

PARTIAL RESULTS REGARDING IDENTIFICATION OF A RESISTANCE SOURCE OF OILSEED RAPE AT *Verticillium longisporum* PATHOGEN

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Abstract

Brassica napus is considered to be one of world's important oil crops which provides not only the edible oil for human consumption but also the protein rich feed for animals and raw materials for industrial processes such as biodiesel production. The aim of our study was to identify some new resistant sources of oilseed rape with resistance to *Verticillium longisporum* disease. For this as biological material we used 65 oilseed rape cultivars. To obtain the phenotypic data regarding the *V. longisporum* resistance, all cultivars were artificially inoculated with the pathogen in laboratory. After the artificial infection, it was observed a large variation of resistance to *V. longisporum* among the tested cultivars. We obtained 15 cultivars which showed a higher resistance to the pathogen than the control variant Express which is tolerant to the disease. For the molecular studies, we used 50 SSR markers which were chosen from previous studies. Using the genotypic data obtained with the SSR analysis and the phenotypic data represented by the AUDPC values resulted after the artificial infection of the each cultivar, we identified a QTL for resistance to *V. longisporum*. The QTL was localized on the first chromosome (LG group 1) with a LOD value of 3,4 and a phenotypic variation (R^2) of 11,4%. The results from this study are the first step in the investigation of the genetic basis of currently available resistance sources.

Key words: oil seed rape, *Verticillium longisporum*, resistance