

Molecular phylogenetic analyses of aminoacyl tRNA synthetases and translational elongation factors

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Woese et al. (1990, PNAS 87: 4576) divided all extant life into three groups (Domains), Bacteria, Archaea, and Eukarya. However, Rivera & Lake (1992, Science 257: 74) suggested that Eukarya is a sub-group of Archaea as the sister group of Eocyte (Crenarchaeota) from the comparative analysis of indels in the alignment of translational elongation factors, EF-Tu/1a and EF-G/2. Thus, the results of phylogenetic analyses are different depending on the tree reconstruction methods and genes used for analysis.

Recent accelerated increase of genome information has promoted genome-wide phylogenetic analyses. The accelerated increase of archaeal genome information is also apparent in recent years. When Woese et al. (1990) proposed 3 domain hypothesis, only two archaeal phyla, Crenarchaeota and Euryarchaeota, were known. However, Nanoarchaeota, Thaumarchaeota, Korarchaeota, and Aigarchaeota have recently been proposed as novel archaeal phyla. Therefore, re-analysis of relationship among Bacteria, Archaea, and Eukarya by using current data is important.

The number of genes used in the genome-wide phylogenetic analysis is, however, limited. In addition, different methods for inferring phylogenetic trees often give different results. We think that careful curation and careful phylogenetic analysis of each gene is important prior to the multi-gene based phylogenetic analyses.

We are performing molecular phylogenetic analyses of various protein genes related to translation, to understand early evolution of life. In this paper, we will report the progress of our phylogenetic analyses on some aminoacyl tRNA synthetases (ARS) and translational elongation factors, and discuss relationship between Archaea and Eukarya.

Keywords: Archaea, Bacteria, Eukarya (Eucarya), Last Universal Common Ancestor, Aminoacyl tRNA synthetase, Translational Elongation Factor