

44-2 - Identification and characterization of three putative compatibility factor genes involved in the plant – *Verticillium* interaction

Identifikation und Charakterisierung drei putativer Kompatibilitätsfaktoren in der Pflanze – Verticillium Interaktion

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The hemibiotrophic soilborne fungus *Verticillium longisporum* represents one of the important pathogenic fungi in oilseed rape (*Brassica napus*) cultivation. So far, only minor genetic variation in resistance to the fungus could be found in oilseed rape germplasm. To develop resistance against the fungus in oilseed rape, we followed a strategy based on the molecular understanding of plant-fungus interaction. In this way, a set of genes were identified from oilseed rape genome, which were highly upregulated at early infection stages in a compatible plant-fungus interaction. Arabidopsis knock-out mutants of the genes exhibited strongly reduced susceptibility to the fungal infection, suggesting their crucial role in the plant-fungus interaction. Here, we report recent results of molecular and functional characterization of three putative compatibility factor genes and their possible role in the modulation of a compatible plant-fungus interaction in Arabidopsis as well as in oilseed rape plants.

44-3 - Impact of cultivar resistance to *Verticillium longisporum* on drought stress tolerance of winter oilseed rape (*Brassica napus*)

*Einfluss der Sortenresistenz gegen Verticillium longisporum auf die Trockenstresstoleranz von Winter-
raps (Brassica napus)*

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Verticillium longisporum (VL) is a vascular pathogen of crucifers with a potential to cause significant yield losses in oilseed rape (OSR). In resistant, VL infected OSR genotypes substantial amounts of vascular occlusions which obstruct xylem vessels have been detected. This mechanism of resistance to the pathogen may however alter the rate of water and nutrient transport and consequently plant response to drought stress. To investigate whether genotypic VL resistance is associated with a reduced drought tolerance, we studied drought resistance of VL-resistant and susceptible winter OSR genotypes under infection with the xylem-colonizing pathogen VL. Analysis of disease parameters (net AUDPC, stunting and fungal biomass by qPCR) showed a significantly lower rate and level of disease development in the resistant genotype SEM across all watering regimes. Likewise, regardless of the water supply at different field capacity levels, high disease severity and stunting effects were observed in the susceptible cultivar Falcon. Furthermore, the amount of fungal DNA was up to 31fold in Falcon as compared to SEM. qPCR results showed that levels of fungal DNA were positively correlated with the intensity of drought stress. At 49 DPI, the respective average fungal DNA in dry hypocotyl tissue at 100, 60, and 30% field capacity was 27.1, 29.0 and 36.0 ng/g in SEM and 839.1, 1,032.4 and 1,096.4 ng/g in Falcon, indicating a more pronounced colonization of plant tissues with VL during drought stress particularly on susceptible *B. napus* varieties. Significant changes in physiological parameters (gas exchange, relative water content, proline content and water use efficiency) and up-regulation of drought stress marker genes confirmed the reaction of both genotypes to drought stress. On the other hand, neither VL alone nor its interaction with drought or the genotype had any significant effect on these physio-