lates, in particular those with MDR1 h and multi-resistant phenotypes, were genetically distinct from *B. cinerea* populations that occur in vineyards. DNA sequencing indicated that the strawberry isolates indeed represented a separate clade, similar to *B. cinerea* and *B. fabae*. A PCR assay was developed that allowed reliable discrimination of 'strawberry type' Botrytis genotypes from *B. cinerea sensu stricto*. 'Strawberry type' genotypes were found to be dominating in German strawberry growing regions, but almost absent from vineyards. We raise the hypothesis that these genotypes have been selected in German strawberry fields partly because of their ability to accumulate more fungicide resistance mutations than *B. cinerea sensu stricto*.

(DPG AK Mykologie)

3) Molecular methods for fungicide resistance detection

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Fungicides resistance is a growing problem since the introduction of target specific fungicides. Determination of the baseline sensitivity of a fungal population and detection of sensitivity changes after market introduction is required for a sustainable use of fungicides. Different monitoring methods are available for detection of fungicide sensitivity of fungal isolates or population including *in vivo*, *in vitro* and molecular genetic techniques. Molecular genetic techniques show with respect to throughput, duration time and amount of pathogen material advantages over *in vivo* and *in vitro* methods. Also additional information on pathogen populations can be obtained by using quantitative methods. Before the usage of a molecular genetic assay for fungicide resistance detection the exact resistance mechanism must be determined. Verification of DNA sequences, specificity and validation with an *in vivo* or *in vitro* assay is also essential to avoid wrong results. CAPS-PCR (Cleaved Amplified Polymorphic Sequences-PCR) is a simple combination of target gene amplification and additional cleavage of the polymorphic site with a restriction enzyme. This method shows limitations with respect to quantification, detection limit and restriction enzyme limitation. From the molecular genetic assays real-time PCR show the greatest sensitivity. With the coupling of allele-specific primers with real-time PCR, a detection limit lower than 1% mutation in a wildtype population (e.g. S524T in the *cyp51*), can easily established with an additional quantification option. Different codons for the same amino acid, e.g. F129L in the cytochrome *b* of *Pyrenophora teres*, or different mutations at the same codon, e.g. P225F/L or H272Y/R in the SdhB gene of *Botryotinia fuckeliana*, would require a complex real-time PCR assay. Newer real-time PCR instruments offer the option of High-Resolution melting. Depending on sequence and instrument the application is limited to genotyping. The limitations of the allele-specific real-time PCR can be solved by pyrosequencing, which is a sequencing-by-synthesis method based on the online detection of pyrophosphate which is released during the elongation of a sequencing primer by DNA polymerase. Besides the quantification option and detection limit between 5–10%, the sequencing of short DNA fragments provides additional information on nearly related pathogen species, for example *M. nivale* and *M. majus*.

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4) *Verticillium*-monitoring of former agriculturally used land for the risk minimization of following planted woods

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On a field in Brandenburg, which was formerly used as agricultural land, there have been planted different species and subspecies of trees in the year 2010. 34 soil assays were taken from the rhizosphere in November 2011 of trees with wilt symptoms, e.g. *Acer*, *Quercus*, *Platanus*. The soilsuspension was examined in the laboratory for the existence of microsclerotia of *Verticillium dahliae*. The objective of this present thesis is to give suggestions for the selection of urban trees concerning their sensitivity to *Verticillium dahliae* and the possibilities for minimizing and fighting against the contamination.

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5) Sweets for my sweet: Carbohydrate metabolism in the parasitic and non-parasitic stage of *U. fabae*

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The mobilization, uptake and metabolism of carbohydrates from host tissue is of crucial importance for obligate biotrophic pathogens like the broad bean rust *Uromyces fabae*. In the course of our studies different genes involved in carbohydrate metabolism during the parasitic stage of *U. fabae* were identified, including an invertase, a haustorium-specific hexose transporter with high affinity for D-Glucose and D-Fructose and different enzymes catalyzing subsequent metabolic conversions of acquired carbohydrates. In contrast, only little is known about the molecular mechanisms of carbohydrate metabolism during the non-parasitic stage. Therefore our research also focused on the identification of enzymatic pathways, providing physiological energy during the germination of spores and subsequent colonization of the host plant. To identify genes involved in sugar metabolism, we use different PCR-approaches based on sequence information from other rust fungi like *Puccinia*- or *Melampsora*-species. The use of real-time PCR also enabled us to quantify the activity of different genes, involved in the metabolism of sugars at different stages of fungal growth. Our research shall provide new insights in the carbohydrate metabolism of obligate biotrophic organisms and help to understand the complex mechanisms and relationships making rust fungi such a successful group of parasites.

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