French regional genetic collaborative projects to improve welfare and resilience of dairy cows

H. Leclerc[1], I. Croué[2], R. Vallée[1], A. Baur[2], A. Barbat[3], S. Fritz[2], M. Philippe[4], M. Brochard[5], F. Guillaume[4], G. Thomas[1], L. Manciaux[6], J.B. Davière[7], L Voidey[8] and N. Gaudillière[9]

[1]IDELE, UMT eBIS, 78352 Jouy-en-Josas, France
Corresponding Author: helene.leclerc@inra.fr
[2]ALLICE, UMT eBIS, 78352 Jouy-en-Josas, France
[3]INRA GABI, UMT eBIS, 78352 Jouy-en-Josas, France
[4]EVOLUTION, 35538 Noyal sur Vilaine, France
[5]MO3 - UMOTEST, 01250 Ceyzériat, France
[6]BCEL-Ouest, 22195 Plérin Cedex, France
[7]SEENERGI, 53942 Saint Berthevin Cedex, France
[8]Apporteur Grand-Est, France
[9]MO3 - Conseil Elevage 25-90, 25640 ROULANS, France

Abstract

Two collaborative projects, GENOSANTE and MO3SAN, considering Holstein (HOL) and Normande (NOR) breeds on the one hand, and Montbéliarde (MON) breed on the the other hand, bring together French companies (breeding companies, milk recording and herd support organizations in HOL and NOR; breeding companies, milk recording and herd support organizations and Livestock health protection groups (GDS) in MON) and research organizations (INRA, Allice, and IDELE). The aim of those projects is to provide selection tools for new traits to improve dairy herd profitability and cow welfare. The two projects focus on three areas of research: ketosis, claw disorders and heath data through events recorded by farmers.

Ketosis is one of the most common disorders in dairy cows due to energy deficit in early lactation. Its prevalence reaches 4% for its clinical form and 12-20% for the subclinical form. Analysis of beta-hydroxybutyrate (BHB) and acetone through MIR spectrum in milk collected since 2012, from 7 to 120 days in milk, were used. Heritability estimates of acetone were 0.12 in HOL, 0.15 in NOR and 0.11 in MON and 0.10, 0.16 and 0.14 for BHB. Genetic and genomic breeding values for ketosis have been estimated routinely since 2016 in HOL and NOR and are under development in MON.

Claw lesions are the 3rd most important health issue in dairy cattle, after mastitis and fertility issues. They impact herds both economically and in terms of animal welfare. 21 lesions are routinely recorded by professional trimmers on touch screens. Seven 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)), with prevalence ranging from 7 to 53% on trimmed cows (depending on the trait and breed), were studied. Heritabilities ranged from 0.02 to 0.08 in HOL, 0.04 to 0.22 in NOR and 0.05 to 0.11 in MON. Genetic correlations revealed two distinct genetic groups for claw lesions: infectious (DD, HHE, and IH) and noninfectious (SHC, SHD, WLF, and SU) lesions. Genetic correlations among lesions of the same group were moderate to high. Genetic evaluation for claw health was implemented late 2017 in HOL, and is under development in NOR and MON.

Common health disorders registered on farm (metritis, retained placenta, milk fever…) are currently under study in HOL.

All these developments aim at improving dairy cow welfare and resilience through genetic and management and are only possible with efficient data flows from phenotype collection in herds to genetic evaluations and management tools for breeders.

Keywords: Collaborative project, dairy cow, ketosis, claw health, health, genomic evaluation.

Introduction

Genetic selection of dairy cattle, initially based on production traits, has been gradually completed by functional and health trait. Presently, genomic selection development brings new perspectives. Genetic trend is expected to increase, thanks to the reduction in generation interval, particularly for low heritability traits such as those related to animal health. To enlarge the panel of traits genetically evaluated, different strategies can be used: 1/ better use of existing information, such as MIR spectra, or 2/ building a new reference population from scratch, by collecting new phenotypes (eg. claw disorders); this second option is of course much more expensive than the first one.

Genosanté and MO3SAN are French collective achievements initiated by the Evolution breeding company in 2015 on the one hand and Umotest breeding company in 2018 in the other hand. To meet these challenges of developing selection tools for new traits to improve dairy herd profitability and cow welfare, they brought together partners representing stakeholders of the whole dairy sector, from upstream (milk recording and herd support organizations (DHI), Livestock health protection groups (GDS) and breeding companies) to downstream (milk processing industry) and R&D partners. It aims at improving animal health by proposing new tools both for management and for selection. The project should also help the milk industry to better answer consumer's requests for less veterinarian treatments and for animal welfare. This project is based on the complementarity of the partners skill's: new phenotypes recording, herd management and health support with DHI, new phenotypes recording and health support with GDS, genotyping and selection with breeding companies, genetic evaluation with joint technology unit (UMT eBIS) (gathering INRA, IDELE and Allice).

Those projects focus on 3 groups of traits that have a significant impact on herd health, animal welfare and herd profitability: Ketosis, Claw health traits and other health traits (metritis, retained placenta, displaced abomasum, milk fever…), this latter group of traits being still under study.

Ketosis: a first trait, with a large phenotyped population available through MIR spectra

GénoSanté project deals with Holstein (HOL) and Normande (NOR) dairy breeds, respectively the 1st (1.5 millions of lactation per year in DHI) and 3rd (190 000 lactation per year in DHI) breed in France, and MO3SAN project deals with Montbéliarde (MON) breed, the 2nd breed (425 000 lactations per year in DHI) in France.

Ketosis is a metabolic disorder of dairy cows at early stage of lactation. It is due to a lack in energy intake relative to the energy required for milk production. In France, its prevalence is estimated at 3 to 4 % for clinical ketosis and at 12 to 20% for subclinical cases. A main impact of this disorder is a decrease in milk production by 300 to 500 kg milk per lactation. Moreover, it is associated to reproduction disorders (delay in cyclicity, lower conception rate) and to other disorders such as mastitis. In 2012, the tool Cetodetect® was implemented, thanks to the European program Optimir (2011-2015), in order to help farmers and technicians to detect early cases of ketosis (Schwartz *et al.*, 2015). This tool is based on a decision tree from beta hydroxybutyrate (BHB) and acetone (acet) concentrations estimated from MIR spectra on milk samples. Lactating cows receive a score between 0 and 5, with 0 corresponding to healthy cows; 1 to 2 to subclinical cases, 3 to 5 to clinical ketosis. This indicator helps farmers to prevent ketosis by adapting the feeding or through treatments in case of clinical ketosis. Génosanté and MO3SAN aim at completing the panel of tools with a genetic evaluation.

A large database

Phenotypes used for the genetic evaluation are milk BHB and milk acetone contents predicted from MIR spectra since 2012 for GénoSanté and 2015 for MO3SAN. These concentrations were log-transformed in order to obtain a normal distribution, assuming that the risks have a multiplicative effect. Only data from the farms working with the DHI participating to those projects were used. The analysis was based on test days of pure breed cows recorded between 7 and 120 days of lactation and in 1st to 5th parity. Contemporary groups of less than 5 animals per herd x test-day were excluded from the analysis. Almost 2.3 million of HOL cows, 400 000 NOR and 178 000 MON cows meet all these requirements (table 1).

Development of a genetic evaluation (polygenic, genomic or single-step)

The model used was a multiple-trait animal model, using each test day as repeated data within and between lactations. It includes fixed effects of herd x year, month x year, stage of lactation x parity (3 classes: 1, 2, 3 to 5), age at 1st calving for nulliparous cows and days dry x parity for multiparous ones, and an effect of the laboratory within year.

The estimated heritabilities (table 2) were 12, 15 and 11 % for acetone concentration in HOL (based on 800 000 cows), NOR (based on 140 000 cows) and MON breeds, respectively, and 10, 16 and 14% for BHB. The estimated repeatabilities were 22, 24 and 20% for acetone, 22, 24 and 20% for BHB.

The heritabilities of these traits are moderate, as for other functional traits such as somatic cell score (Rupp and Boichard, 1997). They are consistent with those estimated in other countries, such as in the Netherlands (Van der Drift *et al.*, 2012), slightly lower than those obtained with models using different lactations as different traits (around 20%, Koeck *et al.*, 2014; Vosman *et al.*, 2015).

In HOL and NOR breeds, a genomic evaluation was performed using a reference population including all females and males with performances and genotyped by one of the partner breeding companies of Génosanté. Performances of females were Yield Deviations, those of males were DYDs computed from YDs of ungenotyped daughters.

Table 1. Description of the data available for ketosis traits in three breeds in spring 2019.

	Holstein	Normande	Montbéliarde
#cows with phenotypes	2 291 428	408 182	178 360
#genotyped cows with phenotypes	121 872	31 801	33 699
#genotyped sires with DYD of ungenotyp. daught.	18 945	2 461	3 439

Table 2. Estimated genetic parameters in three breeds for ketosis traits: log(acetone) and log(BHB) (heritabilities (h^2) and repeatabilities in bold; genetic correlations (rG) above the diagonal and correlations between permanent environment (rPE) below the diagonal).

		Holstein		Normande		Montbéliarde	
		log(acet)	log(BHB)	log(acet)	log(BHB)	log(acet)	log(BHB)
h^2 and rG	log(acet)	**0.12**	0.85	**0.15**	0.89	**0.11**	0.85
	log(BHB)		**0.10**		**0.16**		**0.14**
Repeat and rPE	log(acet)	**0.18**		**0.24**		**0.20**	
	log(BHB)	0.88	**0.22**	0.91	**0.26**	0.66	**0.20**

The size of the reference population was quite large, with more than 140 000 animals in HOL, and 35 000 animals in NOR (Table 1). The model of genomic evaluation was similar to the one used for the French official genomic evaluations. It is based on a MarkerAssisted BLUP, using from 250 to 3000 QTL according to the breed and the trait. These QTLs were first pre-selected with the BayesCπ methodology and then traced with 4-SNP haplotypes. The first evaluation for ketosis was published in August 2016.

In MON breed, due to more recent development (spring 2019) the genetic evaluation will be implemented with a single-step model where all genotype, pedigree, performance and progeny data available through MO3SAN project are analysed simultaneously. Routine evaluation are planned in 2021.

For each animal, a ketosis index was computed, with a 50% weight for BHB and acetone. As expected, a reduction of the risk of ketosis (clinical and subclinical) was observed for cows with a higher GEBV. For instance, in HOL, the average percentage of testdays corresponding to ketosis cases was 9% for cows with a GEBV between +1 and +2, while it reached 33% for cows with a GEBV between - 1 and -2, i.e. a 3.5 times lower risk of ketosis.

Claw health traits: a reference population to be built

Claw lesions are one of the most important health issues in dairy cattle. Hoof and leg disorders are a major welfare problem in dairy farming, often causing pain and lameness in cows (11% of cows with lameness – Delacroix, 2000). Their origin is multifactorial: infectious, traumatic, housing/hygiene, nutrional… Hoof disorders are also associated with high cost and have been identified as the third most costly pathology after mastitis and fertility troubles (Enting *et al*., 1997; Van der Waaij *et al*., 2005). Even without being responsible for clinical lameness, some studies describe that more than 50% of cows show at least one lesion (e.g., Van der Linde *et al*., 2010; Van der Spek *et al*., 2013). Reducing the prevalence of claw lesions is therefore of major interest in dairy farms.

Data collected

Twenty-one claw health traits are collected as described in ICAR Atlas (ICAR, 2015) by professional trimmers on touch screen. Seven of them, having a prevalence of at least 5% were studied: sole hemorrhage circumscribed (SHC), sole hemorrhage diffused (SHD), sole ulcer (SU), white line fissure (WLF), digital dermatitis (DD), heel horn erosion (HHE) and interdigital hyperplasia (IH). Each trait is described by a severity score from 1 to 3, except for DD having a 4th level. The traits DD, HHE, and IH can be classified as infectious traits and SHC, SHD, SU, and WLF as non-infectious traits. Data collection started in April 2014. The trimmers visited farms when called by farmers to trim their cows. Croué *et al* (2017) investigated effect of preselection of cows for trimming because including untrimmed cows as healthy caused bias in the estimation of genetic correlations. A trimming status trait to account for preselection have been used, as it allows consideration of the exhaustive population of cows present at a time a trimmer visited a farm without causing bias in genetic parameters.

Due to the non-exhaustive collection of information on the herd (preselection of cows for trimming) and the limited number of herds using the trimming services proposed by DHI and GDS, the population available to estimate genetic parameters and construct a reference population for genomic evaluation is limited in size. In our studies, we do not considered a severity degree of the lesion. A cow was given a score of 1 for a lesion if the lesion was observed by the trimmer, 0 if it was not. Only data from the farms working with the DHI participating to those projects were used. The analysis was based on data collected from purebred cows recorded between days in milk 1 to 550 of lactation in 1st to 3rd parity for HOL (1 to 5th parity for NOR and MON). Contemporary groups of less than 5 animals per herd x test-day were excluded from the analysis for HOL (4 animals per herd x test-day in NOR and MON). Only hind claw information was kept because front hooves were not often trimmed and showed fewer lesions than hind hooves, the two hind claw must be trimmed. Only the first trimming record of each cow was kept. The model will be updated when the proportion of cows trimmed several times is higher. In spring 2019, almost 120 000 million of HOL cows, 17 000 NOR and 15 000 MON cows me*et al*l these requirements (table 3). For genetic parameters estimation, only 46 787 trimmed cows (+ 54 090 contemporary non trimmed cow) where used in HOL, and the complete population available in spring 2019 in NOR and MON.

Development of a genetic evaluation

The model used was a multiple-trait animal model. It includes fixed effects of herd-date of trimming, parity, stage of lactation (10 classes). The model include a heterogeneous residual variance on trimmer-year effect.

In the HOL population trimmed cows, 82% of the cows had at least one lesion (Croué *et al*, 2017). The HHE and SHD were the most frequent lesions, with prevalence of 53 and 43%, respectively (Table 4a). The least frequent lesion was SU, with a prevalence of 7%. In NOR, the most frequent lesions is still HHE, and in MON, it is SHD with 35 (Table 4b) and 45% (Table 4c) respectively. Some difference between breeds need to be noticed. For DD, MON seems to be less concerned with only 16% of cows whereas 29 and 32% in HOL and NOR respectively. For IH, NOR is more concerned with a prevalence of 21% of cows while 9% or less in HOL and MON. For WLF, the prevalence is variable between breed: 9% in NOR, 16% in HOL and 24% in MON.

Table 3. Description of the data available for claw health traits in three breeds in spring 2019.

	Holstein	**Normande**	**Montbéliarde**
#cows with phenotypes	118 816	17 350	14 985
#genotyped cows with phenotypes	16 982	5 618	2 078
#genotyped sires with DYD of ungenotyp. daught.	3 183	409	662

Table 4a. Prevalence (%) of claw lesions and estimated genetic parameters in Holstein breed for 7 claw health traits: (Digital Dermatitis (DD), Heel Horn Erosion (HHE), Interdigital Hyperplasia (IH), Sole Ulcer (SU), White Line Fissure (WLF), Sole Hemorrhage Circumscribed (SHC) and Sole Hemorrhage Diffused (SHD), heritabilities (h²) in bold on the diagonal with standard errors in bracket; genetic correlations (rG) above the diagonal with standard errors in bracket).

		Infectious traits			Non infectious traits				
	Preval.	**DD**	**HHE**	**IH**	**WLF**	**SU**	**SHC**	**SHD**	**TRIM**
DD	29	**0.07** (0.01)	0.63 (0.07)	0.68 (0.05)	-0.21 (0.08)	-0.04 (0.09)	-0.23 (0.09)	-0.10 (0.11)	0.43 (0.08)
HHE	53		**0.04** (0.01)	0.51 (0.08)	-0.05 (0.09)	0.36 (0.09)	0.15 (0.11)	0.02 (0.12)	0.55 (0.09)
IH	8			**0.08** (0.01)	-0.16 (0.08)	-0.02 (0.08)	-0.01 (0.10)	-0.15 (0.10)	0.37 (0.08)
WLF	14				**0.06** (0.01)	0.51 (0.08)	0.35 (0.10)	0.23 (0.11)	0.10 (0.09)
SU	7					**0.05** (0.02)	0.86 (0.05)	0.26 (0.11)	0.36 (0.09)
SHC	16						**0.03** (0.00)	0.49 (0.11)	0.45 (0.10)
SHD	43							**0.03** (0.01)	0.13 (0.12)
TRIM									**0.02** (0.00)

Table 4b. Prevalence (%) of claw lesions and estimated genetic parameters in Normande breed for 7 claw health traits: (Digital Dermatitis (DD), Heel Horn Erosion (HHE), Interdigital Hyperplasia (IH), Sole Ulcer (SU), White Line Fissure (WLF), Sole Hemorrhage Circumscribed (SHC) and Sole Hemorrhage Diffused (SHD), heritabilities (h²) in bold on the diagonal with standard errors in bracket; genetic correlations (rG) above the diagonal with standard errors in bracket).

		Infectious traits			Non infectious traits				
	Preval.	**DD**	**HHE**	**IH**	**WLF**	**SU**	**SHC**	**SHD**	**TRIM**
DD	32	**0.10** (0.02)		0.86 (0.05)	-0.44 (0.17)	0.02 (0.15)	-0.17 (0.19)		0.30 (0.12)
HHE	35					Not converged			
IH	21			**0.22** (0.03)	-0.46 (0.15)	-0.08 (0.13)	-0.34 (0.17)		0.25 (0.10)
WLF	17				**0.04** (0.01)	0.51 (0.17)	0.36 (0.23)		0.34 (0.16)
SU	11					**0.08** (0.02)	0.70 (0.15)		0.21 (0.13)
SHC	9						**0.04** (0.01)		0.17 (0.18)
SHD	29								Not converged
TRIM	43								**0.16** (0.02)

Table 4c. Prevalence (%) of claw lesions and estimated genetic parameters in Montbéliarde breed for 7 claw health traits: (Digital Dermatitis (DD), Heel Horn Erosion (HHE), Interdigital Hyperplasia (IH), Sole Ulcer (SU), White Line Fissure (WLF), Sole Hemorrhage Circumscribed (SHC) and Sole Hemorrhage Diffused (SHD), heritabilities (h²) in bold on the diagonal with standard errors in bracket; genetic correlations (rG) above the diagonal with standard errors in bracket).

		Infectious traits			**Non infectious traits**				
	Preval.	**DD**	**HHE**	**IH**	**WLF**	**SU**	**SHC**	**SHD**	**TRIM**
DD	16	**0.05** (0.01)	0.71 (0.14)	0.77 (0.12)	-0.12 (0.17)	0.50 (0.17)		-0.30 (0.19)	0.53 (0.13)
HHE	34		**0.07** (0.02)	0.55 (0.14)	-0.08 (0.16)	0.60 (0.13)		-0.46 (0.17)	0.50 (0.12)
IH	9			**0.08** (0.02)	0.15 (0.15)	0.51 (0.14)		-0.08 (0.18)	0.49 (0.12)
WLF	24				**0.11** (0.02)	0.46 (0.14)		0.25 (0.16)	0.22 (0.12)
SU	8					**0.08** (0.02)		-0.14 (0.18)	0.59 (0.11)
SHC	14						Not converged		
SHD	45							**0.07** (0.02)	-0.41 (0.13)
TRIM	53								**0.29** (0.03)

The estimated heritabilities (table 4a, 4b, 4c) are low to moderate, according to the breed and the trait: 0.02 to 0.08 in HOL, 0.04 to 0.22 in NOR and 0.05 to 0.11 in MON. In general, genetic correlations among lesions of the same group (infectious vs non infectious) were moderate to high (between 0.50 to 0.68 and 0.55 to 0.77 in HOL and MON respectively for infectious traits – between 0.23 to 0.86 and 0.36 to 0.70 in HOL and NOR respectively for non-infectious traits). Heritabilities and correlations estimated are consistent with those estimated in other countries, such as in the Netherlands (Van der Spek *et al.*, 2013).

A genomic evaluation (Croué *et al.*, 2019) was performed for the 3 breeds using a reference population including all females and males with performances and genotyped by one of the partner breeding companies of Génosanté and MO3SAN. Performances of females were Yield Deviations, those of males were DYDs computed from YDs of ungenotyped daughters. In spring 2019, the size of the reference population was around 20 000 animals in HOL, 6 000 animals in NOR and 2 700 animals in MON (Table 3). For the last two breeds, these population sizes need to be further increased to make genetic evaluations more reliable and to estimate missing traits (HHE and SHD for NOR and SHC for MON). The genomic evaluations are based on GBLUP. In HOL genome wide association studies (GWAS) have been carried out and have shown a large number of QTL (Croué *et al*, 2019).

For each genotyped animal, an index for RLI (resistance to infectious lesions) and for RLNI (resistance to non-infectious lesions) were computed. In HOL, RLI has a 50% weight for DD, 25% for HHE and 25% for IH, and RLNI has a 40% weight for WLF, 40% for SU and 10% each for SHC and SHD. As expected, whatever the traits (DD figure 1A, IH figure 1B, SU figure 1C and WLF figure 1D) and the breed, animals with poorer index (lower than -1) have a 80% risk of presenting the lesion, while animals with an index of +1 have a risk lower than 10%.

Routine evaluation are available since 2017 for HOL, winter 2019 for NOR and planned for 2021 in MON, with an enlarge reference population in order to improve genomic prediction equation.

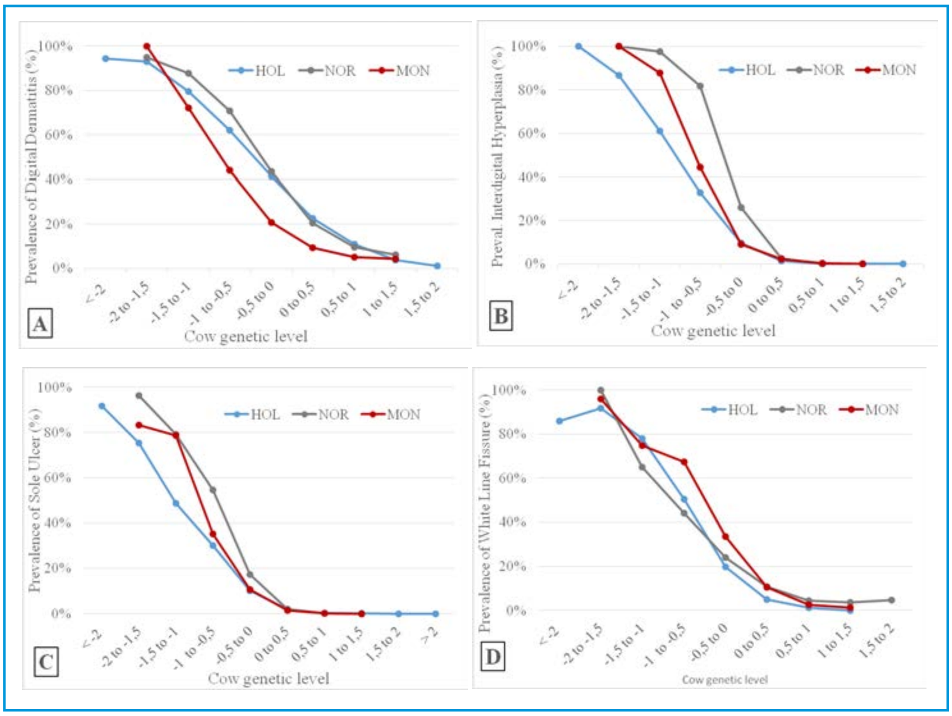

Figure 1. Prevalence of claw traits (A: Digital Dermatitis ; B: Interdigital Hyperplasia ; C: Sole Ulcer; D: White Line Fissure) in function of cow genetic index (minimum number of 10 cows per class).

Conclusion

Génosanté and MO3SAN are collective achievements of partners sharing a common goal, improving the productive health of dairy cows. Evaluations of other new traits are expected over the coming years. All the partners of the program share the benefits. Breeders and AI companies will be able to account for these traits in their breeding process. Genetic evaluations brings also useful information for DHI, which can better understand the major risks for disorders through the estimated environmental effects (eg. herd x year).

Genomic selection is a promising tool to increase resistance to new health traits such as ketosis or claw lesions in dairy cows.

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