Using Proteomics to Understand Ocean Acidification Stress in the Pacific Oyster

Emma Timmins-Schiffman (UW, SAFS) Brook Nunn (UW, Med. Chem.) David Goodlett (UW, Med. Chem.) Gary Dickinson (The College of NJ) Steven Roberts (UW, SAFS)

Crassostrea gigas

- Important aquaculture species in the PNW and worldwide
- Ecological services: water filtration, habitat, food



Ocean Acidification and Bivalves



Energy/resource use

Growth & calcification

- Acidosis and shell dissolution
- CO3²⁻ availability

Characterize how ocean acidification affects the oyster's response to a second stressor



Time





Experimental Design

- Mechanical stress as a proxy for environmental stress
- MS promotes a catecholmine stress response in C. gigas (Lacoste et al. 2001)



Methods: Proteomics

- Expression of genes and proteins change in response to the environment
- Shotgun techniques provide non-biased surveys of molecular physiological changes



Methods: Proteomics

- Shotgun sequencing using LC-MS/MS
- Protein fragments (peptides) are sequenced
- Sequences are identified using a database of proteins



Results: Proteomics



- 2,677 proteins were identified
- Coverage of entire C. gigas proteome: 9.5%

Results: Proteomics









Mechanical Stress



Axis 1

Mechanical Stress





Mechanical Stress





pCO₂ and Mechanical Stress

- Stress Response
 - Heat shock protein 70
 - Caspase
- pH Homeostasis
 - V-type proton ATPase
- Immune Response
 - o Cathepsin B
 - o MAP kinase kinase

Summary

Proteomics can provide insight into the physiological response to ocean acidification.

Summary

Exposure to multiple stressors can impact an organism's ability to mount a successful response to either stressor.



Implications

We should continue to consider multiple stressors when assessing responses to environmental change.



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