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Variability in Gibbs energy of tRNA molecules in mitochondrial genomes of Chordates: neutral selection or evolution towards optimization of translation?

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Motivation and Aim: It is known that translation of frequent codons in prokaryotes and some eukaryotes is optimized by increasing the copy number of corresponding tRNA gene. However, highly streamlined mitochondrial genomes of Chordata mostly hold only one tRNA gene for each amino acid. So how is mitochondrial translation optimized? We hypothesized that stability of tRNA molecules might be an important variable, correlating with codon usage (CU). It is known that translation of frequent codons in prokaryotes and some eukaryotes is optimized by increasing the copy number of corresponding tRNA gene. However, highly streamlined mitochondrial genomes of Chordata mostly hold only one tRNA gene for each amino acid. So how is mitochondrial translation optimized? We hypothesized that stability of tRNA molecules might be an important variable, correlating with codon usage (CU).
Methods and Algorithms: To test this hypothesis we reconstructed secondary structures and Gibbs energy of each tRNA from almost 4000 Chordata mito-genomes, as well as deriving various genomic features for every species. Ecological data was downloaded from the AnAge database. We also conducted reconstruction of ancestral tRNA states, using the CAT evolutionary model, at each internal node of phylogenetic tree to observe the evolutionary trend in stability.
Results: We observed that (i) In different classes of Chordata tRNA stabilities are highly variable: tend to be more stable in Aves versus Mammalia and in Actinopterygii versus Amphibia and Reptilia. GC content of the whole mitochondrial genome demonstrates the same relationship, suggesting that tRNA stability, might be just a neutral consequence of the whole genome GC content. However, comparing tRNA GC content with whole genome – we observed that warm-blooded opposed to cold-blooded Chordata have increased tRNA GC content versus background – it is possibility that tRNA stability might be under stronger selection in species with high basal metabolic rate. (ii) Comparing different species within each class, we observed positive correlations between tRNA stability and whole genome GC content. (iii) Comparing different tRNA molecules within the same genome of each species, we observed a positive correlation between tRNA stability and CU, especially in warm-blooded species. We concluded that tRNA stabilities of warm-blooded Chordata species, tend to be under stronger selection constraints of translation efficiency than those of cold-blooded Chordates.
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References

1. Lehmann G. et al. (2008) Do mitochondrial DNA and metabolic rate complement each other in determination of the mammalian maximum longevity? Rejuvenation Research. 11(2):409-417.
2. Satoh T.P. et al. (2010) Transfer RNA gene arrangement and codon usage in vertebrate mitochondrial genomes: a new insight into gene order conservation. BMC genomics. 11(1):479.