

Phylogenetic relationships of peach (*Prunus persica* L. Batsch) cultivars based on internal transcribed spacer (ITS) sequences of nuclear ribosomal DNA

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Objectives

Peaches and nectarines have been known to be native to China and their place of origin is highlands of the Yellow River, China, 1200~2000 m above sea level. Wild *P. persica* trees has been found in southern Henan, Shanxi, Gansu, fountainhead area of Yellow river and Yangtze river, western Yunnan area, and southern Tibet in China (Wang, 2001). In this research, the ITS region's nucleotide sequence of the 52 peach cultivars selected out of Chinese local derivation cultivars, Chinese improved, Japanese, American cultivars, and outgroup, *Prunus davidiana* and *Prunus mume*, were analysed for phylogenetic relationship.

Materials and methods

52 peach cultivars, including 23 Chinese local and 4 Chinese improved cultivars, 10 Japanese, 12 American and 2 Korean cultivars and 3 related species which are *P. ferganensis*, *P. davidiana* and *P. mume* were used in this study. The ITS region's nucleotide sequence was verified by automatic sequencing using ABI Prism 3700 DNA Analyzer at Genotech Co. (Taejoen, Korea), the nucleotide sequence among the cultivars was analyzed at ClustalW (<http://www.ebi.ac.uk/clustalw/>). Phylogenetic analysis was determined using the ClustalW and Treeview program. ITS1, 5.8s, and ITS2 regions were decided by comparing already studied ITS sequences .

Results

The ITS regions of 52 peach cultivars, from 624 bp to 629 bp, did not show much of differences. ITS 1 region was 229~232 bp, 5.8s rDNA gene was 85 bp, and ITS 2 is 278~281 bp. 5.8s rDNA genes did not have diversity among cultivars (2 sites), ITS 1 and ITS 2 regions had 21 sites and 20 sites, respectively. Based on the phylogenetic analysis, 52 peach cultivars and two related species (*P. ferganensis*, *P. davidiana*) tested in this study were divided into 4 branches