more polymorphic SSR markers, the target interval was reduced from 40 cM to 8 cM. To further enrich the linkage map we explore the syntenic information of the reference genomes of *Brachypodium* and wheat.

## *Poster 61. Fine mapping of the leaf rust resistant Lr14 locus in durum wheat.*

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Leaf rust is a main disease that affects durum wheat production. Resistance to this fungal pathogen is therefore a main objective for durum wheat breeding. The leaf rust resistant allele *Lr14*-Creso from the durum wheat cultivar Creso and its derivative Colosseo is one of the most important leaf rust resistance sources present in the modern durum germplasm, and it has been located in the distal portion of chromosome 7BL (Maccaferri et al. 2008. Theor Appl Genet 91:731-738), with the identification of linked SSR markers (gwm146 and gwm344) suitable for marker-assisted selection. Our target is to fine map and eventually clone *Lr14*-Creso. To this end, a set of ~100 recombinant $BC_2F_{3:4}$ isolines were developed. Additional $BC_3$ isolines were developed in order to confirm and to further study the phenotypic effects of *Lr14*-Creso. New SSRs and 13 conserved orthologous sequence (COS-SNP) derived markers (UBW) were developed and mapped within an interval of 8 cM that includes the QTL peak. The COS-SNP markers have been obtained by exploiting the conserved collinearity between the most distal portions of rice chromosome 6, *Brachypodium* chromosome 1, and wheat chromosome arm 7BL. Using the coding sequence of the rice and *Brachypodium* collinear genes, the corresponding wheat orthologs were retrieved, specific PCR assays (~1 kb) targeting the intron/exon boundaries of the genes were designed, amplified on the genomic DNA of the parents Colosseo and Lloyd and the amplicons cloned in pGEM®-T Easy Vector. 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 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 183 elite accessions (Maccaferri et al. 2010. Mol Breed 26:189-228), which allowed us to validate the presence of *Lr14* and to further improve mapping resolution.

## *Poster 62. Marker development for the wheat leaf rust resistance gene Lr16 using a comparative genomic approach.*

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Wheat leaf rust, caused by the fungus *Puccinia triticina*, is one of the serious diseases of wheat worldwide. *Lr16* is a widely deployed leaf rust resistance gene that is effective against the North American *P. triticina* population when in combination with *Lr34*. Previous studies mapped this gene on the distal end of wheat chromosome bin of 2BS (fraction length (FL) 0.84–1.00). In the current work, we integrated a flanking marker and additional markers that are within a close proximity to the gene. Orthologous conserved markers were developed from bin-mapped expressed sequence tags (ESTs) and from ESTs identified based on colinearity with the *Brachypodium* genome. ESTs with orthologous genes in these collinear regions were used to develop new conserved markers for saturating the region. Seventy-three pairs of primers were developed, and ~30% showed polymorphism in the segregating RIL/DH populations. Efforts are now underway to integrate these polymorphic markers into genetic maps.