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Genetic and environmental effects on claw disorders in large-scale dairy farms

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Introduction

As the level of milk production in dairy cattle increases, correlated responses of health problems need to be studied further. Health problems result in higher culling rates, increased veterinary costs, and losses due to lower production and discarded milk. In recent years, research on health traits has concentrated on fertility and mastitis. In the Nordic countries for example, clinical mastitis has been included in dairy cattle breeding objectives since the late 1970s. Genetic evaluation is based on defining the trait as a binary response in a linear model (Heringstad et al., 2000). In recent years, involuntary cullings because of feet and leg disorders are of similar concern.

Much of the variability in feet and leg health is associated with environmental effects, but several studies have revealed genetic impact in such traits. For selection to be effective, reliable estimates of genetic parameters of claw disorders are needed to determine the amount of genetic variation available. Correlations with other variables of economic importance are also needed. The objective of this study was to determine the effects of milk yield, parity, housing systems and feeding strategies on sole ulcers, horn erosion, digital dermatitis and limax. Further heritabilities and genetic correlations were estimated between these claw disorders and other productive and functional traits.

Material

The data set comprised test day records and claw disorders recorded in 2003 of rear legs from 5634 Holstein cows in 9 large-scale dairy farms from one region within Eastern Germany. Claw diseases were divided in four different categories (digital dermatitis, sole ulceration, horn erosion and limax) and analysed separately. Each cow was given a six-week-possibility in 2003 to fall ill because of feet and leg disorders. Disorders were scored on an all or none basis. If a cow had the health problem, she was given a score of 1; otherwise she was given a score 0. Repeated measurements of same claw diseases were not taken into account and incidences of rear legs right and rear legs left were regarded as same traits. Figure 1 gives an overview of mean incidences of claw disorders in the complete data and in herds with highest and lowest incidences for each trait. For sires of cows with at least 40 daughters in the claw database, correlations between breeding values for functional type traits (official national German breeding values from 02/2004) and breeding values of claw disorders were calculated.

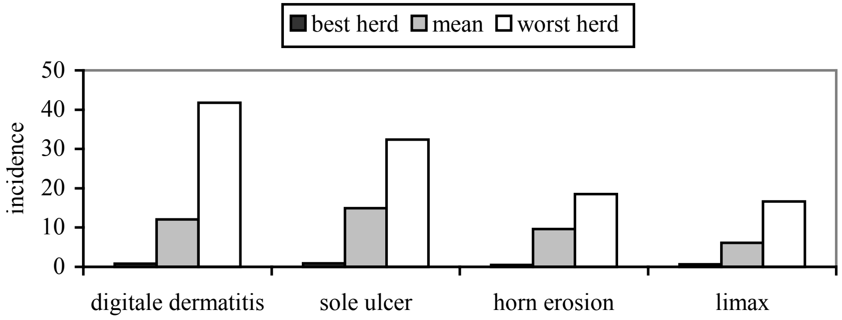

Figure 1: Incidences of claw disorders

Method and Models

Because disorders are binary, the residuals cannot be normally distributed. The best line to describe the relationship between the dependent and independent variables is not likely to be linear, but rather than S-shape. This is the primary reason why the Logit transformation function (GLIMMIX-Makro, SAS) was used to determine the impact of environmental effects on claw disorders. The average in milk yield of control 1 and control 2 after calving was fitted as a covariate in the model. Somatic cells were transformed to Somatic Cell Score using SCS = $\log_2$(somatic cells/10000)+3. The complete model was:

$$\text{Logit}(\pi_{rstu}) = \varphi + \gamma_r + \theta_s + \beta X_{rs} + \gamma_r{*}\beta X_{rs} + \varepsilon_{rstu}$$

π_{rstu} = probability of occurrence for claw disorder
φ = overall mean effect
γ_r = fixed effect of parity
θ_s = fixed herd effect
βX_{rs} = linear regression of milk yield on claw disorder
$\gamma_r{*}\beta X_{rs}$ = linear regression of milk yield on claw disorder within parity
ε_{rstu} = random residual effect

The main objective of this study was to estimate heritabilities of claw disorders using normal (identity), logistic and threshold models. ASReml software (Gilmour et al., 1998) was used to estimate variance components for identity and logistic link functions. The probit transformation from a binomial scale to the underlying liability is well known in the animal breeding literature (Dempster and Lerner, 1950). The theory suggests that heritability on the binomial scale is $h_b^2 = h^2 z^2/p(1-p)$, where h^2 is heritability on the normal scale, z is the height of the ordinate of standard normal distribution at the threshold point and p is the frequency of ones. Heritability estimates after Lerner-Dempster-Transformation are denoted as threshold heritabilities (h^2_{DL}). Genetic correlations between binomial distributed traits (claw disorders) and normally distributed traits (milk yield, SCS) were estimated via ASReml using identity link functions. Vinson et al. (1976) have shown that the genetic correlation computed from multi- or binomial phenotypes of related animals estimates directly that between normally distributed variables.

The generalized mixed model including random animal effect used to estimate variance covariance components for heritabilities and correlations can be described as:

$Y_{ijklm} = g(x) \quad = \quad \mu_i + H_{ij} + P_{ik} + a_{il} + e_{ijklm}$

Y_{ijklm} = the incidence of trait i for cow record l within herd j and parity k

$g(x)$ = a link function (identy, logistic)

μ_i = the overall mean on trait i

H_{ij} = the fixed effect of herd j for trait i

P_{ik} = the fixed effect of parity k on trait i

a_{il} = the random effect of cow l on trait i

e_{ijklm} = the random residual error on the scale of the link function used

Results and discussion

Preliminary analyses were first conducted by using the claw data to determine which environmental effects significantly affected health problems. Herd effect significantly ($P < .01$) affected all disorders, whereas parity was only significant on horn erosion ($P < .05$). The production level in milk yield in the first third of lactation stratified for different parities is associated with higher incidences in claw disorders as illustrated in figures 2 and 3 for horn erosion and digitale dermatitis.

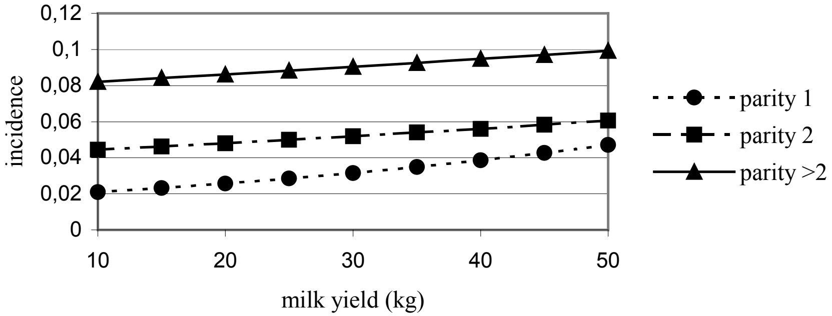

Figure 2: Incidences of horn erosion in dependency of milk yield stratified by parities

As expected, there is an increase of incidences in horn erosions with increasing parities. In contrary, heifers liability to digitale dermatitis doesn't differ from adult cows. This circumstance was observed in several practical studies and can be explained by resistances against some specific bacteria with consecutive parities. High milk yield within first third of lactation increases cows risk to be affected with health problems. Collard et al. (1999) have shown that metabolic stress occurs when the cow's energy intake does not match its requirement and the cow is unable to compensate and mobilises its body reserves too quickly. Increased digestive and locomotive problems were associated with longer and more extreme periods of negative energy balance. In early lactation, cows are fed high energy diets with relatively low ratios of roughage to concentrate. These diets can cause ruminal acidosis, which often leads to laminitis.

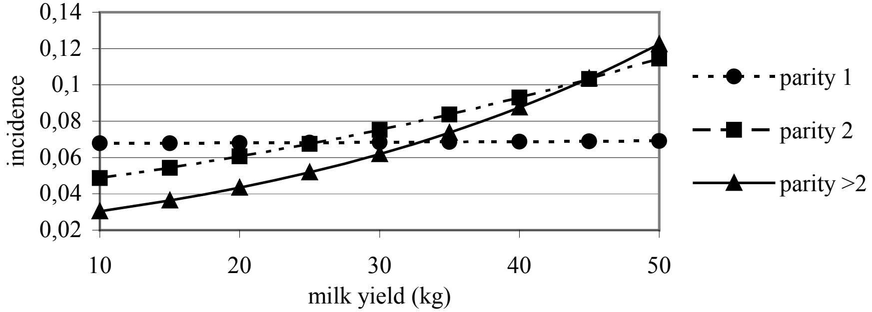

Figure 3: Incidences of digitale dermatitis in dependency of milk yield stratified by parities

Table 1 displays the results of genetic analysis with respect to heritabilities from normal (link=identity, h_N^2), logistic (h_L^2) and threshold models (h_{DL}^2) and genetic correlations between traits from normal models. Heritabilities for claw disorders estimated in normal linear models were in a range from .059 (digitale dermatitis) to .073 (sole ulcer).

Table 1: Genetic parameters for claw disorders. (Linear models: h_N^2 on the diagonal, genetic correlations above the diagonal, correlations between residuals below the diagonal)

	digitale dermatitis	**sole ulcer**	**horn erosion**	**limax**	**milk yield**	**SCS**
digitale dermatitis	**0,059** **±0,012**	0,561 ±0,073	0,337 ±0,139	0,691 ±0,099	0,240 ±0,145	0,151 ±0,176
sole ulcer	0,173 ±0,011	**0,073** **±0,012**	0,443 ±0,115	0,498 ±0,112	0,057 ±0,122	0,276 ±0,159
horn erosion	0,056 ±0,012	0,163 ±0,011	**0,067** **±0,015**	0,668 ±0,111	0,270 ±0,127	0,187 ±0,173
limax	0,195 ±0,010	0,116 ±0,011	0,023 ±0,011	**0,061** **±0,011**	0,336 ±0,140	0,149 ±0,173
milk yield	0,023 ±0,017	0,047 ±0,020	0,022 ±0,019	0,003 ±0,017	**0,277** **±0,031**	0,198 ±0,110
SCS	0,020 ±0,014	0,030 ±0,013	0,033 ±0,016	0,015 ±0,013	-0,230 ±0,021	**0,093** **±0,019**
h^2_L	**0,073** ±0,009	**0,086** ±0,006	**0,104** ±0,014	**0,115** ±0,021		
h^2_{DL}	**0,156**	**0,155**	**0,196**	**0,231**		

It seems that heritabilities are overestimated after Dempster-Lerner-transformation, especially for traits showing low frequencies of diseased cows. A simulation study of this transformation carried out by Gianola (1982) found that heritabilities were systematically overestimated when paternal half-sib data were used.

Maximum Likelihood procedures which can be applied to estimate parameters in logistic models are used in several investigations to analyse categorical traits in dairy cattle (e.g. Rodriguez-Zas et al., 1997). Heritability estimates were slight above normal identity models. However, the binomial distribution, as explained by Freund and Walpole (1980) is approximately normal when the expected value of nθ is equal to 5 or more where n is the smallest subclass number and θ is the incidence of the trait in question. In our study, nθ for limax is 2.9 and for horn erosion 4.5, respectively.

Genetic correlations between individual health traits and milk yield were positive indicating an antagonism, as found out by Lyons et al. (1990). In addition, table 1 contains correlations among six health traits (claw disorders and SCS). The most correlations were large and positive. Genetically, health problems appear to occur together by categories. The genetic correlations suggested that cows genetically susceptible to some type of health problems are likely to be susceptible to other health problems as well.

Breeding values for claw disorders from 41 sires with at least 40 daughters were correlated with official breeding values for functional type traits from national breeding value estimation (February 2004). Results are given in table 2. Not surprisingly, correlations were mostly positive between conformation traits describing the structure of feet and legs and claw disorders. Rear leg rear view is a trait with an intermedium optimum. Values greater 100 indicate steep legs which seems to be favourable. Bulls that transmitted steeper foot angels and straighter legs from the rear view had less daughters with feet and leg disorders. Similar results were found by Boettcher et al. (1997) applying linear and threshold models. Low foot angle, hocking in and wide rumps were mostly associated with clinical lameness.

Table 2: Correlations between breeding values (BV) for functional type traits and breeding values for claw disorders

	sole ulcer		digitale dermatits		limax	
BV for type trait….	% healthy daughters	BV	% healthy daughters	BV	% healthy daughters	BV
Feet & leg score	0,41	0,34	0,39	0,42	0,58	0,54
Rear leg side view	-0,46	-0,37	-0,34	-0,38	-0,49	-0,36
Foot angle	0,26	0,22	0,44	0,46	0,37	0,18
hocks	0,23	0,17	-0,03	-0,02	0,21	0,51
Rear leg rear view	0,25	0,24	0,41	0,37	0,55	0,40

Conclusion

Heritability estimates for claw disorders were low to moderate using normal identity and logit link-functions in evaluation models. Nevertheless, heritability estimates are large enough to make selection for reduced health problems feasible. If such selection were practiced, weighting all traits by their appropriate economic values would be required. Accurate and complete data are a basic requirement if selection for improved health is to be practiced. Further on, a strong relationship was observed between milk yield in the first stage of lactation and claw disorders. Continued selection for high production may increase the proportion of cows in extreme negative energy balance during early lactation causing health problems.

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