

Genetic diversity shaped by transposon variation in chickpea

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Motivation and Aim: Chickpea is a crucial crop for the agricultural sector and serves as a significant contributor to the economy of many developing countries. It finds use as a source of human nutrition and livestock feed alike. However, the sensitivity of chickpea to both biotic and abiotic factors has been on the rise, primarily due to the reduced genetic diversity in cultivars since the mid-twentieth century. In certain years, drought and extreme temperatures have been responsible for up to half of the global crop loss [1, 2], thereby underscoring the need for developing productive and climate-resistant chickpea genotypes. Achieving this objective would be a significant challenge for the crops industry.

Transposable elements (TEs) are mobile genomic elements that enable plants to adapt to environmental conditions. Up to 80 % of a plant cell's genome is comprised of TEs which can influence agricultural traits such as plant growth, size, color and shape of fruits or flowers, flowering time, and resistance to pests [3, 4]. Studying mobile elements in the chickpea genome will facilitate breeding and obtaining climate-resilient varieties. This study evaluates the contribution of TEs to chickpea diversity.

Methods and Algorithms: We collected 190 chickpea genotypes from the Vavilov All-Russian Institute of Plant Genetic Resources in Russia, comprising of 167 landraces collected by Vavilov in 1930s and 23 elite cultivars. We grouped the samples into seven geographic regions based on proximity (i.e., Mediterranean, Lebanon, South of Russia, Turkey, Uzbekistan, India, and Ethiopia). Short-read genome sequencing with the Illumina protocol yielded a dataset with an average coverage of 25x or about 37 Gbp per sample. The reads were processed and aligned to the chickpea reference genome assembly ASM33114v1. PopoolationTE 2 tool was used to predict mobile elements in separate- and joint-analysis modes [5].

We conducted two modes of analysis to study the transposon content of chickpea samples. In the first mode, we analyzed the transposon content of each sample separately, while in the second mode, we analyzed the transposon composition of the entire set. By obtaining lists of mobile elements and their coordinates, we were able to perform further analyses, such as identifying the distributions of TE types and the positions of their insertions in the genome with respect to gene coordinates. We also used the PrimatR statistical package to identify “hot spots” where TE insertions are densely located. Additionally, we studied TE polymorphic positions (TIPs) that are specific to chickpea populations from diverse geographical and climatic collection sites. To assess the contribution of TIPs to phenotypic variation, we conducted GWAS using both GAPIT [6] and the IIIVmrMLM program [7] and data on 12 phenotypic traits measured at two experimental stations, Astrakhan and Kuban, in 2022.

Results: Our findings indicate that the majority of transposable insertion polymorphisms belong to the Copia and Gypsy families, with 41 % and 16 %, respectively. The introns

of genes were found to have the highest frequency of polymorphic positions. 47 TE insertion hotspots were present across all chromosomes, with the lowest number of hotspots observed in chromosomes 5 and 8. Furthermore, we found that the Ethiopian population had a higher incidence of TIPs, which were predominantly found in this population. Finally, a thorough GWAS analysis identified 244 quantitative trait nucleotides (QTNs) that explained 18.1 % to 65.61 % of the variation for different phenotypic traits. The maximum amount of trait variation explained by a single QTN was 13.71 %. Of the 244 QTNs identified, 28 were mapped to genes with known function or located within the 1 kb-flanking region of these genes. These results shed new light on the genetic variation and distribution of TIPs, as well as the presence of QTNs that contribute to the phenotypic variability of certain traits.

Conclusions: Overall, our findings highlight the significant role played by TIPs in the generation of phenotypic diversity in chickpea and hold great potential for future breeding programs, offering a promising avenue for the development of improved cultivars.

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