The Genetic Correlations between Different Claw Disorders in Finnish Ayrshire Cows

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Abstract

This paper describes the genetic correlations between sole haemorrhage, chronic laminitis, white-line separation, sole ulcer, heel horn erosion and corkscrew claw in Finnish Ayrshire cows recorded in the field by claw trimmers between 2003 and 2010. The statistical analyses were done using an animal model and restricted maximum likelihood method by applying the statistical package ASREML. The genetic correlations between claw disorders varied between -0.24 and 0.77. Most of the genetic correlations were positive and from moderate to high. The moderate to high positive genetic correlations between claw disorders indicate that disorders are genetically connected to each other and cows which are genetically susceptible to some disorder are more likely to be affected by other disorder as well.

<u>**Key words:**</u> claw disorder, correlation, Ayrshire

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Introduction

Claw disorders are identified as the third most costly disease in dairy farming after mastitis and infertility (Enting *et al.,* 1997; Kossaibati and Esslemont, 1996). The cost of claw disorder at a cow level varies according to the severity and type of claw disorder and the stage of lactation when the disorder appeared. Poor claw health is also a serious welfare problem, because claw disorders are usually painful and long-lasting (Enting *et al.,* 1997; Van der Waaij *et al.,* 2005).

The claw health is affected by genetic and environmental factors. The heritabilities of claw disorders are low hence improvement of claw health in the short-term can be achieved by improving environmental effects (Van der Waaij *et al.,* 2005). However, in the long-term genetic selection is useful. Claw health of a cow can be improved by direct selection for claw disorders or it can be improved through indirect selection through other genetically correlated traits (Van der Waaij *et al.,* 2005). The efficiency of selection on different claw health traits depends also on the genetic correlations between different claw disorders.

In the literature most genetic correlations among claw disorders are high and positive (e.g König *et al.,* 2005). Genetically, health problems appear to occur in clusters. The high positive genetic correlations between health traits suggest that cows genetically susceptible to some type of health problems are more likely to be affected by other health problems as well (e.g. König *et al.,* 2005; Lyons *et al.,* 1991).

The aim of this study was to evaluate the correlation between different claw disorders in Finnish Ayrshire cows.

Material and Methods

Data

The data set consisted of 116 521 claw trimming observations of 52 720 Finnish Ayrshire cows from 2 033 herds which had claw trimming records in the national data set. The data was collected by claw trimmers between 2003 and 2010 and all the claw disorders were recorded as 0 (absence) or 1 (disorder). Hence all the cows considered healthy in this study were those cows which were trimmed and no claw disorders found. Data included six different claw disorders, namely - sole haemorrhage, chronic laminitis, white-line separation, sole ulcer, heel horn erosion and corkscrew claw (Table 1). Usually the corkscrew claw is recorded if the twist is

over 180° but in Finland all over 90° twists are recorded. Pedigree was traced 5 generations back and only animals with breed code Ayrshire were used.

Table 1. The percentage of claw disorder observations

Claw disorder	%
Sole haemorrhage	14.67
Chronic laminitis	0.90
White-line separation	5.69
Sole ulcer	1.68
Heel horn erosion	4.12
Corkscrew claw	4.16
Total	31.22

Statistical Analysis

Because of the computational problems while fitting multivariate model the genetic correlations were obtained from bivariate mixed model analysis using an animal model and restricted maximum likelihood method with ASREML software (Gilmour *et al.,* 2009).

The model contained the following fixed effects: year-season, lactation stage at the time of trimming and the age at the time of trimming. Herd, claw trimmer, animal, animal permanent environment and residual effects were treated as random. The season was defined as 1=December to February; 2= March to May; 3= June to August; 4=September to November). Lactation stage was defined as 1=1-60d, 2= 61-120d, 3=121-180d, 4=181-240d, 5=241-300d, 6=301-360d, 7=361-430d and 8=431 and over.

Random herd effects were assumed to be: HE ~ MVN ($\mathbf{0}$, $\mathbf{I}\sigma_{he}^2$), where σ_{he}^2 is the herd variance. Random claw trimmer effects were assumed to be: CT ~ MVN ($\mathbf{0}$, $\mathbf{I}\sigma_{ct}^2$), where σ_{ct}^2 is the claw trimmer variance. Random animal effects were assumed to be: AN ~ MVN ($\mathbf{0}$, $\mathbf{A}\,\sigma_a^2$), where σ_a^2 is the additive genetic variance. Random permanent environmental effects were assumed to be: PE ~ MVN ($\mathbf{0}$, $\mathbf{I}\,\sigma_{pe}^2$), where σ_{pe}^2 is the animal permanent environmental variance. Random error terms were assumed to be: E ~ MVN ($\mathbf{0}$, $\mathbf{I}\sigma_e^2$), where σ_e^2 is the environmental variance.

In the bivariate model:

The variances and co(variances) for animal effects were defined as:

$$\mathbf{a} = \begin{bmatrix} \mathbf{a_1} \\ \mathbf{a_2} \end{bmatrix} \sim \text{MVN}\,(\mathbf{0}, \mathbf{G_0} \otimes \mathbf{A}), \text{ where } \mathbf{0} \text{ is a}$$

vector of zeros,

$$\mathbf{G_0} = \begin{bmatrix} \sigma_{a1}^2 & \sigma_{a12} \\ \sigma_{a21} & \sigma_{a2}^2 \end{bmatrix} \text{ is the genetic co(variance)}$$

matrix, $\otimes$ denotes the Kronecker product, $\mathbf{A}$ is the additive genetic relationship matrix including 5 generations. The variances and co(variances) for random effects were defined as:

$$\mathbf{e} = \begin{bmatrix} \mathbf{e_1} \\ \mathbf{e_2} \end{bmatrix} \sim \text{MVN}\,(\mathbf{0}, \mathbf{R_0} \otimes \mathbf{I}), \text{ where } \mathbf{0} \text{ is a}$$

vector of zeros,

$$\mathbf{R_0} = \begin{bmatrix} \sigma_{e1}^2 & \sigma_{e12} \\ \sigma_{e21} & \sigma_{e2}^2 \end{bmatrix}$$

is residual (co)variance matrix and $\mathbf{I}$ is the identity matrix.

Results and Discussion

Genetic correlations

The genetic correlations varied between -0.24 and 0.77 (Table 2). Most of the correlations between claw disorders were positive and from moderate to high. This indicates that these disorders are genetically connected to each other and cows which are genetically susceptible to some disorder are more likely to be affected by other disorder as well.

Only the correlations between sole haemorrhage and heel horn erosion and between chronic laminitis and heel horn erosion were negative. The negative correlations between these traits are unfavourable but these traits had also high standard errors. The highest genetic correlation was found between sole ulcer and chronic laminitis (0.77).

Table 2. Genetic correlations between claw disorders and their standard errors

	CL	WLD	SU	HH	CSC
SH	0.61	0.41	0.51	-0.21	0.27
	±0.13	±0.09	±0.11	±0.13	±0.09
CL		0.55	0.77	-0.24	0.28
		±0.12	±0.11	±0.20	±0.13
WLD			0.72	0.21	0.39
			±0.09	±0.16	±0.09
SU				0.39	0.23
				±0.13	±0.09
HH					0.08
					±0.17

SH=Sole haemorrhage, CL=Chronic laminitis, WLD=White-line separation, SU=Sole ulcer, HH= Heel horn erosion, CSC=Corkscrew claw

There are only few estimates of correlations between different claw disorders for red breeds in literature and other studies have mainly focused on Holstein breed.

Johansson *et al.* (2011) presented a claw health index for Holstein and Red Dairy Cattle (RDC), which was included in Nordic total merit index (NTM), and is routinely run in the joint genetic evaluation for Finland, Sweden and Denmark. The correlations between sole ulcer and corkscrew claw and between sole ulcer and white-line separation were close to those estimates Johansson *et al.* (2011) found for RDC. The correlations between sole ulcer and sole haemorrhage, between corkscrew claw and sole haemorrhage and between white-line separation and sole haemorrhage were little lower than those Johansson *et al.* (2011) presented for RDC. Johansson *et al.* (2011) found a much lower genetic correlation between white-line separation and corkscrew claw (0.08) compared to estimate from this study (0.39).

Conclusions

Most of the genetic correlations between claw disorders are favourable. The moderate or high positive genetic correlations between claw disorders indicate that claw disorders are genetically connected to each other and cows which are genetically susceptible to some claw disorder are more likely to be affected by other claw disorder as well.

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