

# PhD subject at Evo-Eco-Paleo lab

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**Thesis title: Grey-zone of speciation in the green world.**

## Context:

Speciation is a process of accumulating barriers in genomes that reduce the viability and fertility of hybrids. The higher the level of molecular divergence between two lines, the higher the number of expected barriers increases. A relationship between genome divergence and the degree of genetic isolation has recently been shown in 61 pairs of animal lineages. This null relationship between molecular divergence and reduced gene flow revealed three important patterns in speciation: 1) semi-permeable barriers are widespread; 2) different pairs of lineages can be either totally isolated or genetically connected for the same level of divergence and 3) there is a 2% divergence threshold beyond which hybridization is suppressed.

While these patterns are identified in animals, they remain unexplored in plants where the diversity of reproductive systems and dispersal capacities could influence speciation dynamics.

In the proposed thesis, we first wish to improve current methods of inference for detecting gene flow. Secondly, we wish to take advantage of the genome resequencing data available in the NCBI for a large number of plant populations. For each pair of populations, the molecular divergence as well as the probability that the partners of the pair exchange gene flow will be estimated. The overall pattern newly obtained in plants will finally be compared with the known pattern in animals. This pattern will then be dissected within plants to understand the roles of different life history traits related to the reproductive system, mode of dispersal and environment.

This topic will be of interest to profiles wishing to develop or deepen their genome simulation capabilities to compare observation with simulation. The lack of field and laboratory experience means that no unforeseen contingencies related to future containment will jeopardize the proper conduct of the project.

## Objectives:

1. Improve existing inference methods.
2. Collect available sequencing data for different pairs of plants.
3. Infer the relationship between molecular distance and genetic isolation for different clades in plants.

**Potential skills:** Population genetics; Evolutionary biology; Bioinformatics;

**Keywords:** Speciation; demographic inferences; plants; reproductive systems

## Publications of the laboratory related to the subject :

Fraïsse, C., Roux, C., Gagnaire, P.A., Romiguier, J., Faivre, N., Welch, J.J. and Bierne, N., 2018. The divergence history of European blue mussel species reconstructed from Approximate Bayesian Computation: the effects of sequencing techniques and sampling strategies. *PeerJ*, 6, p.e5198.

Roux, C., Fraïsse, C., Romiguier, J., Anciaux, Y., Galtier, N. and Bierne, N., 2016. Shedding light on the grey zone of speciation along a continuum of genomic divergence. *PLoS biology*, 14(12)

Roux, C., Fraïsse, C., Castric, V., Vekemans, X., Pogson, G.H. and Bierne, N., 2014. Can we continue to neglect genomic variation in introgression rates when inferring the history of speciation? A case study in a *M. trichopus* hybrid zone. *Journal of Evolutionary Biology*, 27(8), pp.1662-1675.