

## Master 2 Internship 2022-2023

**Structure:** Laboratoire d'Ecologie Alpine (UGA, USMB, CNRS)      **Director :** Stéphane Reynaud  
**Team:** Macroevolution, Evolutionary Ecology & Biodiversity Dynamics      **Team leader:** Sébastien Lavergne  
**Address :** [LECA](#), UMR 5553, Univ Grenoble Alpes

**Internship supervisor:** François Pompanon, Prof HDR  
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**Starting date :** 01/01/2023 (flexible)      **Allowance :** ~ 580 €/month  
**Potential PhD recruitment thereafter**

### Application

Send CV, Bachelor's degree results and motivation letter by e-mail to F. Pompanon before **30/10/2022**.  
Any preliminary questions are welcome.

## The role of genomic introgressions in the process of animal domestication

### Objectives

The goal is to assess the consequences of hybridization with wild species during the domestication of the goat, by identifying the introgressed genomic regions and evaluating the relative importance of introgressions in relation to selection (positive or relaxed, natural or human mediated).

### Summary

Hybridization plays an important role in species diversification and adaptation, with induced gene transfers leading to rapid genomic changes. During domestication, this process has probably played a much more important role than originally thought. Recent examples show the importance of wild-type alleles in performing essential functions such as adaptation to altitude in yak and sheep [1, 2]. However, the available information is targeted at specific breeds and adaptive or zootechnical traits, and the extent of introgression remains unknown. The candidate will analyse several hundred genomes produced by the international Vargos consortium [3] to identify the genomic regions introgressed from bezoars and ibexes, and evaluate their impact on the structuring of domestic genomes in order to clarify the selective (adaptation, improvement) and demographic (migrations, foundations) history of the goat.

[1] Qiu et al. 2012. Nat. Genet. 44:946–949. [2] Yang et al. 2018. Mol. Biol. Evol. 36:283–303. [3] Denoyelle et al. 2021. Genet Sel Evol. 53: 86

### Methods

The candidate will analyse a dataset of several hundred genomic sequences by bioinformatics approaches (whole genome approaches) and statistics (detection of selected/introgressed regions).

### 5 selected publications of the group

F.J. Alberto, F. Boyer, [...], and F. Pompanon. 2018. Convergent genomic signatures of domestication in sheep and goats. Nature Communications 9: 813.

B. Benjelloun, F. Boyer, [...], and F. Pompanon. 2019. An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. Molecular Ecology Resources, 19: 1497–1515.

L. Denoyelle, P. de Villemereuil, [...] and F. Pompanon. 2021. Genetic variations and differential DNA methylations to face contrasted climates in small ruminants: an analysis from traditionally-managed sheep and goats. Frontiers in genetics, 12: 745284.

T. Cumer, F. Boyer, and F. Pompanon. 2021. Genome-wide detection of structural variations reveals new genomic regions associated to domestication in small ruminants. Genome Biology and Evolution, 13:8.

C. Her, H.R. Rezaei, [...] and F. Pompanon. 2022. The maternal origin of domestic sheep. Animal Genetics, 53:452-459.