

A detailed black and white line drawing of several oysters, some open and some closed, set against a dark blue background. The oysters are scattered across the slide, with a larger cluster in the bottom left corner.

# Understanding Oyster Population Connectivity and Adaptation in Narragansett Bay

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Gomez-Chiarri, Jonathan Puritz**



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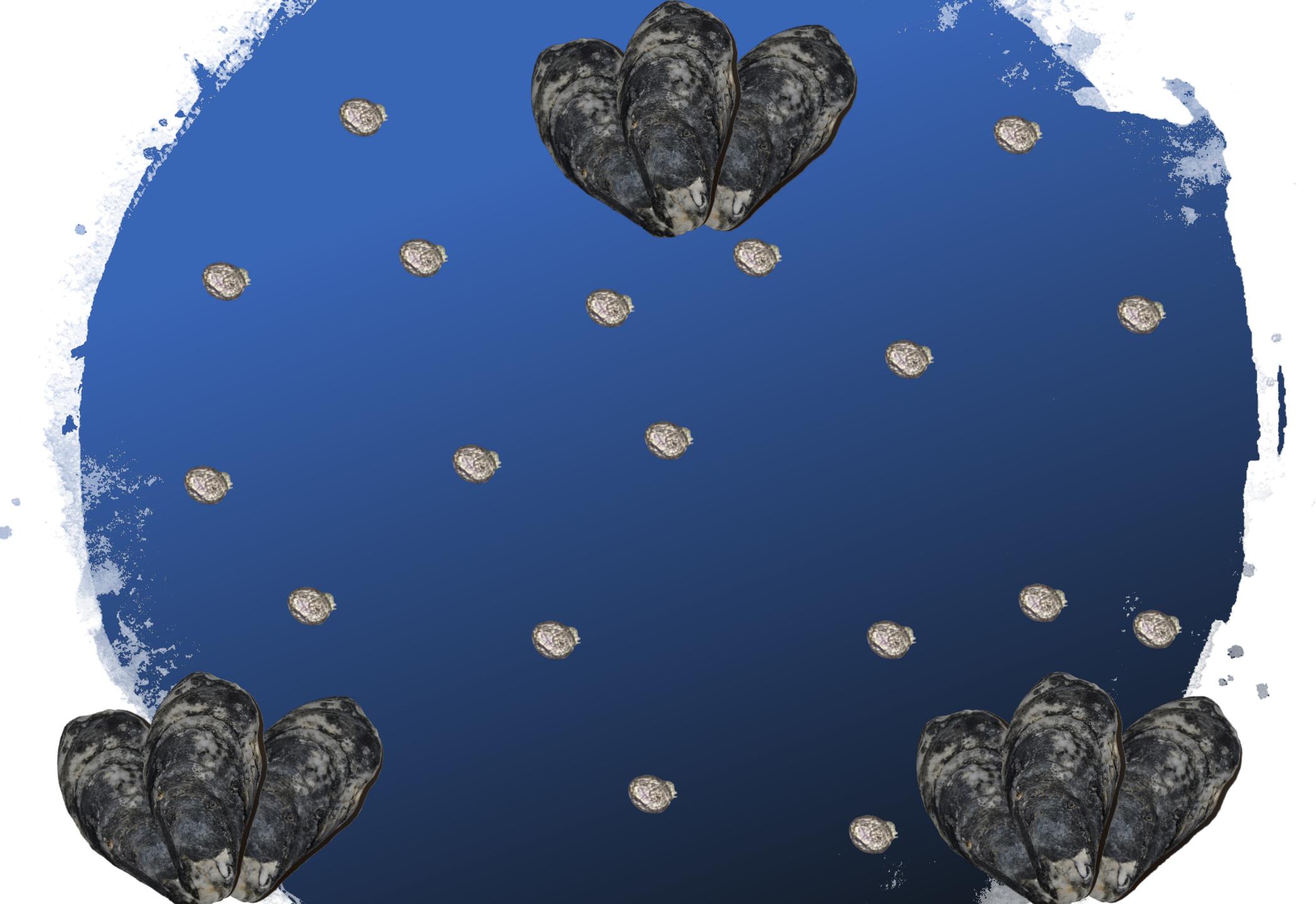
@AZyck

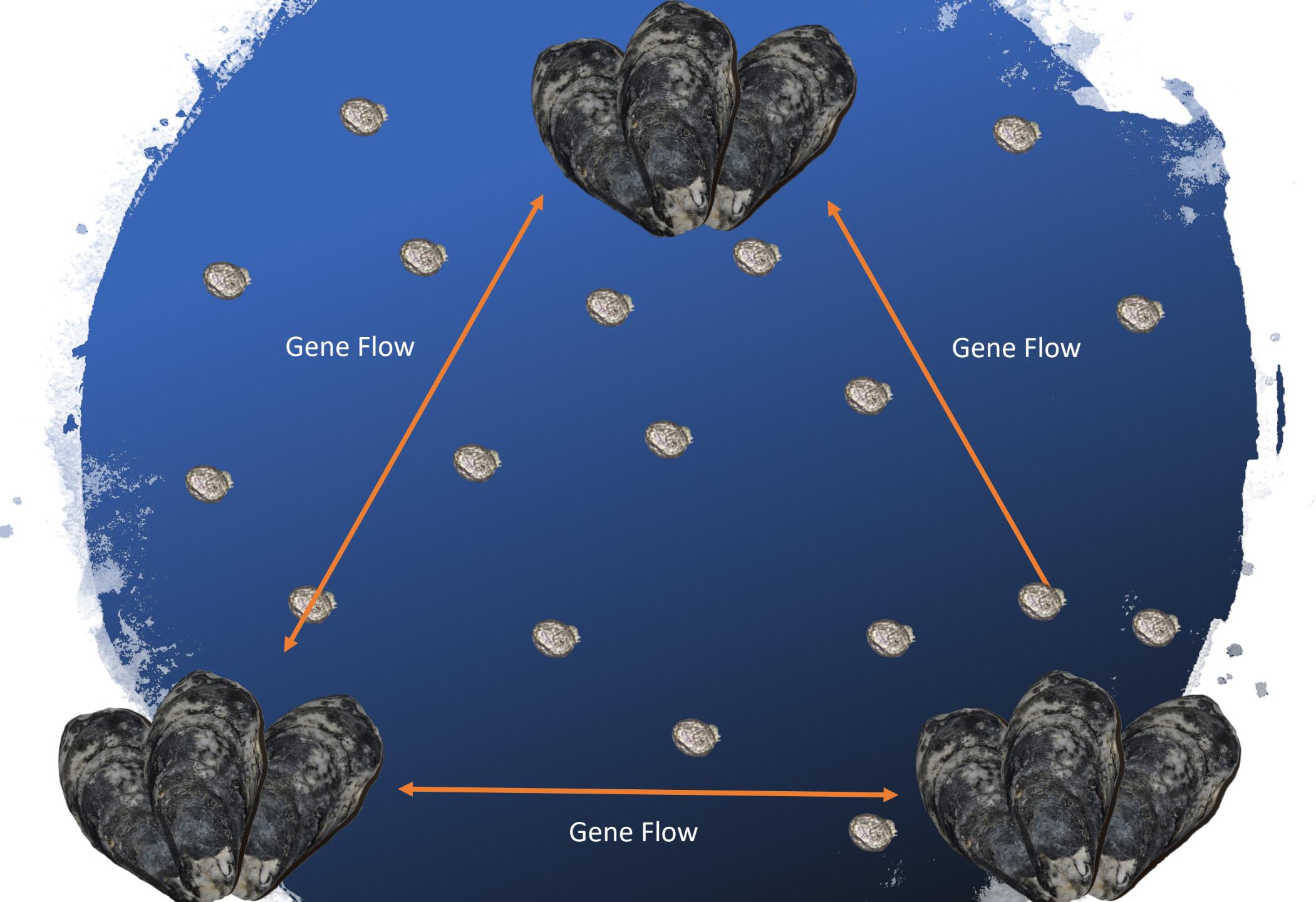


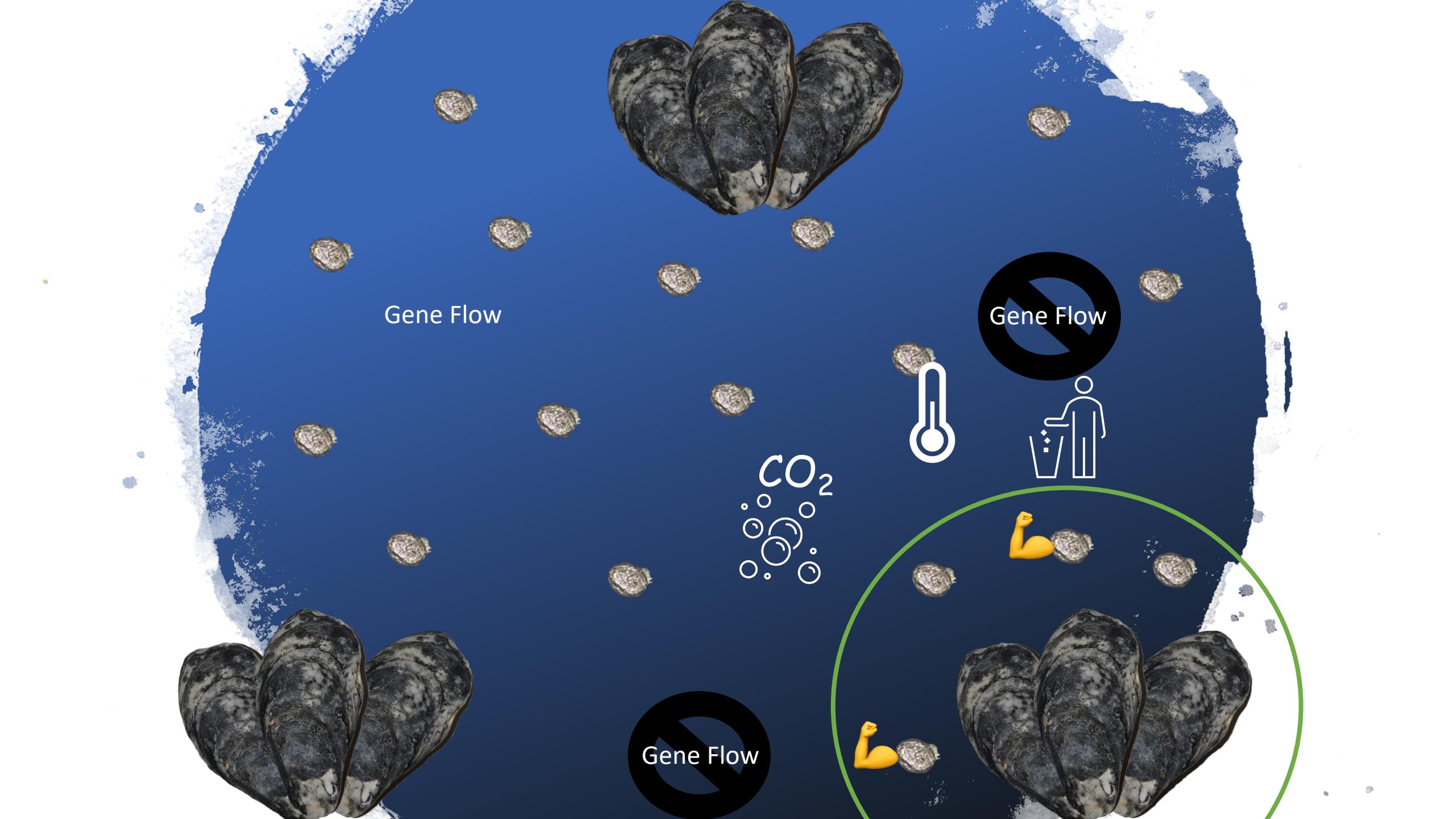
University of Rhode Island  
*Department of Biological Sciences*



Puritz Lab of Marine  
Evolutionary Ecology





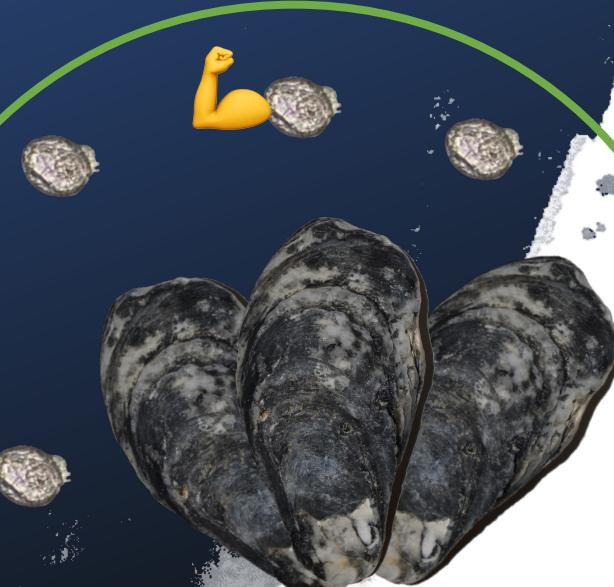


Gene Flow

Gene Flow

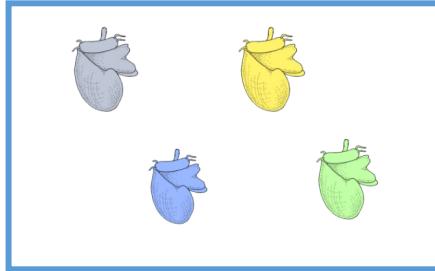
Gene Flow

$CO_2$

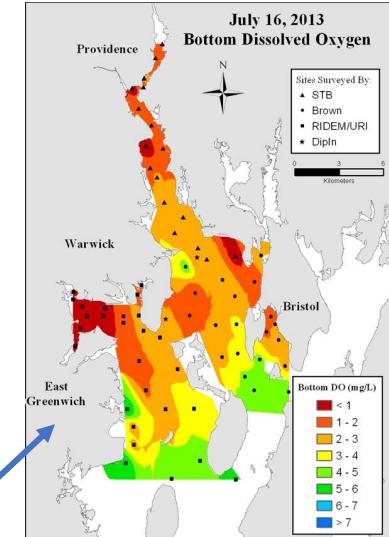


# Linking larval coastal stressor response to population connectivity patterns in adult oysters

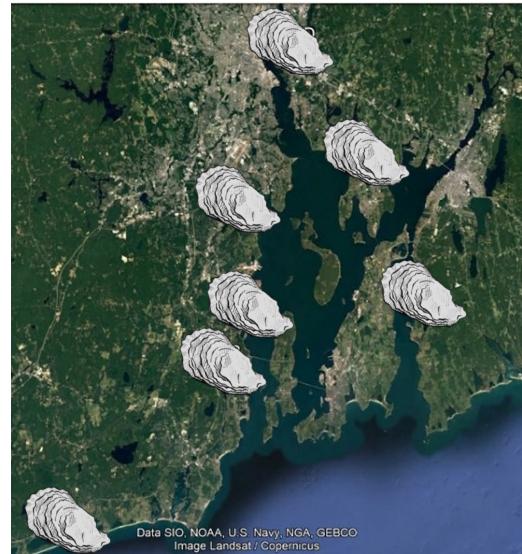
Larval response to  
coastal stressors



Environmental data



Population genetics

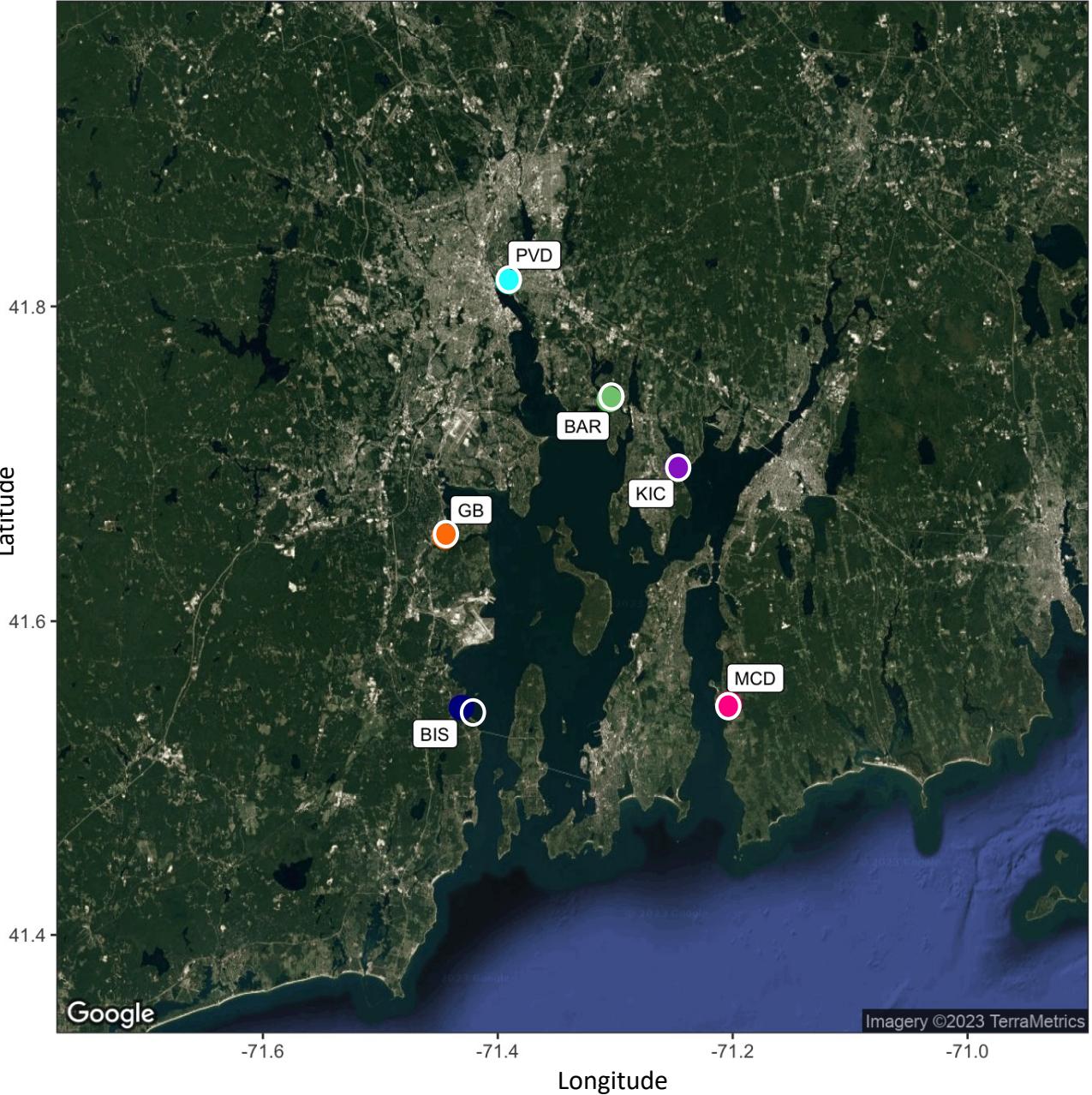


# Oysters and environmental data collected from 6 sites

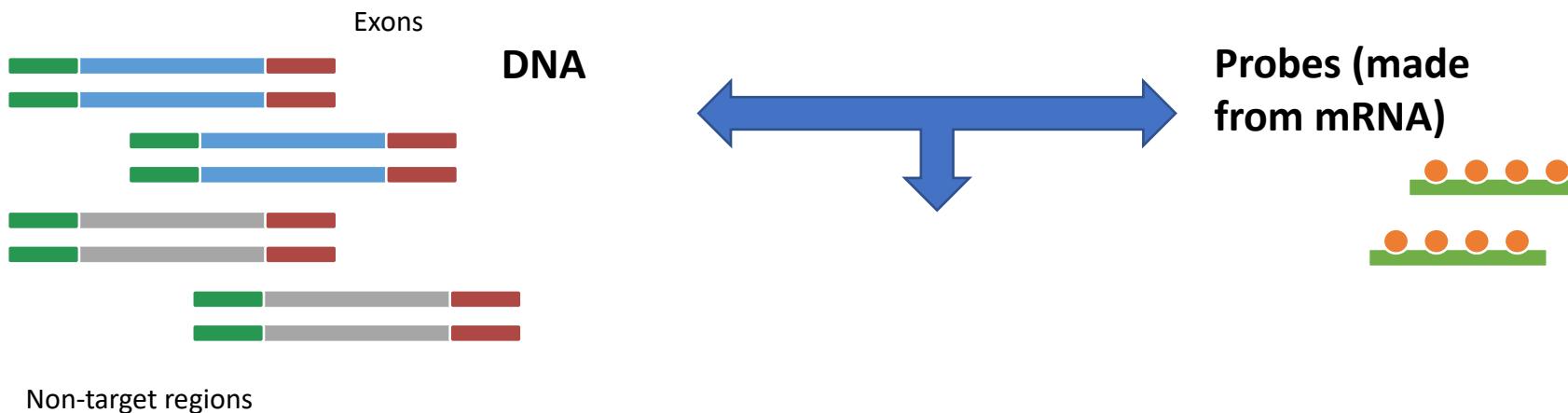
	Sewage Effluent*	Temperature (°C)	Salinity (ppt)	pH	Dissolved Oxygen (mg/L)
PVD	59.860	15.8	18.82	7.68	4.9
GB	14.596	22.27	29.58	7.67	4.57
BIS	8.825	21.39	27.32	7.94	7.05
BAR	17.881	22.08	29.08	7.69	5.37
KIC	56.313	21.5	28.31	7.84	6.07
MCD	12.111	22.24	20.68	7.69	8.76

PVD – Narragansett Bay Commission  
GB, BAR, KIC – URI Watershed Watch  
BIS, MCD – Onset HOBO data loggers

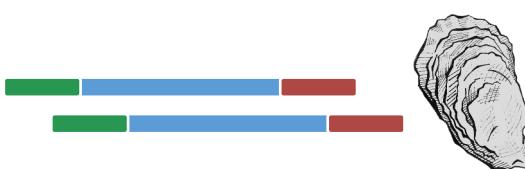
Summary data based on summer averages



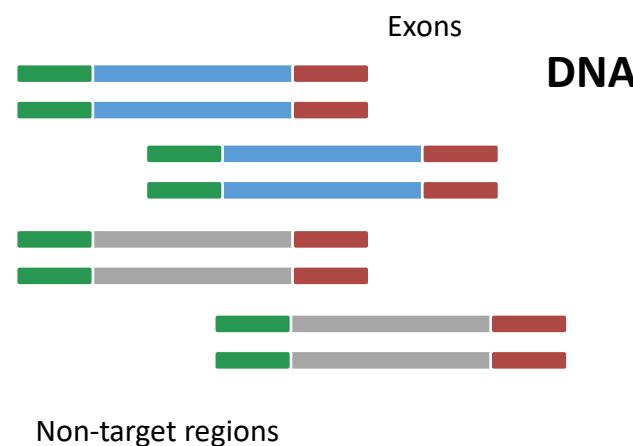
# Expressed Exome Capture Sequencing!



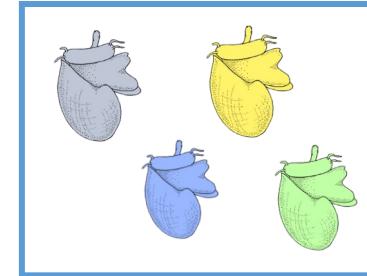
**Selective enrichment of exon sequences  
of your study organism**



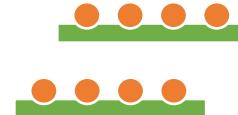
# Expressed Exome Capture Sequencing!



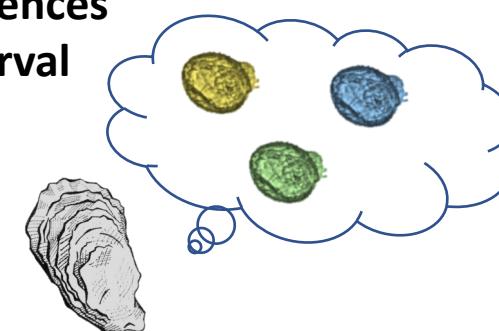
Larval oysters exposed  
to coastal stressors



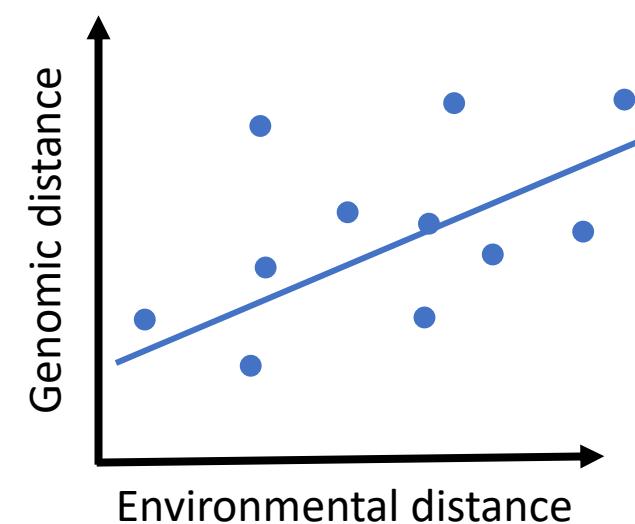
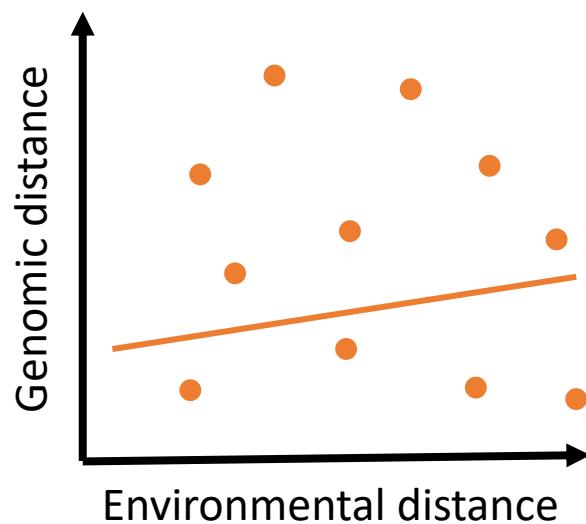
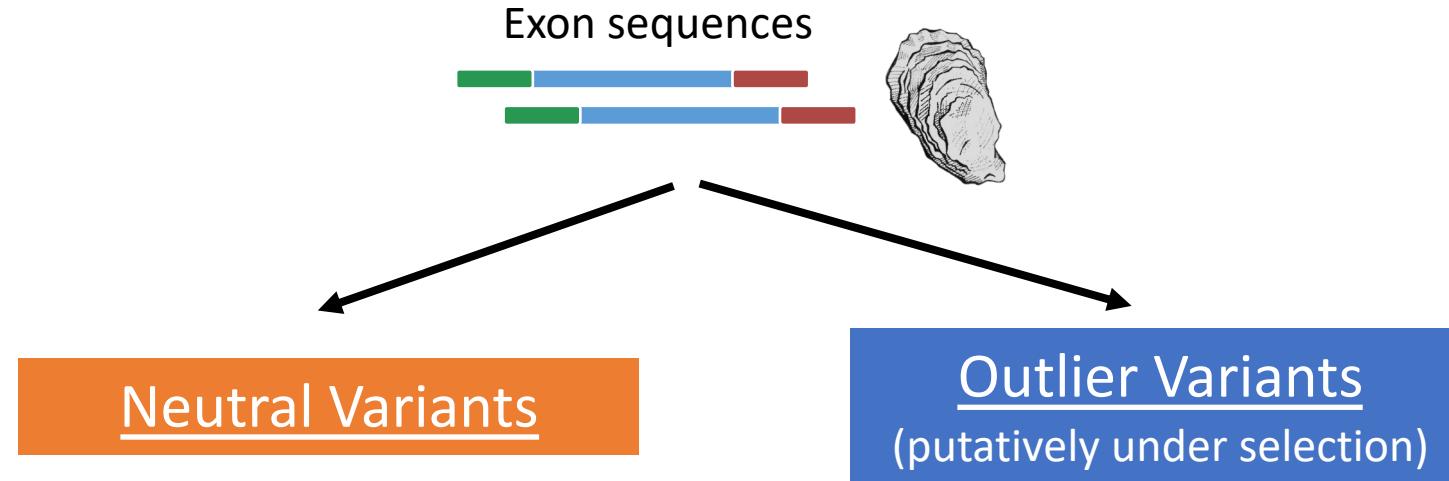
Probes (made  
from mRNA)



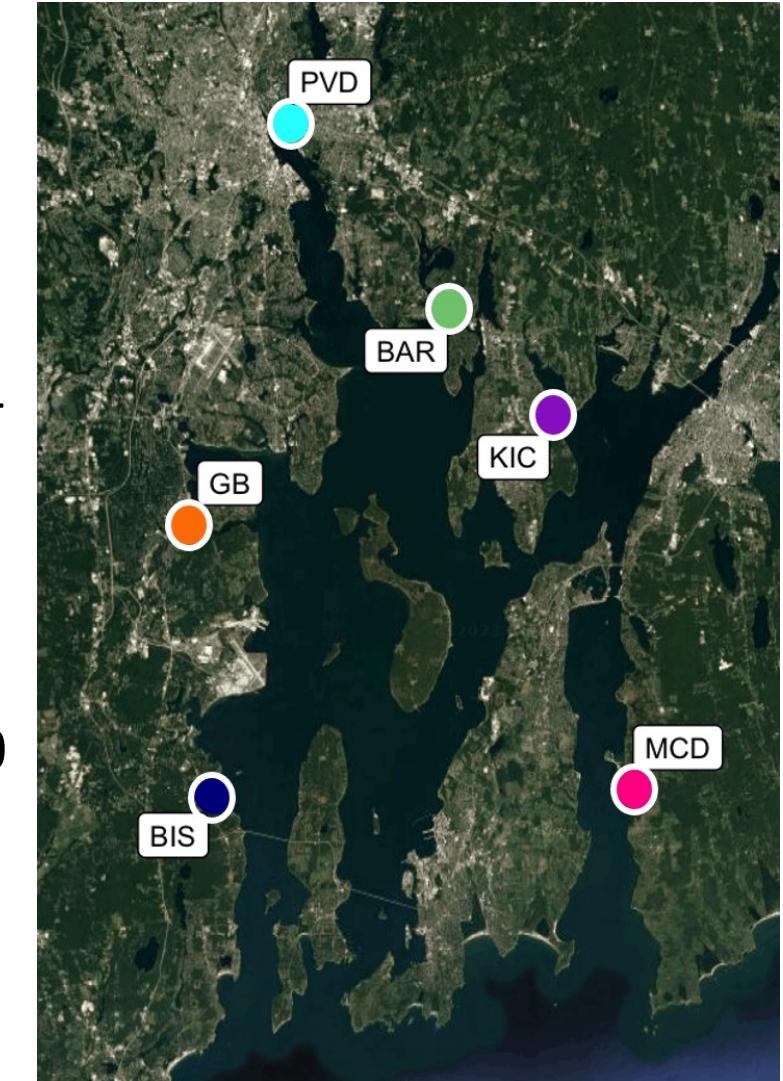
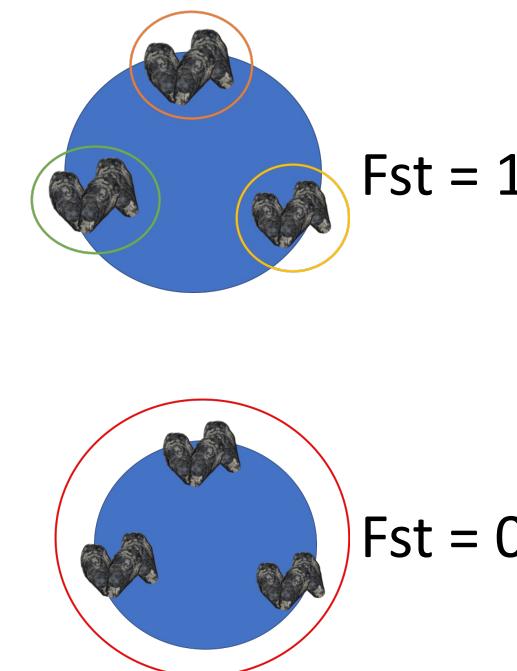
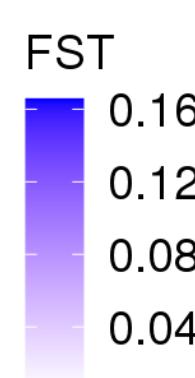
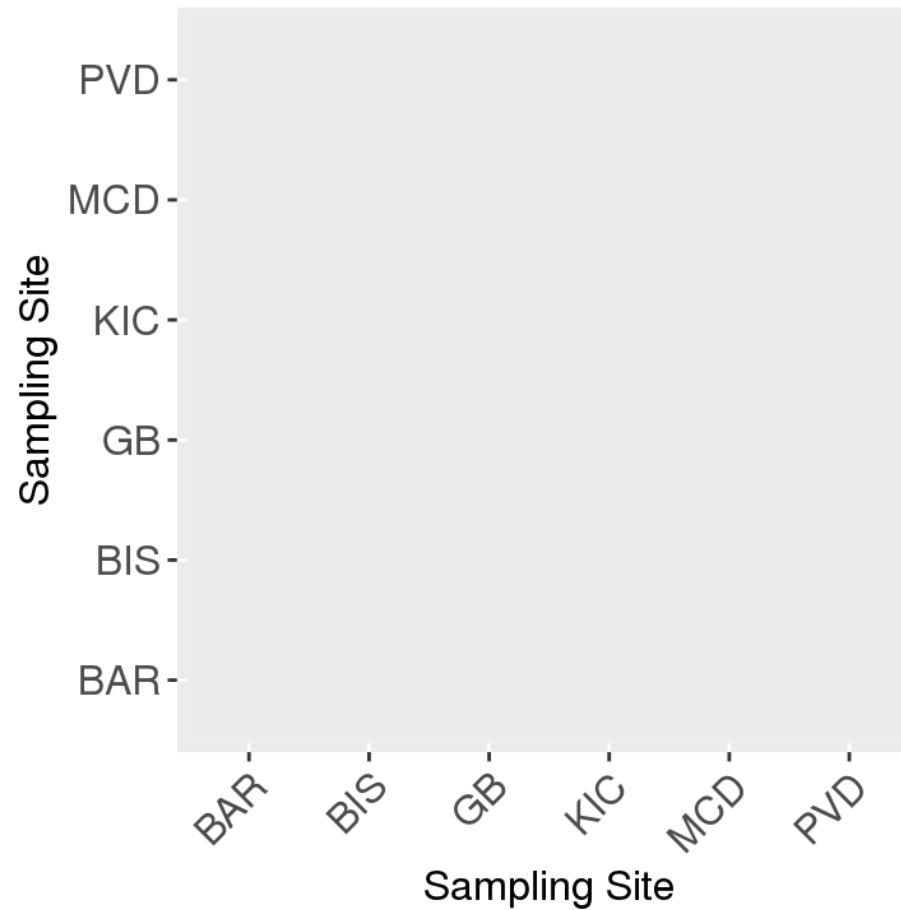
Selective enrichment of exon sequences  
of adult oyster DNA related to larval  
response to coastal stressors



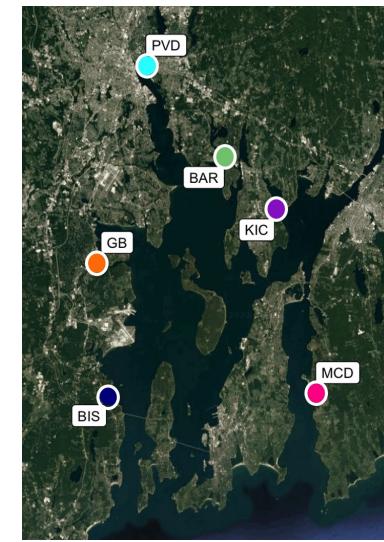
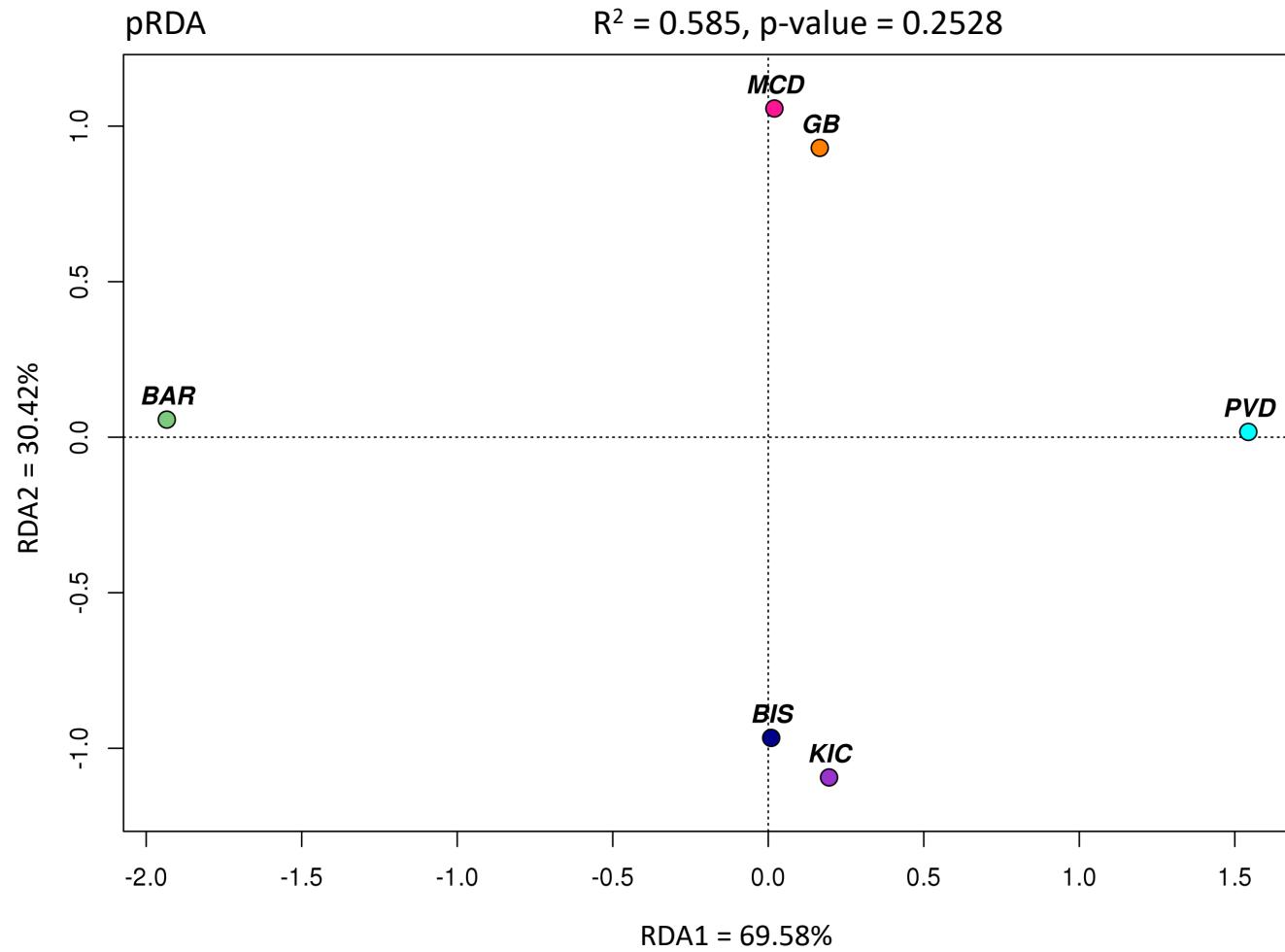
# Population & Seascape Genomics Analysis



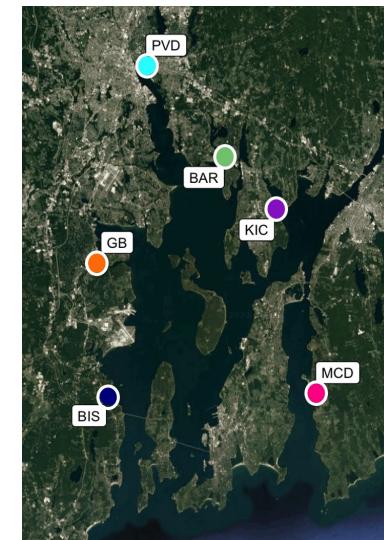
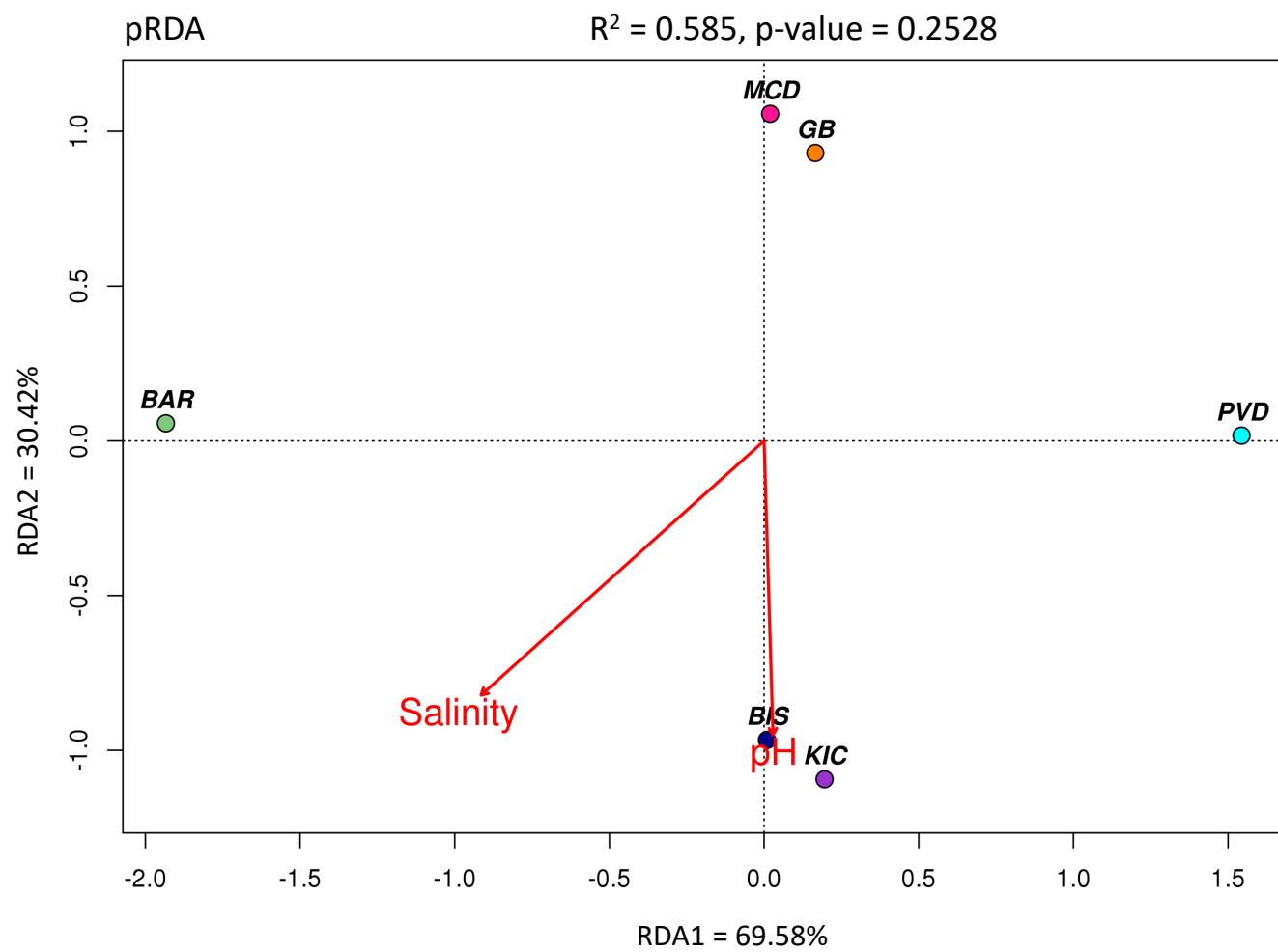
# High levels of population differentiation in variants under selection



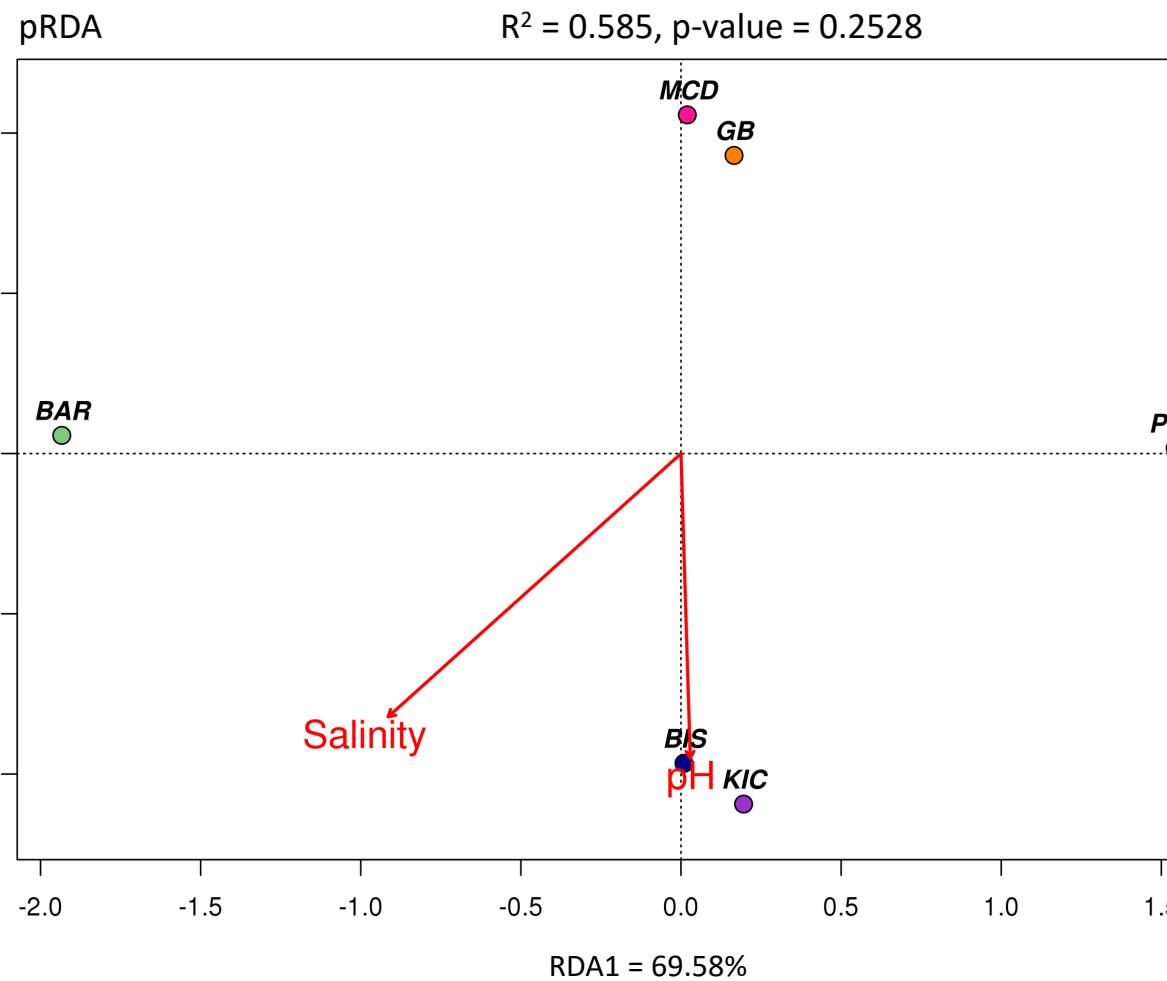
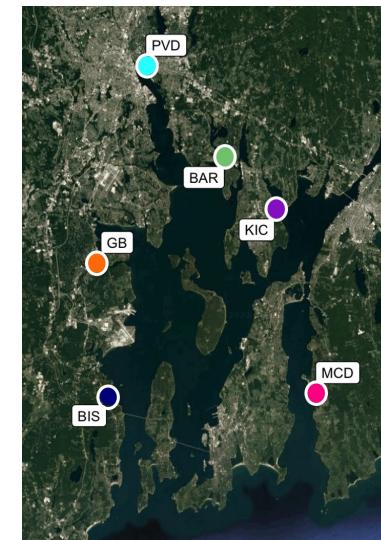
# Salinity & pH may explain population structure in variants under selection



# Salinity & pH may explain population structure in variants under selection

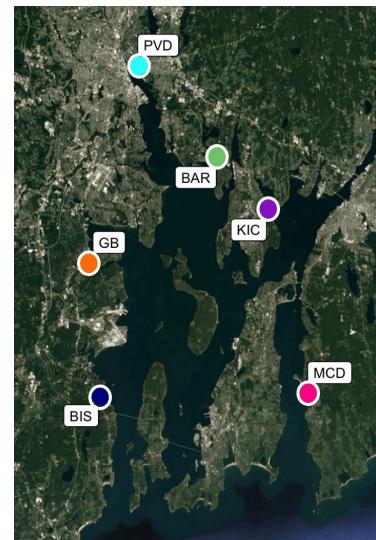
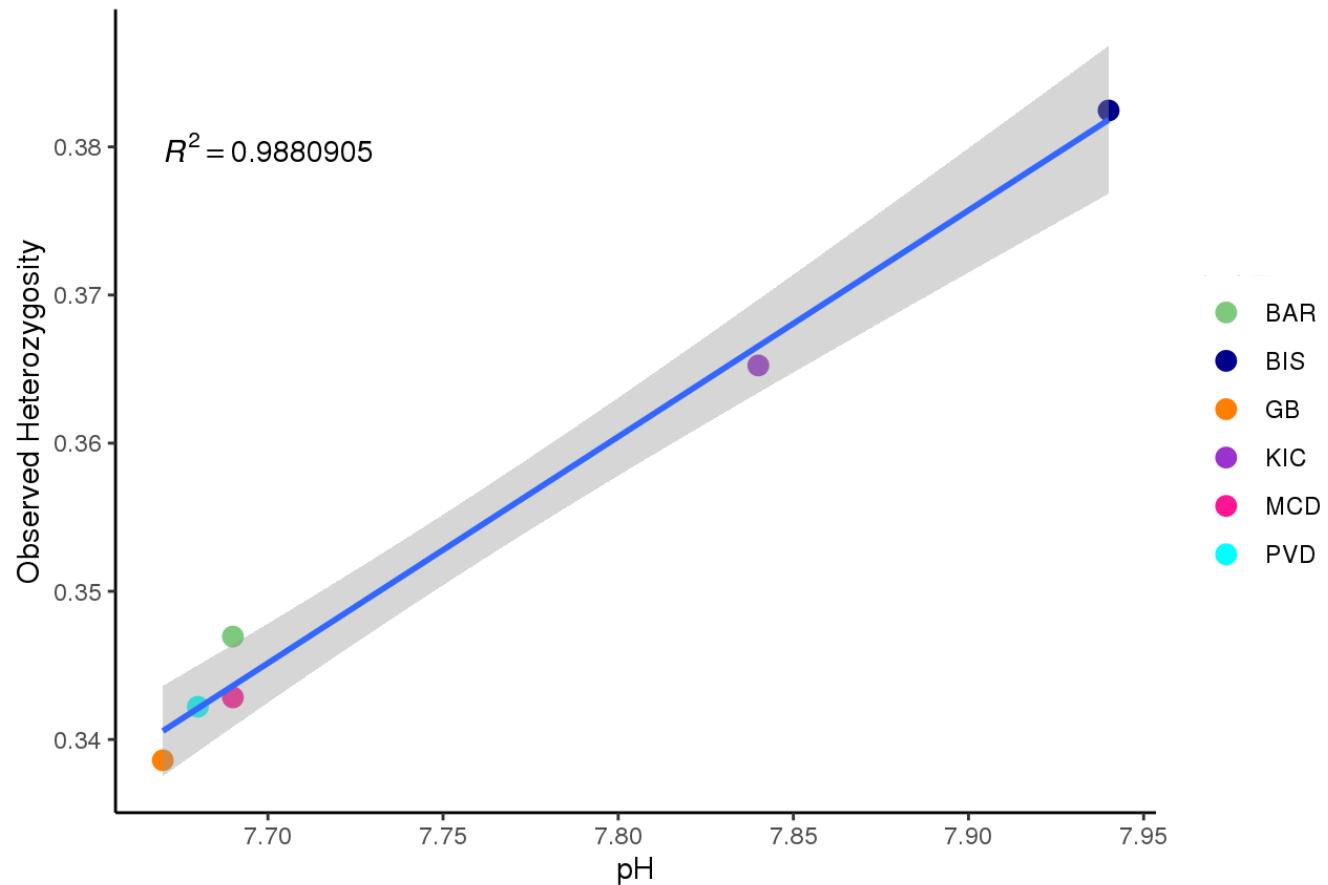


# Salinity & pH may explain population structure in variants under selection



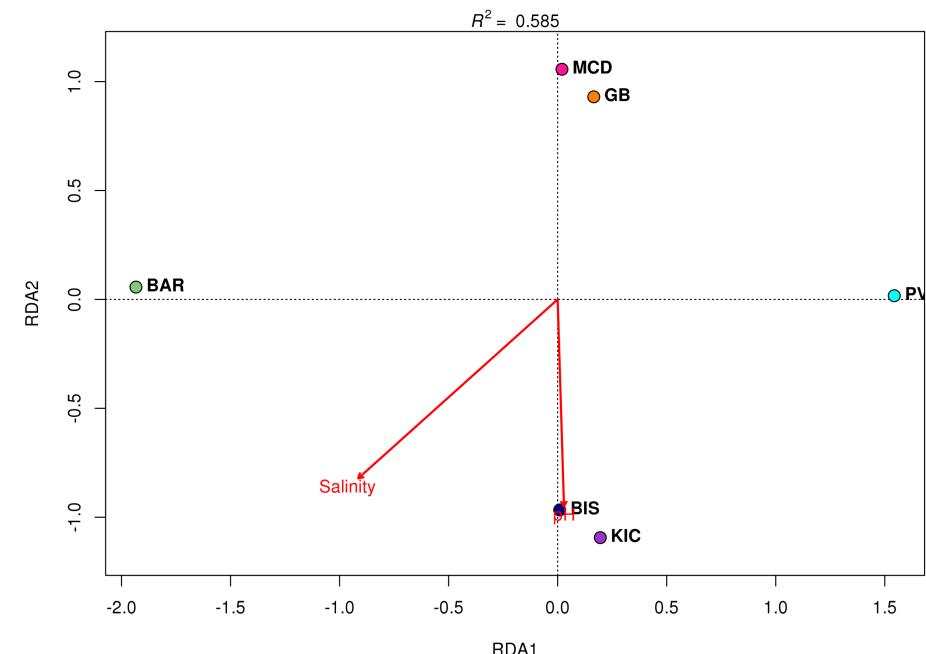
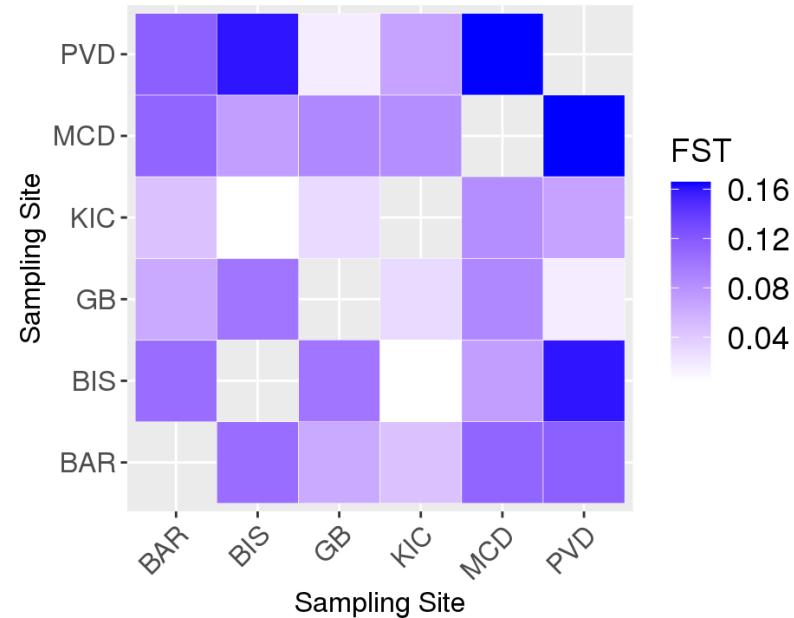
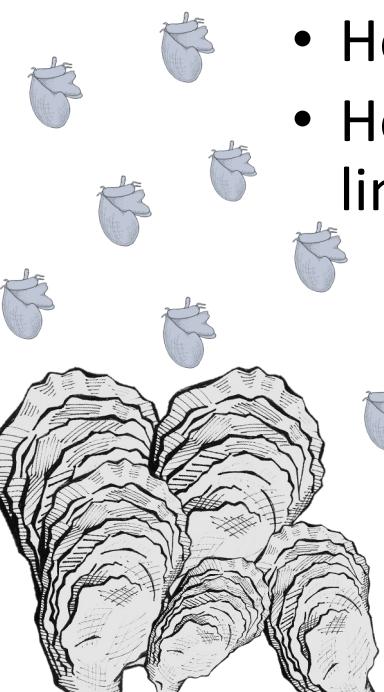
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# Observed heterozygosity increases with pH



# Application of genomic tools for oyster restoration

- Site selection is an important step in restoration
- It can be more accurately informed by understanding:
  - How populations are genetically connected
  - How environmental conditions promote or limit gene flow across populations





Bioinformatic  
pipeline and  
analyses



# Acknowledgements

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- Maggie Schedl
- Jacob Green



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