Development of expressed sequence tag-simple sequence repeat markers for genetic characterization and population structure analysis of *Praxelis clematidea* (Asteraceae)

Q.Z. Wang, M. Huang, S.R. Downie and Z.X. Chen

1College of Chemical and Engineering, Huaqiao University, Xiamen, Fujian, China
2Department of Plant Biology, University of Illinois at Urbana-Champaign, Urbana, IL, USA

Corresponding author: Q.Z. Wang
E-mail: wqz@hqu.edu.cn

Received December 16, 2015
Accepted January 15, 2016
Published May 23, 2016
DOI http://dx.doi.org/10.4238/gmr.15028038

ABSTRACT. Invasive plants tend to spread aggressively in new habitats and an understanding of their genetic diversity and population structure is useful for their management. In this study, expressed sequence tag-simple sequence repeat (EST-SSR) markers were developed for the invasive plant species *Praxelis clematidea* (Asteraceae) from 5548 *Stevia rebaudiana* (Asteraceae) expressed sequence tags (ESTs). A total of 133 microsatellite-containing ESTs (2.4%) were identified, of which 56 (42.1%) were hexanucleotide repeat motifs and 50 (37.6%) were trinucleotide repeat motifs. Of the 24 primer pairs designed from these 133 ESTs, 7 (29.2%) resulted in significant polymorphisms. The number of alleles per locus ranged from 5 to 9. The relatively high genetic diversity (*H* = 0.2667, *I* = 0.4212, and *P* = 100%) of *P. clematidea* was related to high gene flow (*Nm* = 1.4996) among populations. The coefficient of population differentiation (*Gst* = 0.2500) indicated
that most genetic variation occurred within populations. A Mantel test suggested that there was significant correlation between genetic distance and geographical distribution ($r = 0.3192$, $P = 0.012$). These results further support the transferability of EST-SSR markers between closely related genera of the same family.

**Key words:** *Praxelis clematidea*; Invasive plants; EST-SSR; Transferability; Genetic variation