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Application of metabolomics, lipidomics, and kinetic flux profiling to understand the metabolic role in microbial interactions

Shawn R Campagna
University of Tennessee, USA

Our lab uses an interdisciplinary approach that relies heavily on liquid chromatography–mass spectrometry (LC–MS) based metabolomics to understand medicinally and environmentally relevant microbial processes. The primary analytical platform is an UPLC-Orbitrap MS with electrospray ionization source, and the methods employed attempt to measure the concentration (pool size) of ~1000s of analytically tractable, yet chemically diverse, water and lipid soluble metabolites from all kingdoms of life. These methods measure at least one metabolite from all known carbon and nitrogen utilization pathways, the activated methyl cycle, all amino acid and nucleotide biosynthesis pathways, as well as lipids with diverse head groups; and the average coverage for each major pathway is ~65%. The utility of these metabolomics methods can be enhanced by monitoring the incorporation of stable isotope-labeled nutrient sources, either ^{15}N or ^{13}C, into the metabolome using kinetic flux profiling techniques (KFP). When coupled, pool size determination and KFP can be used to determine both the amounts of metabolites within and relative rates of flux through many biochemical pathways *in vivo* and allow a global snapshot of cellular metabolism to be obtained from a single set of experiments. Several vignettes from our work studying bacterial cell-cell signaling (quorum sensing), microbial nutrient cycling by marine organisms, and novel biochemical pathways in yeast will be discussed to highlight the utility of applying these metabolomics tools to probe complex biological systems and to provide insight into the mechanisms that consortia of microorganisms utilize to cooperatively and/or competitively dictate resource utilization.

Biography

Shawn R Campagna received his Ph.D. from Princeton in 2006, after working with Prof. Martin Semmelhack on a joint project with Profs. Bonnie Bassler and Frederick Hughson to characterize the chemical properties of an interspecies bacterial signaling molecule, autoinducer-2. He then performed post-doctoral research with Prof. Joshua Rabinowitz at the Lewis-Sigler Institute for Integrative Genomics at Princeton University where he developed mass spectrometric methods for the identification of novel biochemical pathways and natural products from whole cell extracts. He joined the Chemistry Department at UT Knoxville in 2007 where he has worked to develop new metabolomic and lipidomic techniques.

campagna@ion.chem.utk.edu