Immune suppression of the echinoderm Asterias rubens (L.) following long-term ocean acidification - Bodil Hernrotha,b,∗, Susanne Badenc, Mike Thorndykea, Sam Dupontc

“We compared effects of exposure to predict near-future (2100) ocean acidification (OA; pH 7.7) and normal seawater (Control; pH 8.1) on immune and stress responses in the adult sea star Asterias rubens. Analyses were made after one week and after six months of continuous exposure. Following one week exposure to acidified water, the pH of coelomic fluid was significantly reduced. Levels of the chaperon Hsp70 were elevated while key cellular players in immunity, coelomocytes, were reduced by approximately 50%. Following long-term exposure (six months) levels of Hsp70 returned to control values, whereas immunity was further impaired, evidenced by the reduced phagocytic capacity of coelomocytes and inhibited activation of p38 MAP-kinase. Such impacts of reduced seawater pH may have serious consequences for resistance to pathogens in a future acidified ocean.”

Comparison of phagocytosis in three Caribbean Sea urchins - John DeFilippo, John Ebersole, Gregory Beck\*

“In 1983 large numbers of the sea urchin Diadema antillarum unexplainably began showing signs of illness and dying in the Caribbean, and over the next year they came close to extinction, making it one of the worst mass mortality events on record. Present evidence suggests a water-borne pathogen as the etiological agent. Decades later Diadema densities remain low, and its near extinction has been a major factor in transforming living coral reefs in the Caribbean to barren algae-covered rock. In the ensuing decades, no solid explanation has been found to the questions: what killed Diadema; why did Diadema succumb while other species of urchins on the same reefs did not; and why has Diadema still not recovered?

A recent hypothesis posited by our lab as to Diadema's vulnerability was directed at possible compromised immunity in Diadema, and experimental results found a significantly impaired humoral response to a key component of gram-negative bacteria. Here we use flow cytometry to examine the cellular arm of invertebrate immunity. We performed cytotoxicity and phagocytosis assays as a measure of the cellular immune responses of cells from Diadema and two other species of sea urchins not affected by the die-off. Despite our previous findings of in impaired humoral response, our study found no apparent difference in the cellular phagocytic response of Diadema compared to the other urchin species studied.”

“No causative agent has been discovered, but the outbreak followed water currents and mortality did not decrease with distance, suggesting a water-borne pathogen (Lessios, 1988).”

Sea urchins fight off pathogens with specialized cells called coelomocytes, located in their coelomic fluid, that can mount a proper immune response (deflippo).

Based on the study done by Flippo XXX, Diadema antillarum is “no less capable” of mounting a proper innate immunity response even though there is prior evidence of a diminished humoral response (Beck et al., 2014). The authors in deflippo (XXX) suggest that maybe the humoral arm of the immune system is impaired, that the recovering population has a stronger immune system than the population that died, or an over-activity of the humoral defenses created a selection for a weak humoral response. In this case some of these scenarios are difficult to prove because of lack of immunological studies during the die-off.

Going Deeper: Metagenome of a Hadopelagic Microbial Community - Emiley A. Eloe1, Douglas W. Fadrosh2, Mark Novotny2, Lisa Zeigler Allen2, Maria Kim3, Mary-Jane Lombardo2, Joyclyn Yee-Greenbaum2, Shibu Yooseph2, Eric E. Allen1,4, Roger Lasken2, Shannon J. Williamson3, Douglas H. Bartlett1\*

Bactereoidetes, Proteobacteria which included Alphaproteobacteria and a small percentage of Firmicutes were found in Hadopelagic region of the Puerto Rican Trench (Eloe et al. 2011).

The use of mitochondrial DNA genes to identify closely related avian species - Sansook Boonseub, Shanan S. Tobe, Adrian M.T. Linacre

According to previous studies done with avian species (Boonseub 2009) the cytochrome B region was able to place the animals into their appropriate orders as compared to other molecular clocks like cytochrome oxidase I and ND2 genes.

Bacterial Associates of Two Caribbean Coral Species Reveal Species-Specific Distribution and Geographic Variability -- Kathleen M. Morrow, Anthony G. Moss, Nanette E. Chadwick, and Mark R. Liles

**Microbial Diversity in a Military Impacted Lagoon (Vieques, Puerto Rico) as Revealed by Metagenomics** Lizbeth Dávila-Santiagoa,b,c, Natasha DeLeón-Rodriguezb\*, Katia LaSanta-Pagána,\*, Janet K. Hattb, Zohre Kurtb\*, Arturo Massol-Deyá and Konstantinos T. Konstantinidis

In Anones 2005 and 2014 Proteobacteria, Bacteroidetes and Firmicutes was found at the beach.

In the human impacted Condado lagoon the phylum’s Bacteroidetes and Proteobacteria were found. The authors conducted an analysis to test if these phylums of the Condado lagoon reflected human-gut bacteria and found that low abundances accounted for this type of bacteria suggesting that these bacteria are environmentally adapted and do not emerge from the human-gut.

The Purple Sea Urchin Strongylocentrotus purpuratus Demonstrates a Compartmentalization of Gut Bacterial Microbiota, Predictive Functional Attributes, and Taxonomic Co-Occurrence - Joseph A. Hakim 1,\*, Julie B. Schram 2, Aaron W. E. Galloway 2, Casey D. Morrow 3,

Michael R. Crowley 4, Stephen A.Watts 1 and Asim K. Bej 1,\*

In the sea urchin Strongylocentrotus the most abundant bacteria found were Epsilonproteobacteria that were from the order Campulobacterales.

In the sea urchin Strongylocentrotus an extremely low abundance of Tenericutes was also found.

“The importance of gut bacteria in sea urchin host health was further supported in S. droebachiensis, in which microbial suppression through antibiotics showed a reduced capacity for host incorporation of essential amino acids.” Fong,W.; Mann, K.H. Role of gut flora in the transfer of amino acids through a marine food chain. Can. J. Fish. Aquat. Sci. 1980, 37, 88–96. [CrossRef]

Immune suppression of the echinoderm Asterias rubens (L.) following long-term ocean acidification - Bodil Hernrotha,b,∗, Susanne Badenc, Mike Thorndykea, Sam Dupont

Adult star Asterias rubens when exposed to acidified water, the pH of coelomic fluid was significantly reduced and the immunity impaired evidenced through reduced phagocytic capacity and other markers.

The Composition, Diversity and Predictive Metabolic Profiles of Bacteria Associated With the Gut Digesta of Five Sea Urchins in Luhuitou Fringing Reef (Northern South China Sea) - Qiucui Yao1,2,3,4,5, Kefu Yu1,2,3\*, Jiayuan Liang1,2,3, Yinghui Wang1,2,3, Baoqing Hu5,

Xueyong Huang1,2,3, Biao Chen1,2,3 and Zhenjun Qin1,2,3

Bacteria represented in the five sea urchins (Stomopneustes variolaris, Diadema setosum, Echinothrix calamaris, Diadema savignyi, and Tripneustes gratilla) studied by Qiucui et al. (2019) included Fusobacteria, Proteobacteria, and Bacteroidetes.

“Zha et al. (2018) reported that Fusobacteria could be used as indicators of a host experiencing stress from food resource limitation and heavy predation. Furthermore, many bacterial species of the phylum Fusobacteria have been associated with infections caused by host psychological stress (Bennett and Eley, 1993). Therefore, we inferred that sea urchins in Luhuitou fringing reef might be experiencing some sort of stress.”

“Owing to their positive effects, some sea urchins have been employed in recent years to restore many degraded coral reefs (Stimson et al., 2007). For example, in K¯ane’ohe Bay, the flourishing red algae Kappaphycus and Eucheuma block sunlight and smother the corals, resulting in vast destruction of coral reefs. In order to restore this ecosystem, three organizations have collaborated to rear the juvenile sea urchin T. gratilla and release the organisms in the bay in an attempt to clear the flourishing red algae for the proposed duration of 2009–20251 (Stimson et al., 2007). In the Florida Keys, because the population of D. antillarum has yet to recover from the mass mortality event of 1983–1984 (mentioned above), the species has been captive spawned and released into the wild to restore the coral reef (Sharp et al., 2017). Studies of the behavioral and morphological characteristics and genetic structure of sea urchins have been carried out to provide a scientific reference for development of a restoration plan (Francis-Floyd et al., 2015; Chandler et al., 2017; Sharp et al., 2017).”

“These studies revealed that the bacterial community composition in L. variegatus was significantly different among the pharynx tissue, gut tissue, gut digesta, and fecal pellets (Hakim et al., 2015, 2016) and suggested that only the bacteria in the stomach and intestinal lumen were specifically symbiotic with the sea urchin (Meziti et al., 2007).”­­

“The analysis indicated that the gut digesta in T. gratilla consisted almost entirely of macroalgae fragments, with no evidence of corals and their calcium carbonate skeleton, while the digesta of the other four sea urchin species were dominated by coral and their calcium carbonate skeleton, turf algae, filamentous algae, silt and calcareous algae.”

“These bacteria are considered specialists in the degradation of high-molecular-weight organic matter, i.e., proteins and carbohydrates (Thomas et al., 2011). Complex polysaccharides are resistant to the action of digestive enzymes (Thomas et al., 2011). The members of the phylum Bacteroidetes are believed to complement eukaryotic genomes with degradation enzymes targeting resistant polymers such as plant cell wall compounds (Thomas et al., 2011). The recent sequencing of Bacteroidetes revealed numerous carbohydrate-active enzymes that can degrade a broad spectrum of substrates of plant, algal, and animal origin (Thomas et al., 2011).”

“Another abundant genus, Vibrio, represented the dominant bacteria in the gut digesta of the sea urchin L. variegatus (Lawrence et al., 2010; Hakim et al., 2015, 2016). Members of Vibrio isolated from the gut of sea urchin Strongylocentrotus nudus produced amylase, gelatinase, chitinase, and fucosidanase (Beleneva and Kukhlevskii, 2010), suggesting that they may participate in the host’s food digestion process.”

“According to our gut digesta analysis, T. gratilla primarily feed on macroalgae, while the other four sea urchin species, D. setosum, D. savignyi, E. calamaris, and S. variolaris, mainly feed on coral skeletons, filamentous, turf algae, and other animals.”

“The results of our gut digesta analysis were similar to those in previous studies (Herring, 1972). For example, Herring reported that seagrasses were dominant within the stomach content of

T. gratilla, while the stomach contents in both E. calamaris, D. setosum and S. variolaris were dominated by algae, coral, silt and calcareous algae (Herring, 1972). Carreiro-Silva and

McClanahan (2001) reported that D. setosum and D. savignyi, as scraper, erode coral skeletons, but T. gratilla, as a browser, do not.”

“Many previous studies have showed that diet was one of the key factors shaping the gut bacterial composition of many wild animals (Miyake et al., 2015).”

Bacterial Community in Gut Contents of the Sea Urchin Diadema setosum and the Ambient Sediments from Sichang Island using Metagenomics Approaches - Natnicha Tanrattanapitak and Supanut Pairohakul\*

“In the gut content samples, Bacteroidetes was found as the most abundant phylum whereas in the ambient sediments was predominated by Proteobacteria.”

“Classification in term of class categories, Bacteroidia, Clostridia, Flavobacteria and Gammaproteobacteria were shown to be dominated in the gut content community, respectively as displayed in Figure 1.”

“For example, Zhang et al. (2014) reported that intestine of *Strongylocentrotus intermedius* was dominated with *Psychronomas*, *Shewanella*, *Saccharophagus degradans* and *Nitrosomonas eutropha*, all of which were not be found in the present study.”

“Unkles (1997) found that *Vibrio*, *Pseudomonas*, *Aeromonas* and *Flavobacterium* were predominant taxa in *Echinus esculentus*, except *Vibrio*; however, all the reported genera cannot be detected in this study.”

“In the case of *Lytechinus variegatus*, Nelson et al (2010) found that *Vibrio*, *Pseudomonas* and *Gamma Proteobacteria* were predominated taxa whereas Hakim et al (2016) reported that the dominated taxa were *Vibrio*, *Photobacterium*, *Propionigenium* and *Ferrrimonas*.”

“One of the remarkable results in genus level is that *Fusibacter* of the phylum Firmicutes was identified in the study”

Recovery of the sea urchin Diadema antillarum promotes scleractinian coral growth and survivorship on shallow Jamaican reefs Precht 2010 – Citation only!!!!!

Limitations:

Small sample size in Guayama, perhaps why it was statistically significant.

Suggestions:

Diversity of Algae by different locations and overall diet impact on gut microbiota.