# Genetic relationships of the Japanese persimmon *Diospyros kaki* (Ebenaceae) and related species revealed by SSR analysis

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**ABSTRACT.** Simple sequence repeat (SSR) molecular markers based on 18 primers were employed to study the genetic relationship of Japanese persimmon (*Diospyros kaki*) specimens. Two hundred and sixty-two bands were detected in 30 Japanese persimmon samples, including 14 Japanese and 10 Chinese genotypes of Japanese persimmon (*Diospyros kaki*) and six related species, *D. lotus*, *D. glaucifolia*, *D. oleifera*, *D. rhombifolia*, *D. virginiana*, and Jinzaoshi (unclassified - previously indicated to be *D. kaki*). All SSR primers developed from *D. kaki* were successfully employed to reveal the polymorphism in other species of *Diospyros*. Most of the primers were highly polymorphic, with a degree of polymorphism equal to or higher than 0.66. The results from the neighbor-joining dendrogram and the principal coordinate analysis diagram were the same; i.e., the Chinese and Japanese genotypes and related species were separated and the relationships revealed were consistent with the known pedigrees. We also concluded that 'Xiangxitianshi' from Xiangxi municipality, Hunan Province, China, is actually a sport or somaclonal variant of 'Maekawa-Jirou', and that

'Jinzaoshi' should be classified as a distinct species of *Diospyros*. We found that SSR markers are a valuable tool for the estimation of genetic diversity and divergence in *Diospyros*.

**Key words:** *Diospyros*; Genetic relationships; SSR