

Phylogenetic Diversity in Microbial Communities Associated with Gulf of Alaska Deep-Sea Corals

Kevin Penn, Tom Guilderson, and Naomi Ward

The Institute for Genomic Research

Center for Accelerator Mass Spectrometry, University of California Santa Cruz/Lawrence Livermore National Laboratory

Deep-sea corals inhabit cold and sunless waters where they grow extremely slowly and are vulnerable to destructive fishing practices. Despite their widespread distribution and importance as indicators of climate change, the corals' feeding and reproductive strategies are still poorly understood. Shallow-water corals harbor species-specific bacterial communities; deep-sea coral microbial assemblages have not been previously reported. We examined microbes associated with black and bamboo corals collected on the Gulf of Alaska seamounts. Bacterial genomic DNA from four surface mucopolysaccharide layer samples was extracted and purified, and the 16S rRNA genes PCR-amplified, cloned, and sequenced. A distance-treeing method was used to assign cloned sequences to taxonomic groups within the domain Bacteria.

Coral-associated microbial populations showed considerable phylogenetic diversity; 11 phyla, 15 classes, 26 orders, and 30 families were represented. The four coral samples showed very different microbial community compositions. A Murray Seamount black coral sample was dominated (36% of clones) by α -proteobacteria (*Rhizobiales*, *Rhodobacteraceae*, *Sphingomonadales*), also containing Actinobacteria, *Flexibacteraceae*, *Chlorobiaceae*, and *Spirochaetaceae*. A Murray bamboo coral sample showed a more pronounced pattern of dominance, with 70% of clones belonging to *Rhodobacteraceae* and 26% to *Pseudomonadaceae* (α -proteobacteria). The prevalence in both coral types of *Rhodobacteraceae*, known nitrogen-fixers, suggests that they may be providing fixed nitrogen symbiotically to the corals. A Chirikof Seamount *Antipathes* sp. possessed a completely different microbial community, dominated (46% of clones) by *Mycoplasmataceae*, with minor components of *Flexibacteraceae*, *Verrucomicrobiaceae*, and Proteobacteria. Mycoplasmas are bacterial pathogens not previously reported in association with corals or other deep-sea fauna.

This survey provides preliminary evidence of species-specific bacterial assemblages in deep-sea corals; future sampling of multiple individuals is needed to confirm this relationship.