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Salt tolerance and molecular genetic diversity analysis in chickpea (*Cicer arietinum* L.) from Ethiopia

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Abstract

Salinity is one of the major abiotic stresses reducing chickpea growth and productivity. Genetic improvement for salt tolerance requires knowledge of genetic diversity in available germplasm. However, there is limited information on the extent of genetic variation for salt tolerance among Ethiopian chickpeas. This study was carried out to determine the extent of variability for salt tolerance and molecular genetic diversity of Ethiopian chickpeas. In a hydroponic experiment, 87 chickpea genotypes, which included 69 accessions and 18 released varieties were screened for salt tolerance. Further, the accessions were grouped into five populations namely; North Shewa, North-West Amhara, East Gojam, West Gojam and East Shewa. Plants were cultivated for 15 days in a saline solution containing 100 mM NaCl. Non-treated plants served as control. Data were collected on shoot and root growth parameters. The total dry matter percent reduction was used to classify the level of salinity tolerance of each accession. A significant phenotypic variation was marked and accessions Minjar, 207656, 41119, and 41164 were identified to be salt tolerant. A molecular genetic diversity study was conducted on 87 genotypes along with an additional 20 wild types using eight inter-simple sequence repeat markers. A high level (>95%) of polymorphism has been obtained. East Shewa population had the highest genetic diversity (H= 0.33, I = (0.48), while North Shewa obtained the lowest diversity (H = 0.27, I = 0.41). High genetic diversity was found in salt-tolerant chickpea accessions from the North-west Amhara (H = 0.30, I = 0.44) and East Shewa populations (H = 0.30, I = 0.43). It suggests that using parental materials from those populations could be effective to improve the salt tolerance of chickpeas. Furthermore, wild types exhibited a higher genetic distance from all populations (>0.06). As a result, wild chickpeas could be exploited to improve salt tolerance in cultivated genotypes. The genetic variation for salt tolerance, as well as the molecular genetic diversity found among the chickpea accessions, will aid in the development of chickpea breeding and conservation strategies in Ethiopia.

Keywords: Chickpea, genetic diversity, hydroponics, ISSR-marker

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