Application of a Multivariate Random Regression Sire Model to Estimate Genetic Parameters among Milk Yield, Somatic Cell Count and Laminitis

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Abstract

A multivariate random regression sire model was applied to estimate simultaneously genetic parameters for Gaussian traits (milk yield, SCS) and binary recorded disorders (laminitis). Results revealed moderate heritabilities for SCS and laminitis in the range from 0.10 to 0.19 in the period from day 30 to day 305 after calving. Genetic correlations for individual test days and also for the whole lactation between production (milk yield) and functionality (SCS, laminitis) were positive and indicating an antagonistic relationship. The positive genetic correlations between laminitis and SCS from 0.49 to 0.24 over the whole trajectory suggest that cows genetically susceptible to some type of health problems are likely to be susceptible to other health problems as well.

Introduction

As the level of milk production in dairy cattle increases, correlated increases of health problems need to be studied in more detail. Health problems result in higher culling rates, increased veterinary costs, and economic losses due to lower production and discarded milk. In recent years, research also in Germany has focussed on analyses for directly recorded health traits, such as mastitis or claw disorders (e.g. König *et al.*, 2005).

In animal breeding, there are more and more traits of interest recorded repeatedly per animal or recorded at various times during an animal's life. They may change, gradually and continually, as time progresses. Typical examples are test day records for dairy cows, with milk production at the beginning and the end of lactation having quite different means and variances. Also diseases occur on several points during the lactation; however, the frequencies are different among animals. On a biological basis there could be different genes that are turned on and off as an animal ages causing changes in physiology and performance.

The objective of this study was to assess a multivariate random regression sire model (**RRM**) for the 3 traits milk yield (**MY**), somatic cell score (**SCS**), and laminitis (**LAM**) to infer genetic relationships among production and functional traits for different time points within the lactation.

Material and Methods

Laminitis was recorded in 2005 from 4386 Holstein cows in 9 large-scale dairy farms from one region in Eastern Germany. All observations were from a single farm visit of the same claw trimmer which implies a data structure without repeated measurements. Hence, cows were scored at different time points for days in milk (**DIM**) between day 30 and day 305 after calving. The absence or presence of laminitis was scored as "0" or "1", respectively. Milk yield and SCS were used from the test day closest to the claw trimming date. Because cows in this study have only one observation for all traits in one particular time interval, the RRM can pull out genetic parameters for each day through the connections created by sires (Schaeffer, 2004). An overview of the data is given in Tab. 1.

The RRM sire model for this analysis was

$$y_{ij} = X_{ij} b + \sum_{m=1}^{3} u_{im} \phi_m (\mathrm{DIM}_j) + e_{ij}$$

where *y* is the vector of records on a cow from sire *i* on day *j* in milk (DIM); $X_{ij}b$ models fixed effects including herd-test-day and parity, u_i is the random effect for sire *i* and polynomial coefficient *m*, $\phi_m(\text{DIM}_j)$ denotes the values of the *m-th* orthogonal Legendre polynomial up to order 3 formed from the time covariate DIM including an intercept, and e_{ij} are the residuals. The complete vector of sire effects is assumed to have (co)variance structure $G \otimes A$, where *A* is the relationship matrix among 286 sires, and *G* is the (co)variance matrix associated with the 3 Legendre polynomials.

For the binary trait "laminitis" the threshold liability methodology (Gianola, 1982) was applied. It is assumed that an underlying continuous variable, liability λ_i, exists such that the observed binary variable y_i takes a value of 1 if λ_i is larger than a fixed threshold, and 0 otherwise. The whole analysis was done in a Bayesian framework. A single chain length of 50,000 was generated for a model with a common residual variance within trait for all DIM. The first 5,000 samples were discarded as a burn in, and the remaining samples were used to compute posterior means of model parameters. Convergence of Gibbs chains was monitored by visual inspections of plots of samples.

Daily sire variance of MY, SCS, and LAM at DIM *j* can be written as:

$$\sigma^2_{sj} = \phi_j^{'} G_s \phi_j \qquad \textbf{(1)}$$

where G_s is the 12 x 12 (co)variance matrix of the random sire regression coefficients for the three traits. Heritability of a trait at any time *j* along the lactation trajectory was estimated as:

$$h^2_j = \frac{4\sigma^2_{sj}}{\sigma^2_{sj} + \sigma^2_e} \qquad \textbf{(2)}$$

Genetic correlations among combinations of traits *k* and *l* at times *j* were:

$$r_{gd} = \frac{\phi_d^{'} G_{s_{kl}} 1}{\sqrt{\sigma^2_{sd_k} \sigma^2_{sd_l}}} \qquad \textbf{(3)}$$

where $G_{s_{kl}}$ are random regression coefficients of the sire genetic covariance between traits. Equation **(1)** for different DIM *j* in vectors ϕ' and ϕ was used to estimate genetic covariances between selected DIM and the rest of the lactation for the same trait.

The sum of the additive solutions for sire *i* (for one trait) can be written as:

$$\hat{a}_i^{'} = (\hat{a}_{0\text{i}} \quad \hat{a}_{1\text{i}} \quad \hat{a}_{2\text{i}} \quad \hat{a}_{3\text{i}})$$

These are the estimated breeding values (**EBV**) for the random regression coefficients. Functions of these EBVs can be used for selection decisions. The EBV of sire *i* for one trait, e.g. LAM, on the DIM *j*, denoted as EBV-LAM_j, was calculated as:

$$EBV - LAM_{ij} = \hat{a}_{0\text{i}} + \hat{a}_{1\text{i}} c_{1\text{j}} + \hat{a}_{2\text{i}} c_{2\text{j}} + \hat{a}_{3\text{i}} c_{3\text{j}}$$

where coefficients c are the Legendre polynomials at the respective DIM *j*. An EBV for a complete lactation in the interval of DIM 30 to DIM 305 is obtained by summing the EBVs for each DIM. Estimated breeding values in all traits for the whole period were calculated for all 286 sires.

Results and Discussion

Descriptive statistics for traits and effects are given in Tab. 1. A relatively high percentage of 47.6% of cows had an entry for LAM in one or both rear legs. The system of co-operator herds for progeny testing in this region ensured a reasonable number of progeny per bull for the present analysis, and reliable genetic connectedness across herds.

Table 1. Descriptive statistics for traits.

Trait/effect	Mean	SD	Min	Max
LAM (%)	47.6			
MY (kg)	25.5	9.2	2.1	54.0
SCS[1]	4.6	1.9	-1.1	9.6
DIM (d)	160.2	84.9	30.0	305.0
Daugh./sire	15.3	12.7	1.0	612.0

[1]SCS = log2(somatic cell count / 100,000) + 3

Posterior means of daily heritabilities for MY and SCS increased with DIM (Fig. 1), i.e. from 0.21 to 0.42 for MY, and 0.11 to 0.19 for SCS at days 30 and 305, respectively. The explanation for the lower estimates of heritability at the beginning of the lactation is the lower genetic variance. This is in line with earlier studies (e.g. Negussi *et al.*, 2008).

However, it is in contrast to the results of Liu *et al.* (2001) who reported a fairly homogeneous daily heritability, especially for SCS. Posterior estimates of heritabilities for LAM were relatively constant over the observed period and in the range from 0.10 to 0.12.

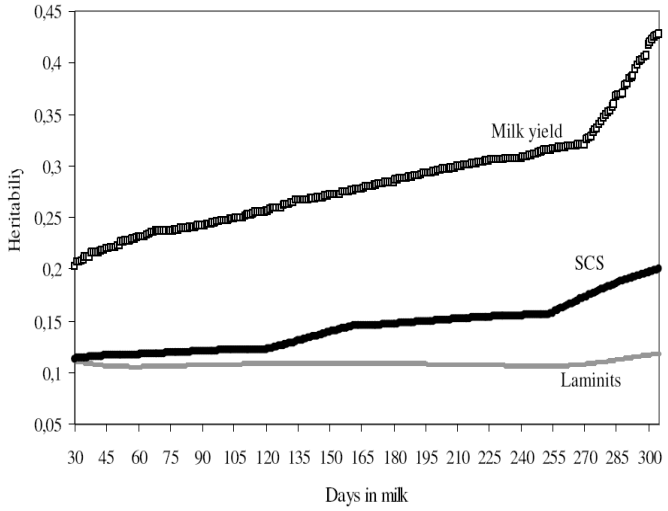

Figure 1. Trajectory of posterior means of daily heritabilities for MY, SCS, and LAM.

Genetic correlations between MY and functional traits (LAM, SCS; Fig. 2) were positive, indicating a genetically antagonistic relationship. For both combinations of traits, the genetic correlation was larger in early compared to later stages of lactation. These findings are in agreement with Negussie *et al.* (2008). In their study, genetic correlations between test day MY and clinical mastitis from the multivariate RRM were all positive and moderate, and highest during early lactation.

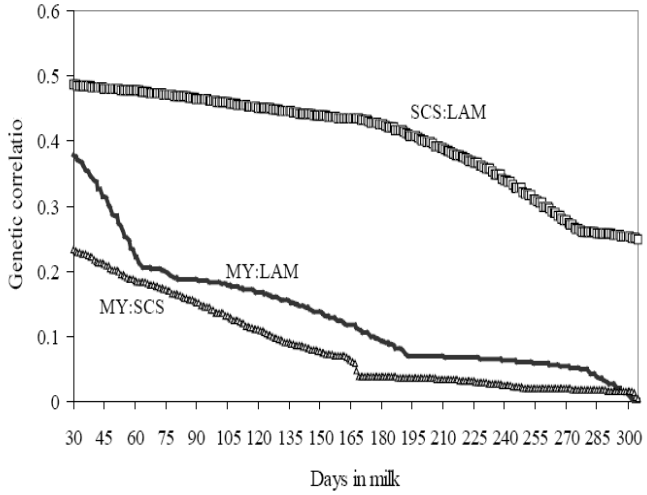

Figure 2. Trajectory of posterior means of daily genetic correlations (posterior means) among MY, SCS, and LAM.

In our study, genetic correlations between LAM and SCS were large and positive in the range between 0.49 and 0.24 over the whole trajectory. Genetically, health problems appear to occur in clusters. The positive genetic correlations suggest that cows genetically susceptible to some type of health problems are likely to be susceptible to other health problems as well.

Estimates of posterior means of genetic correlations between particular days for MY, SCS, and LAM are given in Tab. 2. The correlations between yields or incidences of disorders on days that were close together were high compared with yields or incidences on days that were farther apart. However, moderate positive genetic correlations among individual test days over the whole observed periods justify same selection strategies within all periods of lactation. Genetic correlations were substantially lower when focusing on individual test days at the end of lactation. When interpreting these results and also the genetic parameters at the end of lactation as shown in Fig. 1 and 2, the limited number of observations in this period should be kept in mind.

Table 2. Estimates of genetic correlations (x100) for selected DIM of daily yields for SCS (above diagonal) and LAM (below diagonal).

DIM	30	50	100	150	200	250	300
30		79	61	53	32	30	11
50	88		81	60	36	33	12
100	76	78		85	61	39	16
150	70	74	82		90	40	16
200	51	60	65	84		57	27
250	44	56	57	69	91		45
300	13	13	14	17	30	43	

Correlations among EBV in MY, SCS, and LAM of 286 sires for the complete observed period confirmed previous results (Tab. 3). As shown for individual test days, we found antagonistic relationships. The correlation between EBV-SCS and EBV-MY was 0.20, and 0.29 between EBV-LAM and EBV-MY. Also an increase of lactation milk yield is associated with a greater risk to be affected by any kind of disorder. However, correlations between EBV are always an underestimation of genetic correlations if accuracies of EBVs are lower than 1. The correlation between EBV-LAM and EBV-SCS was 0.39. Selecting

sires which transmit less laminitis has a positively correlated response to reduce incidences of mastitis.

Table 3. Correlations among EBV in MY, SCS, and LAM for the whole observed period.

	EBV	
	SCS	LAM
MY	0.20	0.29
SCS		0.39

Conclusions

The present analysis shows the feasibility of multivariate RRM sire modes and revealed reliable genetic parameters in the case of Gaussian and categorical traits. However, longitudinal data (= repeated measurements) for cows within lactation will enable RRM animal models and should be evaluated in ongoing research studies. Results clearly depict the antagonistic relationship between production (MY) and functionality (SCS and LAM). Previous studies dealt with different models to infer relationships among production and claw disorders, even models considering feedback situations among traits (König *et al.*, 2008) were evaluated. Despite model differences and differences in the definition of traits, e.g. test days versus whole lactation yield, antagonistic relationships were found in all studies. The assessment of selection strategies in a combined breeding goal for production and directly recorded disorders is an imperative task for the near future.

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