RESEARCH INSTITUTION: :"BASELINE AND OIL SPILL IMPACTED MARINE SPONGE MICROBIAL COMMUNITIES AND GENE EXPRESSION ANALYSIS WITH METAGENOMICS"

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SCIENCE ACTIVITIES

1) General Summary

Narrative (1 pages maximum): Please provide a brief overview of the project and goals supported during the conduct of this project. Be sure to highlight any 'lessons learned' that could be applied to the conduct of RFP-I and RFP-II projects (e.g., management, data support, logistics, etc.). Listing accomplishments against project activities, objectives and milestones in bulleted form is acceptable.

The central aim of this proposal was to develop and characterize "sentinel" sponge species and their associated microbiota along with advanced molecular and genomic tools to assess the impact of oil contamination on Western Florida shelf reefs. Marine sponges and their associated microbes are excellent environmental sentinels. Using next generation transcriptomics and metagenomics we can simultaneously trace the direct impact of crude oil (and byproducts) and dispersants on both sponge physiology (a general marker of reef health) and microbial community dynamics (a general marker of regional seawater quality). Evaluating shifts in the composition and function of these organisms and their resident microbes will allow us to determine the overall effects of hydrocarbon loading in the water column that have resulted from the Deepwater Horizon oil spill.

Our primary approach was the application of modern "next generation" DNA sequencing and electron microscopic methods.

We also shifted our experimental strategy slightly from the original proposal, by focusing almost totally on an experimental approach. This was emphasized due to the availability of Dr Becky Thurber's closed tank system at FIU.

Within the first quarter, we formed a working team comprised of the PI's and postdoctoral research scientist Dr Marie Cuvelier, and NSU graduate student Emily Smith (see Table below).

Lessons learned – apply for more shiptime, and coordination with other BP PI's for collections.

2) Results and scientific highlights

Narrative (2 pages maximum): This should be a summary of significant results (positive and negative) and conclusions during the conduct of this project. Listing science results and highlights in bulleted form is acceptable. In each case, please explain the impact of the result.

A major aim was to select and assess an appropriate candidate sponge species as our model taxa. This was not a trivial endeavor, as several taxa are available from the study area and a good match between the experimental applications and species is required. This process is ongoing as well as preliminary SEM ultrastructure microscopy. We were able to perform preliminary scanning electron microscopy of potential candidate species (*Agelas, Cinachyrella*, and *Ircinia*). A large number of filamentous bacteria appeared in the *Ircinia* sample.

We collected and archived marine sponges from Broward county reefs as potential candidates for metagenomic and experimental studies. Co-PI Dr Peter McCarthy from Harbor Branch Oceanographic Institute at Florida Atlantic University sent the two archived samples for NSU for analysis.

Co-PI Dr Pat Blackwelder performed scanning and transmission electron microscopy of potential candidate species (*Agelas, Cinachyrella*, and *Ircinia*). The EM studies have revealed unique structures within *Cinachyrella* that appear in both freshly-collected field samples, and in samples that have been maintained in aquaculture for up to 2-3 weeks. EM micrographs are attached.

- A Sanger clone library from the sponge *Cinachyrella* sp. showed many sequences most similar to *Chloroflexi* and *Actinobacteria*, with a few other sequences belonging to other bacterial groups.
- Graduate student Emily Smith prepared pilot RNA samples from control and treated *Cinachyrella alloclada*. Several of these samples have been sent to the Genomic Sciences Laboratory at North Carolina State University, (Raleigh NC 27606) for pilot Illumina platform RNA sequencing. After an unexpected delay of > 3 months due to purported machine problems at NC State, results have now been transferred to our lab totaling approximately 39 million high quality reads which have at least on reported alignment The reactions have been analyzed by bioinformatics collaborator, David Willoughby of Ocean Ridge Biosciences. In the latter half of 2012, we submitted 16 more X2 and X3 replicates to Argonne National Laboratory for more RNA-sequencing. We are still awaiting the results and analysis.
- Three replicate oil dosing experiments (labeled as X1 X3) were performed on the reef sponge *Cinachyrella alloclada* based on standard CROSERF protocols. Over 80 different sponge samples were exposed to 0.5 ppm oil, oil mixed with 10% Corexit, and Corexit 9500 only.
- Partial 16S rRNA gene sequences were amplified with universal PCR primers in order to globally amplify and characterize as much of the sponge microbial symbiont community as possible. Metagenomic amplicons were sent to the UKY core lab which used 454 Roche GS Titatnium next generation DNA sequening technology. The first X1 experiment generated a total of 153,000 raw sequence reads. This was further narrowed

to a final total of 97,267 high quality 16S rRNA reads. X2 and X3 experiments have produced similar DNA yields, for a total number of >388,000 16S rRNA sequences By the whole project.

 Dr Marie Cuvelier has completed the analysis of XI- X3 data, applying state of the art 16S rRNA analyses, such as QIIME. For example, she has performed comparisons of taxonomic identifications using UCLUST and CDhit options. Rarefaction analysis showed interesting differences between seawater and sponge microbial communities. For example, among all seawater samples, the seawater control had the highest number of predicted OTU's (operational taxonomic units), while among sponge samples, the oildispersant sample at the 24 hr timepoint showed the highest microbial diversity. The analysis also show fairly wide changes in cyanobacteria and actinobacteria diversity in control samples. Only minor trends suggest the greatest increases in bacterial diversity occur in oil/dispersant treated samples. For the most part there are no major shifts in the bacterial community, which refutes the working hypothesis of this project. Consequently, most physiological changes likely stem from within the sponge host

We expect that a minimum of two manuscripts will result from this research.

We have also tested new primers for optimal and most comprehensive amplification of 16S rRNA gene fragments. Through a collaboration with Earth Microbiome Project (EMP), new universal primers have now been utilized.

	Oil (WAF) (0.2 gm/L)	Chemically enhanced (CE) –WAF	Dispersant only (Corexit 9500A)	Untreated seawater control
RNA	Yes	Yes	Yes	Yes
DNA	Yes	Yes	Yes	Yes
Electron microscopy	Yes	Yes	Yes	None
FISH	Yes	Yes	Yes	None
Water samples for bacterialfiltration/genomics	Yes	Yes	Yes	Yes

Table of sponge subsamples taken from each treatment and the intended application of each sample in Experiment X1.

3) Cruises & field expeditions

N/A

Ship or Platform Name	Class (if applicable)	Chief Scientist	Objectives	Dates

- 4) Peer-reviewed publications, if planned (Note: a special section will focus on student and post-doctoral publications)
 - a. Published, peer-reviewed bibliography (Copies of the papers are requested)
 - b. Manuscripts submitted or in preparation (Please note target journal, and anticipated date of publication or submission)

Manuscripts In progress as described above.

5) Presentations and posters, if planned (Please provide copies of each) (Note: a special section will focus on student presentations)

Title	Presenter	Authors	Meeting or Audience	Abstract published (Y/N)	Date
Life at the bottom:	Jose Lopez	R Thurber, P	"Climate-Sustainability	N	Feb 10,
Marine Sponges as	1	Blackwelder	5		2012
Microbial Incubators			Series", Nova Southeastern		
and Bioindicators,			University		
Synergistic Effects of	Jose Lopez	Marie Cuvelier,	Annual Meeting of the	Y	January
Crude Oil and Corexit		Peter Larsen,	Society of Integrative and		2, 2013
Dispersant on a		Patrica	Comparative Biology, San		-
Sponge Holobiont		Blackwelder,	Francisco, CA		
System		Emily Smith, Pete			
		McCarthy, Jack			
		A. Gilbert,			
		Yonggan Wu,			
		David			
		Willoughby,			
		Rebecca Thurber			
Synergistic Effects of	Jose Lopez	Marie Cuvelier,	Gulf Of Mexico: Oil Spill &	Y	January
Crude Oil and Corexit	_	Peter Larsen,	Ecosystem Science		19, 2013
Dispersant on a		Patrica	Conference, New Orleans		
Sponge Holobiont		Blackwelder,	LA		
System		Emily Smith, Pete			
		McCarthy, Jack			
		A. Gilbert,			
		Yonggan Wu,			
		David			
		Willoughby,			
		Rebecca Thurber			

6) Other products or deliverables

Please list (for example: maps, models, tools) and indicate where they can be located/obtained.

- Novel sponge model
- 16S rRNA gene and RNA-seq EST sequences. These will be deposited into various databases such as GenBank, Dryad, MG-RAST
- Electron micrographs of sponge models and microbial symbionts
- Master's thesis (NSU) Emily Smith

7) Data

Reporting on data is done separately through communications with Harte Research Institute; however, please provide a spreadsheet indicating the metadata and ancillary information on the location and status of the archived samples. Also, indicate if there are any issues with respect to data archiving schedule and plan.

PARTICIPANTS AND COLLABORATORS

8) Project participants

Please list the participants of your project, their role(s)* and contact information. This includes some personal information that we will hold closely and for limited purposes. We ask for demographic data – relating to gender, race, and citizenship – so that we can: gauge whether the GoMRI program is fairly reaching and benefiting everyone regardless of demographic category; ensure that those in under-represented groups have the same knowledge of and access to programs, meetings, vacancies, and other research and educational opportunities as everyone else; and we can monitor involvement of international investigators. We will use the demographic data for statistical purposes only. Submission of demographic data is voluntary, but basic data such as name, contact information, and role in the project is required. No personal information will be released. Note: Student/educational information will be collected elsewhere in this report.

* We understand one person may fulfill more than one role; please list all applicable roles using the following standardized titles: Principal Investigator, Co-Principal Investigator, Scientific Participant, Technician, Lab Assistant, Administrative Support.

First Name	Last Name	Role in Project	Institution	Email	Gende r	Race	Citizens hip
Jose	Lopez	PI	Nova	joslo@nova.edu	M	Pacific	
	1		Southeastern	. 0		Islander	
			University				
Rebecca	Vega-Thurber	Co-PI	Florida Intl	rvegathurber@gmai	F	Caucasian	USA
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Peter	McCarthy	Co-PI	FAU at Harbor	PMCCART5@hboi.	М	Caucasian	USA
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			Oceanographic				
			Inst.				
Patricia	Blackwelder	Co-PI	Nova	pblackwelder@rsm	F	Caucasian	USA
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			University				
Willoughby	David	Bioinforamtics	Ocean Ridge	davidw@oceanridg	М	Caucasian	USA
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Wu	Yonggan	Bioinformatics	Ocean Ridge	yongganw@oceanri	М	Caucasian	USA
		Consulatant	Biosciences	dgebio.com			
				-			
Gilbert	Jack	Bioinforamtics	Argonne National	gilbertjack@anl.gov	Μ	Caucasian	USA
		Consulatant	Laboratory				
			<u> </u>				

MENTORING AND TRAINING

9) Student and post-doctoral participants

Please list the student participants of your project, their educational role, and other information. This includes some personal information that we will hold closely and for limited purposes. We ask for demographic data – relating to gender, race, and citizenship – so that we can: gauge whether the GoMRI program is fairly reaching and benefiting everyone regardless of demographic category; ensure that those in under-represented groups have the same knowledge of and access to programs, meetings, vacancies, and other research and educational opportunities as everyone else; and we can monitor involvement of international investigators and students. We will use the demographic data for statistical purposes only. Submission of demographic data is voluntary, but basic data such as name, contact information, and research area is required. No personal information will be released.

First Name	Last Name	/ PhD /	Thesis or research topic	Institution	_	Completion	Gender	Race	Citize nship
		MS / BS				year			
Marie	Cuvelier	Post-doc	Metagenomic analysis		R Thurber	Dec 2012	F	C	
Emily	Smith	MS	Gene expression of dosed sponge samples		J Lopez	Dec 2012	F	C	

- 10) Student and post-doctoral publications, if planned
 - a. Published, peer-reviewed bibliography (Copies of the papers are requested)
 - b. Manuscripts submitted or in preparation (Please note target journal, and anticipated date of submission or publication)

Smith, E. Willougby, D., Blackwelder, P., McCarthy, P.J., Gilbert, J., Cuvelier, M., Vega-Thurber, R., Lopez, J. Transcriptome analysis of marine sponge *Cinachyrella sp.*, possible new model organism for oil and dispersant ecotoxicology. BMC Genomics. In Preparation – target submission date May 2013

11) Student and post-doctoral presentations and posters, if planned (Please provide copies of each)

Title	Presenter	Authors	8	Abstract published (Y/N)	Date

12) Images

Please attach high-resolution image and provide details including a description of the image, location, credit, date, etc. Of note: Image may be used in GoMRI promotions, make sure you have rights to use the image. Note: GoMRI will establish a Flicker site to share these images through the GoMRI website and with media and the public.

Electron micrographs and their descriptions are attached. All SEM photo copyrights are owned by Dr Patricia Blackwelder (Nova Southeastern University).

13) Continuing Research

If you are continuing this research under another grant, please include granting authority and title of award and a very brief synopsis (2-3 sentences).

We have obtained additional funding through an internal Nova Southeastern University Presidential Faculty Research and Development Grant. The project is a continuation of the FIO project entitled "Developing diagnostics for oil exposure in marine sponges" but will primarily be used to support the last stages of graduate student Emily Smith's MS thesis. This project will focus on the bioinformatics analysis of the first set of Illumina RNA-seq data.