

## **ABSTRACT**

We report a map of 4.97 million single-nucleotide polymorphisms of the chickpea from whole-genome resequencing of 429 lines sampled from 45 countries. We identified 122 candidate regions with 204 genes under selection during chickpea breeding. Our data suggest the Eastern Mediterranean as the primary center of origin and migration route of chickpea from the Mediterranean/Fertile Crescent to Central Asia, and probably in parallel from Central Asia to East Africa (Ethiopia) and South Asia (India). Genome-wide association studies identified 262 markers and several candidate genes for 13 traits. Our study establishes a foundation for large-scale characterization of germplasm and population genomics, and a resource for trait dissection, accelerating genetic gains in future chickpea breeding.