



Expressed sequence tag-simple sequence repeat-based molecular variance in two *Salicornia* (Amaranthaceae) populations

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ABSTRACT. *Salicornia* spp is one of the most salt-tolerant vascular plants and is native to salt marshes and estuaries. We developed expressed sequence tag derived-simple sequence repeat (EST-SSR) markers for estimating genetic diversity and marker-assisted *Salicornia* breeding. Six polymorphic EST-SSRs of 40 detected 27 alleles, ranging from three to five alleles per locus. The average number of alleles per locus was 4.33 and 4.17, and the major allele frequency at locus DY529765 was high, being 0.859 and 0.857 in *S. bigelovii* and *S. europaea*, respectively. Gene diversity, heterozygosity and polymorphism information content were highest at locus DY529950 and similar in

these two species. Gene diversity increased with increase in the number of alleles that had a low major allele frequency at a locus. Six polymorphic loci effectively discriminated 46 taxa into three clusters via different analyses. Significant deviation of F_{ST} from zero in three suggested populations for six loci indicated population differentiation and limited gene flow among them. A reduced median network established that taxon SB65 is primitive. SMART (simple modular architecture research tool) analysis of peptide sequences of six EST-SSRs showed that loci DY529765, DY529950 and EC906203 contained transmembrane, TLC, AgrB and NTR domains and might be involved in salinity stress tolerance. These EST-SSRs are a valuable resource for marker development and may be useful in marker-assisted *Salicornia* breeding.

Key words: Gene diversity; Gene flow; Allele frequency; Reduced median network; Salinity tolerance