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PHENOTYPIC PLASTICITY OF ROOT ARCHITECTURE AMONG WILD EMMER WHEAT INTROGRESSION LINES PROMOTE DROUGHT TOLERANCE

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Drought is the major environmental factor limiting wheat production and sustainability worldwide. The wild emmer wheat (*T. turgidum* ssp. *dicoccoides*) genepool harbors a rich allelic diversity for numerous important traits, including drought tolerance. The overall goal of this research is to identify wild alleles for improving root architecture and enhance drought tolerance. A set of Adapted Near Isogenic Lines (NIL) was developed by introgression of wild emmer accession Zavitan into elite durum wheat (T. *turgidum* ssp. *durum*, cv. Svevo). The BC_3F_4 NILs were genotyped using the 90k Illumina array and linked to the wild emmer genome, and phenotyped using high-throughput image-based phonemics approach. A wide range of drought adaptation strategies were found among the NILs. Cluster analysis of morpho-physiological traits revealed five clusters of drought responses. Three drought-tolerant NILs representing different adaptations were selected for detailed characterization. Phenomics experiment including root architecture phenotyping support the drought response strategies. Further, Root phenotyping showed a higher root biomass for all chosen NILs compare to Svevo and high interaction with water availability in one NIL. This NIL showed the highest WUE under water-limited treatment and early vigor in both treatments. Currently we apply RNA-seq to identified candidate genes and reveal their underline mechanisms. While conventional breeding to improve drought tolerance focused on upper ground phenotypes and was limited by narrow allelic variation, the combination of specific wild alleles for vital drought tolerance traits as root architecture can be used for new breeding strategies, oriented drought adaptations for plant productivity.