STAGE DE RECHERCHE M2 ECOLOGIE EVOLUTION GENOMIQUE
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The role of gene flow in rapid adaptation of fungal plant pathogen

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Pyrenophora teres is an important pathogen of barley. It can cause severe damages resulting in 10 to 40% of yield loss. It exists in two different forms: *P. teres* f. *maculata* and *P. teres* f. *teres*. These forms were historically shown to be different based on the symptoms they cause on the leaves: respectively, spot-like lesions and net-shaped ones. More recently, they have been identified as two distinct genetic populations. Since they can infect the same hosts and are found in the same regions of the world, such clear structure is surprising. Moreover, rare hybrids have been identified in the fields and experiments have shown that hybrids between the two forms can be as virulent as their parents in not more. This opens a wide array of questions. How do these populations stay distinct in these conditions? Can we find early-generation hybrids? Using whole genome sequences, are there loci where gene flow is present and others representing islands of divergence?

In order to answer these questions, we are offering a 6 months master project. During this internship, you will work in a highly international setting and in one of the best research institute in the world. You will gain and develop skills in computational and evolutionary biology. These include, for instance, dealing with large datasets and analyzing genomic sequences, skills which are very much in demand in the research world at the moment. You will be offered free accommodation or a 600 € monthly stipend. Finally, if you are motivated and fit in the team, a funded PhD project is designed to follow-up this internship.

Requirements:

- You must have good communication skills, both written and oral in English. This will be the main language used during the internship.
- You must have at least a Bachelor's degree in molecular biology, genetics, genomics, evolution, bioinformatics or any related field. You must be completing or already have a Master's degree in a similar field.
- You must have previous knowledge of bioinformatics, genomics or population genetic.
- You should be able to work autonomously, be curious and display interest for the following topics: evolution, genomics, bioinformatics, host-pathogen coevolution, genome evolution etc.