

P101**EVOLUTION OF MITOCHONDRIAL GENETIC CODE IN METAZOA**

Shin-ichi Yokobori, Laboratory for Cellular Biochemistry, Department of Molecular Biology, School of Life Science, Tokyo University of Pharmacy and Life Science, Hachioji, Tokyo 192-0392, JAPAN. yokobori@ls.toyaku.ac.jp

Most metazoan mitochondrial (mt) genetic system uses atypical genetic code, and number and sorts of encoded genes by its genome is nearly constant. Metazoan mt genetic code has evolved along radiation of metazoans. In this report, I will discuss evolution of genetic code in metazoan mitochondria based on the characteristics of mt genomes as well as characteristics of mt tRNAs.

1) In the course of sequence determination of several urochordate mt genomes, we found that the urochordate mitochondria use AGA and AGG (AGR) as glycine codons. The different mt codon table is used in Urochordata, Cephalochordata, Vertebrata, Echinodermata, and Hemichordata. By comparison of metazoan mt genomes including various deuterostome mt genomes, we suggested that asymmetric nucleotide composition between two strands of metazoan mt genomes and inversion of direction of nucleotide substitution pressure on the metazoan mt genomes are might have played important roles during codon reassignment in metazoan mitochondria.

2) Characteristic features of tRNA such as the anticodon sequence and modified nucleotides in the anticodon loop are thought to be crucial effectors for promoting or restricting codon reassignment. Sufficient tRNA genes for decoding all codons on mt mRNAs are encoded on the most metazoan mt genomes, whereas genes for all tRNA modification enzymes and all aminoacyl tRNA synthetases are encoded by the nuclear genome. Recent findings on basepairing rules between anticodon and codon in various metazoan mitochondria suggested that the complete loss of a codon is not necessarily essential for codon reassignment to take place. Competition between two tRNAs with cognate anticodon sequences towards the relevant codon to be varied could have had a potential role in codon reassignment.