

A631

The Mitochondrial Genome of a Centipede *Bothropolys* sp. (Arthropoda, Chilopoda)

Sin Ju Park^P, Yong Seok Lee¹, Min Ho Yoon¹, Ui Wook Hwang^C

Department of Biology, Graduate School, Kyungpook National University, Taegu 702-701

One of the four major groups in the phylum Arthropoda, the subphylum Myriapoda include four Classes: Chilopoda, Diplopoda, Symphyla and Paupoda. Chilopoda to which centipede belongs, in contrast with two pairs of leg per a segment in Diplopoda, have a pair of leg per a segment. Phylogenetic position of myriapods still remains uncertain within the phylum Arthropoda. It has been argued that Myriapoda has closer relationship with the Hexapoda/Crustacea clade or with Chelicerata, and that Myriapoda are a monophyletic or a paraphyletic group. In spite of such arguments, no complete centipede mitochondrial genome has been achieved except the case of *Lithobius forficatus*(Arthropoda, Chilopoda). Here, we determined partial mitochondrial genome sequences from *Bothropolys* sp. belonging to the same family with *Lithobius*. The newly obtained nucleotide sequences were ca. 5Kb ranging from 16S rDNA to cytochrome C oxidase I. This result could be helpful for examining arthropod phylogeny, especially in defining phylogenetic position of myriapods.

A632

Mitochondria Cytochrome b Gene을 이용한 왜가리과 (Family Ardeidae)의 분자계통학적 분석

서영광^P, 류시현¹, 이진희¹, 박희천^C

경북대학교 생물학과, 대구 702-701

왜가리과(Family Ardeidae)에는 세계적으로 20속 65종이 분포하고 있고, 이 중 한국에는 9속 17종이 분포한다. Genbank에서 얻은 자료와 한국에서 채집된 종을 포함하여, 총 13속 18종의 mitochondria cytochrome b gene을 분석한 결과 왜가리과 (Family Ardeidae)는 단계통을 이루고 있었다. 그리고 *Ardea*, *Bubulcus*, *Butorides* 속이 하나의 group을 형성하였고, *Egretta*, *Syrigma* 속이 하나의 group을 형성하였다. 또한 세계적으로 *Ardea*, *Casmerodius*, *Egretta* 등의 여러 속명으로 혼동되고 있는 중대백로(Great Egret)는 이번 연구에서 Neighbor Joining의 방법으로 분석한 결과, *Ardea cinerea*, *Ardea herodias*와의 거리가 각각 0.08076, 0.08591로 나타났고, *Egretta tricolor*, *Egretta caerulea*, *Egretta thula*와의 거리가 각각 0.12228, 0.12949, 0.12897로 나타나 *Ardea* 속에 포함되어 있다는 결과를 지지하였다.

A633

Mitochondrial Genome and Phylogenetic Position of the Phylum Bryozoa

Kum-Hee Jang^P, Ji Eun Seo¹, Ui Wook Hwang^C

^{PC}Department of Biology, Graduate School, Kyungpook National University, Taegu 702-701; ¹Department of Biology, Woosuk University, Wanju 565-701

Bryozoa have been traditionally allied to the deuterostomes on the basis of the shared tripartite, lophophore in the deuterostome pterobranchs and details of their cleavage pattern and nervous system. Other evidence, however, including from molecular sequence data and the shared possession of chitinous setae, places them with the other protostome groups and particularly close to the eutrochozoans, e.g. molluscs, sipunculans and annelids. Because Bryozoa, the suspension-feeding metazoan exhibits characteristics of both deuterostomes and protostomes. Thus, the morphology and embryology of Bryozoa are phylogenetically ambiguous, and their origin is a major unsolved problem of metazoan phylogenetic relationship. To resolve such problems of bryozoan phylogeny, we employed an approximately 2,600bp mitochondrial genome (mtDNA) sequences from 16S rDNA to COI gene, which was from a bryozoan *Bugula neritina*. Gene arrangements of this region had quite peculiar patterns compared with the previously reported: COI abutted directly with ND6, and tRNA^{Gly}, tRNA^{Pro}, tRNA^{Val(-)}, tRNA^{Met}, tRNA^{Ile}, tRNA^{Asp} were found between 16S rDNA and ND6 in order. Such gene arrangement pattern has never been observed in animal mitochondrial genomes. It implies that bryozoans may have very unique evolutionary history apart from other animal groups. Bryozoan mitochondrial genome research makes it helpful to understand controversies related to bryozoan phylogeny.

A634

Early Larval Stages of *Erimacrus isenbeckii* and a Comparison with Other Zoeal Larvae

Chu Lee^P, Young Bong Moon¹, Im Gi Geon², Jeong Min Shim¹, Hyun Sook Ko³, Young Dae Kim¹, Sang Jun Lee⁴

^{P1}East Sea Fisheries Research Institute, Gangneung 210-861; ²South Sea Fisheries Research Institute, Yeosu 550-820; ³Department of Biology, Silla University, Busan 617-736; ⁴National Fisheries Research and Developmental Institute, Busan 619-902

Ovigerous crabs of *Erimacrus isenbeckii* were collected in the east-northern of Korea and their larvae were reared in the laboratory of East Sea Fisheries Research Institute. The morphological features of the first zoea between the present material and sample of Sasaki & Mihara (1993) show some difference in mouth part setations. Within the family Atelecyclidae, the first zoea of *Erimacrus isenbeckii* resembles that of *Telmessus cheiragonus*, but they can be distinguished in the characteristics of the abdominal somite. The former has the lateral process on the abdominal somites two and three whereas the latter has the lateral process on the abdominal somites two. The purpose of the present study is to describe the morphological characteristics of the two zoeal stages of this species in detail and compare its morphology with zoeas within the family.