

Phylogenetic utilities of nuclear ribosomal DNA and mitochondrial DNA

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Since the tools of molecular biology were introduced to systematics, our view related to phylogeny has greatly changed from the previous view based on detailed analyses of morphology and development. This change has enormously affected on all branches of biology. In particular, the significance and value of development of molecular systematics are much more emphasized in the case of parasites with complex life cycles or few phylogenetically informative morphological characters. However, to choose one or more appropriate molecular markers or useful gene regions for resolving a particular systematic question among the organisms at a certain categorical level is still a very difficult process for new researchers in the field of molecular systematics. The primary goal of this paper, therefore, is to provide new workers in this rapidly expanding field with theoretical information to enable them to choose one or more appropriate molecular markers or useful gene regions, by illustrating general properties and phylogenetic utilities of nuclear ribosomal DNA (rDNA) and mitochondrial DNA (mtDNA) to have been most commonly used for phylogenetic researches so far.

The highly conserved sequence-based molecular markers - nucleotide sequences and secondary structures of three nuclear rRNA coding regions (SSU, LSU, and 5.8S rDNAs) and mitochondrial 12S rDNA, and mtDNA gene rearrangements - are useful for investigating phylogenetic relationships at higher categorical levels (deep branches of evolutionary history) from Kingdom to Order or rarely to Family. Nucleotide sequence of mitochondrial 16S rDNA and amino acid sequences of mitochondrial protein coding genes such as Cytb, COI, COII, ND1, and ND2 are suitable for phylogenetic studies mainly among families or rarely among genera. On the other hand, the hypervariable gene regions - nucleotide sequences of non-coding rDNA regions such as ITS, IGS, mtDNA

control region, and DNA sequences of protein coding genes DNA sequences such as Cytb, COI, COII, ND1, and ND2 - are useful for elucidating phylogenetic relationships at lower categorical levels (recently diverged branches) from Genus to population. In summary, different selective forces have led to the evolution of various molecular markers with varying degrees of sequence conservation. Thus, appropriate molecular markers or gene regions should be chosen with even greater caution to deduce true phylogenetic relationships over a broad taxonomic spectrum. We hope that this paper could play an important role as a helpful and general guide for investigators who desire to resolve phylogenetic problems by using appropriate molecular markers and gene regions.