The microbial world presents systematists with a bounty of blessings together with the cruelest of curses. The paraphyletic group we call the prokaryotes are the oldest, most abundant, and most diverse form of life on Earth. Their ancestors constituted the entire biosphere for at least two-thirds of Earth’s history (Lipps, 1993); they are the dominant or sole form of life in many extreme habitats; and it has been estimated that their biomass in deep subsurface crustal fluids alone may be greater than that of all life on the surface of the planet (Whitman et al., 1998). It is now widely acknowledged that mitochondria and chloroplasts share common ancestry with the α-proteobacteria and cyanobacteria, respectively, and even the eukaryotic nucleus undoubtedly has prokaryotic origins (Katz, 1999). For scientists interested in studying biological diversity, no groups are more important and exciting than the Bacteria and Archaea. So impressive are they that Edward O. Wilson closed his autobiography, Naturalist (Wilson, 1994), by saying if he were starting out today, he would be a microbiologist.

Nevertheless, we know very little about the natural history of the Bacteria and Archaea. Their microscopic size means that microbiologists before the development of molecular biology had very few morphological or other characters with which to infer taxonomic relationships, and species characterization and description required cultivation of pure culture isolates in the laboratory. We also now know that only 1% or less of the microbiota have been grown in the laboratory and those are not representative of the dominant taxa in nature. That’s a taxon sampling problem if there ever was one and suggests that the phenotypic properties of most of life remain to be determined.

With such large room for advancement, it’s not surprising that research on the evolutionary biology of prokaryotes has benefited from molecular genetic and genomic tools more than that of any other group of organisms. A desire to synthesize the current state of affairs, and to build more bridges between microbiologists and our botanical and zoological counterparts, led James R. Brown and me to organize a symposium on this topic for the 1999 annual meeting of the Society of Systematic Biology. We invited Rita Colwell, Director of the U.S. National Science Foundation, to open the symposium and, although unfortunately she was unable to be there, she sent a letter to the attendees which said, in part:

Just as we don’t currently know the complete diversity of prokaryotic organisms on Earth, we are just starting to appreciate the full range of their mechanisms for evolutionary change. Great progress has been made in the past two decades. However, given the fascinating range of mechanisms of recombination in prokaryotes, processes that regulate evolutionary change in this wide array of organisms remain a fertile field of inquiry. In fact, we need to move very quickly to keep up with the speed with which microorganisms are changing. Whether we like it or not, these smallest of organisms have already inherited the earth.

This issue of Systematic Biology presents four papers from the symposium. The first of these, “Genomic and Phylogenetic Perspectives on the Evolution of Prokaryotes”, by James R. Brown, covers the history of progress in microbial systematics as well as various attempts to infer a universal phylogenetic tree. Drawing on examples from aminoacyl-tRNA synthetases, Brown illustrates how complete genome sequences have revealed an immense amount of genetic interchange in the form of lateral gene transfer, protein fusions, and rearrangements, and discusses the implications of this in reconstructing phylogenetic relationships. In “Environmental Diversity of Bacteria and Archaea”, Edward F. DeLong and Norman R. Pace take on the problem of the 99% of life that is still unknown to science. They discuss molecular phylogenetic and genomic tools for interrogating the environment to identify which taxa are the most abundant in natural habitats. For example, Archaea were once thought to be all but absent from most marine habitats, but evidence now indicates they may comprise 20% of the microbial cells in the ocean. As genes representing more and more of the undescribed taxa are recovered, they cause us to rethink systematic hypotheses and to revise our concepts of biodiversity altogether.
Uncovering the driving mechanisms and forces that gave rise to microbial diversity requires applying approaches from population biology. Two alternative, thought-provoking views on how to manage this are presented by Frederick M. Cohan and Jeffrey G. Lawrence. Cohan asks whether population clusters in the bacterial world share the same genetic, phenotypic, and ecological properties as do macro-species. In “Bacterial Species and Speciation”, he argues that genetic exchange and recombination in Bacteria are far less frequent (per generation) but more promiscuous than in sexual organisms. Cohan places emphasis on the role of ecological parameters in defining species clusters, in which periodic selection events purge them of diversity, helping to maintain their integrity as a species group. In contrast, in “Correlating Lateral Transfer with Genetic Headroom”, Lawrence presents evidence that genomic data reveal far more frequent intraspecific combination between strains than between species. The fixation of laterally transferred information, in Lawrence’s view, depends on effective population size. The larger the population size, the greater the leeway to accommodate new genetic information, and in turn, the better a cell can exploit new niches, leading to the creation of new species. Nevertheless, both authors appear to believe that patterns of recombination are intimately associated with the species concept as it applies to prokaryotic microorganisms.

Less than 20 years ago, academic institutions were awarding doctorates for sequencing a single gene from a single taxon. Now that high-power sequencing facilities have turned their attention from the human genome to sequencing microbial ones, it takes about a day to sequence 95% of the entire complement of DNA of a single microorganism. The quantity of data this will soon provide for examining the evolutionary pattern and process of life is almost beyond the imagination. Come and join in the feast.

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