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The First Complete Spider Mitochondrial Genome from a Joro Spider *Nephila clavata* (Chelicerata, Arachnida)  
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Recent concepts of relationships among spiders are mainly based on morphological, ecological, and behavioral characters. In contrast, only a few spider molecular phylogenetic approaches were conducted so far. For molecular phylogenetic studies, mitochondrial genome sequences have been considered as a very useful tool for addressing phylogenetic relationships at various categorical levels in taxonomy. In spite of its importance in phylogeny, no complete spider mitochondrial genome which has been published until now. In this study, thus, we determine the first complete spider mitochondrial genome from a joro spider. Joro spider mtDNA is 14,435 bp in size and contains 13 proteins, 2 rRNAs, 1 A+T rich region, and 4 tRNA genes (tRNA<sup>Ser</sup>, tRNA<sup>Cys</sup>, tRNA<sup>Trp</sup>, and tRNA<sup>Tyr</sup>). In addition, positions and orientations of all the components excluding undefinable tRNA genes were identical to those of previously reported chelicerate mtDNAs. New addition of complete spider mitochondrial genome to arthropod phylogeny study based on complete mitochondrial genome sequences could give more concrete solutions to the arthropod phylogeny problems, such as arthropod monophyly or not as well as phylogenetic position of Chelicerata consisting of Xiphosura (*Limulus*), Eurypterida (*Eurypterus*) and Arachnida (spiders) among arthropods. For the sake of this purpose, here, we reconstructed arthropod phylogeny with addition of complete spider mitochondrial genome sequences by means of three different tree-making algorithm: maximum parsimony (MP), neighbor joining (NJ), and maximum-likelihood (ML) methods.

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*Anas pecilorhycha*와 *Cygnus cygnus* (Aves, Anseriformes, Anatidae)의 전체 미토콘드리아 유전체 염기서열 분석  
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*Anas pecilorhycha*(흰뺨검둥오리)는 우리나라에서 가장 광범위하게 분포하고 있는 종이며 대조적으로 *Cygnus cygnus*(큰고니)는 멸종위기에 처해 천연기념물로 지정되어있는 종이다. 이 종들의 유전자원을 보존하기 위해서 집단유전학과 분자계통학적 연구에서 가장 빈번하게 사용되는 미토콘드리아 유전체의 전체 염기서열분석을 실시하고자 하였다. 미토콘드리아 유전체는 약 14~16kb로 37개의 유전자(13개의 단백질 암호화 유전자, 2개의 리보솜 RNA, 22개의 tRNA와 1개의 A+T rich region)를 가지고 있다. 현재 *A.pecilorhycha*와 *C.cygnus*는 약 15kb에 이르는 long PCR산물을 얻었으며 이로부터 부분적인 염기서열을 결정하였다. *A.pecilorhycha*는 ND에서 CO1까지 약 7kb 염기서열을 분석하였으며 *C.cygnus*는 CO1에서 ATPase6까지 약 3.5kb 염기서열을 분석하였다. 분석된 염기서열들은 지금까지 밝혀진 인근 분류군의 미토콘드리아 유전체들과 비교하고 논의하였다.

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The Mitochondrial Genome Sequences of a Millipede *Nemasoma varicorne* (Diplopoda: Julida)  
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Myriapods have a few tasks to be resolved: Myriapoda monophyly or not and phylogenetic relationships among the four extant arthropod subphyla, Hexapoda, Myriapoda, Chelicerata and Crustacea. A few studies related with complete myriapod mitochondrial genome have been performed so far. The mitochondrial gene arrangements in arthropods known until now appeared to be highly conserved. Thus, when the rearrangements occur, they are known to be powerful markers for inferring deep animal evolutionary history. In this study, we are planning to determine the complete mitochondrial genome sequences of a millipede species *Nemasoma varicorne* (Julida: Nemasomatidae) and to investigate its phylogenetic information content. We, here, determined about 8Kb mitochondrial genome sequences from *N. varicorne*, which corresponds to the half of the total length (15Kb). If we determine the complete mitochondrial genome sequences of the millipede, it will be possible to discern phylogenetic relationships among the four major arthropod groups as well as confidence of myriapod monophyly.

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Phylogenetic Relationships of Five Seahorses Species (Genus *Hippocampus*) Inferred from Mitochondrial 16S rDNA Sequences  
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The molecular phylogeny was used to revise the current systematic scheme of representative seahorse genus *Hippocampus*. The phylogenetic relationships of the genus *Hippocampus* species were elucidated based on nucleotide sequences of the mitochondrial 16S rRNA gene. The families Cichlidae and Pomacentridae were employed as outgroups for this phylogenetic analysis. The results of this study supported new relationships that do not agree to the traditional classification of the genus *Hippocampus*. The phylogenetic tree reconstructed with 16S rDNA sequences revealed a close relationship between *H. histrix* and *H. barbouri*. *H. comes* appeared as a sister taxon of the *H. histrix* + *H. barbouri* clade. Although the phylogenetic position of *H. erectus* and *H. kuda* are still ambiguous even in the present study, our results supported that *H. comes*, *H. barbouri* and *H. histrix* formed unambiguously a monophyletic group. This study has very valuable meaning in that it is the first molecular phylogenetic study performed with *Hippocampus* species.