

LATITUDINAL AND DEPTH PATTERNS OF MICROBIAL ENZYME ACTIVITIES IN THE OCEAN: IMPLICATIONS FOR CARBON CYCLING

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Heterotrophic microbial communities are responsible for cycling an estimated half of marine primary productivity (Azam & Malfatti 2007) modifying, repackaging, and remineralizing dissolved as well as particulate organic matter. Much of this organic matter initially is produced as high molecular weight (HMW) substrates, including polysaccharides, proteins, and lipid complexes. The initial step in degradation of these HMW substrates is extracellular enzymatic hydrolysis, through which the substrates are hydrolyzed to sizes sufficiently small for uptake into the cell (Fig. 1). The structural selectivity of microbial enzymes, as well as the rates at which they function, are therefore critical parameters determining the depth and location at which organic matter is remineralized in the ocean, or conversely, the nature and quantity of substrates that may persist in ocean waters or in sediments over geologic time periods.

Recent genomic and metagenomic work has provided initial insight into the distribution of genes that correspond to extracellular enzymes among specific organisms and communities (e.g. Wegner et al. 2013; Teeling et al. 2016). The ability to hydrolyze high molecular weight substrates varies greatly among microbes: some lack extracellular enzymes, others possess a genetic arsenal capable of hydrolyzing a considerable range of substrates (e.g. Sun et al. 2016). The nature and diversity of hydrolytic enzymes found in marine microbial communities is thus highly variable by location as well as season (Gomez-Pereira et al. 2012; Teeling et al. 2012). Increasing knowledge about genes, genomes, and metagenomes, however, does not yield information about the rates at which enzymes actually function, and organic matter is thereby transformed, in the environment. We have pioneered new methods to measure hydrolysis of polysaccharides and phytoplankton-derived organic matter in the ocean (Arnosti 2003), measuring the rates and patterns of hydrolysis of a diverse range of structurally-distinct HMW substrates. These investigations have demonstrated that there is no simple correlation between substrate structural factors - such as monosaccharide composition - and hydrolysis rate. For example, two glucose-containing soluble polysaccharides (laminarin and pullulan) typically show considerable differences in rates and patterns of hydrolysis in the water column; compositionally-complex heteropolysaccharides, moreover, can be rapidly hydrolyzed despite their chemical complexity (Arnosti et al. 2011).

The rate at which HMW organic matter is cycled, instead, is a function of microbial community capabilities as well as substrate structure. Recent investigations have demonstrated that there are large-scale differences in microbial community composition (microbial biogeography), with fundamentally different communities at temperate and high latitudes, at surface and depth, between coastal and offshore waters, and between sediments and the overlying water column (e.g., Fuhrman et al. 2008; Zinger et al. 2011). Our data from our most recent transect cruises in the Atlantic, Pacific, and Arctic Oceans demonstrate that large-scale patterns in enzyme activities reflect these broad patterns in microbial biogeography. On global scales, the spectrum of enzyme activities (the number of structurally-distinct substrates hydrolyzed) narrows markedly from temperate to high latitudes, as well as from surface to deep waters. Temperature is not the major factor driving these patterns, however, since individual substrates are often hydrolyzed more rapidly in cold than in warmer waters. Moreover, the spectrum of substrates hydrolyzed on particles and aggregates is typically broader than in the waters from which they were derived, suggesting that particle-specialist communities possess a broader range of enzymatic capabilities - not simply higher rates of enzyme activities - than their free-living counterparts.

Key structure-function correlations between microbial communities and their enzymatic activities are being revealed through our ongoing investigations of microbial community composition and activities. Some substrates are hydrolyzed by a wide range of organisms, while other organisms evidently are specialized for the hydrolysis of distinct substrates; their presence and activities drives the turnover of certain types of organic matter. The role of the “rare biosphere” (Sogin et al. 2006) may thus include acting as a reserve for the degradation of substrates that are episodic in their availability in the environment. The capabilities, distribution, and temporal dynamics of microbial communities, as well as the structure and form of organic substrates, are therefore key determinants of organic matter reactivity in the ocean.

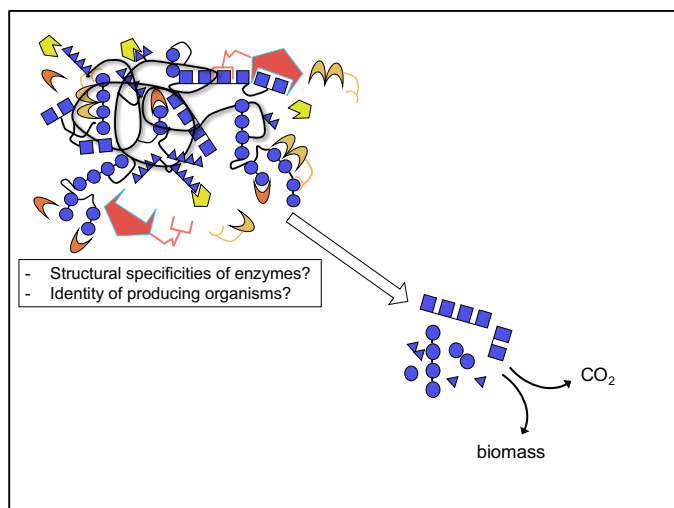


Figure 1: A range of different extracellular enzymes (orange, yellow, red shapes) is required to hydrolyze most high molecular weight substrates (blue shapes) to sizes sufficiently small (blue fragments) for uptake into the cell. The structural specificities of these enzymes, the identity of the producing organisms, and the conditions under which specific enzymes are produced are only beginning to be revealed. Figure modified from Arnosti (2011).

References

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