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Poster Abstract – A.08

IDENTIFICATION OF A MAJOR QTL ON CHROMOSOME ARM 7BL FOR DURABLE LEAF RUST RESISTANCE IN DURUM WHEAT

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Leaf rust is a threat to durum wheat (*Triticum turgidum* L. var. *durum*) production. However, genetic and molecular mapping studies aimed at characterizing leaf rust resistance genes in durum wheat have been undertaken only recently.

In this research, we targeted the genetics of the resistance to leaf rust (*Puccinia triticina* Eriks.) conferred by Creso, an Italian durum wheat cultivar released in 1974 from CIMMYT's and Italian materials. This resistance can be considered as durable having been effective since 1975 in a wide range of environments.

The genetic basis of leaf rust resistance was studied using 176 recombinant inbred lines (RILs) from Colosseo x Lloyd and 62 advanced lines derived from multiple crosses involving Creso or its resistant derivatives in their pedigree. RILs were tested under field conditions with a mixture of Italian leaf rust isolates and at the seedling stage with single isolates. In the field experiment, the percentage of infected leaf area was evaluated at three stages through the disease developmental cycle and the area under disease progress curve (AUDPC) was then calculated. A major QTL (*QLr.ubo-7B.2*) for leaf rust resistance at both adult (field conditions) and seedling stages was identified on the distal region of chr. 7BL. In the field, the QTL showed an R^2 of 72.9% and a peak LOD score of 44.5 for AUDPC. The presence of this major QTL was validated by a linkage disequilibrium-based test using field data of advanced lines from multiple crosses. The association results confirmed the QTL location between *Xbarc340.2* and *Xgwm344.2*, with the corresponding AUDPC R^2 values ranging from ca. 10 to ca. 35% depending on the year. *QLr.ubo-7B.2* maps in a gene-dense region (7BL10-0.78-1.00) known to carry several genes/QTLs in wheat and barley for resistance to rusts and other major cereal fungal diseases, including *Lr14a* and *Lr19*, two major candidates for this gene. The availability of precise genetic stocks for the above genes/QTLs in a homogeneous genetic background will facilitate gene postulation studies and, eventually, positional cloning of new resistance genes.