Genetic and genomic evaluation of claw health traits in Spanish dairy cattle

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Abstract

The purposes of this study were to implement a routine genetic evaluation of claw health traits and to validate the genomic proofs for six claw disorders: dermatitis (DE), sole ulcer (SU), white line disease (WL), concave dorsal wall (CD), interdigital phlegmon (IP), and interdigital hyperplasia (IH). Claw disorders show moderate to high negative correlations with five feet and legs conformation traits, feet & legs (F&L), rear legs rear view (RLRV), foot angle (FA), locomotion (LOC), and bone quality (BQ), which ranged from 0.23 to -0.90. Including feet and legs type traits in a multi-trait evaluation would be a good option in order to increase the reliability of claw health breeding values. Claw trimming information with 593 137 records of six claw disorders of 221 266 cows, daughters of 8 000 bulls, and recorded in 1 418 Holstein dairy herds by 34 trimmers were used to carry out a genetic evaluation for claw disorders considering two scenarios. The first one, a 6-trait analysis with the claw health traits, and in the second one, the type traits were added to the multi-trait analysis. A total claw health index (ISP) was used to compare the results using sires with at least 20 daughters and 50% of reliability. For genomic prediction, a GBLUP with polygenic effect was applied to estimate genomic breeding values. The 1 317 sires reaching a minimum of 50% in reliability of EBV for total claw health index were used as the reference population was applied to estimate genomic breeding values. The inclusion of feet and legs type traits in the multi-trait genetic evaluation increased the reliabilities for claw disorders EBV of proven sires by 8% to 32%. Regarding genomic validation, the correlations between DRP and DGV ranged from 0.15 to 0.36. The regression coefficients were close to 1, except for DE and IH. To achieve a higher accuracy a larger reference population is needed. Therefore, an international genetic evaluation for claw health would increase the sire's reference population. At national level, performing a single-step evaluation could lead to slightly higher reliability.

Key words: claw health, genomic evaluation, multi-trait model, type traits

Introduction

Claw health is one of the major concerns in intensive dairy production farming. Claw disorders causes the worsening of cow welfare and economic losses, because it reduces the cow performance and increases the risk of premature culling (Warnick *et al.*, 2001; Booth *et al.*, 2004; Charfeddine & Pérez-Cabal, 2017). Based on this scenario, an electronic recording system for claw disorders called I-SAP was implemented in Spain in 2012.

Genetic selection provides a tool to improve claw health, but requires genetic variation. Genetic parameters of claw disorders scored by claw trimmers have been estimated previously with a small data set, and heritabilities ranged from 0.01 to 0.05 (Pérez-Cabal & Charfeddine, 2015). Given that claw lesions show a low heritability, the selection of more resistant animals to claw disorders can be achieved by combining those traits with feet and legs conformation (van der Linde *et al.*, 2010). The conformation traits contribute through an indirect selection due to the genetic correlations with claw health traits. However, they could also contribute to a better estimation of EBVs in a joint multi-trait genetic evaluation. At present, improvement of claw health in Spain is being approached by an index which includes only feet and legs traits but the information gathered within the I-SAP program (Charfeddine &

Pérez-Cabal, 2017) allows the update to a new claw health index.

On the other hand, the incorporation of genomic information has allowed the estimation of more accurate predictions for young animals without phenotypes (Odegard *et al.*, 2013).

The objectives of this study were to implement a routine genetic evaluation for claw disorders and to assess the reliability of genomic breeding values in Spanish dairy cattle.

Material and methods

Data

Claw trimming information of six claw disorders was obtained from the I-SAP database (Charfeddine & Pérez-Cabal, 2014). Disorders included in this study were dermatitis (DE) which includes interdigital and digital dermatitis, sole ulcer (SU), white line disease (WL), interdigital hyperplasia (IH), interdigital phlegmon (IP), and concave dorsal wall (CD). Claw health information used complied with the following requirements: records from January 2013 until October 2017, occurred in lactations from first to fifth within the 500 days from calving. Records from heifers were excluded as well as records from hoof trimmers with few data. Only herds with at least 30% of cows trimmed and herd-year-season with more than 10 cows with at least one disorder were included. The final dataset used for the genetic evaluation included a total of 593 137 records for 221 266 cows, daughters of 8,000 bulls and recorded in 418 Holstein dairy herds by 34 trimmers. We performed preliminary analyses (not shown) to compare the inclusion or not of the untrimmed cows, such as reported by Malchiodi *et al.* (2015) and Croué *et al.* (2017), which led to a better estimation of breeding values. Then, we considered both trimmed and untrimmed cows into the final data set. The average of trimmed cows within herds was about 70% of present cows.

Regarding type information, 173 129 cows in the claw health data set had a score for feet and legs (FL), rear legs rear view (RLRV), foot angle (FA), locomotion (LOC), and bone quality (BQ). The pedigree file consisted on 465 889 animals and 10 generations were included.

Total claw health index: ISP

In a previous study (Yánez *et al.*, 2017), a new claw health index called ISP was established based on the economic losses due to claw disorders estimated in Charfeddine & Pérez-Cabal (2017), as follows:

$$ISP = -9,30 \cdot DE - 44,00 \cdot SU - 37,40 \cdot WL$$
$$- 4,52 \cdot CL - 3,55 \cdot IP - 1,45 \cdot IH$$

And if expressed in percentages, the relative importance of each lesion in the ISP was:

$$ISP = -12\% \cdot DE - 57\% \cdot SU - 28\% \cdot WL$$
$$- 1\% \cdot CL - 1\% \cdot IP - 1\% \cdot IH$$

The genetic responses expected with this index were a decrease of the prevalence ranging from 1% (IP) to 95% (SU), which can be translated into a reduction of economic losses of 4.10€/cow/year.

Genetic evaluation

Statistical analyses
A multi-trait animal model, with repeated observations for the claw health traits was used. Two scenarios were considered. In the first one, a 6-trait analysis with the claw health traits were performed. In the second scenario, the conformation traits were added to the multi-trait analysis. The model for claw health traits was:

$$y_{ijklmn} = \alpha + HYS_i + SL_j + LA_k + TRIM_l$$
$$+ PE_m + Animal_n + \varepsilon_{ijklmn}$$

where, y_{ijklmn} is the observed performance of DE, SU, WL, IH, IP, CD (0= non-affected; 1= affected); α is an intercept; HYS_i is the systematic effect of herd-year-season of trimming (8 705 levels); SL_j is the systematic effect stage of lactation (15 levels; one level every 30 days in milk); LA_k is the systematic effect of lactation-Age at calving (52 levels); $TRIM_l$ is the systematic effect of hoof trimmer (34 levels); PE_m is the random permanent environmental effect of the lth cow (221 266 levels); $Animal_n$ is the random additive genetic effect of the nth animal (465 889 levels), and ε_{ijklmn} is the random residual error.

The model for feet and legs traits was:

$$y_{ijkl} = \alpha + HVC_i + LA_j + SL_k + Animal_l + \varepsilon_{ijkl}$$

where, y_{ijklm} is the score of FL, RLRV, FA, LOC, and BQ; α is an intercept; HVC_i is the systematic effect of herd-visit-classifier (11 625 levels); LA_j is the systematic effect of lactation-Age at calving (34 levels); SL_k is the systematic effect stage of lactation at classification (11 levels; one level every 30 days in milk, level 11 grouped cows with DIM>305); $Animal_l$ is the random additive genetic effect of the lth animal (463 889 levels), and ε_{ijkl} is the random residual error.

Genetic parameters were estimated using VCE (Groeneveld *et al.*, 2008) while the genetic evaluation was carried out with MIX99 (Strandén & Lidauer, 1999).

Estimated breeding values were standardized to relative breeding values with a mean of 100 and a standard deviation of 10 and reversed in sign. Thus, higher EBVs indicate sires with daughters more resistant to claw disorders. The potential advantage of adding conformation traits to claw health traits in a multi-trait analysis was tested calculating the Pearson and Spearman correlations between predicted EBV for sires with at least 20 daughters and at least 50% of reliability, as in official proofs, and estimating the improvement of the reliability of proofs.

Genomic evaluation

GBLUP with polygenic effect, as used for the official routine genomic evaluation by the Spanish Holstein Association, was applied to estimate direct genomic values (DGV). A previous test was performed to check for the optimum percentage of polygenic effect in order to combine genomic matrix and the relationship matrix. For the genomic prediction, we assumed that 30% of genetic variance is due to polygenic effect not described by the SNP markers.

Sires reaching a minimum of 50% in reliability of EBVs for total claw health index (1 317 sires) were used as the reference population. The response variable in the genomic predictions was the deregressed proof (DRP), obtained using MiX99 package and weighted by number of daughters per sire to account for differences in reliability of EBV. A 10-fold cross-validation was performed (Efron & Tibshirani, 1993), where sires were randomly assigned into ten subsets of similar size. For validation assessment, two parameters were taken into account, the accuracy calculated as the Pearson correlation between estimated DGV and known DRP, and the prediction bias calculated as the regression coefficient of the DGV on the DRP.

Results and Discussion

Prevalence of claw health traits used in the study and their estimated heritability and repeatability are in Table 1. The most frequent disorders shown in Spanish dairy cattle are DE, SU, and WL. Around 30% of cows showed at least one disorder. Heritabilities were low and ranged between 1% and 13%. Repeatabilities were also low and ranged from 3% to 22%.

Table 1. Prevalence, heritability (h^2) and repeatability (r) with their corresponding standard errors (S.E.), for each claw disorder.

Claw disorder[a]	Prevalence (%)	h^2 (S.E.)	r (S.E.)
DE	10.07	0.06 (0.007)	0.11 (0.007)
SU	11.37	0.06 (0.007)	0.11 (0.007)
WL	8.03	0.02 (0.003)	0.07 (0.004)
CD	1.50	0.02 (0.004)	0.22 (0.005)
IP	0.95	0.01 (0.003)	0.03 (0.004)
IH	0.54	0.13 (0.010)	0.07 (0.010)

[a]DE: Dermatitis; SU: Sole ulcer; WL: White line disease; CD: Concave dorsal wall; IP: Interdigital phlegmon; IH: Interdigital hyperplasia.

Estimated genetic correlations between claw health and type traits are shown in Table 2. Correlations ranged from 0.23, between FA and DE, to -0.90, between IH and RLRV. Correlations with IH were very high, however the standard error of this estimates are quite high due to the low frequency of this disorder.

Reliabilities of proofs were calculated based on the effective daughter contribution. The inclusion of feet and legs type traits in the multi-trait model increased the reliabilities of proofs for claw disorders of proved sires by 8% to 32% (Table 3). Pearson and rank correlations between EBVs for claw disorders estimated within both scenarios varied in the range of 0.91 to 0.98, which mean that EBVs changed slightly by including feet and legs type traits.

Table 2. Genetic correlation between claw disorders and feet and legs type traits.

	DE[a]	SU	WL	CD	IF	IH
F&L[b]	-0.18	-0.30	-0.24	-0.25	-0.26	-0.11
RLRV	-0.20	-0.10	-0.09	-0.12	-0.23	-0.11
FA	0.23	0.15	-0.16	-0.12	-0.11	-0.04
LOC	-0.18	-0.54	-0.30	-0.43	-0.41	-0.90
BQ	-0.09	-0.15	-0.30	-0.02	-0.19	-0.08

[a]DE: Dermatitis; SU: Sole ulcer; WL: White line disease; CD: Concave dorsal wall; IP: Interdigital phlegmon; IH: Interdigital hyperplasia.
[b]F&L: Feet and legs; RLRV: Rear legs rear view; FA: Foot angle; LOC: Locomotion; BQ: Bone quality.

Table 3. Correlation between EBVs and reliability gain of sire's proofs for claw disorders due to the inclusion of type traits in the genetic evaluation.

Claw disorder[a]	Correlation between EBVs		Rel. gain
	Spearman corr.	Pearson corr.	
DE	0.98	0.98	9%
SU	0.96	0.96	10%
WL	0.91	0.91	14%
CD	0.92	0.92	8%
IP	0.93	0.93	32%
IH	0.96	0.96	22%
ISP	**0.97**	**0.97**	**12%**

[a]DE: Dermatitis; SU: Sole ulcer; WL: White line disease; CD: Concave dorsal wall; IP: Interdigital phlegmon; IH: Interdigital hyperplasia, ISP: Total claw health index.

Despite the low heritabilities, when the ISP was computed for sires in the two scenarios, large differences between daughter groups were observed. The percentage of daughters with at least one claw disorder varied between 18% and 34% among the 100 sires with the best and the worst ISP proof.

Results of cross-validation for genomic evaluation are in Table 4. Correlations between DRP and DGV weighted by the number of the effective daughter contribution (EDC) ranged from 0.15 to 0.36, and showed low accuracy for some traits such as DE and IH. Reliabilities were lower than those estimated by Ødegard *et al.* (2013), although in that study they used sire EBV instead of DRP as response variables. The regression coefficients were close to 1, except for DE and IH. To achieve higher accuracy a large reference population is needed. For that, an international genetic evaluation for claw health would increase the sire's reference population. At national level, performing a single step evaluation could lead to slightly higher reliability.

Table 4. Accuracy (R) and b-values (prediction bias) with the corresponding standard error (S.E.), obtained from a 10-fold cross-validation.

Claw disorder[a]	R	b_values	S.E.
DE	0.19	0.72	0.11
SU	0.34	0.99	0.08
WL	0.27	0.94	0.10
CD	0.35	0.94	0.08
IP	0.36	1.03	0.08
IH	0.15	0.76	0.15

[a]DE: Dermatitis; SU: Sole ulcer; WL: White line disease; CD: Concave dorsal wall; IP: Interdigital phlegmon; IH: Interdigital hyperplasia.

Conclusion

The implementation of a routine genetic evaluation for claw disorders is more than justified despite the low heritability, given the large genetic variation between breeding values of the best and worst bulls. The inclusion of feet and legs type traits in a multi-trait animal model increased the reliabilities of proofs for claw disorders, though it may imply a little change in the EBVs. Reliabilities of genomic proofs are low to moderate, which make an international evaluation for claw health traits urgently needed in order to extend the reference population.

Acknowledgments

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