

QTL analysis of durum wheat using microsatellite for genetic map

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Durum wheat (*Triticum turgidum* L. var. Durum) has an allotetraploide genomic structure (genome AABB, $2n = 4x = 28$), characterized by the presence of seven groups of omeologhi. The grain produced is used for the production of different types of food including pasta, couscous, burghul, and bread. In modern breeding programs, agro-morphological evaluations, conducted in multiple environment, are commonly used to identify improved lines. Although this has led to a significant increase in the stability of the evaluated traits, the genetic progress for key quality traits presented in wheat has been considerably slowed down. Recently, molecular markers have played a key role in modern breeding programs and their implementation has become a standard process to select numerous alleles of interest. Molecular maps have been developed to localize the molecular markers and genetic loci capable of controlling the traits of interest.

In contrast to hexaploid wheat (AABBDD), for which have been developed many molecular chromosome maps (Chao *et al.* 2008) and diploid wheat for which were obtained several linkage maps, relatively little attention has been devoted to the durum wheat. Blanco (1998) developed the first interspecies linkage map (*T. durum* x *T. dicoccoides*) based on 65 RILs utilizing RFLP markers, later supplemented with SSR markers. The first intraspecific map, however, was developed by Nachit *et al.* (2001). Recently have been published several maps that integrate different types of molecular markers (Maccaferri *et al.* 2008). Many of these maps were used to identify the locus for quantitative traits (QTLs), especially for

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the traits associated with the quality characteristics as well as the content of carotenoids (Zhang *et al.* 2008), the protein content, test weight (Elouafi and Nachit 2004) and the strength of the gluten. Among these QTLs, many of them have been identified by crosses involving parental lines of wild tetraploid (Gonzalez-Hernandez *et al.* 2004).

Different types of molecular markers based on different techniques have different characteristics that make them particularly useful for different needs. Several maps were constructed by use of older molecular markers such as RFLPs (Random Fragment Length Polymorphism) and AFLPs (Amplified Fragment Length Polymorphism) later saturated the latest generation markers such as microsatellite or SSR (Simple Sequence Repeats), based on sequences and transcribed (EST) until the advent of newer markers DART (Diversity Array Technology) supported by high-throughput technologies.

In order to have a genetic map it is of particularly importance the parents choice, they should show high levels of polymorphism. Furthermore, in order to identify QTLs positions, the parent must have contrasting characteristics for the traits of interest. After the parent have been chosen, different segregant population could be analysed such as F₂,