



UMR 1313 GABI

G2B Team

INRA Jouy en Josas
Domaine de Vilvert
F-78350 Jouy en Josas
www.jouy.inra.fr/gabi



Overall activity

Our main mission is through genetic approaches, to contribute to the sustainability of bovine production in its economic, social and environmental dimensions. Our activities are based on a strong synergy between genomic selection and analysis of genetic variability. These two key topics take full advantage of new genotyping and high-throughput sequencing techniques and bioinformatics.

Highlights

- Development of genomic selection in French dairy cattle
- ISO9001-2008 certification of the cattle genetic and genomic evaluations.
- Identification of causal mutations responsible for defects or embryonic mortality;
- Identification and characterization of the “polled” locus (absence of horns in cattle)
- Founding member of the “1000 bull genomes” Consortium
- New release of the Survival Kit (survival analysis software)

Joint Research Unit

Animal Genetics and Integrative Biology

Bovine Genetics & Genomics (G2B)

Team Leader

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Scientific Questions

1- Bovine genetic evaluation and genomic selection

The team is responsible for cattle genetic evaluation in France, from its conception to its practical implementation. This historic activity is a deciding factor of cattle selection in France and has been ISO9001 certified since 2006. It evolves regularly in terms of traits evaluated and methodologies used.

Genomic selection deeply transforms genetic evaluations. This is the scientific project of the UMT « Genetic and Genomic Management of cattle populations » (UMT 3G) joining together INRA, the French Livestock Institute (Institut de l'Élevage) and Unceia. This project is aimed at : (a) implementing genomic selection in all cattle breeds for all traits; (b) expanding the number of evaluated traits, especially in the fields of animal health, adaptation, and product quality; (c) providing methods and population management tools; (d) developing international partnerships.

Within the Gembal and GenSSeq projects, methodologies for efficient genomic selection robust for low relationships are being developed, taking advantage of varying polymorphism densities (from low density (LD) to the whole genome sequence).

Applications are developed within breed and in a multi-breed context, at the national and international levels. This topic is naturally a part of the INRA «genomic selection» metaprogramme, a source of multidisciplinary activities, exchanges between species, and international partnerships towards the North as well as the South (GenoSouth project).

In this context, it is crucial to regularly update breeding objectives (the Osiris project) and the management of populations for a better sustainability (selected traits, management of diversity), while integrating demands from the industry and society and





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Collaborations and partnerships

Numerous collaborations with the GenPhySe INRA unit (Toulouse) and with the « Physiology and Production Systems » (PHASE) and Animal Health INRA Divisions

Bovseq sequencing project coordinated by Limoges University for the analysis of meat quality traits

Member of and important contributor to the « 1000 bull genomes » project led by Melbourne University.

International collaboration in genetic and genomic evaluations (Eurogenomics, Intergenomics, Interbull, Interbeef)

Links with INRA meta-programmes

SELGEN: multidisciplinary approaches across species, and in interaction with the social sciences on the consequences of genomic selection.

GISA: Analysis of the genetic determinism of mastitis and paratuberculosis

2 – Analysis of genetic determinism of phenotypes

The second major thematic studied by G2B is the genetic determinism of different traits, especially related to the quality of products and adaptation. Experimental designs are built on experimental facilities or commercial farms with our industrial partners of genomic selection. The main projects deal with milk composition (PhenoFinLait), meat tenderness (Qualvigene), mastitis resistance (Le Pin experimental facilities (EF)), precocity, feed efficiency, and methane emission (Bourges and Le Pin EF), foot health (Genopedix), susceptibility to paratuberculosis (Paradigm/Picsar). Special attention is paid to the identification of the genes responsible for genetic defects within the National Observatory of Bovine Abnormalities (ONAB) and through the analysis of whole-genome sequences. The Akelos project is dedicated to horn determinism. Within the CartoSeq, Represeq, GenSSeq, Bovseq projects, many whole-genomes are being sequenced. Sequence or structural variants are being identified. The aim is to track down the causal mutations of a large number of influential chromosome regions (QTL). This top-down approach (from QTL to QTN) is completed with a bottom-up approach (from sequences to phenotypes) developed within the Regulomix and BovReg projects, focusing on the analysis of the impact of DNA variants located in gene regulatory regions, assuming that some of these variants have a biological effect.

Research Infrastructure

Phenotypes supporting our activity originate from the national animal breeding data bases (SIG) and from two experimental facilities in Le Pin and Bourges. The INRA computer centre CTIG is a close partner that provides access to data and computing capacity. Most genotyping data are produced by Labogena, for research as well as for genomic selection. Whole-genome sequences are produced by the GetPlage platform in Toulouse and bioinformatics work is performed in collaboration with the Sigenae group.

Recent Publications

- Allais-Bonnet A., Grohs C., Medugorac I., et al (2013). Novel insights into the bovine polled phenotype and horn ontogenesis in Bovidae. *PLoS One* 8:e63512.
- Fritz S., Capitan A., Djari A., et al. (2013). Detection of haplotypes associated with prenatal death in dairy cattle and identification of deleterious mutations in GART, SHBG and SLC37A2. *PLoS One* 8:e65550.
- Meszaros G., Sölkner J., Ducrocq V. (2013). The survival kit: Software to analyze survival data including possibly correlated random effects. *Computer Methods and Programs in Biomedicine* 110:503-510.
- Boichard D., Chung H., Dasonneville R., et al. (2012). Design of a bovine low-density SNP array optimized for imputation. *PLoS One* 7:e34130.
- Legarra A., Ducrocq V. (2012). Computational strategies for national integration of phenotypic, genomic, and pedigree data in a single-step best linear unbiased prediction. *Journal of Dairy Science* 95:4629-4645.
- Vinet A., Drouilhet L., Bodin L., et al (2012). Genetic control of multiple births in low ovulating mammalian species. *Mammalian Genome* 23:727-740.
- Dockes AC., Magdelaine P., Daridan D., et al (2011). Farming and breeding goals for sustainable animal breeding - views and expectations of stakeholders from the production chains and the general public. *Productions Animales* 24:285-296.
- Meersseman C, Léjard V, Rebours E, Boussaha M, Maftah A, Petit D, Rocha D. 2014. Bovine TWINKLE and mitochondrial ribosomal protein L43 genes are regulated by an evolutionary conserved bidirectional promoter. *Gene*. 537:154-163.

Complete list of publications at www.iouy.inra.fr/gabi

