A Single-Step Genomic Evaluation of Claw Health Traits in French Holstein, Montbéliarde and Normande Breeds

H Leclerc, A Lepers, A Baur, A Barbat, T Tribout, S Fritz

▶ **To cite this version:**

H Leclerc, A Lepers, A Baur, A Barbat, T Tribout, et al.. A Single-Step Genomic Evaluation of Claw Health Traits in French Holstein, Montbéliarde and Normande Breeds. 2023 Interbull Meeting, Interbull, Aug 2023, Lyon, France. pp.207-212. hal-04345892

HAL Id: hal-04345892
https://hal.inrae.fr/hal-04345892

Submitted on 14 Dec 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

A Single-Step Genomic Evaluation of Claw Health Traits in French Holstein, Montbéliarde and Normande Breeds

H. Leclerc[1], A. Lepers[2], A. Baur[1], A. Barbat[3], T. Tribout[3], S. Fritz[1]

[1] Eliance, UMT e-bis, 78352 Jouy-en-Josas, France

[2] IDELE, UMT e-bis, 78352 Jouy-en-Josas, France

[3] INRAE GABI, UMT e-bis, 78352 Jouy-en-Josas, France

Abstract

Claw lesions are the third most important health issue in dairy cattle, after mastitis and fertility issues. 21 lesions defined according to ICAR standards are recorded by trimmers on touch pad since the early 2010s. Seven of these lesions (Digital Dermatitis (DD), Heel Horn Erosion (HHE), Interdigital Hyperplasia (IH), Sole Hemorrhage Circumscribed (SHC), Sole Hemorrhage Diffused (SHD), Sole Ulcer (SU) and White Line Fissure (WLF)), which have a prevalence of more than 10%, and/or may be responsible for lameness, were studied in the Holstein, Normande and Montbéliarde breeds. Breed specificities have also led to study Toe Necrosis (TN) and Corkscrew Claw (CSC). In summer 2022 dataset, more than 440,000 Holstein trimmings (respectively 80 000 Montbeliarde and 62 000 Normande) from 250 000 cows (respectively 44 000 Montbeliarde and 35 000 Normande), including 35,000 genotyped cows (respectively 15 000 Montbeliarde and 10 000 Normande) were available for the development of the genetic evaluation model. 40% of the cows were trimmed more than once, but only 20% were trimmed in different lactations. Estimated heritabilities ranged from 0.01 and 0.22 depending on the trait. Genetic correlations showed two groups of traits that were highly correlated: 1) within the infectious traits (DD, HHE and IH), in particular with high correlations between DD and IH (between 0.65 and 0.80 according to the breed); 2) within the non-infectious traits (SHC, SHD, WLF and SU) with genetic correlations between 0.40 and 0.89 in Holstein; TN and CSC being relatively independent from the other traits. Multiple trait single-step genomic evaluations have been developed for each group of traits to limit computational times, with a negligible effect on estimated genetic values compared to a nine traits genetic evaluation. Implementation of routine evaluation is planned for April 2024.

Key words: claw health, single-step, genomic evaluation, genetic correlations

Introduction

Claw health are a major welfare problem in dairy farming, often causing pain and lameness in cows. In France, it is the third most costly disorder and is responsible for a fifth of culling after mastitis and fertility trouble. Lameness usually has a multifactorial origin. 24 claw health traits as described in ICAR Atlas (ICAR, 2020) can be registered, and 11 of them are mandatory.

Until now, the development of claw health genetic evaluation in France has been private initiatives directly led by breeding companies (Leclerc et al., 2019). A need to harmonise the different initiatives and to bring the Holstein closer to the Eurogenomics golden standards, led to initiate a national project in summer 2022. With data currently available, it is now possible to set up a multiple trait model that takes into account successive trimmings using a single step methodology, and to include new traits of interest as required.

Based on data collected since 2012 in the 3 main breeds (Holstein, Normande and Montbéliarde), the objective of this study was: 1) to select traits of interest from the 24 claw heath traits; 2) to estimate genetic relationships between those traits; 3) to develop a multiple trait model that takes into account successive trimmings using a Single Step Genetic Evaluation.

Materials and Methods

The claw health database

Breeding organizations (Evolution/Synetics, Genes Diffusion, Origen Normande, Umotest) gathered information on 642 540 claw trimming animals (Table 1 with breed distribution), collected by 220 professional trimmers on touch-pad from 2012 to 2022 in 9 091 herds.

Data comes from a limited number of herd, because not all of them are using trimming service, and a large part part of the trimming service is carried out by independent trimmers who do not have the touch-pad to collect claw health data. In addition, the breeder chooses which cows to trim. Therefore, we have non-exhaustive data within herd.

To ensure the quality of the data, only data from herds enrolled in official milk recording, having a lactation rank of one to five5 and a lactation stage of one to 550 are considered. The cows must have at least the two rear claws trimmed and a minimum recovery period of four months after the previous lesion to be considered as a new lesion as mentioned in EuroGenomics Golden Standard (S. De Roo, 2022 - personal comm.).

Analysis of herds with exhaustive trimming has shown that only 12% (Normande) to 21% (Holstein) of cows have no lesions, so we decided to not assume a healthy status / absence of claw disorders of untrimmed cows by default.

were selected: Digital and interdigital Dermatis (DD), Interdigital Hyperplasia (IH), Heel Horn Erosion (HHE), White Line Disease (WDL), Sole Hemorrhage Diffused (SHD) and Circumscribed (SHC), Sole Ulcer (SU), Toe ulcer and Necrosis (TN) and CorkScrew Claw (CSC). These traits present a prevalence of at least 10% in one of the three studied breeds, or for TN an increasing frequency and a large economic impact, culling being in most cases inevitable.

Due to infectious status of Digital Dermatitis, only cows from a herd with affected contemporaries are considered healthy.

Model

Bivariate and Multivariate linear animal models were fitted using REML procedure from the Wombat software (Meyer, 2007), based on selected data described in Table 1. A minimum of 10% of the herd trimmed per year is required to select data for genetic evaluation, but this minimum is increased to 15% with two annual visits for genetic parameter estimation (and 50% in Holstein).

The following linear animal model, with repeated observations within and across lactations, was applied:

$$\boldsymbol{y}=\boldsymbol{X\beta}+\boldsymbol{Za}+\boldsymbol{Zp}+\boldsymbol{e}$$

where **y** is the vector of severity scores for the traits (from 0 = healthy to 3=severe lesion except for TN and CSC which are treated as a binary traits 0/1); **β** the vector of fixed effects consisting of a herd × trimming date effect (with minimum five cows in

Table 1. Description of the datasets used for the differents step of the study

		Holstein	Normande	Montbéliarde
Database	#trimmed cows	451 322	61 975	79 371
Genetic parameters estimation	#trimmed cows	89 930	25 551	38 148
	#trimmed data	142 090	41 017	64 471
	#herd x trimming date	4 258	3 298	3 682
	#animal in pedigree file	190 212	70 719	95 243
Single Step Genetic Evaluation	#trimmed cows	299 679	44 268	45 878
	#trimmed data	532 712	82 265	76 672
	#herd x trimming date	26 228	6 854	4 707
	#animals (♂+♀) in reference pop	46 072	13 291	12 817

Nine claw health traits from the 24 ICAR Atlas

Holstein and four in the other breeds), trimmer × year effect, age of calving × parity effect, calving month × year effect, parity × lactation month × 3 year period effect ; **a** the vector of additive gene
tic effect ~$\mathbf{N}(0,\mathbf{A}\sigma^2_g)$, **p** the vector of random effect of permanent environment ~$\mathbf{N}(0,\mathbf{I}\sigma^2_{pe})$. **X** and **Z** are incidence matrices.

A Single-Step genetic evaluation using HSSGBLUP software (Tribout et al., 2020) using multivariate model similar to variance component estimation was performed on the 9 traits and then split in two groups of traits: a group of three infectious traits (DD, IH and HHE) and 6 traits (SHC, SHD, SU, WLD, CSC and TN) to limit memory requirements and computational time by two to three.

Results & Discussion

The prevalence of the traits is not similar from one breed to another one. In Holstein (Table 2) (Normande & Montbéliarde breed are in Annex), DD and HHE have a higher prevalence than on other breeds. In Montbeliarde breed, it is mainly the prevalence of WLD and CSC that distinguishes it, while in the Normande breed, many traits show higher prevalence than in the other breeds (DD, IH, TN, WL, SU).

In Holstein (Table 2), heritabilities are quite low, between 2% and 10% (between 2 and 8%, in Normande except for interdigital hyperplasia with a moderate heritability of 22% (Table 5 in Annex) and between 4 and 9% in Montbéliarde (Table 6 in Annex), but within the range of similar studies (CRV, 2022 ; Johansson et al., 2011). The repeatability trend is similar between breed, with some traits with moderate repeatability ranging from 0.17 to 0.23 for digital dermatitis, white line disease and sole ulcer and quite high for interdigital hyperplasia and toe ulcer and necrosis ranging from 0.34 to 0.47, illustrating how difficult it is to treat for this lesions in the long term.

The estimated genetic correlations tend to show the existence of 2 groups of traits: A first group of infectious traits with DD, HHE and IH and a second group with mechanical/physical lesions with SHC, SHD, WL, SU, TN and CSC. The genetic correlations within group are high: for instance, between 0.50 and 0.71 between the 3 infectious traits in Holstein. Within group of mechanical lesion, genetic correlations are usually moderate (generally in the range from 0.25 to 0.50), except high correlations between SHC and SU with 0.89, 0.78 and 0.84

Table 2. Holstein genetic parameters estimates (Prevalence of the traits (%), heritabily on diagonal, Genetic correlations (rg) above diagonal – standard error of heritability and range of standard error of genetic correlations, and repeatability) for claw health traits (Digital Dermatis (DD), Interdigital Hyperplasia (IH), Heel Horn Erosion (HHE), White Line Disease (WDL), Sole Hemorrhage Diffused (SHD) and Circumscribed (SHC), Sole Ulcer (SU), Toe ulcer and Necrosis (TN) and CorkScrew Claw (CSC)).

Holstein	**Preval.**	**DD**	**HHE**	**IH**	**TN**	**SHC**	**SHD**	**WL**	**SU**	**CSC**	**repeat.**
DD	**35%**	**0.08**	0.68	0.71	-0.06	-0.08	-0.17	-0.14	0.01	0.00	**0.18**
HHE	**39%**		**0.04**	0.50	-0.12	0.22	-0.10	-0.05	0.28	0.18	**0.09**
IH	14%			**0.10**	-0.10	-0.02	-0.09	-0.06	0.06	0.02	**0.41**
TN	3%				**0.01**	0.48	0.55	0.50	0.58	0.06	**0.34**
SHC	16%					**0.04**	0.44	0.47	0.89	0.19	**0.08**
SHD	25%						**0.02**	0.43	0.40	0.32	**0.05**
WL	17%							**0.05**	0.63	0.20	**0.17**
SU	13%								**0.06**	0.09	**0.17**
CSC	5%									**0.02**	**0.11**
σ_{error} $\mathbf{h^2}$		0.005	0.004	0.006	0.002	0.003	0.003	0.004	0.004	0.003	
σ_{error} $\mathbf{r_g}$	**Min**	0.03	0.04	0.03	0.08	0.03	0.06	0.04	0.04	0.06	
	Max	0.10	0.11	0.10	0.13	0.10	0.11	0.10	0.09	0.13	

respectively for Holstein, Normande and Montbéliarde breed. This suggests that SHD may be a precursor to SU. In the 3 breeds, the correlation between the two different sole haemorrhages (SHC and SHD) is moderate with values between 0.26 and 0.50, clearly showing that they are two different traits.

Impact of splitting the nine traits into two groups of traits is negligible. Correlations between GEBV obtained in a nine traits sets vs a 3+6 traits are over 0.99 for all traits in the three breeds (except for DD and HHE in Montbéliarde breed > 0.984)

More than 1,6 millions of animals were evaluated based on the 500 thousand trimmed data and 46 thousand animals in the Holstein reference population. GEBV are expressed in genetic standard deviation unit. Analysis of the risk factor (% of animals affected) as a function of GEBV shows, for instance in the Normande breed, that number of animals with IH drops from 73% for an index of -1 to 25% for an index of 0, and from 19% of animals with TN to only 1% for similar index than previously.

Composite indexes have been defined for each breed to optimize their uses and to improve the genetic level of the population, taking into account prevalence and estimated incidence costs (Table 3) (synthesis from Dolechek and Bewley, 2018 & 2019; Whay and Shearer, 2017; Willshire and Bell, 2009; Bruijnis et al, 2010; Charfeddine and Perez-Cabal, 2017; and discussion with French veterinarians R. Guatteo and A. Waché – personal comm.).

For infectious traits, the composite SLI (Table 4) has the same weighting for the three breeds. For mechanical traits, breeds specificities have been taken into account (Table 4) by including toe necrosis in selection index in Normande breed, and corkscrew claw in Montbéliarde breed as well as increasing weight on white line disease for this breed.

Table 3. Estimated claw disorders costs in €uro.

	Estimated Cost		
	Direct	Indirect	Total
DD	50€	150€	200€
HHE	25€	0€	25€
IH	50€	50€	100€
SHC	25€	0€	25€
SHD	25€	0€	25€
WD	30€	100€	130€
SU*	50€	200-300€	300€
TN*	50€	300-1000€	450€
CSC	25€	0€	25€

⁂ High culling risk for high severity levels

A claw health index gathers the SLI and SLM, with a balanced weight in Montbéliarde, whereas Holstein and Normande give 60% on SLI and 40% on SLM.

Conclusions

From the nine claw health traits studied, two groups of traits emerge which are more or less genetically independent of each other, and which make it is possible to evaluate them in two sets of 3+6 traits.

Breed-specific composite for claw health have been decided in concertation between breed societies and will be included in future revisions of the Total Merit Index.

The first routine genetic evaluation is currently implemented at GenEval and the official release is scheduled in April 24.

Table 4. Composite of claw health traits: Infectious traits index (SLI), Mechanical trait index (SLM), and Claw Health index (STPI).

	Infectious Traits index (SLI)			Mechanical Traits index (SLM)						Claw Health index (STPI)	
Traits	DD	IH	HHE	SHC	SHD	WL	SU	TN	CSC	SLI	SLM
Holstein	0.60	+0.30	+0.10	0.10	+0.10	+0.40	+0.40			0.60	+0.40
Normande	0.60	+0.30	+0.10	0.05	+0.05	+0.25	+0.40	+0.25		0.60	+0.40
Montbéliarde	0.60	+0.30	+0.10	0.10	+0.10	+0.45	+0.30		+0.10	0.50	+0.50

Acknowledgments

This research project led by Eliance was financially supported by Breeding companies (Evolution / Synetics; Genes Diffusion; Origen Normande and Umotest) with the support of numerous trimming data suppliers, and GenEval for the implementation of the routine evaluation. Previous studies conducted through GénoSanté and MO3San have contributed to the creation of trimming databases and first experiences with genetic evaluation. GenoSanté was labelled by the Valorial competitiveness cluster. It has received funded from the Fonds Unique Interministériel (BPI France, regions of Brittany, Alsace and Pays de Loire). MO3San was labelled by the Valorial competitiveness cluster. It has received funded BPI France (regions of Burgondy, Franche Comté). A seed project POD² funded by Apis-Gene to establish a reference population by providing financial support for genotyping.

References

Bruijnis M.R.N., Hogeveen H., Stassen E.N. 2010. Assessing economic consequences of foot disorders in dairy cattle using a dynamic stochastic simulation model. *J. Dairy Sci.* 93, 2419-2432.

Charfeddine N. and Pérez-Cabal M.A. 2017. Effect of claw disorders on milk production, fertility, and longevity, and their economic impact in Spanish Holstein cows. *J. Dairy Sci.* 100(1), 653-665.

CRV. 2022. E-30 Claw Health Index - Manual quality. https://www.cooperatie-crv.nl/wp-content/uploads/2022/08/E_30-Klauwgezondheid-Augustus-2022-Engels.pdf

Dolecheck K. and Bewley J. 2018. Animal board invited review: Dairy cow lameness expenditures, losses and total cost. *Animal*. 12(7), 1462-1474.

Dolecheck K., Overton M.W., Mark T.B. and Bewley J. 2019. Use of a stochastic simulation model to estimate the cost per case of digital dermatitis, sole ulcer, and white line disease by parity group and incidence timing. *J. Dairy Sci.* 102(1), 715-730.

International Committee for Animal Recording (ICAR). 2020. ICAR claw health atlas, https://www.icar.org/ICAR_Claw_Health_Atlas.pdf

Johansson K., Eriksson J.-Å, Nielsen U. S., Pösö J., Aamand G. P. 2011. Genetic evaluation of claw health in Denmark, Finland and Sweden. *Interbull Bulletin* 44, 225-228.

Leclerc H., Croué I., Vallée R., Baur A., Barbat A., et al. 2019. French regional genetic collaborative projects to improve welfare and resilience of dairy cows. ICAR Techn. Series 24:373-381.

Meyer K. 2007 WOMBAT: a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). *J Zhejiang Univ Sci B.* 8(11), 815-821 doi:10.1631/jzus.2007.B0815

Tribout T., Ducrocq V. and Boichard D. 2020. HSSGBLUP: A Single-Step SNP BLUP genomic evaluation software adapted to large livestock populations. Proc. of the 6th ICQG, Brisbane, Australia.

Whay H.R., Shearer J.K. 2017. The impact of the lameness on the welfare of the dairy cow. Vet. Clin. *North Am. Food Animal Pract.* 33, 153-164.

Willshire J.A., Bell N.J. 2009. An economic review of cattle lameness. *Cattle practice*. 17(2), 136-141.

Annex 1. Normande and Montbéliarde genetic parameters estimates

Table 5. Normande genetic parameters estimates (Prevalence of the traits (%), heritabily on diagonal, Genetic correlations (rg) above diagonal – standard error of heritability and range of standard error of genetic correlations, and repeatability) for claw health traits (Digital Dermatis (DD), Interdigital Hyperplasia (IH), Heel Horn Erosion (HHE), White Line Disease (WDL), Sole Hemorrhage Diffused (SHD) and Circumscribed (SHC), Sole Ulcer (SU), Toe ulcer and Necrosis (TN) and CorkScrew Claw (CSC)).

Normande	Preval.	DD	HHE	IH	TN	SHC	SHD	WL	SU	CSC	repeat.
DD	43%	0.08	0.37	0.80	-0.45	-0.25	-0.26	-0.39	-0.27	-0.19	0.18
HHE	33%		0.02	0.18	-0.29	0.11	-0.01	-0.22	0.31	0.00	0.04
IH	30%			0.22	-0.29	-0.24	-0.23	-0.16	-0.22	-0.15	0.47
TN	5%				0.03	0.23	0.27	0.43	0.22	0.15	0.39
SHC	14%					0.03	0.50	0.31	0.78	0.20	0.06
SHD	29%						0.03	0.45	0.30	0.36	0.06
WL	28%							0.07	0.25	0.36	0.23
SU	18%								0.07	0.10	0.23
CSC	3%									0.05	0.19
σ_{error} h^2		0.010	0.004	0.017	0.008	0.005	0.006	0.010	0.009	0.010	
	Min	0.04	0.12	0.04	0.10	0.06	0.09	0.08	0.08	0.09	
σ_{error} r_g	Max	0.12	0.17	0.12	0.17	0.16	0.16	0.14	0.13	0.16	

Table 6. Montbéliarde genetic parameters estimates (Prevalence of the traits (%), heritabily on diagonal, Genetic correlations (rg) above diagonal – standard error of heritability and range of standard error of genetic correlations, and repeatability) for claw health traits (Digital Dermatis (DD), Interdigital Hyperplasia (IH), Heel Horn Erosion (HHE), White Line Disease (WDL), Sole Hemorrhage Diffused (SHD) and Circumscribed (SHC), Sole Ulcer (SU) and CorkScrew Claw (CSC)).

Montbél.	Preval.	DD	HHE	IH	TN	SHC	SHD	WL	SU	CSC	repeat.
DD	24%	0.04	0.58	0.65		0.26	-0.10	-0.02	0.32	-0.20	0.13
HHE	34%		0.04	0.34		0.44	-0.03	0.14	0.44	0.11	0.06
IH	13%			0.09		-0.01	0.04	-0.02	0.06	-0.08	0.39
TN	2%										
SHC	14%					0.04	0.26	0.36	0.84	0.36	0.08
SHD	33%						0.04	0.17	0.32	0.46	0.06
WL	33%							0.08	0.49	-0.02	0.18
SU	10%								0.05	0.21	0.19
CSC	15%									0.07	0.17
σ_{error} h^2		0.006	0.005	0.009		0.005	0.005	0.008	0.006	0.008	
	Min	0.07	0.08	0.07		0.05	0.08	0.07	0.07	0.08	
σ_{error} r_g	Max	0.12	0.11	0.10		0.11	0.11	0.09	0.11	0.10	