

**Application of EST-SSR marker in detection of genetic variation among purslane
(*Portulaca oleracea* L.) accessions**

ABSTRACT

Express sequence tag (EST)-simple sequence repeat (SSR) was employed to assess the genetic diversity in elite germplasm collections of purslane (*Portulaca oleracea* L.) which is a saline and drought tolerant annual herb containing high amount of vitamins, minerals, and antioxidant properties. The 10 primers gave a total of ninety-five bands among which 95 were polymorphic (100 %). The genetic diversity as estimated by Shannon's information index was 1.85, revealing a high level of genetic diversity in the germplasm. The average numbers of observed allele, effective allele, expected heterozygosity, polymorphic information content (PIC), and Nei's information index were 9.5, 5.14, 0.81, 0.33, 0.77, and 0.79, respectively. The UPGMA dendrogram based on Nei's genetic distance grouped the whole germplasm into eight distinct clusters. The analysis of molecular variance (AMOVA) revealed that 71.87 % of total variation occurred within population while 28.13 % from among populations. Considering all these criteria and results from marker-assisted diversity analysis, accessions that are far apart based on their genetic coefficient (like Ac11 and Ac17; Ac4 and Ac42; Ac16 and Ac31; Ac38 and Ac17; Ac21 and Ac31; Ac30 and Ac10) could be selected as parents for further breeding programs.