

## Masterarbeit (M.Sc.) / Bachelorarbeit (B.Sc.)

### Fachgebiet für Populationsgenetik

#### *Bachelor- und Masterarbeiten*

Das Fachgebiet für Populationsgenetik vergibt ab sofort eine Masterarbeit / Bachelorarbeit in Populationsgenetik in der Analyse von Pathogenen verschiedener Nutzpflanzen. Die Arbeit umfasst gängige Methoden der Populationsgenetik (wie Datenbank-Recherche, Sequenzalignments) sowie klassische und aktuelle populationsgenetische und phylogenetische Analysen.

Thema: Population genomics analysis of crop pathogens

Background: With the advance of sequencing technologies, there is abundance of recently sequenced genomes of important pathogens of crops such as *Mycosphaerella tritici* (fungus pathogen of wheat), *Phytophthora infestans* (oomycete pathogen of potato and tomato) and *Cladosporium fulvum* (fungal pathogen of tomato). These crop pathogens are interesting because they have small genomes which make analyses tractable. From an evolutionary point of view they evolve very fast and possibly violate some classic models of population genetics. We use evolutionary methods to analyse these data in order to understand how these pathogens evolve in time in response to disease management methods (such as changes in crop varieties or application of fungicides) and if classic evolutionary theory can be applied to the evolution of these genomes.

Objectives: The student will be in charge of collecting and assembling available genomic data on our local servers, implement multiple genome alignments and classic population genetics analyses. Additional relevant advanced population genetics methods using coalescent theory and/or phylogenetic methods will be performed.

Methods: Classic Linux, Perl and R codes. Sequencing database queries, filtering of Next Generation Sequencing data and quality control of SNPs, full genome alignments of multiple strains from a given species, classic population genetic analyses, phylogenetic methods, coalescent theory softwares (ms, msms).

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