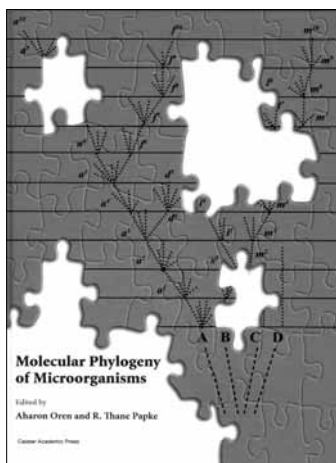


# BOOK REVIEWS

INTERNATIONAL MICROBIOLOGY (2010) 13:219-220

ISSN: 1139-6709 [www.im.microbios.org](http://www.im.microbios.org)



## Molecular phylogeny of microorganisms

AHARON OREN,  
R. THANE PAPKE (EDS)

2010. Caister Acad. Press,  
Norfolk, UK

348 pp, 16 × 24 cm

Price: £ 159

ISBN 978-1-904455-67-7

Charles Darwin introduced the concepts of phylogeny and evolution to the scientific world, and he was optimistic that some time in the future the secrets of phylogeny would be revealed. Life may have diverged from one or more common ancestors to result in the current diversity of living organisms on Earth. Although Darwin did not mention the microbial world in his writings, surely he knew about the diversity of bacteria, protists, fungi, etc., known since the days Antonie van Leeuwenhoek discovered the microscopic world. The different approaches applied today to elucidate the molecular phylogeny of prokaryotes reveal the complex world of the microbes that Linnaeus described under a single taxon: "Chaos infusorium," with six "species":  $\alpha$  *Febrium exanthematicarum contagium*;  $\beta$  *Febrium exacerbatum causa*;  $\gamma$  *Siphilitidis virus humidum*;  $\delta$  *Spermatoci vermiculi Leeuwenhoek*;  $\epsilon$  *Aetherus nimbus mense florescentiae*;  $\zeta$  *Fermenti putredinisque septicum*.

Some of the early phylogenetic studies of prokaryotes were morphology-based. The emergence of technology to determine amino acid sequences in proteins and later nucleotide sequences in RNA and DNA has revolutionized all biological disciplines. At present the existing framework looks reasonable, but new discoveries in the future may again lead to changes in concepts for microbe phylogeny and their classification. *Molecular phylogeny of microorganisms* explores in ten chapters current concepts in molecular phylogeny and their application to understanding the evolutionary history of prokaryotic microorganisms.

The analysis of molecular sequences involves four steps: (i) selection of an appropriate molecule as phylogenetic marker; (ii) acquisition of molecular sequences; (iii) multiple sequence alignment; and (iv) phylogenetic evaluation using

appropriate software tools. Once homologous residues (nucleotides or amino acids) are aligned, phylogenetic trees can be calculated by distance, maximum parsimony, maximum likelihood and Bayesian methods (chapter 2).

The total gene pool of a species, or pan-genome, consists of the *core* genes, conserved in all strains, and *accessory* (or *disposable*) genes found only in some individuals of the species. Only orthologous core loci are useful for phylogenies and for within-species population genetic analyses. Recent estimates of the conserved core genome of all *Bacteria* indicate that it is most likely composed of <50 core genes, of which 31 are ubiquitous (single copy orthologous genes shared by the three domains of life, *Bacteria*, *Archaea* and *Eukarya*). If ubiquity is present in 90% or 80% of the individuals of each prokaryotic phylum, it reaches 60 and 71 genes, respectively. In addition to size and structure variation, phylogenetic markers must be ubiquitous and have functional constancy. Theoretically, the best strategy to obtain a reasonable estimate of the species tree is to consider multiple genealogies inferred from unlinked loci, and to use multiple individuals per species (chapter 3). Other markers used in rRNA-based global phylogenetic studies include gene encoding translation elongation and initiation factors, RNA polymerase subunits, DNA gyrases, heat shock and *recA* proteins. Hsp70 (DnaK) heat shock protein data do not allow a distinct separation of the domains *Archaea* and *Bacteria*. With an increasing number of full genomes and new methods, phylogenomic studies have developed further. Several phylogenomic approaches currently in use are the comparison of gene content, gene order, average character identity, etc. (chapter 4).

How should prokaryote species be classified in higher taxa? There is an official nomenclature of prokaryotes in the International Code of Nomenclature of Prokaryotes, but there is no official classification of them. The most accepted definition of a prokaryotic species as a group of strains, including the type strain, are those that share at least 70% total genome DNA-DNA hybridization and have less than 5°C  $DT_m$  (the difference in the melting temperature between the homologous and the heterologous hybrids formed under standard conditions). A genus can be defined as a collection of species with many characters in common; a family can be defined as a collection of genera that share many characters; a class can be defined as a collection of orders with many common properties, etc., but how many and which characters must they have in common? (chapter 5).

Prokaryotes were the sole inhabitants of this planet for a large part of the history of life. They hold the keys for under-

standing the beginning of life and how different biochemical processes prepared to evolve to more complex organisms such as eukaryotes. Phylogeny not only organizes and classifies objects, but also relates the process by which these organisms became distinct entities. Many investigators have proposed various roots, using a wide diversity of biological data. These models illustrate the difficulty to reach a scientific consensus to define the root of the tree of life. The explosion in genomic data has also revealed the true complexity of evolution (chapters 6, 7). The significance of lateral gene transfer has subtly reconceptualized attempts to construct this universal tree (chapter 8). The accessory genes (remember that with the core genes together they constitute the pangenome of one species) indicate that microbial genomes are changing rapidly. Most of the accessory genes constitute derived characters for the strains in which they are found, but these genes are not found in other organisms and thus, they do not provide a taxonomic marker.

Nevertheless, the presence of a particular transferred gene has been shown, in several cases, to constitute a shared derived character useful in classification. Many transferred genes will be nearly neutral in the recipient, or be under selection only for a short period of time, and may persist in the recipient lineage for less than a few hundred million years. For a gene to survive in the recipient lineage, it must

become essential for the recipient, either because it provides a function that becomes essential or because it replaces the gene that was originally present in the recipient (chapter 9).

Photosynthesis is one of the most successful energy production strategies that have been acquired by non-photosynthetic eukaryotic heterotrophs several times through endosymbiosis. Whereas all plastids are derived from a single ancient fusion of a cyanobacterium-like prokaryote and a eukaryotic cell, plastids have evolved through a tortuous path among eukaryotes. Plastids have been modified to suit the light needs of their host. The coordination of the host and symbiont requires massive loss or transfer of genetic material from the symbiont to the host (chapter 10).

This sums up the outstanding book edited by Oren and Papke, *Molecular phylogeny of microorganisms*, obligatory reading for all microbiologists to understand the essential concepts of microbial systematics and the present tree of life in our planet.

---

**MERCEDES BERLANGA**  
University of Barcelona  
mberlanga@ub.edu

---