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.

Genotypes implicated in salicylic acid, jasmonic acid, and in ethylene signalling were screened and found as resistant as the wild-type plants, demonstrating the dispensability of those pathways in *L. maculans* resistance. Camalexin, on the other hand, is only partially responsible for *L. maculans* containment in *Arabidopsis*, since *pad3-1* and *esa1* clearly showed a susceptible response while wild-type levels of camalexin were present in *lms1*. In work with additional mutants and transgenic lines we have found an abscisic acid (ABA) and callose dependency for resistance in the Arabidopsis - *Leptosphaeria maculans* system. Thus, the plant response is quite different to *L. maculans* compared to the soil-borne *V. longisporum* where for example ethylene and jasmonic acid signalling seems to play important roles. Further mutant and genetic studies are ongoing to get a more thorough understanding of defence responses to these two pathogens. In addition, since *V. longisporum* is a devastating pathogen on *Brassica* oilseed crops in Sweden, efforts are ongoing together with other disciplines at SLU, SJV and Svalöf Weibull AB to obtain a deeper understanding of this plant-fungal system, develop field scoring systems and means of control strategies. Recently, work concerning plant defence in barley to several fungal pathogens have been linked to our group. The focus here is on characterizing mutants, understand important defence factors, gene cloning and gene function.

Suggestions for students projects:

1. In silico comparisons of microarray data on defense signalling in Arabidopsis.

2. Screening of Arabidopsis mutants to Sclerotinia to reveal important defence signalling pathways.

3. Utilize crosses between Arabidopsis ecotypes for genetic mapping of resistance genes to Sclerotinia.

4. Model weather data from SMHI and disease incidence recorded by SJV in order to predict how severe disease attacks will be in future years.

5. Creation of a simple computer system to organize seed, genotypes, primers etc of material generated in the group.

6. Genetic mapping of genes are nearly always ongoing – if interested, it is only to jump in to that work

7. To make construct where we fuse promoters of interest with marker genes such as GUS and GFP and analyse transgenic material carrying such constructs.

8. Yeast-2-hybrid screens will be set up later during autumn 2005 – if interested, it is only to jump in to that work.

9. Develop and run of various real-time PCR analyses.

Discuss your wishes and interest further with Christina Dixelius:

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