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UMR 1313 - GABI

Equipe Genetics and Integrative Biology Team

BIGE

Team leader
Eric Barrey

Global theme
The BIGE team develops new knowledge in equine genetics and genomics.

Applications :
- Genomic selection by sport discipline.
- Identification of causal mutations and development of genotyping tests for traits of interest: hair curl in Curly horses, withers height in sport ponies, risk of exercise-induced myositis in Arabian horses.

université PARIS-SACLAY

Attached to the **Université Paris-Saclay**

Attached to the **ABIES doctoral school** (Agriculture, 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

Scientific questions

The mission of the BIGE team is to provide the equine industry with new knowledge in equine genetics and genomics, enabling it to improve equine populations in terms of the sporting abilities, health and well-being of horse breeds produced in France. The scientific questions we are trying to answer concern :

1- Genetic selection in the context of sports performance and functional longevity

We develop multi-criteria genetic selection methods integrating performance and longevity traits. Sporting or functional longevity corresponds to the length of time an animal performs well and is in good health. It is essential for farm profitability, as an animal that performs well for longer optimizes breeding costs and improves the sustainability of production. Functional longevity depends not only on life expectancy, but also on numerous genetic and environmental factors influencing, for example, health, locomotion and disease resistance.

Examples of related projects:

- **Génomique Equine Normandie (GENi)** : Production of tools to characterize the innate aptitudes of horses in the three major segments of the industry: gallop racing, trotting and sport. These aptitudes relate to sporting skills, but also to the absence of predispositions to under-performance associated with a number of respiratory, infectious, spinal or muscular pathologies.
- **LiFeS** : Identification and characterization of early selection markers associated with functional sporting longevity in the show jumping horse.
- **GenEndurance** : Identification and characterization of biomarkers and genetic determinants to characterize the sporting aptitude for aerobic exercise in endurance racing in Arabian and Arabian crossbred horses.

2- Artificial intelligence for genomic selection

We are conducting interdisciplinary and cross-species projects exploring the possibilities of using predictive deep learning and machine learning models to predict genetic values or phenotypes from high-density genotypes. Generative deep learning models are also being developed to produce artificial genotypes.

Examples of related projects:

- **GenIALearn** : Exploratory project to evaluate the performance of statistical and deep learning methods for the joint prediction of multiple complex traits by integrating massive genotyping data.
- **DeepSelectGene :** PhD project on deep learning from genotype data and application to genomic selection.

3- Analysis of the genetic determinism of complex diseases

We are conducting projects to identify causal mutations and explore the potential role of non-coding RNAs (microRNAs and long non-coding RNAs) as biomarkers and/or therapeutic targets for complex diseases.

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Research facilities :
Partnership with breeders' associations

Examples of related projects:

- **Myopathie récurrente d'exercice (RER)** : Identification of genetic causes of acute exercise-associated myositis in Arabians, French Trotters and Thoroughbreds.
- **Mélanome Equin** : Identification and characterization of oncogenic long non-coding RNAs for early diagnosis and treatment of melanoma and carcoid. Development of an antitumor antisense oligonucleotide treatment active against melanoma and sarcoid skin tumors.
- **MiROC et MARKER-OC-FRAGMALIM** : Identification of microRNA and metabolite biomarkers to better characterize osteochondrosis.

4- Improving knowledge of equine genomics

We are involved in methodological developments aimed at characterizing gene structure and function. We are particularly interested in characterizing the genetic variability of mitochondrial DNA in relation to running performance. Indeed, mitochondria are involved in a wide range of cellular functions, and are not just power plants. From a genetic point of view, there is a real interest in better understanding the variability of the mitochondrial genome and its functional impact.

Examples of related projects:

- **mtDNA-seq** : Projet méthodologique exploratoire ayant pour objectif de développer de nouvelles méthodes adaptées au séquençage du génome mitochondrial utilisant la technologie de séquençage long-read nanopore.
- **Memigenomics** : Développement méthodologique pour analyser à grande échelle la diversité mitochondriale afin de mieux comprendre la biodiversité des populations naturelles et mettre en application le concept de pangénome mitochondrial.
- **mtDNA-seq :** Exploratory methodological project to develop new methods adapted to mitochondrial genome sequencing using long-read nanopore sequencing technology.
- **Memigenomics** : Methodological development for large-scale analysis of mitochondrial diversity to better understand the biodiversity of natural populations and apply the mitochondrial pangenome concept.

Expertises

Our team has developed a broad spectrum of skills, from clinical to genomics, including quantitative genetics, functional genomics, molecular biology and bioinformatics.

Partners

- Institut Français du Cheval et de l'Equitation (IFCE, Saumur).
- Ecole Nationale Vétérinaire d'Alfort - ENVA.
- The Center for Imaging and Research on Equine Locomotor Disorders (CIRALE-ENVA).
- LABÉO, Pôle d'analyses et de recherche de Normandie, Caen.
- Laboratoire des Courses Hippiques - LCH, Verrières-le-Buisson.
- Center d'anthropobiologie et de génomique - Unité CAGT, CNRS, Université Paul Sabatier, Toulouse.
- Evolution, Genome, Behavior, Ecology Laboratory (EGCE), CNRS, Université Paris-Saclay, IRD.
- Andrés Bello University, Santiago, Chile.

Publications

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