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Sequence Analysis of the 5.8S Ribosomal DNA and Internal Transcribed Spacers (ITS1 and ITS2) from Four Taxa of *Oxalis* (Oxalidaceae) in Korea
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A total 691-bp portion of the 5.8S ribosomal DNA and internal transcribed spacers, ITS1 and ITS2, was sequenced in four taxa of the Korean *Oxalis* in order to examine the degree of sequence divergences and phylogenetic relationships among taxa. The sequences of the same DNA region, deposited in the GeneBank, of 16 *Oxalis* taxa were also included in the genetic analysis as an out group and/or comparative data. The sequence divergences both between *O. corniculata* and *O. corniculata* f. *erecta* and between *O. acetosella* and *O. obtriangulata* were appeared to low as less than 10%. However, the sequence divergences both between *O. corniculata* and *O. acetosella* and between *O. corniculata* f. *erecta* and *O. obtriangulata* were appeared to high relatively as around 50%. The strict consensus tree showed the monophyly of the Korean *Oxalis*, and they were grouped into two; one consists of *O. corniculata* and *O. corniculata* f. *erecta*, the other *O. acetosella* and *O. obtriangulata*. The topology of phylogenetic relationships highlighted the strong bootstrap support (100%) for the four taxa of the Korean *Oxalis*.

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한국산 산제비란(난과)의 형태적 변이
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산제비란(*Platanthera mandarinorum*)은 동북아시아 지역에 널리 분포하며, 형태적 변이가 심하여 중국과 일본 등에서 많은 종내 분류군이 보고되어 왔다. 본 연구에서는 한국산 산제비란의 분류학적 연구를 위해 우선 형태적 변이를 조사하였다. 한반도 자생 식물 집단 또는 개체 간의 변이를 조사하고, 동시에 일본의 표본을 비교하였다. 조사 결과, 잎과 화피편의 모양은 집단 내 변이가 심하여 종내 분류군을 나누는 분류형질이 될 수 없지만, 거의 길이와 형태 등은 지리적 분포에 따라 차이가 있음을 알 수 있었다. 지리적 분포와 거의 형태에 따라 한국산 산제비란은 *P. mandarinorum* 내 3변종으로 다음과 같이 정리되었다. *P. mandarinorum* var. *neglecta* (Schltr.) F.Maek.는 전국에 분포하고, 거는 위를 향해 뻗어 있으며 끝부분이 S자형으로 휘어지고, 기부에서부터 3/4 지점까지 두꺼워지다가 얇아진다. *P. mandarinorum* var. *cornubovis* (Nevski) Kitag.는 홍도와 그 북쪽에서 발견되며, 거는 많이 휘어지고 길이는 13~26 mm로 두께 변화는 거의 없다. *P. mandarinorum* var. *brachycentron* (Franch. et Sav.) Koidz. ex Ohwi는 홍도와 제주도에서 발견되며, 거는 약간 휘어지거나 휘어지지 않고 아래쪽이나 뒤를 향하며 길이는 11~17 mm로 두께 변화는 거의 없다.

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A Taxonomic Study of Korean Anacardiaceae Based on Morphology and Numerical Analysis
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Morphological characters of six Anacardiaceae species (*Rhus* and *Toxicodendron*) in Korea were examined to elucidate their taxonomic identities. Based on the morphological review, the new key for the Korean Anacardiaceae was made up. Principle components analysis (PCA) of 28 Korean Anacardiaceae OTUs using 68 morphological characters were applied to taxonomic delimitations. PCA results did not support the previous taxonomic relationship by chemical components. On the other hand, present study showed the importance of plant habit. From the PCA results, six taxa of two genera were grouped distinctly as species clusters including each populations.

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Molecular Phylogeny of Tribe Forsythieae (Oleaceae) Inferred from Plastid DNA *trnK* sequences
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Phylogenetic studies were conducted to define the systematic problems and phylogenetic relationships of tribe Forsythieae (13 taxa of *Abeliophyllum* and *Forsythia*) and its related groups (4 species of *Fontanesia* and *Jasminum*) using plastid DNA *trnK* sequences. The molecular systematic result suggested the monophyly of tribe Forsythieae, and Fontanesia (tribe Fontanesiae) was the very close group of tribe Forsythieae. Phylogenetic relationships between *Abeliophyllum* and *Forsythia* resolved clearly on the phylogenetic tree from plastid DNA *trnK* sequences. Also, present result supported the previous morphological, RAPD, and nrDNA ITS data.