

Origin of Eukarya based on phylogenetic trees of aminoacyl-tRNA synthetase

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Woese et al. (1990; PNAS 87:4576-4579) classified all extant organisms into three domains based on the phylogenetic analysis of 16S/18S rRNA. Phylogenetic relationship of these three domains, especially the phylogenetic position of Eukarya has been argued. Besides the three domain hypothesis, the two domain hypothesis has been proposed, where Eukarya are included in Archaea. With recent increase of genome sequences, phylogenetic analyses of all extant organism using concatenate alignment of universal conserved genes supported the two domain hypothesis (Guy & Ettema 2011; Trends Microbiol. 19:580-587, Williams et al. 2012; Proc. Biol. Sci. 279:4870-4879, Williams et al. 2013; Nature 504:231-236, Williams & Martin Embley 2014; Genome Biol. Evol. 6:474-481). However, the closest archaeal species of Eukarya may be more than one in other analyses (Thiergart et al. 2012; Genome Biol. Evol. 4:466-485, Rochette et al. 2014; Mol. Biol. Evol. 31:832-845). Thus, the origin of Eukarya is uncertain. In this study, we performed molecular phylogenetic analyses of 23 aminoacyl-tRNA synthetases (ARSs), and discussed phylogenetic relationship of all extant organisms. Clarifying evolutionary pathways of ARSs may extend our fundamental understanding of early evolution of life. Organellar ARS traced various evolutionary routes different from cytoplasm ARS. Understanding their routes may clarify the origin of organellar and horizontal gene transfer during evolution of Eukarya. Especially, we focused on the phylogenetic position and eukaryal cytoplasmic ARS. Amino acid sequence data of 23 ARSs (117 species: 56 Bacteria: 23 Archaea: 38 Eukarya) were collected. The ARS gene trees were reconstructed by using the maximum likelihood method (RAxML) and the Bayesian method (PhyloBayes). The root of the individual gene tree was inferred from composite tree of several ARSs. Cytoplasm ARSs in 13 trees (LeuRS, GluRS, TrpRS, CysRS, AspRS, GlyRS α_2 type, SerRS, PheRS α subunit, PheRS β subunit, IleRS, ValRS, Class II LysRS, ThrRS) of 23 trees showed monophyly, however, the other 7 trees showed polyphyly (AlaRS, ArgRS, HisRS, MetRS, ProRS, TyrRS, AsnRS). Cytoplasmic ARS is absent in 2 trees of 3 ARSs (Class I LysRS, GlyRS $\alpha_2\beta_2$ type, GlnRS) and is sister group of bacterial group in GlnRS tree. 9 monophyletic cytoplasm ARSs are ingroup of Archaea in 9 trees and 4 monophyletic cytoplasmic ARSs are ingroup of Bacteria in 4 trees. 7 polyphyletic cytoplasmic ARSs are also ingroups of Archaea and Bacteria. These results support the two domain hypothesis. 3 monophyletic cytoplasmic ARSs are closest to TACK superphylum in Archaea and another 3 monophyletic cytoplasmic ARSs is closest to Euryarchaeota in Archaea. The closest species of monophyletic cytoplasmic ARSs in 9 trees showed that Eukarya derived from both TACK superphylum and Euryarchaeota and suggest that the ancestor of Eukarya originated from the fusion between ancestor of TACK superphylum and ancestor of Euryarchaeota. 4 monophyletic cytoplasm ARSs derived from bacteria are closest to different bacterial species, which showed that independent lateral gene transfer occurred from bacterial genome to the genome of Eukaryal ancestor and transferred genes replaced the cytoplasm ARS in the genome of Eukaryal ancestor. Furthermore, 7 polyphyletic cytoplasmic ARSs showed that independent lateral gene transfer from Archaea or Bacteria occurred during evolution of Eukarya and the genes replaced the cytoplasm ARS. Finally, We propose that the ancestor of Eukarya is fused organism between ancestor of TACK superphylum and ancestor of Euryarchaeota and lateral gene transfer of various bacteria from different lineages have been contributed the formation of Eukaryal cells.

Keywords: phylogenetic analysis, aminoacyl tRNA synthetase, early evolution, origin of Eukarya