

GENETIC ANALYSIS OF YIELD AND ADAPTATION TO LOW WATER AND NITROGEN INPUTS IN DURUM WHEAT

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water stress, low nitrogen, adaptation, grain yield, durum wheat

Durum wheat is a cereal of primary importance cultivated across a number of macro-environments differing in photoperiod, total amount of rainfall and thermo-pluviometrical patterns during the crop cycle. A prerequisite for more sustainable agricultural practices is the release of cultivars requiring lower water and N inputs; therefore, the improvement of water and N-use efficiency is an important goal for improving grain yield and yield stability in durum wheat. Identifying quantitative trait loci (QTLs) effective across a broad range of environmental conditions (Maccaferri et al., 2008 *Genetics* 178: 489-511) facilitates the integration of marker-assisted selection in breeding program.

The purpose of this research is to investigate the genetic basis of adaptation, yield and other agronomic traits of durum wheat in a multi-environment field testing experiment, under different water and N availabilities.

A population of 181 recombinant inbred lines (RILs) was developed by PSB (Bologna, Italy) from the cross between the two Italian elite durum wheat cvs. Meridiano and Claudio, both characterized by high yield potential and stability. A wide range of variation was observed for grain yield, with mean values ranging from a minimum of 1.71 t/ha under reduced water availability (Obregon, Mexico) to a maximum of 6.28 t/ha under rainfed conditions adopting normal rates of N fertilizer (Northern Italy). RILs were evaluated in five field trials varying for water and nitrogen regimes. A preliminary analysis carried out with 213 SSR and DArT markers evidenced two major QTL clusters for grain yield, yield components and several other traits on chrs. 4B and 5A. Favourable alleles were inherited from the parental cultivar Claudio at the 4B QTL region and from Meridiano at the 5A QTL. Additional markers with highly significant effects on grain yield were found on chrs. 2B, 3B, 5B and 7B, with favourable alleles contributed by both parents, thus accounting for the wide transgressive segregation observed among the RILs. Grain yield of the RILs was highly predictable based on the SSR alleles present at four key-chromosome regions.

These results highlight that variation at key-chromosome regions controlling phenology largely influence broad adaptability of tetraploid wheat, similarly to what has been observed in hexaploid wheat (Cockram et al., 2007. *J Exp Bot* 58: 1231-1244), and that large genetic variation for adaptation, yield potential and yield components is present in the elite durum wheat germplasm. Up to now, this variation has been explored to a limited extent.