Metabolic functioning of a ciliate-methanogen symbiosis from anoxic habitats

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Symbioses between anaerobic protists and methanogenic archaea are common in oxygen-depleted habitats ranging from aquatic sediments to gastrointestinal tracts, yet little is known about the mechanisms and dynamics of metabolic interaction between these players. In these putatively syntrophic associations, it has been hypothesized that host fermentation is facilitated by symbiont consumption of fermentative end-products (e.g., H2) during symbiont methanogenesis. However, at present there is very little information about the metabolic pathways employed by both host and symbionts. Here, we report the gene content of a 93% complete genome from the Methanobacterium symbiont of a common anaerobic ciliate from the genus Heterometopus. In addition, we also investigated coupled host-symbiont metabolism during different stages of host growth, as well as when exposed to micro-oxic conditions, with experimental measurement of symbiont CH4 production and assessment of host and symbiont gene expression via transcriptomic sequencing. Given that, in some habitats, protist-associated methanogens can account for a significant portion of CH4 production, data regarding host and symbiont metabolic processes is not only foundational to our knowledge of the physiology and ecology of protist-methanogen symbioses, but may also critical to our understanding of biogeochemical processes in the ecosystems they inhabit.