

The Recent Research Trend using MtDNA and Complete Mitogenome Sequences of Some Insects

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Millions of partial mitochondrial gene sequences from diverse organisms are found in GenBank. Differences in nucleotide and amino acid sequences from various portions of mitochondrial regions are utilized for the purpose of diverse fields such as population genetics, phylogeography, molecular phylogeny, species identification, conservation, disease detection, maternal identification and so on. A recent molecular technical advance has further prompted the scientific field of mitogenomics, and until this year, the complete mitochondrial DNA sequences are reported from more than 500 animals including 37 insect species. These sequence information has greatly devoted to the understanding of mitochondrial genomic structure, rearrangement, and molecular evolution of each categorical organism. With the purpose to know the genomic structure of firefly, our research group has reported a 17,739 bp-long complete mitochondrial genome sequence of *Pyrocoelia rufa* belonging to Coleoptera. One of the unusual features of *P. rufa* mitogenome was the presence of 1,724 bp-long intergenic spacer, composed of twelve 134-bp tandem repeats plus a partial copy of the repeat. Also, we have sequenced a 15,521-bp long mitogenome of mole cricket, *Gryllotalpa orientalis*, belonging to Orthoptera. The *G. orientalis* contains most common gene order and arrangement, found in several insect species, but differ from *Locusta migratoria*, another orthopteran species sequenced in their entire mitochondrial genome. Phylogenetic analysis with available complete insect mitogenome sequence has shown a resolving power to the diversification events within Endopterygota, but less powerful in the earlier insect diversification events. Also, with the purpose to know genetic divergence and pattern of evolution among close species we are working on some bumble bee species belonging to Hymenoptera and some of the achievement will be introduced in the presentation.