

MAPPING QTLs FOR ROOT MORPHOLOGICAL TRAITS IN DURUM WHEAT

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ABSTRACT

Durum wheat (*Triticum turgidum* L. var. *durum*, $2n=4x=28$, AABB) is an economically and nutritionally important cereal crop in the Mediterranean region and its production is largely influenced by environmental stresses, such as drought, heat and nutrient deficiency. Roots are an important part of the plant architecture that is involved in foraging for the available water and nutrients in the rhizosphere. A deep and thick root system is generally considered as a more favourable element allowing the crop to maintain its water status even under water stress. Nonetheless, little is known about the molecular and genetic basis for root growth in durum wheat. The availability of molecular marker technology has provided plant breeders with a new set of tools to evaluate plant diversity at a DNA level. In the present study, chromosome regions involved in the control of root architecture were investigated by testing a recombinant inbred lines (RIL) population consisting of 123 F_{8,9} lines derived from the cross between two durum wheat varieties (Creso and Pedroso) contrasting for root traits. The genetic map comprised more than 500 molecular markers spanning greater than 1800 cM. QTL analysis showed that a relatively limited number of chromosome regions were involved in the root morphology. The most relevant regions were identified on chromosome 2A, 6A, 5A and 1B for traits related to length, area and volume of roots.

Key Words. Durum wheat, Root morphology, QTL, Recombinant inbred lines.

INTRODUCTION

Durum wheat (*Triticum durum* Desf.) is one of the major cereal crops in the Mediterranean region. Its production area is gradually increasing in spite of abiotic constraints as drought stress. The most important task in planning a breeding programme for the improvement of drought resistance is the formulation of the drought-resistant ideotype. Rooting depth is among the most important traits required to sustain plant function under low water availability conditions. A deep and voluminous root system should permit seedlings to extract soil moisture in a greater soil volume. The influence of root architecture on yield and other agronomic traits, especially under stress conditions, has been widely reported in all major crops (Passioura, 1972; Ludlow & Muchow, 1990; Price et al., 2002; Tuberosa et al., 2002; de Dorlodot et al., 2007). The objective of the present paper was to map the QTLs of root morphological traits in durum wheat.

MATERIALS AND METHODS

A recombinant inbred lines (RIL) population consisting of 123 F8:9 lines derived from the cross between two durum wheat varieties (Creso and Pedroso) contrasting for root traits were used to identify chromosome regions involved in the control of root architecture. The 123 RILs derived from the cross Creso x Pedroso along with the two parents were grown hydroponically in growth chamber in 2009 at Foggia for analyzing the root morphological traits and mapping QTLs by using the MapQTL5 software based on the genetic linkage map constructed by Marone et al. (2009). The experiment was conducted using a randomised complete block design with five replications. In the present study several morphological traits were recorded using the root analysis software WinRHIZO (version 4.0b, Regent Instruments Inc., Quebec, Canada) but we refer only for the following traits (i.e. Total Root Length, - Length-, Projected Root Area –Projarea-, Root Surface Area –Surfarea-, Average Root Diameter -Avgdiam-, Root Length per Volume –Lenpervol-, Total Root Volume -Rootvol-).

RESULTS AND DISCUSSION

Genetic variability of root traits

The ANOVA (not shown) revealed the presence of significant differences ($P < 0.01$) among the durum wheat RILs for all the investigated traits ($P < 0.01$). The mean values of the investigated traits, their range of variation, standard deviation (SD) and standard error (SE) values are reported in Table 1. A normal frequency distribution was found for all analysed traits, indicating that different loci could be involved in the genetic control of these traits.

Table 1. Mean, minimum and maximum values, SD and SE of the root traits.

	ID	Creso	Pedroso	RILs			SD	SE
				Mean	Min.	Max.		
Length (cm)	1	234.6	361.6	290.7	99.2	497.0	72.9	3.78
ProjArea (cm ²)	2	8.4	13.5	10.5	3.3	15.8	2.2	0.11
SurfArea (cm ²)	3	26.5	42.4	33.1	10.4	49.6	6.9	0.36
Average Diameter (mm)	4	0.36	0.38	0.37	0.20	0.64	0.05	0.00
LenPerVol (cm/cm ³)	5	234.6	361.6	290.7	99.2	497.0	72.9	3.78
Volume (cm ³)	6	0.239	0.398	0.305	0.087	0.635	0.067	0.003

Mapping QTL for root traits

The linkage map used for QTL analysis included SSR, STS and DArT markers for a total of ca. 500 markers covering more than 1800 cM (Marone et al., 2009). Single-marker regression and composite interval mapping QTL analysis showed that a relatively limited number of chromosomes were involved in the root morphology. The most relevant regions were identified on chromosomes 2A, 6A, 5A and 1B for traits 1,2,3 and 5 while for traits 6 the region involved were on chromosomes 2A and 6A. The observed phenotypic variation explained by these QTLs, considering every regions identified for each traits, is more than 60%.

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