Strategies to assess the biochemical properties of extracellular hydrolases in aquatic environments

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Metagenomic, metatranscriptomic, and single cell genomic tools have done much to expand our ability to determine the range of metabolic capabilities of microbial communities, but these tools ultimately rely on our ability to infer enzyme function from DNA sequences. Hydrolytic enzymes are particularly important for organic matter degradation, but determining their function based solely on DNA sequence homology can be difficult. We present results of a biochemical characterization of the first peptidase ever expressed and characterized from an uncultured Archaeon to test the hypothesis that DNA homology of hydrolases to those of cultured organisms is a useful way to infer functions. We also demonstrate that the bulk biochemical properties of mixed pools of hydrolases present in environmental samples can be elucidated using inhibition experiments. We show that the amino acids which are removed from detrital organic matter more quickly are those which bind better to the active sites of a wider range of peptidases. These results demonstrate how the biochemical properties of environmental hydrolases influence global patterns of organic matter diagenesis.