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AgroParisTech
INSTITUT DES SCIENCES ET INDUSTRIES DU VIVANT ET DE L'ENVIRONNEMENT
PARIS INSTITUTE OF TECHNOLOGY FOR LIFE, FOOD AND ENVIRONMENTAL SCIENCES

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UMR**1313**

GiBBS

Leader
Xavier Rognon
Tatiana Zerjal

Overall Activity
At GiBBS, we lead research in genetics, bioinformatics and biostatistics methods, by associating these with real problems and applied studies performed by our team or via partnerships.

Outstanding Results
- Organization of the "Deep Learning and Genomics" seminar
- Regeneration Rosetta: a web application for "Gene expression and chromatin accessibility" (2019)
- Diversity and genetic progress in dairy cattle using ROH (2019)

Member of the **Paris-Saclay University**

université PARIS-SACLAY

Member of the **doctoral school**: **ABIES (**Agriculture, Biology, Agriculture, Environment, Health)

SAPS
Sciences Animales
PARIS SACLAY

Member of **SAPS** (Animal Sciences Paris-Saclay)

Génétique animale et biologie intégrative (GABI) Genomics, Biodiversity, Bioinformatics, Statistics Team

Scientific Questions

### 1 – Biodiversity, genetic resources and population genetics

Our research covers all fields associated with genetic diversity and genetic resources. We characterize, valorize and manage the diversity of various species, endangered species, large breeds and cryoconserved resources. Finally, we are members of an international cooperation network associated with the FAO.

Related Projects: GDivSelGen (SELGEN Metaprogramme); IMAGE & GenResBridge (Europe H2020).

2 – Biostatistics and bioinformatics

Our biostatistics and bioinformatics activities have two goals. We develop methods (Bayesian statistics, network inference, multivariate methods), software and pipelines (variant calling, annotation, structural variation detection) for the analysis of -omics data and their interpretation. We also provide support and advice in statistics and bio-informatics for biologists in or outside of GABI.

Related Projects: EnorPREG (ANSES); BioMARQ'LAIT (CASDAR); RECEPT (ApisGene)
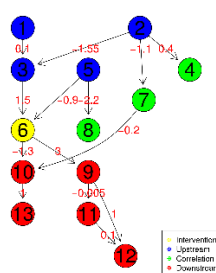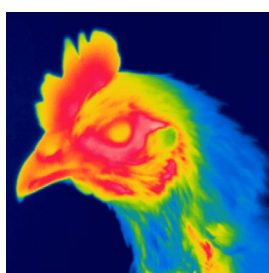
IMAGE Innovative Management of Animal Genetic Resources

📍 **Île-de-France - Jouy en Josas – Anthony Research Center**

Domaine de Vilvert
78350 Jouy en Josas

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Research Facilities:
- National databases and data collected on the field.
- Poultry experimental unit (PEAT, Nouzilly).
- Network of Biological Resource Centers (CRB- CRB-Anim, Infrastructure project).

Partnerships:
- Europe: the IMAGE cryopreservation infrastructure project; the GenResBridge project on animal, plant and forest genetic resources
- Europe, Taiwan: Studies on population genetics and genomics in poultry (chickens, quails);
- Africa, India: Studies on population genetics on local cattle, poultry, guinea fowl populations;
- USA : Biostatistics, Data integration and visualization.

3 – Animal experimentation and experimental lines

Our experiments on poultry (chickens, quails) are performed as part of long-term selection experiments for food efficiency, egg production and adaptation capacity. The team maintains a large number of chicken populations for their biological and genetic relevance. All these populations are used as models in functional genomics or population genomics studies.

Related Projects: ChickStress (ANR)

Expertise:

Population genetics and genomics; in situ and ex situ genetic resource management methods; animal experimentation; biostatistics; data analysis; bioinformatics.

Recent Publications: All our publications are accessible at: https://www6.jouy.inrae.fr/gabi

Doublet AC, et al. The impact of genomic selection on genetic diversity and genetic gain in three French dairy cattle breeds. Genet Sel Evol. 2019, 51:52.

Ducrocq V, et al. Genomics for ruminants in developing countries: from principles to practice. Front Genet. 2018, 9:251.

Flori L, et al. A genomic map of climate adaptation in Mediterranean cattle breeds. Mol Ecol. 2019, 28:1009-1029.

Hubert JN, et al. Cancer-and behavior-related genes are targeted by selection in the Tasmanian devil (Sarcophilus harrisii). PLoS One. 2018, 13:e0201838.

Leroy G, et al. Stakeholders and the management of animal genetic resources across the world. Livest Sci. 2017, 198:120-128.

Li J, et al. A missense mutation in TYRP1 causes the chocolate plumage color in chicken and alters melanosome structure. Pigment Cell Melanoma Res. 2019, 32:381-390.

Monneret G, et al. Identification of marginal causal relationships in gene networks from observational and interventional expression data. PLoS One. 2017, 12:e0171142.

Neou M, et al. Pangenomic classification of pituitary neuroendocrine tumors. Cancer Cell. 2020, 37:1-12.

Rau A,et al. Exploring drivers of gene expression in the Cancer Genome Atlas. Bioinformatics. 2018, 35:62-68.

Rau A, et al. Regeneration Rosetta: An interactive web application to explore regeneration-associated gene expression and chromatin accessibility. G3 (Bethesda). 2019, 9: 3953-3959.

Thélie A, et al. Chicken semen cryopreservation and use for the restoration of rare genetic resources. Poult Sci. 2018, 98: 447-455.

Wang S, et al. Breeding policies and management of pedigree dogs in 15 national kennel clubs. The Vet J. 2018, 234:130-135.

Zerjal T, et al. Assessment of surface temperature variation under chronic high temperature in four experimental layer chicken lines differing for heat resistance and feed efficiency traits. 10th ESPG. 2017.

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