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

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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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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

Table 1. Differences in mean liability to respiratory disease between the class with the highest (maximum) and the class with the lowest (minimum) posterior mean for each of the effects

Effect	Classes, n	Maximum	Minimum	Difference in posterior mean
Birth-year	7	2006	2001	0.30
Birth-month	12	October	April	0.17
Sex of calf	2	Heifer	Bull	0.08
Born with difficulty	2	Yes	No	0.22
No. of calves in HYM ¹	11	9	1	0.25

¹HYM = herd-year-month.

average herd size in Norway is another important factor, as RD is more frequent in larger herds. Differences in production systems, climate, breed, pathogens, herd-size, data recording system, field data vs. data from experimental herds may explain the large differences in RD frequency between studies.

Although the posterior distributions of all systematic effects had large standard deviation (SD) relative to their mean values, some tendencies were observed (Table 1). Liability to RD increased with year, which may be due to improved reporting of calf diseases. April had the lowest and October the greatest effect on liability to RD. Calves born in spring and early summer (March through June) tended to have a lower liability to RD than calves born during the winter (October to February). Further, posterior mean of liability to RD was slightly greater for heifer calves than for bull calves, and calves born with difficulties had a greater posterior mean than other calves. The results also indicated that liability to RD increased as the number of calves born in the same HYM increased from 1 to 9.

Mean, SD, and 95% credibility intervals of the posterior distributions of variance components and heritability of liability to RD are given in Table 2. Differences between herds were paramount, with herd accounting for more than 30% of the variance in the underlying scale. Posterior mean (SD) of heritability of liability to RD was 0.05 (0.018). The posterior distribution of heritability of liability to RD had a slightly longer tail to the right (Figure 1). This may be because low incidence of RD, and thus little phenotypic variability, makes inference about genetic parameters imprecise. It is clear, however, that the true value of heritability is

unlikely to exceed 0.12. No previous estimates of heritability of RD in dairy calves were found in the literature. Using linear models, Muggli-Cockett et al. (1992) and Snowden et al. (2005) estimated heritability of RD in beef calves at 0.10 and 0.07 to 0.19, respectively. Because heritability estimates from linear models are dependent on disease incidence, these results cannot be compared directly with ours. Snowden et al. (2005) converted their estimate to the underlying scale using the approximation of Robertson and Lerner (1949), and found a heritability of RD of 0.48, which is much higher than our estimate.

Predicted probability of RD for sires varied from 0.44 to 1.15% (Table 3); that is, the lowest-ranking sire had a predicted probability of RD that was more than twice as high as that for the highest-ranking sire. However, the 95% credibility intervals overlapped (Table 3), which is not surprising in light of the low incidence of the disease. With improved and more extensive re-

Table 2. Mean, standard deviation, and 95% credibility interval (CI, 2.5 and 97.5 percentiles) of posterior distributions of sire variance, herd variance, and heritability of liability to respiratory disease

Parameter	Mean	SD	95% CI
Sire variance (σ_s^2)	0.01	0.005	0.006 to 0.024
Herd variance (σ_h^2)	0.48	0.032	0.417 to 0.543
Heritability [$h^2 = 4\sigma_s^2/(\sigma_s^2 + 1)$]	0.05	0.018	0.024 to 0.093

Figure 1. Posterior distribution of heritability [$h^2 = 4\sigma_s^2/(\sigma_s^2 + 1)$] of liability to respiratory disease.

Table 3. The 5 highest- and 5 lowest-ranking sires based on predicted probabilities (%) for respiratory disease (RDprob) and the corresponding 95% credibility interval (CI, 2.5 and 97.5 percentiles)

Sire rank	RDprob,%	95% CI
1	0.44	0.25 to 0.74
2	0.44	0.27 to 0.72
3	0.45	0.31 to 0.65
4	0.46	0.28 to 0.75
5	0.47	0.26 to 0.81
724	1.00	0.72 to 1.38
725	1.01	0.73 to 1.38
726	1.03	0.60 to 1.71
727	1.06	0.66 to 1.66
728	1.15	0.63 to 2.03

cording of calf diseases, the precision in genetic evaluation of sires could be improved.

Although heritability is low (0.05), selection could be reasonably accurate if the trait were recorded in large progeny groups, as in the Norwegian Red breed. This trait can be observed in both sexes, potentially doubling the amount of information available for sex-limited traits such as mastitis and fertility, the latter having a lower heritability than RD (Andersen-Ranberg et al., 2005). The frequency of RD and other calf diseases is very low in the Norwegian Red population and, therefore, under the present conditions, there is not much scope for genetic improvement.

Information on calf diseases may also provide potential early indicators of general disease resistance. Heringstad et al. (2005) found that the genetic correlations among mastitis, ketosis, milk fever, and retained placenta, 4 very different diseases, were positive, which indicates the existence of some general disease-resistance factor with a genetic component. In the future it could be of interest to examine genetic associations between RD in calves and other diseases (e.g., mastitis) in dairy cows. Possible carryover effects on other traits, such as growth, fertility, and production later in life is another reason why data on RD, and other calfhoo diseases, may be valuable from a breeding perspective.

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