



## Genetic diversity of wild *Prunus cerasifera* Ehrhart (wild cherry plum) in China revealed by simple-sequence repeat markers

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Genet. Mol. Res. 14 (3): 8407-8413 (2015)

Received November 6, 2014

Accepted March 26, 2015

Published July 28, 2015

DOI <http://dx.doi.org/10.4238/2015.July.28.7>

**ABSTRACT.** Simple-sequence repeat (SSR) markers were employed to assess the genetic diversity of wild *Prunus cerasifera* Ehrhart (wild cherry plum) in China. Fourteen SSR primer pairs generated a total of 94 alleles (90 were polymorphic, accounting for 95.74%), with a mean of 6.71 alleles per locus. The number of alleles detected at each locus ranged from 2 at BPPCT 028 to 13 at BPPCT 002, with an average of 6.71 alleles per locus. Nei's genetic diversity ranged from 0.0938 to 0.4951 and Shannon's information index ranged from 0.1706 to 0.6882, with averages of 0.3295 and 0.4899, respectively. The SSR data indicated moderate genetic diversity of *P. cerasifera* in China. In the unweighted pair group method with arithmetic mean phylogenetic tree, the 40 forms of *P. cerasifera* were divided into 3 genetic clusters.

However, the 3 clades determined using SSR data were not consistent with the classification based on morphological characters, such as fruit color. Because of the endangered status and the moderate genetic diversity of *P. cerasifera* in China, both *in situ* and *ex situ* conservation strategies should be adopted.

**Key words:** Conservation; Endangered species; Genetic diversity; Simple-sequence repeat; Wild *Prunus cerasifera*