

Genetic determinants of rapeseed (*Brassica napus* L.) resistance against *Plasmodiophora brassicae* Wor. infection.

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## **Abstract**

*Brassica napus* is one of the world's most important oil crops. Its cultivation faces challenges from several significant *Brassica* diseases, including clubroot, which accounts for an estimated 10% yield loss worldwide. Clubroot is caused by the soil-borne obligate endobiotrophic rhizarian *Plasmodiophora brassicae*. This pathogen stimulates the outgrowth of the infected roots, leading to the development of prominent galls. The affected plants exhibit systemic symptoms, leading to non-optimal flowering and premature senescence.

Due to the high longevity and durability of *P. brassicae* resting spores, controlling the disease proves challenging. Consequently, breeding resistant varieties, which relies on the identification of the genetic factors involved in the response to infection, remains one of the most effective control strategies.

In this study, a clubroot resistance locus from *B. napus* cultivar 'Tosca' is mapped to a genomic region encompassing approximately 100 kbp. The local sequence polymorphism and differential gene expression patterns between clubroot-resistant and susceptible lines are evaluated. Based on the results, the duplicated, highly polymorphic TNL-family gene is designated for functional studies. The ectopic expression of the coding regions of the TNL genes in *Arabidopsis thaliana* strongly supports the hypothesis of their involvement in disease resistance.

Furthermore, a comparative analysis of the resistance locus structure among a broader panel of Brassicaceae genomes is conducted. The results highlight the high evolutionary dynamics of the region, particularly in the case of the TNL gene.

The results of this study provide valuable resources for direct incorporation into resistance breeding schemes and open up many new possibilities for further basic and applicational research.