

SEARCHING FOR THE GENETIC BASIS UNDERLYING THE GROWTH OF BARLEY ROOT SYSTEM IN ARTIFICIAL COMPACTED SOIL LUMPS

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soil compaction, root system traits, barley cultivars, GWAS, sustainability

Soil compaction is defined as the reduction of air-filled pore space leading to the densification of soil and the distortion of soil structure affecting soil density, water conductivity, and nutrient availability (Oldeman et al., 1991). These conditions affect root morphology, root development and plant growth leading to evident modification of root architecture including decrease of root length, increase of diameter width, root tortuosity, increase of root hair and lateral root formation.

In this study, artificial compacted soil lumps were created starting from powdered fine silty, mixed, mesic Udic Ustochrepts soil with a composition in texture classes as sand 14%, silt 50%, and clay 36% (Rizza et al., 2018). Dried sand, vermiculite and water were added to the powdered soil in rapport 1:0.2:1 respectively. The mixed soil was aliquoted in small plastic baskets and dehydrated at 60°C to obtain artificial soil lumps with a 30% of water content. A panel of 139 barley cultivars both 2 rows and 6-rows, genotyped with Illumina 9K iSelect Chip, were sowed in each lamp and three lumps for each genotype were prepared. After 5 days from germination all plants were extracted from the lumps, root systems were washed, scanned and analyzed with Winrizho software. Three root morphology traits (Total Root Length, TRL; Average of Diameter Width, ADW; Seminal Root Number, SRN) and Shoot:Root (S/R) ratio were chosen for subsequent genomic analysis.

4,942 biallelic and polymorphic SNP markers were used to investigate population structure, genetic diversity, haplotype detection and GWA studies.

All root morphology traits showed a normal distribution and modest level of broad sense heritability (H^2), confirming the role of root plasticity in plant root architecture and adaptation. The highest value H^2 was reported by the S/R ratio (40.2%), while the AWD showed the minimum value of 3.9%. No correlations were observed among TRL, AWD, S/R ratio, SRN traits. The GWAS analysis conducted with a General Linear Model (GLM) approach revealed significant association only for TRL trait showing an association with two SNPs on chromosome 4H and 5H. Both SNPs were already detected and genetically mapped in QTL associated to root length by Amad Naz *et al.* (2014). MTAs (Markers Trait Associations) based on haplotype blocks were identified for TRL, ADW the S/R ratio and SRN, according to the critical LD value. The haplotype blocks were constructed with a maximum of 8 SNPs in LD associated to TRL on 5H, spanned on 294kb. Further analyses are in progress to investigate haplotype blocks for all traits.