
Microbial life through the lens of molecules

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Abstract

The seminal discovery that evolutionary information can be retrieved from the monomer sequence of biological macromolecules had a profound impact in biology. One of the most immediate and powerful applications was the possibility to establish a natural classification of all organisms by using the information contained in universal conserved gene markers. Carl Woese successfully developed this approach using small subunit (SSU) rRNA molecules as universal identity markers and leading to establish the first universal molecular phylogenetic trees (with the incidental discovery of the archaea). This so-called ‘Woesian’ revolution soon paved the way to yet another revolution, that of environmental microbiology. Microbiologists knew that only a tiny fraction of the microbial diversity in natural ecosystems was amenable to culture in the laboratory. Initial molecular analyses based on amplification, cloning and (Sanger) sequencing SSU rRNA genes from environmental samples led to the discovery of a wide diversity of novel lineages that have been densely populating universal phylogenetic trees ever since. The advent of high-throughput sequencing techniques making possible massive SSU rDNA metabarcoding and the direct sequencing of environmental community genomes (metagenomes) have only confirmed and amplified our initial suspicions that most biological diversity is microbial and that this diversity is far more extensive than we ever thought. In turn, enriching taxonomic sampling with novel environmental lineages is fundamental to help reconstructing the tree of life and unraveling past evolutionary history. High throughput molecular techniques allow sampling natural microbial communities at unprecedented levels, such that microbial ecology can now embrace classical ecological theory.

Keywords: evolutionary information, phylogenetic trees, sequencing techniques, biological diversity

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