

Isolates from wheat predominantly clustered with isolates from finger millet and ryegrass in genetic distance analysis suggesting evolutionary relationship.

Twenty-seven wheat lines were assessed for resistance to wheat blast in a standardized screening assay in the greenhouse. Inoculations were performed on the leaves and ears in separate experiments to test the organ-specific responses. Leaf infection was not correlated with ear symptoms. Upon ear inoculation at flowering stages, cultivar MILAN showed the highest resistance to *M. grisea*, but this was associated with a relatively high susceptibility to *Fusarium* head blight (FHB, *Fusarium graminearum*). Conversely, SUMAI 3 and GONDO-CBRD were susceptible for *M. grisea*, but relatively more resistant to *F. graminearum*. Differential interactions of *M. grisea* and *F. graminearum* with these three wheat cultivars were studied on ears by confocal laser scanning microscopy (CLSM) at different time points of disease development. At 24 h post-inoculation (hpi), hyphae of both pathogens were observed in anthers, some following the filament towards the ovary. At 48 hpi, the tips of palea and stigma were uniformly invaded, while only *F. graminearum* showed initial infection of the rachilla. Colonization with both pathogens on anthers, filament, stigma and palea was similar on the three wheat cultivars. A hypothesis is that differences in resistance of the three cultivars are expressed in more interior tissues in the spikelets. In the resistant MILAN/*M. grisea* interaction a strong accumulation of H₂O₂ within 48 h post-inoculation (hpi) was detected in the palea, which was not found in the two susceptible cultivars. The histochemical localization of H₂O₂ in the palea tissue indicates the involvement of active oxygen species (AOS) in the resistance response of wheat plants against *M. grisea*. This study indicates the existence of resistance in wheat lines specific for wheat blast caused by *M. grisea*, with no cross-reactivity to another important ear pathogen, *F. graminearum* causing *fusarium* head blight.

138-Kamble, A.¹; Koopmann, B.²; von Tiedemann, A.²

¹ University of Pune, India

² Georg-August-Universität Göttingen

Comparative analysis of defense responses in *B. napus* against *V. longisporum* during host and chemically induced resistance

Verticillium longisporum is a soilborne vascular fungal pathogen of oilseed rape and poses a major threat to its cultivation. Lignification of cell walls is a common defense response and has been shown to also enhance resistance against vascular pathogens. The incorporation of phenylpropanoid derived monolignols in lignin and lignin like polymers following infection results in strengthening of cell walls and improves structural rigidity thus limiting the degradation of cell walls by exogenous enzymes and also limits diffusion of enzymes and toxins from the fungus to the host. In the present investigation, we compared the expression of resistance in respect to the phenylpropanoid metabolism in a susceptible ('Falcon') and a resistant genotype (SEM 05-500256) of *Brassica napus*.

Our earlier work on β aminobutyric acid (BABA) induced resistance in *B. napus* against *V. longisporum* demonstrated early and significant increase in phenylalanine ammonia lyase (PAL) activity in hypocotyls suggesting higher synthesis and accumulation of phenylpropanoids. This increase in PAL activity was found to correlate with large numbers of phenol storing cells surrounding the vessels. Similar kind of defense responses were also reported in case of genotypic resistance in *B. napus* against *V. longisporum* wherein resistance was correlated with higher levels of soluble and cell wall bound phenolics, phenol storing cells and lignin formation in hypocotyls. We also observed a strong and significant increase in salicylic acid (SA) during the susceptible interaction of *B. napus* against *V. longisporum* which correlated with a higher amount of pathogen DNA found in the hypocotyls. These results suggested the possibility of pathogen mediated diversion of the cinnamic acid pool (a common precursor for both SA and lignin biosynthesis) towards SA, to the expense of a rapid and effective lignin biosynthesis hence weakening the plant defense response against fungal invasion. Our present study is based on this hypothesis and we are investigating the role of SA as a negative regulator of resistance in *B. napus* response to *V. longisporum*. Work is in progress to examine the level of salicylic acid, qualitative and quantitative profiling of soluble and wall bound phenolic compounds using HPLC, activities of enzymes of the phenylpropanoid pathway, such as PAL, peroxidase, cinnamate 4-hydroxylase and a histochemical analysis to get more insight into the phenolic profiling, alterations in the chemical composition and regulation of lignin biosynthesis.