20-6 - Differenzielle Rolle der Salicylsäure bei der basalen und kultivarspezifischen Resistenz von Raps (*Brassica napus* L.) gegen *Verticillium longisporum*

Differential role of salicylic acid in basal and cultivar-related resistance of oilseed rape (Brassica napus L.) to Verticillium longisporum

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Verticillium longisporum is a soil-borne vascular pathogen causing 'Verticillium stem striping' in oilseed rape. This disease is estimated to induce significant yield losses in oilseed rape (*Brassica napus*) ranging from 10-50 % (Dunker et al. 2008). Due to the lack of effective fungicides, breeding for resistant cultivars is an essential strategy to manage this disease. The level of salicylic acid (SA), a signaling component in plant defense to pathogens, was strongly modulated in hypocotyl and stem tissues of oilseed rape by infection with *V. longisporum* (Kamble et al. 2013). Responses to *V. longisporum* infection of *Nah*G transformed oilseed rape ('Drakkar'), as well as a susceptible ('Falcon') and resistant ('SEM') *B. napus* cultivar were conducted to obtain an insight into the role of SA in the *B. napus*-*V. longisporum* pathosystem. A remarkably increased susceptibility was observed on SA-deficient transgenic *Nah*G oilseed rape plants to *V. longisporum*, which indicated that SA plays a role in basal resistance in *B. napus* against *V. longisporum*. Regarding the cultivar-related resistance, a faster increase of SA was observed in the resistant cultivar, leading to less growth of *V. longisporum* in hypocotyls and indicating that elevated SA is crucial for disease defense in the early infection phase. However, the increase of SA in later stages of infection may be at the expense of accumulation of precursors of lignin, e.g. *p*-coumaric acid, ferulic acid and sinapic acid, which are considered to play a crucial role in resistance against *V. longisporum* in the later infection phase. *PR1* and *PR2* genes, SA-dependent plant resistance marker genes, were up-regulated in both resistant and susceptible cultivars after fungal infection, however, they do not have quantitative relation to resistance.

Literature

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20-8 - Morphologische und molekulare Charakterisierung europäischer Arten des *Diaporthe*/ *Phomopsis* Komplexes, die mit Soybean Seed Decay assoziiert sind

Morphological and molecular characterization of European species of the Diaporthe/Phomopsis complex associated with Soybean Seed Decay

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The genus *Phomopsis* (teleomorph *Diaporthe*) comprises phytopathologically relevant funghi which cause diseases on a wide range of economically important crops including soybean. This group of pathogens has been reported to be involved in several soybean diseases, including *Phomopsis* Seed Decay (PSD) (*Phomopsis longicolla*), Stem Blight (*D.*

phaseolorum var. *sojae*) and Stem Canker (*D. phaseolorum* var. *caulivora* and *D. phaseolorum* var. *meridionalis*), resulting in significant yield and quality losses. Accurate species identification of DPC is critical in understanding disease epidemiology and for developing effective control measures. Also, it has been documented that MAT primers are useful in mating-type diagnosis in a wide range of *Diaporthe* and *Phomopsis* species. In this study, we focused on morphological (color and shape of colonies, existence of alpha, or beta conidia, or both, and their characteristics, production of perithecia, and size of conidia) and molecular analyses of species from DPC-damaged European soybean seeds obtained from several locations throughout Austria, France, and Germany. In addition, the European DPC isolates were classified according to their mating-type loci using Primers MAT1-1-1FW/RV and MAT1-2-1FW/RV. Surface sterilized soybean seeds were placed on APDA and incubated for 30 d at 24°C. Putative isolates of the DPC were purified using the single spore method. Genomic DNA was extracted from mycelium of each single-spore isolate. Thirty-two strains of Diaporthe and Phomopsis were isolated and phylogenetic relationships were determined using the translation elongation factor 1-alpha (TEF1) and nuclear ribosomal DNA internal transcribed spacers (ITS) sequences. By combining morphological and molecular data, four species including *Phomopsis longicolla*, *Phomopsis* sp., *Diaporthe caulivora* and *Diaporthe eres* could be distinguished on soybean seeds. Also, results from mating-type experiments revealed that MAT primers used in this study allowed mating-type diagnosis of the 28 isolates. Further studies for controlling these pathogens using biological control agents are currently in progress.

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