Linking Microbial Phylogeny and Functional Gene Diversity to Microbial Mat Ecosystem Function Following Environmental Disturbance

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The ability of ecosystems to adapt to environmental perturbations depends on the duration and intensity of change and the overall biological diversity of the system. In this study, a microbial mat ecosystem located on San Salvador Island, The Bahamas was used as a model to examine how environmental disturbance affects microbial community resistance, their protein synthesis potential (PSP), ecosystem function as measured by biogeochemical cycling, community stability, and resilience. This ecosystem experienced a large shift in salinity (230 to 65 g kg\(^{-1}\)) during 2011–2012 following the landfall of Hurricane Irene on San Salvador Island. High throughput sequencing and analysis of 16S rRNA and rRNA genes from samples before and after the pulse disturbance showed significant changes in the diversity and an increase in PSP of abundant and rare taxa, suggesting overall compositional and functional sensitivity to environmental change. Together, these findings show complex community adaptation to environmental change and help elucidate factors connecting disturbance, biodiversity, and ecosystem function that may enhance ecosystem models. Based on these findings, a long-term study was conducted to answer questions about the impacts of seasonal and pulse disturbance on the community resistance, ecosystem function and stability, and resilience using a comparative metagenomic approach. Over the course of four years the microbial mat community was monitored and vertical sections were taken at eight time points. We found that a wide range of environmental factors play a role in shifting the microenvironment of the mat resulting in compositional changes over time leading to vertical niche differentiation within the mat. Community composition did not significantly change on Archaea and Bacteria phyla level but on class level. The microbial community of the deepest layer was resistant to environmental disturbance, while upper layers changed in community composition and did not return to its pre-disturbed state, suggesting that the community was not resilient to the disturbance event after one year. Assessing apparent functional capacity of the archaeal metagenomes over time, showed that the metagenome of the first three time points were distinct from all other time points and pre-and post-disturbance metagenome were different.