Evolution of races within f.sp. lycopersici of Fusarium oxysporum

Race 1 isolates of *Fusarium oxysporum* f.sp. *lycopersici* (Fol) are characterized by the presence of *AVR1* in their genome. The product of this gene, Avr1, triggers resistance in tomato cultivars carrying resistance gene *I*. In Fol race 2 and race 3 isolates, *AVR1* is absent and hence they are virulent on tomato cultivars carrying *I*. In this study, we analyze an approximately 100 kb genomic fragment containing the *AVR1* locus of race 1 isolate Fol004, and compare it to the sequenced genome of Fol race 2 isolate 4287 (Fol4287). A genomic fragment of 31 kb containing *AVR1* was found to be missing in Fol4287. Further analysis suggests that race 2 evolved from race 1 by deletion of this 31 kb fragment due to a recombination event between two transposable elements bordering the fragment. A worldwide collection of 71 Fol isolates represents races 1, 2 and 3, all known VCGs and five different geographical origins was subjected to PCR analysis of the *AVR1* locus, including the two bordering transposable elements, avirulence genotypes. Based on phylogenetic analysis using *EF1-a*, five evolutionary lineages for Fol were identified that correlate well with VCGs. More importantly, we show that Fol races evolved in a stepwise manner within each VCG by the loss of function of avirulence genes in a number of alternative ways.

Interaction between the fungal pathogen Fusarium graminearum and the aphid Sitobion avenae in wheat ears

We investigate how the fungal pathogen *Fusarium graminearum* (Fg), known to cause Fusarium Head Blight disease and producer of deoxynivalenol (DON), and the grain aphid *Sitobion avenae* influence each other feeding both on the nutrients of grain ears. Experiments elucidated that pre-exposure of wheat ears to grain aphids five days prior to inoculation had a positive influence on the subsequent ear colonization by Fg, leading to more symptomatic spikelets and a higher fungal biomass in the ears six days after spray inoculation. Investigation of the plant responses showed an upregulation of defense genes due to Fg infection, but the defense was higher when the ears had been previously infested with aphids. Conversely, the influence of the fungus and DON on grain aphids showed that the aphids, although they do not specifically prefer Fg- or DON-contaminated ears, were able to survive on common field concentrations of DON without a loss of survival and reproduction. Interestingly, we also noticed that the grain aphid can tolerate DON much better than the pea aphid *Acyrthosiphon pisum* which has a host specificity for vegetables. In conclusion, these results indicate that grain aphids *S. avenae* can favor a subsequent Fg infection in wheat and that they are able to thrive well on common field concentrations of DON. The high sensitivity of pea aphids to DON compared to grain aphids might point to an adaptation of *S. avenae* to cope with DON in wheat ears.

Lineages in Nectriaceae: Generic status of Fusarium

The ascomycete family Nectriaceae (*Hypocreales*) includes numerous important plant and human pathogens, several of which are used extensively in industrial and commercial applications as biodegraders and biocontrol agents. Members of the family are unified by phenotypic characters such as uniloculate ascomata that are yellow, orange-red to purple, not immersed in a well-developed stroma and with phialidic asexual morphs. Presently, the generic concepts in Nectriaceae are still poorly defined, since sequence data are only now becoming available for many of these genera. To address this issue we performed a multi-gene phylogenetic analysis using partial sequences of the *act1*, *act2*, *cmdA*, *hisH3*, ITS, LSU, *rpb1*, *rpb2*, *tef1* and *tub1* gene regions for available type and authentic strains representing known genera in Nectriaceae, including several genera for which no sequence data were previously available. Supported by morphological observations, the data resolved more than 40 genera in the Nectriaceae. We re-evaluated the generic status of several genera, including the genus *Fusarium*, which were shown to represent several genera previously introduced for these fungi. Additionally, two new genera are introduced for fungi previously treated as *Fusarium*.