

Z 101 Three New Gastrotrichs of Genus *Chaetonotus* (Chaetonotidae)

Ji Min Lee* and Cheon Young Chang
(대구대학교 자연과학대학 생물학과)

Three new species belonging to genus *Chaetonotus*, which were collected from the washings of submerged plant material and bottom debris at mountain streams of Korea, are reported. *Ch. (Euchaetonotus)* sp. 1 is most similar to *Ch. (E.) armatus* Kisielowski in the trigonal head, the shape and arrangement in 5 longitudinal rows of dorsal scales as well as general body shape, but discernible from it in the presence of two pairs of dorsal bristles, well-developed cephalion and the arrangement or length of spines. *Ch. (Euchaetonotus)* sp. 2 seems to be most close to *Ch. (E.) hoanicus* Schwank in bearing the five-lobed head, the similar scales with concave posterior edge in 10-11 longitudinal rows on trunk, but differs from it in the shape of keeled scales without spiny process at the head and neck region, and the starting points of spines on the trunk scales. The most remarkable peculiarity of *Ch. (Hystricochaetonotus)* sp. is two parallel longitudinal rows of 5-6 long spines at the trunk region, as shown in *Ch. (H.) decemsetosus* Marcolongo. However, *Ch. (H.)* new species is differentiated from it by the number of spiny scales and the shape of simple spine without barb or lateral denticle.

Z 102 Discrimination of Korean *Scapharca* Species (Bivalvia, Arcoida) by mtDNA Analysis

Sang-Youp Lee*, Sang-Hae Kim
(인제대학교 생명공학부)

The genus *Scapharca* consist of three species in Korea; *Scapharca broughtonii*, *S. satowi*, *S. subcrenata*. In order to distinguish the molecular genetic characteristics of these species, cytochrome C oxidase subunit I (CO I) gene of mitochondrial DNA was analyzed by analysis of nucleotide sequences and PCR-RFLP. And also, the unidentified arkshell spat imported from China was analyzed by the same methods. The nucleotide sequences of arkshell spat from China was completely equal to *S. satowi*. The degree of nucleotide sequence transposition between *S. satowi* and *S. broughtonii* was 5%, that between *S. satowi* and *S. subcrenata* 11%. The phylogenetic tree was constructed by using UPGMA method. Effective discrimination of *Scapharca* species was achieved by the RFLP for PCR-amplified 646 bp fragment. Digestion with HaeIII produced no fragment in *S. broughtonii*, and two fragments in *S. satowi*. Digestion with Hinf I produced two fragments in *S. broughtonii*, and no fragment in *S. satowi*. So RFLP using HaeIII and Hinf I is useful to distinguish from the *Scapharca* species in Korea.