Structure and Evolution of animal mitochondrial tRNAs

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Abstract

Transfer RNAs are ancient molecules whose origin goes back to the beginning of life on earth. As key partners in the ribosome-translation machinery, tRNAs read genetic information on messenger RNA and deliver codon specific amino acids for peptide bond synthesis to the ribosome. They are present in all types of cells as well as in organelles. Animal mitochondria tRNAs show a low level of primary sequence conservation and exhibit "bizarre" secondary structures, lacking complete domains of the classical cloverleaf. The knowledge about their tertiary folds and the stabilizing networks remains fragmentary. They are hard to detect and frequently missed in genome annotations. Here, an automated annotation procedure for mitochondrial tRNA genes in Metazoa, based on sequence and structural information, and integrated into a novel whole genome annotation pipeline, is described. The established tRNAdb system was adapted to handle mitochondrial tRNA sequences. This provides a data storage system with adequate capacity and functions for a deep data analysis. The Leontis-Westhof rules for isosteric base pairs were implemented to identify conserved tertiary interactions. The new annotation method, applied to re-annotate thousands of available metazoan mitochondrial genomes, allows comparative studies that cover the whole metazoan kingdom. The analysis of this comprehensive set of mitochondrial tRNA genes gives new insights into the evolution of structures of mitochondrial tRNA sequences as well as into the mechanisms of genome rearrangements. This reveales frequent losses of tRNA genes, but also frequent independent losses of individual parts of tRNA genes,

and wide-spread conserved overlaps of tRNA genes. Hotspots of structural diversity, concerning the presence or absence of D- and T-stems, are found throughout the whole Metazoa. Minimized tRNAs in Nematoda were analyzed in detail. A careful re-annotation of their genomes reveales functional truncated sequences without D- and T-stems. Direct evidence for several recent tandem duplication-random loss events is gained, demonstrating that this mechanism has an impact on the appearance of new mitochondrial gene orders. Tertiary interactions, confirmed in nuclear encoded tRNAs, could be identified throughout mitochondrial sequences in teleost fishes and mammals. Even if the results show a high flexibility for mitochondrial sequences, possible and impossible tertiary cores can be assigned to the different mitochondrial tRNA families.