

RETURN TO DICHOTOMY: BACTERIA AND ARCHAEA

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ABSTRACT

We briefly reviewed the argument about the phylogenetic tree of life on the earth, and the validity of the group archaeobacteria or *Archaea*. We explained our proposal about dichotomic division of the general phylogenetic tree of life. We also proposed the way of handling eukaryotes in the prokaryotic phylogenetic tree.

1. PHYLOGENETIC TREES OF LIFE

In 1977 Woese and Fox (1977) have reported the cataloguing analysis of small subunit ribosomal RNA of methanogenic bacteria. They found that methanogenic bacteria belong to an unique group different from eukaryotes and common bacteria (eubacteria). They proposed a group archaeobacteria to represent the third group. Thermophilic sulfur-dependent bacteria, and extremely halophilic bacteria were also included in archaeobacteria (Fox et al., 1980). They suggested that the life on the earth should be divided into three not two nor five (Woese and Fox, 1977).

Until 1989, there was no way to determine the root of the general phylogenetic tree. In 1989 two groups have reported the way to determine the root of the global phylogenetic tree (Gogarten et al., 1989; Iwabe et al., 1989). They used duplicated genes to determine the root in the tree. Several genes have been used to determine the root. It was concluded that the root is between eubacteria and archaeobacteria with eukaryotes on the archaeobacterial branch (Iwabe et al., 1989; Miyata et al., 1991). The root was adapted to the phylogenetic tree derived from rRNA sequences (Woese et al., 1990, Fig. 1). Woese et al. proposed the names of these three groups: *Archaea*, *Bacteria* and *Eucarya* for archaeobacteria, eubacteria and eukaryotes, respectively (Woese et al., 1990).

2. RELATION BETWEEN EUKARYOTES AND ARCHAEBACTERIA

On the other hand, the relation between eukaryotes and archaeobacterial groups is an unsettled question. Sequence analysis of rRNAs suggests that archaeobacteria are monophyletic (Gouy and Li, 1989) and the eukaryotes have separated before the division of archaeobacterial groups. Protein sequences did not give conclusive results. Recently Lake analyzed the elongation factor sequences (Rivera and Lake, 1992; Lake, 1994). They suggested that the eukaryotes are more closely related to eocytes (thermophilic archaeobacteria) than halophiles.

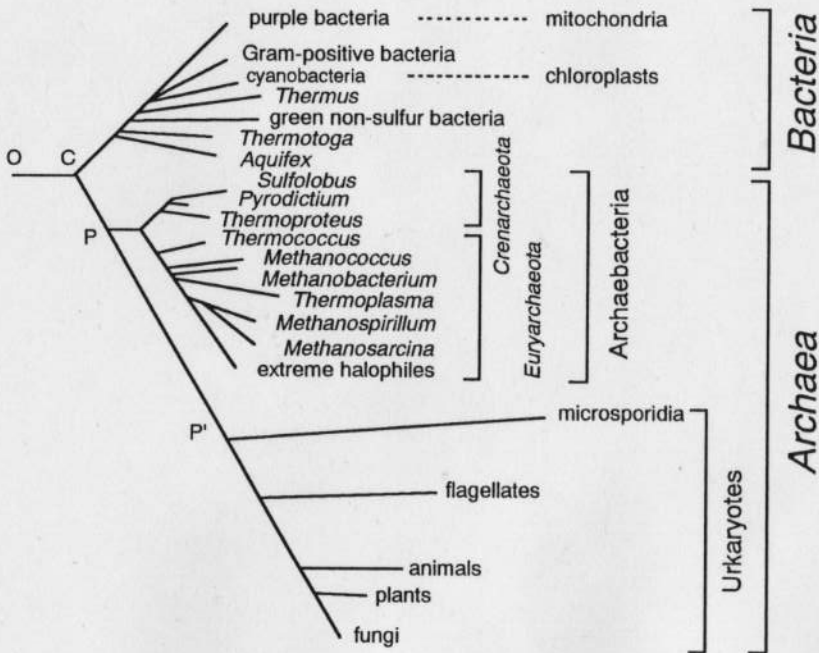


Figure 1. Phylogenetic tree and the dichotomic division of life.

The results suggest that the nuclear genes of eukaryotic cell like rRNA are closely related to archaebacteria and may be included in archaebacteria. It is rather natural to include eukaryotes in archaebacteria.

3. DICHOTOMIC DIVISION OF LIFE ON THE EARTH

We pointed out that the most primitive division of the life is the separation between eubacteria and archaebacteria at the position indicated by the letter c in Fig.1 (Yamagishi and Oshima, 1993). We proposed the dichotomic division of life: Bacteria (eubacteria) and Archaea. The dichotomic division is shown in Fig.1. We proposed to include the nuclear genomes or genes of eukaryotes in Archaea (Yamagishi and Oshima, 1993). Because the separation of archaebacterial group and urkaryotes is so small, these two groups should not be taken as the most primitive division. Thus life on the earth should be divided into *Archaea* and *Bacteria*

4. POSITION OF EUKARYOTES IN THE PROKARYOTIC TREE

The next problem is how to handle eukaryotes. Phylogenetic analysis of rRNA and protein sequence of chloroplasts and mitochondria supported the symbiotic theory of these organelles in eukaryotic cells. Chloroplasts of green plants are closely related to and included in cyanobacteria (Giovannoni et al., 1988; Turner et al., 1989). Mitochondria are included in alpha subdivision of proteobacteria (Purple bacteria, Yang et al., 1985; Olsen et al., 1994). Each component of the eukaryotic cells is assigned to the prokaryotic phylogenetic tree.

We also propose that the eukaryotes should not be positioned in the phylogenetic trees as a whole. Instead, each component of the eukaryotic cells, or each gene of the eukaryotic cells should be placed at each suitable position in the prokaryotic phylogenetic tree (Yamagishi and Oshima, 1993). We also think it appropriate to use the word *urkaryotes* proposed by Woese et al. (Woese and Fox, 1977) to represent nuclear genomes or genes of eukaryotes.

What about eukaryotes as a whole, then? We think it appropriate to treat eukaryotes like molecules, which are the counterparts of atoms (Yamagishi and Oshima, 1993). Each prokaryotic species is accepted as an atom or element. Thus the eukaryotic cells can be expressed as the combination of each component of prokaryotes. For example, green plants contain nucleus, mitochondria and chloroplasts. The nucleus probably consists of cells or Archaea whose precise positions in the phylogenetic tree are not known. Though, there are still many possibilities including that the nucleus is made of several prokaryotic components from *Archaea* and *Bacteria*. Then the nucleus itself must be expressed as the combination of prokaryotic components. Accordingly, the universal phylogenetic tree contains only prokaryotes and prokaryotic component of eukaryotes. Eukaryotes should not appear in the phylogenetic tree as a whole.

Accepting these ideas on eukaryotes, life on earth should be divided into two groups, *Archaea* and *Bacteria*. In Fig.1, we used the word *archaeobacteria* to represent the groups of *Crenarchaeota* and *Euryarchaeota* (Woese et al., 1990). The phylogenetic nomenclature, *Archaea* should be used to mean that the group consists of three subgroups: *Euryarchaeota*, *Crenarchaeota* and *Urkaryotes*. It is also convenient to use the common name *archaeobacteria*, though it is not a taxon name, for the group contains *Crenarchaeota* and *Euryarchaeota*.

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