law (EU Directive 96/23 and 90/676, 2001), German farmers or their veterinarians are obliged to record all drugs used and every veterinary treatment of livestock. Therefore, one of the aims of this study was to examine such records for their suitability in genetic analysis. Furthermore, another approach of treating health data was established in this study. In principle, there are three ways to define the traits that describe udder health. Firstly, the incidence of mastitis cases can be treated as a binary trait per lactation. Secondly, the number of mastitis cases can be counted per lactation and thirdly, a continuous trait can be defined after assigning "sick days" to cases of mastitis. However, this latter approach is somewhat arbitrary since it is normally unknown how many days the cow is sick per case of mastitis. Despite this uncertainty, some authors have argued that such an approach would be a valid approximation (e.g. Kehr et al., 2007) and thus this approach was followed in the present study in assuming a predefined number of days sick (DS) per case of mastitis. For sake of comparison, also the first approach was applied.

Material and Methods

Data and trait definition. Health data of 23,101 cows in first to third lactation, located in 21 contract herds in Northeast Germany, were used to analyze udder health. Average herd size

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and milk yield were 781 cows and 9,960 kg, respectively. Data was recorded by farmers and veterinarians. A total of 80,701 records, i.e. udder health problems, recorded between day one and 305 days post partum were used.

Only lactation records from Holstein cows with a valid link to the German milk recording database at VIT, Verden, were considered for analysis and milk yields and SCS were extracted from this data base as well. Lactation records were merged with health data. Lactation records without a match in the health data base were defined as non-diseased lactations.

A binary trait (binS) was defined such that a "1" denoted at least one mastitis case per lactation and a "0" represented no sickness throughout the entire lactation. The second trait was days sick (DS) which was defined as the sum of all days per lactation a cow was considered to be sick. Assumptions followed the rules used by Kehr *et al.* (2007): With the first incidence a cow was defined as ill for 14 days. In case of a second incidence record between day eight and 14 the cow was considered not to have recovered. In this case the period of illness was extended for seven days (Total = 21 DS). If an incidence record occurred in the extension period of seven days, the period was extended for another seven days. Incidence records occurring after an already defined period of illness were considered to be a new sickness period and treated as described above.

Statistical analysis. Environmental and genetic effects on binS were analyzed by a single-trait threshold animal model using ASReml 3.0 (Gilmour *et al.* 2008) applying a probit link function. The model included the fixed effects of parity, herd-year-season, 305 day milk yield (MY) and SCS, as well as a random animal effect and a permanent environmental effect.

DS, SCS, and MY were analyzed by a multiple-trait model using a linear animal model and the VCE 6.0 software (Groeneveld *et al.* 2008). For all traits, the fixed effects of parity and herd-year-season, as well as a random animal effect and a permanent environmental effect were included. Taking into account that culled animals had a lower risk for increased values of DS, days-at-risk was additionally used in the DS model.

Results

As shown in Table 1 the incidence rate, i.e. at least one incidence record per lactation, as well as DS and SCS were lowest in first lactation (31.4 %, 7.44 d and SCS = 2.43) and increased to 49.4 %, 15.5 d and SCS = 3.16 in third lactation.

Table 1: Characteristics of data used in genetic analysis (DS – days sick)

	1	**2**	**3**	**all**
Total lactations, n	15,924	12,005	7,069	34,998
Incidence rate, %	31.3	43.1	49.4	39.0
Mean DS, d	7.44	12.83	15.5	10.92
Mean days at risk, d	291.7	286.8	282.5	288.2
Age at calving, mo	26	39	53	-
Mean 305 day milk yield, kg	8,726	10,048	10,364	9,509
Average SCS	2.43	2.8	3.16	2.7

Analysis of binS for all lactations resulted in an estimate of the heritability of 0.09. This estimate is at the upper end of the range found by several authors (Vallimont *et al.* 2009, Sørensen *et al.* 2009, Zwald *et al.* 2004, Heringstad 2000). Table 2 presents estimates of heritabilities, genetic and phenotypic correlations for DS, SCS and MY multivariate analysis, carried out separately for all three lactations. DS showed low heritabilities for all parities, reaching a maximum at 0.10 when including the combination of second and third lactation. Heritabilities for SCS and MY varied between 0.13 to 0.17, and 0.47 to 0.23, respectively. Genetic correlations between DS and SCS were high but differed from unity, indicating that SCS only is an auxiliary trait for udder health. Genetic correlations for DS and MY vary between 0.35 and 0.40, thus being considerably higher than the correlation for SCS and MY which range from 0.0 to 0.25. This finding indicates that the genetic relationship between milk yield and udder health is more antagonistic than anticipated from a common analysis using SCS only.

Moderate phenotypic correlations between DS and SCS are pointing out that udder health problems not necessarily lead to an increased SCS.

Table 2: Heritabilities (h^2), genetic (r_g) and phenotypic (r_p) correlations with standard errors for Days Sick (DS), SCS and Milk yield (MY).

		lactation									
		1		**2**		**3**		**2 + 3**		**all**	
h^2	**DS**	0.06	0.01	0.08	0.02	0.07	0.02	0.10	0.02	0.08	0.01
	SCS	0.13	0.02	0.17	0.03	0.17	0.04	0.17	0.04	0.16	0.01
	MY	0.47	0.03	0.33	0.03	0.23	0.01	0.31	0.01	0.37	0.01
r_g	**DS and SCS**	0.67	0.09	0.72	0.07	0.99	0.01	0.79	0.01	0.77	0.03
	DS and MY	0.39	0.11	0.36	0.12	0.35	0.16	0.40	0.16	0.35	0.03
	SCS and MY	0.10	0.04	0.00	0.07	0.25	0.16	0.11	0.16	0.10	0.04
r_p	**DS and SCS**	0.35		0.48		0.48		0.48		0.43	
	DS and MY	-0.01		-0.01		-0.05		-0.03		-0.02	
	SCS and MY	-0.09		-0.16		-0.16		-0.16		-0.13	

Conclusion

It is well known that udder health traits show low heritabilities which has been confirmed by this study. The comparison of different trait definitions for udder health, i.e. as a binary trait or a quantitative measurement involving some assumptions (DS) leads to similar estimates of the heritability. The results indicate that the trait definition as DS focuses on the ability of the cow to deal with a disease while SCS gives information about the immune response. In contrast to the genetic correlation between MY and SCS, the genetic correlation between MY and DS points to a very clear genetic antagonism between milk yield and udder health. As other authors have concluded before, data recording systems for udder health have to be developed so that genetic evaluations can be based on SCS as well as on incidence records (Carlen *et al.* 2004).

The results also indicate that the data recorded by farmers and their veterinarians are of good quality, making them suitable for genetic analyses. Further research is needed to compare different trait definitions and relations to other qualitative and quantitative traits.

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