

restriction site variations of eight PCR-amplified chloroplast regions. 16 individuals were examined by maximum parsimony analysis, representing seven species of *Typha*. *Sparganium erectum* was used as the outgroup. The ITS and cp DNA trees are suggested the following relationships: (1) *Typha latifolia* is sister to clade consisting of all other *Typha* species (2) *T. domingensis* is closely related to *T. angustifolia* species (3) *T. orientalis* and *T. laxmanni* form monophyletic groups respectively (4) *T. glauca* clade forms monophyletic group in ITS tree whereas paraphyletic group in cp DNA tree (5) *T. angustifolia* is closely related in ITS tree whereas is detected the disjunction between Eurasia and North America in cp DNA tree.

A210 A Phenetic Analysis of *Typha* Using Morphological Characters

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We used principal components analysis (PCA) and UPGMA cluster analysis to determine taxonomically definable limits and to estimate the phenetic relationships among *Typha* species in the world using 24 quantitative characters. A scatter plot of the first two principal components (50.2% of total variance) resolved 9 clusters among 230 specimens of *Typha* examined by useful characters such as leaf apex angle, leaf width, gap between staminate and pistillate inflorescences, staminate inflorescence length, and pistillate inflorescence length. The clusters corresponded to eight currently recognized species except that *Typha angustifolia* and *T. domingensis* are incompletely separated with overlap. UPGMA also represented that individuals of *Typha* species form discrete clusters according to 9 cluster species. Although *T. angustifolia* and *T. domingensis* were not discrete in the results of PCA and UPGMA, *T. domingensis* is distinguished from *T. angustifolia* by qualitative morphological

characters such as nonauriculate leaf sheaths, bracteoles shape, club shape of abortive ovary, and subulate anthers.

A211 A Development of Specific DNA Marker for the Identification of the Cultivated Korean Ginseng (재배 인삼에 대한 DNA 마커 개발 연구)

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본 연구에서는 Random Amplified Polymorphic DNA(=RAPD) 방법을 사용하여 우리나라에서 재배되는 인삼(금산, 풍기, 개성, 강화)과 및 중국에 분포하는 장뇌삼(*Panax ginseng*) 5개체군 43개체에 대하여 UPGMA와 maximum parsimony 분석을 통하여 유연관계를 분석하였다. 외군으로는 미국산 *Panax quinquefolius*를 사용하였다. 총 120개의 RAPD primer에 대하여 20개의 primer에서 83개의 polymorphic DNA band가 관찰되었다. 그 중에서 62개는 한국과 중국에 분포하는 개체간에서 차이를 나타내고, 21개는 외군인 미국산 *Panax quinquefolius*와의 polymorphism을 나타내준다. UPGMA 분석결과 금산 개체군은 다른 지역에 비해 가장 낮은 변이를 나타내었다. 국내에서 재배되는 개체들은 지역별로 유집은 이루어지지 않았으나, 개성과 강화 지역에서 수집된 개체들은 높은 유연관계를 보여주었다. Maximum parsimony 분석결과는 지역별로는 구분이 되지 않았으며, 금산과 중국의 장뇌삼은 높은 유연관계를 나타내었다. 본 연구결과 다양한 PCR 기법을 이용하여 우리나라에서 재배되는 재배삼들의 지역간의 변이를 분석할 수 있었고, 이러한 결과는 우리나라 인삼과 근연종(*P. japonica*, *P. quinquefolius*)과의 유연관계 비교분석과 인삼속 전체의 계통관계 정립에 기초자료가 될 것으로 보인다.

A212 Molecular phylogeny and character evolution of *Jasminum* (Oleaceae)

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Jasminum is the largest genus in the

family Oleaceae. The species numbers are estimated from 150 to 450 depending on the authors. Several species are widely cultivated in all over the world. However, most species are distributed in Asian/African sub-/tropic regions. The genus is traditionally classified into two groups, section *Alternifolia* and the opposite-leaved group, based on the arrangement of leaves. The opposite-leaved group further classified into three sections: *Unifoliolata*, *Pinnatifolia* and *Trifoliolata*, based on the number of leaflets. Recent molecular sequence data suggest that the *Menodora* may include within *Jasminum*. In order to evaluate the phylogenetic relationships between *Menodora* and *Jasminum* and to estimate the evolutionary directions of leaf character in *Jasminum*, we sequenced the *trnT*-L-F regions (\approx 1600bp) of chloroplast genome and nuclear ITS regions (\approx 700bp) from including 16 species of *Menodora*, 70 species of *Jasminum*, and 10 outgroup genera. Both nuclear ITS and chloroplast *trnT*-L-F sequence data support the monophyly of three major clades including *Menodora*, alternate-leaved *Jasminum* and opposite-leaved *Jasminum*. The genus *Menodora* was nested within *Jasminum* and form a sister clade to the alternate-leaved *Jasminum*. Traditionary recognized three sections within the opposite-leaved *Jasminum* were not monophyletic and mixed each others in some species. The monophyly of *Menodora* was further supported by an unique 300bp insertion mutation in the chloroplast *trnT*-L noncoding region.

A213 Molecular phylogeny of the genus *Hypericum* (Hypericaceae) from Korea and Japan: an evidence from nuclear rDNA ITS sequence data

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Hypericum includes approximately 350-400

species, distributed in worldwide. Among them, 26 species are distributed in Korea and Japan. Although there has been considerable effort to resolve sectional circumscription and relationship of the genus *Hypericum*, much controversy still remain regarding these taxonomic issues in the genus. As a part of our ongoing phylogenetic study of the genus *Hypericum*, here we performed the phylogenetic analysis of the nuclear ribosomal DNA internal transcribed spacer(ITS) sequences from 24 Korean and Japanese species and three other outgroup species. The sampling included most of previously described species both from Korea and Japan. The ITS phylogeny suggest that *Hypericum* species from Korea and Japan grouped into three monophyletic sections (*Hypericum*, *Roscyna* and *Trigynobrathys*). *H. sampsonii* was treated to section *Hypericum* or to section *Drosocarpium* by previous morphological study, but ITS tree support the species as a member of section *Roscyna* or the distinct fourth section rather than section *Hypericum*. The taxonomically problematic *H. kamtschaticum* was a sister species of *H. erectum* within the section *Hypericum*. This result is in agreement with recent suggestions based on morphological and cytological studies. Phylogenetic relationships among species from Korea and Japan are mostly resolved on the ITS tree.

A214 생식기관 형태에 기초한 모데미풀의 계통분류학적 연구

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지금까지 모데미풀은 분류학적 위치에서 특산속으로의 처리에 많은 논란이 있으며 화분연구 및 그의 연구에서도 정확한 결론을 내리지 못하였다. 따라서 본연구는 한국 특산속 식물인 모데미풀의 계통분류학적 위치를 분명히 하기 위하여 모데미풀의 생식기관형성 초기부터 성숙종자단계까지의 재료를 사용하여 파라핀법으로 생식기관 해부형태를 조사하였다. 실험결과 모데미풀은 생식기관의 발달과정에