# Trophic Relationships in Modern Microbial Mats Determined Using Protein Stable Isotope Fingerprinting

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The carbon isotopic composition ($\delta^{13}C$) of bulk organic matter has been used to identify the primary carbon metabolisms in a variety of modern environments. This metric may not be as useful in microbial mat systems, where closely associated microbial communities, often employing flexible carbon metabolisms, make it difficult to distinguish producer from consumer isotopically. Protein Stable Isotope Fingerprinting (P-SIF) is a recently developed method which allows measurement of the $\delta^{13}C$ values of whole proteins, separated from environmental samples and identified taxonomically via proteomics. Here we used P-SIF to determine the trophic relationships in two modern microbial mat samples, one each from Yellowstone National Park and Lake Huron USA. In both cases, values of $\delta^{13}C$ of producers and consumers were indistinguishable and indicative of primary production via the Calvin-Benson-Bassham cycle (CBB). The finding that the consumers of CBB-derived carbon were isotopically indistinguishable from their source of organic matter cautions against using the $\delta^{13}C$ of bulk organic matter as an indicator of inferred trophic level in microbial mats or other complex microbial communities that may be engaged in cross-feeding. Similarly, such isotopic signatures illuminate the challenges for determining from the geologic record whether such environments were net $O_2$ sources or sinks (net autotrophic or net heterotrophic) [1].

[1] Voorhies, A. *et al*.. (2012) Geobiol 10: 250-267.