

THOUSAND KERNEL WEIGHT AND NUMBER OF STERILE SPIKELETS IN DURUM WHEAT: TWO SIDES OF THE SAME COIN?

RICCI A., MACCAFERRI M., STEFANELLI S., COLALONGO C., SANGUINETI M.C.,
TUBEROSA R.

Dept of Agroenvironmental Science and Technology (DiSTA), University of Bologna, Viale Fanin
44, 40127 Bologna (Italy)

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Association mapping was used to dissect the genetic basis of grain yield (GY) in a collection of 189 elite durum wheat accessions evaluated during 2004 and 2005 in 15 Mediterranean environments highly different for GY. Association mapping results evidenced the Colosseo-like haplotype as the favourable one for the main QTL for trait thousand kernel weight (TKW) on chr. 5A. (Maccaferri M. et al. 2011 Journal Experimental Botany. 62: 409-438). A population of 176 RILs from the cross Colosseo (C) x Lloyd (L) was used to obtain a linkage map based on 162 SSR and 392 DaRT markers for a total length of 2,022 cM. The CxL RIL population was evaluated for TKW in four field trials (2006 fall sowing, 2009 both fall and spring sowing, 2010 fall sowing). Moreover, in 2010 the CxL RIL population has been tested for several traits related to GY, including the number of sterile spikelets (St-Spk). Phenotypic data were analyzed by composite interval mapping (CIM) and QTLs were identified for both traits in the proximal portion of chr. 5AS (deletion bin 5AS1-0.40). Seven of the 120 SSRs tested between the parents of the mapping population, have been mapped in the 5AS region and the QTL analysis showed the presence of two QTLs for TKW and St-Spk with similar LOD profiles and QTL peak position. The region spans an interval of 12 cM. Therefore, there is the possibility that both TKW and St-Spk are under the genetic control of the same locus (pleiotropy). *QTKw.ubo-5A* may represent a locus controlling spikelet fertility during differentiation rather than a locus for grain weight *per se*. This needs to be confirmed with more detailed genetic materials and experiments. With regard to the genetic materials both BC₃ progenies and congenic lines derived from heterogeneous inbred families were obtained through MAS on both parental cvs. Colosseo and Lloyd.

Moreover, SNP markers from conserved orthologous regions (COS-SNP) were developed through synteny-based analysis by exploiting the conserved colinearity between *O. sativa* chr. 12-*Brachypodium* chr. 4 and *O. sativa* chr. 9-*Brachypodium* chr. 4, respectively. SNP discovery between Colosseo and Lloyd showed low variability (7%) in the peri-centromeric region of chr. 5AS. Finally, we are using the “sequence capture” method in combination with “next generation sequencing” in the attempt to discover COS-SNP markers from at least 200 genes selected based on the collinearity with the target region.