

**A721**

**Large expansions of the V4 and V7 regions by slippage related inserted sequence and their phylogenetic implication in Superorder Peracarida (Malacostraca, Crustacea)**

Chong Pyo Choe\*, John M. Hancock‡, Ui Wook Hwang\*, Sa Heung Kim\*, and Won Kim\*

\*Department of Molecular Biology, Seoul National University, Seoul 151-742, Korea; ‡MRC Clinical Sciences Centre, Royal Postgraduate Medical School, Hammersmith Hospital, London

Size variations in the V4 and V7 regions of the small subunit ribosomal RNA gene were examined from representatives of the major four orders of superorder Peracarida (Malacostraca, Crustacea). Although there were some exceptions in the V4 region, most taxa showed the expanded V4 and V7 regions compared to other malacostracan groups. Despite the difference of primary structure, predicted secondary structure of the expanded V4 and V7 region showed comparable patterns from the analyzed taxa. The typical secondary structures of the V4 region of the peracaridna groups except one species of Cumacea were not changed by inserted sequence. The secondary structure of the V7 region was changed with some more phylogenetically informative patterns. Many statistically significant ( $P < 0.01$ ) motifs were found by motive search. These motifs implied that the inserted sequences in the V4 and V7 regions causing the size variation were generated by slippage-replication mechanism. However, any phylogenetic relatedness among the motifs was not found, thus the possibility of the origin of the inserted sequences shown in the V4 and V7 regions from a common ancestor could not be inferred with the simple motive search. The pattern analysis of the size variations in the V4 and V7 regions and the changed shape of the V7 region from the peracaridan groups had some restrictive phylogenetic information and the phylogenetic relationship was inferred. It equally implied that sequence insertions of the V4 and V7 regions were originated from a common ancestor. The possibility that the inserted sequences are the products of homoplasy is quite small because the primary sequences of the V4 and V7 regions is too different in each group. Analysis of the slippage motifs on secondary structure of the V7 region shows that there are three types of motifs according to the role in the formation of secondary structure. A hypotheses is suggested to explain the process of secondary structural change by slippage motifs.

**A722**

**A New Species of Genus *Zelinkaderes* (Zelinkaderidae: Cyclorhagida: Kinorhyncha) from Korea, with a Brief Revision of the Genus**

Young Hee Song\*, Ji Min Lee and Cheon Young Chang

Department of Biology, Taegu University

As a result of examining the kinorhynch specimens collected from the sublittoral sand bottom at Kuryongp'o, they were turned out to be a new species belonging to genus *Zelinkaderes* Higgins, 1990. Three species are now recognized in the genus: *Z. submersus* (Gerlach, 1969), *Z. floridensis* Higgins, 1990, and *Z. klepali* Nebelsick, 1995. The new species is most similar to *Z. klepali* Nebelsick in the number and arrangement of cuspidate spines, but distinguished by lacking acicular spine on segment 11. A brief revision of this genus is supplied with a character comparison table and scanning electron microscope photographs, moreover with a key to the species of *Zelinkaderes*.