PROPOSALS ON THE GROUP OF ARCHAEBACTERIA AND NAMING OF THE LAST COMMON ANCESTOR

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Since the proposal of archaebacteria or *Archaea* (1,2), there have been arguments concerning the taxonomic validity of the group (1-4). Very recently, Rivera and Lake reported that eukaryotes and eocytes (thermophilic archaebacteria) are immediate relatives (5), which in turn supported their eocyte tree. On the basis of their eocyte tree, they insisted that archaebacteria should be divided into three groups, halobacteria, methanogens and eocytes (thermophilic archaebacteria), and that the eukaryotes and eocytes comprise a monophyletic superkingdom the kalyotes.

They obtained very good evidence to prove that eukaryotes and eocytes are closely related, because the two groups contained an 11-amino acid sequence in the EF-1 sequences while the other groups lacked the 11-amino acid insert.

Nevertheless, we support the grouping of archaebacteria, after a modification, for the reasons as described below. Although their analysis provided the evidence to determine the topology of the phylogenetic tree, their data is essentially all or non evidence. The kind of data does not provide the information about the mutual phylogenetic distance between each group, which are more important for taxonomic grouping. In phylogenetic trees calculated from ribosomal RNA sequences, mutual separation of halobacteria, methanogens, thermophilic archaebacteria(eocytes), and eukaryotes are small. On the other hand, separation between eubacteria and archaebacterial groups including eukaryotic nuclear are significantly longer than other branches. We propose that the

highest taxonomic grouping should be done based on the evidence, that all the living organisms should be divided into Bacteria and Archaebacteria (*Archaea*), and that Archaebacteria should include halobacteria, methanogens, thermophilic archaebacteria, and nuclear genes of eukaryotes. This is the modification of the definition of domain *Archaea* that was originally proposed by Woese *et al.* (2) to include the nuclear genes of eukaryotes in Archaebacteria (*Archaea*).

The common ancestor of all the living organisms on the earth has been frequently called progenote, which is originally defined by Woese, as the entities, still in the throes of completing the evolution (refinement) of the links between genotype and phenotype (6). Recently several authors showed the evidence that the common ancestor had developed the modern genetic system and insisted that the common ancestor is not the progenote. We propose a name of the common ancestor, "commonote".

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