

Evolutionary genomics: the metazoan mitochondrial dna

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One of the most important aspect of the mitochondrial genome evolution in Metazoa, is the constancy on size and gene content of the mtDNA whose plasticity is maintained through a great varieties of gene rearrangements probably mediated by tRNA genes. It was generally accepted that there is a trend to maintain the same genetic structure within the phylum but more recent reports show that a consistent number of transpositions are also observed between closely related organisms. Base composition of mtDNA is extremely variable. Often the GC-content is low and, when it increases, the two complementary bases distribute in a asymmetric way, creating, particularly in vertebrates, a negative GC-skew. We have found in mammals that the base composition of the coding strand and the degree of gene variability are related to the asymmetric replication mechanism of mtDNA. A quantitative measurement of mtDNA evolutionary rate, has revealed that the various component have different evolutionary rates. tRNA genes are among the most conserved but, when compared to nuclear counterparts, they evolve 100 times faster. Finally we describe molecular phylogenetic reconstructions, some of which have revealed unexpected findings, and may change our vision for the classification of the living organisms.