

QTL CLUSTER FOR GRAIN SIZE AND PHENOLOGY TRAITS REVEAL CANDIDATE GENES INVOLVED IN GRAIN YIELD OF DURUM WHEAT

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Grain yield (YLD) reflects the combination of thousand kernels weight (TKW) and grain number per area. TKW is mainly and tightly underpinned by grain length (GL), grain width (GW) and area (AREA). YLD can be maximized by growing varieties which heading time (HT) allows the crop to avoid stresses during grain-filling phase. HD is a critical stage that marks the transition into the grain-filling period, during which grain weight is defined.

In the present study, a high-density genetic linkage map based on iSelect 90K SNP markers was realized using the durum wheat Liberdur x Anco Marzio recombinant inbred line (RIL) population that was evaluated to detect QTL and candidate genes controlling YLD, GL, GW, AREA, HT and plant height (PH).

The two parents showed significant differences for HT, PH, AREA in all three seasons, and for TKW, GL and GW in two trials. The parental Anco Marzio has generally larger grains compared to those of Liberdur, which were narrower. High heritability values, exceeding 0.55, were found for HT, GL and AREA while TKW heritability values ranged from 0.45 to 0.72.

The genetic map consists of 5,134 SNP markers that were grouped in 21 linkage groups. A total of 2,085 markers were localized on the A genome, whereas 3,049 were mapped on the B genome. The entire map covered 2,207.9 cM with an average chromosome length of 157.7 cM.

A total of 30 putative QTL were detected on ten chromosomes in the RIL mapping population. Among them, there were 9 QTL for TKW (2 QTL), GL, GW (2 QTL), AREA, HT and PH (2 QTL), distributed on 1B, 2A, 3A and 6B chromosomes, which were detected in at least two years and across years. Out of the 30 detected QTL, ten were co-located in two different QTL cluster regions of chromosome 2A. The first region included 6 QTL in the genetic interval between 34.4 and 36.4 cM, while the second comprised 4 QTL in the interval between 87.5 and 89.6 cM. QTL cluster regions were found also on chromosome 1B, 3A, 4B, 6B (2 cluster), and 7B.

The candidate genes research in the QTL clusters region found three particularly noteworthy, as previously reported to be directly involved in grain yield: TRITD2Av1G019250, encoding for pseudo-response regulator (*Ppd-A1*) in the 2A chromosome; TRITD4Bv1G171270, encoding for a Big Grain 1 protein in the

4B cluster, and two candidate genes encoding for an acid β -fructofuranosidase (TRITD6Bv1G005370 and TRITD6Bv1G005450), both in the 6B. Interestingly, in all cluster in which a QTL for AREA was detected, candidate genes involved in auxin metabolism were found.

To investigate on the adaptability mechanisms of durum wheat to drought and salt stress, the parental lines Anco Marzio and Liberdur have been included in a set of cultivars that will be evaluated in a high-throughput phenotyping platform. This evaluation will be funded by the project “E-Crops: Technologies for digital and sustainable agriculture (Progetto ARS01_01136 - PON Ricerca e Innovazione, 2014 2020 - Area AGRIFOOD)”.