

# DISTINGUISHED SCIENTIST SEMINAR SERIES

## Mining Soil Metagenomes for Meaning

James M. Tiedje

Center for Microbial Ecology, Michigan State University

Friday, January 14, 2011 10:30 a.m. – 12 p.m.

Building 15, Room 253, Berkeley Lab

### BIOGRAPHICAL SKETCH



JAMES TIEDJE is University Distinguished Professor of Microbiology and Molecular Genetics and of Crop and Soil Sciences at Michigan State University, and is Director of the Center for Microbial Ecology, one of the original NSF-funded Science and Technology Centers. His group has made contributions to understanding denitrification, soil microbial community structure, and novel bacteria that live by halo-respiration on chlorinated chemicals. Recently he has used genomics and metagenomics to better understand ecological functions, speciation, and niche adaptation. He has served as Editor-in-Chief of *Applied and Environmental Microbiology* and Editor of *Microbial and Molecular Biology Reviews*. He has served on the Board on Life Sciences of the National Research Council, chaired EPA's Science Advisory Panel, and serve on DOE's Biological and Environmental Research Advisory Committee. He was President of the American Society for Microbiology and of the International Society of Microbial Ecology, and chaired the Soil Biology Division of the International Soil Science Society. He is a Fellow of the AAAS, the American Academy of Microbiology, the Soil Science Society of America, and a member of the U.S. National Academy of Sciences.

### SPEAKER'S SCHEDULE

10:30 am – 12:00 noon  
Talk and Discussion, B50 Auditorium

12:00 noon - 1:30 pm  
"Brown Bag" style lunch - post-docs  
Lower Level Room, Cafeteria

2:00 pm  
One-on-one meetings as scheduled

### 2010-2011 Distinguished Scientist Seminar Series

May Peter G. Cook  
2011 CSIRO Land and Water - Waite Campus  
Australia

### ABSTRACT

Because of its diversity, the soil is arguably the most challenging frontier in biology. Soil houses the most complex microbial communities because of its ancient history; complex sets of interrelating gradients; and protective, isolating, and relatively resource-poor and stable physical structure. This results in an incredibly diverse set of gene sequences, at least on the scale at which soils are normally sampled. These genes and their host microbes catalyze vital functions ranging from biogeochemical cycles, to greenhouse gas flux, to water quality, to plant and animal health. The new molecular and omic technologies provide scientists with the opportunity to understand and eventually better manage some of these communities, but today's challenge lies in analyzing the massive amount of currently short sequences. I will discuss three components that underpin the understanding of soil communities: their compilation of subcommunities, the species and pangenome perspective, and the initial efforts to link sequence and function. I will use examples from agricultural, permafrost, tropical, rhizosphere, and native ecosystems that include both shotgun and gene-targeted (amplicon) sequencing of key (eco)functional genes, *nifH* and *bphA*, for nitrogenase and aromatic degradation, respectively.

### CONTACT US

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