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Abstract

Drought is a major constraint in wheat (*Triticum aestivum* L.) grain yield. The present work aimed to identify quantitative trait nucleotides (QTNs)/ candidate genes influencing drought tolerance-related traits at the seedling stage in 261 accessions of a diverse winter wheat panel. Seeds from three consecutive years were exposed to polyethylene glycol 12% (PEG-6000) and a control treatment (distilled water). The Farm-CPU method was used for the association analysis with 17,093 polymorphic SNPs. PEG treatment reduced shoot length (SL) (-36.3%) and root length (RL) (-11.3%) compared with control treatments, while the coleoptile length (CL) was increased by 11% under drought conditions, suggesting that it might be considered as an indicator of stress-tolerance. Interestingly, we revealed 70 stable QTN across 17 chromosomes. Eight QTNs related to more than one trait were detected on chromosomes 1B, 2A (2), 2B, 2D, 4B, 7A, and 7B and located nearby or inside candidate genes within the linkage disequilibrium (LD) interval. For instance, the QTN on chromosome 2D is located inside the gene *TraesCS2D02G133900* that controls the variation of CL_S and SL_C. The allelic variation at the candidate genes showed significant influence on the associated traits, demonstrating their role in controlling the natural variation of multi-traits of drought stress tolerance. The gene expression

of these candidate genes under different stress conditions validates their biological role in stress tolerance. Our findings offer insight into understanding the genetic factors and diverse mechanisms in response to water shortage conditions that are important for wheat improvement and adaptation at early developmental stages.

Keywords: drought tolerance, seedling, winter wheat, GWAS, candidate genes, PEG, FarmCPU, breeding