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

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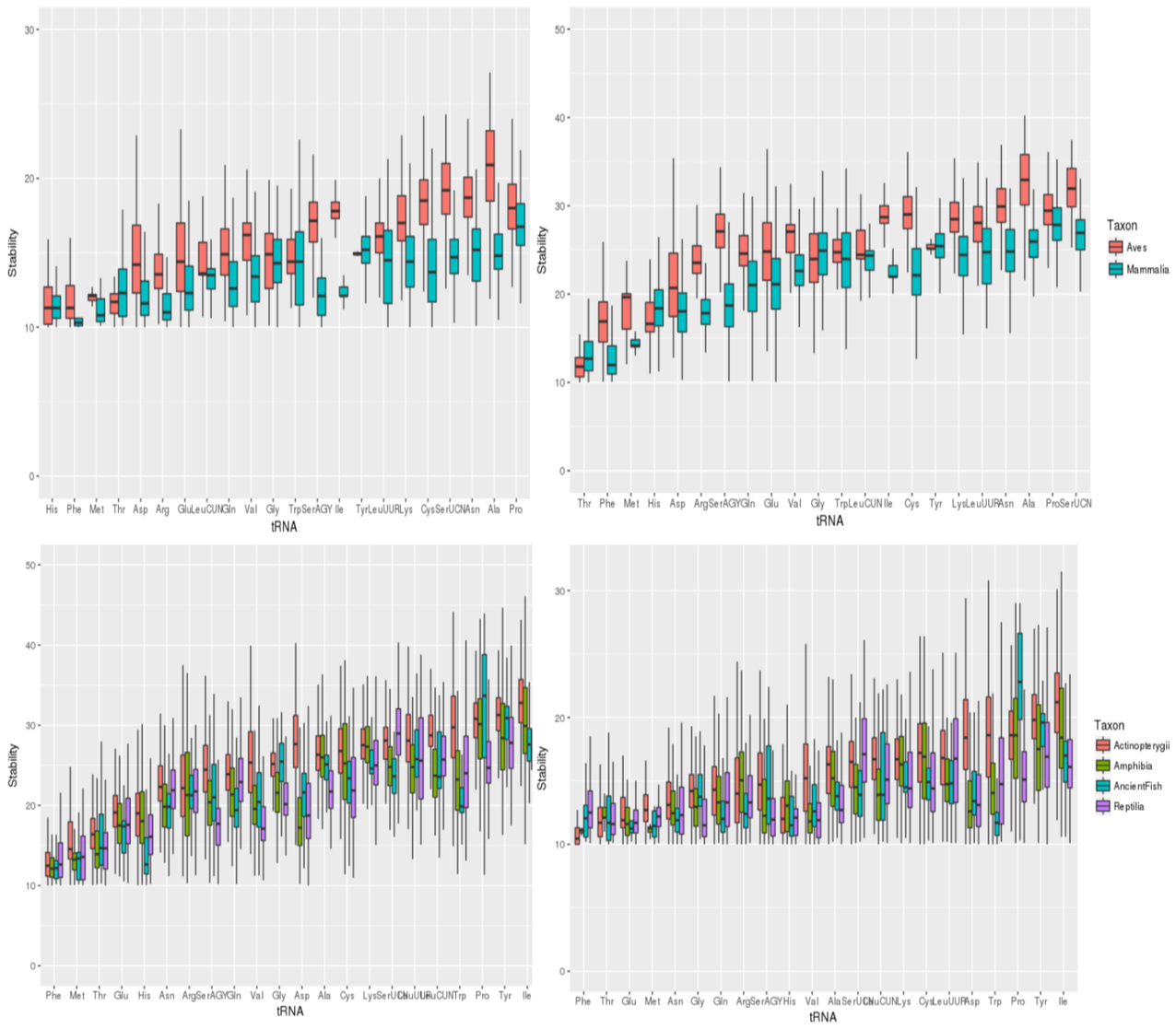
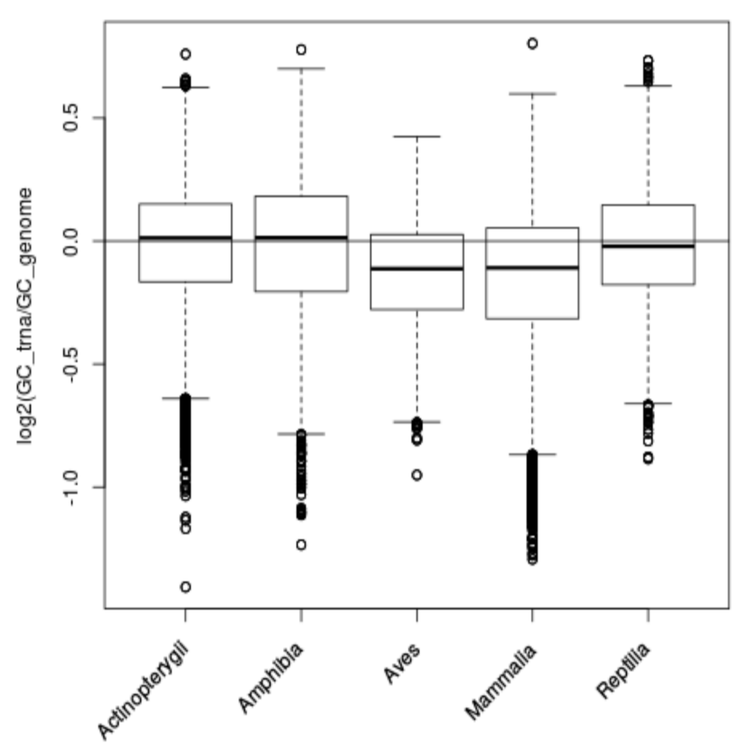
It is known that translation of frequent codons in prokaryotes and some eukaryotes is optimized by increasing the copy number of corresponding tRNA gene. However, highly streamlined Chordate mitochondrial genomes mostly hold only one tRNA gene for each amino acid. So how is mitochondrial translation optimized? We hypothesized that stability of tRNA molecules is an important variable, correlating with codon usage (CU). To test this hypothesis we reconstructed secondary structures and Gibbs Energy of each tRNA from ~4000 Chordata mito-genomes based on a manually curated database of tRNA secondary structures [1]. We also reconstructed ancestral states, using CAT evolutionary model, at each internal node of phylogenetic tree to observe evolutionary stability trend.



Observations

In different classes of Chordates tRNA stabilities are highly variable: more stable in Aves than Mammalia, in Actinopterygii than Amphibia and Reptilia. GC% of the whole mito-genome demonstrates the same relationship, suggesting, tRNA stability, might be just a neutral consequence of the whole genome GC%. However, comparing tRNA GC% with whole genome - we observed that warm-blooded opposed to cold-blooded Chordates have increased tRNA GC% versus background - it is possibie tRNA stability might be under stronger selection in species with high basal metabolic rate.Comparing different species within each class, we observed positive correlations between tRNA stability and whole genome GC %. 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. Conclusion: warm-blooded Chordate tRNA stabilities tend to be more selectionally constrained for translation efficiency than those of cold-blooded Chordates. Mechanistics account for 40-60% of stability, depending on species.



Codon usage

Previosly a positive correlation has been shown between codon usage and position on genome for mitochondrial tRNAs [2]. We observed the following trend for stability, codon usage and position on genome: more stable tRNAs are positioned further away from origin of transcription. As for codon usage when analyzed together tRNAs show a weak positive correlation with codon usage - the more codons the more stable the secondary structure. When analyzed separately some tRNAs fail to show that trend, they correlate negatively - those are the tRNAs for chaos-inducing amino acids (A,R,G,Q,S,P,E,K). Explains ~15%.

Ancestral state reconstruction and analysis

We reconstructed the ancestral states of all analyzed tRNAs. Then for each node of evolutionary tree we calculated average stacking energy for reconstructed ancestral states using btwisted.

For evolutionary distance and stacking energy there is a weak relationship - the closer to tips of the tree the more stable the secondary structure.

Stability is also affected by the ecological parametres of species - basal metabolic rate, body mass, generation time, which are intercorrelated [3]. They are all intercorrelated between them, correlated to GC% of the genome. BMR as we have observed has a weak positive effect on stability. Ecological parametres explain ~10% of secondary structure stability in tRNAs.

References

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[2] Satoh T.P. et al. Transfer RNA gene arrangement and codon usage in vertebrate mitochondrial genomes: a new insight into gene order conservation // BMC Genomics. 2010. № 1 (11). C. 479.

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