



Microbial diversity of sunken woods provides insights into ocean chemosynthetic communities dispersion

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Different sources of imported, organic matter carried down to the deepest parts of all seas could enhance the species richness of sediment-dwelling communities where organisms are highly food-limited relying primarily on organic material from upper layers. Furthermore, when deposited in marine sediments, large organic falls undergo sufficiently steady decay for oxygen to be depleted, attracting anaerobic living forms. The phylogenetic resemblance and overlap in species of metazoans living in woods or large animal remains with those of highly reduced environments like hydrothermal vents and cold seeps has led to the hypothesis that deep-sea organic rich matter deposits could play a major role in the dispersion and evolution of chemoautotrophic communities in marine waters. In spite of their potential importance no studies have dealt with free-living microbial diversity and activities at sunken woods. We have used culture-independent methods to study the microbial communities on both, artificially immersed and natural wood samples, located at geographically isolated coastal and deep-sea environments. SSCP of the 16S rRNA gene (rDNA) served to fingerprint the Archaea and Bacteria communities living on and within the woods to determine their resemblance among samples. Posterior rDNA cloning and sequencing of target samples gave clues on the actual diversity and phylogenetic resemblance of the main metabolic players responsible of energy and carbon flows. Our results broad our narrow knowledge on the microbial biofilms that develop around woods in marine environments and give clues on the ecological importance of these organic island deposits for the dispersion of chemosynthetic communities at the ocean basin.