**Identification of the SNP markers for drought tolerance and related agronomic traits in chickpea under multi-environments using GWAS analysis**

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Drought tolerance is a complex trait that involves numerous genes. Identifying key causal genes or linked molecular markers can facilitate the fast development of drought-tolerant varieties. Using genome-wide association study (GWAS) is a powerful approach to identifying the genetic factors underlying the intraspecific phenotypic variations. To address this, we cultivated 185 chickpea accessions in two distinct locations in Lebanon over two years, subjecting them to both irrigated and rain-fed environments. We measured 11 traits, including morphological, yield, yield components and tolerance score. SNP genotyping revealed 1344 variable SNP markers distributed across the chickpea genome. A genome-wide association study (GWAS) revealed several marker-trait associations (MTAs) associated with the traits evaluated. Within the rainfed conditions, 11 significant markers were identified, each associated with distinct chickpea traits. Another set of 11 markers exhibited associations in both rainfed and irrigated environments, reflecting shared genetic determinants across these conditions for the same trait. We identified 28 genetic regions containing SNPs significantly associated with several different drought traits, which was an indication of pleiotropic effects. Among the identified genes are *CPN60-2, hsp70, GDSL(GELP), AHL16, NAT3, FAB1B, bZIP, and GL21*. These genes collectively contribute to the multifaceted response of chickpea plants to drought stress.