Genetic Parameters For Claw Health And Foot And Leg Conformation Traits In Finnish Ayrshire Cows

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Introduction

Impaired mobility from poor claw health is associated with direct and indirect costs. Indirect costs include involuntary culling, loss of milk production and increased calving interval (Barkema et al. (1994); Green *et al.* (2002); Garbarino *et al.* (2004)). Cows which had claw or foot disorder produced 30.8-310.5 kg less milk per year in a study of Finnish Ayrshire cows (Rajala-Shultz *et al.* (1999)). After infertility and mastitis, claw disorders are the third most expensive disorder in dairy farming (Enting *et al.* (1997)). Poor claw health is also a serious welfare problem, because claw disorders are usually long term and painful (Alban (1995); Enting *et al.* (1997)).

Claw health is affected by both genetic and enviromental factors. Heritability of claw health is low hence it can be improved by improving management (van der Waaij *et al.* (2005)). However, long-term improvement of claw health can be accomplished by genetic selection. Finland, Denmark and Sweden are developing a claw health index, which makes use of a sub-index for all health traits that considers claw and leg disorders as combined trait. This will be included in the Nordic total merit index. Genetic parameters of claw health and genetic parameters between claw health and conformation traits might be breed specific so it is important to estimate these in all Nordic countries. Including correlated information from foot and leg conformation traits is useful to increase accuracy because conformation data is available earlier and more animals have conformation records than claw health records. Genetic parameters for claw disorders have been estimated mainly by linear mixed models (e.g. Laursen *et al.* (2009)). The phenotypic observation is binomial and hence binomial model could give better estimates.

The objective of this study was to evaluate the genetic parameters of claw health and foot and leg conformation traits using a binomial mixed model for claw health in Finnish Ayrshire cows.

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Materials and methods

The dataset analysed in this study was from years 2000 to 2008 and consisted of 42,738 cow-level observations of 15,734 Finnish Ayrshire cows. Data was recorded by hoof trimmers and was merged with foot and leg conformation data recorded by breeding advisors from Faba service. Hoof trimmers usually visit farms one to four times a year and during those visits they usually trim all cows. In Finland national Healthy Hooves project was established in 2003 and since then the claw trimming records have been collected routinely. Claw trimmers mark the claw disorders to the form during their visits and farmers or dairy advisors save them to the database with special program. Claw disorders were categorized into 10 groups (Table 1). In this study all claw disorders were combined for one binomial claw health trait i.e. the cow was either healthy or had a claw disorder. Conformation traits were evaluated with linear scoring method using a scale from 1 to 9.

Table 1: Percentage of cows with claw disorders

Disorder	Cows, %	Disorder	Cows, %
Sole haemorrhages	18.76	Digital dermatitis	0.18
Chronic laminitis	1.59	Corkscrew claw	4.81
White line separation	6.65	Other claw disorder	0.61
Sole ulcer	1.83	*Preventive treatment = healthy*	58.96
Interdigital dermatitis	0.66	*One or more claw disorders*	41.04
Heel horn erosion	5.95		

The binomial claw health data and the conformation data were analysed using an animal model and restricted maximum likelihood method with ASREML (Gilmour *et al.* (2006)). Because claw health is a binary character, the residuals cannot be normally distributed. The best function to describe the relationship between the dependent and independent variables is not linear, but rather S-shaped. This is the reason why a linear logistic model with mixed effects was used. Heritabilities were estimated from univariate analyses. Genetic correlations were obtained from bivariate mixed model analyses between a binary claw health trait and linear conformation trait one at a time. Different models were used for analyzing claw health and conformation traits.

For binomial claw health trait: $\text{logit}(Y_{ijklmno}) = \mu + YS_i + AG_j + LA_k + HE_l + CT_m + AN_{n(1)} + PE_o$, where μ is the overall mean, YS_i is the fixed effect of year-season (i=1-36), AG_j is the fixed effect of the age at the time of trimming (j=1-193), LA_k is the kth lactation stage at the time of trimming (j=1-8), HE_l is the random herd effect (l=1-1657), CT_m is the random claw trimmer effect (m=1-77), $AN_{n(1)}$ is random animal effect and PE_o is random animal permanent environment effect.

For each linear conformation trait: $Y_{ijklmno} = \mu + YS_i + AG_j + LA_k + HE_l + CT_m + AN_{n(2)} + e_{ijklmno}$, where μ is the overall mean, YS_i is the fixed effect of year-season (i=1-60), AG_j is the fixed effect of the age at the time of observation (j=1-151), LA_k is the kth lactation stage at the time of observation (j=1-8), HE_l is the random herd effect (l=1-1657), CT_m is the random observer effect (m=1-90), $AN_{n(2)}$ is random animal effect, and $e_{ijklmno}$ is the random error term. In bivariate analysis $AN_{n(1)}$ and $AN_{n(2)}$ jointly ~N(0,G□□), where A is a relationship matrix including all available generations and G is unstructured genetic covariance matrix.

Results and discussion

Heritability and variances. Heritability estimates for claw health and foot and leg conformation traits are presented in Table 2. Estimated heritability for claw health using binomial logistic model was 0.07 and in accordance to estimates from literature (e.g. Laursen *et al.* (2009)). Claw health was also estimated with linear model to compare the results from linear and logistic models. Estimated heritabilities using linear models were 0.04 for claw health and ranged from 0.08 to 0.18 for foot and leg conformation traits. When linear heritability estimate for claw health was transformed to the underlying continuous scale (Falconer and McKay (1996), p. 304) the heritability estimate was same than with logistic model (0.07). Similar estimates were obtained using bivariate models (results not shown).

Table 2: Estimates of heritability and additive and phenotypic variances in claw health and foot and leg conformation traits from univariate analysis

Traits	h^2±S.E.	$SE_h{}^2$	σ^2_A	σ^2_P
CH	0.07±0.01	0.0141	0.37	5.18
RLRV	0.09±0.02	0.0167	0.19	2.24
HA	0.18±0.01	0.0119	0.29	1.63
BS	0.32±0.01	0.0117	0.55	1.73
FEA	0.17±0.02	0.0188	0.23	1.41
FA	0.08±0.01	0.0144	0.17	2.04

CH= claw health, RLRV= rear legs rear view, HA= hock angle, BS= apparent bone structure, FEA= fetlock angle, FA= foot angle

Genetic and phenotypic correlations. Estimates of genetic and phenotypic correlations for claw health and foot and leg conformation traits are presented in Table 3. The genetic correlation between claw health and hock angle was moderate and positive (0.36 ± 0.06). Moderate negative genetic correlations were found between claw health and bone quality, between claw health and fetlock angle and between claw health and foot angle. The genetic correlation between claw health and rear legs rear view was close to zero. The estimates found in the literature differ greatly for genetic correlation parameters between claw disorders or claw health and foot and leg conformation traits. For example in Laursen *et al.* (2009) study genetic correlation between claw health and rear leg rear view was 0.21 and in the study of Boettcher *et al.* (1998) it was -0.68. Koenig *et al.* (2005) had four different claw disorders in their study and genetic correlation estimates between them and foot angle ranged from -0.22 to -0.61. Van der Waaij *et al.* (2005) had six different claw disorders in their study where genetic correlation estimates between claw disorders and rear legs rear view ranged from -0.35 to 0.22. The phenotypic correlations between claw health and foot and leg conformation traits were all close to zero as in many other previous studies (e.g. Laursen *et al.* (2009)).

Table 3: Estimates of genetic and phenotypic correlations between claw health and foot and leg conformations

	CH, Genetic correlations ± S.E	CH, Phenotypic correlations ± S.E
RLRV	-0.02±0.09	-0.02±0.01
HA	0.36±0.06	0.04±0.01
BS	-0.35±0.10	-0.04±0.02
FEA	-0.30±0.07	-0.01±0.01
FA	-0.48±0.08	-0.05±0.01

CH= claw health, RLRV= rear legs rear view, HA= hock angle, BS= apparent bone structure, FEA= fetlock angle, FA= foot angle

Conclusions

Estimated heritability for claw health using binomial logistic model was quite low. The moderate size of genetic correlations, together with higher heritabilities of indicator traits, showed that hock angle, apparent bone structure, fetlock angle and foot angle are useful indicator traits for improved claw health. The results suggest that genetic evaluations are useful for claw health, especially when evaluated simultaneously with indicator traits. Differences in genetic correlations between Nordic countries should be compared, before applying to a joint Nordic model.

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