



Genetic variation and genetic structure of the endangered species *Sinowilsonia henryi* Hemsi. (Hamamelidaceae) revealed by amplified fragment length polymorphism (AFLP) markers

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Genet. Mol. Res. 14 (4): 12340-12351 (2015)

Received June 24, 2015

Accepted September 11, 2015

Published October 14, 2015

DOI <http://dx.doi.org/10.4238/2015.October.14.1>

ABSTRACT. Comprehensive research of genetic variation is crucial in designing conservation strategies for endangered and threatened species. *Sinowilsonia henryi* Hemsi. is a tertiary relic with a limited geographical distribution in the central and western areas of China. It is endangered because of climate change and habitat fragmentation over the last thousands of years. In this study, amplified fragment length polymorphism markers were utilized to estimate genetic diversity and genetic structure in and among *S. henryi*. In this study, Nei's genetic diversity and Shannon's information index were found to be 0.192 and 0.325 respectively, indicating a moderate-to-high genetic diversity in species. According to analysis of molecular variation results, 32% of the genetic variation was shown to be partitioned among populations, demonstrating a relatively high genetic divergence; this was supported by principal coordinate analysis and unweighted pair-group method with arithmetic average analysis. Moreover,

the Mantel test showed that there was no significant correlation between genetic and geographical distances. The above results can be explained by the effects of habitat fragmentation, history traits, and gene drift. Based on the results, several implications were indicated and suggestions proposed for preservation strategies for this species.

Key words: *Sinowilsonia henryi* Hensi.; Genetic variation; Genetic structure; Amplified fragment length polymorphism (AFLP) marker