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한국산 참나무속 참나무아속(너도밤나무과)의 수리분류학적 연구

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본 연구에서는 한국산 참나무속 참나무아속(*Quercus* subg. *Quercus*) 6종 및 잡종 추정 개체들을 대상으로 수리분류학적 분석을 수행하여 형태학적 주요 식별형질의 변이 양상을 파악하고자 하였다. 잎, 견과, 각두 포린 등의 형태에 관한 49개의 형질들을 사용하여 전국에서 채집된 155개체를 대상으로 주성분분석을 수행한 결과, 한국산 본 아속 개체들은 (1) *Q. acutissima-Q. variabilis*, (2) *Q. dentata*, (3) *Q. aliena*, (4) *Q. mongolica*, 그리고 5) *Q. serrata* 개체들로 구성된 5개의 집단으로 구분되었고 잡종 추정 개체들은 대부분 추정 부모종 사이에 위치하였다. 동일한 data matrix를 사용한 유집분석에서도 비슷한 양상이 나타났다. 수리분류학적 분석에서 하나의 집단을 형성한 *Q. acutissima*와 *Q. variabilis*는 잎 하면 털의 종류 및 분포양상에서 뚜렷이 차이를 나타내므로 이를 종합해 볼 때 한국산 참나무아속 6종은 뚜렷이 구분되는 것으로 판단된다. 한편, 잡종 추정 개체들은 대체로 추정 부모종간 중간형을 띠는 것으로 나타났다. 한국산 본 아속 식물을 식별하고 잡종화 양상을 이해하는데 있어 잎의 크기와 모양, 엽신 하부의 형태, 거치의 크기와 형태, 소지의 직경, 견과의 모양, 각두 포린의 길이 등의 형질이 특히 유용하였다.

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A Taxonomic Study of the Genus *Spirogyra* (Zygnematales, Chlorophyta) in Korea

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A taxonomic study of the genus *Spirogyra*(Chlorophyta) were investigated to clarify their taxonomic limit and the variation range among species on the basis of comparative morphological, cytological and the numericalanalyses by unialgal cultures and fields samples collected from various freshwater habitats in Korea. 25 characters selected on morphological feature of the species were examined on 568 individuals for morphological comparisons and numerical analyses. Most characters showed a broad variation within species of which ranges were overlapped among taxa. In principal component analysis, width and length of vegetative cell, shape of septum, chloroplast number, width and length of female gametangium, size and shape of zygospore, and cell wall ornamentation of the spore showed a comparatively high vector. As a result, a total of 14 species and 1 variety including 1 new species and 11 unrecorded species in Korea were identified in this study. The number of chromosomes of Korean *Spirogyras* ranged from n=12 in *S. varians* to n=38 in *S. africana*.

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Phylogenetic Analysis of the Genus *Polygonatum* (Liliaceae) in Korea Based on Nuclear Ribosomal DNA ITS Region Sequences

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The phylogenetic analysis of 12 taxa of Genus *Polygonatum* distributed in korea were carried out by comparing their nucleotide sequences spacer(ITS) of nuclear ribosomal DNA. The lengh of the ITS1 and ITS2 regions varied from 138 to 243 bp and from 160 to 226bp, respectively. The 5.8S coding region was 156 bp long. The G+C contents of ITS1 ranged from 48.6 to 75.2% and ITS2 ranged from 50.0 to 80.2%. The pairwise distance between *P. stenophyllum* and *P. sibiricum* was 0.0044 showing the lowest value among any other pairs. On the other hand, the pairwise distance between *P. thumbergii* and *P. robustum*, *P. stenophyllum* was 0.1106 showing the highest value among any other pair. This results showed that ITS sequence ahalysis was a useful tool for elucidating phylogenetic relationship.

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Phylogeny of a New Candidate of *Griffithsia* from Korea Based on Morphological and Molecular Evidences

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A new candidate of *Griffithsia* from Korea was investigated by means of morphology and multigene analysis. Samples of the new candidate were taken from six locations: Chaguido, Gangjeong, and Moonseom in Jejudo, Geojedo and Wando on the South Coast, and Gampo on the East Coast. The new candidate is distinguished by having one carpogonial branch and very small thalli (≈0.5 cm), although it is similar to *G. japonica* and *G. okiensis* from Japan. Plastid protein-encoded *psaA*, *psbA*, and *rbcL* gene sequences were determined for nine *Griffithsia* including four different samples (Gampo, Geojedo, Moonseom, and Wando) of the new candidate and eight putative relatives, containing samples from the type locality of *G. japonica* and *G. okiensis*. All four samples of the new candidate were identical in the three plastid genes. However, the three coding gene sequences of the new taxon were different enough to warrant its natural entity. Trees from individual and concatenated data showed that the new taxon was more closely related to *G. okiensis* than to *G. japonica* and these three taxa were monophyletic. Our results are in accordance with reproductive morphology that tetrasporangia of the former group are naked or surrounded by involucres produced directly from axial cell, while tetrasporangia of the latter group are protected by involucres produced from stalk cells of tetrasporangial fascicles.