

A722

**A Revision of the Genus *Synagelides*
Strand, 1906 (Araneae: Salticidae)
from Korea**

Byung-Woo Kim* and Joo-Pil Kim

Dept. of Biology, Dongguk University, Seoul
100-715; The Arachnological Institute of Korea,
Seoul 133-040

Two species, *S. agoriformis* Boesenberg et Strand, 1906 and *S. zhilcova* Proszynski, 1976 of the genus *Synagelides* from Korea are revised with accurate illustration and identification key. The latter species is newly recorded in the Korean spider fauna. These species can be easily identified by the copulatory openings and the position of the genital organs with copulatory canal and spermatheca.

A723

**New Records of Two Echinoids
(Echinodermata: Echinoidea) in
Korea**

Sook Shin*

Dept. of Biology, Sahmyook University, Seoul
139-742

Some echinoids were collected at a depth of 20m in Cheju Island, Korea. Of which two species were identified as *Diadema setosum* (Leske, 1778) belonging to family Diadematidae, order Diadematoida and *Toxopneustes pileolus* (Lamarck, 1816) belonging to family Toxopneustidae, order Echinoida. These species turned out to be new to the Korean fauna and were redescribed on the morphological characteristics with illustrations.

A724

**Phylogenetic Analysis of HERV-W LTR
Elements in Humans and Primates**

**Seung-Heui Jeon, Joo-Young Choi,
Joo-Mi Lee, Jun-Seop Kim, Won-Ho Lee,
and Heui-Soo Kim**

Division of Biological Sciences, College of Natural
Sciences, Pusan National University, Pusan
609-735, Korea

Human endogenous retroviruses W family (HERV-W) includes multiple sclerosis-associated retrovirus (MSRV) sequences identified in particles recovered from monocyte cultures from patients with multiple sclerosis. Long terminal repeat (LTR) of HERV-W family have been found to be coexpressed with sequences of closely located genes. We identified thirteen HERV-W LTR elements from the cDNA libraries of human fetal brain and placenta, and analyzed them along with sequences on the human X chromosome and other primate species (Old and New World monkeys). A phylogenetic analysis by neighbor-joining method revealed the close relationships between and within the species with a high degree of sequence similarity. The result suggests that HERV-W LTR elements have evolved independently during primate evolution.

A801

**Concerted Evolution of Duplicated
 α -Amylase Gene in *Drosophila*
melanogaster by Intrachromosomal
Gene Conversion**

**Seung-Hyun Sung*, Seon-Ock Woo and
Dong-Sang Suh**

Dept. of Genetic Engineering, Sungkyunkwan
University, Suwon 440-746

The duplication of the genes is one of the simplest cases of a multigene family and the conversion between duplicated genes limits their independent evolution. Demonstration

of the existence of inversion between the duplicated genes supports the concerted evolution of the gene copies. Rapid rates of gene conversion were observed between duplicated α -amylase coding sequences in *Drosophila melanogaster*. It has been reported that the interspecific sequence divergence between the coding regions is greater than the divergence between gene copies within a species and duplicated coding sequences can to facilitate mitotic recombination. In order to detect intrachromosomal inversion of α -amylase gene, primers were selected from the highly divergent flanking regions of *Amy-p* and *Amy-d* and using the established PCR method, the evidence of inversion was clued and developed. The frequency of inversion in natural population was $7.018 \pm 0.001 \times 10^{-3}$ and six homozygous lines of inversion mutants were made by curly method. These homozygous lines had activity of AMY¹ isozyme and southern analysis revealed that inversion was occurred in α -amylase genes. The both inverted amy genes were amplified by developed PCR method and were cloned in plasmid vector. We analyzed those sequences confirming the gene rearrangement as well as the inversion between two duplicated genes. And also the results of nucleotide substitutions between *Amy-p* and *Amy-d* in standard type and inversion types suggested the improvements of the fact that gene recombination involved gene conversion and mismatch repair leads to gene exchange and then concerted evolution is caused by frequent gene exchange in natural population. This study could provide a clear demonstration that recurrent gene conversion as well as gene rearrangement indeed lead to the concerted evolution of the gene pair.

A802

Phylogenetic Relationship among Selected Taxa of Genus *Goodyera* Based on nrDNA ITS1 Sequences

Che-Hoan Kim*, Yong-Uk Chung, Ji-Hoon Song, Yong-Hwan Jung, Sang-Hyun Han and Moon-You Oh

Department of Biology, Cheju National University, Cheju 690-756

Phylogenetic relationship among five species of Genus *Goodyera* (*G. schlechtendaliana*, *G. chejuana*, *G. macrantha*, *G. maximowicziana* and *G. velutina*) distributed in Mt. Halla (Cheju) was analyzed by comparing the nucleotide sequences of the internal transcribed spacer 1 (ITS1) region. The nrDNA ITS1 region was amplified with the universal ITS primers (ITS1 and ITS2) by polymerase chain reaction (PCR). The length of the nrDNA ITS1 region identically represented in 238 base pairs (bp) among selected taxa. The G+C contents of the nrDNA ITS1 region ranged from 45.4% (*G. macrantha*) to 46.6% (*G. schlechtendaliana*). In the comparing of the nucleotide sequences among selected taxa, fifteen sites of point mutation (base substitution) were found. The pairwise distance between *G. macrantha* and *G. maximowicziana* was 0.0043 showing the lowest value among any other pairs.

A803

Phylogenetic Relationships among Araliaceae in Cheju Island Based on the Internal Transcribed Spacer 1 Sequences of Nuclear Ribosomal DNA

Sang-Hyun Han*, Yong-Hwan Jung, Mi-Hee Ko, You-Sung Oh, Yu-Kyong Kim, Sun-Kyong Lim and Moon-You Oh

Department of Biology, Cheju National University, Cheju 690-756

We analyzed the phylogenetic relationships among Araliaceae plants growing in Cheju island. Seven genus (*Aralia*, *Dendropanax*, *Acanthopanax*, *Kalopanax*, *Tetrapanax*, *Hedra* and *Fatsia*) including 8

species of Araliaceae were sampled from Cheju island and nuclear ribosomal DNA (nrDNA) internal transcribed spacer (ITS) of 6 species sequenced. The nrDNA fragment flanking ITS 1 was amplified by PCR and compared with their conformations by single-stranded conformation polymorphism (SSCP) analysis. There were three significantly different types. With the ITS 1 sequences, we constructed the phylogenetic tree to conclude the intergenic relationships. The computed multiple alignments showed no difference in partial sequences of two coding regions; 5.8S and 18S nrDNA included in amplified products. The length of ITS 1 appeared from 221 bp to 223 bp and (G+C) contents included in the range of flowering plants. The ITS 1 tree was branched into three subgroups; *Acanthopanax-Kalopanax-Panax-Aralia*, *Dendropanax-Fatsia* and *Hedera*, though the results were not identical to SSCP types exactly. More informations on other molecular data should be added to say the evolutionary relationships among them.