French beef breeds at the forefront of genomics

French breeding schemes for beef cattle were already reputed worldwide for their efficiency. An even more efficient selection for breeding animals is now possible thanks to the addition of genomic information to the data used until the present time (performances and pedigree).

Genotyping efforts carried out in recent years have enabled the three main French beef breeds to have sufficiently large reference populations available to overcome this important hurdle in selecting breeding animals.

The IBOVAL indexes that integrate genomic data are now more precise and consequently are disseminated at an earlier stage in the animal's life.
1
The practical implementation and distribution of services

For an animal of the charolaise, limousine or blonde d'aquitaine breeds, the genomic component, calculated from equations established on the reference population, is combined with the estimation of its genetic potential which combines genealogies and performances. In this way we make the most of all the available information sources, whether it is genomic data from the reference population or polygenic data obtained from all the performances and genealogies available in the selected population. Thus a “consolidated” IBOVAL index is produced which has the advantage of being more precise than each of its components.

In each of the breeds, one or several societies are commercialising this new technology. They are the principal contacts for clients, breeders or organisations. They provide support through all the steps from the biological sampling needed for genotyping to the presentation of the results. These societies act within a framework defined by the Breed Societies, in particular regarding animals that can be genotyped and that must be part of the defined “Target Population”.

The official publication of the results (in the databases and on various reports) is transparent for users because its mode of expression is identical to the breeding values presented previously. It is simply more accurate or published earlier in the animal's life.

2
Medium term perspectives (new breeds, new traits)

For the 6 other beef breeds evaluated in France (salers, aubrac, parthenaise, rouge des prés, gasconne and bazadaise) as well as for new traits, reference populations sufficiently large to access a routine genomic evaluation are not yet available. Work in progress aims to:

- increase reference populations in each breed and for different traits;
- establish links between several breeds by valuing the common markers or even better, by directly taking into account the “causal mutations”.

Furthermore, the two-step computation method currently used will soon be replaced by a single step method. This will enable optimal combination of phenotypes of genotyped and non-genotyped individuals. We expect a gain in precision from this, particularly for individuals where only their relatives are genotyped.

For Philippe Dru, a Limousine breeder based in the Loire Valley (GAEC Petit-Pont in Montereul-sur-Loir):

« Compared to existing tools, the value of using genomics in my herd is to be able to select breeding animals at an earlier age, with more precision, and safeguard my mating plans while accelerating genetic progress. It’s also an extra commercial argument to get the most from my breeding animals. »