

Hydrocarbon utilization by uncultured sediment microbes

Brett J. Baker, Nina Dombrowski, Kiley W. Seitz, Ian Rambo, Andreas P. Teske

Hydrocarbons (alkanes and polycyclic aromatic hydrocarbons (PAHs)) are predominant in sediments impacted by naturally occurring seeps, hydrothermal influence, and petroleum mining activities. Microorganisms derive carbon and energy from the degradation of hydrocarbons. To resolve pathways for anaerobic hydrocarbon degradation among uncultured archaea and bacteria we have reconstructed genomes from hydrocarbon-rich estuary (Mesquite Bay in South Texas) and deep-sea (Guaymas Basin, Gulf of California) sediments. We have reconstructed genomes comprising 28 distinct archaeal and bacterial phyla from Guaymas. The archaea at both sites included members of the Bathyarchaeota, which appear to be involved in anaerobic butane oxidation. Newly obtained members of the novel “GoM-Arc1” archaeal group, related to anaerobic methane-oxidizing (ANME) archaea, encode novel pathways for short-chain hydrocarbon oxidation via the alkyl-coenzyme M reductase and other enzymes with homology to those involved in methanogenesis. In Guaymas sediments methane oxidation appears to be mediated by ANME-1 archaea. Interestingly, genes encoding enzymes that activate hydrocarbons for anaerobic degradation were detected in Bacteroidetes, Chloroflexi, Latescibacteria (WS3), and KSB1 phyla. These findings elucidate the biodiversity of hydrocarbon degradation and expand the hydrocarbon substrate specificity of archaea and bacteria in nature.

For MB:

From the rps3 phylogeny (recovered from the 4 metagenomes)

Syntrophobacter fumaroxidans: [syntrophic propionate](#)-degrading [sulfate](#)-reducing bacterium

Dehalococcoides mccartyi (*D. mccartyi*) are specialist “strict organohalide respiring bacteria,” and are restricted to reductive dehalogenation