

MOLECULAR AND FUNCTIONAL INSIGHTS INTO AN UNIDENTIFIED DISEASE IN FLOWER GARDEN BANKS NATIONAL MARINE SANCTUARY: EXPLORING IMMUNE PATHWAYS AND DISEASE PHENOTYPES

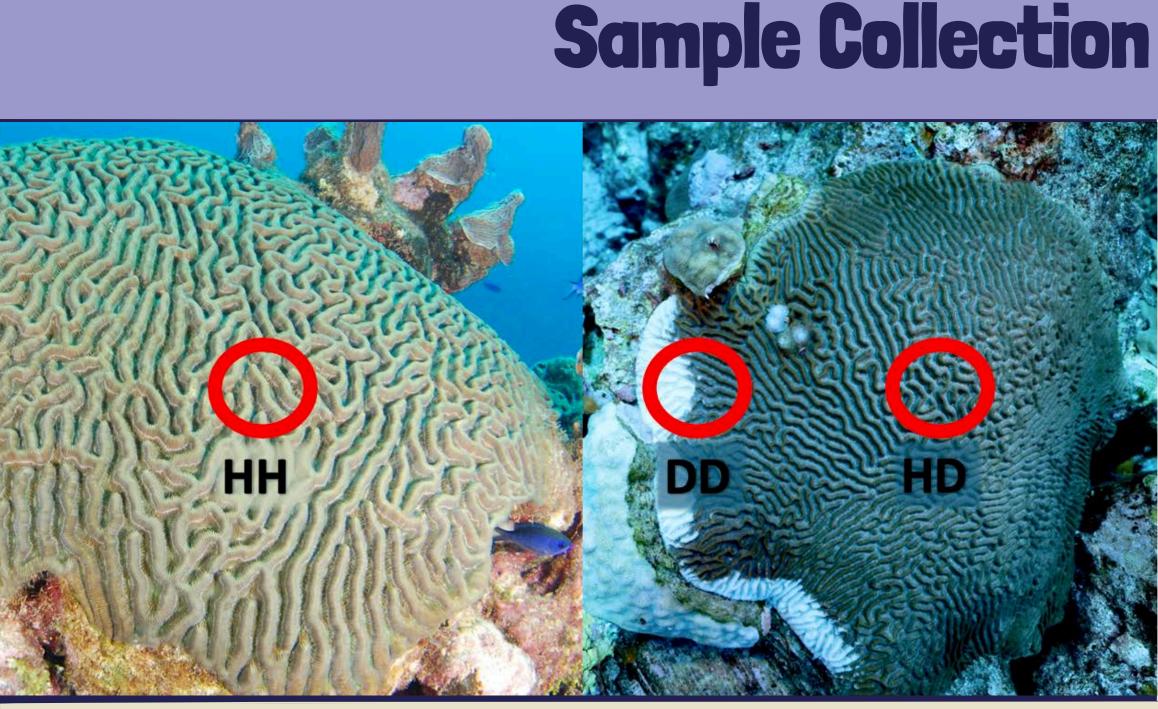
Background

In August 2022, an unidentified white syndrome disease was observed at the East and West Banks of Flower Garden Banks National Marine Sanctuary [1]. In September 2022, samples of Pseudodiploria strigosa were collected.

Disease characteristics [1]:

- Acute tissue loss
- Multi-focal lesions
- Lesions along colony margins

Research Goal Link genes to phenotypes of disease from various types of data



Methodology

Total RNA extracted from flash frozen coral tissue. Kit: Invitrogen RNAqueous.

RNA sequencing: 150bp paired-end, poly-A trail enrichment on the Illumina Novaseq 6000 platform.

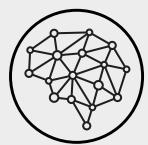
A *de novo* transcriptome was assembled and reads were mapped: *FastP - Trinity* - BUSCO - BBsplit - Salmon



Histology traits were measured across 5 slides per sample by Dr. Ashley Rossin.



DeSEQ2: Identified differentially expressed genes across health state comparisons.



Weight Gene Co-Expression Analysis (WGCNA) to identify networks of genes correlated to histology traits: average symbiont area and average vacuole area.



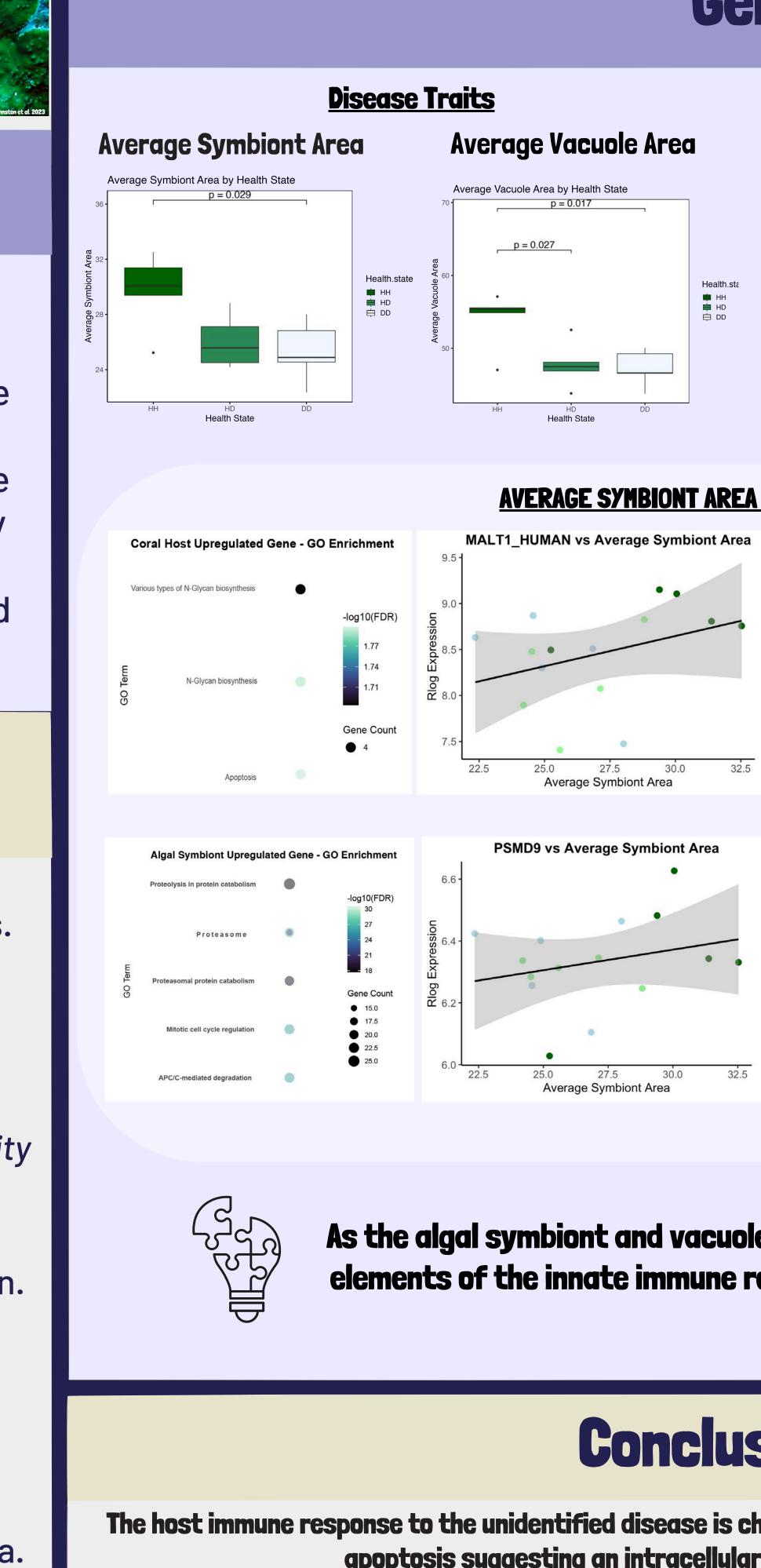
Gene Annotation & GO Enrichments: Transcripts are annotated using NCBI Uniprot Database. GO enrichment analysis was done using the STRING Database.

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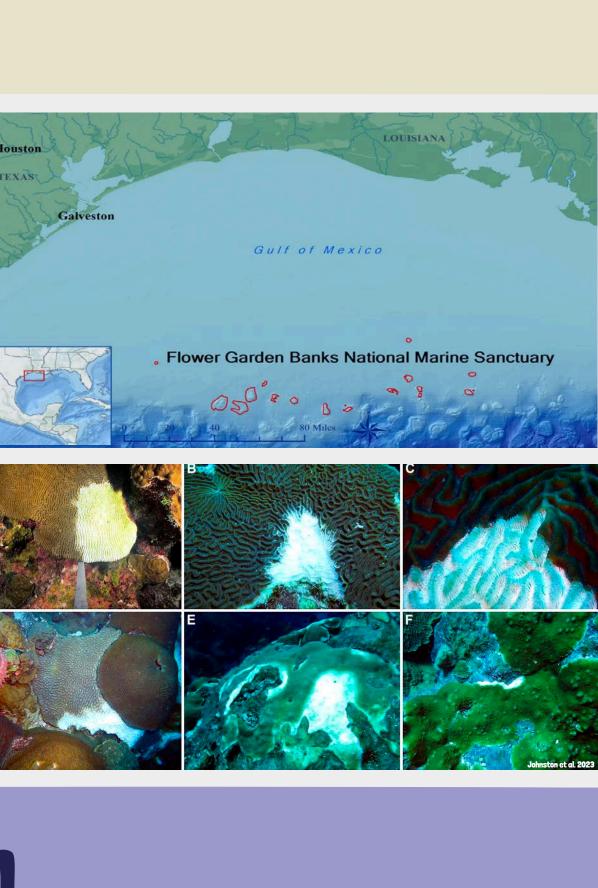
The Importance of Gene Expression Analysis

Genes will increase or decrease in expression in response to different stimuli such as disease, heat stress and other environmental variables. Understanding gene expression in both the coral host and its algal symbiont in response to disease—even an unidentified one-can offer valuable insights into mechanisms of the disease.



The HD portion of the colony is mounting the strongest response against the disease, creating the potential for recovery.

In March 2023, more samples (and species!) were collected. In May 2024, the majority of the above diseased colonies had recovered from the disease!



n = 15 *Pseudodiploria* strigosa 5 of HH: healthy sample from a healthy colony **5 of HD:** healthy sample from a diseased colony **5 of DD:** diseased sample from a diseased colony

An Integrative Framework to Study Coral Disease

Transmission Electron Microscopy (TEM)

The coral holobiont is highly complex. To fully understand what occurs during a disease, it is essential to integrate all components of the holobiont—coral host, algal symbionts, and microbial and viral communities—into our analyses. Additionally, incorporating microscopy techniques, such as histology and transmission electron microscopy (TEM), provides tangible, observable phenotypes associated with disease that we can correlate to gene expression.

Gene & Disease Trait Relationship

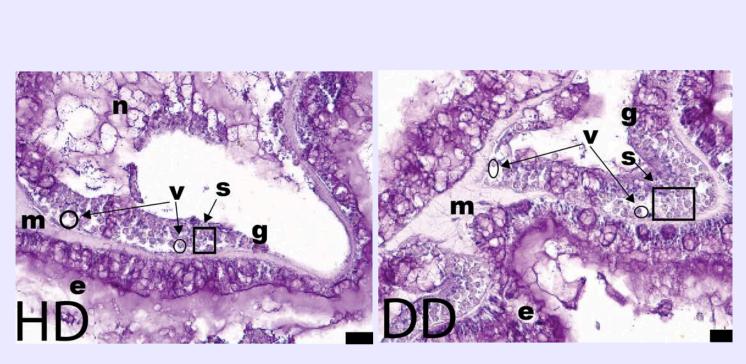


Figure 1 Symbols are denoted as follows: e: epidermis, m: mesoglea, g: gastrodermis, s: algal symbionts, square surrounds smaller and degraded symbionts, v: vacuolization, oval surrounds symbionts with larger

lucosa–associated Coral Host Upregulated Gene - GO Enrichment lymphoid tissue lymphoma translocation protein Transcriptional Regulation Gene Cou **Function:** Activates innate Transcription Initiation mmunity and NF-KB signaling; linked to RNA Polymerase suppression of apoptosis HH = Supporting the coral's ability to Nucleotide Excision Repair maintain cellular integrity and health HD, DD = Actively promoting DNA Repair Mechanisms programmed cell death to prevent further spread of disease **26S proteasome non-ATPase** Igal Symbiont Upregulated Gene - GO Enrichme regulatory subunit 9 Proteasomal protein catabolism Function: Regulates protein KEAP1-NFE2L2 pathway degradation as part of the 26S roteasome complex. Glutamate-ammonia ligase HH = Supporting the coral's ability o maintain cellular integrity and **).** DD = Actively promoting ummed cell death to preve APC/C-mediated degradation further spread of diseas

As the algal symbiont and vacuole degrade with disease, the host immune response involves activation of apoptosis and elements of the innate immune response, and genes involved in recycling and elimination of degraded proteins and cells.

Conclusions

The host immune response to the unidentified disease is characterized by elimination of degraded proteins, and apoptosis suggesting an intracellular pathogen and oxidative stress.

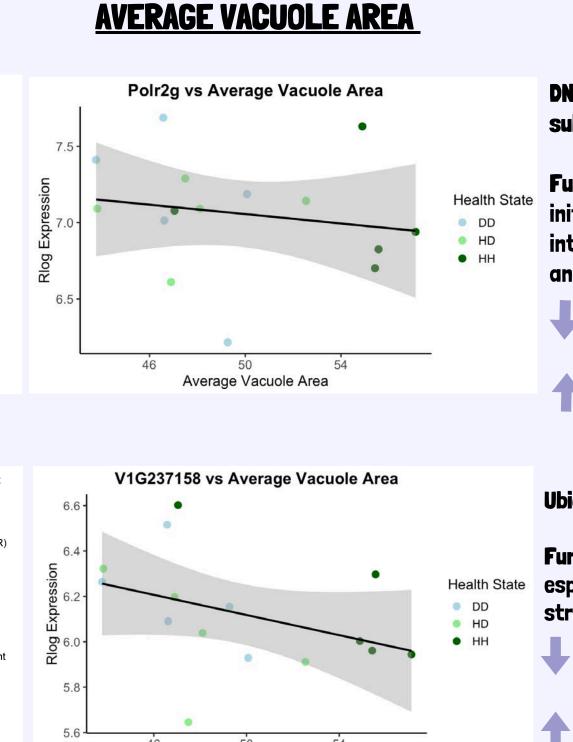




The Importance of a Holistic Analysis

Histological Characterization of Disease

- High intensity of necrosis across diseased samples (DD)
- Vacuolization of symbionts (symbiont to vacuole ratio) not significant in diseases samples.
- Vacuoles and algal symbionts are shrinking in diseased colonies (HD, DD)
- Disease does not follow a consistent pattern of vacuolization and exocytosis



verage Vacuole Area

DNA-directed RNA polymerase II subunit RPB7

Function: Supports transcription initiation and stabilizes the nteraction between the polymerase

- and RNA during elongation. **HH = Stable state with minimal need for**
- transcriptional reprogramming. HD, DD = Indicates increased host
- transcriptional activity, likely reflecting stress, immune response, or breakdown of symbiosis.

Ubiquitin-conjugating enzyme E2 S

Function: Tags proteins for degradation, especially during cell cycle control and stress.

- HH = Stable state with reduced need



