

Morphological characters were re-examined for section *Maingola* and section *Alcimandra* which has been considered to be closely related to the former. In result, section *Alcimandra* was combined with section *Maingola* because there was no distinctive character to separate these two sections. Although section *Alcimandra* is distinguished from others in having long stamen to hide gynoecium, many exceptions are found in the family. Recent molecular phylogenetic studies have also demonstrated the close affinity between sections *Maingola* and *Alcimandra*. *Magnolia macklottii* complex has been problematic because some taxonomically important characters show a wide range of variation. Principal component analysis was carried out for the matrix of 52 OTUs X 28 characters. Two varieties, *Magnolia macklottii* var. *macklottii* and *Magnolia macklottii* var. *maingayi*, were recognized in the complex mainly by the presence/absence of hairs in fruits. Leaf shape and hairs in twig appeared to be variable. Therefore, six species including five varieties were recognized in section *Maingola*.

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**Phylogeny of the Berberidaceae
Based on *ndhF* Gene Sequence Data**

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A molecular phylogeny of the Berberidaceae was reconstructed using the *ndhF* gene sequences from 22 taxa representing 17 ingroup genera and five outgroups. All of the phylogenetic trees generated by maximum parsimony, distance and maximum likelihood method unanimously recognized monophyly of four base chromosomal groups (i.e., X=10,

X=8, X=7, and X=6). Among the chromosomal group the X=10 (*Nandina*) and X=8 (*Caulophyllum*, *Leontice*, and *Gymnospermium*) group formed a very strong clade, but the phylogenetic position of the X=7 (*Berberis*, *Mahonia*, and *Ranzania*) group was not fixed. The largest chromosomal group, the X=6 group consisted of five distinctive clades; (1) *Jeffersonia* and *Plagiorhegma*, (2) *Achlys*, (3) *Bongardia*, (4) *Epimedium* and *Vancouveria*, (5) *Podophyllum*, *Sinopodophyllum*, *Dysosma*, and *Diphylleia*. Except the basal position of the *Jeffersonia* clade, the phylogenetic relationship among the rest clades was unresolved. More data are in need to clarify the phylogenetic position of the X=7 group and evolutionary relationships among the four clades within the X=6 group.

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**Phylogeny and Relationships
between Asian and Australian
Indigofera (Leguminosae) Based on
Nuclear Ribosomal DNA ITS
Sequences**

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The internal transcribed spacer (ITS) regions of 18-26S nuclear ribosomal DNA was sequenced to address the phylogenetic relationships and to measure the extent of differentiation among eighteen *Indigofera* species from Asia and Australia. ITS1 had 230-240 base pairs long while ITS2 had 210-215 bp long. The 5.8S rRNA coding gene was 161 bp long. Sequence divergences calculated by Kimura's two parameter method among species ranged from 0.3 to 12.5%. Six most parsimonious tree were produced from sixty five phylogenetic

informative nucleotide sites, which had a consistency index of 0.80 and a retention index of 0.75 with 242 tree length. And bootstrap and Jackknife analyses was performed to confirm its phylogenetic strength. ITS sequence data suggested that Australian species were diverged from SE Asian species. The bootstrap analysis showed strong monophyletic relationships among genus *Indigofera* comparing with the most related genera.

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A Genealogical Pattern of *Ginkgo biloba* L. on the Base of RAPD Analysis in Korea

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Ginkgo biloba L. has been cultivated for their conservative values and economic importances. This study was intended to reveal their regional and genealogical relationships, and to find genetic markers by using Random Amplified Polymorphic DNA(RAPD). We have collected seventy six plants of *Ginkgo* older than at least 200 years. Among them, forty four plants were compared for their genetic characteristics. On the base of the RAPD analysis, we expect to trace the genealogy of *Ginkgo* which has been planted during last one thousand three hundred years in Korea. Although we have not found out any specific marker yet, the phenogram of RAPD pattern of Korean *Ginkgo* was constructed by UPGMA and neighbour-joining methods.

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Cuticle Micromorphology of Leaves on the Genus *Fagus* L. (Fagaceae)

and Its Taxonomic Implications

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참나무과에 속하는 너도밤나무속(*Fagus* L.)은 북반구 온대지방에 분포하고, 전세계적으로 10여종이 알려져 있다. Shen, C. F.(1992)는 너도밤나무속을 나무의 수형과 수피, 각두와 포린의 형태 등을 가지고 2개의 아속과 4개의 절로 분류하였다. 너도밤나무속의 cuticle층의 미세구조에 대해서는 현생종과 화석 식물에 대한 비교 연구를 위해 다수 행하여 졌다 (Jones, 1984, 1986; Smiley C. J. & Huggins L. M. 1981). 그러나 너도밤나무속에 대한 Cuticle의 미세구조의 분류학적 유용성에 대해서는 언급된바 없다. 따라서 본 연구는 너도밤나무속에 속하는 8종(*F. engleriana*, *F. japonica*, *F. sylvatica*, *F. longipetiolata*, *F. lucida*, *F. hayatae*, *F. crenata*, *F. grandifolia*)의 잎의 큐티클 형질을 조사하였다. 그 결과 잎의 큐티클 층의 미세구조 중 표피세포의 형태, 왁스(wax)층의 발달유무, 기공의 형태, 기공의 크기, 기공 주위의 돌기물의 유무, 부세포의 형태, 공변세포의 돌출여부, stomata rim의 발달여부, areole line상의 모공의 유무 등이 뚜렷한 차이를 보였다. *Fagus* 아속(Subgenus *Fagus*)은 areole line위에 모공이 존재하고, 단모가 있으며, stomata rim이 뚜렷이 발달하였다. *Engleriana*아속(Subgenus *Engleriana* Camp ex Shen)은 표피세포가 다각형이며, 단모가 있으며, 왁스층이 잘 발달하였으며, 기공 주위에 둥근 돌기가 있고, 뚜렷한 부세포가 없으며, 기공의 형태는 원형이며, areole line 상의 모공은 없다. 이러한 잎의 큐티클 미세구조는 너도밤나무속내의 분류군의 분류학적 해석에 매우 유용한 것으로 밝혀졌다.

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Gynodioecy in *Lycopus lucidus* Turcz. (Lamiaceae) in Korea: A Confirmation for the Gender Dimorphism Based Mainly on Floral Morphology