Genetic Correlations between Claw Health and Feet and Leg Conformation Traits in Swedish Dairy Cows

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1. Introduction

With the fast increase in dairy herd size over the last decades, and a change from tie stalls to free stalls it is imperative from an economic and welfare point of view to have a good claw health reducing the risk for lameness. Of Swedish Red (SR) cows and Swedish Holstein (SH) 5.9 % and 8.1 %, respectively, are culled due to feet and leg diseases (Swedish Dairy Association, 2008) and genetic selection for better claw health is desirable. Among most common claw diseases occurring as herd problems dermatitis (DD) and heel horn erosion HH are hygiene related diseases and sole haemorrhage (SH) and sole ulcer (SU) are related to laminitis which is a metabolic and trauma related disease. An earlier Swedish study failed to use reports from veterinary practitioners on lameness and proposed to use records collected at maintenance claw trimmings (Ral *et al.*, 1995). Claw diseases, locomotion, abnormal claw conformation and treatments have now been recorded by Swedish claw trimmers on a voluntary, national basis since 2002. Heritabilities of claw diseases are low, as for other diseases, ranging from 1 to 10 % across traits (Naeslund *et al.*, 2008, Van der Waaij *et al.*, 2005). However, conformation traits for feet and leg have considerably higher heritability (Boelling *et al.*, 2007; Pérez- Cabal & Alenda, 2002; Wiggans *et al.*, 2004). The aim of this study was to investigate correlations between claw diseases and feet and leg conformation traits as an alternative for indirect genetic selection for improved claw health.

2. Material and Methods

2.1 Claw Health Data

Records of the most common claw diseses: dermatitis (DD), heel horn erosion (HH), sole haemorrhage (SH) and sole ulcer (SU) scored as absent (0), slight (1) or severe (2) by Swedish claw trimmers from 2003 through 2007 were used in the present study.

Naeslund *et al.* (2008) found high genetic correlations between DD and HH, and between SH and SU and suggested treating DD and HH as one trait (DDHH) and to treat SH and SU as another trait (SHSU). Diseases were combined such that the one with the highest score was kept resulting in a combined disease frequency slightly higher than the two diseases separately, but lower than the sum of the two diseases. In the current study it was also tested to combine all four diseases into one combined claw health trait (TOTAL) again combining diseases in such a way that the highest score was kept.

Many cows were trimmed more than once within lactation and also trimmed in several lactations. However, for this analysis only the information from the first trimming in the first lactation was used.

The edited data set included 58 457 Swedish Red (SR) and 65 789 Swedish Holstein (SH). Frequency of DD, HH, SH, SU, DDHE, SHSU, and TOTAL of fist trimming in first lactation of SR and SH are shown in Table 1.

Table 1. Frequency of dermatitis (DD), heel horn erosion (HH), sole haemorrhage (SH), sole ulcer (SU), dermatitis+heel horn erosion (DDHH), sole haemorrhage + sole ulcer (SHSU), dermatitis +heel horn erosion+sole haemorrhage+sole ulcer (TOTAL) on a 0-1-2-scale for Swedish Red (SR) and Swedish Holstein (SH) in first lactation.

Trait	SR			SH		
	0	1	2	0	1	2
DD	93.32	5.61	1.06	92.52	5.99	1.49
HH	82.32	15.00	2.67	84.96	12.78	2.26
SH	74.94	17.21	7.84	72.21	19.40	8.39
SU	96.15	2.47	1.38	94.73	3.28	1.99
DDHH	79.05	17.40	3.55	80.89	15.61	3.50
SHSU	72.90	18.30	8.80	69.33	20.89	9.78
TOTAL	61.25	27.27	11.48	59.34	28.32	12.34

2.2 Feet and Leg Conformation Data

In 1993 the type classification system in Sweden changed from a subjective 4-point scale to the current linear 9-point scale. Twenty-one single conformation traits are currently recorded and have since 2004 been genetically evaluated jointly with Denmark and Finland (Fogh *et al.*, 2004). For this study 5 feet and leg type traits were considered – these were rear leg side view (RLSV), rear leg rear view (RLRV), hock quality (HQ), bone structure (BS), and foot angle (FA). Data were sparse in the beginning and it was decided only to use data from 2000 onwards for the current study.

After editing, the two data sets contained 99 835 and 104 227 first lactation cows with type trait records for SH and SR, respectively. The scale for the 5 type traits with means and standard deviations are listed in Table 2 for SH and SR, respectively.

Table 2. Feet and leg conformation traits with trait definition and mean and SD for Swedish Holsteins (SH) and Swedish Red (SR).

Trait	Scale	SH		SR	
		Mean	SD	Mean	SD
Rear leg side view	1=straight, 9=sickled	5.03	0.95	5.34	0.95
Rear leg rear view	1=toes out, 9=parallel bowed-legged	6.24	1.13	6.14	1.19
Hock quality	1=filled, 9=dry	5.83	1.25	6.04	1.21
Bone structure	1=coarse, 9=fine & thin	6.39	1.09	6.24	1.13
Foot Angle	1= low, 9= steep	5.06	1.04	5.05	0.99

2.3 Joint data and method

Pedigree was traced 5 generations back and for the current analyses only animals with breed code SH and SR was used. The edited data set for claw health and conformation were merged breed wise. Variance components were estimated in bivariate linear animal models using the DMU-software (Madsen & Jensen, 2000).

2.4 Models

The model for claw health data:

$$Y_{ijklmn} = Age_i + Sta_j + Mo_k + Tra_l + HYS_m + cow_n + e_{ijklmn} \quad [1]$$

where $Y_{ijklmno}$ = claw trimming observation on cow n; Age_i = fixed effect of calving age in months, j=20,..,36; Sta_j = fixed effect of stage

of lactation in months at time of claw trimming, i=1,..,18; Mo_k = fixed effect of month of calving; Tra_l = fixed effect of training of claw trimmer, k=1,..,4; HYS_m = random effect of herd*calving year*season, where year*season goes from first of July one year to last of June the next year, ~ND(0, σ^2_{hy}); cow_n = random effect of cow, ~ND(0, $\mathbf{A}\sigma^2_A$); $e_{ijklmno}$ = random residual. ~ND(0, σ^2_E).

The model for feet and leg conformation traits:

$$Y_{ijklm} = Age_i + Sta_j + Mo_k + HYS_l + cow_m + e_{ijklm} \quad [2]$$

where Y_{jklmn} = Type trait observation recorded on cow *m*; Age_i = fixed effect of age of first calving in month, i = 20,..,36; Sta_j = fixed effect of lactation stage. j = 1,..,8; Mo_k = fixed effect of month of classification, k = 1,..,12; HYS_l = fixed effect of herd*year*season, where year*season goes from first of July one year to last of June the next year (≥3 observations) or classifier*year*season (<3 observations); cow_m = random effect of cow, ~ND(0, $\mathbf{A}\sigma^2_{a(tt)}$); e_{ijklm} = random residual, ~ND(0, σ^2_E).

3. Results and Discussion

Heritabilities and genetic correlations for feet and leg conformation traits and genetic correlations between claw health data and feet and leg conformation data are presented in Table 3 and Table 4 for SH and SR, respectively. Heritabilities for feet and leg type traits were in the range from 0.10 to 0.31 and in accordance to estimates from the literature (e.g. Boelling *et al.*, 2007; Pérez- Cabal & Alenda, 2002; Wiggans *et al.*, 2004). Genetic correlations between conformation traits were low except for the correlation between HQ and BS that was as high as 0.87 for SH and 0.92 for SR.

For SH all correlations between feet and leg type traits and claw health were in the range -0.08 to 0.27 and non-significant different from zero, except for the correlations between RLSV and claw health traits as well as the correlations between DD and FA and DDHE and FA. Van der Waaij *et al.* (2005) found genetic correlations in a similar range (-0.22 to 0.16) while slightly higher (-0.54 to 0.02) correlations between breeding values were obtained by Koenig *et al.* (2005). Correlations between the combined disease traits and the conformation traits were similar to the single traits indicating no advantage in correlations by combining the disease traits.

The genetic correlations between feet and leg type traits and claw health were in general higher for SR than for SH and many of the correlations were significantly different from zero. As selection for type traits has taken place over several decades it can be speculated if a slight indirect selection for better claw health has taken place for SR and if that is the reason for a lower frequency of SR cows culled for feet and leg problems.

Several Interbull member countries do have a genetic evaluation for locomotion traits (Lawlor and Klei, 2008) while genetic evaluation of claw health data from claw trimmings is internationally rather scanty. Van der Waaij *et al.* (2005) estimated genetic correlations between locomotion and claw health and obtained correlations in the range -0.71 to 0.13 indicating that claw health and locomotion are rather different traits.

4. Conclusions

The genetic correlations between claw health traits and feet and leg conformation traits were low for SH and most were non-significantly different from zero. SR on the other hand showed in general higher correlations between feet and leg type traits and claw disorders. The correlations are, however, still low and indirect selection for better claw health using type traits is not possible for neither SH or SR. Present results emphasizes the great importance of keeping records of claw health by claw trimmers in favor of conformation traits.

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Table 3. Heritiabilities (bold) and genetic correlation with (SE) among type traits and between claw disorders and type traits for Swedish Holsteins (SH).

Trait[1]	RLSV	RLRV	HQ	BS	FA
DD	*0.13 (0.06)*	0.12 (0.07)	-0.04 (0.07)	0.02 (0.06)	*0.15 (0.07)*
HH	*0.23 (0.07)*	-0.03 (0.07)	-0.01 (0.07)	0.07 (0.07)	0.07 (0.08)
SH	*0.18 (0.08)*	-0.08 (0.08)	-0.08 (0.08)	-0.02 (0.08)	-0.03 (0.09)
SU	*0.28 (0.07)*	0.16 (0.08)	-0.08 (0.08)	0.10 (0.07)	-0.03 (0.08)
DDHH	*0.21 (0.06)*	0.06 (0.07)	0.001 (0.07)	0.07 (0.06)	*0.16 (0.07)*
SHSU	*0.22 (0.07)*	-0.03 (0.08)	-0.08 (0.07)	0.03 (0.07)	-0.05 (0.08)
TOTAL	*0.27 (0.06)*	-0.04 (0.07)	-0.07 (0.07)	0.04 (0.06)	0.03 (0.07)
RLSV	**0.21**	-0.06 (0.04)	*0.25 (0.04)*	*0.09 (0.03)*	*-0.39 (0.04)*
RLRV		**0.14**	*0.15 (0.04)*	*0.15 (0.04)*	0.03 (0.05)
HQ			**0.11**	*0.87 (0.01)*	-0.07 (0.05)
BS				**0.23**	-0.001 (0.04)
FA					**0.16**

Significant genetic correlations in *italic.*

[1] DD = dermatitis, HH = heel horn erosion, SH = sole haemorrhage, SU = sole ulcer, DDHH = dermatitis + heel horn erosion, SHSU = sole haemorrhage + sole ulcer, TOTAL = dermatitis+heel horn erosion+sole haemorrhage+sole ulcer, RLSV = rear leg side view, RLRV = rear leg rear view, HQ = hock quality, BS = bone structure and FA = foot angle.

Table 4. Heritiabilities (bold) and genetic correlation with (SE) among type traits and between claw disorders and type traits for Swedish Red (SR).

Trait[1]	RLSV	RLRV	HQ	BS	FA
DD	0.09 (0.08)	0.09 (0.09)	*-0.19 (0.08)*	-0.23 (0.08)	0.03 (0.09)
HH	*0.17 (0.07)*	-0.11 (0.08)	*-0.31 (0.07)*	*-0.24 (0.07)*	-0.05 (0.09)
SH	*0.16 (0.07)*	-0.06 (0.07)	-0.10 (0.07)	*-0.19 (0.06)*	*-0.25 (0.08)*
SU	0.11 (0.08)	0.14 (0.09)	-0.15 (0.08)	*-0.17 (0.08)*	0.12 (0.09)
DDHH	*0.16 (0.07)*	-0.03 (0.07)	*-0.29 (0.07)*	*-0.26 (0.06)*	-0.06 (0.08)
SHSU	*0.16 (0.06)*	-0.01 (0.07)	-0.10 (0.07)	*-0.18 (0.06)*	*-0.17 (0.08)*
TOTAL	*0.19 (0.06)*	-0.01 (0.07)	*-0.18 (0.07)*	*-0.23 (0.06)*	-0.10 (0.08)
RLSV	**0.25**	*-0.22 (0.04)*	-0.02 (0.03)	*-0.12 (0.03)*	*-0.38 (0.04)*
RLRV		**0.17**	*0.18 (0.04)*	*0.10 (0.03)*	*0.18 (0.05)*
HQ			**0.10**	*0.92 (0.01)*	*-0.11 (0.04)*
BS				**0.31**	-0.08 (0.04)
FA					**0.23**

Significant genetic correlations in *italic*.

[1] DD = dermatitis, HH = heel horn erosion, SH = sole haemorrhage, SU = sole ulcer, DDHH = dermatitis + heel horn erosion, SHSU = sole haemorrhage + sole ulcer, TOTAL = dermatitis+heel horn erosion+sole haemorrhage+sole ulcer,RLSV = rear leg side view, RLRV = rear leg rear view, HQ = hock quality, BS = bone structure and FA = foot angle.