



## P0910: Genome-Wide Association Mapping of Root Extension in a Collection of European Winter Barley Cultivars

Root extension in cereals is an extremely plastic trait exhibiting high variation in relation to the genetic background and to environmental conditions. The study of root system is particularly important in the Mediterranean area, where genetic improvement of drought tolerance on winter barley is a relevant breeding target. Here we aimed at exploring the natural genetic variation in root extension in a collection of European winter barley cultivars (67 two-rowed and 75 six-rowed, released between 1921 and 2006). For each genotype, three plants were grown in cylindrical pots (rhizotrons) with diameter of 10 cm and 50 cm height, filled with siliceous sand. Plants were collected at the 4 leaf stage (Zadocks stage 14), when roots were separated from shoots and scanned. The obtained images were analyzed by using the winRHIZO software to calculate the total root extension, as the sum of lengths of primary and secondary roots. The whole experiment was replicated three times, showing repeatability of 0.53. The same collection was previously genotyped for >7000 iSelect SNP markers, providing a powerful tool for association mapping of root traits. Genotype-phenotype association with the R-GAPIT package identified a significant genomic region on chromosome 5H-bin7, that has been scrutinized for candidate genes and alleles with a putative role in the trait under study.

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