

**Genetic diversity analysis among collected purslane (*Portulaca oleracea* L.)
accessions using ISSR markers**

ABSTRACT

Genetic diversity and relationships among 45 collected purslane accessions were evaluated using ISSR markers. The 28 primers gave a total of 167 bands, among which 163 were polymorphic (97.6%). The genetic diversity as estimated by Shannon's information index was 0.513, revealing a quite high level of genetic diversity in the germplasm. The average number of observed allele, effective allele, expected heterozygosity, polymorphic information content (PIC) and Nei's index were 5.96, 1.59, 0.43, 0.35 and 0.35, respectively. The UPGMA dendrogram based on Nei's genetic distance grouped the whole germplasm into 7 distinct clusters. The analysis of molecular variance (AMOVA) revealed that 89% of total variation occurred within population, while 11% were found among populations. Based on the constructed dendrogram using ISSR markers those accessions that are far from each other by virtue of genetic origin and diversity index (like Ac1 and Ac42; Ac19 and Ac45; Ac9 and Ac23; Ac18 and A25; Ac24 and Ac18) are strongly recommended to select as parent for future breeding program to develop high yielding and stress tolerant purslane variety in contribution to global food security.