

Chinawat Yapwattanaphun 2003: Phylogenetic Analysis of Some Plants in the Genus *Garcinia* Using ITS Sequence Data and AFLP Analysis.

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AFLP analysis was used to evaluate the genetic variation of the mangosteen (*Garcinia mangostana* L), which is an asexual and agamosperous fruit tree. Twenty-three samples of *G. mangostana* were collected from Thailand, Indonesia and Malaysia. In addition, two related species of *G. mangostana*, *G. hombroniana* Pierre and *G. malaccensis* Hook, were used to evaluate the variation within species. A total of 477 scorable bands were obtained using 10 primer pairs in 23 plants of *G. mangostana* and 41 polymorphic bands were detected from 9 primer pairs. It is remarkable that intraspecific variations exist in *G. mangostana*, although the level of polymorphisms was relatively low when compared to the two related species. Since *G. mangostana* is agamospermy and always produces seeds without fertilization, it seems likely that all mangosteen trees are somatic clone. The genetic variations among *G. mangostana* are probably due to the somatic mutation while the variations in *G. malaccensis* and *G. hombroniana*, which are considered to be facultative agamosperms, are due to sexual reproduction. We concluded that AFLP analysis is a useful tool to detect genetic variation of mangosteen. The phylogenetic relationships among 17 *Garcinia* species including *G. mangostana* (mangosteen) were analyzed by comparing sequences of the internal transcribed spacer (ITS) region of nuclear ribosomal DNA (nrDNA). Both parsimonious and neighbor joining (NJ) analyses revealed that *G. mangostana* is closely related to *G. malaccensis* said to be a progenitor of mangosteen. Although another suspected progenitor of mangosteen, *G. hombroniana*, was more far distant from *G. mangostana* than *G. malaccensis* phylogenetically. *Garcinia hombroniana* formed a cluster with *G. rostrata*, *G. speciosa* and *G. silygifolia*, and this cluster was connected with a cluster of *G. mangostana* and *G. malaccensis*. The ITS sequence analysis showed that *G. atroviridis*, *G. cowa*, *G. dulcis*, *G. malaccensis*, *G. mangostana*, *G. rostrata* and *G. vilersiana* have nucleotide additivity (two different nucleotides at the same locus) at several sites in the ITS region. The occurrence of these species might be related to hybridization with ancestors, but the genomic compositions, even chromosome numbers, of these species are still unknown.

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