A803 A Phylogenetic Analysis in the Rosaceae based on ITS Sequence Data

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Phylogenetic relationships of 21 *Prunus* species (*P. yedoensis, P. sargentii, P. pendula* for. *ascendens, P. serrulata* var. *quelpaertensis, P. buergeriana, P. maximowiczii, P. serrulata* var. *spontanea, P. japonica* var. *nakaii, P. padus, P. takesimensis, P. serrulata* var. *tomentella, P. persica, P. serrulata* var. *pubescens, P.* X *choreiana, P. armeniaca* var. *ansu, P. mume, P. tomentosa, P. perisica* for. *rubroplena, P. salicina, P. glandulosa* for. *sinensis, P. leveilleana*) and a cultivar of *P. yedoensis* and one outgroup (*Rosa majalis*) were analysed by comparing their nucleotide sequences from the internal transcribed spacer (ITS) 1 and ITS 2 regions. The length of the ITS 1 region was ranged from 222 to 254 base pairs (bp) and the ITS 2 region from 207 to 245 bp. Sequence alignment and relationship analysis is in progress.

A804 Indistinctness of Species Concept between *Dendropanax morbefera* Leville and *D. trifidus* Makino Based on Phylogenetic Studies

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Molecular phylogenetic diversity between *Dendropanax morbifera*, Korean endemic plant as used garden tree and as painting sap to furniture, and *D. trifidus*, Japanese endemic and as well that was investigated. Until now on, there were few reports that these two species are surely different and can classify with any morphological characters. Only some taxonomists described can that they are differentiated with little difference of its fruit shape and sap color. Nevertheless open question which they are really different species has left. To reveal this question, we have worked molecular phylogenetic study. At first, nuclear internal transcribed spacer 2 region within 5.8S and 18S ribosomal DNA coding region was amplified, and then these amplified fragment were analyzed with using single stranded conformation polymorphism (SSCP), heteroduplex analysis (HTA) and DNA sequencing. SSCP analysis showed two significant patterns in both of all. Its result could be able to classify them to two groups, but it was impossible to divide two species. Results from nucleotide sequencing and single stranded conformation polymorphism showed us these two species may be same. Now, corresponding to this study, previous study of PCR-RAPD and morphology we arrived at a point of conclusion that it is meaningless to classify these two species.