

## STUDY OF ROOT AND SHOOT MORPHOLOGICAL TRAITS IN A COLLECTION OF DURUM WHEAT CULTIVARS

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Root architecture can be targeted in breeding programs to develop crops with more efficient capture of water and nutrients, and therefore more resistant to drought, climate change and suitable for sustainable agriculture.

A collection of 138 T. durum cultivars, selected from the CerealMed panel, and 2 common checks (Iride and Svevo) were grown in ryzotrons in controlled conditions (growth chamber), in order to study morphological traits of the shoot and root apparatus. The root images were taken at five-leaves stage with a scanner and then the root measurements were performed using the Win-RHIZO system (version 4.0b; Regent Instruments Inc., Quebec, Canada). Several morphological traits of the roots were recorded using the root analysis software, as length (cm), surface area (cm<sup>2</sup>), mean diameter (mm), volume (cm<sup>3</sup>), and number of tips, forks, and crossings. For shoot traits, maximum shoot lengths (cm), number of shoots, number of leaves and shoot biomass (g) were evaluated.

The cultivars evaluated in the present study have been genotyped and a set of 13,475 single nucleotide polymorphism (SNP) markers have been used for genome-wide association study.

The mixed linear model revealed a total of 134 QTLs distributed on all 14 durum wheat chromosome, from 4 on chromosomes 1A, 4A and 5A, to 20 on 2B, considering all the phenotypic traits. 50 QTLs were identified for shoot traits, from 6 for plant height to 24 for total biomass, while 72 QTLs were identified for root traits, from 7 for diameter and surface area to 14 for root biomass. Twelve QTLs were involved in the control of root to shoot ratio. It was possible to observe some regions associated specifically to root traits, as the QTLs on chromosome 6A, position 16-20 Mb, for root biomass, average diameter and number of forks, and position 503 Mb for number of tips, number of crossings and root to shoot ratio. In other cases, we found the co-localization of QTLs involved in the control of both root and shoot traits, as the QTL on chromosome 6A, position 598 Mb, for root biomass, root surface area, shoot biomass and total biomass. Besides novel QTLs, some of the QTLs identified in the present study found correspondence with regions previously mapped, providing a validation of the mapping approach herein used.

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