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Variational Analysis of *Pyrus ussuriensis* Complex by DNA Markers

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Origin center of *Pyrus ussuriensis* is Far Eastern Asia. Korean populations of *P. ussuriensis* are distributed in central region of origin center. Gene pool of Korean populations of *P. ussuriensis* is composed of nine varieties. Taxonomic circumscriptions of these infraspecific taxa are very ambiguous. In order to analyse these infraspecific variations, it is adopted to RAPD method as a DNA marker. RAPDs counted in electrogram are treated to MEGA program. And then compare RAPD data with morphological data. As a result, it is analysed to genomic variation pattern and arranged to circumscriptions of infraspecific taxa. Geographical genetic map of Korean *P. ussuriensis* are obtained from relationships of RAPD data and geographical distribution pattern of populations.

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Molecular Phylogeny of Magnoliaceae Based on *ndhF* Sequences

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Sequences of the chloroplast gene *ndhF* from 82 taxa, representing a broad spectrum of the family Magnoliaceae, were analyzed to estimate phylogenetic relationships of the family. Sequence divergences reach to 0.87 % in the subfamily Magnolioideae and 2.73 % in the family Magnoliaceae, which are considerably low in comparison to other angiosperm families. *Magnolia macrophylla* and *M. dealbata*, which are members of section *Rytidospermum*, are placed at the base of phylogenetic trees. Of the remaining taxa, several lineages are clearly recognized even though their relationships are not completely resolved. Subgenus *Yulania* clearly forms a well-defined clade. In the clade of subgenus *Yulania*, *Magnolia acuminata*, which is a sole North American member of the subgenus, is separated from all other Asian species of the subgenus. Section *Gynopodium* of the genus *Magnolia* is tied with genera *Mangliastrum* and *Pachylanax*. Genera *Michellia* and *Elmerrillia* form a clade with sections *Maingola* and *Alcimandra* of genus *Magnolia* and they are closely related to subgenus *Yunania* and the clade of the genus *Mangliastrum-Pachylanax*-section *Gynopodium*. Sections *Blumiana* and *Aromadendron* are tied with the sections *Gwillimia* and *Lirianthe*, even though they are treated as different subgenera. Sequence analyses also support that section *Rytidospermum* is polyphyletic, which was claimed in the previous study using cpDNA RFLP. The molecular data suggest that currently recognized classification system of Magnoliaceae should be revised.