

EDITORS' PREFACE

As the millenium approaches, it is becoming safe to make assertions about the most significant developments of the twentieth century. In microbial systematics, the use of DNA sequence comparisons culminating in Woese's revelation of three domains of cellular life must surely rank high on any list. Considering that, at the beginning of the century, DNA had not been demonstrated to be the repository of genetic information and that, as the century draws to a close, we have complete genomic sequences for a number of organisms shows just how far we have come.

Evidence for the three domains sprang from the still young field of molecular biology and, although it is not universally accepted (see Lake's chapter, for example) it has dramatically changed our way of thinking about the evolution and relationships of cellular life (see Doolittle's introductory chapter).

Another young field of study, palaeoecology, has contributed to our appreciation of the antiquity of cellular life on this planet. The world formed some 4.5 GYr (4.5×10^9 years) ago. The surface cooled and liquid water formed during those first 0.5 GYr, but it was widely believed that the extensive meteoric bombardment, which also resulted in the visible cratering on the moon, was of such ferocity that liquid water would have been evaporated to condense again later. However, cyanobacteria seem to have been active earlier than 3.5 GYr (see Schopf's chapter). Cyanobacteria are not simple or 'primitive' cells and our understanding of bacterial evolution does not place their appearance early. This is, for many, an astonishingly short time period for life to have begun and evolved so far and it does present paradoxes that have not yet been satisfactorily resolved. It does, at least, cast doubt on the idea that liquid water was completely removed during the meteoric bombardment. Evidence for the first multicellular organisms appears in the geological record at about 0.7 GYr, so for the majority of the Earth's history life was an unicellular phenomenon. All the major chemical cycles must have been in place during this time, so macroscopic life evolved into a functioning ecosystem. It should not be a great surprise to learn that the microbial cycles are those which drive life on the planet.

The techniques of molecular biology, particularly DNA sequencing, are providing data in ever greater quantities with which diverse organisms can be compared. Historically, taxonomy has been developed by comparing very similar organisms with very small (usually phenotypic) differences in order to deduce their relationships. It becomes exponentially more difficult to deduce relationships as the similarity decreases and the number of characters in common falls to a tiny fraction of the total number of

characters available. The phrase 'cellular life' has been used here principally to avoid a discussion of what, exactly, constitutes life. The origin of the viruses is still very much an open question and suffers greatly from the paucity of characters in common, not just with cellular life, but even between the major groups of viruses (see the chapters by Holmes and Simmonds).

Molecular biology has allowed us to recover vast numbers of characters, many of which are shared by all cellular life. By far and away the most studied gene has been that encoding the small-subunit (16S) ribosomal RNA. If Darwinian evolution (descent with modification) is the dominant evolutionary model through the history of life, then sufficient quantity of sequence data of this type will allow us to build bifurcating phylogenetic trees establishing the relationship of one taxon with another. The tantalizing prospect is that there is another model of evolution visible in the predominantly asexual microbial world that owes much to lateral transfer and promiscuous genetic exchange (i.e. between quite unrelated partners) which would render such a tree an artefact of the gene chosen to build it, and in which the evolutionary relationships are a network (allowing for anastomization) rather than a simple tree. Issues of this kind were addressed in a previous symposium volume (52: *Population genetics of bacteria*) to which the reader's attention is drawn. Such models will not be resolved until large sections of genomes of a taxonomically diverse set of organisms are available for analysis.

Unicellular eukaryotes are a poorly understood group of microbes; for those of us who work with them it is depressingly common to find 'microbe' and 'bacteria' being used as synonyms. There is now no doubt that the eukaryotic cell evolved by successive mergers of cells (see chapters by Sogin, Gray, Douglas and Gogarten). The resulting organisms are capable of staggering morphological richness (see Moore's chapter on the fungi, for example), but also of 'reverting' to a phenotype regarded as primitive in order to exploit an available niche (see Fenchel's chapter on eukaryotic anaerobes, for example). It is going to be fascinating to see how these intertwined genetic histories resolve themselves into an evolutionary history.

Biodiversity remains high on the political agenda, especially following the 1992 Earth Summit in Rio de Janeiro. There are comparatively few microbial taxa named but their diversity cannot be doubted. Indeed, our appreciation of what is meant by the words 'microbial biodiversity' is still developing (see Giovannoni's chapter). Microbes are capable of almost any physiological process (see Dijkhuizen's chapter), many of which are beyond the capacity of their multicellular descendants. The simple system of counting 'species' is only a single facet of the jewel of biodiversity. A greater appreciation of microbial evolution will surely help to understand just how rich and varied life truly is.

Modern systematics, through the study of evolution and the use of

phylogenetic principles, is an exciting and vibrant field. It is the cornerstone of modern biology and will be of interest to both the specialist and general reader. In this fast moving field, the editors have placed the authors under a great deal of time pressure to deliver state-of-the-art chapters. We would like to thank them for producing such current and readable accounts so quickly.

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INTRODUCTION

It is a pleasure to remember of earlier Society for General Microbiology symposia. I hope you recognize the title of this essay. It is the same as that of the 1971 Symposium, for his erudite but discursive introductory chapter in the 1970 volume (Stanier, 1970). That symposium 'Organization and Evolution of Prokaryotic and Eukaryotic Cells' was about comparing and contrasting cells of the two sorts, and about how the one might have given rise to the other. Issues still very much alive and central to this meeting of the Society are still at the heart of a century later.

It was a time of a crucial juncture in the development of our thinking about the origin of life. One 'fact', the existence of two and only two basic types of organism, prokaryotes and eukaryotes, seemed solidly established. A central evolutionary concept, that eukaryotic organisms arose by endosymbiosis and respiration are the degenerate descendants of photosynthetic cyanobacteria, anciently established within the eukaryotic lineage, was moving towards acceptance and 'proof'. In addition, molecular biology (including molecular phylogenetic reconstruction) was about to revolutionize microbiology and comparative biochemistry on the resolution of cellular evolutionists.

It was a time, I think, at a crucial juncture in the development of our field. Although some of what Stanier believed 25 years ago was actually wrong, we have accepted a simple prokaryotic/eukaryotic dichotomy. Although we have accepted the bacterial origins of chloroplasts and mitochondria, we have begun to move towards the endosymbiont hypothesis within a broader context as a theory for the origin of eukaryotic cells. Once more a new era of biological methodology, this time based on the comparison of molecular sequences, is about to overwhelm us all.

Thus I will be on the issues which Stanier addressed, presenting what I believe to be the current consensus about them. I will then highlight the weak points and make some suggestions about how the next generation might work. Many of the more contentious issues will be discussed in more detail by other contributors to this volume.