Genetic analysis of phenylpropanoid metabolites associated with resistance against *Verticillium longisporum* in *Brassica napus*

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Verticillium longisporum is causing one of the most important diseases of winter oilseed rape in northern Europe. Long-term control of *V. longisporum* can only be achieved by using cultivars exhibiting effective resistance. In general, resistance to *V. longisporum* is a quantitatively inherited trait. A major quantitative trait locus (QTL) for resistance was mapped in a doubled haploid (DH) rapeseed population on chromosome C5 and a minor QTL on chromosome C1. Resistance has been found to be correlated with the concentration of soluble and cell-wall bound phenolics in the hypocotyl of the *B. napus* mapping population after infection. Especially, single peaks from HPLC analysis of the cell wall-bound phenolics fraction explained up to 60% of the phenotypic variation of the resistance reaction. The QTL for these compounds also co-localize with the major QTL for resistance on chromosome C5. The lignin monomer composition was studied by GC/MS in 81 DH lines of the mapping population and revealed a significant increase in the G/S lignin monomer ratio in the hypocotyls of susceptible, but not in resistant plants after infection.

The variation in G/S lignin monomer ratio and susceptibility showed a Pearson correlation of 0.54 after *V. longisporum* inoculation. Changes in the lignin composition have also been observed in studies using a limited number of genotypes for different host-pathogen-system interactions including *V. dahliae* interaction with resistant tomato and pepper genotypes where lignification and reinforcement of cell walls was speculated to be involved in resistance reactions of plants against fungal infections. However, in contrast to these studies we found an increase of G/S lignin ratio only in susceptible, but not in resistant genotypes suggesting that these changes are rather indirect effects of successful fungal invasion of the hypocotyl tissue and not directly causally linked to resistance. To evaluate the relevance and contribution of phenylpropanoid metabolites to resistance against *V. longisporum* in rapeseed and link phenotypic to genotypic information we are performing a GC/MS analysis in a mapping population of 100 DH lines. In addition, to improve resolution of genetic mapping for these metabolomic traits and resistance a high-density genetic map is currently under development.