

SEMINAR-IV

GENES, PROTEINS, AND MOLECULAR MARKERS FOR IMPROVING
ROOT TRAITS IN WHEAT (*Triticum aestivum* L.)

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Executive Summary

Wheat (*Triticum aestivum* L.) production in the world is challenged by different biotic and abiotic stresses, which are increasing with climate change. Unravelling the molecular genetics quantitative trait loci (QTL), candidate genes and proteins of root traits is essential wheat root trait improvement through breeding. One hundred and three recombinant inbred lines (RILs) RILs of Synthetic W7984 × Opata M85 and 14 pairs of near-isogenic lines (NILs: pairs of genetically identical lines except for genomic regions (GRs)) of wheat were used to phenotype root traits in a semi-hydroponic system. The composite interval mapping method was used to discover QTL for root traits from RILs. Candidate genes and proteins for root traits were identified from NILs through genotype-phenotype association analysis, and label-free proteomics, respectively. The RILs exhibited significant variation in root traits; 14 QTL for eight root traits were identified mainly on chromosome groups 5, 6 and 7. Important QTL for shallow root (*Q.rd.uwa.7BL: Xbarc50*) and high RM (*Q.rm.uwa.6AS: Xgwm334*) were validated in two independent F₂ populations of Synthetic W7984 × Chara and Opata M85 × Cascade, respectively. Separately, 10 of 14 NIL pairs showed significant variation between their isolines for root traits; 15 putative candidate genes for root traits, including outstanding genes *TraesCS4A02G185300* and *TraesCS4A02G442700* encoding UDP-glycosyltransferase and *TraesCS4A02G330900* encoding leucine-rich repeat receptor-like protein kinase were identified on targeting GRs on chromosomes 4BS, 4BL, 4AS, and 7AL of NILs. Furthermore, three candidate protein biomarkers for total root length and root dry mass in NIL pairs targeting GRs on chromosomes 4A and 7A—asparagine synthetase (*TraesCS4A02G109900*), signal recognition particle 19 kDa protein (*TraesCS7A02G333600*) and 3,4-dihydroxy-2-butanone 4-phosphate synthase (*TraesCS7A02G415600*)—with consistent gene expressions at protein and mRNA transcription (qRT-PCR) levels were identified. Our research provides an improved understanding of molecular control of root traits and potential for marker-assisted root breeding in wheat.

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