Plant pathogenic fungi and their plant-host interactions

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Our work comprise of both genetic characterisation of fungal populations as well as studies to enhance our understanding on plant defence to different types of fungal pathogens. In East Africa we are taking part in two projects where we are trying to elucidate the genetic structures of *Cercospora* species that are attacking maize, sorghum as well as wild sorghum relatives, together with *Mycosphaerella fijiensis*, the cause of black Sigatoka on East African highland cooking banana. This fungal genetic approach has been taken as a first step which will be followed by addressing various breeding strategies in the region.

We are also working with several *Brassica* pathogens where we are partners in genetic diversity and phylogeny programmes as well as are running defence signalling and functional genetics projects on *Arabidopsis*. *Leptosphaeria maculans* and *Verticillium* species primarily *V. longisporum*, are two pathogens that have a central role in our work, but *Sclerotinia sclerotiorum, Alternaria brassicae, A. brassicicola, Botrytis cinerea* and *Peronospora parasitica* are use for comparative studies. Eleven *L. maculans* susceptible (*lms*) *Arabidopsis* mutants have been isolated which displayed differential susceptibility responses. *lms1* was crossed with Col-0 and Ws-0 and mapping data for both populations showed the highest linkage to a region on chromosome 2. Further fine-mapping is now ongoing using various recombinant inbred lines and additional mapping populations. Three genes have hitherto been cloned. To further reveal important signalling pathways in this pathosystem a massive screening of Arabidopsis mutants have taken place.

***Mycosphaerella fijiensis,* a severe fungal pathogen on banana (*Musa* spp.)**

We are working with the most serious fungal pathogen on banana, *Mycosphaerella fijiensis*. In the project we have several objectives, one of them is to define the population structure of the fungus, in order to develop an integrated disease management strategy. For the population studies we use different molecular markers, such as AFLP, CAPS and microsatellites. We are planning to apply these markers on a set of recently obtained isolates from Uganda. We are also planning to sequence part of the ITS region of selected isolates to confirm the species identity. Several student projects can be outlined within the project, see below.

1. The application of AFLP markers. Routinely, we use a set of four primer combinations. These primer combinations will be tested on our isolates. Restriction-ligation and two rounds of PCR amplification will be conducted before electrophoresis on a sequencing machine. The obtained data will then be analysed using the programs GeneScan and Genotyper.

2. The application of microsatellites and sequencing of the ITS region of selected fungal isolates. The student will start with PCR amplification of microsatellites using fluorescently labeled primers and continue with electrophoresis of the obtained PCR products on a sequencing machine. The microsatellites will be further analysed by the

softwares GeneScan and Genotyper. PCR amplification of part of the ITS region will be done in parallel. Sequencing of the ITS region will be performed directly on the obtained PCR products or via a TOPO cloning step. The obtained sequences will then be analysed using Factura, AutoAssembler and BLAST.

3. The application of CAPS markers to the isolate collection and, if possible, to a larger collection of isolates obtained from our collaboration partner in England. The CAPS markers will be produced via PCR and allele frequencies can be determined after ordinary agarose electrophoresis.

The amount of work included in the student project depends on the number of credits. This number will be decided after discussions between the student and the supervisor.