

## Research Topic for the ParisTech/CSC PhD Program

**Subfield:** Biology (Molecular Biology, Animal Genetics, Genomics)

**ParisTech School:** AgroParisTech

**Title:** Identification and experimental validation of bovine regulatory polymorphisms

**Advisor:** Dr. Dominique Rocha, Directeur de Recherche INRA

Laboratoire Génétique Animale et Biologie Intégrative,

Equipe Génétique et Génomique Bovine

Centre INRA, Jouy-en-Josas, France

Phone: 00 33 1 34 65 24 22

Email: dominique.rocha@inra.fr

Website: www.jouy.inra.fr/gabi

### **Short description of possible research topics for a PhD:**

An increasing number of genomic loci have been associated with diseases or phenotypes of interest. More recently, genome-wide linkage mapping of gene expression levels have showed that allele-specific differences in gene expression are common and can be attributed to *cis*-acting regulatory polymorphisms. These studies often reveal regions containing several polymorphisms and distinguishing the real causative genetic variants remains difficult. It is therefore crucial to develop strategies to predict and validate functionally relevant polymorphisms to pinpoint more rapidly potential causative genetic variants underlying phenotypes of interest.

In the proposed PhD project we will develop a high-throughput approach to experimentally validate and characterise regulatory polymorphisms that potentially alter phenotypes of interest. As a proof-of-principle, we will apply this approach in an unusual model species, *Bostaurus*.

Combining whole-genome sequencing, RNA-Seq and phenotypic data available for dairy and beef animals we will first identify putative regulatory variants. We will then select some of these candidates for experimental validation using a novel *in vitro* screen. Our team is a founding member of the 1,000 Bovine Genomes Consortium and international collaborations (for *e.g.* with Australia, Canada) are planned.

The regulatory genomics approach that we will develop should allow us to discover significant genetic markers for important traits for dairy and beef cattle.

### **Required background of the student:**

Molecular biology skills are required. Experience in cell culture and bioinformatics will be an advantage.

### **A list of 5 representative publications of the group:**

Bourneuf E. *et al.* (2017). Rapid discovery of *de novo* deleterious mutations in cattle enhances the value of livestock as model species. *Sci. Rep.* **7**: 11466.

Sanchez M.P. *et al.* (2017). Within-breed and multi-breed GWAS on imputed whole-genome sequence variants reveal candidate mutations affecting milk protein composition in dairy cattle. *Genet. Sel. Evol.* **49**: 68.

Ramayo-Caldas *et al.* (2016). Multi-breed and multi-trait co-association analysis of meat tenderness and other meat quality traits in three French beef cattle breeds. *Genet. Sel. Evol.* **48**: 37.

Boitard S. *et al.* (2016). Uncovering adaptation from sequence data: Lessons from genome resequencing of four cattle breeds. *Genetics* **203**: 433-450.

Daetwyler H.D. *et al.* (2014). Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. *Nat Genet.* **46**: 858-865.