

DEVELOPMENT OF A HIGH-DENSITY CONSENSUS MAP IN DURUM WHEAT

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A well-saturated genetic map is an important tool for plant breeding and many technologies are available to increase the abundance of molecular markers suitable for genetic analysis, such as DArT markers.

A consensus map of durum wheat (*Triticum turgidum* L. var. *durum*) was constructed based on segregation data from six mapping populations, including Creso x Pedroso, Ofanto x Cappelli, Cirillo x Neodur, Svevo x Ciccio, Messapia x MG4343 and Latino x Primadur. All listed genotypes are durum wheat varieties, except MG4343, which is an accession of *Triticum turgidum* var. *dicocoides*. The composite map contained a total of 1916 markers, comprising SSR, EST-SSR, STS, TRAP, RFLP, morphological and biochemical markers. The total map length spanned 3021 cM spread over 25 linkage groups and showed a mean distance between neighbouring loci of 1.6 cM. Among all markers, 640 were common at least in two populations while 1276 were mapped in a single population. The comparison of marker order in the consensus and the individual maps, revealed a good co-linearity, except for few putative inversions in the frame of few cM.

A small fraction (8%) of the markers deviated significantly from the expected Mendelian ratio; clusters of loci showing distorted segregation ($P < 0.01$) were found on chromosomes 5A, 6A, 1B, 2B, 4B, 5B, 6B, and 7B.

The analysis of map location of putative homoeologous loci suggest the occurrence of several rearrangements in chromosomes 4A, 5A, 6A, and 7B. The putative translocation on chromosome 7B was previously described.

This consensus map represents a very useful tool, providing a more complete coverage of the durum wheat genome, to facilitate genomic researches such as evolutionary studies, QTL fine mapping for map-based cloning, evaluation of the degree of linkage disequilibrium and association analysis of important agronomic traits.