Department of Biology

The College of Arts + Sciences | Indiana University Bloomington

Norman Pace Lecture

Norm Pace

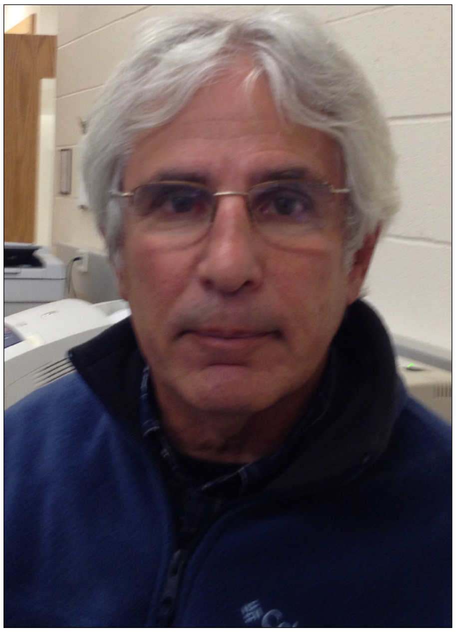
Tue., Apr. 5, 2022, from 4 to 5 p.m.

Attend in person: Myers 130

Attend virtually on Zoom (find meeting registration details at http://go.iu.edu/29K7)

Mitchell Sogin, Ph.D.

Distinguished Emeritus Senior Scientist
Josephine Bay Paul Center for Comparative Molecular Biology and Evolution
Marine Biological Laboratory at Woods Hole, Massachusetts



Mitch Sogin

Setting the Pace of Discovery

The article "Protozoa as indicators of pollution" [John Moor, *Scientific Monthly*, 74:7-9, 1952] stated, "The protozoan fauna (as a matter of fact, the whole microbiome) is poor in species and individuals." This represents one of—if not the first—published definitions of the term microbiome; however, our contemporary understanding of the microbiome traces back to pioneering molecular strategies in the Pace laboratory. Early practitioners of biodiversity (a form of political ecology) treated the microbial world as an afterthought with only 5000 named taxa. Nearly 100 years after discovery of the microbial world, scientists could only identify and classify microbes by morphology, cell-staining characteristics, physiological properties, and by the chemical reactions they perform. The limited morphological complexity discernable through light microscopy and the requirement to grow microbes in the laboratory for identifying phenotypic features that can serve as taxonomic determinants constrained our ability to differentiate between kinds of microbes. A half century ago, interactions between the Pace and Woese laboratories revolved about evolutionary questions that spanned RNA processing to discovery of new kingdoms of microorganisms. Pace took Woese's presentation of "Phylogenetic measurement in 'procaryotes' by primary structural characterization" [*J. Molec. Evolution* 1, 173-184, 1972)] to the next level through the development of molecular tools for defining microbial community structure, dynamics (ecology), and adaptation to their environment in "The analysis of natural microbial populations by ribosomal RNA sequences" [*Adv. Microbial Ecol. 9:1-55*] and "A molecular view of microbial diversity and the biosphere" [*Science* 276:734-740 1997]. These advances laid the foundation for contemporary microbiome research. Today's high-throughput marker gene analyses (rRNA sequencing) and binning of assembled contigs from shotgun metagenomic datasets have begun to unveil an astonishingly complex evolutionary history and ecology for single-cell organisms in ecosystems that span the deep subseafloor to the human microbiome.

The **Pace lecture series** (established in 2018) honors IU alumnus (BA '64 Bacteriology, with honors) and former Professor and Distinguished Professor of Biology (1984 to 1996) Norman R. Pace, one of the world's most influential biologists. Pace revolutionized microbial ecology in ways that allowed the "unseen 99 percent" to be revealed. He is known for his groundbreaking research in biochemistry and in microbial ecology and evolution. He has been a pioneer and leader in two very different fields: (1) he co-discovered catalytic RNAs, and (2) he was a pioneer in developing the methods and philosophy of sequence-based studies of microbes in their natural environments, ushering in the age of metagenomics and microbiome research.