

Analysis of Molecular Evolution in Mitochondrial tRNA Gene Sequences

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1 Introduction

When studying about molecular evolution, it is very important to make phylogenetic trees from correlation of each sequence. We therefore developed a computational method [1] based on principal component analysis (PCA) and multidimensional scaling analysis (MDS). Our method is based on that used by the Casari *et al.* [2] to predict functional residues in ras-rab-rho super family. We have extended it to the analysis of tRNA gene sequences and have used it to identify the groups of bases specific to particular species by applying its basic procedure recursively. The advantages of our method are as follows; (1) it allows comparison of the whole sequence; (2) Gene sequences are represented as vectors in a generalized sequence space; (3) the bases of each sequence are projected individually onto the same sequence space. Applying this method to the sequences of all the mitochondrial tRNA genes, we expect to detect not only bases that are always conserved but also bases that are often conserved.

2 Results

We classified mitochondrial tRNA gene sequences by each 21 tRNA species (containing tRNA_f^{Met}). In all the graphs of each 21 tRNA species, sequences divided four groups. They are “vertebrates,” “arthropoda,” “plants and single cells/fungi,” and “echinoderms and nematoda/trematoda.” The “echinoderms and nematoda/trematoda” group located in the middle of the other groups. This means that echinoderms, nematoda and trematoda are turning point among the other species. Then, we detected many characteristic bases in all the mitochondrial tRNA gene sequences of various species. Most of characteristic bases are in elbow region of tRNA (Fig. 2). The bases in the elbow region play an influential role in determining the dynamics of the molecule [3]. Thus, the results suggest that preserving the dynamics of the molecule of each tRNA is important to molecular evolution.

References

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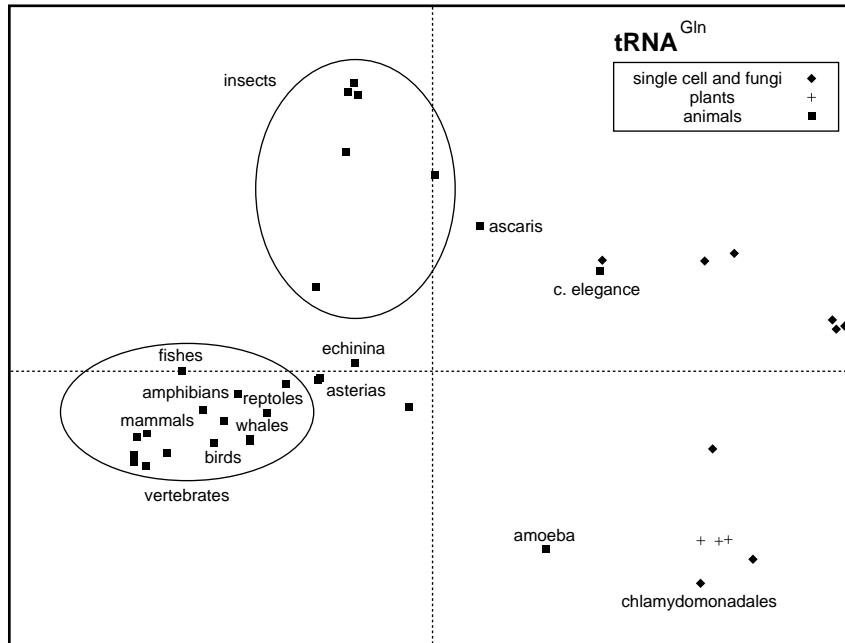


Figure 1: Plots of sequence of tRNA^{Gln}. Sequences are grouped by species related closely and separated by species related distantly.

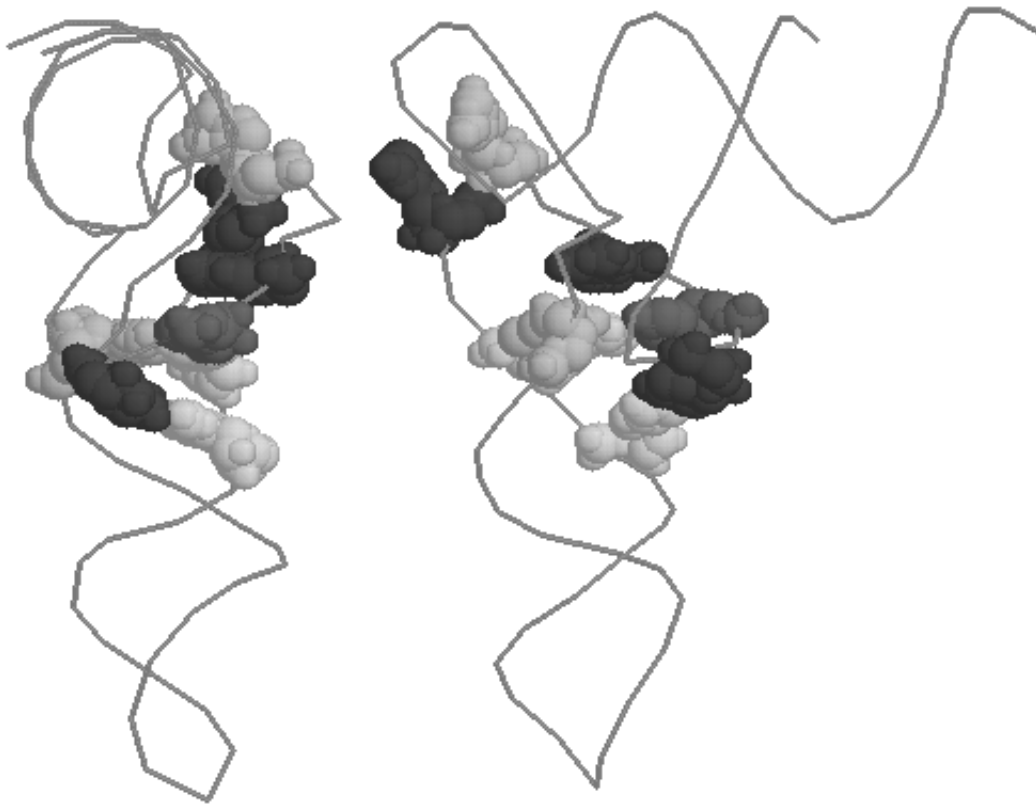


Figure 2: Characteristic bases (spacefill model) represented on the common 3-dimensional backbone model of tRNA.