JUSTIFICATION FOR SUPPLEMENT

REU Supplement: Modeling Salinity-Driven Biogeochemical Fluxes in Shallow Coastal Lagoons

(Supplement to award DEB-1149447, "CAREER: Linking Microbial Phylogenetic and Functional Gene Diversity to Microbial Mat Ecosystem Function Following Environmental Disturbance")

Summary of Existing Work

The purpose of the work supported under DEB-1149447 is to examine the relationship between biodiversity and ecosystem function to better understand ecosystem stability or resiliency during environmental change. Given that microorganisms are the foundation of ecosystem processes, we have been focused on understanding the environmental cues that drive temporal variation of the microbial community (abundance and activity) and the effect on ecosystem resiliency following environmental disturbance. We have been testing our hypotheses in a small lagoon on San Salvador Island, The Bahamas. This lagoon is an excellent model ecosystem because much of the biogeochemical cycling occurs within a highly diverse and tightly metabolically coupled microbial mat that is temporally exposed to wide ranges in salinity (30-300 psu). We have collected samples from this site bi-annually since 2012 and have captured a range of environmental conditions, including before and after 2 major hurricane disturbances. We have observed shifts occurring in the activity of rare and abundant populations of microbes during these changes and currently have a manuscript submitted outlining how these changes affect ecosystem function. While the current award focuses on primary productivity as the main endpoint of analysis, preliminary data suggest that climate-driven disturbances are causing fluxes in overall biogeochemical cycling resulting in possible temporal bursts of greenhouse gas production from this ecosystem. This REU supplement would provide an excellent opportunity for undergraduate students to explore the potential greenhouse gas feedback loop occurring in this ecosystem and provide data that, while independent of the ongoing study, will be fundamentally synergistic to the overall project.

Student's Involvement in the Research Project

The current award is supporting a graduate student involved in analyzing molecular-based 16S rRNA and metatranscriptomic data related to previously established aims. Supported through University of South Carolina (UofSC) funds, a second graduate student with a background in software engineering is working in collaboration with the NSF-funded graduate student to build ecosystem models based on collected molecular and environmental data. In this REU supplement, I am requesting support for two undergraduate students to work independently yet synergistically with the two established graduate students to examine temporal fluxes in overall biogeochemical cycling occurring in the lagoon ecosystem. While, the two undergraduate students will work on different aspects of this project they will be necessarily linked, with one student involved in quantitative PCR analysis of biogeochemical cycling (C,N,O,S) genes and transcripts and the other student involved in developing the algorithms for integration of resultant data into our developing ecosystem models. While nucleic acids have already been extracted for samples taken between 2012-2015 (for studies related to the ongoing study), the undergraduate student involved in this aspect of the project will work with the PI and the NSFsupported graduate student to design and perform properly controlled and replicated QPCRbased studies using our established laboratory protocols to examine the abundance and expression of biogeochemical cycling genes in these samples. The samples were taken within a range of salinities during day and night from the same area of the lagoon and consist of replicate cores separated into one-millimeter layers to a depth of eight millimeters. Thus, these samples will allow the undergraduate student to analyze gene abundance and expression over

temporal and spatial scales under different environmental conditions. While the first student is collecting gene abundance and expression data, the second undergraduate student will be working in collaboration with the modeling-focused graduate student to develop, test, and implement algorithms for the integration of the gene abundance and expression data into ecosystem models that are being developed for the overall project. Once QPCR data is generated, the modeling-focused undergraduate student will work collaboratively with the molecular-focused undergraduate student to integrate the newly collected data into the models. Lastly, to help the undergraduate students gain a deeper understanding of the ecosystem dynamics and to gain experience with the logistics of fieldwork, both students will be involved in 2016 sampling trips. Thus, while all students (undergraduate and graduate) will be working independently, their work is extremely synergistic and will require continuous communication/collaboration. This will not only help the undergraduate students understand the interdisciplinary nature of field/lab-based ecosystem studies but will also help them develop the skills needed for collaborative projects. The end goal of the student involvement in this project will be the development and publication of a peer-reviewed manuscript outlining their findings.