

Short Communication: Genetic Analysis of Respiratory Disease in Norwegian Red Calves

B. Heringstad,*†¹ Y. M. Chang,‡ D. Gianola,*§ and O. Østerås#||

*Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, PO Box 5003, N-1432 Ås, Norway

†Geno Breeding and A. I. Association, PO Box 5003, N-1432 Ås, Norway

‡Division of Genetic Epidemiology, Cancer Research UK Clinical Centre, St James's University Hospital, Leeds, LS9 7TF, United Kingdom

§Department of Dairy Science, University of Wisconsin, Madison 53706

#Norwegian Cattle Health Services, TINE Norwegian Dairies B.A., PO Box 58, N-1430 Ås, Norway

||Department of Production Animals, Clinical Sciences, Norwegian School of Veterinary Science, PO Box 8146, Dep. N-0033 Oslo, Norway

ABSTRACT

A genetic analysis of respiratory disease (RD) in Norwegian Red calves was conducted. This is the first genetic study of calf diseases based on data from the Norwegian health recording system, and RD was chosen because it is the most frequent disease in calves. Records on absence or presence of RD before 180 d of age for 250,212 calves (progeny of 728 Norwegian Red artificial insemination sires) were analyzed with a threshold model. A total of 0.7% of the calves had veterinary treatment of RD before 180 d of age. Heritability of RD in the underlying scale was 0.05, with a 95% credibility interval from 0.02 to 0.09. The “worst” sire had a predicted probability of RD that was more than twice as high as that of the “best” one (1.15 vs. 0.44%). Their 95% credibility intervals for predicted probability of RD, however, overlapped. With improved and more extensive recording of calf diseases, the precision in genetic evaluation of sires could increase considerably. The frequency of RD is very low in the Norwegian Red population at present, so there is not much scope for genetic improvement. However, this study indicates that reasonably precise genetic evaluation of sires for resistance to RD could be feasible.

Key words: calf, heritability, respiratory disease, threshold model

Most genetic studies of health and diseases in dairy cattle have focused on lactating cows, and little research has been done on quantitative genetics of calf diseases. In a review, Shook (1998) stated that genetic studies of calf-hood diseases in commercial herds were nonexistent, and concluded that more knowledge was needed for making decisions about the inclusion of these traits

in breeding programs. There are some genetic studies of postnatal mortality in dairy calves (Erf et al., 1990; Hansen et al., 2003), and Maltecca et al. (2006) found that crossbreeding with Jersey leads to an improvement in calf health and survival relative to performance in purebred Holsteins. No genetic study of specific diseases in dairy calves could be found in the literature.

In beef cattle, bovine respiratory disease (RD) is the most common and costly disease affecting calves and genetic variation has been detected for this trait. Using data from a large experimental herd at Clay Center (Nebraska), Muggli-Cockett et al. (1992) and Snowden et al. (2005) found estimates of heritability ranging from 0.07 to 0.19 for RD in preweaned beef calves.

Clinical disease data are integrated into the Norwegian Dairy Herd Recording System and involve records of all veterinary treatments applied on an individual cow basis. In recent years, effort has been made toward including calves and young animals into this health recording system. Although not all herds report calf diseases yet, there are data available for genetic studies. The objective was to conduct a quantitative genetic analysis of RD in Norwegian Red calves. In this first genetic study of calf diseases based on data from the Norwegian health recording system, RD was chosen because it is the most frequent disease in calves.

Data included all Norwegian Red calves born from January 1, 2000, through June 30, 2006. Because not all herds report calf diseases, recording of dehorning, which is treated as a health record, was used to test whether herds reported disease records on calves. Only data from herds with records of dehorning were included in this study. Data were restricted further to include only progeny of Norwegian Red AI sires with at least 50 calves in the data set. The final data set had information on 250,212 calves, the progeny of 728 sires.

Here, RD includes diseases with any clinical symptoms in the respiratory tract. The Norwegian cattle population is free from bovine infectious rhinotracheitis (IBR), with the last case reported in 1993 (Mørk and

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¹Corresponding author: bjorg.heringstad@umb.no

Hellberg, 2005); bovine viral diarrhoea virus (**BVDV**), with the last case in 2005 (Nyberg et al., 2006), and probably also *Mycoplasma bovis*, because it has not been detected (Lie et al., 2007). The most prevalent agents in relation to RD in the Norwegian population have been bovine respiratory syncytial virus (**BRSV**) and parainfluenza-3 virus (**PI-3**; Lie et al., 2007).

Respiratory disease was defined as a binary trait (0 or 1) based on whether the calf had at least one veterinary treatment of RD before 180 d of age. About 0.7% of the calves had RD, and average age at treatment was 51 d. In 50% of the RD cases the calf was less than 40 d old, and about 90% of the cases took place before 120 d of age. About 19% of the calves, of which 85% were bull calves, were sold or culled from the herd before they were 180 d old (on average at 91 d). The risk of RD may have been somewhat understated for these calves because they had a shorter period at risk. Bull calves (51% of the records) had a slightly lower frequency of RD than heifer calves (0.63 vs. 0.73%). In Norway, calving difficulty is recorded in 4 categories: 1 = easy calving, 2 = slight problems, 3 = difficult calving, or 4 = "unknown," with 91.0, 4.5, 2.0, and 2.5% of the records in category 1, 2, 3, and 4, respectively. This information was used to define a binary variable: calf born with difficulty, which was scored as "yes" if calving difficulty score was 2 or 3, and "no" otherwise. Calves born with difficulties (6% of the calves) had a greater frequency of RD compared with other calves (1.08 vs. 0.65%). Respiratory disease is more frequent in larger herds. The mean frequency of RD was 0.54% in herd-year classes with fewer than 10 calves and 1.60% in herd-year classes with more than 30 calves. Therefore, a variable to take into account the number of contemporary calves was defined: number of calves born in the same herd \times year \times month (**HYM**) was counted and recoded into 11 classes (1, 2, ..., 10, >10), where >10 was defined as 1 group because 91% of the calves were born in HYM classes with <11 calves.

The pedigree file had information on sires and maternal grandsires of the 728 bulls with progeny in the data set, traced back as far as possible, and included a total of 1,241 males.

A threshold-liability model (e.g., Gianola and Foulley, 1983) was used for analysis of the binary RD data. The threshold model postulates an underlying continuous variable, liability (λ), such that the observed binary response (RD) takes value 1 if λ exceeds a fixed threshold and 0 otherwise. The threshold and the residual variance (σ_e^2) are not identifiable in binary data analysis, so these parameters were set equal to 0 and 1, respectively. A linear sire model was used for analysis of liability to RD. In matrix notation, the model can be written as $\lambda = \mathbf{X}\beta + \mathbf{Z}_h\mathbf{h} + \mathbf{Z}_u\mathbf{u} + \mathbf{e}$, where λ is a vector of

unobserved liabilities to RD; β is a vector of systematic effects, including year and month of birth (7 and 12 classes, respectively), sex of calf (2 classes), calf born with difficulty (2 classes), and number of calves born in the same HYM (11 classes); \mathbf{h} is a vector of herd effects (6,801 levels); \mathbf{u} is a vector of sire transmitting abilities; \mathbf{e} is a vector of residuals, and \mathbf{X} , \mathbf{Z}_h , and \mathbf{Z}_u are the corresponding incidence matrices.

A Bayesian approach using Markov chain Monte Carlo methods (e.g., Sorensen and Gianola, 2002) was implemented. Independent uniform priors were assigned to each of the elements of β . Herd and sire effects were assigned the normal prior distributions $\mathbf{h} \sim N(0, \mathbf{I}\sigma_h^2)$ and $\mathbf{s} \sim N(0, \mathbf{A}\sigma_s^2)$, respectively, where \mathbf{I} is an identity matrix, \mathbf{A} is the additive relationship matrix, and σ_h^2 and σ_s^2 are the herd and sire variances, respectively. Independent scale inverse chi-square priors were used for the unknown variance components (σ_h^2 and σ_s^2). Draws from the posterior distribution of the parameters were obtained using a Gibbs sampler. Inferences were based on 400,000 samples for each parameter, collected after a burn-in of 20,000 iterations. The effective sample size was 4,700 for σ_s^2 and 11,000 for σ_h^2 .

Genetic evaluations of sires (posterior means) were computed in the liability scale, and used to predict probabilities of RD (sire evaluation in the probability scale) with corresponding 95% probability intervals. The probability of no RD in a large future progeny group of sire j was assessed as $\Pr(y_j = 0 \mid \mu, s_j) \approx \Phi(\mu + \bar{s}_j)$, where y_j is the binary response taking the value 0 if the calf is healthy and 1 otherwise; μ is the population mean liability; \bar{s}_j is the posterior mean of transmitting ability in the liability scale for sire j ; and $\Phi(\cdot)$ is the cumulative standard normal distribution function.

The mean frequency of RD in Norwegian Red calves (0.7%) was much lower than in other studies. In a study of Jersey \times Holstein crossbreeds in the United States, Maltecca et al. (2006) reported that 33% of the calves had some degree of RD during the first 7 d after birth. In preweaned beef calves, Snowden et al. (2005) found incidences of RD (from birth to weaning at an average of 194 d) varying from 3.3 to 23.6% between years, with an overall average of 10.5% from 1983 through 2001. Their study included 9 purebred and 3 composite breeds, and the mean incidence of RD varied from 8 to 19% among breeds. Respiratory disease is a complex of illnesses, caused by many different microorganisms, showing different clinical signs, and several predisposing causes and environmental risk factors have been associated with RD (Snowden et al., 2006). The most prevalent agents in relation to RD in the Norwegian population are BRSV and PI-3, as Norway is free from IBR, BVDV, and probably *Mycoplasma bovis*. The small

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