Genetic Analysis Of Diarrhea And Respiratory Diseases In Austrian Fleckvieh Heifer Calves

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Introduction

A routine registration system is an essential prerequisite for the reduction of disease frequencies by both, management and breeding. However, in Scandinavian countries with a long history of health registration and also in Austria, where health registration just started recently, the main focus is on lactating cows. While support for management (Egger-Danner et al. (2007a)) is also provided for replacement stock, no routine breeding value estimation exists for this group of animals in either country. Continued non-consideration of calfhood diseases could however lead to increased disease incidence. Gastrointestinal and respiratory diseases were shown to be among the main health problems during the calves' first months of life (e.g. Gulliksen et al. (2009); Svensson et al. (2003)). In dairy cattle, genetic parameters were only estimated for respiratory diseases in Norwegian Red calves (intraherd heritability 0.05 on the underlying scale; Heringstad et al. (2008)). The aim of this study thus was the genetic analysis of diarrhea and respiratory diseases in female Austrian Fleckvieh (dual purpose Simmental) calves by means of a Bayesian probit threshold sire model.

Material and methods

Data. All data were provided by ZuchtData EDV-Dienstleistungen GmbH being responsible for the Austrian Dairy Herd Recording System. Health data were collected within the Austrian project "Health monitoring in cattle" in which diagnoses from veterinarians are recorded. Only records from herds actively participating 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. (2007b) and Koeck et al. (2010). In total, records from 35,506 Austrian Fleckvieh heifer calves born between January 1, 2007 and April 3, 2009 were provided. The data set was restricted to sires and herd classes with a minimum of 10 and 5 heifer calves, respectively. After edits, the final data set included a total of 32,523 Fleckvieh heifer calves from 2,078 herds. The sire pedigree file had information on 1,187 males, including the 455 sires with heifer calves in the data set. Diarrhea and respiratory diseases were defined as binary traits (1 or 0) based on whether or not the calf had at least one veterinary treatment within the first 180 days of age.

Model. A Bayesian probit threshold sire model using the RJMC routine implemented in the DMU software (Madsen and Jensen (2008)) was used for analyzing the binary disease data.

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The threshold model postulates an underlying continuous variable, liability (λ). The observed binary response (diarrhea, respiratory diseases) takes a value of 1 if λ exceeds a fixed threshold and 0 otherwise. In matrix notation the model can be described as

$\lambda = \mathbf{X\beta} + \mathbf{Z_h h} + \mathbf{Z_u u} + \mathbf{e}$,

where λ is the vector of unobserved liabilities to diarrhea and respiratory diseases, **β** is a vector of the systematic effect of year (2007-2009) and season (January-March, April-June…) of birth (10 classes), **h** is a vector of herd effects (2,078 levels), **u** is the vector of sire transmitting abilities, **e** is a vector of residuals, and $\mathbf{X}$, $\mathbf{Z_h}$ and $\mathbf{Z_u}$ are corresponding incidence matrices. A Bayesian approach using Gibbs sampling was applied. Inference was based on a chain length of 300,000 samples collected after a burn-in of 50,000 iterations.

Results and discussion

Mean frequencies of diarrhea and respiratory diseases were 2.8% and 3.5%, respectively and are thus similar to values reported for both sexes and selected herds in Sweden and Norway (Svensson et al. (2003); Gulliksen et al. (2009)). However, mean frequency of respiratory disease of calves in the Norwegian Cattle Health Recording System was reported to be much lower (0.7%; Heringstad et al. (2008)) suggesting an inferior quality of routinely recorded data. In accordance to Gulliksen et al. (2009), diarrhea mainly first occurred early in life while first occurrence of respiratory diseases was more equally distributed (Figure 1).

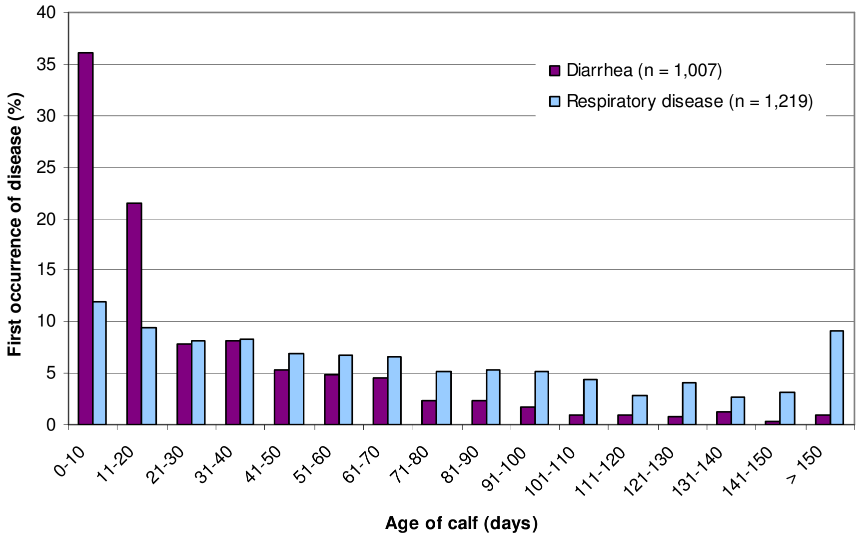

Figure 1: Age distribution for first occurrence of diarrhea (n = 1,007) and respiratory diseases (n = 1,219) in 35,506 calves until 180 days of age

The results from the Bayesian probit threshold model are given in Table 1, where mean and SD of the posterior distributions of variance components and heritability of liability to diarrhea and respiratory diseases are shown. The posterior means (SD) of heritability of liability to diarrhea and respiratory diseases were 0.027 (0.015) and 0.039 (0.017). The intraherd heritability for respiratory diseases is in accordance with the value of 0.05 reported for Norwegian Red calves (Heringstad et al. (2008)). Applying a logit threshold sire model, a lower heritability (<0.01) was found for digestive diseases in Danish Holstein heifers before first calving (Fuerst-Waltl and Sørensen (2009)). As illustrated by Figure 2, both distributions of the heritabilities of liability to diarrhea and respiratory diseases were reasonably sharp but showed long tails to the right. As suggested by Heringstad et al. (2008), low frequencies of both diseases and consequently rather low phenotypic variability resulting in imprecise inference about genetic parameters may have caused the latter finding.

Table 1: Means and standard deviations (SD) of the posterior distributions of sire and herd variance and of heritability of liability to diarrhea and respiratory diseases

	Diarrhea		Respiratory diseases	
	Mean	SD	Mean	SD
Sire variance	0.010	0.006	0.015	0.007
Herd variance	0.490	0.048	0.498	0.045
Heritability[1]	0.027	0.015	0.039	0.017
Heritability, intraherd[2]	0.040	0.022	0.058	0.025

[1] Heritability: $h^2 = 4\sigma_s^2 / (\sigma_s^2 + \sigma_h^2 + 1)$

[2] Heritability, intraherd: $h^2 = 4\sigma_s^2 / (\sigma_s^2 + 1)$

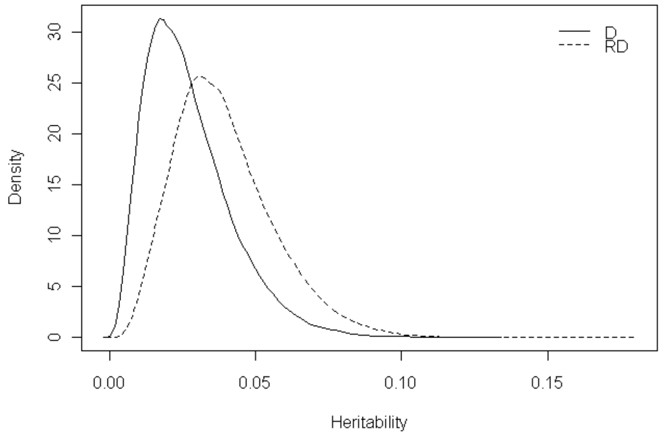

Figure 2: Posterior distributions of heritability [$h^2 = 4\sigma_s^2 / (\sigma_s^2 + \sigma_h^2 + 1)$] of liability to diarrhea (D) and respiratory diseases (RD)

Conclusion

With regard to calf diseases, ethical issues and the economic impact on cattle breeding should not be neglected. Calf diseases are however not considered in any breeding program so far. In Austrian Fleckvieh, relatively low frequencies of digestive and respiratory diseases are observed. Heritabilities for these traits are rather low, but in the range of other functional traits, for which genetic improvement is achieved. However, in younger calves, where especially diarrhea is a problem, treatments for groups of calves may take place which are not assigned to individual calves and are hence not recorded. Besides, currently ear tag numbers of male calves are not available for veterinarians using herd management programs. Thus, it is possible that actual frequencies of these calfhood diseases are underestimated. As diseases at an early age are likely to be connected with diseases during adulthood (Heringstad et al. (2008)), more effort should be put on improving the calves' health data quality. Monitoring of the population and of extreme bulls might be very useful for breeding organizations to avoid deterioration in these traits.

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