

GENOMIC SELECTION ACCESSIBLE TO ALL RUMINANTS



KEY FIGURES

14 cattle breeds
4 sheep breeds
2 goat breeds

The French collective organisation opens genomic selection to all ruminants

A more efficient selection of breeding animals is from now on possible thanks to the joint process of genotypes with pedigree and performance data. This technological advance has led to the distribution of more precise breeding values that are published at an earlier stage of the animal's life.

The implementation of this technology, effective in major dairy cattle breeds since 2009 and in Lacaune dairy sheep breed since 2015, is currently being deployed for the other breeds and the other industries.

France is one of the only countries in the world to offer this technology in cattle, sheep and goats, thanks to a professional organisation structure which is closely linked to Research and Development. This facilitates the sharing of technological progress and the fast transfer of innovations on the ground.

But what exactly is “genomic selection”?

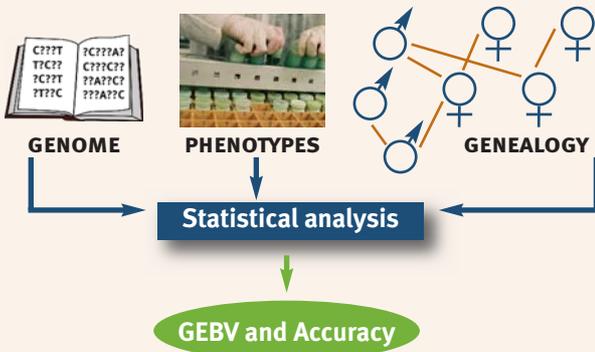


Example of the Bovine SNP 50 chip: this chip contains 24 zones, each one allowing analysis of a different animal. A zone is composed of microbeads which make it possible to read one of the 54,000 selected markers.

1

Technology and genetic evaluation

Genomic selection consists of choosing breeding animals from evaluation results that include not only the data of performances and pedigree but also known data on the genome of the animals.



2

Consequences for breeding schemes

By reading its DNA, it is possible to estimate a genetic breeding value for an animal:

- from birth (or even at the embryo stage),
- for a wide range of traits, some of which were previously available at a very late stage in the animal's life like fertility or longevity,
- with better precision than that obtained at the same age with only performances and pedigree data.

The efficiency gain for the collective selection programmes is linked on one hand to a shortening of the interval between generations, in particular thanks to early use of the best males and females as elite breeding animals, and on the other hand to the gain in precision of estimated genetic breeding values for natural mating females and males.

At the level of breeding scheme management, multiple changes are induced. They must take into consideration technical parameters (reproduction methods, generation intervals...) as well as economical factors specific to each industry.

Genomic selection can also help with controlling genetic variability, provided each young breeding animal is disseminated in a sensible controlled manner while quickly replacing males.

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Today, for a reasonable cost, we can genotype an animal for several tens of thousands of DNA markers on a device called a "SNP chip".

The development of genomic evaluations requires a reference population, which means a group of genotyped animals that also have reliable recorded performances available. The bigger this reference population is, and the more accurately measured performance records are, the more precise the genomic evaluation results will be.

For a given trait, the variant effect of each marker on the performance recorded on the reference population is measured. These effects are combined with other known data (pedigree, performance) in order to obtain genomic breeding values.

3

A rich supply for better sustainability

Genomic selection opens interesting perspectives for the evaluation of new traits, of which the measuring costs are too high to be carried out on the entire recorded herd: in this case the annual monitoring can be concentrated on a few thousand to tens of thousands of animals. This is the reason why ambitious phenotyping programmes are in progress in every sector. The traits measured relate to aptitudes that up to now have been difficult to select, such as robustness of animals, health and feed efficiency.

4

Medium term perspectives

Other applications of genotyping exist and will become widespread. Therefore, a genotyping result can enable the control of an animal's parentage, even to offer a parent, among a list of candidates.

Genomic selection is a young science. It will benefit again in the coming years from many methodological advances. For example, INRA is taking part in an international research programme that studies over a thousand complete bovine genomes. As knowledge of genomes progresses, new mutations responsible for interesting performance traits (double-muscle, polled...) and for genetic anomalies (infertilities, ataxias...) are identified. These mutations become integrated into the SNP chips. In this way, new genotyped animals will also have data available on these genetic particularities which can be managed within the selection populations.