

## **A CONSENSUS MAP FOR QUALITY TRAITS IN DURUM WHEAT BASED ON GENOME-WIDE ASSOCIATION STUDIES AND DETECTION OF ORTHO-META QTL ACROSS CEREAL SPECIES**

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Since crop quality is a complex trait, either related to end-use properties or to nutritional content and regulated by different compounds, the genetic determination of quality traits is rather complicated. Due to the high environmental influence on crop quality traits, the search for genes related to them is more complex such as the transfer of these characters, despite the presence of novel genomic tools.

GWAS detects the association between genotype and trait of interest using conserved linkage disequilibrium (LD) present in a selected panel of accessions. Recently, association or LD mapping, utilizing genome-wide markers, has been adopted in wheat because of two main advantages: 1) association mapping does not require the cost and time associated with the population and genetic map development, and 2) GWAS provides high mapping resolution as it efficiently uses the multiple historical crossover events occurred in the diverse association panel used.

The present work focused on the identification of durum wheat QTL hotspots from a collection of genome-wide association studies, for quality traits, such as grain protein content and composition, yellow color, fiber, grain microelement content (iron, magnesium, potassium, selenium, sulfur, calcium, cadmium), kernel vitreousness, semolina, and dough quality test. For the first time a total of 10 GWAS studies, comprising 395 marker-trait associations (MTA) on 57 quality traits, with more than 1,500 genotypes from 9 association panels, were used to investigate consensus QTL hotspots

representative of a wide durum wheat genetic variation. MTA were found distributed on all the A and B genomes chromosomes with minimum number of MTA observed on chromosome 5B (15) and a maximum of 45 on chromosome 7A, with an average of 28 MTA per chromosome. The MTA were equally distributed on A (48%) and B (52%) genomes and allowed the identification of 94 QTL hotspots. Synteny maps for QTL were also performed in *Zea mays*, *Brachypodium*, and *Oryza sativa*, and candidate gene identification allowed the association of genes involved in biological processes playing a major role in the control of quality traits.