

FINE MAPPING OF A LEAF RUST RESISTANCE GENE DERIVED FROM EMMER WHEAT (TRITICUM TURGIDUM SSP. DICOCCUM)

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Leaf rust is a fungal disease responsible for yield losses in many crops, including wheat. Cultivation of resistant varieties and therefore the identification of new resistant genes represent the most efficient strategies to improve current crop.

T. turgidum ssp. *dicoccum*, one of the earliest domesticated wheats derived from wild emmer, acts as a donor of genes for resistance to pathogens. The *T. dicoccum* accession MG5323 was identified as conferring a good level of resistance to different pathogens. A fine mapping strategy was started to identify the gene involved in the leaf rust resistance identified on the short arm of chromosomes 1B. Firstly, molecular markers were analysed to reduce the genetic interval. Secondly, the expression analysis of the putative candidate genes selected on Svevo genome was conducted both in silico and in vivo. Thirdly, the available MG5323 genome sequence was analysed and compared with the tetraploid genomes available, Zavitan (*T. dicoccoides*) and Svevo (*T. durum*). Finally, the presence of conserved domains and the effect of the polymorphisms were also evaluated. Our results allow us to narrow down the physical interval, to reduce the number of candidate genes and to highlight the occurrence of inversion and rearrangement in the tetraploid genomes. Further investigations on the MG5323 mutant population will provide the foundation to clone these genes in *T. dicoccum*.