



## IN GOATS GENOMIC SELECTION IN FRANCE



### KEY FIGURES

**3 600**  
genotypes

**30 %**  
of worldwide  
genotypes

## Genetic progress in the goat sector

The genetic improvement of goats started in the 60s in two main breeds, Alpine and Saanen, with the establishment of milk recording and a breeding scheme. This scheme, performed in pure breed, relies on Artificial Insemination. Each year, planned matings enable the procreation of young breeding males of which the genetic value (index) will be estimated on their descendants.

Approximately forty bucks of each series are kept after performance testing and their sperm is distributed to farms. Originally focused solely on milk protein content, the selection goal gradually grew to include other production traits (protein percent, fat content and fat percent), morphology traits (udder morphology essentially) and the Somatic Cell Count criterion.

Annual genetic gain over the last ten years is approximately 13kg for milk and 0.5kg for protein content, which is between 0.15 and 0.20 unit of genetic standard deviation (depending on breed and trait).





# 1

## Construction of a chip

In 2010, the goat genome sequencing and the creation of an international consortium led by INRA for France and the Beijing Genomics Institute were determining stages in the construction of a genotyping tool.

INRA initially contributed to the sequencing of animals from 3 French goat breeds (**alpine, aaanen, créole**) then played a central role in the international data aggregation that led to the final choice of SNP to integrate into a chip. In 2011, Illumina started producing the 50K goat chip. This tool opened new perspectives regarding the understanding of the genetics of traits and of genomic selection in the goat species. In France, the first stage of genomic selection was the creation of a reference population. 825 progeny-tested artificial insemination bucks of the alpine and Saanen breeds evaluated were genotyped for this purpose.

### METHODOLOGY

A study of the genetic structure of the goat population showed that it was less suited to genomic selection than the main cattle breeds. Furthermore, in spite of their common origin, the Alpine and Saanen breeds are now relatively distant from a genetic point of view, which questions the value of a multi-breed approach.

In view of these initial results and the relatively modest size of the goat reference population, the INRA retained the single step approach which consists of estimating the genomic values directly, in one single step, from female performance and male genomic data.

Taking into account the major gene aS1-casein in the model of evaluation brings further improvement to the efficiency of protein content predictions of 8% in Alpine and 14% in Saanen.

At the same time, a first theoretical study on the optimisation of the goat scheme showed that taking genomic data into account could enable an increase in genetic gain of 46% for milk quantity and milk contents.

# 2

## Implementation

The establishment of genomic selection is programmed for the 2018 campaign for the two breeds as well as all of the traits currently evaluated.

Since the first studies, 234 additional bucks have been genotyped. From here to implementation, all the new series of tested bucks will also be genotyped in order to consolidate the reference population.

The long-term perspectives are:

- The construction of a chip for parentage assignment, integrating genes with major effects on the key traits and which will be genotyped concomitantly;
- The better inclusion of major genes (aS1-casein or DGAT1) in the genomic predictions;
- The use of data coming from genome sequencing in genetic evaluation;
- The management of the genetic variability with the help of genomic data.

# 3

## Consequences for the scheme

Genomics will lead to a reorganisation of the breeding scheme at different levels:

- Planned matings: an earlier genomic index for the elite females will lower the average age of buck dams;
- The choice of young males for insemination: the availability of a reliable and early genomic index for young males born from planned matings will induce a more efficient selection;
- Semen production: in the traditional scheme the whole stock of doses is collected before the estimation of the buck's genetic value is available. With genomics, the buck's semen production will be aligned with his genetic profile;
- The use of young males for insemination: they will be used as soon as they are capable of producing semen without having to wait for the progeny testing results. This will reduce the male generation interval;
- The selection objective, which could integrate new traits, in particular those which are not very heritable and therefore difficult to improve upon in a traditional scheme (functional traits, resistance to disease): the creation of specific reference populations for the inclusion of new criteria will modify the organisation of the collection of phenotypes.

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