

Methanogenic bacteria: a new primary kingdom?

from J. F. Wilkinson

BIOLOGISTS until recently have divided living organisms into two main groups—plants (including bacteria) and animals. The development of the electron microscope made it clear that a more fundamental dichotomy existed in terms of cell structure and the prokaryotic and eukaryotic types of organism were defined. This latter division has been amply confirmed at different levels of cell organisation, but it has usually been considered quite wrongly to represent a fundamental division into two primary phylogenetic groupings—the Prokaryotae and the Eukaryotae. However, it has become clear in recent years that a eukaryotic cell has a composite nature (for example, Stanier *Symp. Soc. gen. Microbiol.* **20**, 1; 1970). It is generally assumed that chloroplasts and mitochondria are descended from a quite different ancestral line from the rest of the eukaryotic cell, which therefore represents the eventual result of an essentially symbiotic relationship between two cell types. Thus it becomes necessary to assume that there may have been at least two ancestral cell types represented by the prokaryote and the cell type that led to the eukaryote; mitochondria and chloroplasts may or may not represent two further cell types.

Can we obtain any information concerning the evolutionary relationships between such ancestral cell types and is it true that all present-day prokaryotes and eukaryotes fall into two basic groupings? To answer these questions, it is necessary to find suitable structures which are common to all living organisms and to compare them. The more conserved such structures are during evolution, the more suitable they are for the purpose. The molecular biologist naturally seeks some defined polymer in which the base sequence can be determined. A good case can be made that the most satisfactory single molecule available for this purpose is rRNA; it is a component of all self-replicating systems including chloroplasts and mitochondria, it is readily isolated and its sequence seems to change only slowly with time allowing the detection of relatedness amongst very distant species (Sogin *et al. J. molec. Evol.* **1**, 173; 1972; Woese *et al. Nature* **254**, 83; 1975; Fox *et al. Int. J. Syst. Bact.* **27**, 44; 1977). In particular, we now have information on 16S (18S) rRNA from a fairly large range of organisms.

Although initial results using this method tended to confirm the dichotomy of living organisms, a major surprise has

arisen from the analysis of a relatively obscure group of organisms—the methane-producing or methanogenic bacteria (Fox *et al. Proc. natn. Acad. Sci. U.S.A.* **74**, 4537; 1977). These strictly anaerobic bacteria have in common the ability to produce methane from CO₂ and H₂ and to obtain their energy by means of this pathway. They have proved to be a difficult group of bacteria to obtain in pure culture, but there has been an increase in research into them in recent years spurred on by their possible use in energy conversion from waste organic matter. They have been found to be a fairly diverse group morphologically, comprising both Gram-positive and Gram-negative bacteria. Indeed, they have often been considered as a heterogeneous collection of organisms which happened to have a common metabolic property—the ability to produce methane from CO₂ and H₂. However, a study of 16S rRNA from 10 species available in pure culture has shown that they rather represent a closely-related phylogenetic grouping which is quite distinct from all other bacteria so far analysed in this way. A measure of their distinctiveness is that two very different prokaryotes, the blue-green algae (bacteria) and the enteric bacteria, are much more closely related to each other than either are to the methanogenic bacteria. Further, the methanogens seem no more related to other bacteria than they are to the eukaryotic component represented by 80S ribosomes. Is it too much to suggest that this difference represents two quite distinct ancestral prokaryotic groupings? It may be too early to say definitely in view of our restricted information on methanogens, but there is some further contributory evidence. Quite apart from metabolic factors related to the ability to synthesise methane and their strictly anaerobic existence, methanogens contain no peptidoglycan in their cell wall, the pattern of base modification in their 16S rRNA is, for the most part, different from that in other bacteria and their tRNA lacks the so-called common sequence TΨGC present in all other organisms tested, be they prokaryotes or eukaryotes (quoted in Fox *et al. Proc. natn. Acad. Sci. U.S.A.* **74**, 4537; 1977).

Arising from this work, it has been suggested by Woese and Fox (*Proc. natn. Acad. Sci. U.S.A.* **74**, 5088; 1977) that there are three aboriginal lines of descent represented by three 'urkingdoms' or 'primary kingdoms'.

The methanogenic bacteria.

This group may have developed at an early stage in the evolution of the

Earth when there was an anaerobic atmosphere rich in CO₂ and H₂ (3 to 4 billion years ago) and they may have played a very important part in the transformation of the environment during this period. Consequently, the name suggested for this urkingdom is the archaeobacteria.

All other prokaryotes so far characterised. This group has three major divisions—the blue-green algae (bacteria), the Gram-positive bacteria and the Gram-negative bacteria. This urkingdom is called the eubacteria and it is the kingdom to which the chloroplast progenitor is derived. Unfortunately, no data seem to be available on mitochondrial rRNA. **The cytoplasmic component of eukaryotes.** This urkingdom, for which the name suggested is the urkaryotes, presumably represents the engulfing species of the composite eukaryotic cell. If it is granted that these are the three major lines of descent and if later evidence supports this view, what is the relationship between these lines of roughly similar levels of organisation? Do they have a common ancestor no longer represented by organisms on this planet? Little is known about the likely age of the eukaryotic cell, but there is some evidence that the prokaryotic cell types have been reasonably stable for at least three billion years (Shopf *Exobiology—Frontiers of Biology* **23**, 16; 1972). If all three urkingdoms did have a common ancestor, represented by a simpler cell structure than the prokaryote, the evolution of this structure into our major cell lines must have occurred within a relatively short time; during this period the structure of substances such as rRNA must have been very much more labile than they have been in the longer period that has followed. It is clear that the recognition of these three lines of descent represents an exciting phase in the history of biology and there remains much to be done in clarifying the position. □

The trouble with kinase crystals

from C. C. F. Blake

A COMMON question asked of X-ray crystallographers is: can you be certain that the structure of a protein in the crystal is the same as that in solution? Although no blanket answer can be given, the indications are that in most cases the crystalline structure is very similar to that in solution. However, as Koshland pointed out many years ago, protein structures are intrinsically finely balanced so that in the presence of ligands different structural states are taken up that are essential for activity.

C. C. F. Blake is a Lecturer in Molecular Biophysics in the University of Oxford.

J. F. Wilkinson is Professor of Microbiology at the University of Edinburgh.