

PHYSICS AND ASTRONOMY SEMINAR SPRING 2009

METAPROTEOMICS OF NATURAL MICROBIAL COMMUNITIES

NATHAN VERBERKMOES
Chemical Science Division
Oak Ridge National Laboratories

Microbial communities play key roles in the Earth's biogeochemical cycles. Our knowledge of the structure and function of these communities is limited because analyses of microbial physiology and genetics have been largely confined to isolates grown in laboratories. Recent acquisition of genomic data directly from natural samples (Tyson, *Nature*, 2004) (Venter, *Science*, 2004) has begun to reveal the genetic potential of communities and environments. The ability to obtain whole or partial genome sequences from microbial community samples has opened up the door for microbial community proteomics. Microbial community proteomics (metaproteomics) is a key technology for studying and gaining insight into microbial physiology in mixed natural microbial communities. We have developed and applied a combined proteogenomic approach using genomics and mass spectrometry-based proteomic methods for characterizing the proteome from microbial communities (Ram, *Science*, 2005; Lo, *Nature* 2007). The key to this technology is the combination of robust multidimensional nano liquid chromatography with rapid scanning tandem mass spectrometry followed by a suite of informatic tools. The model system for the development of these techniques is a low complexity natural acid mine drainage (AMD) microbial biofilm community previously characterized by cultivation-independent genomic methods. The development of the approach on a model low complexity system has allowed us to extend the approach to more complex microbial communities and environments such as soil, ground water, ocean and the microflora associated with the human gut. Key technological advances are needed to obtain "deep" and "wide" proteome coverage in more diverse and complex systems.

Monday, March 16, 2009, 4:00 pm
Brown Hall 261

Refreshments served at 3:45 pm