Microbial communities in lithifying and non-lithifying microbial mats, Eleuthera, Bahamas

Laura K. Baumgartner
Department of Marine Sciences
University of Connecticut
1080 Shennecossett Rd., Groton, CT
UNITED STATES
Laura.Baumgartner@Uconn.edu

Pieter T. Visscher
Department of Marine Sciences
University of Connecticut
1080 Shennecossett Rd., Groton, CT
UNITED STATES

Christophe Dupraz
Institute of Geology
University of Neuchâtel
Rue Emile-Argand 11, 2007 Neuchâtel
SWITZERLAND

Kristen M. Przekop
Department of Marine Sciences
University of Connecticut
1080 Shennecossett Rd., Groton, CT
UNITED STATES

John R. Spear
Molecular, Cellular, and Developmental Biology
University of Colorado
347 UCB, Boulder, CO
UNITED STATES

Norm R. Pace
Molecular, Cellular, and Developmental Biology
University of Colorado
347 UCB, Boulder, CO
UNITED STATES

Microbe-induced calcification and lithification create biosignatures that survive into the fossil record and could be used as indicators of life. However, the actual mechanisms of these processes are still unknown in many systems, making interpretation of these biosignatures difficult. In a hypersaline lagoon in Eleuthera, Bahamas, lithifying and non-lithifying microbial mats coexist under similar physical and chemical conditions[1]. Thermodynamic predictions and *in situ* activity measurements suggest that sulfate-reducing bacteria dominate lithification in these mats. These bacteria may affect calcium carbonate precipitation through alteration of the saturation index or the creation and destruction of exopolysaccharides (EPS). Other groups, such as cyanobacteria, sulfide oxidizers, and aerobic and anaerobic heterotrophs may also cause the precipitation or

dissolution of carbonates. Therefore, as part of an ongoing study of lithification mechanisms in this system, we examined the relationship between lithification and the microbial community by extracting DNA from lithifying and non-lithifying mats. This DNA was amplified and sequenced with broad-spectrum PCR primers. The mats are fairly diverse, although bacterial sequences dominate. The most prevalent bacterial sequences represent alpha proteobacteria, delta-proteobacteria (including sulfate-reducing bacteria) and chloroflexi (including known green non-sulfur bacteria). In addition, while both spatial and temporal changes are observed in the mat communities, the overall presence or absence of certain division- level groups appears to be fairly consistent, suggesting a core community of organisms that carry out key functions in the system.

1. Dupraz, C., Visscher, P.T., Baumgartner, L.K., and Reid, R.P. 2004. Sedimentology 51, 745–765.