carapace spine, a spinous tip of the antenna, and no chromatophore on the base of a dorsal carapace spine in the subfamily Philyrinae.

A801 Random Amplified Polymorphic DNA Variation of Porphyra dentata (Bangiales, Rhodophyta) in the Southern West Coast of Korea

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The RAPD-PCR technique was used to analyze DNA level variation in 12 isolates of *Porphyra dentata* . Of thirty-eight arbitrary primers tested,five primers were able to generate reproducible amplication products. The main band of amplication patterns was shared between populations of *P. dentata* and a population of *P. pseudolinearis* used as an outgroup, the band sharing indices (BSI) between these two species, however, were much lower and the genetic distance indices (DI) were much higher. The level of BSI was relatively high among nine populations of *P. dentata* and DI was relatively low among nine populations. These results suggest that the RAPD-PCR method provides evidence for identification and estimation of genetic differentiation among populations within a species of the genus *Porphyra*.

A802 Phylogenetic relationship in the nuclear ribosomal DNA internal transcribed spacer(ITS) region of Acanthopanax

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The Araliaceae, Acanthopanax are distributed over 600 species of 60 genius, which the most of their are an arbores and herbs in the world. In Korea about 20 species have been reported, continuously made clear a new species and a variety. DNA homology analysis of the Acanthopanax is study, because these are many difficult to classify on their morphological characters. We studied phylogenetic relationship of korea 22 Acanthopanax species analysing ITS sequence of rDNA and rbcL gene. About 600 ~700 base pairs of rDNA region were PCR-amplified and sequenced. The data obtained was compared with GenBank data base. The comparison of ITS sequences in the species through multiple alignments had homology with the known sequences. In addition same method was applied to rbcL gene.

A803 Molecular phylogeny and evolution between Prunus yedoensis and its related species inferred from ITS and rbcL gene sequences

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Molecular phylogeny and evolution between *Prunus yedoensis* and its related 5 species, which have been estimated the parents of *P. yedoensis* were analyzed by comparing nucleotide sequences of ITS of nrDNA and *rbc*L gene of cpDNA. The ITS regions of the nrDNA and *rbc*L gene were amplified directly by symmetric polymerase chain reaction using universal primers. Sequence alignment required 11.1 and 3.9% sequence variation sites in ITS regions and *rbc*L gene, respectively. Interestingly, the variation sites showed differently between *P. yedoensis* native (Jeju, Korea) and the cultivars. Five-bp deletions were found in the ITS1 region of the four individuals of *P. yedoensis* native plants. On the other hand, five-bp deletions were detected in the ITS2 regions of the six individuals of the cultivated *P. yedoensis* compared with the sequence of the other *Prunus* species. In most parsimonious trees, four specimens of

P. yedoensis from Jeju were clearly distinguished from the cultivar plants. On the other hand, the analyses of the ITS and *rbc*L gene sequences showed that *P. pendular* for. *ascendens* was more closely related to the population of *P. yedoensis*, making the latter one of the putative parents of *P. yedoensis*. These results suggest that ITS and *rbc*L gene sequences analyses are useful approaches for inferring molecular phylogeny and evolution between *P. yedoensis* and its related species.

A804 Comparison of genus Polgonatum using ITS(Internal Transcribed Spacers)and rbcL gene

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The genus *Polgonatum* belongs to Polygonatae of Liliaceae, which contains about 58 species in the world. In Korea 14 species and 2 varieties have been reported in this genus. The phylogeny of the genus *Polgonatum* is still in debate, because these are many different opinions on their morphological characters. We studied phylogenetic relationship of korea 14 *Polgonatum* species analysing ITS sequence of rDNA and *rbc*L gene. About 650~680base pairs of rDNA region were PCR-amplified and sequenced. The data obtained was compared with GenBank data base. The comparison of ITS sequences in the species through multiple alignments had homology with the known sequences. In addition same method was applied to *rbc*L gene.

A805 DNA Fingerprinting and Identification of Three Angelica Species using AFLP(amplified fragment length polymorphism) Markers

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This study was conducted to investigate genetic variability of herb medicine, to develop the three Angelica species-specific DNA marker and to estimate phylogenetic relationships among *Angelica gigas* Nakai, *A. sinensis*(Oliv.) Diels., *A. acutiloba* Kitagawa using AFLP(amplified fragment length polymorhism) markers as a fingerprinting technique. Two EcoRI and two MseI primers used in 8 primer combinations generated a total 262 bands, of which 25 were clearly polymorphic among the accessions. Three primer combinations were selected according to their reproducibility, number of polymorphic bands and polymorphism detected between three Angelica species. we propose that genomic fingerprinting techniques such as AFLP can be used as rapid, highly discriminatory screening techniques to determine the herb medicine.

A806 Identification and Phylogeny of Long Terminal Repeat Elements of Human Endogenous Retrovirus HERV-S

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A new human endogenous retroviral family (HERV-S) has recently been identified from human X chromosome. It is 6.7 kb in length and has a typical retroviral structure with LTR-gag-pol-env-LTR. Using the PCR and sequencing approach, we investigated LTR elements of the HERV-S family from a human genomic DNA. Four LTR elements (HSL-1, HSL-5, HSL-10, HSL-11) were identified and have a high degree of sequence similarity (96-99%) with