



# FAANG-Europe

## Analysis of Allele Specific Expression in Farm Animals



An increasing number of genomic loci have been associated with diseases or phenotypes of interest. However, because of the extent of linkage disequilibrium (LD), these studies often reveal linkage to a genomic region containing a large number of polymorphisms and it remains difficult to identify the real causative genetic variant. In addition, several studies have showed that allele-specific differences in gene expression are common and that these differences can be attributed to cis-acting regulatory polymorphisms, close to genes for which altered mRNA expression was detected. Identifying polymorphisms in promoter regions and in LD with polymorphisms displaying allele-specific expression (ASE) could therefore be a way to discover putative regulatory polymorphisms. The Applicant (Gabriel GUILLOCHEAU) has developed during the first year of his PhD a bioinformatics pipeline to identify Single Nucleotide Polymorphisms (SNPs) showing ASE. He has applied this pipeline to identify more than 125,000 SNPs showing allele-specific imbalance using RNA-Seq and whole-genome sequences (WGS) from cattle samples generated in his current laboratory (INRA, GABI Unit, Jouy-en-Josas, France). We would like to collaborate with Prof. David HUME and colleagues at the Roslin Institute (Edinburgh, United Kingdom) to apply this pipeline to study allele-specific imbalance in different farm animal species. Colleagues at the Roslin Institute have created gene expression atlases in different species (river buffalo, goat, sheep) and generated large amount of RNA-Seq and WGS data suitable to analyse ASE.

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