

Mitochondrial Protein Phylogeny Joins Myriapods with Chelicerates
(다지류와 협각류의 근연관계를 보여주는 미토콘드리아 프로테오믹 계통)

Ui Wook Hwang

Department of Biology, Teachers College, Kyungpook National University, Daegu 702-701

(E-mail: uwhwang@knu.ac.kr; uwhwang@hanmail.net)

The animal phylum Arthropoda is of paramount significance for the study of body plan evolution given its abundance of morphologically diverse species and the profound understanding of *Drosophila* development. A major obstacle, however, represents the lack of consistently resolved phylogenetic relationships between the four extant arthropod subphyla Hexapoda, Myriapoda, Chelicerata and Crustacea. Recent molecular studies have converged on strongly supporting a sistergroup relationship between Hexapoda and Crustacea, but failed to resolve the phylogenetic position of Chelicerata and Myriapoda. The mitochondrial genome of the centipede species *Lithobius forficatus* was sequenced and then investigated its phylogenetic information content. The *Lithobius* mitochondrial genome is 15,437 bp long. Gene content and arrangement correspond to that of conservatively evolving arthropod mitochondrial genomes with two exceptions. Most crustacean and insect mitochondrial genomes differ from *Lithobius* with regards to the position of the tRNA^{Leu(UUR)} gene, which in the former is located between the COXI and COXII genes but in *Lithobius* between the tRNA^{Leu(CUN)} and ND1 genes. This is consistent with the previous demonstration that the COXI/tRNA^{Leu(UUR)}/COXII arrangement is a synapomorphy of the Pancrustacea. The second difference concerns the position of the tRNA^{Cys} gene, which in most arthropods resides between tRNA^{Trp} and tRNA^{Tyr}, but within the non-coding region of the *Lithobius* mitochondrial genome. Two alignments having 2560 aa sites (relaxed option) and 1528 aa sites (stringent option) were generated from conserved regions of 12 mitochondrial proteins from *Lithobius* and additional arthropod taxa. ATPase 8 was excluded in the alignment construction due to the short length and hypervariability. Annelid, mollusc and vertebrate species were added for outgroup comparison. Molecular phylogenetic analyses of conserved regions (2560 and 1528 aa sites) from the arthropod mitochondrial proteome were performed using maximum parsimony, neighbor joining, and maximum likelihood

methods, which yields highly resolved and congruent trees. Most significantly, a sister group relationship between Myriapoda and Chelicerata is strongly supported. A close link between myriapods and chelicerates has never been considered from a morphological perspective. It is however striking to note that the same grouping is tentatively supported in various analyses of nuclear ribosomal genes. In addition, a recent analysis of hemocyanin protein in myriapods revealed higher structural similarity between myriapod and chelicerate hemocyanins than with crustacean or insect hemocyanins. Independent molecular data thus provide consistent support for a chelicerate/myriapod sistergroup relationship arguing against a monophyletic Mandibulata. A plausible model was proposed to explain the apparently parallel evolution of similar head morphologies in insects and myriapods. Future research will need to examine the possibility of morphological synapomorphies for a chelicerate/myriapod clade.