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 arragement under the parsimonious criteria supports (((Insecta, Crustacea) Chelicerata) Myriapoda) relationship as well as arthrpod 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 coincedently indicate that Myriapoda (or only Chilopoda) is the earliest-diverged extant arthropod.

A707

One-Step PCR Amplificaton of Complete Arthropod Mitochondrial Genomes

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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 niponese* (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

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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*

lischkei). These sequences were then analyzed together with the published sequences of other 17 prosobranchian gastropods including five vetigastropods. Phylogenetic trees were constructed by neighbor-joining, maximum likelihood, and maximum parsimony methods. The 18S rDNA sequence data provide supports for (1) the monophyly of Vetigastropoda (2) monophylies of three vetigastropod clades, Trochoidea, Fissurelloidea, and Pleurotomarioidea (3) the basal position of the Pleurotomarioidea within the vetigastropod clade (4) the branching order of (Pleurotomarioidea (Fissurelloidea (Haliotoidea, Trochoidea))).

A709

A New Species of the Genus *Chelomalpheus* (Crustacea: Decapoda: Alpheidae) from Korea

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A new snapping shrimp of the genus *Chelomalpheus* Kim, 1998 is described with illustrations. It was found in the burrows of the mud shrimp, *Upogebia major* (De Haan) inhabiting the mud flat of Namyang Bay in Yellow Sea. Two closely related species, *C. koreanus* Kim and *C. yamashitai* (Hayashi) previously reported as the genus *Carvipelta*, have been known to occur in the burrows of thalassinids. The present species is the third report in this genus and characterized by having the following characteristics: the presence of triangular rostrum projected dorsally in lateral view; dorsal margin behind rostrum flattend posteriorly with longitudinal ridge laterally; major chela with palm having a heavy immovable spine on on inferior margin medially and with entirely reduced immovable finger; the presence of a long flap comprised of 11 or 12 joints on the uropodal exopod distally. The relationship among the 3 species are discussed and the biology of the new species is briefly presented.

A710

Identification of Anopheles Species Using ITS2 and mtCOI Gene Sequences

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We determined nucleotide sequences of internal transcribed spacer 2 (ITS2) and/or mitochondrial cytochrome c oxidase I (mtCOI) gene from 7 *Anopheles* mosquito species;*An. sinensis, An. pullus* (= *An. yatsushiroensis*), *An. anthropophagus, An. lindesayi japonicus, An. sineroides, An. koreicus,* and *Anopheles* sp. From the most variable regions found in a sequence alignment of ITS2, species-specific primers were designed for identifying the *Anopheles* species. The specific primers designed worked successfully and can be utilized as a useful tool for identifying *Anopheles* species including sibling species. In addition, we found that *An. yatsushiroensis* is a synonym of *An. pullus* based on the ITS2 and mtCOI gene sequences. Through the individual rearing experiment of *An. pullus*, it was reconfirmed that their F1 progenies were typical *An. yatsushiroensis* in morphology. How can we account for their morphological differences and dominant occurrence of *An. pullus* in winter? Further detailed studies are necessary to give answers to these questions. Besides, phylogenetic relationships among 7 *Anopheles* mosquito species were briefly discussed on the basis of ITS2 and mtCOI gene sequence data.

A711