Internship proposal (Second year of master degree)

Title: Setting up and automating a procedure for the routine assessment of genetic diversity in domestic animal populations

Fields: Population genetics/genomics, bioinformatics, informatics.

Skills: Mastering of the linux environment (bash / shell) and scripts; Knowledge of basic population genetics concepts; Experience in environment managing is welcome (Conda…).

Description:

Artificial selection of domestic animals leads to the use of a small number of individuals (i.e. the best), which, through genetic drift and inbreeding, leads to limited effective populations sizes and low levels of genetic diversity. Reversely, genetic diversity is necessary for selection, whether natural or artificial, and therefore guarantees the evolution of populations to reach new breeding goals or to adapt to new environments. In addition, inbreeding can lead to the appearance of genetic defects (i.e. inbreeding depression). It is therefore necessary to control the level of genetic diversity in domesticated populations on an ongoing basis to ensure their survival and health. This is especially true for local breeds, which are often small in number and may be at risk because of subsequent increased drift and inbreeding.

Within the framework of the RAGEMO project, we propose to set up an observatory of genetic diversity based on the use of molecular tools. The aim is to offer breeders and breed associations, particularly local ones, a routine assessment of the level of diversity of their animals based on genotyping carried out on DNA chips (50K SNPs). This will be based on measurements at different scales, ranging from individual inbreeding to heterozygosity and kinship. Parentage analysis will also be performed to retrieve pedigrees when they are not available. Finally, we will propose to check the assignment of individuals to a breed using supervised classification approaches (e.g. Admixture). This question is often asked by breeders of local breeds for the management of their herd, when introducing new individuals. A large number of methods and software packages have been developed to carry out these analyses, so during this internship we will test different alternatives and choose the most relevant ones, as well as those that will allow the routine implementation of these analyses at the national level. This last point requires the implementation of an efficient workflow that could be carried out on an external infrastructure using, for example, an environment manager (e.g. Conda).

We are therefore seeking for a candidate who can handle high-density genotyping data. In addition, computer skills will be required to develop the necessary workflow for data retrieval, analysis via different software and encapsulation for large-scale production.
Duration: 6 months

Localizations:

INRAE Toulouse – Unité GenPhyse équipe Dynagen (Dynamique Evolutive des Génomes)

OR

INRAE Jouy-en-Josas – Unité GABI équipe GiBBS (Génomique, Biodiversité, Bioinformatique et Statistiques)

Start: From January to March (2023)

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