

EXPLORING PRELIMINARY PROTEOMIC VARIATION FOR STRESS RESPONSE IN PACIFIC OYSTERS (*CRASSOSTREA GIGAS*)

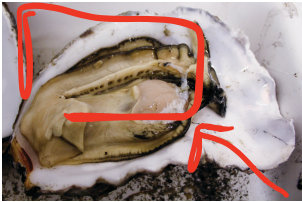


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BACKGROUND



- *C. gigas* provides ecosystem services, basis for aquaculture operations in Washington¹
- Susceptible to ocean acidification and ocean warming^{2,3}
- Limited set of experiments examining oysters' response to multiple stressors that reflect wild conditions

OBJECTIVE: Understand how different environments drive different protein expression in response to stress

EXPERIMENTAL DESIGN

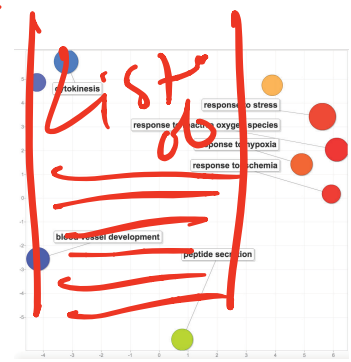
Figure 1. Map of study sites in and around Puget Sound, WA. Inset: Oysters placed in both eelgrass and bare patches at each site to assess the impact of larger-scale ecological interactions on stress response.



- Five experimental sites: Case Inlet, Fidalgo Bay, Port Gamble Bay, Skokomish River Delta, and Willapa Bay
- Outplanted 150 adult sibling *C. gigas*, 30 per site
- Eelgrass presence: assess effect of large-scale ecological interactions
- Continuous environmental chemistry monitoring
- Gill tissue collected after one month for proteomic analyses

DATA-INDEPENDENT PROTEOMICS

OBJECTIVE: Match peptide spectra in ten oyster samples with stress-related proteins present in the *C. gigas* proteome^{4,5}



(clockwise) Figure 2. Overrepresented gene ontology terms for stress-related proteins subsetted from all proteins found in *C. gigas* samples. Size of bubble is representative of frequency in data.

Figure 3. Coefficients of variation for stress-related proteins. Size of bubbles corresponds to coefficient value.

FINDING: Evidence for variation in stress response across five sites and eelgrass conditions

FUTURE DIRECTIONS

- Preliminary insight demonstrates how stress-response is impacted by different environmental conditions
- Use data-specific peptide spectra
- Repeat proteomic analyses with increased sample size
- Develop targeted assay for stress-related proteins

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Handwritten red notes: Acknowledgments, Dave, SAF's Fund