

## GENOME WIDE ASSOCIATION MAPPING IDENTIFIES MAJOR QTLS AFFECTING SEMINAL ROOT TRAITS IN BARLEY (H. VULGARE L.)

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A better knowledge about the genetic basis of root trait variation is crucial to successfully target root traits in breeding programs. In this study we investigated the genetic control of seminal root traits in a barley germplasm collection (WHELBI collection) representative of the genetic variation in this species. Phenotypic data concerning root system were collected in a collection of 485 cultivars, landraces and wild barley accessions using a semi-hydroponic system at the seedling level (13 days from germination). Traits analyzed included seminal root number (SRN), root growth angle (RGA), total root length (TRL) and root dry weight (RDW). All traits showed a relatively high heritability: SRN  $h^2 = 0.87$ , RGA  $h^2 = 0.81$ , TRL  $h^2 = 0.80$  and RDW  $h^2 = 0.55$ . Genome Wide Association mapping identified different QTLs for all traits distributed on all chromosomes. These results represent the starting point for the identification of the genes underlying the identified QTLs and for their use in genetic improvement programs.