

THE FUNCTIONAL POTENTIAL OF CORAL-ASSOCIATED MICROBIAL COMMUNITIES IN *PSEUDOPTEROGORGIA AMERICANA* FROM LA PAGUERA, PUERTO RICO

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Coral-associated microbial communities are increasingly recognized as important components of the coral holobiont that influence coral health and disease. It has been suggested that these communities contribute to the health of the coral ecosystem through energy and nutrient cycling; others suggest that microbial communities provide corals with protection against infectious disease. To date however, there are few studies that directly address the functional role of these communities. In the present study, we examined the functional potential of the coral-associated microbial community found in the surface mucopolysaccharide layer (SML) of a common Caribbean coral, *Pseudopterogorgia americana*. The SML samples were collected in March of 2006 off the coast of La Paguera, Puerto Rico. DNA was extracted and amplified for use in a functional gene array, the GeoChip, which contains 24,000 probes targeting 10,000 functional genes involved in approximately 150 functional groups associated with biogeochemical processes. We examined the presence of these genes in community DNA from the SML of healthy *P.americana* colonies. Our preliminary data indicate that this microbial community possesses 1189 genes known to play a role in numerous biogeochemical processes. These processes include carbon degradation/fixation (159 genes), dissimilatory sulfite reduction (94 genes), metal homeostasis (203 genes), methane generation and oxidation (50 genes), nitrogen fixation/reduction (145 genes), ammonification (94 genes), and organic chemical degradation (444 genes). Our data, although preliminary, suggests that the coral-associated microbial community found in the SML of *P. americana* may play an active role in maintaining the coral holobiont through cycling of key nutrients, metals and organic contaminants. In on-going studies, we are evaluating the functional potential of healthy as well as diseased *P. americana* samples in triplicate using both SML and tissue samples.

This research is supported by the College of Graduate Studies and a National Science Foundation Biodiversity Surveys and Inventories grant.

The mucous samples were collected in March of 2006 off the coast of La Paguera, Puerto Rico and stored in 5M GIT Buffer at -20C. The community DNA was extracted using a CTAB/Phenol/Chloroform protocol and amplified using the Amersham Biosciences TempilPhi amplification kit (25-6400-01).

Category	Gene Category	# Genes	% Total	Example Genes
CDEG	Carbon Degradation	126	10.60	cellulase, chitinase, laccase
CFIX	Carbon Fixation	33	2.78	cdhE, cooF, ACSAB
DSR	Dissimilatory Sulfite Reduction	94	7.91	dsrA, dsrB
MET	Metal Homeostasis	203	17.07	Ni, Cd, Co, Zn, Pb, Al, Hg
MGEN	Methane Generation	19	1.60	mcr, mcrA, mcrG
MOX	Methane Oxidation	31	2.61	mmo, mmoA, pmo, pmoA
NFIX	Nitrogen Fixation	48	4.04	nifD, nifH
NIT	Ammonification, Ammonia Assimilation	94	7.91	amoA, amoB, amoC, gdh
NRED	Nitrogen Nitrate/ Nitrite Reduction	97	8.16	nir, nirK, nirS, norB, narB
ORG	Organic Chemical Degradation	444	37.34	benzene, parathion
		<u>1189</u>	<u>100.00</u>	