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Mitochondrial Genomics and Metazoan Phylogeny

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Mitochondrial genomics is one of the most promising scientific fields because it could be applied to a variety of fields such as molecular evolution, molecular phylogeny, mitochondrial genome-defect related human diseases, bio-energy production, and phylogeography and so forth. Typical metazoan mitochondrial genomes are circular, are 14-18 kb in size, and encode 13 proteins, 2 rRNA [small and large subunit rRNAs (12S and 16S rRNAs)], and 22 tRNA genes (trnA, trnC, etc.) but no introns. The 13 polypeptides are involved in ATP synthesis coupled with electron transfer during O₂ consumption [ATP synthetase subunits 6 and 8 (ATP6 and ATP8), cytochrome C oxidase subunits I-III (COI-COIII), apocytochrome b (Cytb), and NADH dehydrogenase subunits 1-6 and 4L (ND1-6 and ND4L)]. Besides coding regions, there are also noncoding sequences in animal mitochondrial genomes and, more specifically, a major noncoding segment, which in deuterostomes (D-loop) contains a combination of sequence elements that are related with control of both replication and transcription. In recent years, the comparison of complete mitochondrial genome information such as nucleotide and amino acid sequences of mitochondrial genes and gene arrangement has become a very powerful tool for reconstructing metazoan phylogeny. In addition to the two phylogenetic markers on the mitochondrial genomes, alternative start codons, tRNA and rRNA secondary structures, genetic code variations, and features of control region of mitochondrial genome replication and transcription, etc. could give us important signals for elucidating the evolutionary relationships of many major metazoan groups. Complete mitochondrial genome sequences have been published totally for 509 species from 12 metazoan phyla so far: 391 vertebrates, 7 echinoderms, 1 hemichordate, 2 cnidarian, 10 platyhelminthes, 16 nematodes, 64 arthropods, 1 pentastomid, 12 mollusks, 2 annelids, 3 brachiopods, and 1 phoronid (nearly complete). Although complete mitochondrial genome sequences were determined and characterized from over 500 metazoan animal species, most of them were from species biasedly belonging to the subphylum Vertebrata, especially aves and fishes. Thus, it is the fact that, in invertebrates, relatively poor mitochondrial genome studies have been conducted compared with the cases in vertebrates. Thus, my recent research interests lie in 1) determining complete mitochondrial genome sequences from at least one representative species of each phylum in all the 35 animal phyla, and 2) in reconstructing entirely metazoan animal phylogeny based on the whole mitochondrial genome information, and finally 3) in constructing a powerful, synthetic and multi-purpose online mitochondrial genome bank. From 12 of 35 animal phyla, no mitochondrial genome studies have not been performed in complete mitochondrial genome scale. In my laboratory, I and my colleagues have additionally sequenced and analyzed whole mitochondrial genomes from several phyla among the 23 unexplored phyla. The newly obtained mitochondrial genome informations were used for elucidating various metazoan phylogenetic problems debated continuously such as formation of newly suggested Lophotrochozoa and Ecdysozoa and elucidation of unresolved relationships within each group, phylogenetic relationships among four or five arthropod subphyla, phylogenetic position of Collembola (Arthropoda, Hexapoda), and so on. For phylogenetic analysis, a concatenated multiple alignment set of amino acid sequences predicted from 12 protein-coding genes (excluding ATP8) in mitochondrial genomes was employed and then was subjected to Bayesian analysis using MrBayes ver 3.0b4. The resultant Bayesian tree reconstructed with mitochondrial proteomes will be discussed in details, and utility of mitochondrial phylogenomics for examining phylum-level deep metazoan phylogeny will be mentioned too. Here, I will present four important discoveries observed from the mitochondrial proteome phylogeny: phylogenetic positions of Pycnogonida, Collembola, and Myriapoda, crustacean polyphyly, Pentastomida phylogenetic position, and lophophorate phylogeny. In addition, I also mention a plan for construction of an online mitochondrial genome bank. Complete mitochondrial genome sequences from 23 unexplored animal phyla obtained newly and metazoan animal phylogeny reconstructed with complete mitochondrial genome information could be deposited in the online mitochondrial genome bank established by us. To establish online mitochondrial genome bank depends on bioinformatics field because it additionally needs to develop a variety of stand-alone and web-based sequence analysing and trimming programs specific to mitochondrial genomes. It makes it possible to do efficient and rapid monitoring system of papers and data related with mitochondrial genomes.