

DAIRY CATTLE GENOMIC SELECTION IN FRANCE



KEY FIGURES

230 000
females with
genomic breeding
values

Genomic selection for all

In France, for most of the dairy cattle breeds, selection is now based on genomic data. From the earliest age, males destined for insemination and females have full and sound breeding values, obtained thanks to genotyping.

Genetic progress for functional traits is clear: the youngest generations show substantial genetic advantage in fertility, mastitis resistance and longevity.

Bulls are present in large numbers, quickly replaced and present a large diversity of profiles. Inbreeding is still on the increase, but at a more moderated rate than previously.

Breeders have more and more confidence in genotyping their females to make their herd replacement decisions based on genomic breeding values.



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Genomic selection in practice

In 2016, selection of all dairy cattle breeds in France integrates genomic data. All genotyped animals have genomic indexes available for a wide range of traits linked to production, morphology, functional aptitudes (cell count and mastitis resistance, fertility, longevity, calving ease) and in the near future this will include traits also relating to health, hardiness, product quality.

The advantages of genomics are numerous : earliness and accuracy of evaluation, comprehensiveness of evaluated traits, finer management of genetic variability, faster genetic gain...

The computation methods of breeding values are constantly improving, as was the case in 2015 for the **holstein**, **montbeliarde** and **normande** when a substantial technological leap was achieved (increase in size of reference populations, inclusion of genomic relationships...).

2

Adaptations for each breed

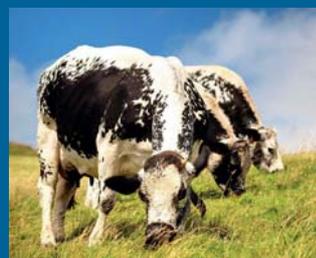
By sharing and consolidating a reference population of 30 000 bulls in collaboration with European partners (Eurogenomics consortium), France has focused on rapidly achieving very reliable genomic indexes for the **holstein** breed. This common international foundation and the breeding values achieved by French bulls encourage recognition of our programmes.

The **pie-rouge** breed benefits from its pedigree relations with holstein and has therefore an indirect genomic evaluation available.

Thanks to the international collaboration at the heart of Inter-genomics, the genomic evaluation of the **brune** breed is based on a constantly growing reference population and produces more and more precise indexes.

For the **normande** and **montbeliarde** breeds, the simultaneous evaluation of genotyped males and females integrated into the reference population is another recent adaptation of the index calculation method to different situations on the ground.

The **abondance**, **tarentaise**, **simmental** and **vosgienne** breeds are due to publish their first official genomic indexes in 2016. The GemBal project run by the UMT 3G partnership between INRA, Allice and the Institut de l'Élevage, coupled with the efforts made by the breed organizations to genotype animals has enabled the creation of sufficiently large reference populations to reach a satisfactory precision in the indexes.



VOSGIENNE BREED: 2500 COWS AND GENOMIC INDEXES

In this context, the Vosgienne breeders were very enthusiastic about the possibilities offered by genomic selection.

They encouraged genotyping of all milk recording females of the breed in order to construct a reference population of over 1000 animals, a solid foundation for genomic evaluation. Today, all Vosgienne animals are genomically indexed with an acceptable level of precision for a wide range of traits. Breeders can implement more informed choices as well as mating plans that are better adapted to their needs, compatible with hardiness, diversity and production systems. This collective effort has resulted in the Vosgienne breed being the smallest breed in the world, in numbers, to benefit from genomic selection.

SIZE OF REFERENCE POPULATIONS

	PRIM'HOSLSTEIN	MONTBÉLIARDE	NORMANDE	BRUNE
Bulls	30 000	2 600	2 300	6 000
Cows		20 000	10 000	
	ABONDANCE	TARENTEISE	SIMMENTHAL	VOSGIENNE
Bulls	345	301	339	56
Cows	1 885	1 273	215	1 076

3

New perspectives

Genomics opens the way for selecting on new traits. For example, a population of several tens of thousands of genotyped cows for whom hoof trimming data have been collected can lead to reliable indexes on foot health.

In the same way, we can envisage selecting on more and more complex traits, such as milk composition (fatty acid profiles, proteins, minerals), cheese-making qualities, resistance to a variety of diseases, or feed efficiency.

At the same time researchers continue to increase index reliability: single step evaluation, use of group markers (haplotypes), identification based on sequencing data of a growing number of causal mutations included in the statistical models of evaluation.

TESTIMONY

Vincent Ducrocq, Director of Research at INRA

“Clearly, the genomic revolution is far from over in dairy cattle. New approaches will allow us to increase selection efficiency whatever the breed or trait. Collective collaboration needs to be maintained because the necessary investments, as much for genotyping as for phenotyping, are substantial.”