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AgroParisTech

UMR **1313 - GABI**

Animal Genetics and Integrative Biology (GABI)

Genetics for sustainable cattle breeding

GBoS

Team learder

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Global theme

The main mission of GBoS is to provide knowledge and tools that contribute, through genetics, to the sustainability of cattle production in its economic, social and environmental dimensions.

université PARIS-SACLAY

Attached to the **Université Paris-Saclay**

Attached to **ABIES doctoral school** (Agriculture, Alimentation, Biology, Environment, Health)

SAPS Sciences Animales PARIS SACLAY

SAPS member
Sciences Animales Paris-Saclay

CARNOT France Futur Élevage

Member of Institut Carnot
France Futur Elevage

The main mission of the GBoS team is to provide knowledge and tools contributing, through genetics, to the economic, social and environmental sustainability of cattle production. The team is made up of around forty INRAE staff, as well as Idele and Eliance personnel within the e-BIS joint technology unit (UMT). The team is also co-director, with Idele, of the Observatoire National des Anomalies Bovines (ONAB).
The team's research falls into three main scientific areas: (a) understanding and characterizing bovine genomes; (b) studying traits and functions (health, adaptation, environmental impact, product quality, genetic anomalies); (c) prediction and selection.

Questions scientifiques

Focus 1 - Understanding and characterizing bovine genomes

This line of research aims to deepen our understanding of bovine genomes by combining systematic sequencing and the study of the effects of genetic variation. Thanks to advanced sequencing technologies, in particular long-read, the aim is to map the structural variants of genomes and gain a better understanding of the "pangenome", i.e. all the genetic variations present in a population, beyond the reference genome. This axis also includes an epigenetic dimension, with a focus on methylation marks to explore the relationship between genetics, epigenetics and animal performance. International collaborations reinforce this approach, while developing innovative tools such as cell lines to test the effect of certain genetic variants. Finally, the team is also exploring genotyping by sequencing as a promising alternative to current genotyping techniques, to anticipate the future needs of genomic selection.

Related projects : H2020 RUMIGEN ; PEPR ADAAPT ; ANR & APIS-GENE PolyPheMe ; APIS-GENE InViTroupeau ; Carnot F2E CASCAD

Focus 2 - Character and function studies

This axis explores the genetic determinism of traits important for the adaptation of cattle to the requirements of agroecology, in particular their health, robustness, efficiency and climatic adaptation. The aim is to gain a better understanding of the genetic basis of these traits, and to guide selection towards animals adapted to different environments. The data collected includes a variety of phenotypes and complex biological information from national and European projects. Work on health concerns the study of resistance to emerging diseases such as strongyles, besnoitiosis and tuberculosis, as well as more common diseases such as mastitis, leg disorders and paratuberculosis. With regard to adaptation and efficiency traits, the team is studying longevity, precocity, heat tolerance, methane emissions and product quality (milk and meat). At the same time, research into new traits, such as animal welfare, is planned using high-throughput phenotyping tools (sensors, milking robots, mid-infrared milk spectra, etc.). The team also works with the industry and veterinary partners to identify genetic abnormalities in cattle, contributing to the Observatoire National des Anomalies Bovines (ONAB). This initiative enables us

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UMR **1313 - GABI**

Highlights
- Study of pangenomes
- Functional validation
- Genetic determinism of methane emissions, thermotolerance, microbiota composition, disease resistance and methylation
- GxE interactions
- Integration of new information to improve accuracy of genomic assessments

Research facilities

Our activity is based on a strong synergy between population management and analysis of genetic variability. Phenotypes come from the national zootechnical database and the experimental unit at Le Pin. The Centre de Traitement de l'Information Génétique is a close partner providing data access. Sequences are produced on the GetPlage platform in Toulouse, and bioinformatics work is carried out in collaboration with Sigenae. The majority of genotyping comes from the genomic selection activity.

to precisely characterize the mutations responsible for certain anomalies, including horning, in order to improve understanding and management.

Related projects : H2020 RUMIGEN ; PEPR ADAAPT ; CASDAR ALONGE ; APIS-GENE & BPI Methane2030 ; APIS-GENE CaiCalor, GMYOSEO2, PRECOBEEF2, METHABREED, BESNALP, GIVERNI, WelCow, FROM4ALL, SéViTal, ACROPOLLED ; projet GLOBAL de l'UE du Pin (diverses sources de financement)

Focus 3- Predictions and Selections

This third axis focuses on improving genomic prediction and selection tools for cattle. The team is exploring new ways to improve the accuracy of genomic evaluations, by integrating functional annotations of genetic variants, non-additive effects and non-genetic information such as epigenetic marks or microbiota. Other research aims to personalize selection indexes according to interactions between genetics and the environment (GxE), in order to adapt selection to the specific features of livestock farms and to future climatic conditions. Another challenge is the management of genetic diversity and inbreeding. Finally, the aim is to make these tools directly usable on the farm to help breeders optimize the renewal of their herds according to their specific environment, with the aim of improving the adaptation and resilience of cattle.

Related projects: H2020 RUMIGEN ; PEPR CoBreeding, ADAAPT ; APIS-GENE TRANSEVAGENOC, SéViTal ; Carnot F2E GS-Mint ; MP CLIMAE Vaacherin and GenAttac consortium.

Expertise

Genome structure and function; Genetic determinism of traits; Genetic evaluation; Population management.

Partners

Idele & Eliance via the Unité Mixte Technologique eBIS; INRAE: GA, Phase and SA departments; Veterinary schools; Bovine breeding operators; International consortia and networks.

Publications

https://eng-gabi.jouy.hub.inrae.fr/the-teams/gbos/gbos-publications