Genetic basis of local adaptation of Maritime pine in Corsica

Nom et contact des encadrants:

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Contexte scientifique et objectifs:

This Master subject aims to conduct research proposed in the project "Tree fitness in a changing world: making use of genomic resources to increase forest and fruit tree productivity and resilience". This project is funded by the INRAE department ECODIV, https://www.inrae.fr/en/divisions/ecodiv and developed in collaboration with Myriam Heuertz (INRAE, UMR Biogeco) and Ivan Scotti (INRAE, URFM).

Understanding the mechanisms of adaptation of trees to their environment is crucial for preserving forests in the face of global warming. Most studies on forest trees to date focus on signatures of positive selection, i.e., the role of advantageous **genetic variants** in increased tree growth and survival. In contrast to previous studies, this Master project will test the role of negative selection, i.e., whether fewer **disadvantageous genetic variants** results in better-adapted plants. The importance of negative selection has been highlighted by theoretical models but empirical evidence is scarce and constraint mostly to humans and a few model organisms. Here we extend the study of negative selection to natural populations of a forest tree.

The **Maritime pine** (*Pinus pinaster* Aiton) is an iconic conifer of great ecological and economic importance. In Corsica it has wild populations living in contrasting environments, which constitutes an ideal case study for analysing adaptation. The main goal of this Master thesis is to study the processes involved in the local adaptation of the Maritime pine across contrasting environments in Corsica. The knowledge of the dynamics of deleterious mutations will be an innovative way to inform breeding programmes *in situ* and *ex situ* conservation strategies of this important pine tree.

The candidate will make use of available data on genome-wide polymorphisms across environmental clines in *P. pinaster* in Corsica. A sample of 30 populations (c.a. 500 trees) covering the full distribution of the species onn the island has been sequenced by the host lab using gene capture methods (3 Mbp). Annotations in ggf format based on the reference genome of the close relative *P. taeda* have been also recently produced. For the same individual trees, estimates of survival, growth and phenology have been measured.

The project will be supervised locally by Rosalía Piñeiro and Santiago González-Martínez.

The core of this proposal relies on bioinformatics skills in order to estimate selection estimates from the genetic data and identify which factors drive differences across populations and environments. Software will include:

GENETREE https://github.com/cjevol/geneTree

est-SFS https://sourceforge.net/projects/est-usfs/

polyDFE https://github.com/paula-tataru/polyDFE

Informations additionnelles: For further information on the project and available genetic data, please send an email to the supervisors (we communicate fluently in French, too).

Montant de la gratification: Standard INRAE, ca. 600 EUR/month.

Exigences particulières: Interest in forests and plant evolution. The candidate will gain experience in bioinformatics analysis and population genetics of genome-wide DNA sequences.

Date limite de candidature, date de retour sur les candidatures: Applications will be examined until a suitable candidate is found.