Estimation of Genetic Parameters for Claw Disorders in Dairy Cows Using a Random Regression Model

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Introduction

Disorders and diseases of the bovine hoof lead to economic losses due to involuntary culling, high costs of veterinary care, lower milk production and discarded milk. Claw disorders can be diagnosed at the time of hoof trimming (e.g. König *et al.,* 2005; Pijl and Swalve, 2006), and data stemming from a detailed collection of these diagnoses can be subject to various kinds of analysis with respect to environmental and genetic factors.

Random regression models (RRM) have been widely used for genetic analysis of production traits and somatic cells score (e.g. Bohmanova *et al*., 2008) as well as for fertility traits (Averill *et al*., 2006). The basic idea of the RRM consists of fitting average lactation curves for a subpopulation and animal specific curves describing deviations from the average curves (Swalve, 2000). Several functions can be used to fit fixed and random regressions (e.g. Ali and Schaeffer (1987); orthogonal Legendre polynomials).

Heritabilities have been estimated for claw disorders and ranged from 6 to 12 % using linear models whereas were varying between 8 and 33 % when applying threshold models (Pijl & Swalve, 2006; Swalve *et al*., 2008).

Material and Methods

Genetic parameters were estimated using a data set collected by René Pijl between 2000 and 2009 from 166 herds located in NW and NE Germany (Swalve *et al*., 2008). The data comprised only 26,112 Holstein cows, mostly in family farms with herd sizes of 50 to 120 with a total of 79,181 observations. At the time of trimming, claws of the cows were evaluated for indications of a disease, scored and recorded electronically. Since sub-clinical as well as clinical cases were recorded, the term "disorder" is more appropriate than "disease". Disorders were coded by either zero or one; i.e. the nature of the data was binary. The most important disorder was laminitis with an incidence rate of 37 %.

The traditional threshold model postulates a linear model between the discrete observable phenotype (y_i) and a non-observable, continuous and normal distributed underlying variable (z_i) satisfying the following condition: $z_i = \eta_i + e_i$

$$y_i = \begin{cases} 1 & \text{if } z_i > \tau \\ 0 & \text{if } z_i =< \tau \end{cases}$$ where $z_i \sim N(\mu_i, \sigma^2_e)$ and τ is a threshold value.

$$\eta = Xb + Z_p p + Z_a a$$

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Where b is the vector of fixed effects, a and p are the vectors of random effects; X, Z_p and Z_a are design matrices for fixed and random effects.

$Var(p) = P = I_p \otimes P_0$, $\quad Var(a) = G = A \otimes G_0$

where P_0 and G_0 are permanent environmental and additive genetic (co)variance matrices, respectively. I_p is the identity matrix, A is the relationship matrix and $\otimes$ is direct product. Under a random regression model (RRM), G_0 is a matrix of order $k \times k$ that contains the variance components for the random regression coefficients and it can be estimated directly from the data (Meyer, 1998). $\hat{G} = \Phi G_0 \Phi`$ where $\hat{G}$ is an approximation of G_0 and the matrix Φ of order $t \times k$ contains the coefficients of the function used and evaluated at t standardized trajectory points (days in milk). Heritabilities on the liability scale at time t are defined as $h_t = (\hat{G} *4)/(\hat{G}+\sigma^2_p + \sigma^2_e)$ where $\sigma^2_e = 1$ applying a probit link function. Using a logit link function, the residual variance has to be corrected by the factor $\pi^2/3$ (König *et al*., 2005).

The comparison of models with and without random regressions was performed using the likelihood ratio test (LRT) as described by Mielenz *et al*. (2006) and Akaike's (AIC) information criteria (Akaike, 1973). The information criteria can be described as AIC=-2logL+2p where p is the number of variance components and logL is the logarithm of the restricted maximum likelihood function. A lower AIC indicates a better fit. The following models were used to estimate the genetic parameter for laminitis.

$$PR(Y_{hijkm}) = \theta(\mu + HV_h + LA_i + DCL_j + a_k + p_k) \quad (1)$$

$$PR(Y_{hijklm}) = \theta(\mu + HV_h + LA_i + DCL_j + s_l + p_k) \quad (2)$$

$$PR(Y_{hijklm}) = \theta(\mu + HV_h + LA_i + DCL_j + \sum_{c=0}^{n} b_{lc}.s_{lc} + p_k) \quad (3)$$

θ= link function, PR = probability of occurrence and μ = Overall mean.

Y_{hijkm} or Y_{hijklm} = treatment of claw disorder (1 = positive 0 = negative)
HV_h = fixed effect of herd-visit h (h=1,..., 791)
LA_i = fixed effect of lactation number i (i = 1, 2, …, ≥ 4)
DCL_j = fixed effect of milk day j (j = 1, …, 7: with classes of 50 days)
a_k = random animal effect for animal k (additive genetic variance)
p_k = random permanent environmental effect of animal k
s_{lc} = c-th random regression coefficient of sire l for genetic effect (c=0 to n)
b_{lc} = c-th term of legendre polynomial of random curve for sire k (n=1 or 2) where

$$b_{.0} = \sqrt{\frac{1}{2}}\ x^0,\ b_{.1} = \sqrt{\frac{3}{2}}\ x^1, b_{.2} = 0.5\sqrt{\frac{5}{2}}\ (3x^2 - 1) \text{ with } x = \left[2(\text{dim} - 5)/(350 - 5)\right] - 1$$

Results and Discussion

Estimates of heritabilities, their standard errors along with AIC values to compare the fit of the models are given in Table 1. The best model according to the AIC criterion and the likelihood ratio test was the sire RRM (2^{nd} order Legendre polynomial) applying the probit link function. The sire RRM was significantly better than the sire or animal model without

random regression. König *et al*. (2008) applied a sire RRM for the analysis of laminitis data and found that heritabilities were relatively similar across lactation and ranged between 0.10-0.12. In this study, the heritability ranged between 0.15-0.23. An earlier study by our group (Swalve *et al*. 2008), using data that was included in the present study, yielded estimates of heritabilities in the range of 0.13-0.20 for laminitis. Huang *et al.* (1995) reported a heritability for laminitis cases of 0.14. Across all models used in this study, estimates of heritability were higher using the probit function than when applying the logit function.

Table 1: Estimates of heritabilities and AIC values from sire and animal models and mean heritability from a sire RRM for the incidence of laminitis

	Models without random regressions				Sire RRM			
	Sire model		Animal model		Legendre order=1		Legendre order=2	
	logit	probit	logit	probit	logit	probit	Logit	Probit
h^2	0.17	0.20	0.16	0.19	0.17	0.20	0.18	0.21
SE	0.019	0.021	0.011	0.013	-	-	-	-
AIC	20480	17527	20602	17551	20461	17505	20444	15223

RRM estimates of heritabilities, genetic and phenotypic correlations for selected days throughout the lactation are presented in Table 2. Genetic correlations between individual time points (days in milk) were between 0.64 and 0.99. Genetic correlations between very early days in the lactation and mid-lactation or late lactation time points are relatively small. After 80 days in milk, the genetic correlation with later points in time stabilizes at > 0.90. In comparison to the results of König *et al.* (2008), estimates of the correlations in this study were higher, probably due to the larger data set.

Table 2: Estimates of heritabilities (on diagonal), additive genetic correlations (above diagonal), and phenotypic correlations (below diagonal)

	Days in milk						
Days in milk	30	70	100	150	200	250	320
30	0.21	0.97	0.92	0.84	0.79	0.78	0.84
70	0.17	0.19	0.98	0.94	0.91	0.90	0.94
100	0.15	0.16	0.19	0.98	0.95	0.93	0.94
150	0.14	0.16	0.17	0.21	0.99	0.99	0.99
200	0.13	0.16	0.17	0.18	0.22	0.99	0.99
250	0.12	0.16	0.17	0.19	0.19	0.22	0.99
320	0.13	0.15	0.16	0.17	0.18	0.19	0.21

Estimates of heritabilities for laminitis cases from different sire RRM in comparison to models without random regression are displayed in Figure 1. Fitting Legendre polynomials of order 2 resulted in a pronounced curvilinear shape of the estimates. Heritability estimates were high at the beginning of lactation which may be taken as a hint on the difficulty to obtain estimates at the margins of the trajectory. Highest estimates were found for 150 to 250

days in milk. Hence, at least for laminitis, this should be the period to collect information if hoof trimming data is recorded as a basis for genetic evaluations.

Figure 2 presents curves of estimated breeding values for the seven most frequently used sires. Apart from differences in the average level of EBVs, it can be seen that differences between sires are especially visible in the period that exhibits highest heritabilities.

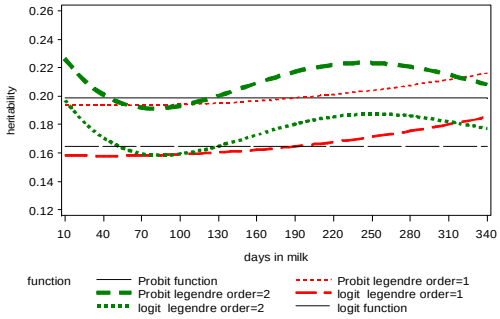

Figure 1: Estimates of heritabilties for laminitis cases from different models

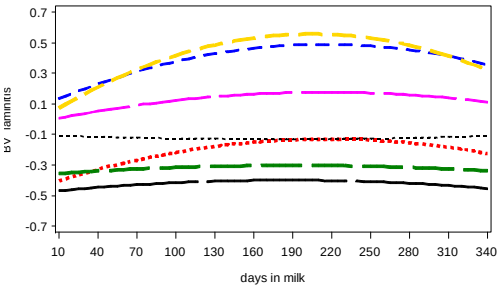

Figure 2: EBV curves for the most frequent bulls

Conclusion

The results show the feasibility of applying random regression models to claw disorder data that has been collected at hoof trimming. Compared to many estimates of heritabilities for disease resistance or disorders, the heritabilites found in this study for the incidence of laminitis are high. Using a random regression model for improved handling of the effect of days in milk, a period (DIM 150 to 250) could be identified which yields optimal results with respect to the genetic differentiation between animals.

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