INTRODUCTION

Long ago, we realized that the number of stars in the firmament was uncountable, and the light they shed is from the far distant past. Our planet’s microbial universe is equally awesome: Thinking about the number of organisms living in one human gut is discomfiting, and we are probably inhaling spores that have been blowing in the wind for years. Advances in genome-sequencing technology now allow previously uncultured organisms to be probed in their natural environments, whether they live intimately with us in our guts or in the far, deep sludge of the ocean’s abyss (see Roussel et al., p. 1046). This special issue examines some of the challenges in understanding the significance of all this diversity to the patterns and dynamics of arguably the most important organisms on Earth.

Although the organisms remain unseen, Falkowski et al. (p. 1034) point out that the microbial world drives some of the largest-scale phenomena on the planet, including photosynthesis, nitrogen cycling, and pandemics of infectious disease. In the opening Editorial, Tiedje and Donohue (p. 985) comment on ways in which this catalytic power might be harnessed to supply the needs of human societies.

Rapid-sequencing technology has also revealed unimaginable degrees of diversity. Paradoxically, the more diversity we find among microbes, the less simple it becomes to assign microorganisms to species. In a News story (p. 1031), Bohannon examines the phylogenetic entanglements caused by dizzying exchanges among the genomes of bacteria, archaea, and their viruses and discusses ongoing efforts to classify microbes with respect to their environments. Certainly, the fascinating microcosms harbored by marine sponges seem to defy biogeography. In a News story, Vogel (p. 1028) describes the remarkable similarity of microbial communities in sponges throughout the world. Nevertheless, Green et al. (p. 1039) argue that rather than investigate the distribution of individuals, we should instead be looking for the geographic distribution of traits.

Despite its uniformity to the human eye, the open sea offers not just a chance for microorganisms to swim but also niches generated by changes in light levels and salinity, marine “snot” and more resistant particles, and homes on the surfaces of animals. Hunt et al. (p. 1081) investigate the effect of niche partitioning in open water in a report showing that the habitat preferences of marine vibrios have taxon-specific patterns. But there are yet more layers of complexity in open-sea communities, and Strom (p. 1043) reviews the interdependencies of microbes in the plankton. Potentially, interrelationships can reach deep scales of detail; for example, Andersson and Banfield (p. 1047) have traced the path of genetic debris left by viruses preying on microbes in biofilms. Other examples of mechanisms used to forge microbial relationships are explored in Science Signaling (www.sciencemag.org/microbialecology): Dow discusses how closely related plant pathogens use similar signaling molecules in distinct ways, Lee describes how microbes in the gut dampen the immune response, and Wartha and Henriques-Normark discuss how mast cells make extracellular traps to kill microbes.

The shock of finding seemingly endless variation in microbial genomes has thus quietly revolutionized thinking about evolution and the species concept, as well as strengthened realization of the importance of the ecological services supplied by the microbial universe.

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Lost in Microbial Space
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