



BiRT
BioResources &
Technologies Tulln



Bioinformatics

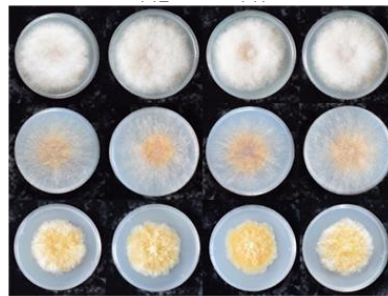
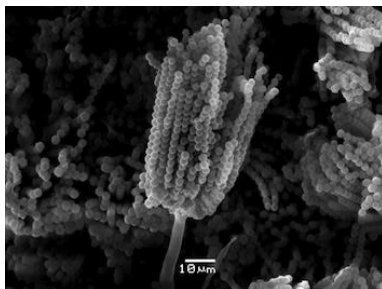
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Cooperative Master Thesis



What makes *Fusarium* aggressive?

Genetic, epigenetic and bioinformatic genomic analysis of different *Fusarium graminearum* strains with variable virulence on wheat

Description

Different strains of the wheat pathogen *Fusarium graminearum* which were cultivated in different labs around the world over several years, were re-sequenced using Illumina high throughput sequencing. Despite the fact that these strains originate from the same original type strain, their descendants show strongly differing phenotypes in respect to growth, reproduction, secondary metabolite production and plant pathogenicity. The aim of the thesis is to identify structural mutations or putative epimutations (in epigenetic regulators) that are linked to the different phenotypes and identifying putative genes or regulatory regions. The majority of work will be done computationally but some wet lab-work will also be required.

Required skills:

- Lab courses in microbiology and molecular biology, e.g. MoBi courses LMBT or Lab Course Agricultural Genetics, or equivalent
- Experience with any Linux OS
- Any skills in programming, data analysis and/or R are welcome, e.g. as introduced in the courses “Essentials for Bioinformatics Data Analysis” and “Sequencing Data Analysis”
- Interest in genetics and epigenetics of microorganisms (fungi)

The student will learn how to work on Linux systems with high throughput sequencing data, data handling, genome mapping, variance analysis, genome wide interpretation and visualization of data using free software including R. Additionally, some lab work on fungi will be done.

General information: Travel expenses to Tulln will be refunded. Extension of the student's engagement beyond the required six months Master Thesis period will be paid by a student employment contract.

Start: as soon as possible (Sept.2019)