

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.

Barley lesion mimic double mutants - initial characterization"

A population (40 000 plants) of the barley mutant 3550, have been mutated and screened for changed phenotype. The mutations were induced by NaN_3 which usually give rise to small mutations, for instance a frame shift. Seven different mutants were identified, they have been screened with the fungus *Bipolaris sorokiniana* on the leaves (spot blotch) and the susceptibility evaluated. The susceptibility towards the fungus *B. sorokiniana* will also be evaluated in the roots (common root rot). Barley is one of the world's most important crops and yield loss due to this fungus is a serious threat to efficient farming. The working task will be to do a common root rot test, evaluate if the genes are recessive or dominant by classical genetics and to extract DNA for further mapping project.

Alternativa studentuppgifter

- Utvärdera mottagligheten i rötterna. Enkelt försök, plantor odlas vertikalt på ett filterpapper och conidier från svampen ingjutna i en agarbit appliceras på rötterna. Tillväxten av svampen mäts med skjutmått eller med kvantifieringsprogram.
- Ta reda på om den muterade genen är dominant, recessiv eller co-dominant. Korsningar till andra korn linjer är gjorda skall "bara" vara att så ut och räkna. Lite klassisk genetik, ganska komplicerad.

- DNA från ett litet antal av dessa korningar kan extraheras. Kan komma att användas vid eventuell senare kartering. Studenten får i alla fall öva på ett sätt att extrahera DNA.
- En annan grupp mutanter har screenats hos Svalöf Weibull AB av Morten Rasmussen. Dessa behöver också karaktäriseras.