

unidentified species were collected. A new species of the Genus *Tanytarsus* and *Chironomus javanus* (Kieffer), an unrecorded species from the Korean fauna were identified, and are fully described with illustrations. *Tanytarsus* sp. nov. was 3th dominant species in the reclaimed rice fields, occurring from late April to the end of September, with the peak density (71.8 adults/m²/day) at 3rd week of June. The absolute density of the new species population was 1,990 adults/m²/season in average of 1997-1999.

A715 Mitochondrial Cytochrome b Gene Sequence Diversity in the Korean Hare, *Lepus coreanus* Thomas (Mammalia, Lagomorpha)

Hung Sun Koh, Tae Young Chun^{*}, Hye Sook Yoo and Ya-ping Zhang

Dept. of Biology, Chungbuk University, Korea;
Kunming Institute of Zoology, Chinese Academy of Sciences, China

Partial sequences of the mitochondrial cytochrome b gene of the Korean hare (*Lepus coreanus*) were analyzed to determine the degree of genetic diversity. Nine haplotypes were observed, and the maximum Tamura-Nei nucleotide distance among them was 2.8%, indicating that the genetic diversity of *L. coreanus* is moderate. In order to clarify the Korean hare's taxonomic status and relationship with the Manchurian hare (*L. mandschuricus*) and the Chinese hare (*L. sinensis*), these nine haplotypes of the Korean hare were compared with 13 haplotypes from other five species of eastern Asian *Lepus* including *L. mandschuricus* and *L. sinensis*. The Korean hare was distinct in its cytochrome b gene, and it is confirmed that *L. coreanus* is a valid species, as noted by Jones & Johnson (1965).

A716 A New Record of Scyphomedusa (Semaestomeae, Pelagiidae) from Geojedo Island, Korea

Jung Hee Park

Department of Life Science, College of Natural Sciences, The University of Suwon

Some scyphomedusae were collected from the coasts of Geojedo Island (Changson), Korea on 26th June 2000. They were found in groups together, and identified into *Chrysaora melanaster* Brandt, 1838 of the order Semaestomeae. Bell light brown, about 90mm wide, flatter than hemispherical in preservation. 32 reddish-brown radial lines upon exumbrella. Oral lobes with finely frilly margin, about 3-4 times as long as bell diameter, 4 in number. Tentacles reddish brown color, laterally compressed, 3-5 per octant. Radial canals 16, rhopalia 8, lappets 48 in number and no ocelli. It is similar with *Dactylometra quinquecirrha* in many taxonomic characters. But it is readily distinguished from the latter which has 16 radial lines. As a result, 3 scyphomedusae are reported from Korean waters so far.

A717 Zoeal Stages of *Philyra kanekoi* Sakai, 1934 (Crustacea: Decapoda: Leucosiidae) Reared in the Laboratory

Hyun Sook Ko

Department of Biology, Silla University

The zoeal stages of *Philyra kanekoi* Sakai, 1934 from hatching were obtained by laboratory rearing. Three zoeal stages were described and illustrated in detail. Zoeal morphology is compared with that of other described species of the family Leucosiidae and a provisional key was provided. Morphological comparisons with congeneric species revealed that zoeas of *P. kanekoi* to be more similar to zoeas of *P. pisum* and *P. platychira* than to zoeas of three other *Philyra* species. But the present material could be identified by having no dorsal

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

Sung-Je Choi¹ and Jong-Ahm Shin²
Kohung Fisheries Technology Institute, Yosu Regional Maritime Affairs and Fisheries Office¹; Department of Aquaculture, Yosu National University²

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*

Hyelyun Lim¹ and Euisoo Yoon²
Department of Life Science, Kongju National University

The Araliaceae, *Acanthopanax* are distributed over 600 species of 60 genus, which the most of their are an arboreans 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

Yong Hwan Jung¹, Sang Hyun Han, You Sung Oh and Moon You Oh
Department of Biology, Cheju National University

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 *rbcL* gene of cpDNA. The ITS regions of the nrDNA and *rbcL* 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 *rbcL* 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