

Oligocarpa 절의 14개 분류군들은 5쌍의 중부동원체염색체, 2쌍의 차중부동원체염색체 및 1쌍의 말부동원체염색체들로 구성된 기본적으로 동일한 핵형을 가지며, 이들 핵형은 부수체의 존재 여부와 그 위치에 있어 절간에 뚜렷한 차이를 나타낸다. 특히 *Cimicifuga* 절에 속한 10개 분류군들의 핵형은 부수체가 없거나 1개에서 4개의 염색체쌍에 부수체가 존재하는 핵형까지 중간에 다양한 변이를 나타내며, 이러한 부수체의 수 변이는 지리적 분포 양상과 관련이 있는 것으로 판단된다. *Macrotys* 절의 단일종인 *C. racemosa*의 핵형은 말부동원체염색체의 centromeric index가 3.5로 매우 낮다는 점에서, *Oligocarpa* 절 3종의 핵형은 말부동원체염색체의 장완에 부수체가 있다는 점에서 속내 다른 절들과 구분되었다. *Pityrosperma* 절과 *Podocarpa* 절 [= *Actaea* sect. *Podocarpae*]의 핵형은 상기 3절의 핵형과 달리 7번 염색체쌍이 차단부동원체염색체로 밝혀졌다. 북미에 분포하는 *Podocarpa* 절의 경우, *C. americana*의 핵형은 3번 중부동원체염색체쌍과 말부동원체염색체쌍에 부수체, *C. laciniata*의 핵형은 7번 차단부동원체염색체쌍에 부수체가 존재하는 점에 의해 다른 절 분류군들과 구분되었다.

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Molecular Phylogeny of *Polygonum* section *Echinocaulon* (Polygonaceae)

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Polygonum sect. *Echinocaulon* (Polygonaceae) is a highly variable and taxonomically difficult taxon consisting of 21 species. We have examined the ITS and *trnL-trnF* sequences from 18 taxa of sect. *Echinocaulon* to infer phylogenetic relationships among the taxa within the section. In all ITS and *trnL-trnF* trees, the taxa previously included in sect. *Echinocaulon* failed to form a monophyletic group: *P. bungeanum* was placed as sister to sect. *Persicaria*, suggesting that *P. bungeanum*

should be transferred from sect. *Echinocaulon* to sect. *Persicaria*. The consensus tree obtained from the combined molecular data sets revealed the presence of five major lineages in the section; these include (1) *P. perfoliatum*-*P. senticosum* var. *senticosum* clade, (2) *P. dissitiflorum* clade, (3) *P. sagittatum* clade, (4) a clade comprising *P. dichotomum* var. *dichotomum*, *P. praetermissum*, *P. hastatosagittatum*, *P. muricatum*, *P. strigosum*, *P. meisnerianum* var. *meisnerianum* and *P. stelligerum*, and (5) a clade including *P. arifolium*, *P. debile*, *P. breviochreatum*, *P. thunbergii* var. *thunbergii*, *P. thunbergii* var. *maackianum* and *P. biconvexum*. Relationships of the taxa depicted in the consensus tree are, in general, in agreement with those previously suggested by the comparative flavonoid chemistry. In addition, the results strongly suggest that *P. sagittatum* may once have had a more continuous range in the northern Hemisphere and fragmented into two widely separated disjunct populations of eastern Asia and eastern North America during Pleistocene glaciation.

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Taxonomic Revision of *Magnolia* section *Maingola* Dandy (Magnoliaceae) and the Multivariate Analysis of *Magnolia macklotii* Complex

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Magnolia section *Maingola* Dandy is distributed in tropical Southeast Asia from India (Assam) to Malay Archipelago extending Borneo. It is distinguished from other taxa in Magnoliaceae by the combination of terminal brachyblast, cylindrical fruit, and free stipule.

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