

# Development of a Single Step Genomic Evaluation of health traits and relationships with dairy traits in French Holsteins

H. Leclerc<sup>1,2\*</sup>, A. Barbat<sup>2</sup>, R. Vallée<sup>3,2</sup>, F. Guillaume<sup>4</sup>, L. Manciaux<sup>5</sup>,  
J.-B. Davière<sup>6</sup> and M. Philippe<sup>4</sup>

<sup>1</sup> ALLICE, 149 rue de Bercy, 75012 Paris, France; <sup>2</sup> Univ. Paris Saclay, INRAE, AgroParisTech, GABI, 78350 Jouy-en-Josas, France; <sup>3</sup> IDELE, 149 rue Bercy, 75012, France; <sup>4</sup> EVOLUTION, CS 10040, 35538 Noyal sur Vilaine, France; <sup>5</sup> INNOVAL, CS 80038, 35538 Noyal sur Vilaine, France; <sup>6</sup> SEENERGI, CS 84215, 53942 St Berthevin, France; [\\*helene.leclerc@inrae.fr](mailto:helene.leclerc@inrae.fr)

## Abstract

Selecting for better health has become of primary importance for the dairy industry. In France, where no national database exists for health traits (except mastitis), a collaborative project has been implemented to explore and evaluate farmer health records. Around 10% of herds record health events accurately. Genetic parameters of 4 disorders have been studied here: Displaced Abomasum (DA), Milk Fever (MF), Metritis (MET) and Retained Placenta (RP). Heritabilities are low (1-2%), but health traits have moderate genetic correlations with some dairy traits (0.15-0.45). Based on EBV obtained with ssGBLUP for the four health traits, the daughters' incidence of best EBV bulls versus worst bulls is reduced by a factor of 2 minimum.

## Introduction

Health traits are of increasing importance for dairy farmers, both for economic reasons (treatments' cost/production loss), for working time and for animal well-being. Since 2000, French laws require breeders to record all treatments in a diary. The pathology causing a treatment may also be recorded. Rapidly, a growing number of breeders started recording using one of the available IT application (software, web...), thus making disease data available to their support organisations. In 2015, a collaborative regional project named "GénoSanté" was initiated by the *Evolution* Breeding Company, together with milk recording and herd support organisations (DHI) of Western France, breeding companies and R&D organisations. The aim of this project was to improve animal health through new tools both for management and selection (Leclerc et al, 2019), adding extra-value to information recorded by farmers in health management diaries. In 2015, a study on a subset of IT application showed that 15% of herds recorded health events exhaustively (Bourrigan et al., 2015) and suggested that these data could help to develop references for management tools and genetic evaluations. The objectives were: 1/ to validate the feasibility of using breeders recorded health data for genetic purpose; 2/ to estimate genetic relationships between some available health traits of interest and other dairy traits; 3/ to develop a Single Step Genetic Evaluation of those health traits.

## Materials & Methods

**The health database:** 742,973 multi-breed health events (mastitis discarded), corresponding to 178 treatments reasons, collected by farmers from 2008 to 2021 in 16,619 herds were available. Due to lack of supervision in the data acquisition system, the consistency of data was checked by cross-referencing all the data available for those animals with the national genetic databases. Six different categories of animals were established: calves less than 1

month old, calves from 1 to 6 months old, heifers over 6 months old, pregnant heifers, cows, and males. A list of possible diseases was defined for each category. For instance, calving pathologies such as uterine prolapse are only possible for the “cow” category. Inconsistent data (2.1%) and uncategorized data (3.9%) were discarded. Data from herds with less than 20 lactations per year were excluded (5.6%), as well as data from collective treatments that did not allow to assess individual sensitivity (22.9%). Among health disorders, four traits were selected: Displaced Abomasum (DA), Milk Fever (MF), Metritis (MET) and Retained Placenta (RP). Lameness and ketosis disorders recorded in herd diaries were not studied here, genetic evaluations for ketosis (through milk MIR spectra of Acetone and Beta-Hydroxybutyrate (BHB)) and lameness (from claw lesions) being already available (Leclerc et al, 2019).

**Completeness at herd level:** To ensure that data available are from reliable herds, a minimum of 3 different health disorders and health events recorded for at least 15% of the lactating cows per year were required to consider the health status of the herd as complete for that year, regardless of breeds. A minimum of 5 consecutive years of completeness was required to select a herd, to ensure this period covers the cow productive lifespan and to have a dataset quality suitable for the estimation of genetic parameters.

**Traits’ definition:** Health disorders were defined as binary traits (0=no case / 1=at least one case) based on whether or not the cow had at least one disease case recorded during the lactation period (0-60 days after calving for DA, 0-7 d for MF, 0-150 for MET, 0-14 d for RP). MET and RP periods are similar to those used in Canada (Koeck et al., 2012). Breeders are more or less sensitive to certain diseases, so only herds with at least one case recorded in the considered year, the previous or the following one have contemporaries’ cows considered as “no case” (617 herds considered for DA, 756 for MF, 767 for MET and 845 for RP). Information from the national database was added for other traits on 409,031 lactations (parity 1 to 5) from 2006 to 2021 (Table 1): Milk production traits, recorded between 7 and 40 days in milk (DIM) (kg of milk, Fat%, Pro%, SCS, acetone and BHB estimated from MIR spectra on milk sample ( $100 \cdot \log_2([\text{acetone or BHB}] + 1)$ )); number of insemination (#INS), interval between calving and first insemination (ICFINS), interval between calving and last insemination (ICLINS), and number of mastitis cases in the lactation (#MAS).

**Analysis:** This study, focused on Holsteins’ data from the exhaustive herds, was split into 3 parts: 1/ variance components estimation within the 4 health traits (herd diaries database); 2/ estimation of genetic correlations between the 4 health traits, and acetone/BHB (Milk database), udder health, fertility and production traits (national database); 3/ genomic evaluation of the 4 health traits by SGBLUP.

**Pedigree and genotyped animals:** Animal pedigree was built by tracing the pedigree of the 167,498 cows with data on 5 generations (339,406 animals). A total 23,132 animals genotyped (or imputed) on the Illumina Bovine SNP50 BeadChip were used for ssGBLUP.

**Table 1. Summary statistics of analyzed traits.**

Trait	N°	#Lact	Mean	Std	Trait	N°	#Lact	Mean	Std
DA (0/1)	a	193,650	0.011	0.102	#MAS	c	409,031	0.44	0.85
MF (0/1)	a	257,482	0.018	0.134	Milk (kg)	b	351,492	32.71	8.26
MET (0/1)	a	215,837	0.063	0.243	Fat%	b	351,492	4.08	0.71
ND (0/1)	a	285,252	0.062	0.241	Pro%	b	351,491	3.03	0.30
#INS	c	351,565	2.21	1.55	SCS	b	351,491	2.42	1.88
ICFINS (days)	c	351,565	91.64	38.15	Acetone	b	239,402	20.89	13.57
ICLINS (days)	c	289,916	134.22	73.13	BHB	b	223,954	15.15	12.17

**Model:** Bivariate and Multivariate linear animal models, with repeated observations across lactations, were fitted by a REML using Wombat software (Meyer, 2007). Multivariate analysis were performed among the 4 health traits, and bivariate for other traits combinations.

$$y = X\beta + Za + Zp + e \quad (1)$$

where  $y$  is the vector of observations for the traits;  $\beta$  the vector of fixed effects consisting of a herd $\times$ year (a,b,c), calving age $\times$ parity (a,b,c), calving month $\times$ year (a,b), length of dry period $\times$ parity (a,b), parity $\times$ DIM (a) [a,b,c as described in table 1];  $a$  ( $\sim N(0, A\sigma^2_g)$ ) and  $p$  ( $\sim N(0, I\sigma^2_{pe})$ ) the vectors of additive genetic and permanent environment,  $X$  &  $Z$  the incidence matrices.

A SingleStep genetic evaluation using HSSGBLUP software (Tribout et al., 2020) using univariate model similar to variance component estimation was performed on the 4 health traits.

## Results

Around 2/3 of health data remained after data edits. It was used to qualify the completeness of 10,019 herds and 8.6% of herds (867) have fulfilled the 5 consecutive years of completeness. The disease frequencies of the 4 health traits were low, from 1.1% for DA to 6.3% for MET (Table 1). MF frequency were highly dependent of parity (close to 0 in 1<sup>st</sup> and 2<sup>nd</sup> up to 9% in 5<sup>th</sup>). Heritability estimates of the 4 health traits in linear model were between 1 and 2% (Table 2). MET genetic correlations were high with RP (0.64) to moderate with DA (0.31).

**Table 2. Heritability (SE in parenthesis), repeatability, genetic correlations (SE) (above the diagonal) and phenotypic correlations (below the diagonal) within four health traits.**

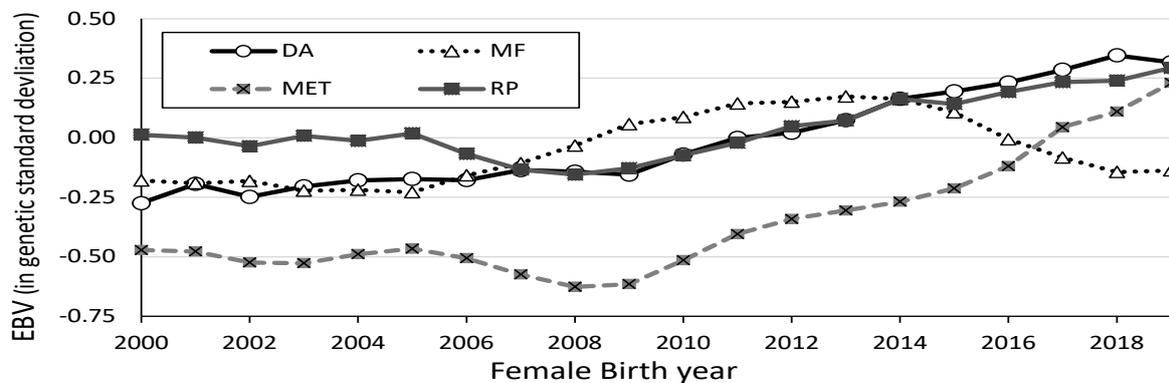
Trait	h <sup>2</sup>	r <sub>p</sub>	Correlations			
			DA	MF	MET	RP
DA	0.020 (0.002)	0.020		0.09 (0.08)	<b>0.31</b> (0.08)	0.14 (0.07)
MF	0.015 (0.002)	0.029	0.013 (0.003)		-0.05 (0.09)	0.04 (0.07)
MET	0.010 (0.001)	0.027	0.036 (0.003)	0.012 (0.003)		<b>0.64</b> (0.06)
RP	0.018 (0.002)	0.034	0.033 (0.003)	0.012 (0.002)	0.122 (0.002)	

Genetic correlations between health traits and other dairy traits are shown in Table 3 (For production traits (grey cells), a negative correlation means a favourable relationship). DA and MF have favourable correlations with ketosis (Acetone & BHB) and fertility traits. MET, and RP to a lesser extent, have positive genetic correlations with #INS and ICLINS. Acetone and BHB have moderate favourable correlations with SCS and Pro% and unfavourable with Fat%.

**Table 3. Genetic parameters between health traits, dairy and fertility-mastitis traits.**

Trait	h <sup>2</sup>	r <sub>p</sub>	Genetic correlations					
			DA	MF	MET	RP	Acetone	BHB
Milk	0.122 (0.004)	0.218	-0.13	-0.02	-0.12	-0.11	0.06	0.03
Fat%	0.214 (0.004)	0.262	0.03	0.07	-0.05	-0.11	0.13	<b>0.25</b>
Pro%	0.274 (0.004)	0.311	<b>-0.16</b>	-0.08	-0.08	-0.11	<b>-0.25</b>	<b>-0.28</b>
SCS	0.079 (0.003)	0.141	<b>0.15</b>	0.10	<b>0.17</b>	0.01	<b>0.18</b>	<b>0.20</b>
Acetone	0.112 (0.004)	0.150	<b>0.28</b>	<b>0.27</b>	0.01	-0.02	-	<b>0.95</b>
BHB	0.101 (0.004)	0.152	<b>0.18</b>	<b>0.27</b>	-0.10	-0.06	<b>0.95</b>	-
#INS	0.044 (0.003)	0.107	<b>0.18</b>	-0.03	<b>0.45</b>	0.13	-	-
ICFINS	0.081 (0.003)	0.162	<b>0.22</b>	<b>0.21</b>	0.10	0.09	-	-
ICLINS	0.060 (0.003)	0.120	<b>0.22</b>	<b>0.20</b>	<b>0.36</b>	<b>0.18</b>	-	-
#MAS	0.076 (0.003)	0.152	-0.04	<b>0.15</b>	0.14	0.06	-	-

Genomic EBV for 4 health traits have been estimated in an univariate ssGBLUP. Based on 636-779 bulls with at least 20 daughters, in comparison with the 25% worst bulls, the 25% best ones have on average an incidence divided by 2 (MET=8.6% vs 4.2% / RP=8.9% vs 3.9% / MF=3.1% vs 1.3%) to more than 10 (DA=2.2% vs 0.2). The female genetic trend (Figure 1) show a favourable evolution of the genetic level for DA, MET and RP since 2008.



**Figure 1. Female genetic trends for DA, MF, MET and RP.**

## Discussion

Farmer-observed health events recorded in diaries can be used to develop genetic evaluation, even if the number of farms is very limited. At the end, 8.6% of herds value 41% of consistent data (a 3 years completeness period would value 18% of herds – 56% of data). This could be improved by focusing DHI effort to increase participation. Highlighting the benefits of disease recording for herd management and genetic evaluations is essential.

Linear model was preferred to threshold model due to practical consideration on multivariate model and ssGBLUP software although the latter is generally recommended with binary traits, such as health traits. Heritability estimates for the 4 health traits (1-2%) were, slightly lower than in Koeck et al. (2012), but consistent with the review of Pryce et al. (2016). High genetic correlations between some of the 4 health traits (MET-RP and DA-MET) are consistent to the ones on Canadian study (Koeck et al., 2012) with lower standard errors. Moderate but favour-able correlations between the 4 health traits and functional/other health traits give a promising situation that could, if the latter group of traits are used as predictors, increase the reliabilities of EBV for health traits. The favourable genetic trends observed for DA, MET and RP since 2008 could be an indirect effect of the inclusion of functional traits in Total Merit Index.

## Acknowledgments

GénoSanté was labelled by the Valorial competitiveness cluster. It has received funded from the Fonds Unique Interministériel (BPI France, regions of Brittany, Alsace, Pays de Loire).

## References

- Bourrigan X., Blériot G., Bouissel C., et al. (2015) *Renc. Rech. Ruminants* 22 :41-44.
- Koeck A., Miglior F., Kelton D.F. and Schenkel F.S. (2012) *J. Dairy Sci.* 95:4099-4108. <https://doi.org/10.3168/jds.2011-5127>
- Leclerc H., Croué I., Vallée R., Baur A., Barbat A., et al. (2019) *ICAR Techn.* 24:373-381.
- Meyer K. (2007) *J ZHEJIANG UNIV-SC B* 8(11):815-821 DOI:[10.1631/jzus.2007.B0815](https://doi.org/10.1631/jzus.2007.B0815)
- Pryce J.E., Parker Gaddis K.L., Koeck A., Bastin C., Abdelsayed M. et al. (2016) *J. Dairy Sci.* 99:6855-6873. 4099-4108. <https://doi.org/10.3168/jds.2016-10854>
- Tribout T., Ducrocq V. and Boichard D. (2020) *Proc. of the 6th ICQG*, Brisbane, Australia.