Unravelling Chickpea’s Genetic Landscape with the Cicer Super-Pangenome

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Chickpea (Cicer arietinum L.) - an important legume crop cultivated in arid and semiarid regions—has limited genetic diversity. Efforts are being undertaken to broaden its diversity by utilizing its wild relatives, which remain largely unexplored. In this direction, we developed the Cicer super-pangenome based on the de novo genome assemblies of eight annual Cicer wild species. We identified 24,827 gene families, including 14,748 core, 2,958 soft-core, 6,212 dispensable, and 909 species-specific gene families. The dispensable genome was enriched for genes related to key agronomic traits. Structural variations between cultivated and wild genomes were used to construct a graph-based genome, revealing variations in genes affecting traits such as flowering time, vernalization, and disease resistance. These variations will facilitate the transfer of valuable traits from wild Cicer species into elite chickpea varieties through marker-assisted selection or gene-editing. This study offers valuable insights into the genetic diversity and potential avenues for crop improvement in chickpea. Furthermore, to enhance the accessibility and utilization of these genomic resources, we developed a user-friendly, public repository ‘CicerPanDB’. This comprehensive database hosts all genome assemblies, gene models, and structural variations identified between wild and cultivated Cicer species, supporting global research and breeding programs aimed at enhancing chickpea’s agronomic traits and resilience to climate variability.

***References:***

*TBC*

*(max. 5 references (first author followed by et al., year of publication, journal abbreviation, volume and pages)*