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P07

PATHOLOGY SESSION - Oral presentation

Detection of *Leptosphaeria maculans* races on winter oilseed rape in different geographic regions of Germany and efficacy of monogenic resistance genes under varying temperatures

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Abstract: Blackleg disease, caused by *Leptosphaeria maculans* is one of the most important fungal diseases in oilseed rape production word-wide (Fitt et al. 2006). Genetic resistance is an important tool to control this disease. Seedling resistance is conferred by single major genes. Due to its sexual propagation, *L. maculans* isolates evolve rapidly from avirulent to virulent strains on cultivars harbouring major resistance genes. Therefore, resistance of oilseed rape against *L. maculans* conferred only by major resistance genes was often overcome and led to severe yield losses in the past in France and Australia (Rouxel et al. 2003; Sprague et al. 2006). Therefore, we cultivated two oilseed rape (OSR) cultivars in 4 different geographical regions in northern Germany in the growing seasons 2011/12 and 2012/13: i) one cultivar harboring no known major gene against *L. maculans* (Lirabon) and ii) one resistant cultivar (Exocet), harboring the major gene *Rlm7*. In autumn and spring we collected true leaves with typical Phoma lesions to gain isolates of *L. maculans*. Isolates obtained from leaves of Lirabon were considered to represent the whole range of virulent isolates in a region. Single spore isolates were tested on a French differential set consisting of 7 OSR genotypes with known major resistance genes for the presence of the avirulence genes *Avr1, 2, 3, 4, 7* and *9* in a cotyledon inoculation test. Thereby, the frequency of virulent isolates in a region was determined. Isolates gained from Exocet were considered to represent the frequency of *Rlm7* resistance breaking isolates, which was tested in the cotyledon inoculation test with a *Rlm7* harboring cultivar (Caiman). The frequency of virulent isolates on *Rlm1, 2, 3, 4* and *9* was very high with over 80%. The frequency of virulent isolates on *Rlm7* was very low (< 5%). We assume that choice of cultivars with different compliment of resistance genes leads to a different spectrum of virulent isolates per region. Furthermore we tested the efficacy of major resistance genes against *L. maculans* under varying temperatures for cotyledons and stems in controlled-environment experiments. Therefore, the resistant cultivars Caiman with *Rlm7* resistance and Uluru with *LepR3* resistance as well as Lirabon as susceptible control were used. For each resistant cultivar an avirulent and a virulent *L .maculans* isolate were selected. Cotyledon resistance was tested with spore suspension, whereas adult resistance was tested at the stem base by inoculation with a mycelium plug. The plant-pathogen interactions were examined at different temperature regimes. Incompatible interactions found on cotyledons of Uluru turned to be compatible, whereas only an increase of *L. maculans* DNA was found for cotyledons of Caiman at higher temperatures (≥27 °C). Major gene resistance actively reduced disease severity in stem tissue. Especially Caiman was strongly dependent on its *Rlm7* resistance gene, whereas resistance of Uluru relied more on quantitative resistance. High temperature treatment did not change incompatibility into compatibility at stem bases.

Key words: *Leptosphaeria maculans*, race distribution, efficacy, major resistance genes, Rlm7, LepR3

References:

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