

illustrated. The present species resembles *Phyllopodopsyllus medius* among the reported species of the genus *Phyllopodopsyllus* in respects to the segmentation of the antennule, the setal formula of exopodites of the second, third and fourth leg. But the present species is easily distinguishable from *Phyllopodopsyllus medius* by the setal formula of endopodites of the second, third and fourth leg.

A704

한국산 각질해면류 (보통해면 강:
망각해면 목)의 한국 2 미기록종

이 경진*, 심 정자
한남대학교 생물학과

1994년부터 2000년까지 한국 제주도, 거문도, 가거도에서 SCUBA를 이용하여 채집된 망각해면류를 동정·분류한 결과 각질해면과 (Spongiidae)의 2종 *Spongia tubulifera* Lamarck, 1814와 *Hyattella intestinalis* Lamarck, 1814가 한국 미기록종으로 밝혀져 보고하고자 한다. *S. tubulifera*는 수심 10-15m에 분포하는 종으로 바위를 두껍게 덮어싸면서 부정형의 덩어리 형태로 성장하며, 표면에 돌출된 많은 봉오리의 끝에는 대공이 열려져 있다. *H. intestinalis*는 수심 20-25m에 분포하는 종으로 바위를 덮어싸며 성장하고, 몸 전체에 불규칙한 많은 구멍이 대공처럼 열려져 있다. 이로써 한국 각질해면과에는 모두 4종이 보고되며, 특히 *Hyattella*는 국내에 처음 보고되는 속 (genus)이다.

A705

*Dimorphostylis*속의 한국산
올챙이새우류(Cumacea) 1신종후보에
관하여

이창욱*, 이경숙
단국대학교 기초과학부 생물학전공

1998년 6월부터 2000년 7월까지 황해와 남해 연안에서 채집된 올챙이새우류를 동정, 분

류한 결과 *Dimorphostylis*속의 1신종후보 (*Dimorphostylis* n. sp.)가 밝혀졌기에 보고하고자 한다. 본 종은 그동안 한국연안에서 보고된 *Dimorphostylisasiatica* Zimmer, 1920, *D. valida* Harada, 1960 그리고 *D. acroplicata* Harada, 1960과 매우 유사하나, 갑각에 나타나는 주름의 양상, 꼬리의 길이 그리고 꼬리에 장식된 가시의 크기와 수에 있어서 독특한 조합을 보인다. 특히, 이들 4종의 수컷 모두는 꼬리 끝에 3개의 가시(apical spines)를 가지는데, 본 종은 3개의 가시 중 가운데 가시가 매우 작은 것이 큰 특징이다.

A706

Is Myriapoda the Earliest-diverged
Extant Arthropod ?

Ui Wook Hwang^{*1,2}, Chan Jong Park¹
and Won Kim¹

School of Biological Sciences, Seoul National University, Seoul 151-742¹; Dept. of Parasitology, Yonsei University College of Medicine, Seoul, 120-752²

Arthropod phylogeny has been still unclear, in which phylogenetic position of Myriapoda remains as the most enigmatic question. In the traditional view based on morphological and paleontological evidences, the sister group of Myriapoda has been believed to be Insecta. In contrast, recent molecular evidences have supported Myriapoda + Chelicerata or the earliest diversification of Myriapoda in arthropod evolution. In order to elucidate the phylogenetic position of Myriapoda with a variety of information derived from arthropod mtDNA, we determined the first complete myriapod mtDNA sequence (15,437 bp) from a centipede, *Lithobius forficatus*. Its gene arrangement is similar to those shown in typical arthropods. Especially, it is completely same with that of *Limulus polyphemus* except for tRNACys gene (C) position. *Lithobius* C is located immediately after the A+T rich region and thus tRNATrp gene (W) and tRNATyr gene (Y) are directly abutted contrasting with WCY generally

shown in the other arthropods known so far. WY arrangement is observed over a wide range of primitive animal groups such as 1 nematode, 2 annelids, 5 molluscs, and even 1 cnidarian. This strongly suggests that WY is a plesiomorphic character rather than an autapomorphic character (translocation of C from WCY) occurred in the myriapod evolutionary lineage. Consequently, gene arrangement under the parsimonious criteria supports (((Insecta, Crustacea) Chelicerata) Myriapoda) relationship as well as arthropod monophyly. In addition, phylogenetic analysis based on nucleotide sequences of first and second codon positions from 6 mitochondrial protein coding genes (COI, II, III, ND2, ND3, and ATPase6) are in accordance with the conclusion inferred from gene arrangement. Both gene arrangement and mtDNA sequence data coincidentally indicate that Myriapoda (or only Chilopoda) is the earliest-diverged extant arthropod.

A707

One-Step PCR Amplification of Complete Arthropod Mitochondrial Genomes

Ui Wook Hwang^{1,2}, Chan Jong Park¹, Tai Soon Yong² and Won Kim¹

School of Biological Sciences, Seoul National University, Seoul 151-742¹; Dept. of Parasitology, Yonsei University College of Medicine, Seoul, 120-752²

A new PCR primer set which enables one-step amplification of complete arthropod mitochondrial genomes was designed from two conserved 16S rDNA regions for long PCR technique. For the purpose, partial 16S rDNAs amplified with universal primers, 16SA and 16SB were newly sequenced from 6 representative arthropods, *Armadillidium vulgare* and *Macrobranchium niponense* (Crustacea), *Anopheles sinensis* (Insecta), *Lithobius forficatus* and *Megaphyllum* sp. (Myriapoda), and *Limulus*

polyphemus (Chelicerata). The genomic locations of two new primers, HPK16Saa and HPK16Sbb, correspond to positions 13314-13345 and 12951 - 12984 in the *Drosophila yakuba* mitochondrial genome, respectively. The usefulness of the primer set was experimentally examined and confirmed with 5 representative arthropods excepting *A. vulgare* having a linearized mitochondrial genome. With this set, therefore, we can easily and rapidly amplify complete mitochondrial genomes with small amount of arthropod DNA. Although the primers suggested here were examined only with arthropod groups, a possibility for successful application to work with other invertebrates is very high, since the high degree of sequence conservation shown in the primer sites in other invertebrates. Thus, this primer set can serve various research fields, such as molecular evolution, population genetics and molecular phylogenetics based on DNA sequences, RFLP, and gene rearrangement of mitochondrial genomes in arthropods and other invertebrates.

A708

Phylogeny of the Vetigastropoda (Mollusca: Gastropoda) Based on the 18S rDNA Sequences

Sook Hee Yoon¹, Byung Lae Choe¹ and Won Kim²

Department of Biological Sciences, Sung Kyun Kwan University, Suwon 440-740¹; School of Biological Sciences, Seoul National University, Seoul 151-742²

The 18S rDNA has been used as one of the most frequent and reliable indicators for elucidating phylogenetic relationships among both closely and distantly related taxa. In order to investigate the phylogeny of Vetigastropoda, the complete 18S rDNA sequences were determined for three new vetigastropods (*Macroschisma dilatatum*, *Tugali gigas*, and *Chlorostoma argyrostoma*