

Genetic relationship of peach (*Prunus persica* L. Batsch) cultivars based on simple sequence repeat (SSR) markers

Jae-ho Yoon*, Won-seob Song, Deok-chun Yang¹⁾,
Yeong-ook Jin, Shaohua Li²⁾, Aimin Zhang³⁾

Division of Plant Science and Production, Sunchon National University,

¹⁾College of Life Science, Kyunghee University,

²⁾Institute of Botany, Chinese Academy of Sciences

³⁾Institute of Genetics and Development Biology, Chinese Academy of Sciences

Objectives

By using results on the variability of SSRs, we surveyed the genetic relationships among 96 of Chinese, Japanese, Korean and the US cultivars, and also observed genetic similarity with other geographical regions.

Materials and methods

96 peach and nectarine cultivars were used in this study and largely dividing into Chinese cultivars and foreign cultivars. The materials cover 23 local, 7 improved common, 9 flat, 8 dwarf (*P. persica* var. *densa*) and 5 ornamental (*P. persica* var. *duplex*) cultivars from China, and 20 Japanese, 20 American and 3 South Korean cultivars. The genetic distance between cultivars was estimated with Nei's parameter (Nei, 1972) implemented by the SimQual procedure of NTSYSpc V. 2.1 program (Rohlf, 1994). Dendrogram was constructed from data matrix by clustering the unweighted pair group method average (UPGMA) with the SAHN-clustering. The values of PIC were calculated (polymorphic information content) for each marker by using the formula below to identify polymorphism of markers.

Results

33 SSRs detected polymorphisms among 96 peach and nectarine cultivars and revealed total 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. Most peaches and nectarines were classified according to their geographical origins except some Chinese cultivars. The 96 peach and nectarine cultivars were classified into 6 groups.