Exploring Relationships between Calving Difficulty and Reproductive Disorders in Austrian Fleckvieh Cows using a Recursive Threshold Model

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Introduction

The relationships among calving difficulty (CD) and reproductive disorders are complex. It is well established that dystocia increases the risk of retained placenta and puerperal metritis (Sheldon et al. (2008)). Some studies reported that genetic associations exist among CD and reproductive disorders. For example, Schnitzenlehner et al. (1998) estimated a low positive genetic relationship between maternal CD and retained placenta. Heringstad (2009) and Koeck et al. (2010) found positive genetic correlations among various reproductive disorders. Further, cows with uterine infections appear to have a higher risk of ovarian cysts (Peter (2004)). Structural-equation models allow disentangling covariance structures as outlined by Gianola and Sorensen (2004). Our objective was to study phenotypic and genetic relationships between CD, early reproductive disorders (ER) and late reproductive disorders (LR) in Austrian Fleckvieh cows using a recursive threshold model.

Material and methods

Data. Data for CD were from the Austrian Dairy Herd Recording System. Health data were provided by the Austrian project "Health monitoring in cattle" in which diagnoses from veterinarians are recorded. Only records from herds participating actively in the health-recording system were considered. A detailed description of the health recording system and data validation is given by Egger-Danner et al. (2007) and Koeck et al. (2010). Records from the first five lactations of Austrian Fleckvieh cows calving between January 1, 2007 and November 30, 2008, were included. Age at first calving was required to be between 19 and 43 months, and records of cows with a calving interval shorter than 300 d or longer than 800 d were excluded. Only cows with observations for CD and health data were included. Records from multiple births, fetotomy or with unknown sex of calf were discarded. Only one record per cow was considered (the first), irrespective of parity. The data set was restricted further to sires with at least 10 daughters, and herd-year-season classes containing at least 3 calving cows. The edited data set included a total of 12,292 cows from 1,248 herds. Farmers score CD in 4 categories: 1 = no assistance, 2 = slight assistance, 3 = needed

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assistance and considerable force, and 4 = caesarean. Because caesareans occur rarely, they were combined with the third category. About 44 % of the cows did not need help, 50 % needed slight assistance and 6 % had a difficult calving. Absence or presence of each of the reproductive disorders was coded as 0 or 1 based on whether or not the cow had at least one veterinary treatment within the first 30 d after calving for ER, which included retained placenta, puerperal diseases and metritis, and within 31 to 150 d after calving for LR including metritis, silent heat/anestrus and cystic ovaries. Mean frequencies of ER and LR were 4.4% and 13.4%, respectively. The sire pedigree file had information on 1,073 males, including the 312 sires with daughters in the data set.

Recursive threshold model. A trivariate recursive threshold model was used for analysis of the trichotomous trait CD and the binary traits ER and LR. The threshold model postulates an underlying continuous variable, liability (l). The observed categorical variable is j if $T_{j-1} \leq l < T_j$, where T_j are thresholds, and j = 1,2, …, J indexes the category to which the observation belongs. The threshold T_1 was set to zero for each of the traits for the sake of parameter identification. The recursive model assumes that liability to CD affects liabilities to ER and LR. Further, it was assumed that liability to ER has a recursive effect on liability to LR. In matrix notation the recursive threshold model can be described as: $\Lambda y = X\beta + Z_h h + Z_s s + e$

where $\Lambda = \begin{bmatrix} 1 & 0 & 0 \\ -\lambda_{21} & 1 & 0 \\ -\lambda_{31} & -\lambda_{32} & 1 \end{bmatrix}$ is a matrix of structural coefficients among traits 1 (CD), 2

(ER), and 3 (LR); λ_{ij} describes the rate of change in trait i with respect to trait j; y concatenates vectors of unobserved liabilities to CD, ER and LR; β is a vector of effects of age at calving-parity classes (8 levels) for all traits, year-season of calving (6 levels) for all traits, and sex of calf (2 levels) for CD; h is a vector of herd-year-season of calving effects (2,819 levels); s is a vector of sire effects; e is a vector of residuals; and X, Z_h, and Z_s are the incidence matrices. Age at first calving was grouped into <27, 27 to 28, 29 to 30 and >30 months, to form 4 levels for 1st parity. For older cows, age-parity classes were parities 2, 3, 4, and 5. Seasons were: January-March, April-June, July-September and October-December. The SirBayes package (Wu et al. (2007)) was used for analysis. A Bayesian approach using Gibbs sampling was applied, with a normal prior distribution for β and independent inverse Wishard prior distributions for h and s. Based on visual examination of trace plots and additional diagnostic checks, a chain length of 150,000 samples was run, after a burn-in of 10,000 iterations, and all these samples were used for inference. Parameters from the recursive model pertain to the system, and they need to be converted in order to be comparable to their counterparts in the standard mixed model, following the relationships described by Gianola and Sorensen (2004).

Results and discussion

A preceding study in Austrian Fleckvieh found that reproductive disorders occurring mainly around calving, such as retained placenta, puerperal diseases, and metritis were highly correlated; also, silent heat/anestrus and cystic ovaries seem to share some of the same genetic background (Koeck et al. (2010)). Because of this, as well as to temper the well known extreme category problems of threshold models (Moreno et al. (1997)) composite traits such as ER and LR were used in this study.

Posterior distributions of the recursive effects are shown in Figure 1. These effects were all positive and the HPD95% (Highest Posterior Density at 95% probability) regions did not include 0. Posterior means of recursive effects were 0.27 from CD to ER, 0.10 from CD to LR and 0.04 from ER to LR. The positive estimates indicate direct causal effects, where an increase in liability to CD increases liabilities to ER and LR. Also, cows with ER are more likely to have LR.
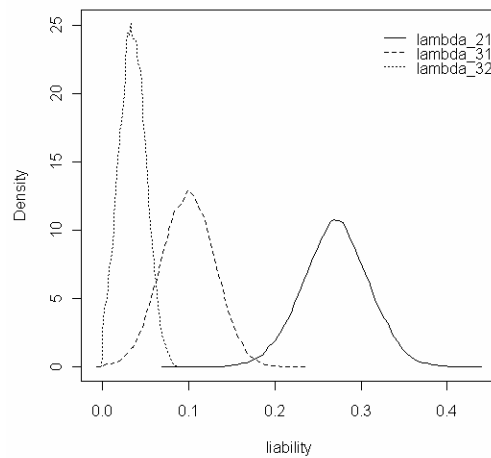
Figure 1: Posterior distributions of recursive effects (from the right) from liability to CD to ER (lambda_21), from CD to LR (lambda_31) and from ER to LR (lambda_32).

Posterior means (standard deviations) of the heritability of liability to maternal CD, ER and LR was 0.07 (0.01), 0.06 (0.03) and 0.07 (0.02), respectively (Table 1). These estimates were in agreement with previous threshold model estimates (López de Maturana et al. (2009); Heringstad (2009); Koeck et al. (2010)).

Table 1 also shows posterior means and standard deviations of genetic correlations. Moderate genetic correlations of 0.34 were obtained between maternal CD and ER and maternal CD and LR. The posterior standard deviations were large and results should therefore be interpreted with caution. In first lactation cows, Schnitzenlehner et al. (1998) reported a positive, albeit non-significant, genetic correlation of 0.26 between maternal CD and retained placenta. In our study, a moderate positive genetic correlation of 0.31 was found between ER and LR. This agrees with a previous estimate in Austrian Fleckvieh cows (Koeck et al. (2010)).

Table 1: Posterior mean and standard deviation (SD) of heritability (on the diagonal) and genetic correlations (above the diagonal) for maternal calving difficulty (CD), early reproductive disorders (ER), and late reproductive disorders (LR)

	CD	ER	LR
CD	0.067 (0.016)	0.341 (0.177)	0.337 (0.162)
ER		0.064 (0.029)	0.310 (0.193)
LR			0.066 (0.022)

The sire of the calf (direct effect) was not included in the model for CD, because the available software program precluded this. In the study of Koeck et al. (2010), correlations between estimated breeding values revealed a negative (P-value = 0.12) relationship between direct CD and ER. Thus, both genetic effects, direct and maternal, should be considered for CD in further studies.

Conclusion

Recursive effects from CD to ER and LR were positive and significant. Moreover, a positive causal effect from ER to LR was detected. Moderate genetic correlations between maternal CD and either ER or LR suggest that genetic selection for maternal calving ease will also improve resistance against early and late reproductive disorders.

Acknowledgments

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