Pycnopodia helianthoides immune response to Sea Star Wasting Disease

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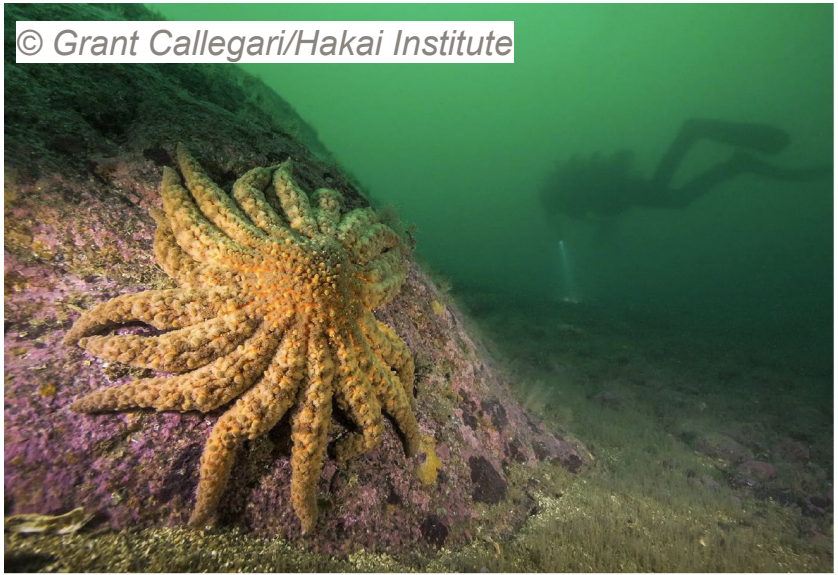
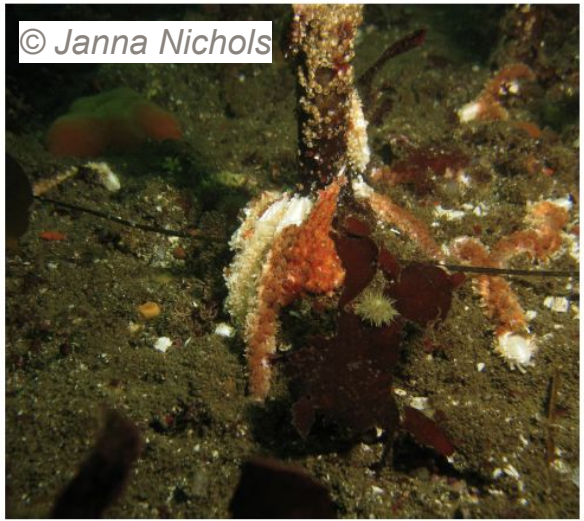
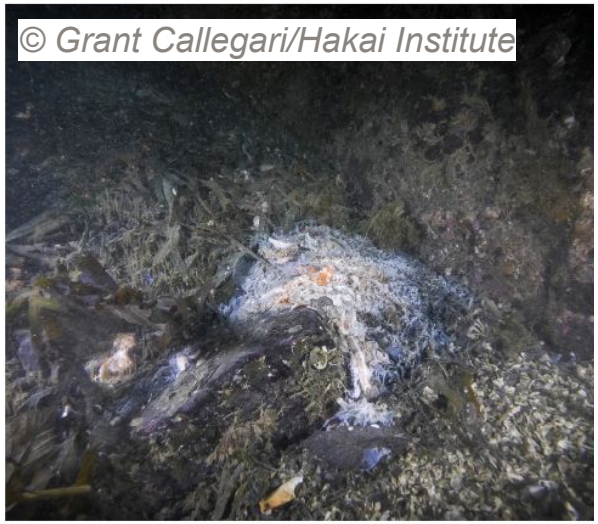
Pycnopodia helianthoides (Sunflower Star)



The Nature Conservancy; Roadmap to Recovery for the Sunflower Sea Star

Sea Star Wasting Disease





P. helianthoides lost **~5.75 billion** stars

Unknown cause

Objectives

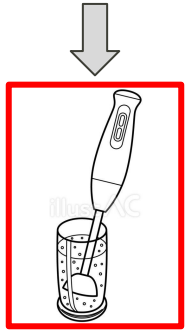
Understand stress/immune response of stars

- Transcriptomics

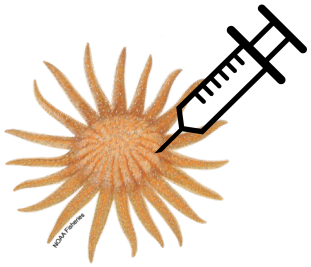
Identify causative agent(s)

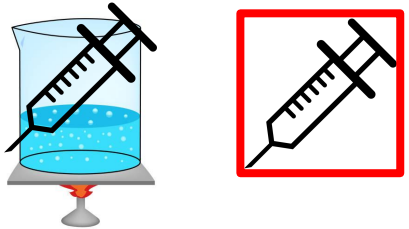
- Transcriptomics; other ‘omics

Experimental Design

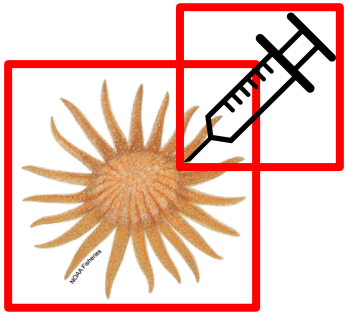


Control
N = 7





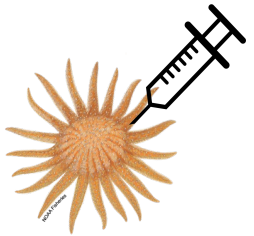
Exposed
N = 7



Experimental timeline

EXPOSED stars injected with live homogenate

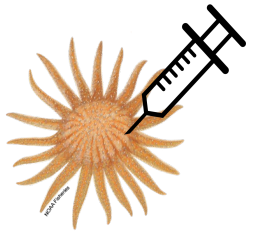
Exposed (n=7)



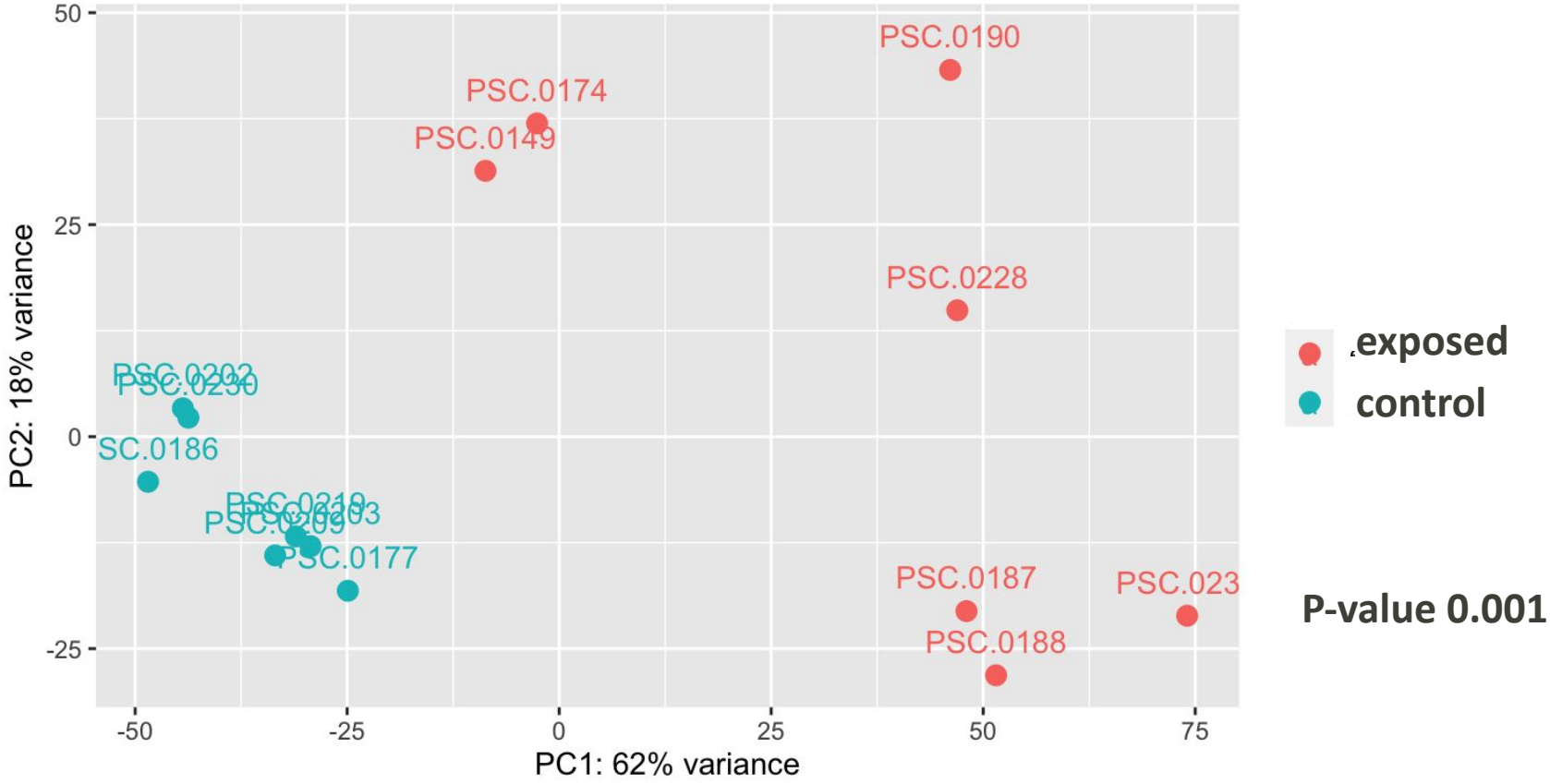
D 0 — D 8 — D 10 — D 11 — D 12 — D 13 — D 14 — D 15

CONTROL stars injected with heat-killed homogenate

Control (n=7)



RNAseq Samples



P-value 0.001

Identifying Genes of Importance

- Disease resilience
- Identify resistant populations in wild
- Test for infection if unknown pathogen

Differentially Expressed Genes (DEGs)

- Compare gene expression between treatments
  - Differential expression → tells how treatment impacts physiology

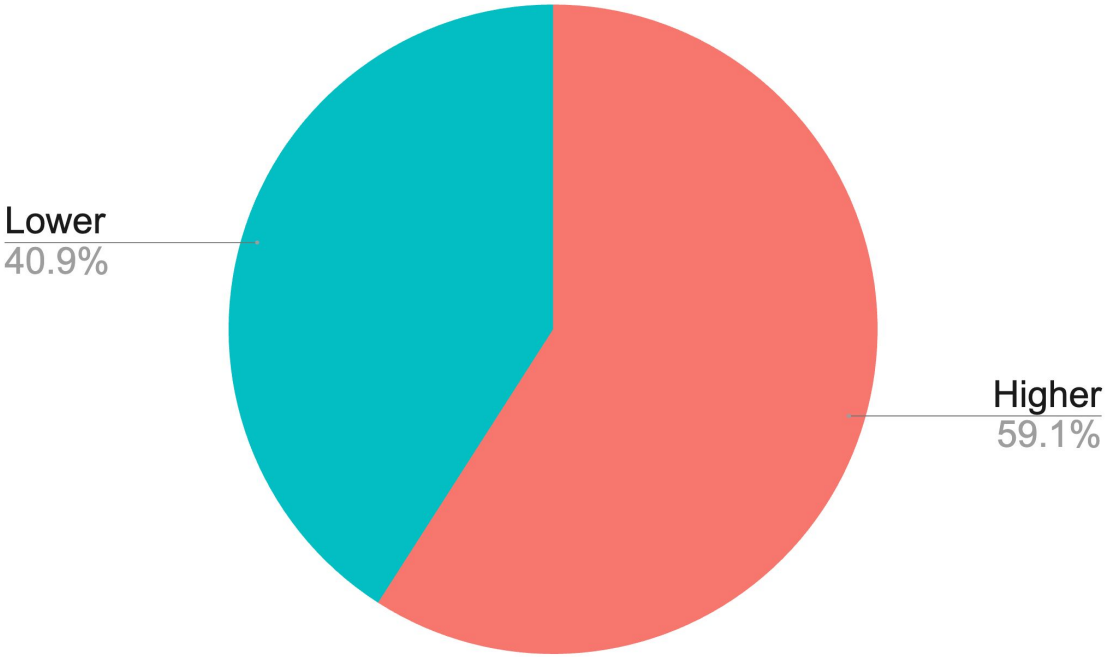
DEGs Expression Levels in Exposed Stars

26581 total genes

7117 differentially expressed

4204 higher expression in exposed stars

2913 lower expression in exposed stars



treatment
treatment
control
exposed
3
2
1
0
-1
-2
-3
PSC.0177
PSC.0186
PSC.0202
PSC.0203
PSC.0209
PSC.0219
PSC.0230
PSC.0149
PSC.0174
PSC.0187
PSC.0188
PSC.0190
PSC.0228
PSC.0231

Enrichment

148 enriched biological processes

90 enriched significantly <0.05pval

Biological Process	Gene
Response to wounding	PIK3B
Positive regulation of tumor necrosis factor production	Ripk1 Rinp Rip
defense response to Gram-positive bacterium	OPTN
Positive regulation of interleukin-6 production	SPON2
Viral mRNA export from host cell nucleus	Thoc6

Previous Work Comparison

	Fuess *et al.* 2015	This Study
Total Genes	29, 476	26, 581
Reference	*P. helianthoides* transcriptome, *de novo* assembly	*P. helianthoides* genome gene list (Schiebelhut *et al*, 2023)
DEGs	3, 773	7, 117
Enriched Biological Processes	13	90

Key Takeaways

There is a difference in gene expression between control and exposed stars

Transcriptomics and new genome can help to identify potential pathogen(s)

Transcriptomics can help us understand differences between populations and species

Upcoming Work

Is there an impact of star age/size on response to exposure to wasting disease?

Multi-species Experiment Summer 2023

- Compare immune response across species: *Pycnopodia helianthoides*, *Pisaster ochraceus*, and *Dermasterias imbricata*
- Earlier stages of disease exposure

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Questions?

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