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## Application of metabolomics and kinetic flux profiling to understand the metabolic function of aquatic microbial consortia

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Recent advances in liquid chromatography–mass spectrometry (LC–MS) based metabolomics and lipidomics have furthered understanding of medicinally and environmentally relevant microbial processes. The utility of metabolomics methodsis enhanced by monitoring the incorporation of stable isotope-labeled nutrients, either 15N or 13C, into the metabolome using kinetic flux profiling techniques (KFP). The coupling of metabolite concentration (pool size) measurements 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 the combination of these methods allow a global snapshot of cellular metabolism to be obtained. Our laboratory's primary analytical platform is a set of UPLC—Orbitrap MSs with electrospray ionization sources, and the methods employed attempt to measure pool size of a large set of analytically tractable water and lipid soluble metabolites from all kingdoms of life. The set of 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. Several vignettes from our work studying aquatic microorganisms will be discussed, with a focus on understanding the utility of metabolomics to understand mixed populations of viruses, bacteria, cyanobacteria, and algae. The information gained from these meta-metabolomics experiments is often enhanced when coupled with other systems biology tools, such as meta-transciptomics; and the integration of multi-omics techniques to study the metabolism of aquatic microbial consortia will be discussed.

### Biography

Shawn R Campagna received his PhD 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. He is currently an Associate Professor and Head of the UTK Biological and Small Molecule Mass Spectrometry Core.

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