



UMR 1313 GABI

BIGE team

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Team

The Integrative Biology and Equine Genetics team is located in Jouy-en-Josas, Toulouse and ENVA Maisons-Alfort. It is made up of 9 members who share a complementary panel of expertise from quantitative genetics to clinical studies including bioinformatics, exercise physiology, molecular biology and functional genomics.

Overall Activity

The BIGE team works on the improvement of equine populations including both sports aptitudes and health.

They also produce improved knowledge on the genomic mechanisms that influence sports performances and the pathologies that limit the use of horses. Thus, the practical result is to provide tools that help improve the management of the horses' sports careers to promote genetic progress and to provide genetic counseling to reduce the incidence of pathologies that have a genetic component.

Unité mixte de recherche

Génétique Animale et Biologie Intégrative (GABI)

Integrative Biology and Equine Genetics (BIGE)

Team leader

Eric Barrey (eric.barrey@jouy.inra.fr)

The team's expertise includes quantitative genetics approach, breeding evaluation of breeding, molecular genetics, functional genomics and integrative biology approaches of muscular exercise.

Scientific Questions

The research objectives of BIGE are:

- Optimizing equine selection methods and improving individual phenotyping of aptitudes.
- Improving the knowledge of the structure and function of the equine genome.
- Increasing the knowledge of the mechanism involved in the interaction between the microbiota and its host metabolism and physiology, being in a better position to obtain robust predictive biomarkers and develop strategies to increase the performance, preserving animal health.
- Studying the biological processes and molecular mechanisms involved in the normal and pathological musculoskeletal development, notably for the recurrent exercise-induced rhabdomyolysis and osteochondrosis.
- Identifying the genetic and epigenetic regulating mechanisms of mitochondrial activity, in particular to explore the role of mitochondrial microRNAs imported and putatively encoded by mtDNA.

Current Projects

GenEndurance (Eric Barrey and Céline Robert): study the relationships between endurance race performances, genetics and phenotype (morphology, gaits, biochemistry, metabolomics) in Arab horses (<http://genendurance.over-blog.com>).

SoGen (Anne Ricard and IFCE): Genomic selection, search for molecular markers in sport horses for jumping ability, morphology and gaits. Simultaneously, large phenotyping for morphology and gaits is developed

GenoTrot, the "trotting gene" DMRT3 (Anne Ricard and SECF): this gene plays a role in the development of coordination for a symmetrical gait such as ambling and trotting. First found in Islandic horse as favorable for ambling, the mutation is fixed in Standardbred horses, the American horse for trot and ambling races. In the French trotter, the gene is still polymorphic. The unfavorable allele carriers have lower probability to be qualified but heterozygote horses have higher earnings in late performances in races. The study will verify these first results and characterize gaits to understand the mechanism. good performers. The genetic variability of DMRT3 on the ability to qualified for trot racing and the ability to perform for long career is studied in Trotteur Français.





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Collaborations and Partnerships

The International Consortium on the Horse Genome, supported by Havemeyer Foundation: high density genotyping Chip 670K, Annotation of Equus Caballus 3

GenOeuf : (BDR INRA Jouy: JP. Ozil and B Banrezes): Role of microRNA in genomic regulation and mitochondrial activity of the ovum 4 hours after fertilization.

MITOMICS: members of the World Mitochondria Society (Chaired by Pr Marvin Edeas and Volkmar Weissig) et

Andes Biotechnologies (Veronica Burzio, Chili): research on the regulation functions of long and small non-coding RNA encoded by the mitochondrial genome.

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EcaOmics (Núria Mach): Modulation of the intestinal microbiota and its fermentation capacity may provide new avenues for managing energy metabolism and health status during endurance exercise. The objective is to predict the energetic and health status of endurance horses through the integration of metagenomics with omic data.

MetaFoil (Núria Mach): The interaction between the intestinal microbiota composition and weaning stress in horses is not yet elucidated. We present a longitudinal study aimed at assessing how the pre- and post-weaning microbiota coevolves with its host behaviour.

StromaEq (Núria Mach): Relationship between microbiota and the parasitic small strongyles in within the infected host remains to be defined. Thus, our global objective is to study the three-way interactions between the horse, gastrointestinal microbiota and cyathostomins parasites in order to gain a holistic understanding of host-pathogen relationship.

Recurrent Exertional Rhabdomyolysis (Marine Beinat) : recurrent exercise-induced myositis (RER) affects nearly 10% of pure-bred horses during their sports career. It seems that this is due to abnormal intracellular calcium homeostasis of the skeletal muscles, which leads to acute muscle contractures that damage the muscle fibers. A research program has been undertaken to characterize the genomic mechanisms of this exercise myopathy, to identify genomic and metabolomic markers and, on the long-term, to develop a genotyping test for myopathy. to better characterize the etiopathology of this muscular disorder that is observed on 10 et 15% of the pure bred horses like Arabian and Trotteur Français. We look for candidate genes in Arabian horses.

MitomiR (Eric Barrey) : numerous nuclear microRNA are localized with the mitochondria in man, mouse, and rat, respectively in myocytes and hepatocytes. The project aims to identify the putative regulation functions of these miRNA in mitochondria in the equine muscles. We investigate whether microRNAs can be encoded by the mitochondrial genome.

Osteochondrosis (Céline Robert): to identify new genomic biomarkers in the synovial fluid for improving the characterization of osteochondrosis.

Recent Publications

Ricard A. Does heterozygosity at the DMRT3 gene make French trotters better racers? *Genet Sel Evol.* 2015 Feb 26;47:10. doi: 10.1186/s12711-015-0095-7.

Desjardin C, Vaiman A, Mata X, Legendre R, Laubier J, Kennedy SP, Laloe D, Barrey E, Jacques C, Cribeu EP, Schibler L. Next-generation sequencing identifies equine cartilage and subchondral bone miRNAs and suggests their involvement in osteochondrosis physiopathology. *BMC Genomics.* 2014 Sep 17;15:798. doi: 10.1186/1471-2164-15-798.

Le Moyec L, Robert C, Triba MN, Billat VL, Mata X, Schibler L, Barrey E. Protein catabolism and high lipid metabolism associated with long-distance exercise are revealed by plasma NMR metabolomics in endurance horses. *PLoS One.* 2014 Mar 21;9(3):e90730. doi: 10.1371/journal.pone.0090730.

Kornaš S, Sallé G, Skalska M, David I, Ricard A, Cabaret J. Estimation of genetic parameters for resistance to gastro-intestinal nematodes in pure blood Arabian horses. *Int J Parasitol.* 2015 Mar;45(4):237-42. doi: 10.1016/j.ijpara.2014.11.003.

Ricard A., S. Danvy, Legarra A. Computation of deregressed proofs for genomic selection when own phenotypes exist with an application in French show-jumping horses. *Journal of Animal Science* 2013, 91: 1076-1085.

Barrey E, Saint-Auret G, Bonnamy B, Damas D, Boyer O, Gidrol X. Pre-microRNA and mature microRNA in human mitochondria. *PLoS One.* 2011;6(5):e20220. doi:10.1371/journal.pone.0020220.

A complete list of publications is available at: www.jouy.inra.fr/gabi

