



## Genetic diversity analysis of *Capparis spinosa* L. populations by using ISSR markers

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Genet. Mol. Res. 14 (4): 16476-16483 (2015)

Received July 15, 2015

Accepted September 20, 2015

Published December 9, 2015

DOI <http://dx.doi.org/10.4238/2015.December.9.19>

**ABSTRACT.** *Capparis spinosa* L. is an important medicinal species in the Xinjiang Province of China. Ten natural populations of *C. spinosa* from 3 locations in North, Central, and South Xinjiang were studied using morphological trait inter simple sequence repeat (ISSR) molecular markers to assess the genetic diversity and population structure. In this study, the 10 ISSR primers produced 313 amplified DNA fragments, with 52% of fragments being polymorphic. Unweighted pair-group method with arithmetic average (UPGMA) cluster analysis indicated that 10 *C. spinosa* populations were clustered into 3 geographically distinct groups. The Nei gene of *C. spinosa* populations in different regions had Diversity and Shannon's information index ranges of 0.1312-0.2001 and 0.1004-0.1875, respectively. The 362 markers were used to construct the dendrogram based on the UPGMA cluster analysis. The dendrogram indicated that 10 populations of *C. spinosa* were clustered into 3 geographically distinct groups. The results showed these genotypes have high genetic diversity, and can be used for an alternative breeding program.

**Key words:** *Capparis spinosa* L.; Inter-simple sequence repeat; Genetic diversity