A201 Molecular phylogeny of Quercus (Fagaceae) based on 160 nuclear ITS sequences

Kyung Choi*[1], Chong-Wook Park[2], Byung-Yun Sun[3], Jae-Hong Pak[4], Myong Gi Chung5 and and Ki-Joong Kim[1]
[1]Department of Biology, Yeungnam University; [2]Department of Biology, Seoul National University; [3]Department of Biology, Chonbuk National University; [4]Department of Biology, Kyungpook National University; 5Department of Biology, Gyeongsang National University

The genus *Quercus* comprises approximately 500 species distributed throught the Northern Hemisphere and economically important genera of woody plants. There are three major distribution centers in the world including North America, Europe and Eastern Asia. The Eastern Asia has the highest species diversity and almost 250 species are recognized in this region. Many primitive species of *Quercus* are also recognized in this region. In order to elucidate the phylogeny of the genus, we reconstructed the phylogeny of the *Quercus* species based on the 160 nuclear ITS sequences from 136 individuals. Subgenus *Cyclobalanopsis* forms a basal clade which is sister clade to the subgenus *Quercus* . The white oak, section *Quercus* sensu Nixon is not a monophylectic group. The section *Quercus* can be recognized two major groups, *Cerris* and *Quercus s.str*. ITS data suggest the basal placement of Eurasian white oak, *Cerris* group within subgenus *Quercus* . Also, the intermediate oak, section *Protobalanus* is not a monophyletic group. The four major infrageneric groups (*Cyclobalanopsis*- (*Cerris* -(*Lobatae*- (*Quercus s.str* +*Protobalanus*)))) are recognized within the genus *Quercus* based on the ITS sequences. Moreover, more than two copies of ITS sequences are recognized from a single individual of many species.

A202 Genetic Diversity and Population Structure of Wild and Cultivated Brown Sea Mustard, Undaria pinnatifida

Man Kyu Huh*[1], Sung Gi Moon[2] and Hong Wook Huh[1]
[1]Department of Biology Education Pusan National University; [2]Department of Biology Kyungsung University

Genetic diversity has been studied extensively in the cultivated brown seaweed, *Undaria pinnatifida* (Harvey) Suringar. Compared with other ecologically and economically significant species, population structure of this species has not been studied. Starch gel electrophoresis was used to investigate the allozyme variation and genetic structure of ten Korean populations of this species. The percentage of polymorphic loci was 33.3%. Genetic diversity was high at the species level (Hes = 0.146); whereas, that of the population level was relatively low (Hep = 0.068). Nearly 86% of the total genetic diversity in *U. pinnatifida* was apportioned within populations. The sexual reproduction, perennial, high fecundity, and colonization process are proposed as possible factors contributing to high genetic diversity. The indirect estimated of gene flow based on Gst was 1.54.

A203 한국 특산 노랑무늬붓꽃(붓꽃과: 금붓꽃계열)의 생식생물학적연구

박경원*, 홍석표
경희대학교 문리과대학 생물학과

한국특산식물인 노랑무늬붓꽃(*Iris odaesanensis* Y. N. Lee)의 자연집단 중 경상북도 청송군 주왕산의 해발 400m의 계곡집단과, 경상북도 영주시 소백산의 해발 1430m지점의 능선의 집단을 대상으로 생식생물학적 연구를 하였다. 주왕산 집단의 주요한 수분매개자(pollinator)는 '산흰줄범하늘소(*Clytus raddensis* 58.33%)' 이었으며, 소백산 집단의 주요한 수분매개자는 '줄진하늘소붙이(*Chrysarthia viatica* 74.41%)' 이었다. 종자에

는 뚜렷한 부속체(elaiosome)가 있었다. 종자의 분산매개자(dispersal vector)로 주왕산 집단에서 ′짱구개미(*Messor aciculatum*)′가 관찰되었다. 또한 노랑무늬붓꽃의 꽃의 해부학적 구조와 수분매개자간의 적합성(fitness)에 대하여 간략하게 고찰하였다.

A204 Systematic significance of seed morphology in tribe Hyoscyameae (Solanaceae): An interpretation of homology

Jin-Hyub Paik* and Suk-Pyo Hong
Laboratory of Plant Systematics, Department of Biology, Kyung Hee University, Seoul 130-701, Korea

The Seed micromorphological studies including anatomy of seven genera in the tribe Hyoscyameae (*Scopolia* Jacq., *Anisodus* Link et Otto, *Atropanthe* Pascher, *Przewalskia* Maxim., *Atropa* L., *Hyoscyamus* L., *Mandragora* L., except *Physochlaina* G. Don.) were carried out using the SEM (including an enzyme etching pre-treatment) and LM. Characteristics of the seeds and their surface cells between/among the investigated taxa are described and compared. In general, the seeds are reniform/subreniform, rectangular or circular in outline and 2.0-5.4㎜ long in size. The seed-coat ornamentation is basically reticulate/ruglo-reticulate, and the lumen is 250-445 X 130-400㎛ in size. Three patterns of the external seed testa can be recognized: 1. The cell walls of the spermoderm are straight (in *Scopolia* s. str. and *Atropanthe*), 2. sinuate (in *Anisodus* and *Przewalskia*), or 3. semi sinuate (in *Atropa*, *Mandragora* and *Hyoscyamus*). The seed testa is usually 120-180㎛, but rarely up to 400㎛ (in *Atropanthe*) in thickness. On the baisis of anatomical data of studied taxa can be distingushied into six groups. The results are compared with the earlier postulated phylogenies of these taxa in the tribe Hyoscyameae, and the possible transformation of seed characters is also briefly discussed.

A205 경기만 염습지의 식물상

심현보*, 서석민, 최병희
인하대학교 생명과학과

경기만 연안과 도서지역의 염습지 식물상을 조사하였다. 조사는 1999년 4월부터 2001년 10월까지 14개 지역의 36개 염습지를 대상으로 자연염습지, 사구, 폐염전, 제방으로 나누어 이루어졌다. 본 조사에서 염생식물은 16과 29속 40종이 확인되었는데, 이 중 자연 염습지에만 서식하는 식물은 지채, 천일사초, 퉁퉁마디, 방석나물, 나문재, 해홍나물, 칠면초 등 7종이었으며, 갯방풍, 갯사상자, 갯쇠보리, 모래지치, 갯씀바귀 등 5종은 사구에서만 서식하였고, 28종은 염습지와 제방 모두에서 자라고 있었다. 또한 염습지의 특성에 따라 자연염습지에 14종, 사구에 23종, 폐염전에 33종이 분포하고 있었다. 염습지 식물중 나문재속(*Suaeda*)의 칠면초(*S. japonica*)와 해홍나물(*S. martima*)이 거의 모든 지역에서 가장 넓게 순군락을 형성하고 있었다. 본 조사에서 나문재속의 국내 미기록종으로 판단되는 식물이 채집되었는데, 이 식물은 같은 속의 다른 종과 개화기, 줄기의 분지, 잎의 형태, 종자의 모양 및 생육지 등에 차이를 보였다. 이들 지역에서 조사된 관속식물은 총 255종이며, 이 중 귀화식물은 39종이었는데, 염생식물을 제외한 나머지 관속식물은 주로 제방에 자라는 해안성 식물이었다.

A206 Phylogentic Relationship among several Genera of Dictyotaceae (Dictyotales) based on 18S rRNA and Partial rbcL Gene Sequences

Wook Jae Lee and Kyung Sook Bae
Korean Collection for Type Cultures, Korea Research Institute of Bioscience & Biotechnology

The partial sequences of the rbcL gene, RuBisCo spacer region and the 18S rRNA gene of representatives of the Dictyotaceae were determined and compared to determine their phylogenetic relationship. The 1861 bases pairs of 18S rDNA sequences were aligned and examined. The aligned 422 bases of partial rbcL gene sequences give similar phylogenetic relationship among taxa as the 18S rDNA sequences. The genera of