

IDENTIFICATION AND MAPPING OF A NEW LEAF RUST RESISTANCE GENE DERIVED FROM *TRITICUM TURGIDUM* VAR. *DICOCCUM*

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Leaf rust, caused by the fungus *Puccinia triticina* (formerly *P. recondita* f. sp. *tritici*) is one of the most important diseases for wheat, causing significant yield losses annually in many wheat growing regions of the world. The utilization of resistance genes is the most viable and economical strategy to minimize the yield losses.

Nevertheless the source of resistance gene is rather limited in durum wheat genetic background, a situation that requires the search of new resistance genes in related wheats.

In order to investigate the genetic basis of leaf rust resistance, we are currently developing a genetic linkage map on a RILs population (122 F9 lines) derived from a cross between the susceptible durum wheat cultivar Latino and the resistant accession MG5323 of *T. turgidum* var. *dicoccum*.

The phenotypic characterization (Infection Type and Relative Disease Severity) of the RIL population by means of artificial inoculation of two *P. triticina* (Jerez 05 and 16081-1) isolates was performed in greenhouse experiment carried out in Italy and Spain.

More than 400 microsatellite markers with known position and well distributed on the whole genome were tested on parents of the segregant population, and 79% of the markers analysed were found polymorphic.

A genetic linkage map for QTL analysis was developed using of 300 SSR markers distributed within 14 linkage group and spanned greater than 2000 cM.

The QTL analysis carried out using the disease response data (IT and RDS scoring) of all the RILs allowed us uncover one major QTL localized in a genomic region where no previously identified leaf rust resistance genes (Lr genes) have been positioned. This major QTL was mapped on the short arm of 1B chromosomes and SSR markers strictly associated were identified. This result therefore suggests the identification of a new resistance gene to leaf rust in the *durum* wheat genetic background.