

From direct imaging to microarrays: Stable isotope probing of microbial function in complex communities

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Isotopic analysis can provide insight into a diverse array of processes, particularly when coupled with other methods. In this presentation, I will review isotopic tracer methods used to gain insights into microbial function. In the past decade, stable isotope probing (SIP) has become an important set of tool for linking microbial identity to function in complex microbial communities. SIP was originally the designation for methods that determined what microbes incorporated a label substrate using high velocity centrifugation to separate DNA based on the extent of labelling. More recently, SIP has evolved into a range of methods for identifying the fate of the label. New approaches include direct imaging of microbial cells, which I refer to as nanoSIP; the use of microarrays to isolate microbe-specific 16s RNA for isotopic analysis, which our group has dubbed chipSIP; protein-specific isotopic analysis, referred to as protein-SIP. Much of my talk will focus on nanoSIP and chipSIP, which our group performs with a Cameca NanoSIMS 50, a high spatial resolution secondary ion mass spectrometry (SIMS) instrument. I will talk about SIP methods in the context of my interest in microbial mats and insect hindguts. A shared feature of this research is that it is multidisciplinary. In the collaborations I participate in, we combine SIP experiments with other physical and chemical data, sequencing, time course and manipulations experiments, microscopy, focused ion beam (FIB) sectioning, catalyzed reporter deposition fluorescence *in situ* hybridization (CARD-FISH), and elemental label FISH (EL-FISH). Combined with other methods, SIP methods provide critical insight into microbial function, particularly in complex systems.