Mammalian Evolution and Phylogeny from Complete Mitochondrial Genomes

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Yu-Hsin Lin

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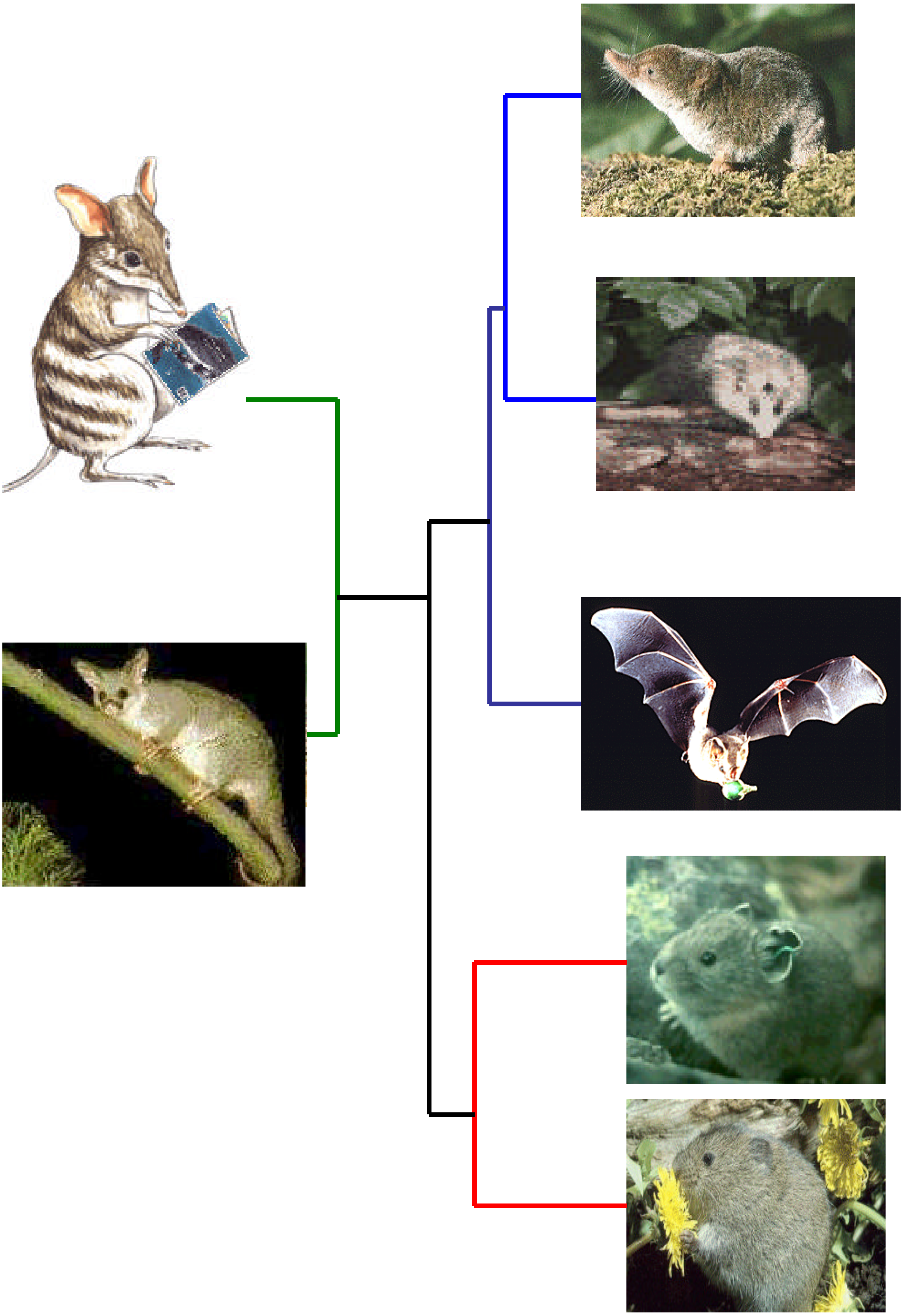
Complete mitochondrial genomes and mammalian phylogeny



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ABSTRACT

The evolutionary tree of mammals is being resolved quickly. Complete mitochondrial DNA sequences are valuable data for deep mammalian phylogenetic relationships. From this study, the use of long-range PCR followed by short-range PCR and sequencing was proven to be a successful strategy for sequencing complete mt-genomes. This method is more efficient and cheaper than current cloning approaches. This method is also able to avoid most of the nuclear mitochondrial copies. Long branch attraction is a problem confusing the deep mammalian phylogeny. By sequencing complete mt-genomes of key taxa (2 marsupials, 2 bats, a pika, a gymnure, a rodent and a shrew) to break up long branches, this study resolve some ambiguous relationships in mammalian phylogeny.

The 8 mammalian mitochondrial DNA sequences from this study give additional support for the 4 groupings (Xenarthrans, Afrotheria, Supraprimates and Laurasiatheria) of placental mammals from current molecular studies. Some of the ambiguous relationships of higher mammalian relationships also get improved resolution. Bats are a monophyletic group but megabats may be paraphyletic. Eulipotyphla is a monophyletic group and deepest in the Laurasiatheria. Rodents are monophyletic and apart from a problem with the tree shrew, are sister to lagomorphs (Glires).

With the new gymnure complete mt-DNA available, the aberrant hedgehog mt-genome is returning to its traditional position in the placental tree and joins other Eulipotyphla (mole, shrew). This monophyletic Eulipotyphla is observed for the first time in the mammalian mitochondrial tree. The Erinaceidae (hedgehog and gymnure) and murid rodent seem to be under different processes of evolution and are attracted to the outgroups. By comparing trees without outgroups (unrooted trees) and with outgroups (rooted trees) and by constraining group(s) with unstable positions, the influence of marsupials/platypus outgroups on Erinaceidae and murid rodent can be investigated. The results from this study suggest that there is a long branch attraction problem between marsupials/platypus outgroups and murid rodent and Erinaceidae; the basal postions of Erinaceidae and murid rodent found in previous studies may be long branch attraction artifacts.

The resolved mammalian tree will be the basis for further molecular studies for estimating the time of divergence of extant mammalian orders, for the prediction of protein secondary structure, for the processes of transition of nucleotides and amino acids sequences in the tree, etc. Having a resolved mammalian tree is not the end for this research, rather a pivotal step for understanding evolution in molecular level.

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