

## **MAPPING QTLs FOR ROOT MORPHOLOGICAL TRAITS IN DURUM WHEAT**

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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 information available on the genetic control of root traits in the field and their relationships with yield is limited, mainly due to the difficulty of measuring root characteristics in a large number of plants. The introduction of DNA-based molecular markers, allows for unprecedented opportunities to identify the genetic factors underpinning the variation of quantitative traits and to investigate to what extent linkage and/or pleiotropy may influence traits association. This work represents a first attempt to study chromosome regions involved in the control of root architecture by testing a recombinant inbred lines (RIL) population 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. The mapping of the QTLs of root morphological traits in durum wheat should facilitate breeding for drought resistance.