



**MARKER-ASSISTED SELECTION  
AND THE GENOMIC SELECTION**

**PRESS RELEASE**



*December 2008*

In fall 2008, the consortium of French breeding companies (BC) adopted the most modern and effective second generation marker-assisted selection (MAS2) programmes in the Holstein, Montbéliarde and Normande breeds. **This method is based on the most recent advances in bovine genome knowledge.**

**This consortium of French BC includes AMELIS, CREAVIA, GDO, GNA, JURA BETAÏL, MIDATEST, and UMOTEST, joined recently by DYNAM'IS, under the aegis of the UNCEIA, and it is associated with INRA and LABOGENA for this large scale use of genomics.**

## From the MAS to the genomic selection

The rapid and effective implementation of this new selection tool has been made possible by the exemplary long-term cooperation since the mid 1990s, between INRA, UNCEIA, these Breeding Companies and LABOGENA.

This partnership enabled first generation marker-assisted selection to be implemented as soon as the early 2000s, which made **France a pioneer in the field.**

The experience acquired by both scientific and technical teams and by the BC, guarantees the effective implementation of MAS2 and Genomic Selection.

**The system that has been set in place ensures the control by farmers of future selection programmes.**

This research has benefited from the nationally managed information system which provided access to animals and their information.

Setting up this research programme and its application has also been **made possible thanks to considerable collective financial investment by these BC**, directly and indirectly via the research-oriented industry joint-venture APIS-GENE in the AGENAE framework.

Thus, in **CartoFine project**, cofinanced by a grant of the National Research Agency (ANR) and **APIS-GENE**, 3,300 bulls have been genotyped for **54,000 markers** with the Illumina beadchip.

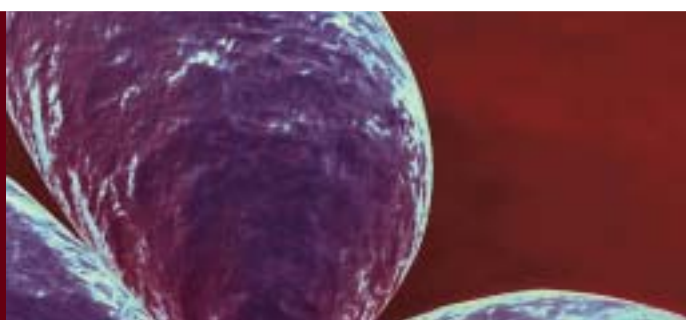
This project paved the way of the second generation MAS.

More recently, APIS-GENE cofinanced the AMASGEN project that concentrates on methodological developments and the validation of genomic selection.

**In response to the expectations of French breeding companies involved in the project, the different partners have increased their investments.**

The UNCEIA has strengthened its technical team, the LABOGENA laboratory has invested in an Illumina genotyping platform for the analysis of several hundred animals a week and the INRA provides its methodological support and computing resources necessary for the monthly genetic evaluation of the breeding animals.

Marker-assisted selection in dairy cattle is symbolic of the complementary nature of the various links in the French



agricultural research and development system.

**After the first generation MAS since 2001, close contact between BC and research continues today by access to MAS2 technology, relying on strong and recognised scientific and methodological bases.**

This technology enables every participating BC to work out its own strategy for the selection and marketing of semen to make the best possible use of these new tools.

Today, MAS2 is an **exclusive tool** reserved for the BC of the consortium, as a result of the research contract which binds the participating BC, UNCEIA, INRA and LABOGENA.

The accuracy of these estimated breeding values is at least as high as competing systems proposed abroad, and high enough to prevent any technical limitation for marketing of breeding animals.

A mandatory judicial expert's report is in progress to determine the conditions for marketing semen from breeding animals evaluated by MAS2.

## **The French partners of the MAS programme**

**The INRA** brings all its expertise and scientific know-how to provide the fastest and most efficient transfer of MAS technology in the field of the genetic evaluation of breeding animals.

[www.inra.fr](http://www.inra.fr)

**LABOGENA** carries out all the genotyping analyses with Illumina technology using the cattle beadchip with 54,000 markers. There are plans to carry out more than 10,000 analyses a year.

[www.labogena.fr](http://www.labogena.fr)

**the UNCEIA** is in charge of the everyday MAS implementation and integrates requests from the BC in the evolution of methods or ways of return to the Selection Companies.

[www.unceia.fr](http://www.unceia.fr)

## **THE BREEDING COMPANIES**

members of the project finance the implementation of this selection method and use the MAS results in their breeding programmes (research, genotyping, support).

**AMELIS**  
[www.amelis.fr](http://www.amelis.fr)

**GNA**  
[gna@gna.fr](mailto:gna@gna.fr)

**CREAVIA**  
[www.genoe.fr](http://www.genoe.fr)  
[www.urceo.fr](http://www.urceo.fr)

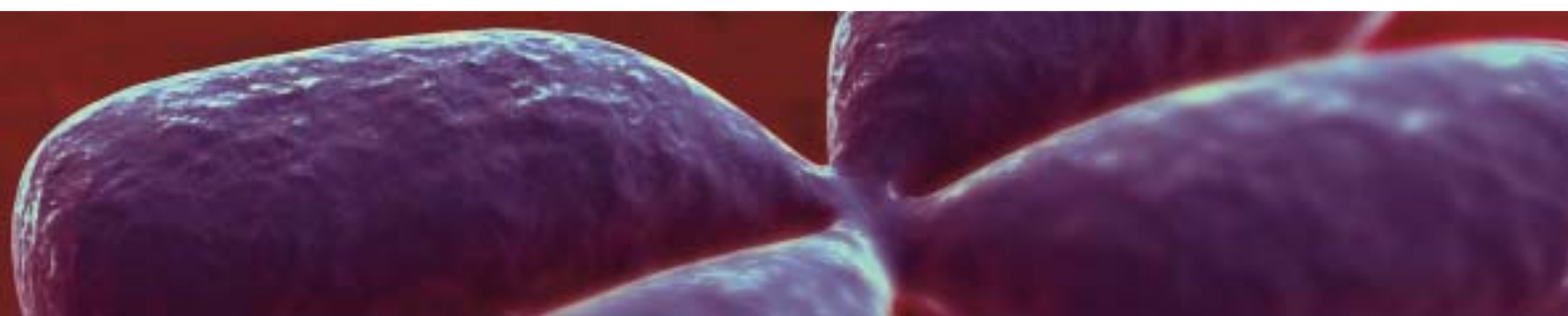
**JURA BETAİL**  
[www.jurabetail.fr](http://www.jurabetail.fr)

**DYNAM'IS**  
[www.dynamis.fr](http://www.dynamis.fr)

**MIDATEST**  
[www.midatest.fr](http://www.midatest.fr)

**GDO**  
[www.genesdiffusion.com](http://www.genesdiffusion.com)

**UMOTEST**  
[www.umotest.com](http://www.umotest.com)



## Scientifically recognised effectiveness

Scientists today agree in saying that work in genomics will give **rise to many developments in the field of genetic evaluations** and in the optimisation of breeding programmes for dairy cattle, **but not all MAS tools or genomic selection tools in the world are actually based on the same markers, on the same reference population or on the same methodologies.**

In other words, if the interest of genomics in selection programmes has proved its worth, **the effectiveness of each MAS tool demands to be checked on real data.**

The effectiveness of the French MAS tool has been verified on a group of 764 young bulls recently progeny tested (468 Holsteins, 152 Normandes et 144 Montbéliardes).

For this, MAS2 evaluations were computed in the conditions prevailing in 2004 for this group of bulls and compared to results after progeny test.

**The results show the great effectiveness of the French tool on all the traits studied.**

The reliability (coefficient of determination or CD) of the proofs of these young bulls evaluated in the conditions of 2004 ranged from 0.50 to 0.65. It was much higher than that obtained in classical genetic evaluation without markers, ranging from 0.20 for fertility to 0.40 for milk protein content.

**Table 1 > average reliability obtained with the french system on young Holstein bulls without progeny performance**

characters	Average reliability for young bulls borned after January 2007 1st
Milk quantity	0,61
Protein	0,59
Fat	0,56
Cells account	0,60
Fertility	0,48
Udder Height	0,51
Milking speed	0,53

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