Prokaryotic Diversity and Function at a Newly Discovered Shallow-water Gas Vent Site in the Tyrrhenian Sea

Sushmita Patwardhan[1], Donato Giovannelli[3,4], Costantino Vetriani[2,3]

[1]Department of Marine and Coastal Science, Rutgers University, New Brunswick, NJ, USA; sushmita.patwardhan@gmail.com
[2]Department of Biochemistry and Microbiology, Rutgers University, New Brunswick, NJ, USA
[3]Institute of Earth, Ocean and Atmospheric Sciences, Rutgers University, New Brunswick, NJ, USA
[4]Earth-Life Science Institute, Tokyo, Japan

Despite their wide distribution, shallow-water geothermal environments have not been explored as extensively as their deep-sea counterparts. Tor Caldara is a newly discovered shallow-water gas vent in the Tyrrhenian Sea, Italy. The study site is a shallow submarine gas vent off the coast with a maximum depth of 3 meters. There is a significant amount of outgassing of carbon dioxide and hydrogen sulfide. A unique feature of this vent site is the absence of a thermal anomaly. In this study, we surveyed the prokaryotic diversity of the established filamentous biofilms growing in the vicinity of the venting, encrustation seen around the orifice of the gas vents as well as the sediment in the venting area. Data show that the sediment community is most diverse and includes members of Proteobacteria, Acinetobacteria Bacteroidetes, Planctomycetes, Acidobacteria, Firmicutes, Cyanobacteria etc. The crust community is slightly less diverse comprising predominantly members of Proteobacteria, Cyanobacteria and Bacteroidetes. The established filamentous biofilm community is the least diverse and most specialized and is dominated primarily by Epsilonproteobacteria, Gammaproteobacteria and Bacteroidetes. In conjunction with the 16S rRNA-based assessment of diversity, we enriched and isolated bacteria using different culture conditions. Two novel bacterial strains, TC3T and TC8T, 92.76% and 91.25 % similar to Sulfurimonas gotlandica and Magnetovibrio blackemorei respectively, were isolated. TC8T was further characterized. The integration of culture-based and molecular analyses is providing qualitative and quantitative insight into prokaryotic diversity and function at the shallow-water vent in Tor Caldara.