Genetic Parameters of Claw Health Traits in Spanish Dairy Cows

N. Charfeddine[1] and M. A. Pérez-Cabal[2]
[1] Dpto. Técnico CONAFE, Ctra. de Andalucía, Km. 23,6. 28340 Madrid. Spain
[2] Departamento de Producción Animal, Universidad Complutense de Madrid, 28040 Madrid, Spain
Email:Nouredine.charfeddine@conafe.com

Abstract

Genetic parameters for claw health disorders were estimated with linear and threshold models in Spanish dairy cattle using around 50,000 trimming observations, recorded on 35,337 cows. Six claw diseases were recorded: Interdigital and digital Dermatitis (DE), Sole ulcer (SU), White line separation (WL), interdigital Hyperplasia (HP), interdigital Phlegmon (PH), and Chronic laminitis (CL). An Overall claw disorder (OCD) was also defined, indicating the presence or absence of at least one of the six claw disorders. Estimates of heritability with linear model ranged from 0.01 for CL and PH to 0.05 for OCD. However, heritabilities estimated with threshold model ranged from 0.06 for PH to 0.39 for HP. Genetic correlations among claw disorders confirm the existence of two groups of traits, one related to horn disorders compound by SU, WL and CL and, other related to infection lesions which bunchs DE, HP and, PH. The results are in accordance with other studies in different populations, and therefore data recorded for the first time in Spain can be considered liable.

Key words: Claw disorders, dairy cow, genetic parameter, linear and threshold models

Introduction

Lameness is the most important reason for culling in Spanish dairy farms after fertility and mastitis. One third of cows within herd have at least one claw lesion, and most of those lesions become chronic overtime (Charfeddine and Pérez-Cabal, 2014). Due to the intensive selection for yield production and the increase in herd size over the last decades, claw health is getting worse and an overuse of antibiotics is being increased. Moreover, claw disorders not only reduce productivity but also harm animal welfare, which represents an important issue in dairy production. Then, nowadays claw diseases are becoming a big source of economic loss to the dairy farmer. These losses are mainly due to a reduced milk production (Green *et al.*, 2002) and poor fertility performance of lame cows (Barkema *et al.*, 1994). Apart from improving herd management, a better claw health can be achieved through selection. Selection for improving claw health in Spain is being addressed by feet and legs type traits but it has been shown in other population that there are low correlations between conformation traits and claw disease traits (Van der Waaij *et al.*, 2005). In 2012, a centralized electronic recording system for 6 claw disorders, called I-SAP, was implemented in Spain (Charfeddine and Pérez-Cabal, 2014) and accurate genetic parameters for claw disorders in Spanish dairy cattle are required for genetic evaluation. The objective of the present study is to estimate genetic parameters of claw disorders in Spanish dairy cattle.

Materials and Methods

Data

Claw trimming data collected from July 2012 to June 2013 including 78 257 records registered by 21 trimmers in 834 dairy herds during 5979 visits were used. Six claw diseases are recorded: Interdigital and digital Dermatitis (**DE**), Sole ulcer (**SU**), White line separation (**WL**), interdigital Hyperplasia (**HP**), interdigital Phlegmon (**PH**), and Chronic laminitis (**CL**). Claw health data were scored in heifers and lactating cows as a categorical trait (0:

absence of disorder, 1: mild lesion, and 2: severe lesion) for each claw. A detailed description of each claw disorder recorded with I-SAP is given by Charfeddine and Pérez-Cabal (2014). Since trimmer who scores hind and fore claws may be a different person and the 85% of lesions were present in rear claws, only rear leg claw disorders were included. A general claw disorder trait was also considered, called Overall Claw Disorder (**OCD)**, indicating the absence or the presence, as mild or severe lesion, of at least one of the six claw diseases. When there is more than one disorder, the highest score is kept for OCD.

For the analyses, claw health data were restricted to herds with at least 50% of present cows were trimmed, and to trimmers with at least 2,000 records throughout all the period considered. Besides, visits with less than 5 cows trimmed were also excluded. After editing 49,963 claw health records, corresponding to 35,337 cows, offspring of 2,759 sires in 566 herds, were used. The data set had repeated records for a given cow because trimmers visit the farm more than once a year and lesion status could change from one observation date to the next. Average number of trimming in the final data set was 1.4 per cow.

Pedigree information was provided by the Spanish Holstein Association (CONAFE). Pedigree of cows with records was traced back for all generations available. A total of 116,298 animals were included in pedigree file. A statistic description for all traits used in the analyses is shown in Table 1.

Table 1. Statistical summary of claw health data.

Trait[1]	**Mean**	**SD**	**Min**	**Max**
DE	0.067	0.25	0	2
SU	0.100	0.33	0	2
WL	0.045	0.23	0	2
CL	0.029	0.19	0	2
HP	0.002	0.05	0	2
PH	0.007	0.11	0	2
OCD	0.232	0.46	0	2

[1]**DE**: Dermatitis, **SU:** Sole ulcer, **WL:** White line separation, **CL:** Chronic laminitis, **HP:** Hyperplasia, **PH:** Phlegmon, **OCD:** Overall claw disorder.

Statistical models

Genetic parameters for claw health traits were estimated fitting two different animal models: a standard linear model and an ordinal threshold model. This was done in order to test the goodness of our data set with respect to other populations.

The linear predictor common to both models was:

$$\eta_{ijklm} = \alpha + HVT_i + LCA_j + DIM_k + PE_l + Animal_m$$

where, η_{ijklm} is a function of the expected liability claw disorder of a specific cow; α is an intercept; HVT_i is the systematic effect of herd-visit-trimmer (1,679 levels); LCA_j is the systematic effect lactation-calving age (31 levels); DIM_k is the systematic effect day in milk at trimming (6 levels: from 0 to 60d; from 61 to 120d; from 121to 180d; from 181 to 240d; from 241 to 305d; and more than 305d); PE_l is the random permanent environmental effect of the lth cow (35 337 levels); $Animal_m$ is the random additive genetic effect of the mth animal (116 298 levels). The joint distribution of random effects included in the linear predictor was:

$$\begin{pmatrix} \mathbf{PE} \\ \mathbf{Animal} \end{pmatrix} \sim N\left(\mathbf{0}, \begin{pmatrix} \mathbf{I}\sigma^2_{\text{PE}} & 0 \\ 0 & \mathbf{A}\sigma^2_{\text{Animal}} \end{pmatrix}\right)$$

where, **PE** and **Animal** are the vectors of permanent environmental and genetic additive effects, respectively; **I** is an identity matrix of 35,337 order; **A** is the additive genetic relationship matrix between animals; σ^2_{PE} and σ^2_{Animal} are the corresponding variances. Permanent environmental and genetic additive effects were assumed to be independent of residuals. The specification for the linear model is completed as $y_{ijklm} = \eta_{ijklm} + \varepsilon_{ijklm}$ and the distribution of residuals was $\boldsymbol{\varepsilon} \sim N\left(\mathbf{0}, \mathbf{I}\sigma^2_{\varepsilon}\right)$.

In the ordinal threshold model, the claw disorder is a categorical trait assuming that the observation of each disorder takes the value t:{0, 1, 2} if an underlying continuous variable falls between thresholds T_{t-1} and T_t (Gianola and Foulley, 1983).

The specification for the threshold model is as follows:

$$\Pr\left(y_{ijklm} = t \mid HVT_i, LCA_j\ ,\ DIM_k\ ,\ PE_l\ ,\ Animal_m\right) = \Phi\left[T_t - \eta_{ijklm}\right] - \Phi\left[T_{t-1} - \eta_{ijklm}\right]$$

where y_{ijklm} is the response of the claw disorder; t = 0, 1, 2 indexes the category of the claw disorder; Φ(.) is the standard normal cumulative distribution function of the standard normal, and T_t and T_{t-1} are fixed thresholds satisfying the order constraint $-\infty<T_0<T_1<\infty$. In the threshold model, a random residual effect was assumed to be normally and independently distributed, with mean 0 and variance 1.

For multi-trait linear animal model parameters were estimated by REML using the VCE 6.0 software (Neumaier & Groeneveld, 1998; Groeneveld *et al.*, 2008). To estimate parameters with the threshold model, MCMC Gibbs sampling has been carried out bivariately with TM software (Legarra *et al.*, 2011). For each population, Gibbs sampling was carried out through a unique chain of 80,000 iterations, discarding the first 30,000 iterations and retaining one every 10 samples.

Results & Discussion

Claw health disorders frequencies

Claw disease frequencies calculated at cow level in final data set are shown in Table 2. SU had the highest prevalence, whereas HP had the lowest. This prevalence were lower than that calculated on the same population as the average of prevalence at herd level by Charfeddine and Pérez-Cabal (2014) because, as it was explained in materials and methods section, herds with percentage of trimming cow lower than 50% were removed from our final data set. Incidences of claw disorders observed in our data were in a wide range, as reported in the literature. Although we observed incidences lower than observed by Somers *et al.* (2003), Van Der Waaij *et al.* (2005), and Stoop *et al.* (2010) in Holstein cows in The Netherlands, the figures reported were slightly higher than those found by Uggla *et al.* (2008) for Swedish Holstein.

Table 2. Cow-level prevalence (%) of the claw disorders in rear legs.

Disorder	Prevalence (%)
DE	6.64
SU	9.13
WL	4.05
CL	2.68
HP	0.16
PH	0.56
OCD	21.43

DE: Dermatitis, **SU:** Sole ulcer, **WL:** White line separation, **CL:** Chronic laminitis, **HP:** Hyperplasia, **PH:** Phlegmon, **OCD:** Overall claw disorder.

Heritability of claw health traits

The heritabilities of claws disorders estimated with linear model ranged from 0.01 (CL and PH) to 0.05 (OCD). However, heretabilities estimated with threshold model were in the range from 0.06 for PH to 0.39 for HP (Table 3). These estimates are in accordance with those reported in the literature, which range from 0.01 to 0.17 for heritabilities estimated with linear model on the observed scale (Swalve *et al.*, 2008; Van der Linde *et al.*, 2010; Weber *et al.*, 2013). Estimated heritabilities estimated with threshold models on the underlying continuous scale range from 0.07 to 0.33 (Swalve *et al.*, 2008; Buch *et al.*, 2011; Weber *et al.*, 2013). Threshold estimates, as expected, are higher than linear model estimates, as well as standard errors estimated with the threshold models. As observed in the literature, HP showed a high genetic component (Van der Waaij *et al.*, 2005; Swalve *et al.*, 2008). Heritabilities estimated support that substantial genetic variation does indeed exist, which warrant genetic selection in order to improve claw health.

Table 3. Heretabilities (h^2) and standard error (S.E.) of claw health disorders estimated with linear and threshold models.

	Linear model		Threshold model	
	h^2	S.E.	h^2	S.E.
DE	0.02	*0.004*	0.14	*0.031*
SU	0.04	*0.004*	0.15	*0.024*
WL	0.02	*0.003*	0.09	*0.021*
CL	0.01	*0.002*	0.07	*0.019*
HP	0.04	*0.003*	0.39	*0.068*
PH	0.01	*0.002*	0.06	*0.019*
OCD	0.05	*0.004*	0.11	*0.007*

DE: Dermatitis, **SU:** Sole ulcer, **WL:** White line separation, **CL:** Chronic laminitis, **HP:** Hyperplasia, **PH:** Phlegmon, **OCD:** Overall claw disorder.

Repeatability of claw health traits

Repeatabilities estimated with the linear model ranged from 0.03 (PH) to 0.18 (CL). However, repeatabilities estimated with threshold model ranged from 0.33 (PH) to 0.69 (HP) (Table 4). The high values for all lesions suggest that once a cow is diagnosed with any lesion she will be more likely to exhibit the same lesion again. Repetabilities estimated indicate that the use of repeated measures for the same cow will improve reliabilities of genetic breeding values.

Genetic and phenotypic correlations between claw health traits

Genetic and phenotypic correlations among the seven traits estimated with linear and threshold model are shown in Table 5 and Table 6, respectively. In general, very similar patterns of correlations are revealed under both models. With linear model, genetic correlations ranged from -0.61 to 0.98, and, genetic correlations estimated with threshold model ranged from -0.62 to 0.97. As Weber *et al.* (2013) reported, it must be noted that genetic correlations estimated using a threshold model are associated with high standard errors.

Genetic correlation between DE and SU is very low, close to zero with both models. Correlation between DE and WL and CL are low and negative. HP shows high correlation with DE and low and negative correlations with SU, WL, and CL. However genetic correlations between SU, WL and CL are high ranged from 0.36 to 0.98 with both models. Those estimates confirm that there are two groups of claw health disorders with different genetic background for each group. Traits related to horn lesions with feeding background are SU, WL and. CL. Traits related to infectious lesions with hygiene background are DE, HP, and PH. This is in agreement with results reported in others studies (Häggman and Juga, 2013; Johansson *et al.*, 2011).

Table 4. Repetabilities (r) and standard error (S.E.) of claw health disorders estimated with linear and threshold models.

	Linear model		Threshold model	
	r	S.E.	r	S.E.
DE	0.10	*0.006*	0.42	*0.032*
SU	0.17	*0.006*	0.51	*0.019*
WL	0.11	*0.005*	0.42	*0.030*
CL	0.18	*0.006*	0.58	*0.035*
HP	0.05	*0.004*	0.69	*0.135*
PH	0.03	*0.004*	0.33	*0.212*
OCD	0.15	*0.005*	0.38	*0.016*

DE: Dermatitis, **SU:** Sole ulcer, **WL:** White line separation, **CL:** Chronic laminitis, **HP:** Hyperplasia, **PH:** Phlegmon, **OCD:** Overall claw disorder.

Phenotypic correlations among claw disorders are low and negative, as reported in others studies (Häggman and Juga, 2013; Odegard *et al.*, 2013). A reason could be that hoof trimmers only marked the worst disorders. The highest phenotypic correlations, as expected, are between the combined trait OCD and the most frequent disorders, DE, SU, WL, and CL. Phenotypic correlations and their standard errors estimated with threshold model are higher than phenotypic correlations and standards errors estimated with the linear model.

Conclusions

The heritability estimates for claw disorders using both linear and threshold model are low to moderate, indicating that concerted selection may reduce the prevalence of claw lesions. Genetic correlations among claw disorders confirm the existence of two groups of traits, one related to horn disorders and the other related to infection lesions. In order to implement a future genetic evaluation, further studies regarding the most appropriate model (linear or threshold) are in process. In the meanwhile, these results are in accordance with other studies in different populations, and therefore data recorded can be considered reliable.

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Table 5. Genetic correlations above diagonal and phenotypic correlations below diagonal between claw health traits estimated with linear model (with SE).

	DE	**SU**	**WL**	**CL**	**HP**	**PH**	**OCD**
DE	-	-0.08 *(0.061)*	-0.30 *(0.044)*	-0.27 *(0.049)*	0.10 *(0.018)*	0.33 *(0.095)*	0.39 *(0.039)*
SU	-0.05 *(0.001)*	-	0.98 *(0.052)*	0.95 *(0.057)*	0.00 *(0.016)*	-0.69 *(0.131)*	0.98 *(0.008)*
WL	-0.04 *(0.001)*	-0.01 *(0.01)*	-	0.63 *(0.115)*	-0.22 *(0.034)*	-0.05 *(0.364)*	0.93 *(0.034)*
CL	-0.03 *(0.001)*	0.01 *(0.001)*	0.03 *(0.001)*	-	-0.03 *(0.020)*	-0.61 *(0.071)*	0.78 *(0.024)*
HP	-0.01 *(0.001)*	-0.01 *(0.001)*	-0.01 *(0.001)*	-0.01 *(0.001)*	-	0.18 *(0.056)*	0.04 *(0.034)*
PH	-0.01 *(0.001)*	-0.02 *(0.001)*	-0.02 *(0.001)*	-0.01 *(0.001)*	0.01 *(0.001)*	-	0.16 *(0.013)*
OCD	0.44 *(0.007)*	0.60 *(0.004)*	0.37 *(0.001)*	0.32 *(0.001)*	0.07 *(0.001)*	0.18 *(0.001)*	-

Table 6. Genetic correlations above diagonal and phenotypic correlations below diagonal between claw health traits estimated with threshold model (with SE).

	DE	**SU**	**WL**	**CL**	**HP**	**PH**	**OCD**
DE	-	0.05 *(0.137)*	-0.30 *(0.151)*	-0.12 *(0.147)*	0.72 *(0.060)*	0.48 *(0.136)*	0.61 *(0.008)*
SU	-0.18 *(0.020)*	-	0.79 *(0.050)*	0.75 *(0.059)*	-0.10 *(0.128)*	-0.73 *(0.083)*	0.97 *(0.008)*
WL	-0.23 *(0.026)*	-0.02 *(0.021)*	-	0.36 *(0.136)*	-0.45 *(0.146)*	-0.62 *(0.116)*	0.91 *(0.020)*
CL	-0.18 *(0.030)*	0.09 *(0.024)*	0.09 *(0.031)*	-	-0.37 *(0.153)*	-0.64 *(0.108)*	0.85 *(0.032)*
HP	0.16 *(0.073)*	-0.07 *(0.064)*	-0.15 *(0.075)*	-0.20 *(0.073)*	-	-0.45 *(0.166)*	0.38 *(0.161)*
PH	-0.29 *(0.106)*	-0.24 *(0.055)*	-0.12 *(0.068)*	-0.16 *(0.065)*	0.09 *(0.101)*	-	-0.21 *(0.195)*
OCD	0.94 *(0.030)*	0.97 *(0.029)*	0.85 *(0.039)*	0.79 *(0.043)*	0.29 *(0.043)*	0.11 *(0.009)*	-