



Diversity, population structure, and evolution of local peach cultivars in China identified by simple sequence repeats

Z.J. Shen^{1,2}, R.J. Ma², Z.X. Cai², M.L. Yu² and Z. Zhang¹

¹College of Horticulture, Nanjing Agricultural University, Nanjing, China

²Institute of Horticulture, Jiangsu Academy of Agricultural Sciences, Nanjing, China

Corresponding author: Z. Zhang

E-mail: zhangzh@njau.edu.cn

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ABSTRACT. The fruit peach originated in China and has a history of domestication of more than 4000 years. Numerous local cultivars were selected during the long course of cultivation, and a great morphological diversity exists. To study the diversity and genetic background of local peach cultivars in China, a set of 158 accessions from different ecological regions, together with 27 modern varieties and 10 wild accessions, were evaluated using 49 simple sequence repeats (SSRs) covering the peach genome. Broad diversity was also observed in local cultivars at the SSR level. A total of 648 alleles were amplified with an average of 13.22 observed alleles per locus. The number of genotypes detected ranged from 9 (UDP96015) to 58 (BPPCT008) with an average of 27.00 genotypes per marker. Eight subpopulations divided by STRUCTURE basically coincided with the dendrogram of genetic relationships and could be explained by the traditional groups. The 8 subpopulations were juicy honey peach, southwestern peach I, wild peach, Buddha peach + southwestern peach II, northern peach, southern crisp peach, ornamental peach, and *Prunus davidiana* + *P. kansuensis*.

Most modern varieties carried the genetic backgrounds of juicy honey peach and southwestern peach I, while others carried diverse genetic backgrounds, indicating that local cultivars were partly used in modern breeding programs. Based on the traditional evolution pathway, a modified pathway for the development of local peach cultivars in China was proposed using the genetic background of subpopulations that were identified by SSRs. Current status and prospects of utilization of Chinese local peach cultivars were also discussed according to the SSR information.

Key words: Peach; Simple sequence repeat (SSR); Local cultivar; Genetic relationship; Population structure; Evolution