

Re: Article: Is the Term 'Prokaryote' Obsolete?

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Robert Karl Stonjek wrote:

Is the Term 'Prokaryote' Obsolete?

The following points are made by Norman R. Pace (Nature 2006 441:289):

1) The explosive accumulation of gene sequences over the past few decades has brought a new perspective on life and its history. Some of the results indicate that we need to reassess our understanding of the course of evolution at the most fundamental level. The current textbook paradigm for biological diversity and evolution is based on the prokaryote/eukaryote model. This posits that there are two kinds of cells: prokaryotic, those without nuclei (specifically, without nuclear membranes) and eukaryotic, those with a classical membrane-bounded nucleus. The model further posits that the former gave rise to the latter. The historical antecedents of this model are complex and rooted in the nineteenth century; for example, German biologist Ernst Haeckel positioned "monera" (masses of protoplasm without a nucleus, later termed "prokaryotes") at the base of his four-kingdoms phylogenetic tree.

2) The recognition that the main eukaryotic organelles, mitochondria and chloroplasts, were derived from bacteria by symbiosis between the bacteria and an ancestral eukaryotic cell prompted speculation on a similar origin for the eukaryotic nucleus. And the discovery of archaea -- microbes that in many molecular ways resemble eukaryotes more than bacteria -- resulted in proposals for archaeal origins for nuclear and cytoplasmic components of eukaryotic cells. Such proposals have sustained the concept that prokaryotes evolved into eukaryotes -- an evolutionary model invoked by the terms themselves.

3) Molecular-sequence comparisons, first of ribosomal RNA genes in the late 1970s and of many other genes since, replaced analyses based on morphological subjectivities (such as the presence or absence of a nuclear membrane) with credible maps of evolutionary relationships between genes. These sequence comparisons have rendered the prokaryote/eukaryote model obsolete. Ribosomal RNA, because of its ubiquity and slow rate of evolution, provides the most reliable view of the earliest evolutionary events. Comparisons of ribosomal RNA sequences show a three-domain tree of life. Although some details of ribosomal RNA-based trees remain controversial, the

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basic three–domains structure and the relationships between the domains are generally accepted and are supported by observed biochemical variati