

Analysis of Genetic Diversity Among Korea, China, Japan and America Peach Cultivars (*Prunus persica* L. Batsch) Determined with SSR Markers

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The genetic relationships among 96 germplasm originating from different eco-geographical of china and variants of *P. persica* were evaluated. Using 33 simple sequence repeat markers (SSRs) screened from 108 published SSR markers developed for peach or sweet cherry. The 33 SSRs detected polymorphisms among 96 peach and nectarine genotypes and revealed a total of 283 alleles with an average of 8.6 alleles per locus. The polymorphism information content (PIC) value ranged from 0.40 (BPPCT041) to 0.98 (BPPCT009) with an average of 0.80.

UPGMA cluster analysis based on Nei's genetic distances classified genotypes into 6 groups, corresponding to their eco-geographical origin and the variants. Group I consisted of Chinese northern and northwestern local cultivars, and was divided into two subgroups, white and yellow peaches. Group II contained mainly Chinese southern local, Japanese, and North American cultivars and can be divided into four subgroups: Japanese white peach cultivars, Chinese flat peach cultivars, American yellow cultivars, and some Chinese local ornamental peach cultivars. Groups III, IV and V were comprised of Chinese local ancient cultivars, and contained "*P. ferganensis* and 'Renmiantao'", "Chinese dwarf cultivars" and 'Fenshouxing', respectively. Group VI had only 'Baishanbitao', a Chinese ornamental cultivar.

Chinese dwarf (*P. persica* var. *densa*) and ornamental cultivars (*P. persica* var. *duplex*) had great genetic distance to cultivated peaches and nectarines, confirming their taxonomic placement of variant of *P. persica*. However, 'Xinjiangdatianren', a cultivar of *P. ferganensis*, was genetically closer to an ancient Northern local ornamental cultivar 'Renmiantao', suggesting that *P. ferganensis* should be a variant of *P. persica* as *P. persica* var. *ferganensis*. Chinese Northern and Northwestern local cultivars clustered together with a greater diversity than that from Chinese Southern local ones, indicating that the Chinese Northern and Northwestern eco-geographical types should be equal in evolutionary status and more ancient than Chinese Southern local cultivars. Moreover, the Japanese and American clustered together with Chinese Southern local peaches, confirming their close phylogenetic relationship with Chinese Southern local cultivars.

Key words: *Prunus persica*, Simple sequence repeats, Phylogenetic, Relationship