

## Metazoan Pylogeny and Mitochondrial Genomics

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Mitochondrial genomics (organelle genomics) is one of the most recently arising, promising scientific fields because it could be applied to a variety of scientific fields such as molecular evolution and phylogeny, population genetics, mitochondrial genome-related human diseases, bio-energy production, and phylogeography and so forth. From ca. over 500 metazoan animal species, complete mitochondrial genome sequences were determined and characterized so far. However, most of them were from species belonging to the subphylum Vertebrata (Phylum Chordata), especially birds and fishes. It means that complete mitochondrial genome studies from only a few invertebrate species have been conducted so far: no complete mitochondrial genomes have published from 21 of 35 metazoan animal phyla so far.

My recent research interests lie in the following three points: 1) to determine complete mitochondrial genome sequences from at least one representative species of each phylum in all the 35 animal phyla, 2) to reconstruct entire metazoan animal phylogeny based on the whole mitochondrial genome information, and 3) to construct a powerful, synthetic and multi-purpose online mitochondrial genome bank. In order to get to the research purposes, we have tried to determine whole mitochondrial genome sequences from the unexplored phyla or subphyla and then, with them, to elucidate various metazoan phylogeny problems debated continuously such as monophylies of Lophotrochozoa and Ecdysozoa, monophyly of lophophorates, phylogenetic relationships among five major arthropod subphyla (including an unidentified Antarctic acari) and so on. For exploring the phylogenetic and evolutionary implications with the new data, we compared gene rearrangement patterns and primary and secondary genome sequence information between phyla or subphyla, and also conducted a variety of phylogenetic analyses (four different tree-making methods: Bayesian, maximum likelihood, maximum parsimony, and neighbor joining analyses) with a concatenated multiple alignment set of amino acid sequences predicted from 12 protein-coding genes excepting for ATPase 8 gene. Through the present talk, new metazoan mitochondrial genome data, and their unique genome features (i.e. phylum or subphylum-specific features), and their phylogenetic and evolutionary implications will be suggested and discussed in detail. In addition, utility of mitochondrial phylogenomics for elucidating debated metazoan deep phylogeny will be discussed.