PhD position in landscape epi / genomics

<u>Title:</u> Genetic and epigenetic spatial population structure of local chicken breeds

Genetic diversity is crucial for populations to adapt to various environments. These adaptive capacities are of major importance in the light of the ongoing climate change that will drastically affect the environmental conditions, influencing biotic (feed, diseases and pathogens distribution) and abiotic components (temperature, rainfall…). Livestock, in particular, are likely to suffer from these issues and numerous studies are ongoing to improve animal adaptation to harsher environmental conditions. In this context, local chicken breeds appeared to be a valuable option to consider, as they represent a large reservoir of genetic diversity valuable for adaptation, particularly in local breeds raised in harsh production environments over a long period of time and presenting characteristics that enable them to cope with these conditions. The study of their genetic diversity and its links with environmental conditions can give some clues for the future challenges that breeding should meet to cope with climate change and set the necessary agroecological transition.

In this context, we propose to study the spatial genetic and epigenetic structure of at least 16 European local chicken breeds and the determinants of their adaptation to various environments. We will focus on both, 1) very localized breeds (ie found in a single restricted area) along a large environmental gradient in terms of climatic conditions raised in free-range conditions, and 2) more cosmopolitan breeds raised in contrasted conditions (raised free-range but bred in-house vs full free-range). This study is innovative since it will both consider the genetic and the epigenetic features of adaptation to understand the link between the environment, the genetic composition of the breed and the methylation profile. This last feature will be investigated with a recently developed approach, GBS-MeDIP, allowing for precise and high throughput epigenotyping (Rezaei et al., 2022). Genotyping will result from both already existing data (Restoux et al., 2022) and newly sampled and genotyped individuals. Links between all compartments will be investigated using classical landscape genetics tools and tailored multivariate approaches like redundancy analysis (Capblancq et al., 2021).

We will aim at functionally characterize local chicken breeds by understanding how environment shape both genetic and epigenetic diversity and how these interact with each other. This may be of particular interest in defining the appropriate unit for future conservation, in particular if we found, for example, some genotypes more prone to change their methylation profiles than others, giving clues about their potential plasticity. On the other hand, if we found distinct methylation profiles in a single breed (ie with a common genetic background), it can be useful to consider this within-breed level of diversity for future conservation purpose (Xia et al., 2016).

References:

Rezaei, S., Uffenorde, J., Gimm, O., Feizi, M. A. H., Miemczyk, S., Coutinho, L. L., ... & Pértille, F. (2022). GBS-MeDIP: A protocol for parallel identification of genetic and epigenetic variation in the same reduced fraction of genomes across individuals. STAR protocols, 3(1), 101202.

Restoux, G., Rognon, X., Vieaud, A., Guemene, D., Petitjean, F., Rouger, R., ... & Tixier-Boichard, M. (in press). Managing genetic diversity in breeding programs of small populations: the case of French local chicken breeds. Genetics, Selection and Evolution.

Capblancq, T., & Forester, B. R. (2021). Redundancy analysis: A Swiss Army Knife for landscape genomics. Methods in Ecology and Evolution, 12(12), 2298-2309.

Xia, H., Huang, W., Xiong, J., Tao, T., Zheng, X., Wei, H., ... & Luo, L. (2016). Adaptive epigenetic differentiation between upland and lowland rice ecotypes revealed by methylation-sensitive amplified polymorphism. PLoS One, 11(7), e0157810.

Skills:
Population and landscape genomics; epigenetics; data management; bioinformatics; Statistics

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Duration:
36 months

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