GEODUCK AS INDICATORS OF ENVIRONMENTAL CHANGE

Laura H. Spencer¹, Micah Horwith², Alex Lowe³, Emma Timmins-Schiffman⁴, Brook L Nunn⁴, Sean Bennett¹, Steven Roberts¹
University of Washington ¹School of Aquatic & Fishery Sciences, ³Department of Biology, ⁴Genome Sciences, ²Washington State Department of Natural Resources,

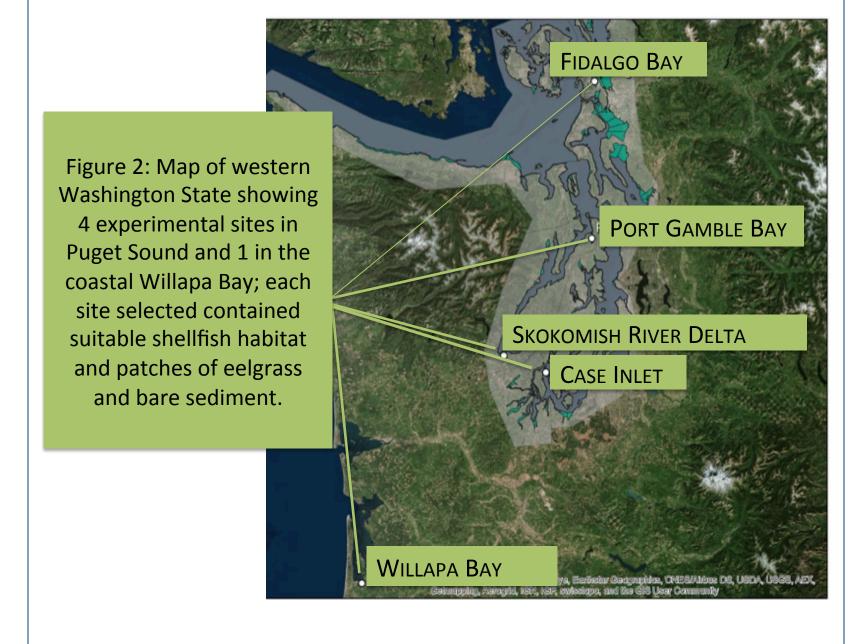
THE ANIMAL

Pacific geoduck (Panopea generosa)

- Largest clam native to the Pacific Northwest
- Important commercial fishery (wild & farmed)
- Sedentary, calcifying, sub-tidal
- Likely to be impacted by rising ocean temperature and pCO₂

THE TRIALS

- 5 sites throughout western Washington
- 2 treatments per site: eelgrass bed, bare sediment
- 4 replicates per treatment
- 2 month-long trials in June and August 2016
- Continuous water quality measurements: pH, temperature, salinity, depth, chlorophyll
- Gill tissue sampled for protein extraction



THE QUESTIONS

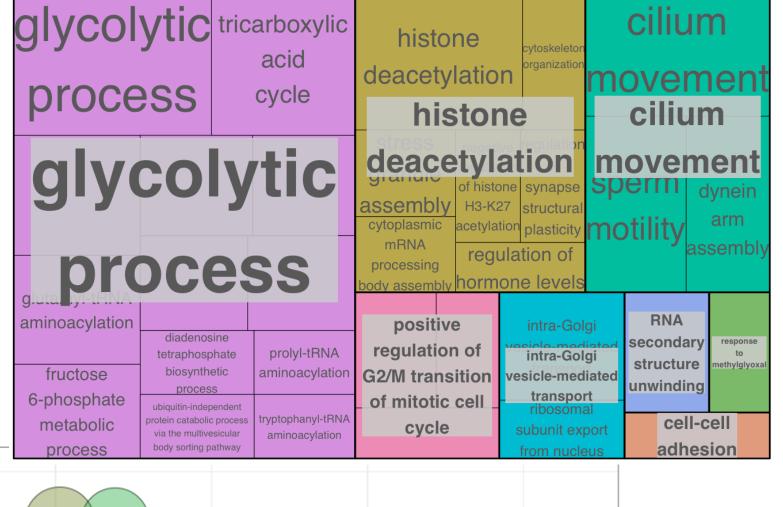
- Can we detect an environmental signature via differences in protein expression?
- Does treatment (eelgrass, no eelgrass) or geographical site correlate with expression of stress-related proteins?
- What is the overall variability in gill tissue protein expression?

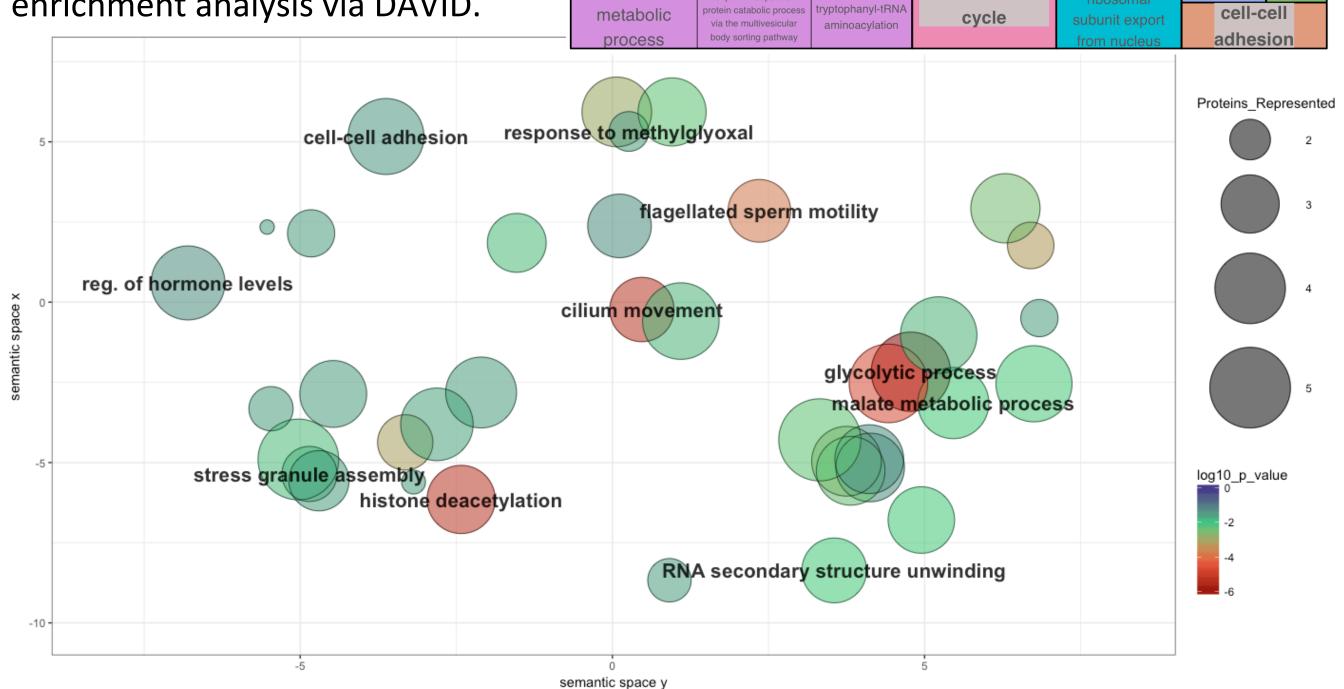
THE PRELIMINARY RESULTS

Shotgun proteomics reveals protein groups differentially expressed in eelgrass beds

Right: Gene Ontology (GO) Tree generated using REVIGO showing differentially expressed biological process categories.

Below: Scatterplot of GO terms; clusters represent closely related categories, size indicates number of proteins represented, color represents p-value from protein enrichment analysis via DAVID.





THE METHODS

Shotgun proteomics for discovery analysis

EXTRACT
PROTEINS &
FRAGMENT

Mass Spec Sample Prep

- Sonication and cell lyses
- Protein quantification
- Mini-Trypsin digestion
- Desalting and peptide isolation
- Add standards

IDENTIFY AND QUANTIFY PEPTIDES

Data-Independent Tandem Mass Spectrometry

- Orbitrap Fusion Lumos machine
- Does not require pre-selected precursor ions
- Captures all peptides within designated mass/charge ratio

IDENTIFY
PROTEINS IN
SAMPLES

PECAN

- Survey peptides against annotated background proteome
- Generate summary file for direct use in Skyline

QUANTIFY RELATIVE PROTEIN ABUNDANCE

Skyline

- View summary statistics for peptide abundance
- Export statistics for processing and visualization



Contact

Laura H Spencer
School of Aquatic and Fishery Sciences, University of Washington
Ihs3@uw.edu
laurahspencer.github.io/LabNotebook

Thank you.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship Program. Special thanks to the teams at the Roberts Lab, the MacCoss Lab of Biological Mass Spectrometry at the University of Washington Department of Genome Sciences, and University of Washington Proteomics Resource.





