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FINE MAPPING OF THE LEAF RUST RESISTANT *Lr14* LOCUS IN DURUM WHEAT

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Leaf rust (Puccinia triticina Eriks.), durum wheat (Triticum durum Desf.), Lr14, synteny, association mapping

Leaf rust (*Puccinia triticina* Eriks. & Henn.) is a main disease affecting durum wheat production in the Mediterranean region. Resistance to this fungal pathogen is a main objective for durum wheat breeding. Improving the resistance to leaf rust can be effectively accomplished through mapping of the resistance loci from valuable sources and using marker-assisted selection (MAS) in breeding programs. The leaf rust resistant allele *Lr14-Creso* from durum wheat cv. Creso and its derivative Colosseo is one of the most important leaf rust resistance sources present in the modern durum wheat germplasm and it has been located in the distal portion of chr. 7BL (Maccaferri et al., 2008. TAG 117: 1225-1240; Marone et al., 2008. Mol Breed 24: 25-39). The identification of several closely linked SSR markers provides the necessary molecular tools to conduct MAS. Our target is to fine map *Lr14-Creso*. The RIL Colosseo x Lloyd population (176 lines) has been used to enrich the QTL region with new molecular markers derived from wheat ESTs. Phenotypic data were collected in the field and also at the seedling stage. A high heritability of the disease response was observed in both cases ($h^2 > 0.80$). The population allowed for mapping the locus at a good resolution level (5 cM).

A set of ca. 100 recombinant $BC_2F_{3:4}$ lines have been developed to fine mapping the QTL. Additional BC_3 lines have been developed in order to confirm and to further study the phenotypic effects of *Lr14-Creso***.** New SSRs and 13 EST-STS markers (UBW and MAG markers) were developed and mapped within an interval of 14 cM that includes the QTL peak.

The EST-STS markers have been obtained by exploiting the conserved colinearity between the most distal portions of rice chr. 6, *Brachypodium* chr. 1 and wheat chr. 7BL. Using the coding sequence of the rice and *Brachypodium* colinear genes, the corresponding wheat orthologs were retrieved using PpETS software. Specific PCR assays (ca. 1 kb) with the primers targeting the intron/exon boundaries of the genes were designed using Primer3, amplified on the genomic DNA of the parents Colosseo and Lloyd and the amplicons cloned in pGEM®-T Easy Vector. Eight clones for each parent were sequenced. Sequencing of the amplicons allowed for the identification of the SNPs differentiating the two homeologous copies of each gene (genome-specific SNPs) as well as the varietal-SNPs between Colosseo and Lloyd. These SNPs were then used to develop markers that, at the same time, were 7B specific and that were polymorphic between the two parents. The detailed synteny analysis and the map of the region including the newly developed markers will be reported. The results are supported by an independent association mapping study

carried out using a panel of 164 elite accessions (cultivars and advanced breeding lines). This allowed us to validate the presence of *Lr14* and to further improve the mapping resolution. The newly developed *UBW* markers tagging the *Lr14-Creso* allele are presently used in MAS activities.