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

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Two collaborative projects

- GÉNO SANTÉ in **Holstein** and **Normande** Breed

1st French Breed:
1,5 millions of lact.
per year in DHI

3rd French Breed:
190 000 lact. per
year in DHI

- MO3 Plateforme Innovation SAN in **Montbéliarde** Breed

2nd French Breed:
425 000 lact. per
year in DHI

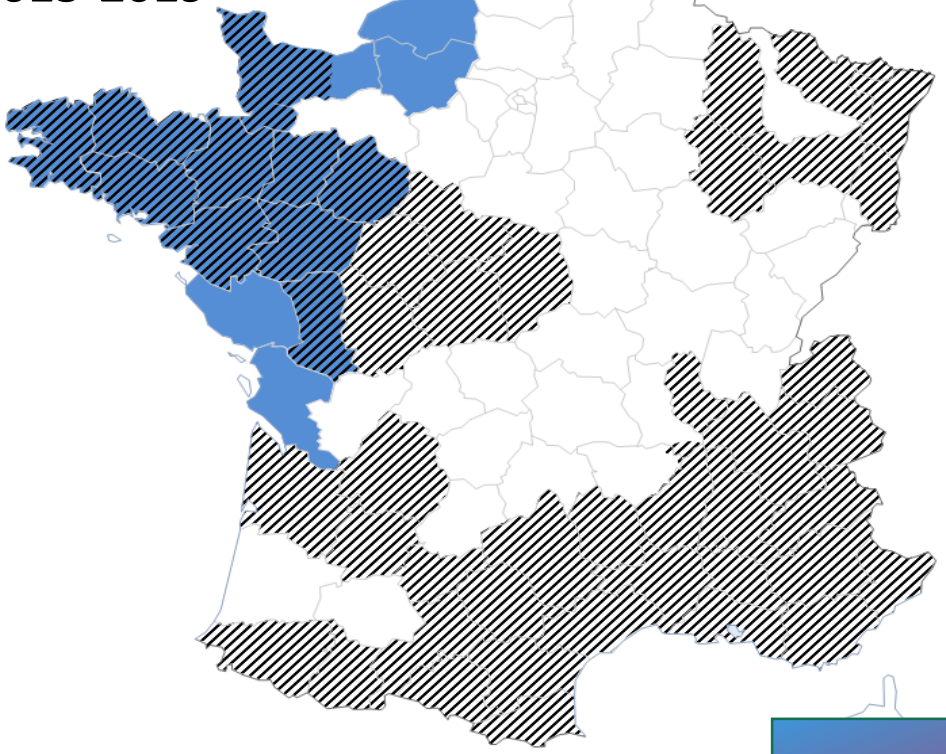
3 (groups of) traits having a significant impact on herd health, animal welfare, and profitability of herd:

✓ Ketosis
✓ Claw health traits
✓ Other health traits

… based on regional network

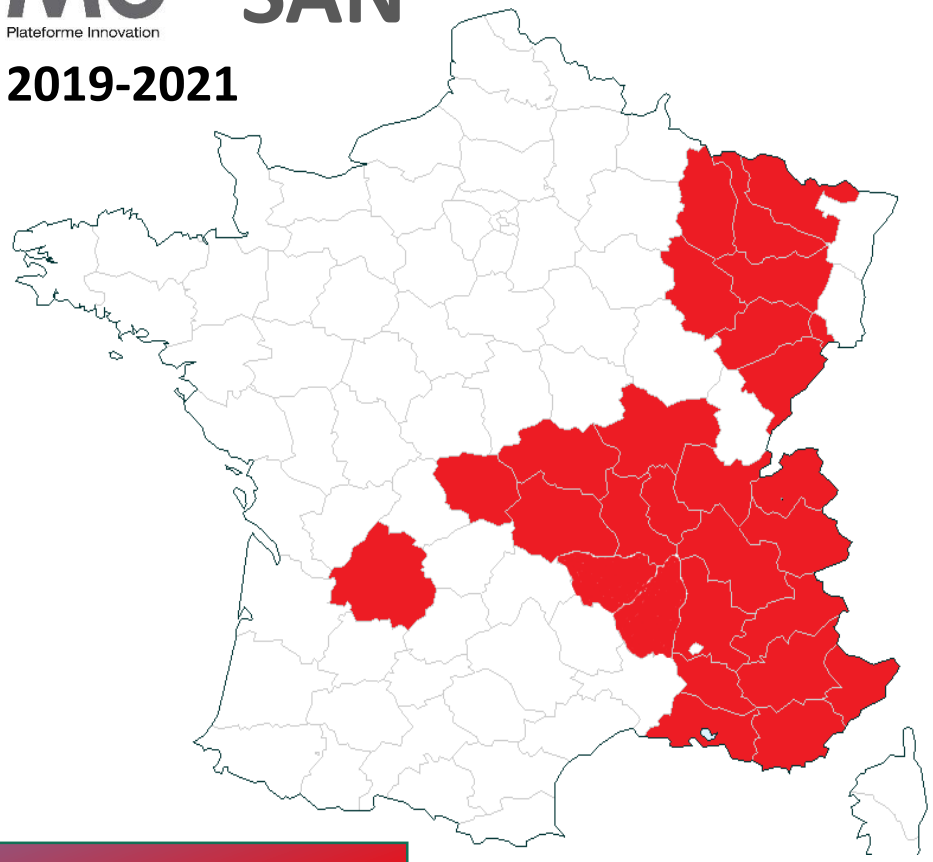
GÉNO SANTÉ

2015-2019



MO3SAN
Plateforme Innovation

2019-2021



Phenotypes available

Genomic index available for genotyped animals + local claw health data

Collective achievements

Industry partners

From upstream

- Breeding compagnies
- Milk recording / DHI organisations)
- Sanitary Defense Group (GDS)

To downstream

- Milk processing industry

Scientific partners

- INRA
- IDELE
- ALLICE

Gathered in UMT ebis

Two projects bringing together stakeholders from dairy cattle sector!

3 traits to improve by Management and Genetic selection

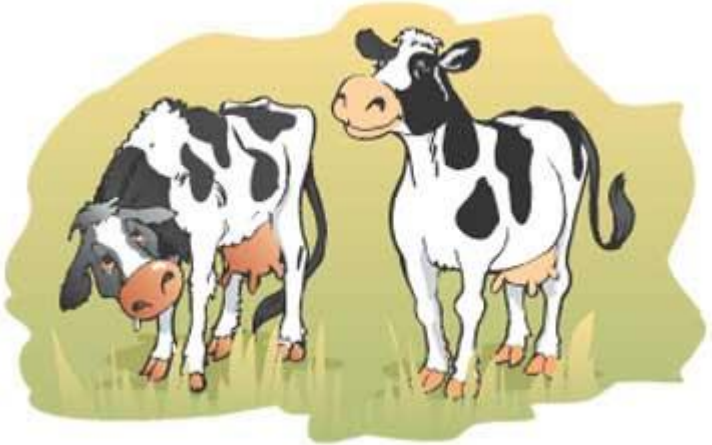
1/ Ketosis

What is ketosis? How to control it?

The main metabolic disease of dairy cows in early lactation

➔ What impacts?

- Decrease in **milk production** (-300 to -500 kg/lact)
- Impact on **reproduction** (cyclicity delayed and success at first service reduce up to 20%)
- Increased risk of **retained placenta** and **displaced abomasum** (x4 to 8)
- Increase in **clinical mastitis** (x3)



➔ How often?

- **Clinical ketosis: 3 to 4 % of cows**
- **Sub-clinical ketosis: 12 to 20 % of cows**

Aim: Prevent and reduce the risk of ketosis in dairy herd

- **Management:** From Cetodetect/CetoMir indicator and specific technical services
- **Genetic:** a genetic evaluation of ketone bodies to improve genetic level of animals by selection.

Population evaluated

A large population

- **Phenotype:** ketone bodies estimated from MIR analysis at monthly test-day
  - **acetone**
  - **β-hydroxybutyrate (BHB)**
- **Population:** Performances since 2012 for west part of France / 2015 for east part
- Use log-transformed concentrations for genetic evaluations
- **1 trait for validation and interpretation of the results: Cetodetect®/CetoMIR® indicator** determined by a decision tree from acetone and BHB concentrations (→ health status of animals)

Data edits

- Herds enrolled in **official milk recording**
- **Purebred** animals
- **Lactations 1-5**,
- **Days In Milk 7 to 120**

	Holstein	Normande	Montbéliarde
#cows with phenotypes	2 291 428	408 182	178 360

Genetic Evaluation (step 1: polygenic)

Genetic parameter estimation

- **2 traits, animal** model, **repeated data** over lactations

h^2 and rG

	Holstein		Normande		Montbéliarde	
	log(acet)	log(BHB)	log(acet)	log(BHB)	log(acet)	log(BHB)
log(acet)	0.15	0.89	0.12	0.85	0.11	0.85
log(BHB)		0.16		0.10		0.14

Repeat. and rPE

	Holstein		Normande		Montbéliarde	
	log(acet)	log(BHB)	log(acet)	log(BHB)	log(acet)	log(BHB)
log(acet)	0.22		0.26		0.20	
log(BHB)	0.88	0.18	0.91	0.24	0.66	0.20

Low to moderate heritability, Acetone and BHB highly correlated but low repeatability (⇨ each performance brings much information)

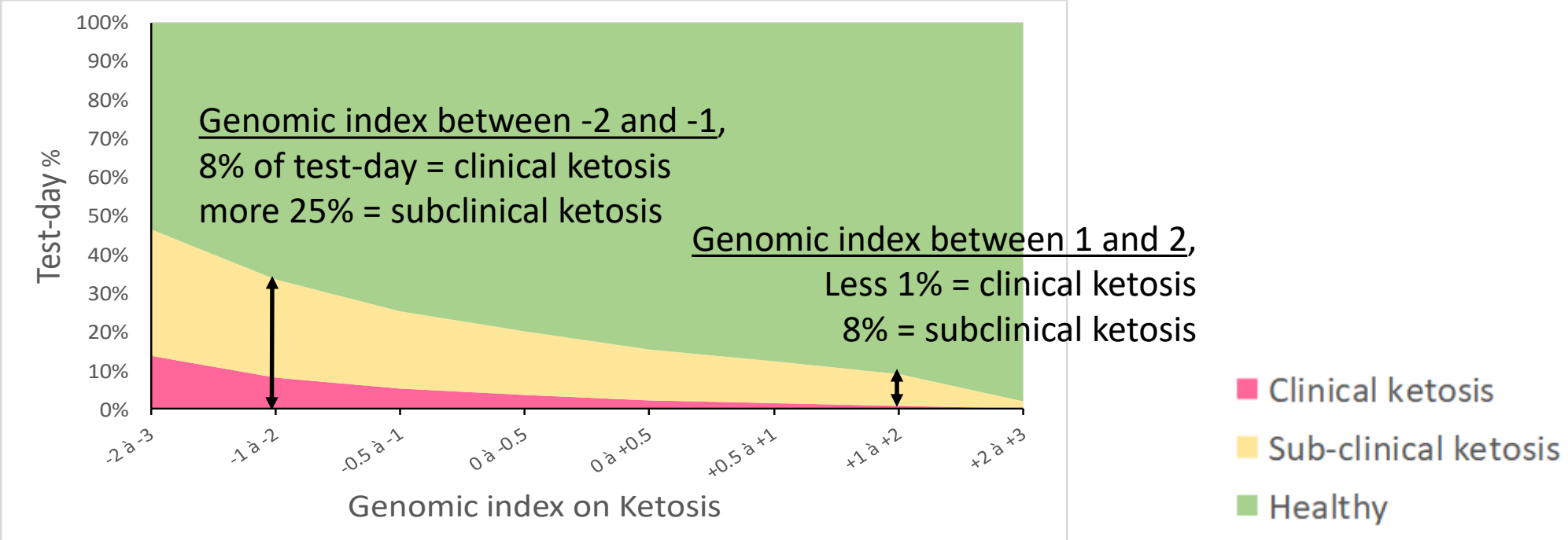
For routine evaluation : single trait, animal model with **repeatability**

Genetic Evaluation (step 2: Genomic evaluation)

GBLUP Genomic Evaluation with **Reference pop** = males + females

	Holstein	Normande	Montbéliarde
#genotyped cows with phenotypes	121 872	31 801	33 699
#genotyp. sires with DYD of ungenotyp. daught.	18 945	2 461	3 439

Incidence of ketosis as a fonction of female genomic index



Ketosis - Sum up

Phenotype readily available, with limited costs
Large population (possibly all cows enrolled in official milk recording)

Be careful to have homogenous phenotypes

Polygenic/Genomic Evaluation:

Available since Aug. 2016 for Holstein
Available since Aug. 2016 for Normande
Expected in 2020 for Montbéliarde
(in a single step model)

3 traits to improve by Management and Genetic selection

2/ Claw health

Claw health 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)
- ✓ Hoof disorders are also associated with high costs and have been identified as the third most costly disease in dairy farming after mastitis and fertility trouble
- ✓ Multifactorial origin:
  - ✓ Infectious
  - ✓ traumatic,
  - ✓ housing/hygiene,
  - ✓ nutrional

- ✓ 21 claw health traits (as described in ICAR Atlas) – 11 traits mandatory

Data collection

- ✓ 80 trimmers collecting data on tactile tab since Sprint 2014 / Autumn 2016
- ✓ Severity scoring from 1 to 3 except for Digital Dermatitis (1 to 4)
- ✓ All trimmers have the same initial training from one single training center

Population evaluated

A limited population

- **Limited** % farm using trimming service (independent trimmers do not take part)
- non-exhaustive data - Breeders choose cows
- Too few cows trimmed 2 times or more (14% in 2017)

Data edits

- Herds enrolled in **official milk recording, Purebred** animals
- **Lactations 1-3** in **Holstein**, **(1-5 in Normande - Montbéliarde**)
- At least **5 animals** in the visit in **Holstein**, **(4** in **Normande - Montbéliarde**)
- **Days In Milk 1 to 550**

	Holstein	Normande	Montbéliarde
#cows with phenotypes	118 816	17 350	14 985

Model adaptation

To take into account preselection of cows, we included a **trimming status** in the model. If **we** considered **not trimmed cows as healthy,** the **genetic correlation are biased.** With a trimming status, they are considered present in the herd but not seen. (Croué et al., JDS 2017)

Genetic parameter Estimation

- **Multiple trait, animal** model

h^2 and Rg **Holstein**

		Infectious traits			Non infectious traits				
	Preval.	DD	HHE	IH	WLF	SU	SHC	SHD	TRIM
DD	29	***0,07***	0,62	0,68	-0,21	-0,04	-0,23	-0,1	0,43
HHE	53		***0,04***	0,50	-0,05	0,36	0,15	0,02	0,55
IH	8			***0,08***	-0,16	-0,02	-0,01	-0,14	0,37
WLF	14				***0,06***	0,51	0,35	0,23	0,10
SU	7					***0,05***	0,86	0,26	0,36
SHC	16						***0,03***	0,49	0,45
SHD	43							***0,02***	0,12
TRIM									***0,02***
	std h^2 = 0.003 à 0.009								
	std rG	0,05 - 0,09	0,07 - 0,09	0,05 - 0,08	0,08 - 0,09	0,08 - 0,09	0,05 - 0,11	0,10 - 0,12	0,08 - 0,12

Source : Croué et al., JDS 2017

Based on 2017 data: 46 787 trimmed cows (+ 54 090 contemporary non trimmed cows)

Low heritability, highly correlated within infectious and non infectious groups of traits

Genetic parameter Estimation (2)

Normande

		Infectious traits			Non infectious traits				
	Preval.	DD	HHE	IH	WLF	SU	SHC	SHD	TRIM
DD	32	***0,10***		0,86	-0,44	0,02	-0,17		0,30
HHE	35								
IH	***21***			***0,22***	-0,46	-0,08	-0,34		0,25
WLF	17				***0,04***	0,51	0,36		0,34
SU	11					***0,08***	0,70		0,21
SHC	9						***0,04***		0,17
SHD	***29***								
TRIM	43								***0,16***
	std h² = 0.012 à 0.020 except for IH 0.030								
	std rG	0,06 - 0,15		0,06 - 0,15	0,15 - 0,17	0,13 - 0,17	0,15 - 0,23		0,10 - 0,16

10 782 trimmed cows
(+ 14 066 contemporary
non trimmed cows)

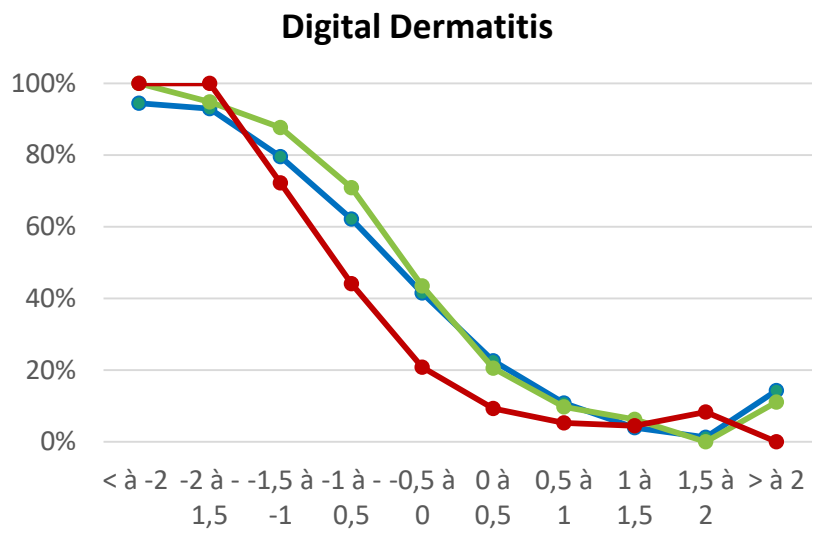
Montbéliarde

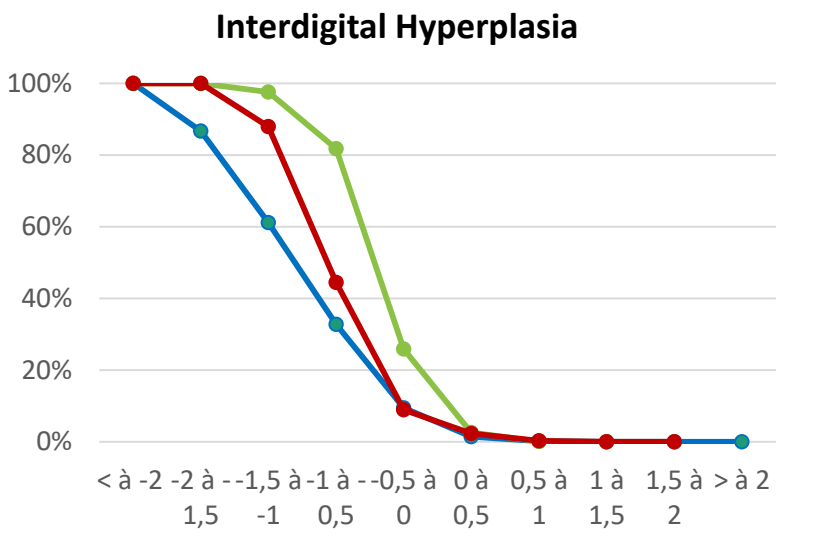
		Infectious traits			Non infectious traits				
	Preval.	DD	HHE	IH	WLF	SU	SHC	SHD	TRIM
DD	***16***	***0,05***	0,71	0,77	-0,12	0,50		-0,30	0,53
HHE	34		***0,07***	0,55	-0,08	0,60		-0,46	0,50
IH	9			***0,08***	0,15	0,51		-0,08	0,49
WLF	***24***				***0,11***	0,46		0,25	0,22
SU	8					***0,08***		-0,14	0,59
SHC	14								
SHD	45							***0,07***	-0,41
TRIM	53								***0,29***
	std h² = 0.01 à 0.02 except for TRIM 0.027								
	std rG	0,12 - 0,17	0,12 - 0,16	0,14 - 0,17	0,15 - 0,17	0,13 - 0,17		0,16 - 0,19	0,11 - 0,14

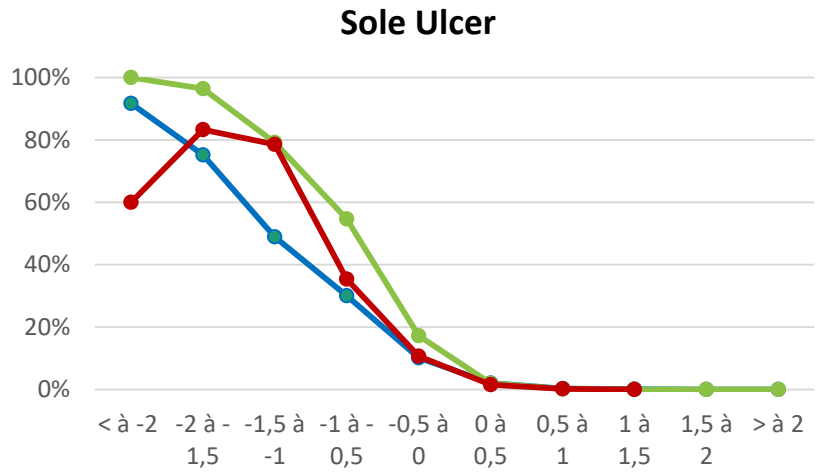
10 164 trimmed cows
(+ 9 040contemporary non
trimmed cows)

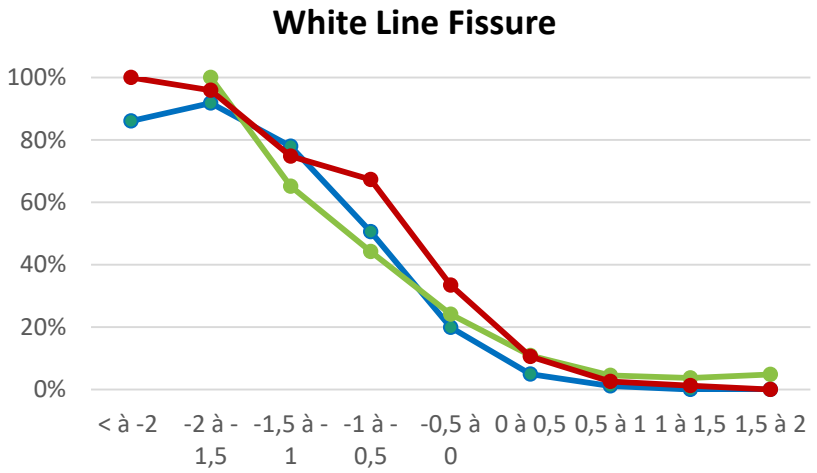
Prevalence of claw traits in function of cow genetic index

(N=106 877 / N=12 395 / N=11 369)









Genetic Evaluation (step 2: Genomic evaluation)

GBLUP Genomic Evaluation with **Reference pop** = males + females

	Holstein	Normande	Montbéliarde
#genotyped cows with phenotypes	16 982	5 618	2 078
#genotyp. sires with DYD of ungenotyp. daught.	3 183	409	662

Routine Genomic Evaluation:

Available since Nov. 2017 in Holstein

Expected in winter 2019/2020 in Normande

Expected in 2020/2021 in Montbéliarde (in a single step model)

Need to **enlarge reference population** in **Normande** and **Montbéliarde** in order to improve genomic prediction equation

GWAS / QTL detection

Lot of QTL found, including 8 with logBF>10 (Croué et al., JDS 2019)

Take Home Message

- ✓ **Management tools** and **Genetic Evaluation** are already available (or coming soon) for **ketosis** and **Claw Health traits**
- ✓ A 3rd group of traits **"Common health disorders",** registered on farm (metritis, retained placenta, milk fever…) are currently under development in **Holstein** and are planned in **Normande** and **Montbéliarde**

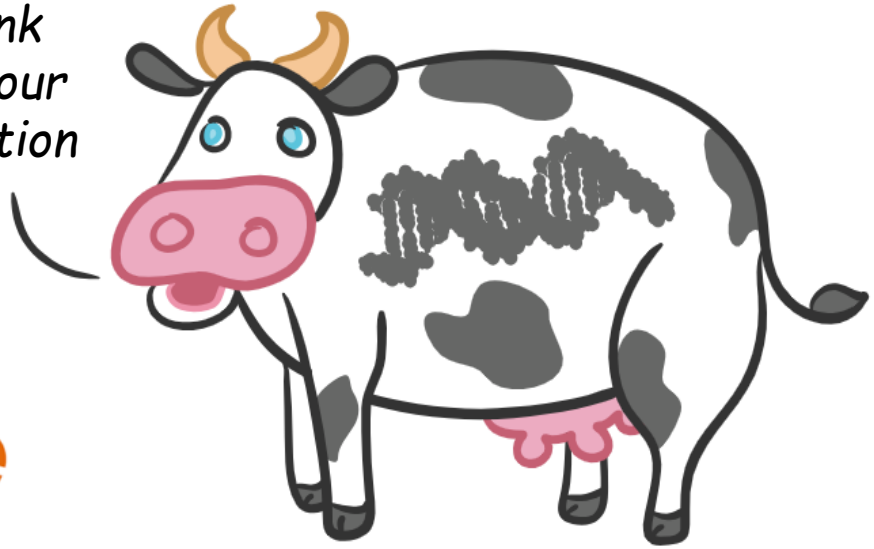
One main issue is to have exhaustive health data during the productive life of the cow (3 to 5 years)

Objectives: Improve **dairy cow welfare** and **resilience**

Only possible with a **efficient data pipelines** from phenotypes collection in herds to genetic evaluation and management tools for breeders

Acknowledgment

Thank for your attention



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