Restoring Oysters Sustainably Requires Good Genes: Genomic Evidence from Delaware Bay and Hudson River

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photo by Josef Galatioto

Restor… …quires

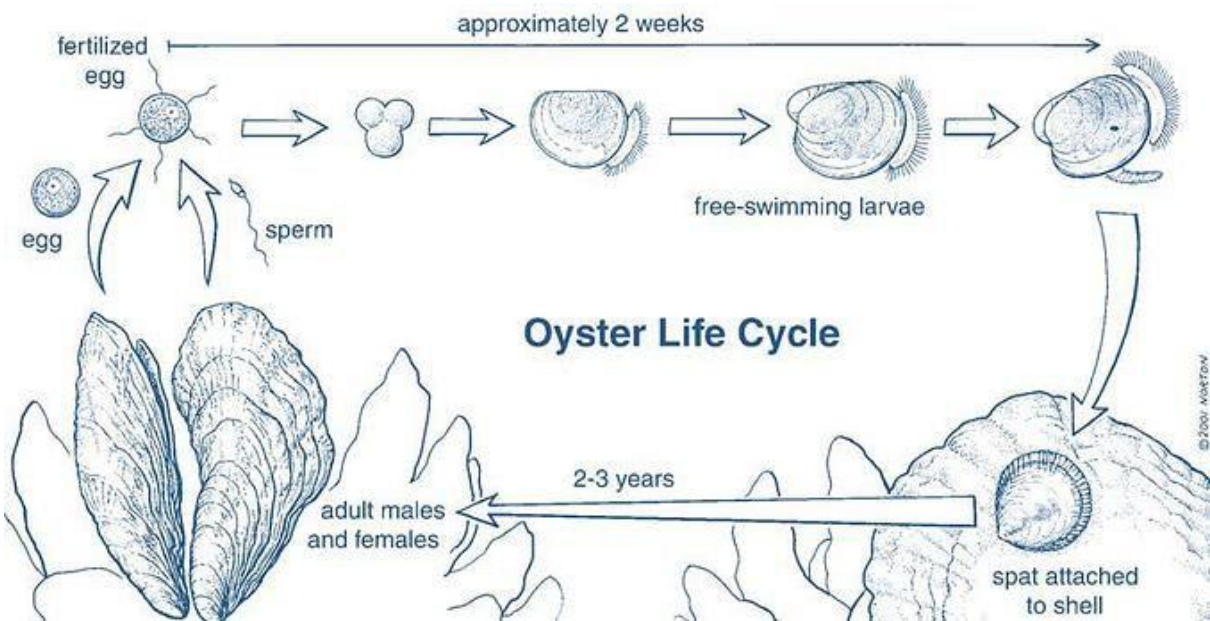
De… …ver

photo by Josef …

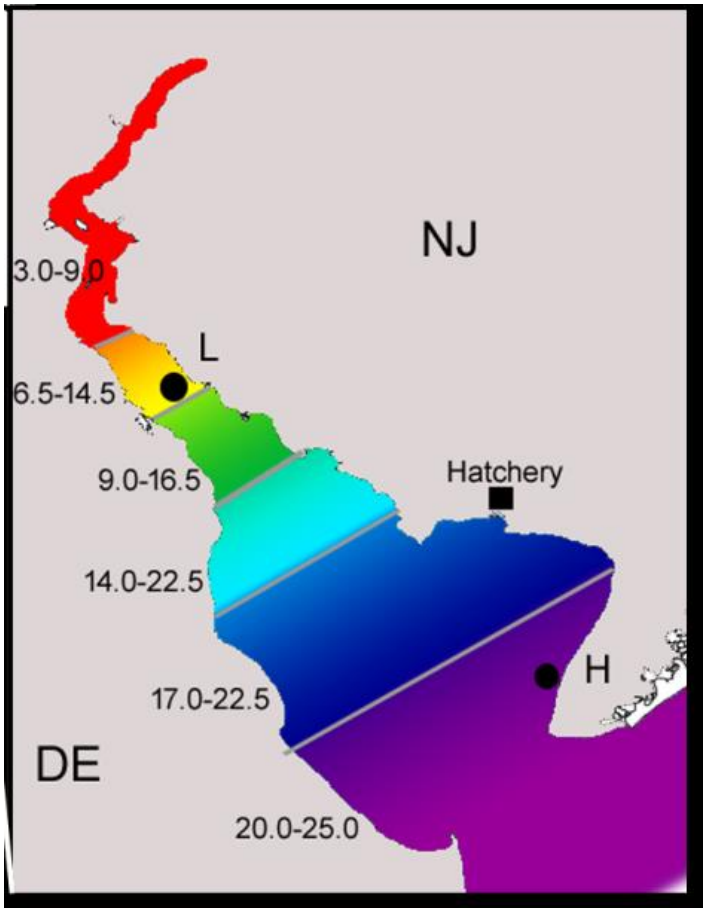
Eastern Oyster Natural History

Crassostrea virginica

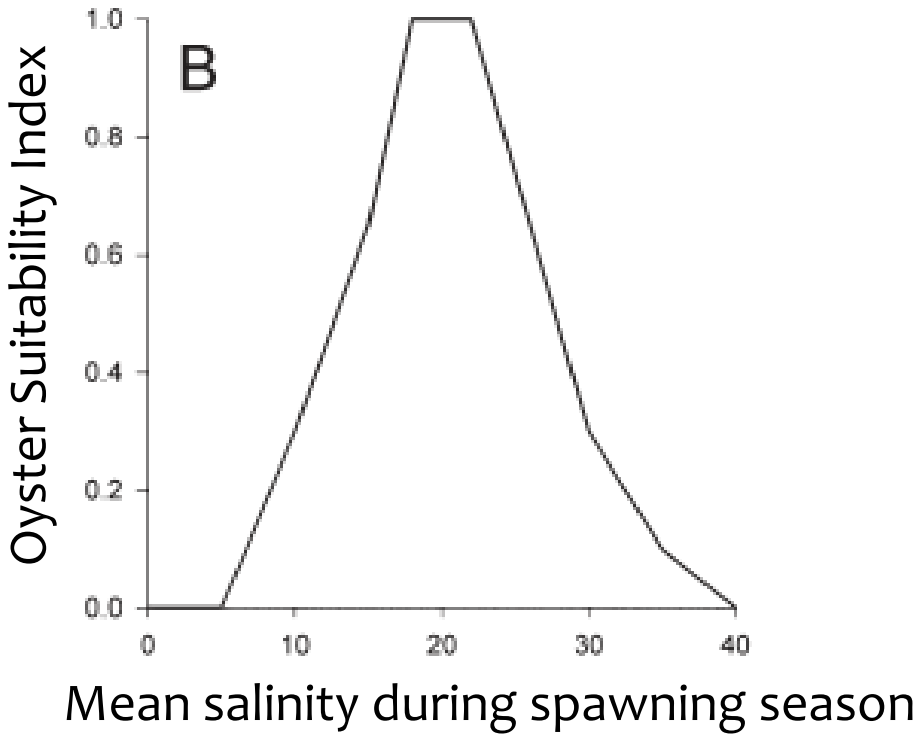
- Canada to Mexico
- High fecundity
- Larval dispersal
- Phenotypic plasticity
  - Shell morphology
  - Depth
  - Euryhaline



Osmoregulatory Plasticity



Swannack et al. 2014 JSR



Questions for Today

* How much does oyster population fitness depend on phenotypic plasticity vs. evolutionary mechanisms that depend on genetic diversity?

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Questions for Today

* How much does oyster population fitness depend on phenotypic plasticity vs. evolutionary mechanisms that depend on genetic diversity?
  - Delaware Bay adaptive gene expression plasticity
* Is larval dispersal limited in the upstream direction, allowing some measure of local adaptation?
  - Hudson River oyster population structure
* Do hatchery produced cohorts have reduced genetic diversity and if so, does it matter?
  - Wild broodstock vs. aquaculture strain vs. wild

Why Restore Oysters?

* Legacy of oysters in NYC

Detroit Publishing, Library of Congress, Circa 1900

Ecosystem Services

* Water quality from filter feeding (1-3 liters / hr / oyster)
* Habitat provisioning
* Coastal protection
  - Attenuation of wave strength

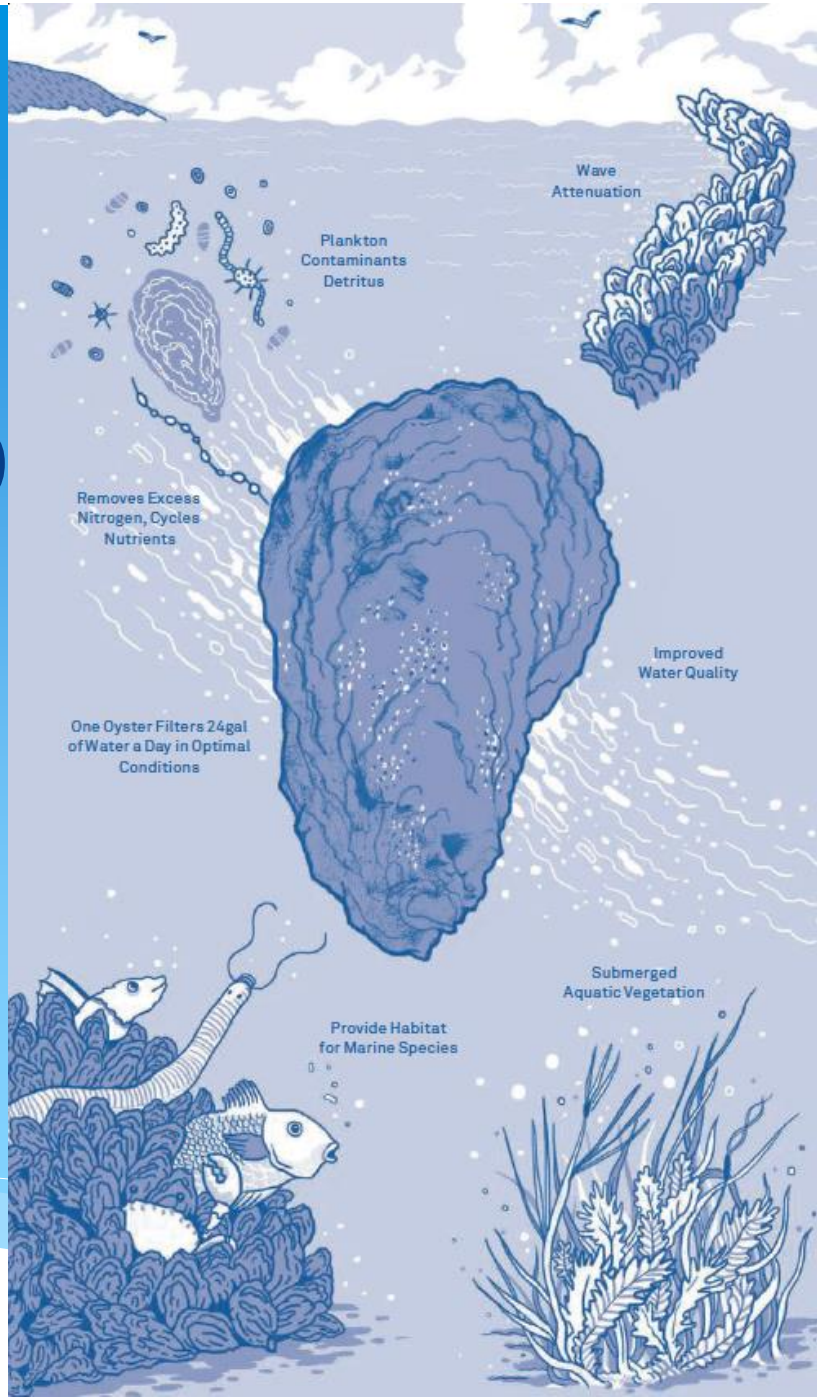

Illustration from BOP Oyster Gardening Manual

NY/NJ Oyster Restoration

* Billion Oyster Project, Harbor School

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* Oyster Research Restoration Project, HRF & partners

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* Tappan Zee Bridge Reconstruction Mitigation, AKRF Inc. with partners
* The River Project, Pier 40
* Naval Weapons Station Earle, NY/NJ Baykeepers
* Rebuild by Design competition – Staten Island living oyster fringe reef, SCAPE landscape architects
* Jamaica Bay by NYCDEP

Oyster Restoration Goals?

* NOT for consumption in Hudson/Raritan Estuary

* Short-lived eco-services from hatchery plantings
  - Local benefits, high maintenance, research pilot

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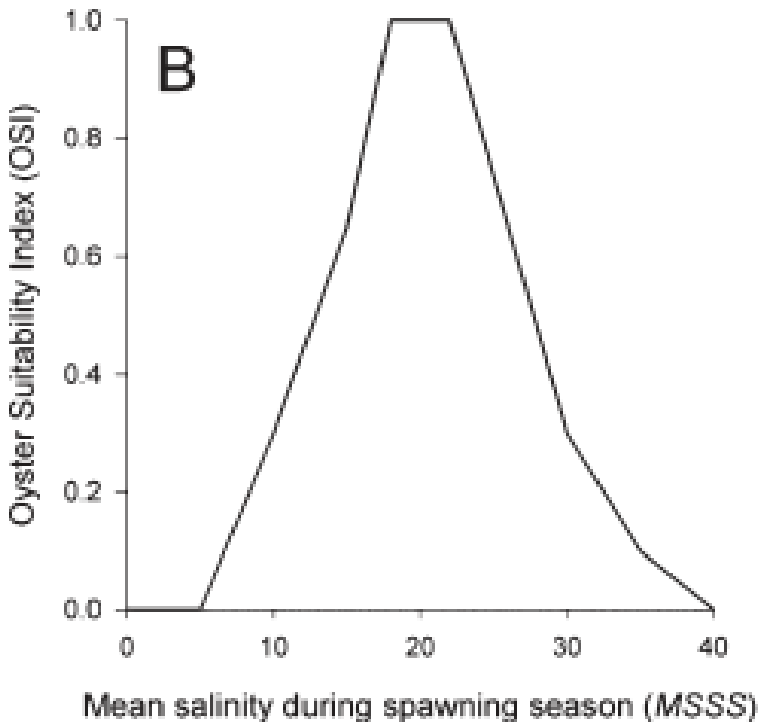
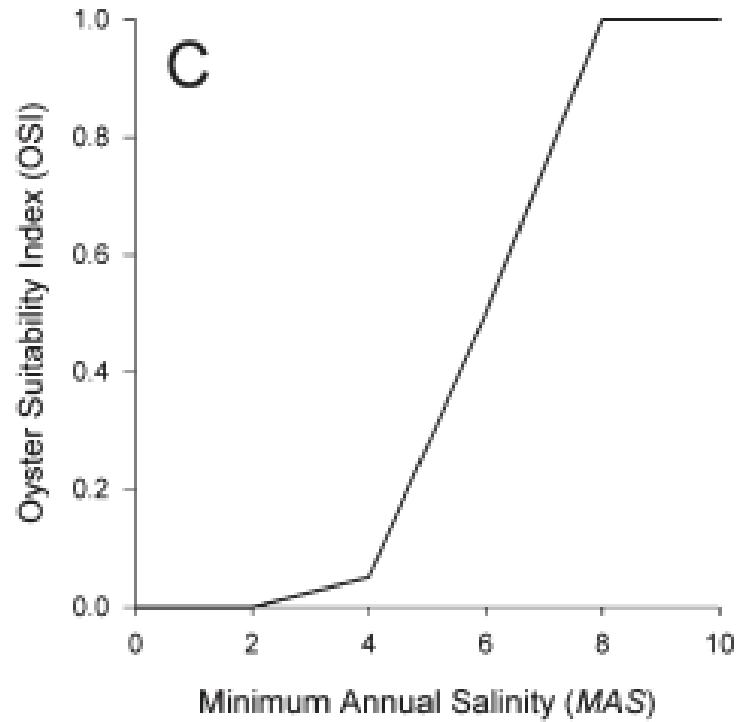
* NOT for consumption in Hudson/Raritan Estuary
* Short-lived eco-services from hatchery plantings
  - Local benefits, high maintenance, research pilot
* Jump-start population recovery (stock enhancement)
* Rebuild self-sustaining reefs

Just How Plastic are Oysters?

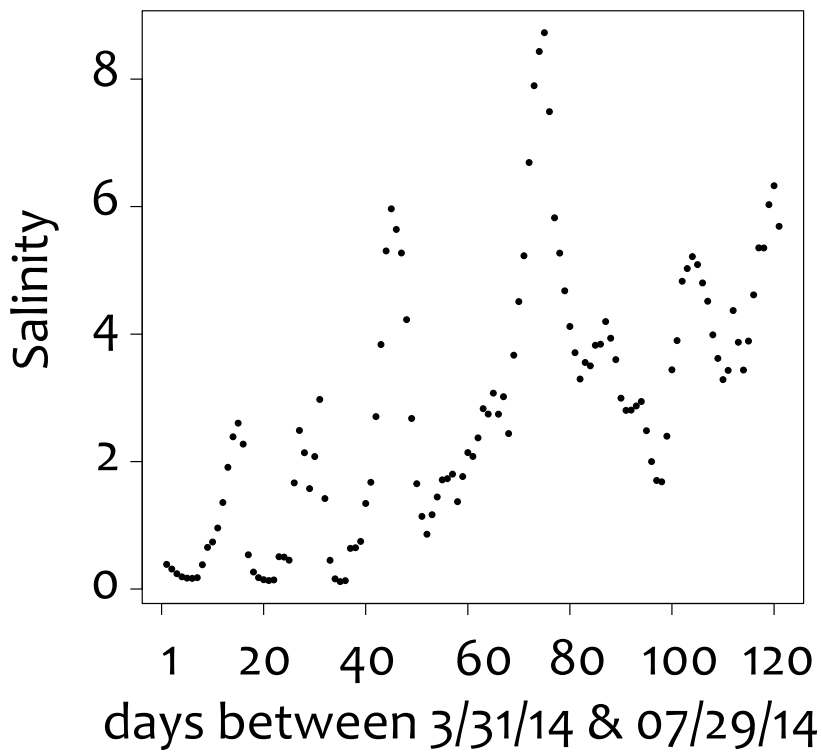
Swannack et al. 2014 JSR





Just How Plastic are Oysters?

Tappan Zee Daily Mean Salinity
at 2 m depth



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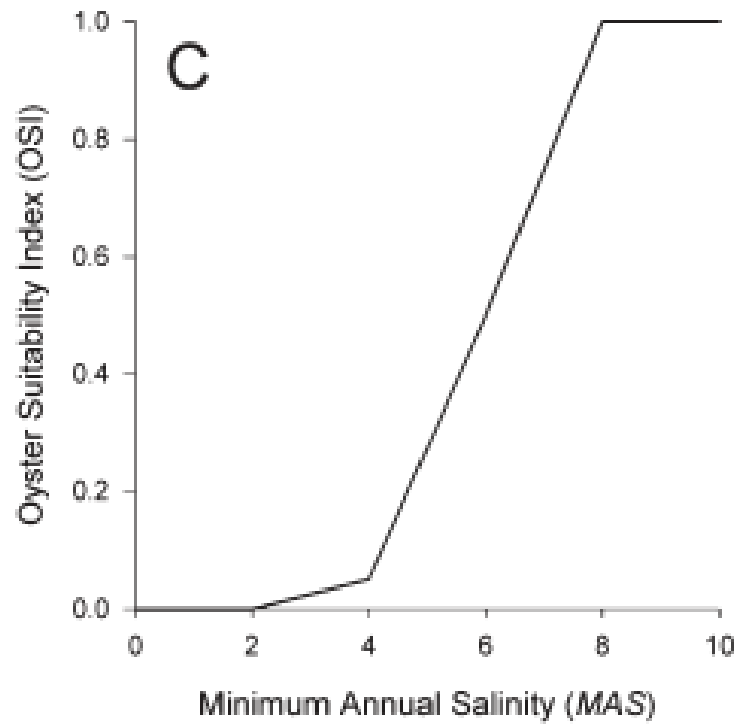
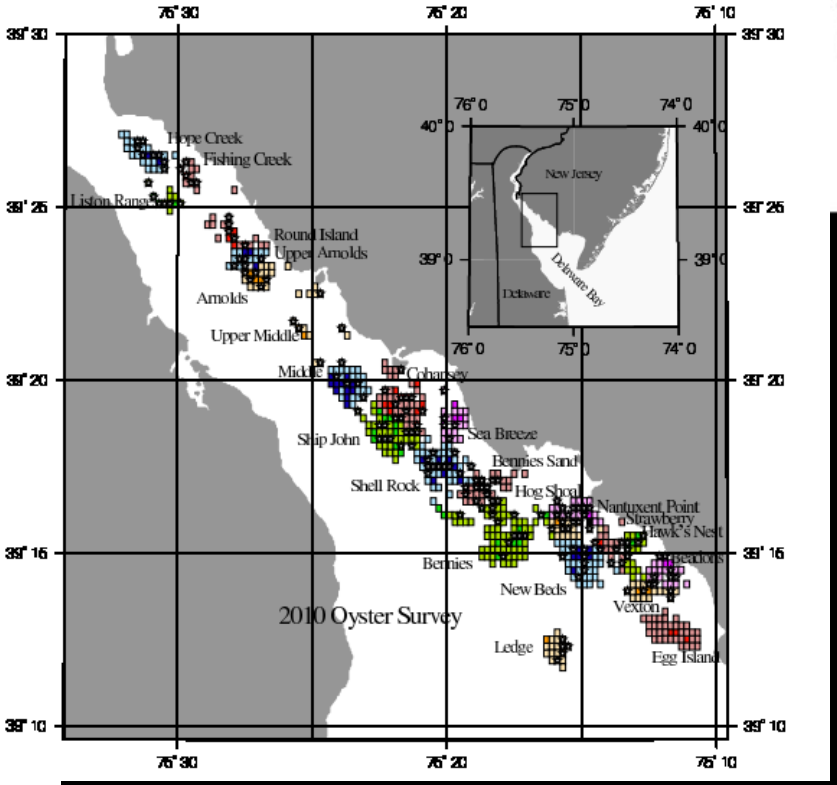
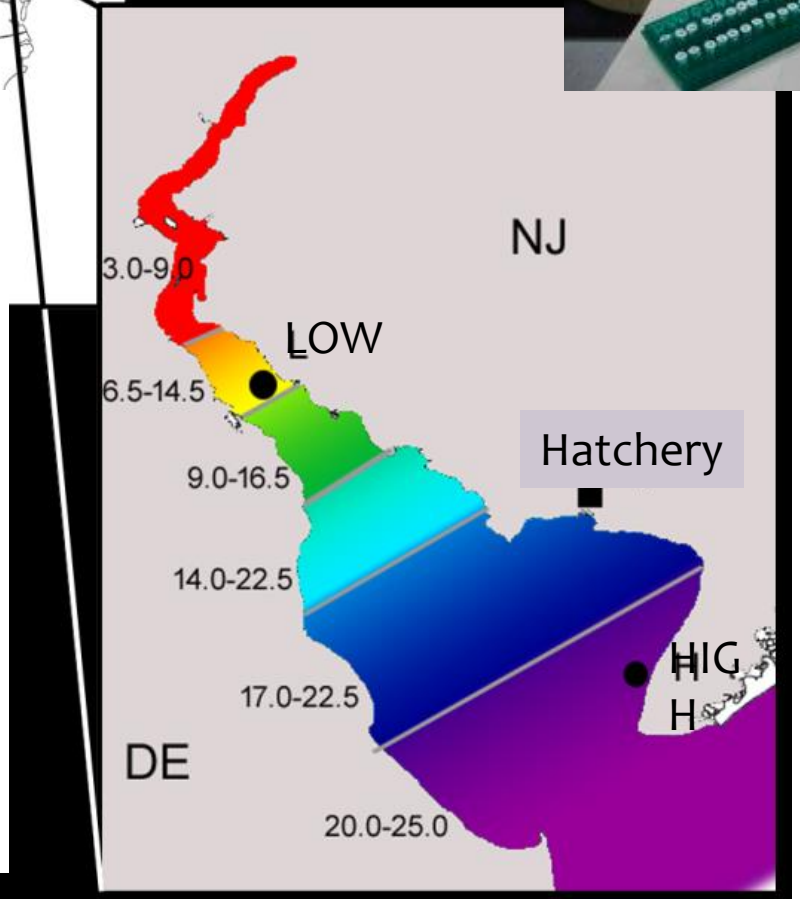


Delaware Bay Oysters

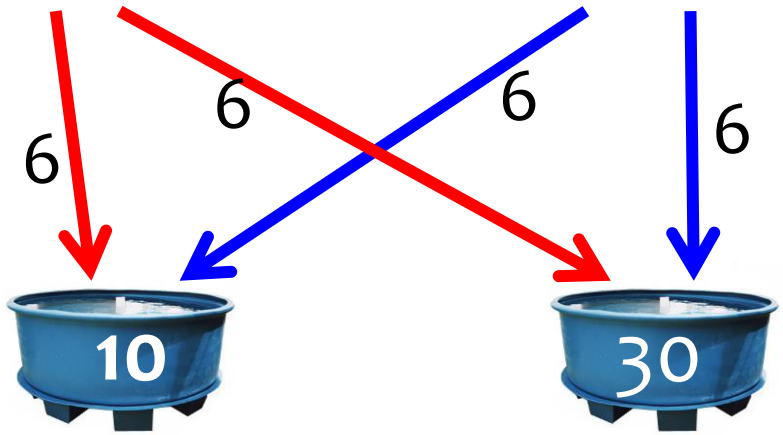




Gene ExpressionMethods

Delaware Bay Source Reefs

Low salinity (10) Mod. salinity (25)



http://www.dnr.state.md.us/

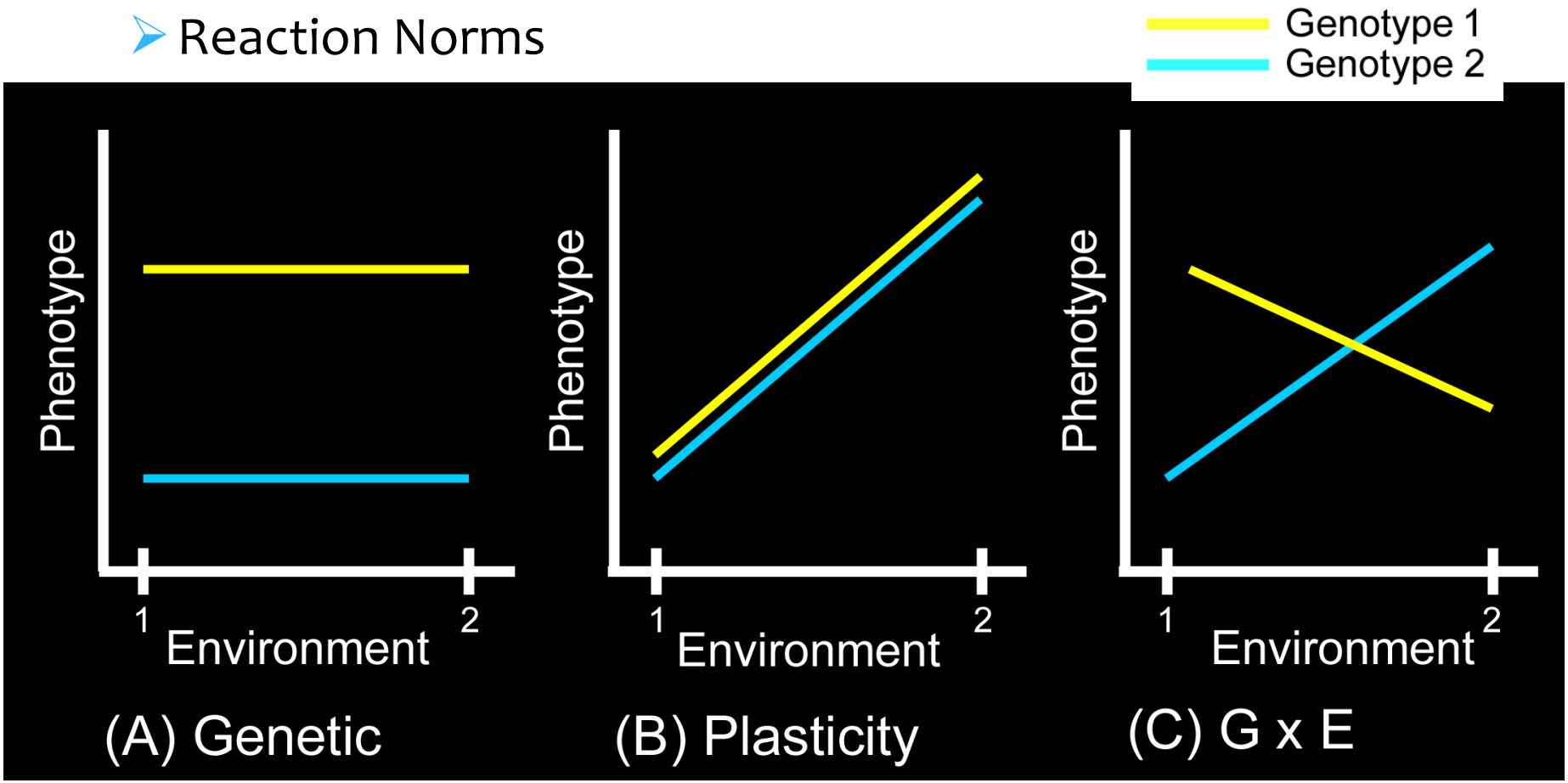
9 week salinity acclimation,

then RNAseq adults

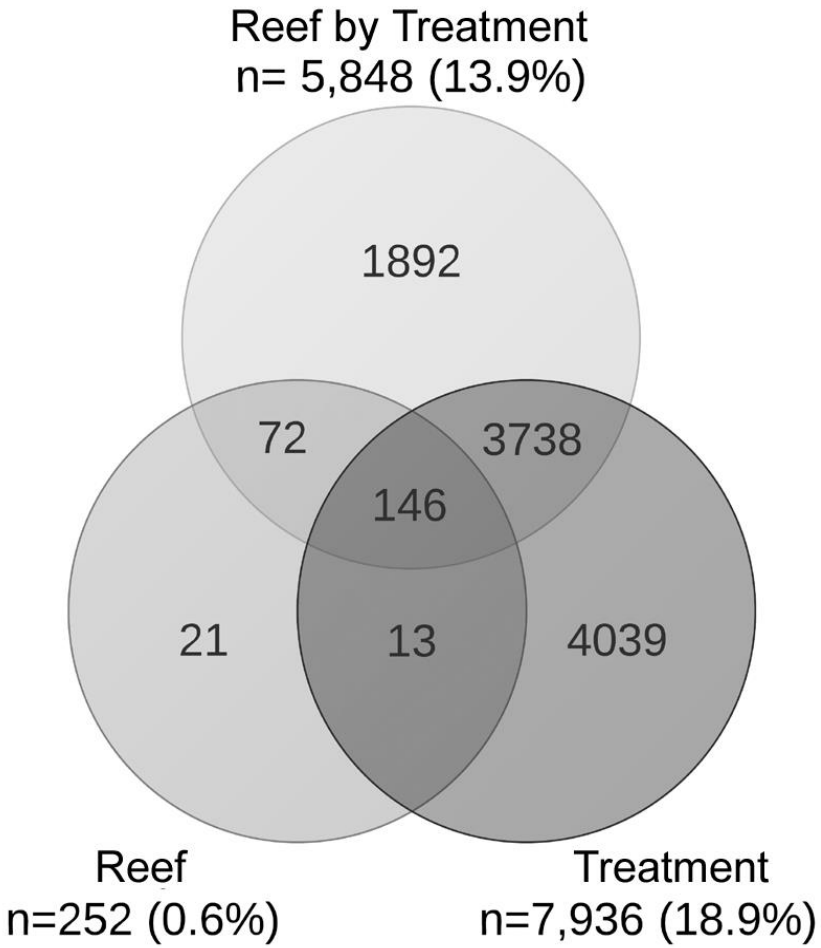
EdgeR testing for differential expression

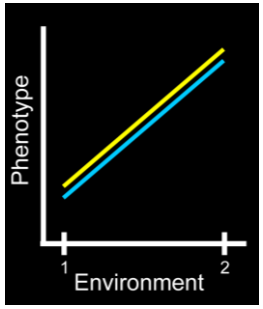
Background

* Response to environmental variation
  - Reaction Norms



Differential Expression Results





Plasticity

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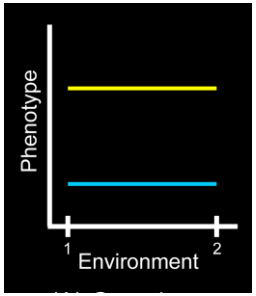
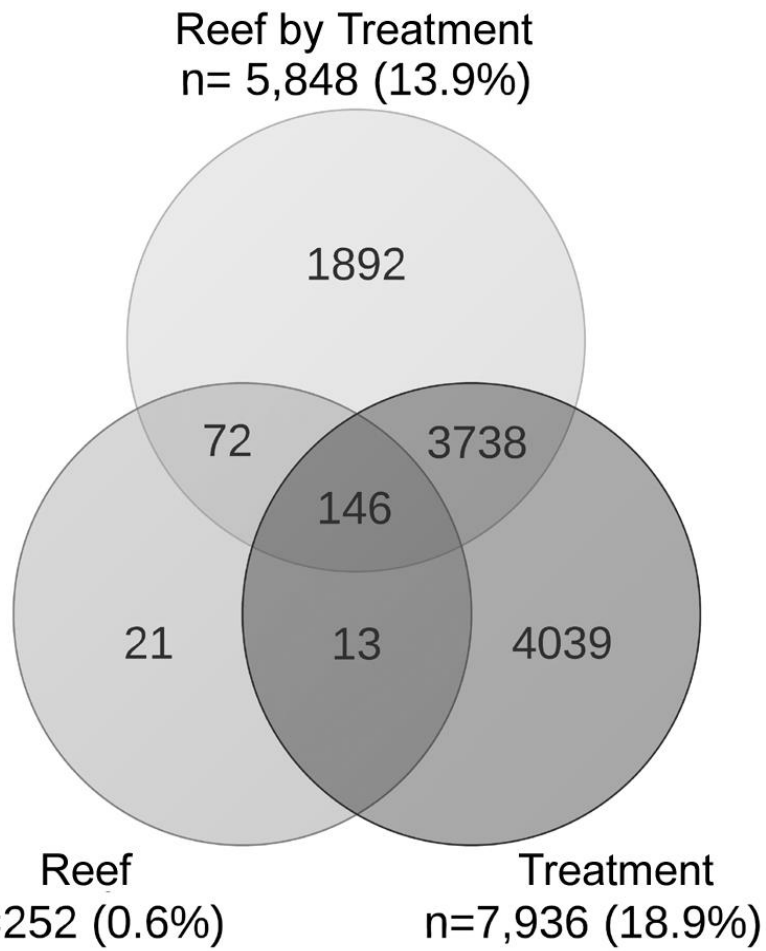
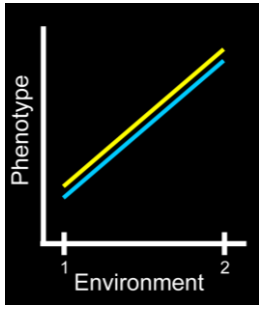


Reef Effect





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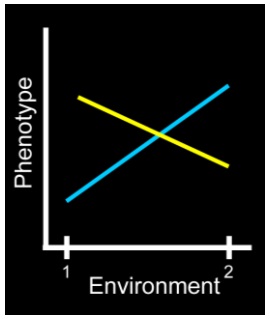
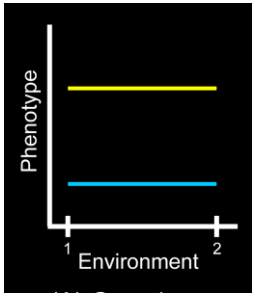


G x E



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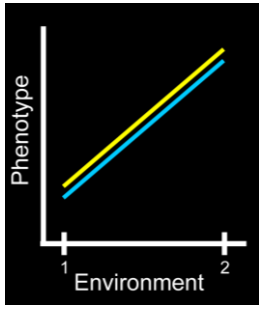
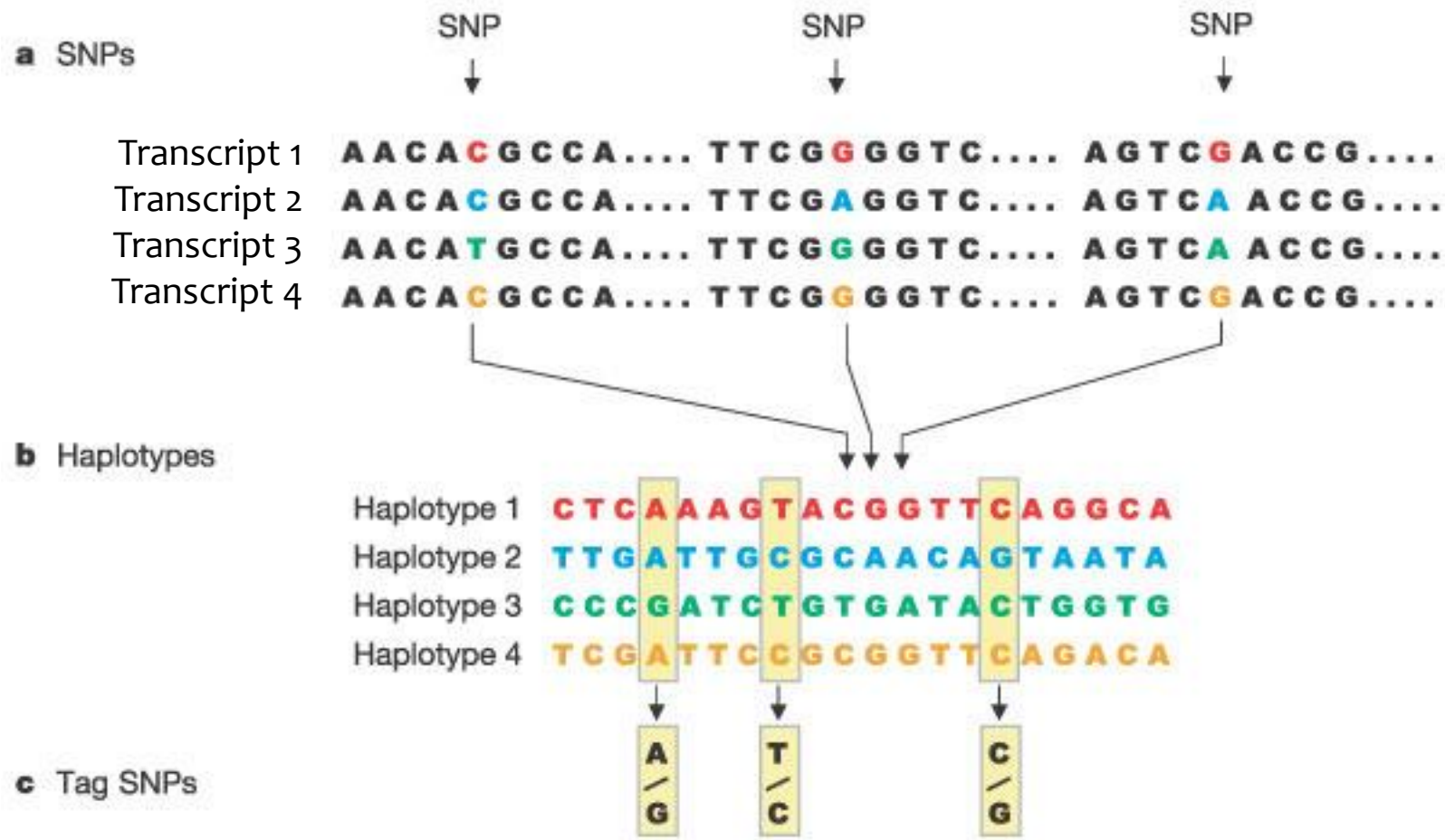


Plasticity

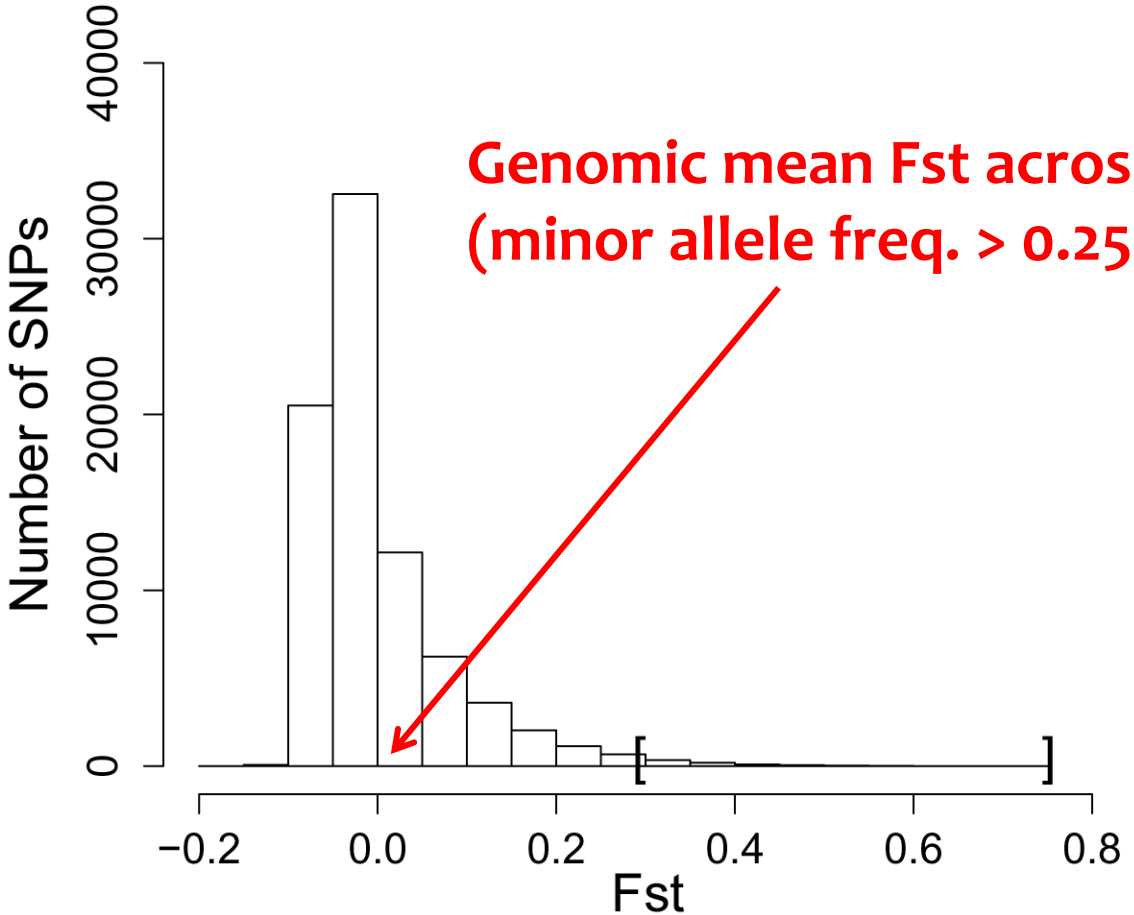
Osmoregulatory Flexibility

* Gene expression plasticity is not the whole story
* Evolutionary processes also important

Single Nucleotide Polymorphisms



Allele Frequency Differentiation Between Reefs Estimated with Fst



Genomic mean Fst across 79,660 SNPs = 0.0025 (minor allele freq. > 0.25)

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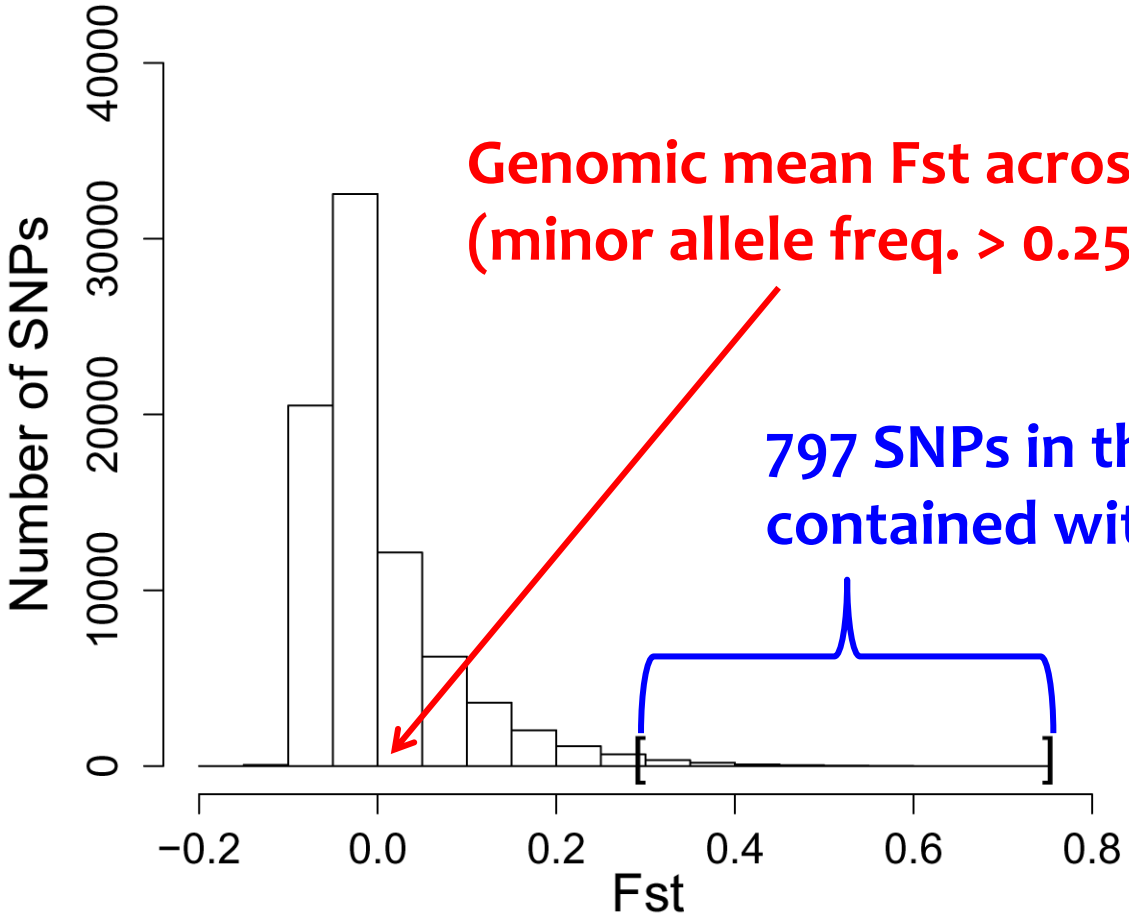


Genomic mean Fst across 79,660 SNPs = 0.0025 (minor allele freq. > 0.25)

797 SNPs in the top 1% of distribution, contained within 627 transcripts

Expectations with Directional Selection

* With strong selection for one sequence (allele) among many variant sequences at a locus, expect that locus to show:

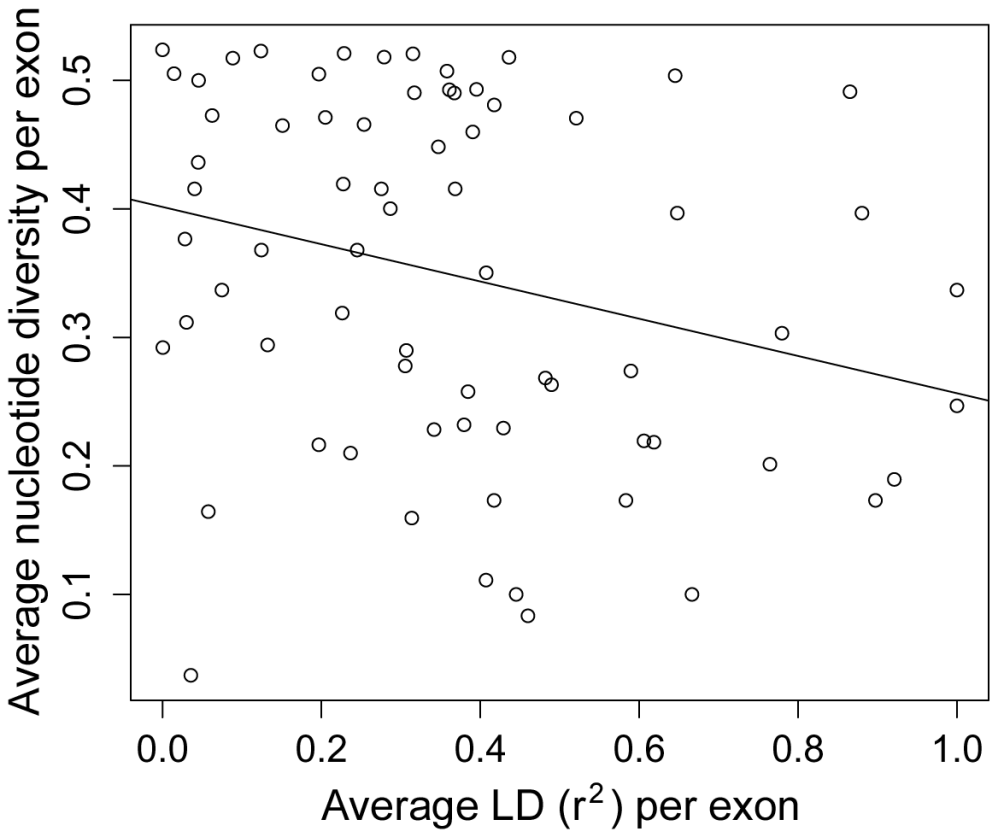
  - Reduced nucleotide diversity
    - Low-salinity reef mean = 0.34
    - High-salinity reef mean = 0.41
    - paired t-test, $p = 0.035$

Expectations with Directional Selection

* With strong selection for one sequence (allele) among many variant sequences at a locus, expect that locus to show:
  - Reduced nucleotide diversity
  - Elevated allele frequency correlations (linkage disequilibrium)

Signature of Selection
at Low Salinity Reef only

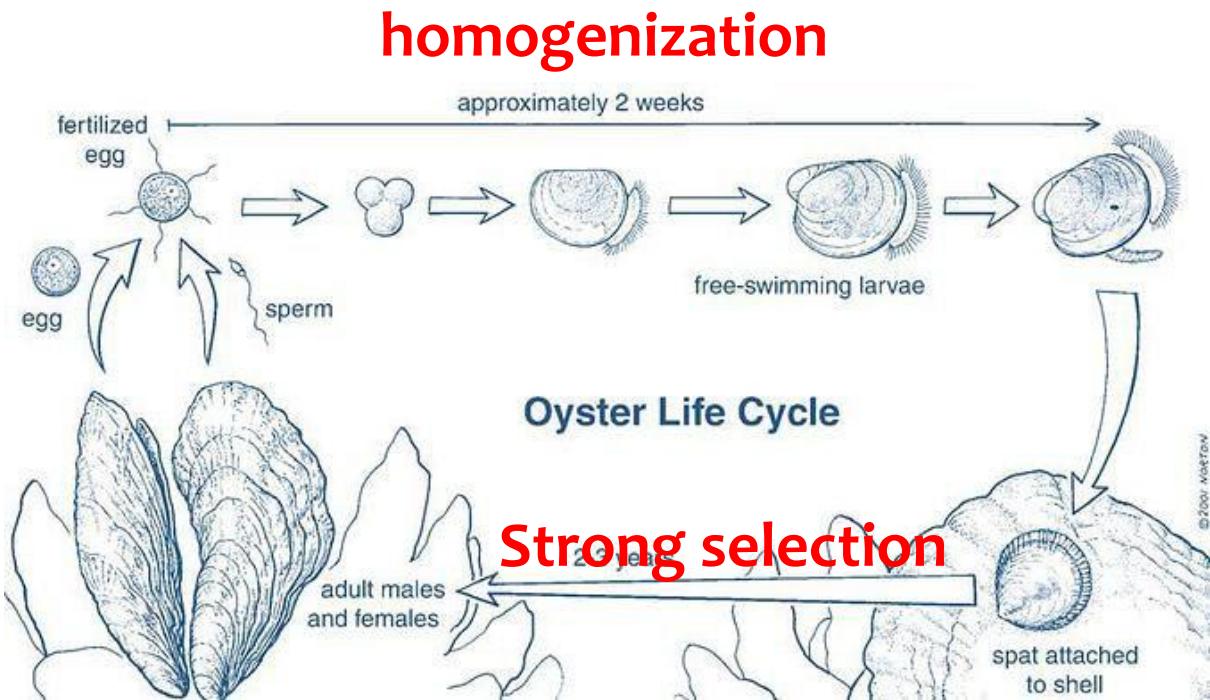
For 627 transcripts that contained one or more high-Fst SNPs:



Pearson correlation test, p=0.019

What is the timescale for this natural selection?

* Recurrent within-generation selection
  - Similar to patterns described for blue mussels and barnacles



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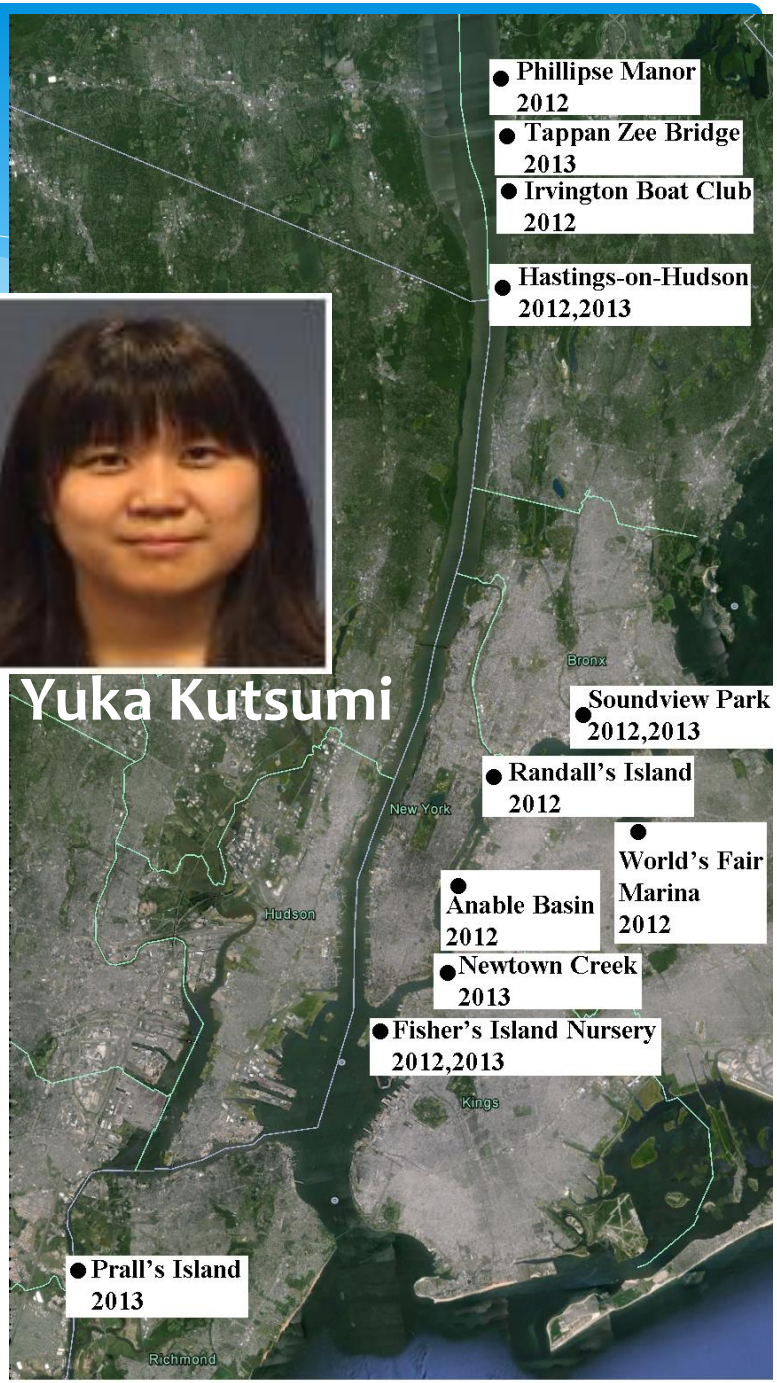
* Multigenerational Darwinian adaptation
  - Only likely if gene flow is limited
  - Biophysical larval tracking models suggest dispersal asymmetry
  - Quantitative genetic simulations ongoing to test these distinct mechanisms

HRE Oysters

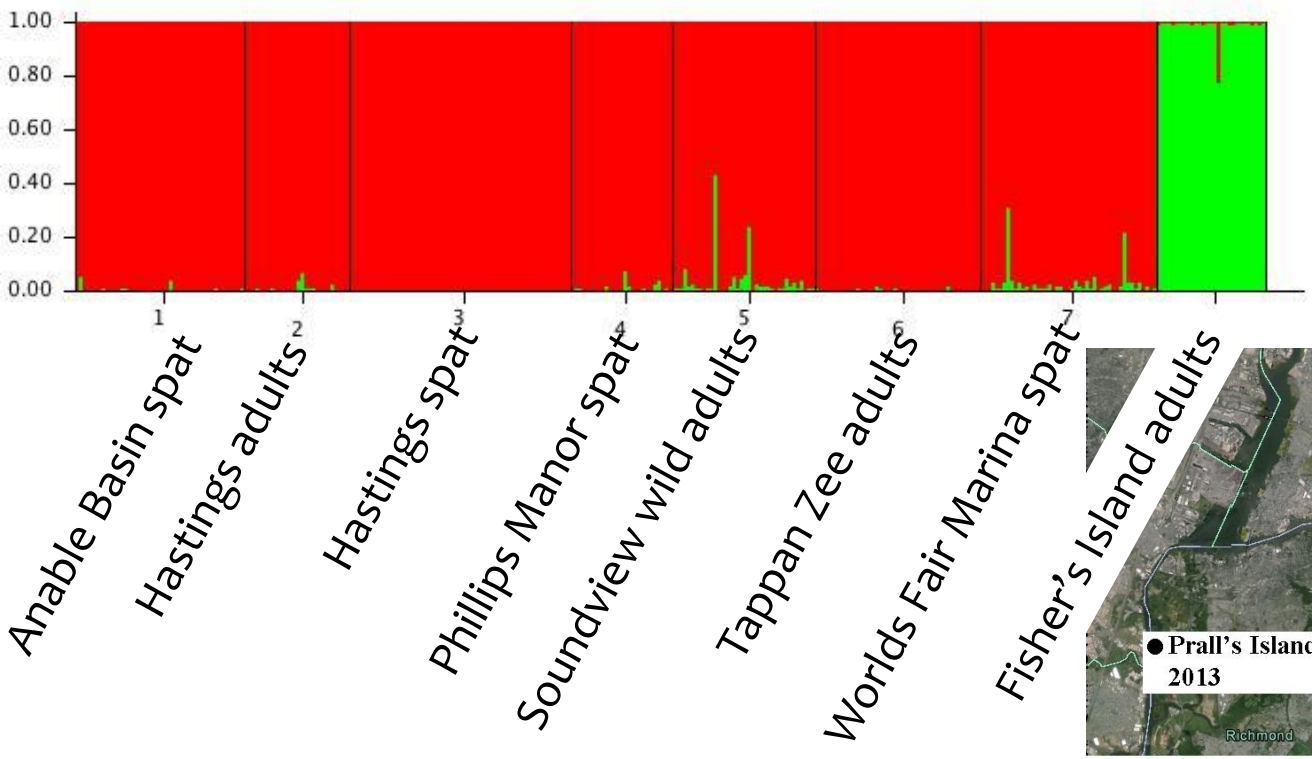
* 2012 and 2013 collections
* Spat and adults
* Thanks to
  - Jeff Levinton, Stonybrook U.
  - Paul Cooper, PrincetonHydro
  - NYCDPR (Pralls Island)
  - NY/NJ Baykeepers
  - NY oyster gardeners
  - HRF & ORRP

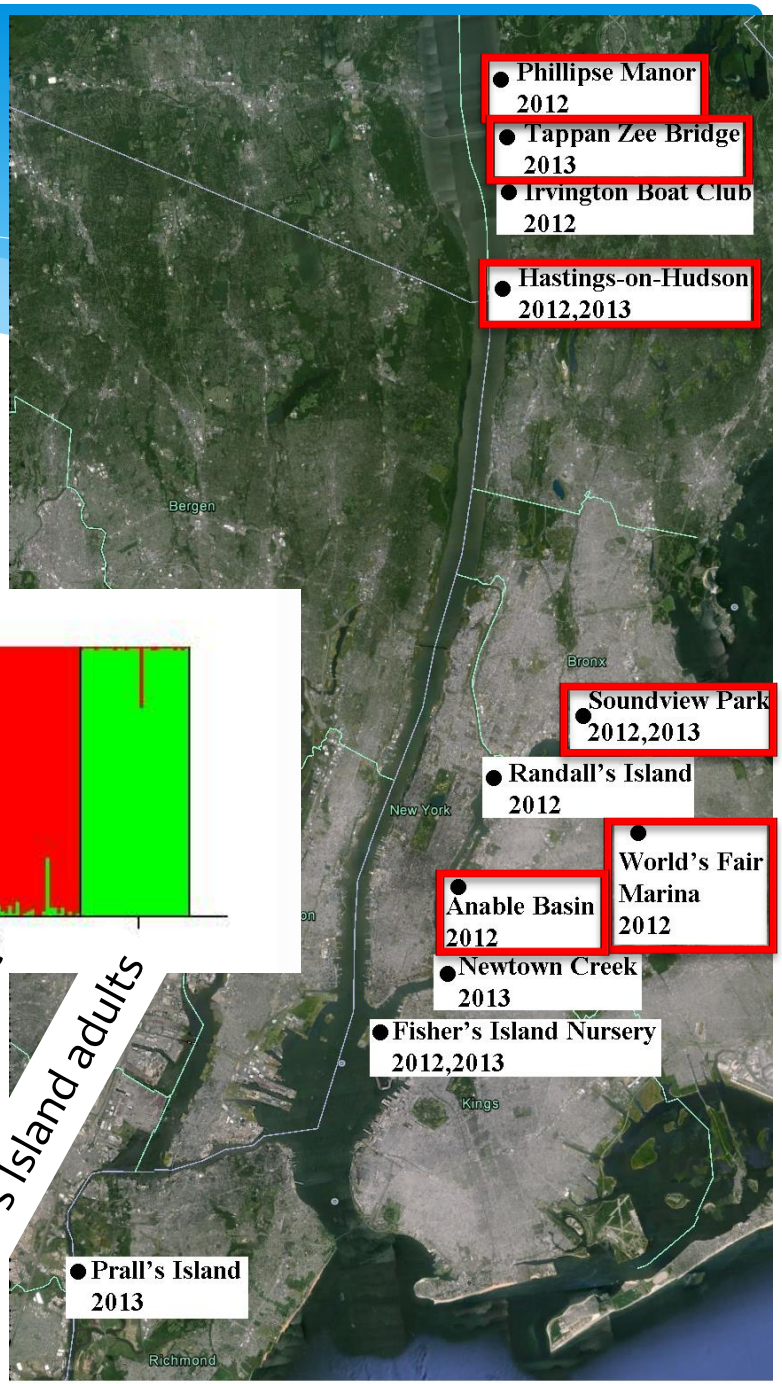
Yuka Kutsumi



Eight Microsatellite Markers, 2012 samples

- Bayesian assignment test clustering using STRUCTURE
- Best support for K=2 differentiated populations





Population Genomic Methods

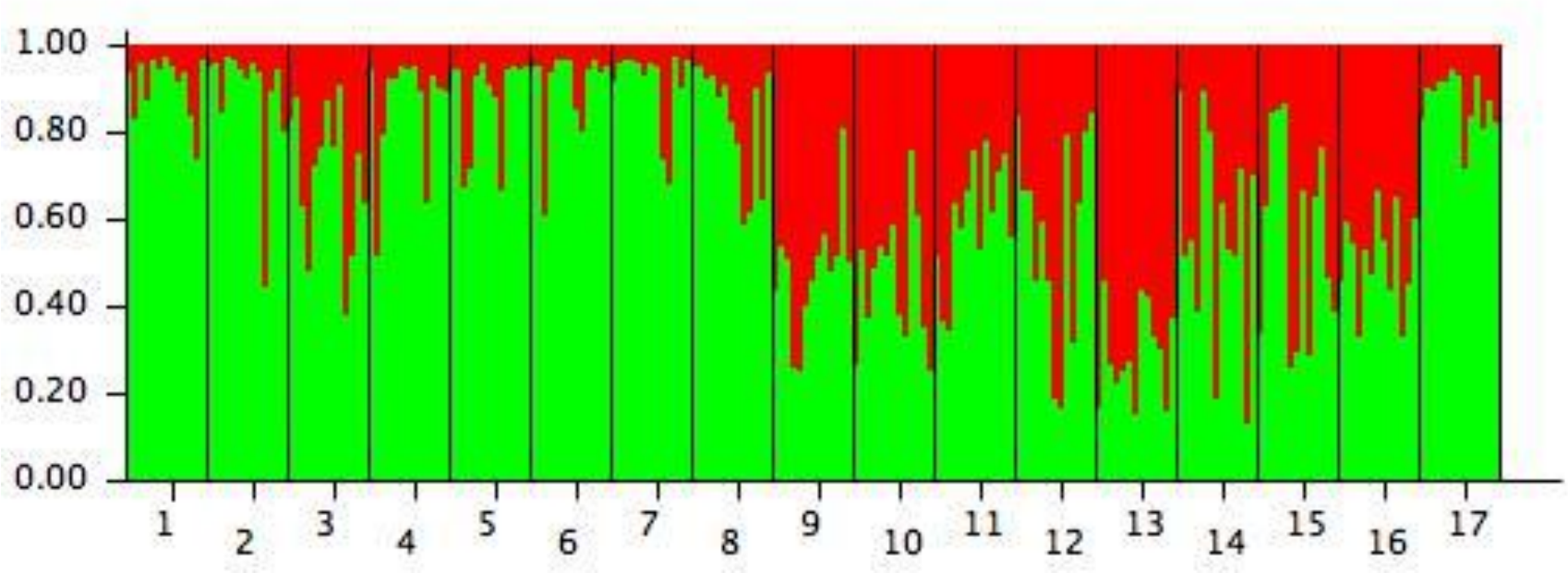
* Double-digest RADseq
  - Barcoded individuals
  - Single-end sequencing
  - 100 bp reads
* n = 13 – 24 per sample
* SNPs or haplotypes
* Filters:
  - 89 bp trimmed reads
  - No missing data
  - Minor allele freq. > 0.01

http://www.bayjournal.com/

Limited Connectivity?

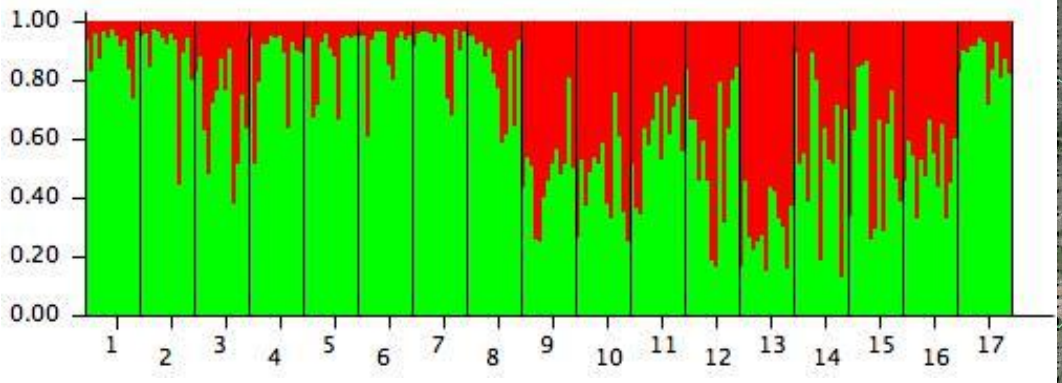
Wild oyster samples

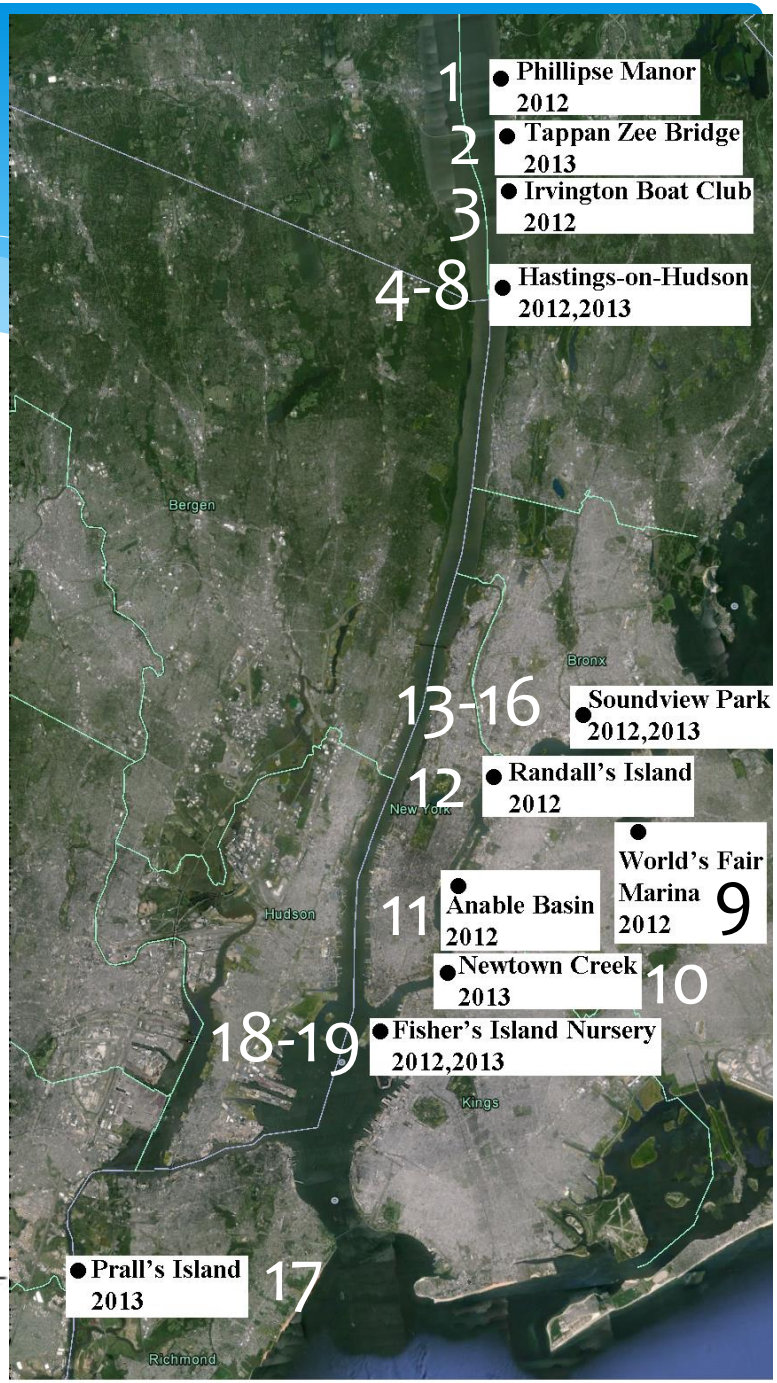
- n = 13 each, no missing data allowed at 430 loci
- Bayesian assignment test clustering using STRUCTURE
- Best support for K=2 differentiated populations



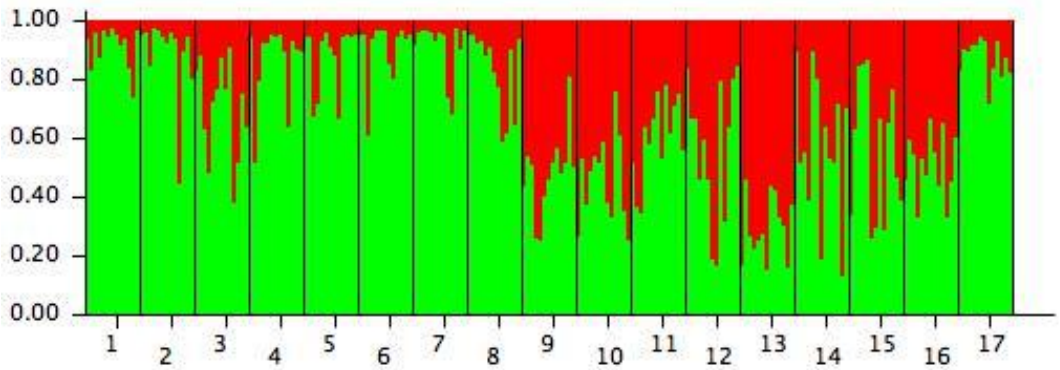
Limited Connectivity?

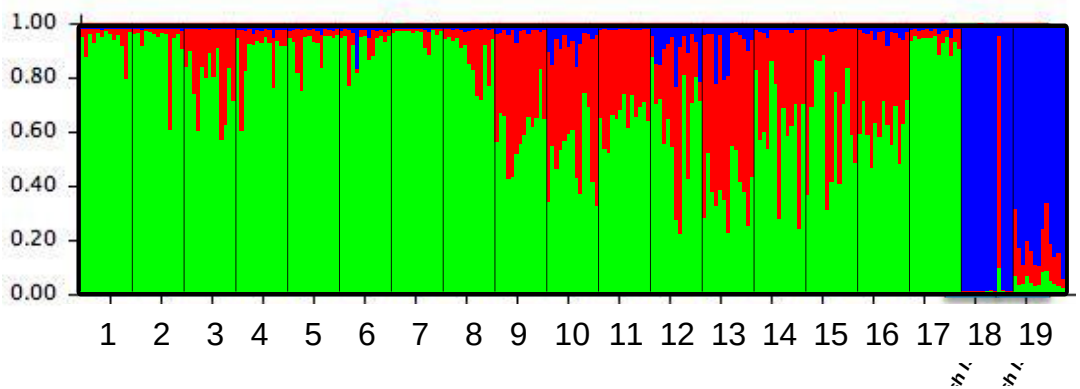
Upper Hudson and lower Hudson samples have different level of historical admixture

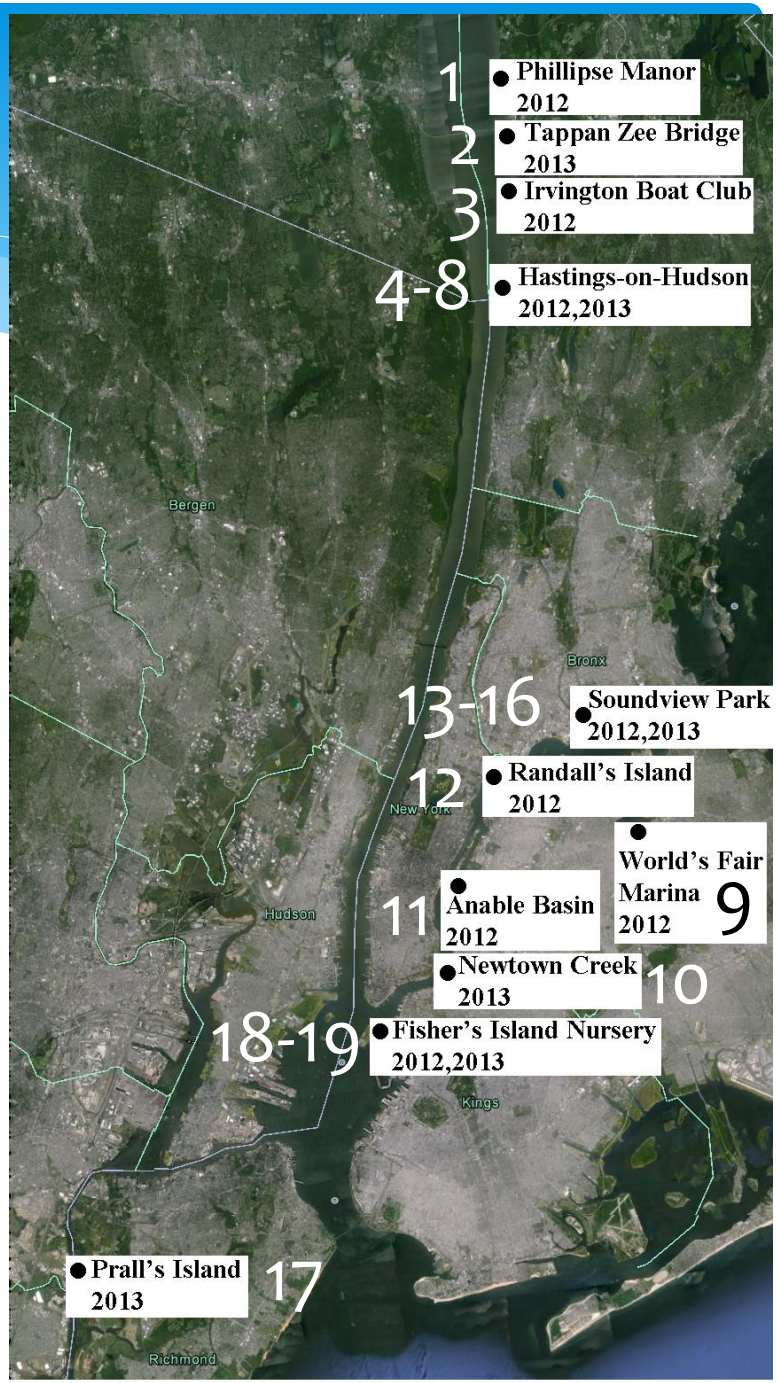




Fisher's Island Introgression?

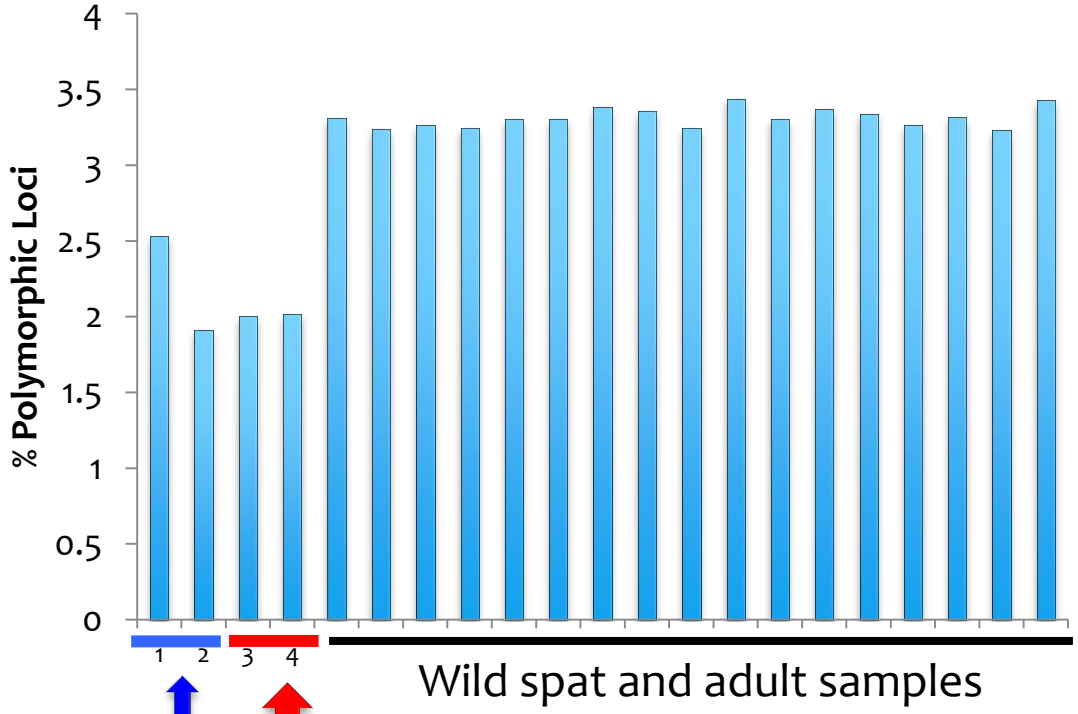






Does Hatchery Production Reduce Diversity?
Percent Polymorphic Loci

* N=13 individuals per sample
* 430 loci with *no missing data*



Wild broodstock cohort outplanted at 2 locations

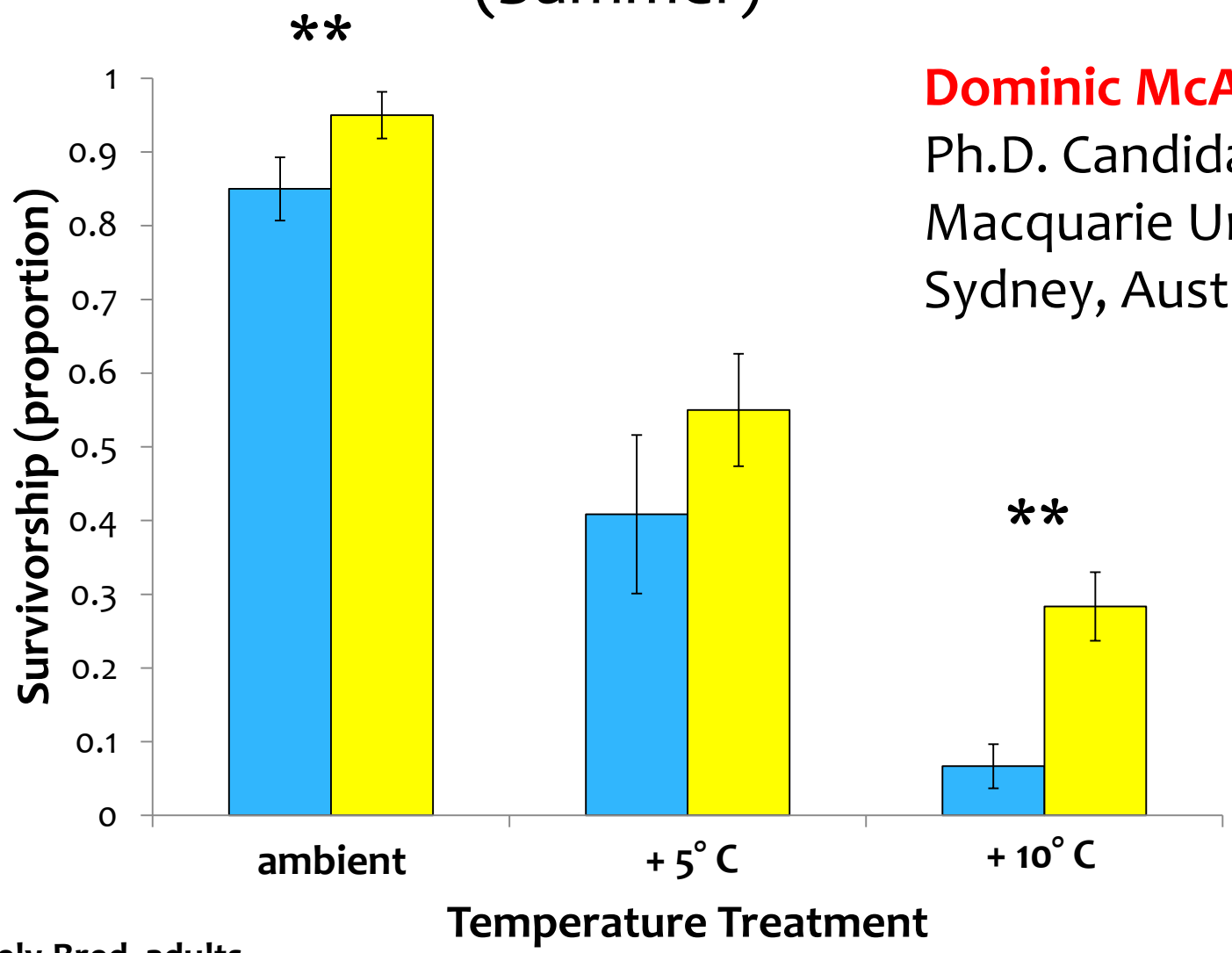
Fisher's Island

Where to Go from Here?

* Oyster performance comparisons
* Compare hatchery-produced and wild across diverse natural environments:
  - Growth rate
  - Survivorship
  - fecundity

Rock Oyster Survivorship after 3 months

(Summer)



Dominic McAfee
Ph.D. Candidate
Macquarie University
Sydney, Australia

** P < 0.05

Selectively Bred adults

Wild adults

Summary and Conclusions

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  - For gene expression, plasticity & evolutionary mechanisms both contribute to broad realized niche

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  - Yes in Hudson River, but don't know degree of isolation yet

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* How much does oyster population fitness depend on phenotypic plasticity vs. evolutionary mechanisms that depend on genetic diversity?
  - For gene expression, plasticity & evolutionary mechanisms both contribute to broad realized niche
* Is larval dispersal limited in the upstream direction, allowing some measure of local adaptation?
  - Yes in Hudson River, but don't know degree of isolation yet
* Do hatchery produced cohorts have reduced genetic diversity and if so, does it matter?
  - Bottlenecks, yes. We need tests of whether bottlenecked and 'specialist' oysters are less reliable for building sustainable reefs

Thanks

* Cornell University
  - Dr. Patrick Sullivan (statistics)
  - Research Assistants: Hilary Kates, Katie Kirk, Courtney Verscaj, Katie Wurtzell
  - Field work: Harmony Borchardt-Wier, Chaz Hyseni, Nils Wendel, Sarah Crestol,
  - Bioinformatics: Dr. Dan Ilut, Andrew Bange
* Haskin Shellfish Research Laboratory, Delaware Bay work
  - Dr. David Bushek and others
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  - NY Sea Grant
  - Cornell University
  - Atkinson Center for a Sustainable Future
  - Sigma Xi
  - Cornell Center for Comparative and Population Genomics

For this Talk:
Hudson River Foundation
Dominic McAfee
Hare Lab

Best Management Practices for Shellfish Restoration

Prepared for the ISSC Shellfish Restoration Committee

2011

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Kennedy et al. JSR 2011

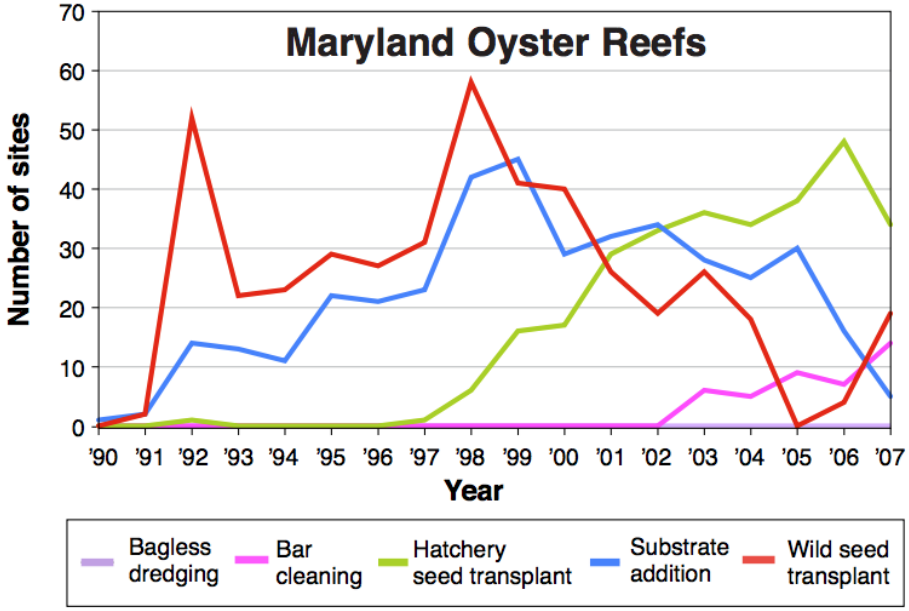

Figure 2. Number of sites that had a restoration activity in MD 1990-2007.

The Nature Conservancy

SAVING THE LAST GREAT PLACES ON EARTH

2012 update

EM SERVICES APPROACH

A PRACTITIONERS GUIDE TO THE

Design & Monitoring of Shellfish Restoration Projects

The Nature Conservancy
SAVING THE LAST GREAT PLACES ON EARTH

2012 update

A PRACTITIONERS GUIDE TO THE

Design & Monitoring of Shellfish Restoration Projects

* Recommendations (in recruitment-limited systems):
  - Transplant broodstock when possible
  - For hatchery-based stock enhancement use locally collected broodstock for spawning
  - Use pair-wise crosses of broodstock to maximize parental contributions, minimize genetic bottleneck
  - Characterize the genetics of broodstock and the hatchery-produced cohort