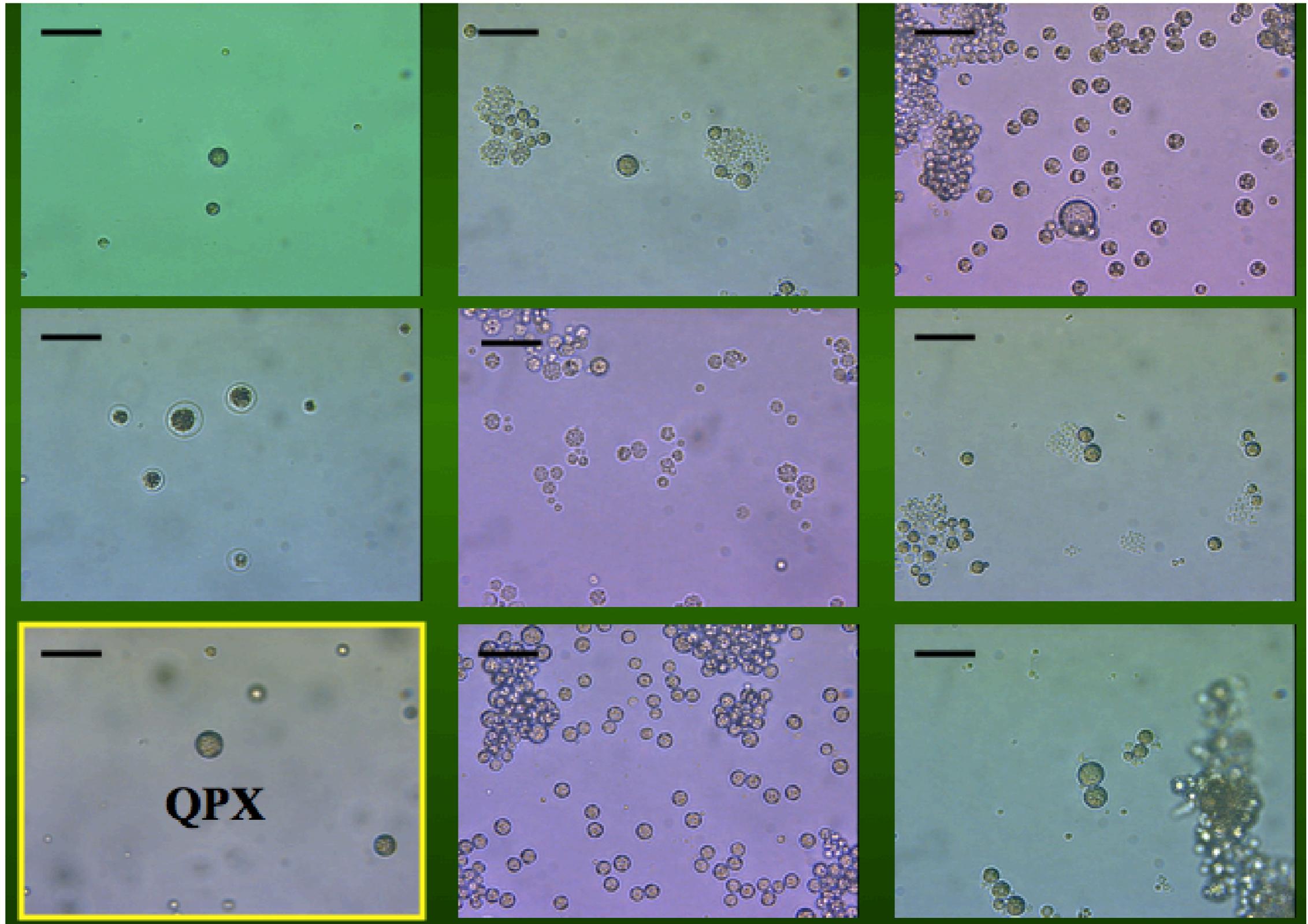


Labyrinthulids

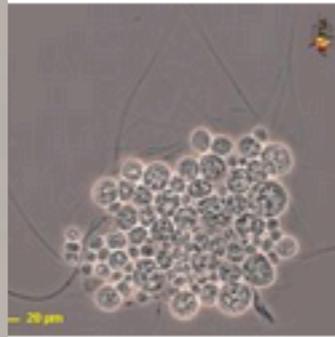




★★★★☆

TRUSTED

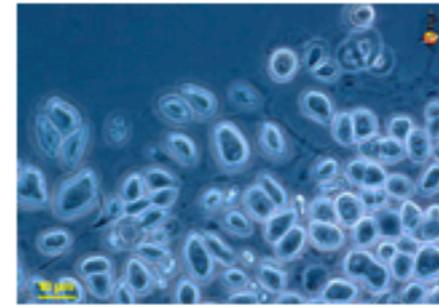
add to a collection



★★★★☆

TRUSTED

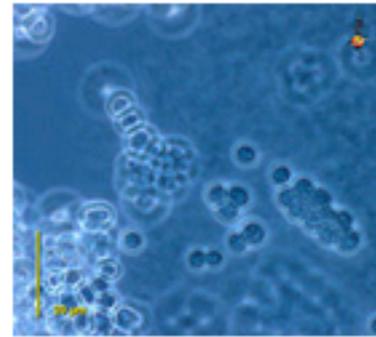
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★★★★☆

TRUSTED

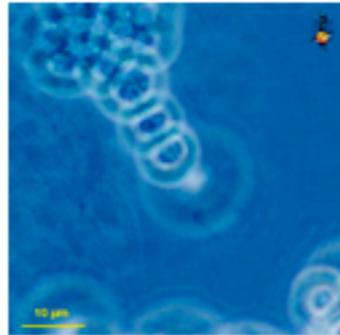
add to a collection



★★★★☆

TRUSTED

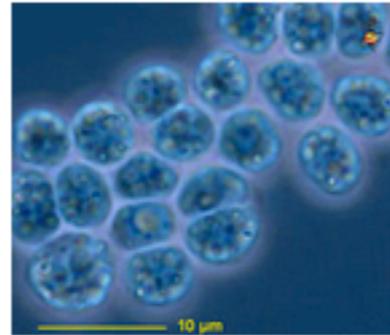
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★★★★☆

TRUSTED

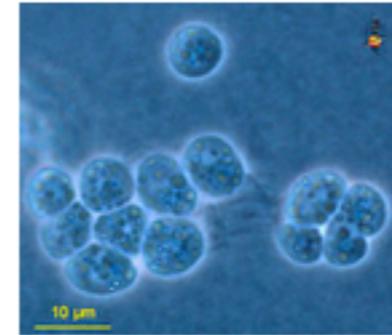
add to a collection



★★★★☆

TRUSTED

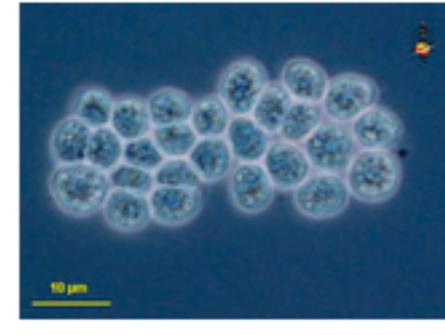
add to a collection



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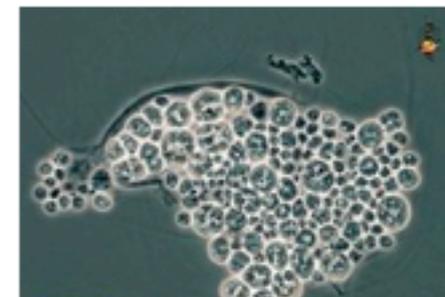
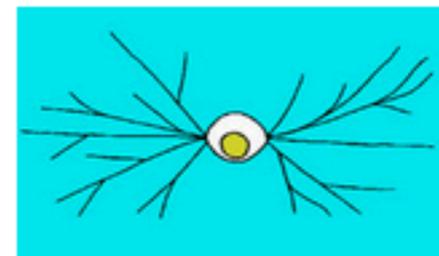
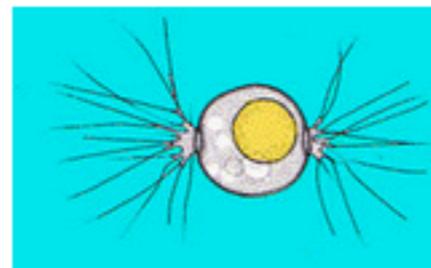
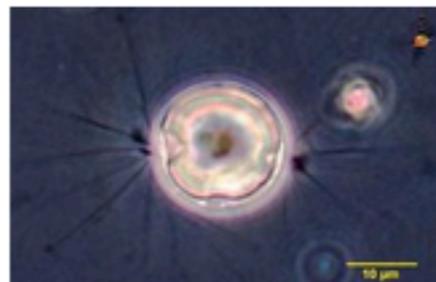
add to a collection



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add to a collection



Labyrinthulids

Labyrinthulidae (synonym labyrinthulid) is a family of mainly marine unicellular protists.

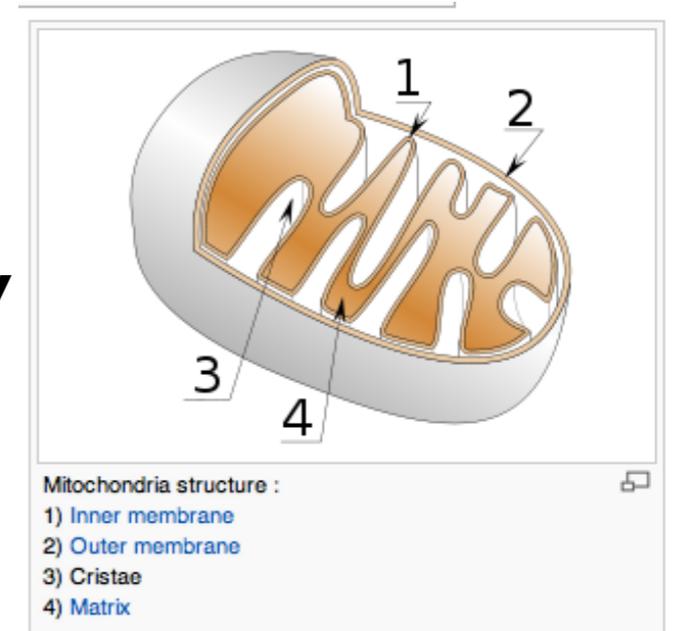
The labyrinthulids are characterized by tubulocristae mitochondria.

Members of the order Labyrinthulida were originally placed in the slime mould category, but their genetics demonstrate their relation to the stramenopiles.

Labyrinthulids

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ORDER Labyrinthulida

 [UniProtKB \(114\)](#) |  [Branch \(372\)](#) |  [Taxonomy help](#)

Taxon identifier	35131
Scientific name	Labyrinthulida
Common name	-
Synonym	-
Other names	<ul style="list-style-type: none">› Labyrinthomorpha› Labyrinthomorphids› Labyrinthulomorpha› Labyrinthulomycota› slime nets
Rank	ORDER
Lineage	<ul style="list-style-type: none">› cellular organisms› Eukaryota› stramenopiles
See also	<ul style="list-style-type: none">› NCBI

Taxonomy navigation

-  › [stramenopiles](#)
-  › [environmental samples](#)
- › [Labyrinthulidae](#)
- › [Thraustochytriidae](#)
- › [unclassified Labyrinthulida](#)

Thraustochytrid-like isolates from marine bivalve mollusks

DQ890358	<i>Crassostrea ariakensis</i>	China	visceral mass	<i>T. aureum</i>
DQ890359	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. caudivorum</i>
DQ890360	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. caudivorum</i>
DQ890361 ¹	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. aureum</i>
DQ890362 ²	<i>Mya arenaria</i>	Oregon	labial palps and gills	<i>T. aureum</i>
DQ890363	<i>Mya arenaria</i>	Oregon	labial palps and gills	<i>T. aureum</i>
DQ890364 ²	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. aureum</i>
DQ890365	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. aureum</i>
DQ890366	<i>Mya arenaria</i>	Oregon	labial palps and gills	<i>T. aureum</i> **
DQ890367	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. aureum</i> **
DQ890368	<i>Crassostrea virginica</i>	Chesapeake Bay	hemolymph	<i>T. aureum</i> **
DQ890369 ¹	<i>Crassostrea virginica</i>	Chesapeake Bay	hemolymph	<i>T. aureum</i>
DQ890370	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. aureum</i>
DQ890371	<i>Mya arenaria</i>	Oregon	labial palps and gills	<i>T. aureum</i>
DQ890373	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. aureum</i>
DQ890374	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>L. haliotidis</i>
DQ890375	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. caudivorum</i>
DQ890376	<i>Mya arenaria</i>	Oregon	labial palps and gills	<i>T. aureum</i>
DQ890377	<i>Mya arenaria</i>	Oregon	labial palps and gills	<i>T. aureum</i>

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DQ890374	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>L. haliotidis</i>
DQ890375	<i>Mercenaria mercenaria</i>	Virginia	mantle	<i>T. caudivorum</i>
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Thraustochytrid-like isolates from marine bivalve mollusks



Thraustochytrid-like isolates from marine bivalve mollusks

Maille Lyons, Christopher Dungan, Steven Roberts

INTRODUCTION

Interest in thraustochytrid biology, ecology, and systematics has resurfaced in recent years due to their elevated production of omega-3 fatty acids (Miller et al. 2007, Jain et al. 2007, Fan et al. 2008), their importance in marine microbial communities (Ramaiah et al. 2005, Bongiorno et al. 2005, 2008), and their role as pathogens of aquatic invertebrates (Anderson et al. 2003, Kvinge et al. 2007, Lyons et al. 2007, Scharer et al. 2007). As a group, thraustochytrids are unicellular, eukaryotic protists whose classification is not clear. They may be classified in either the kingdom Chromista (following Dick 2001 and Ragukumar 2002) or Chromista (if following Cavalier-Smith 1998, Cavalier-Smith et al. 1999, Smith et al. 1994). The corresponding phylum, class, order, and family designations are not consistent between the two classification systems. There are at least five genera of thraustochytrids

<http://goo.gl/a9x81>

Dynamics

Limnol. Oceanogr., 50(6), 2005, 1983–1988
© 2005, by the American Society of Limnology and Oceanography, Inc.

Lethal marine snow: Pathogen of bivalve mollusc concealed in marine aggregates

M. Maille Lyons and J. Evan Ward

Department of Marine Science, University of Connecticut, 1080 Shennecossett Rd., Groton, Connecticut 06340

Roxanna Smolowitz and Kevin R. Uhlinger

Marine Biological Laboratory, 7 MBL St., Woods Hole, Massachusetts

Rebecca J. Gast

Biology Department, Woods Hole Oceanographic Institution, Woods

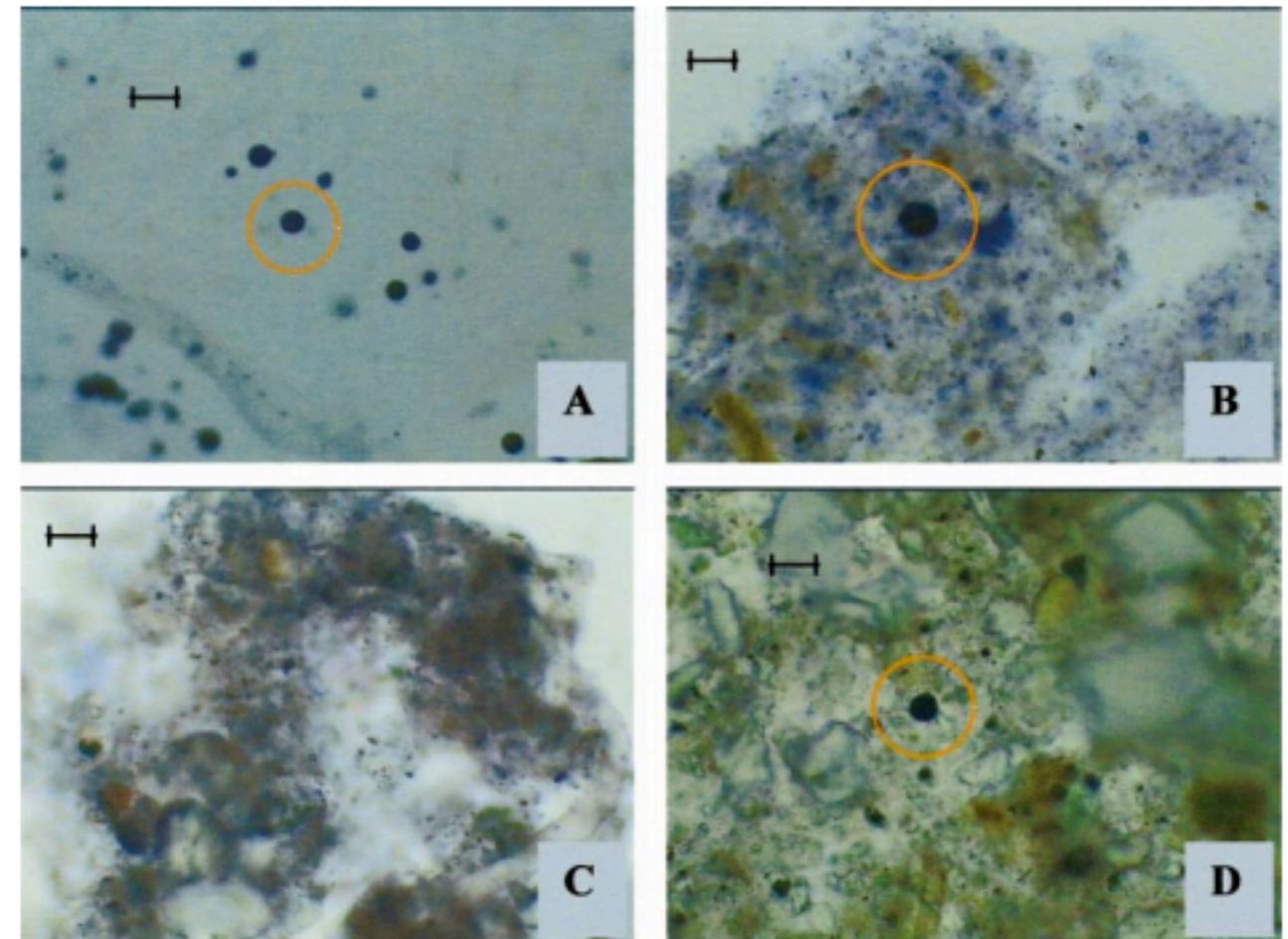
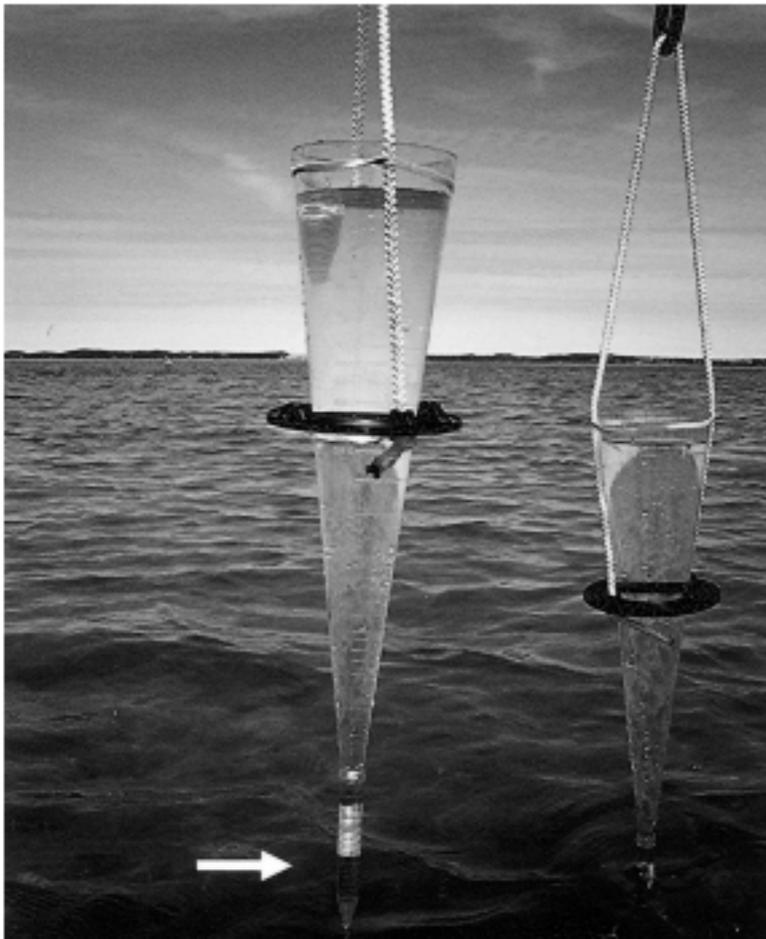
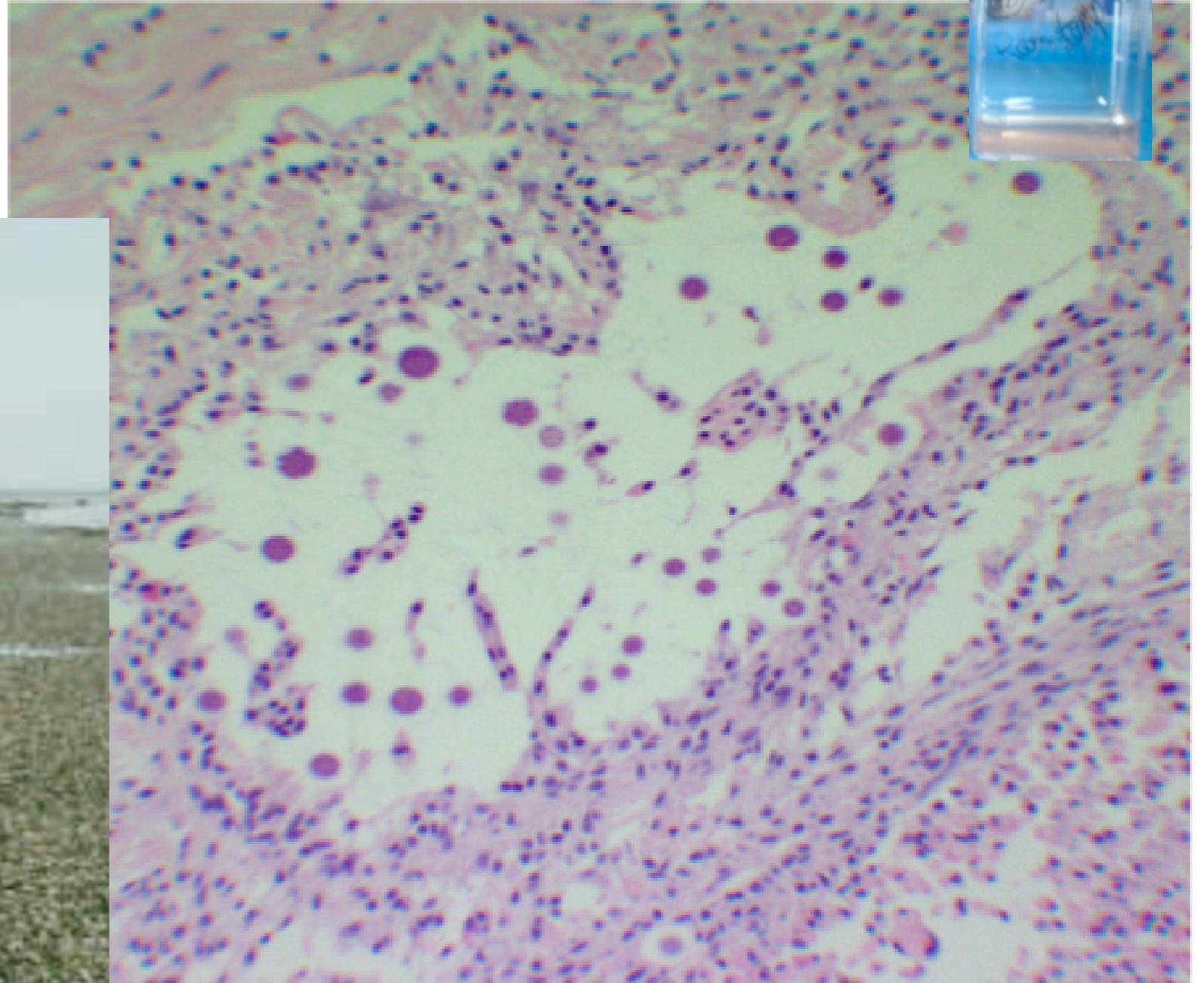


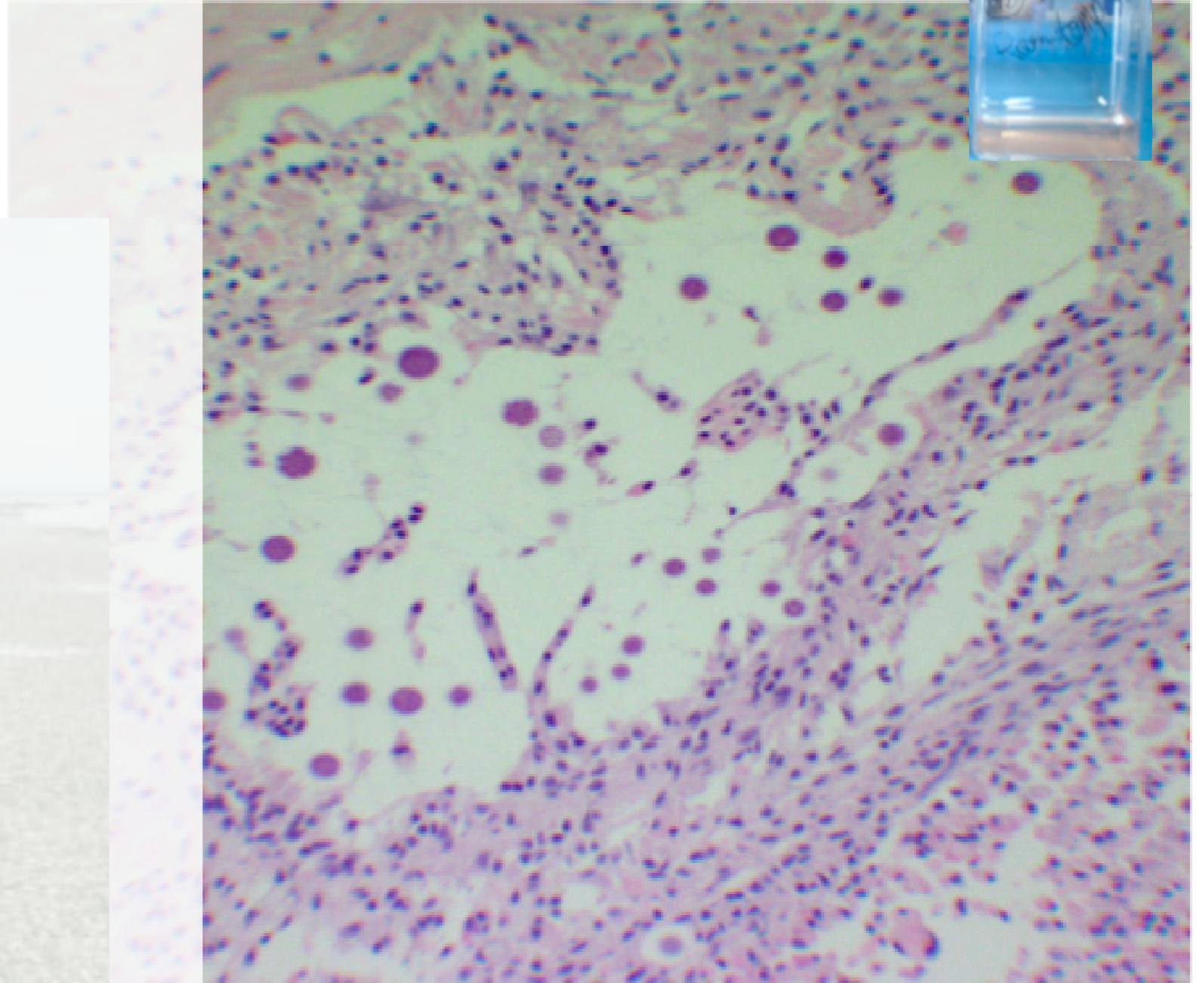
Fig. 2. Examples of in situ hybridization results for Quahog Parasite Unknown (QPX). (A) Positive results for QPX culture. (B) Positive results for laboratory-generated aggregates made with seawater and QPX culture (positive control). (C) Negative results for laboratory-generated aggregates made with seawater with no culture added (negative control; no dark round spheres present). (D) Positive results for natural aggregates collected near quahog beds infected with QPX. Each darkly stained sphere within a red circle is one QPX thallus. Scale bars, 25 μm .

QPX



Roxanna Smolowitz

QPX



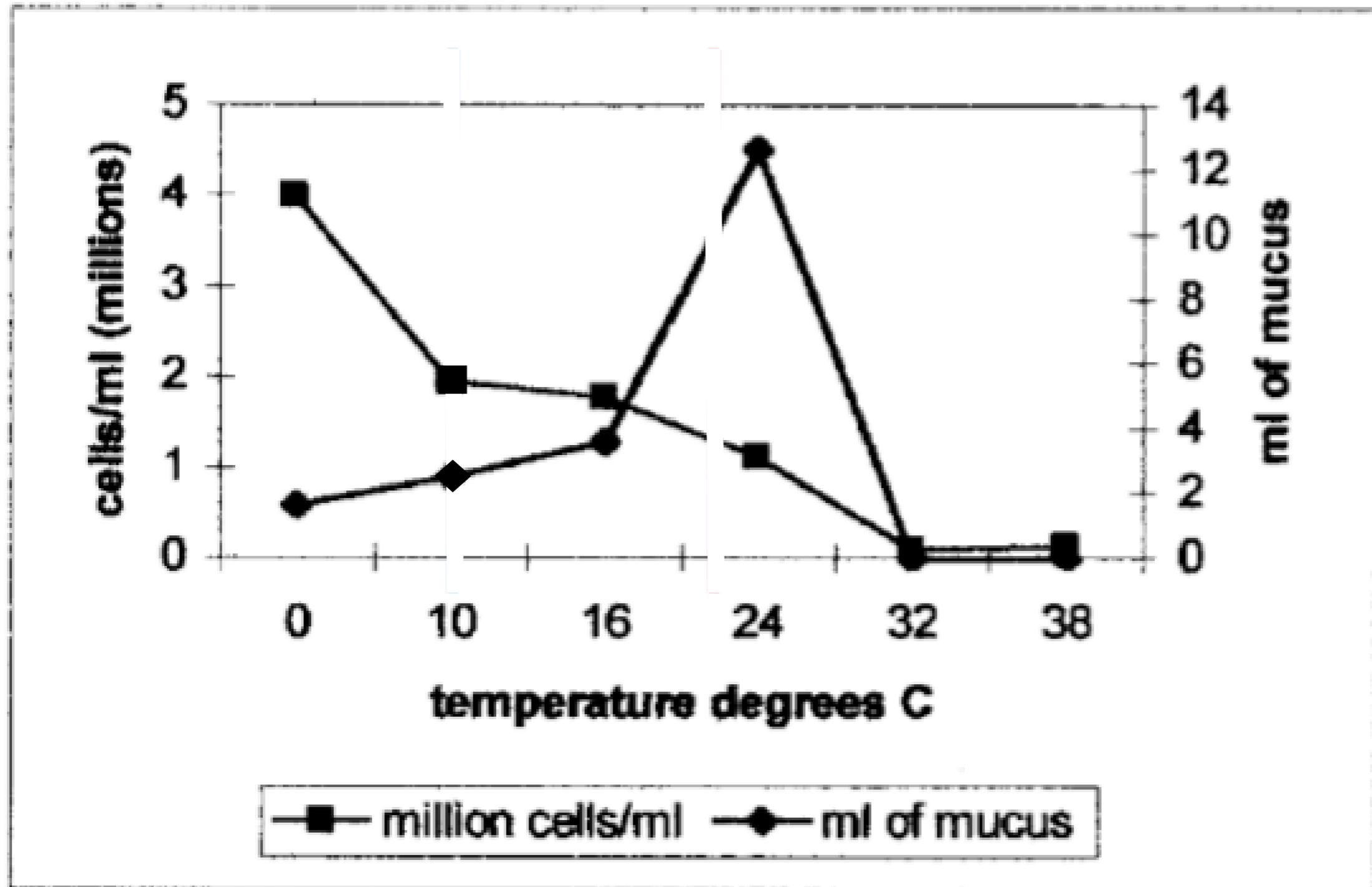
QPX

- Single-celled relative of slime mold that has both animal and fungal characteristics
- QPX secretes a thick layer of mucus to ward off the clam's immune response
- Killing nine out of every ten clams in some plots when it first hit the Massachusetts coast in 1993



Captain Andrew Cummings stands atop clams he and others dug out of their Wellfleet plots to quell a QPX outbreak last winter. Cummings estimated the removal claimed nearly 2 million clams. (Photo courtesy of Captain Andrew Cummings)

QPX Biology



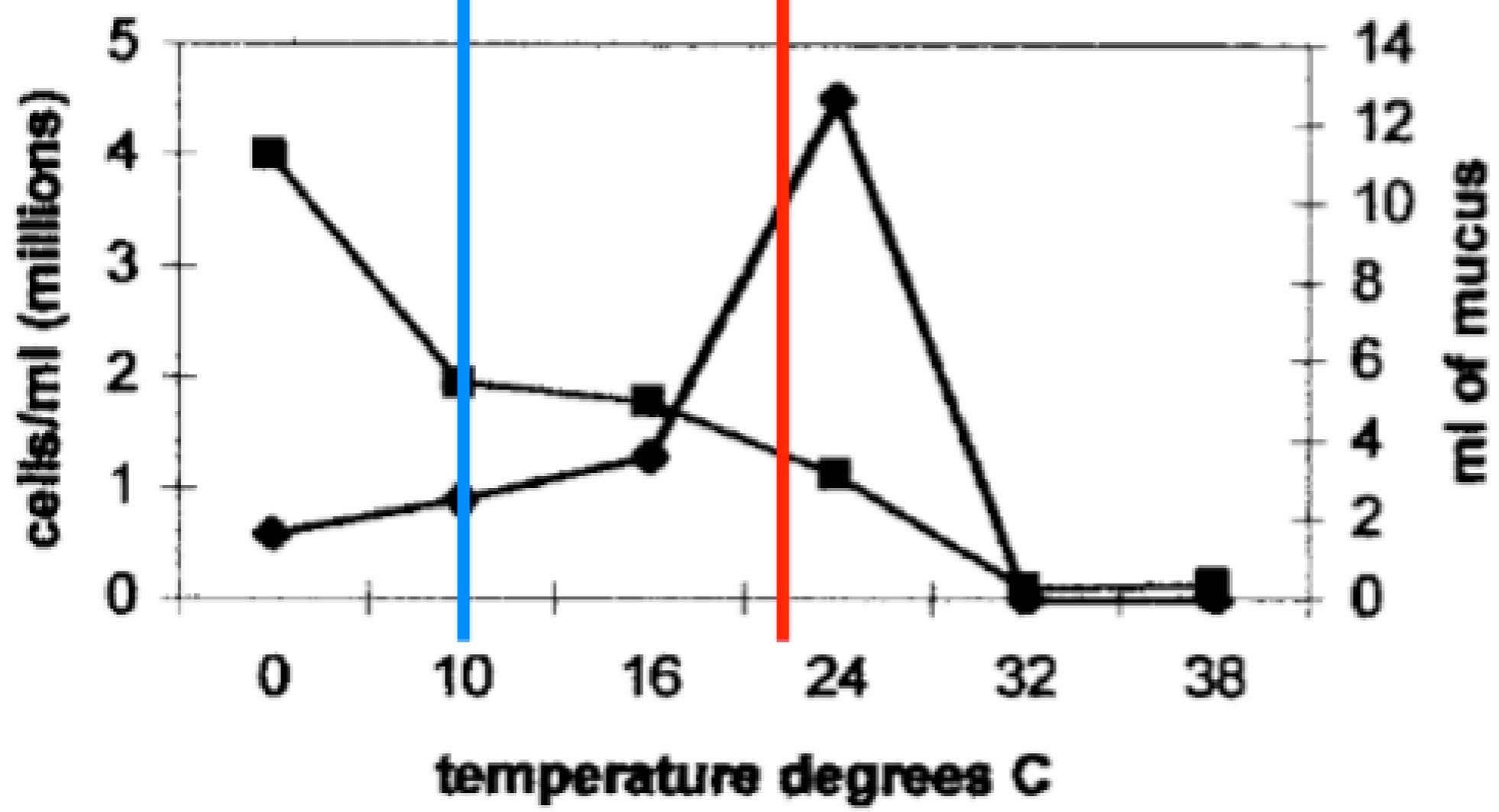
An Experiment

Rationale

- Understand more concerning **QPX** physiology
 - Environmental influence
 - Differences across strain
 - Pathogenecity

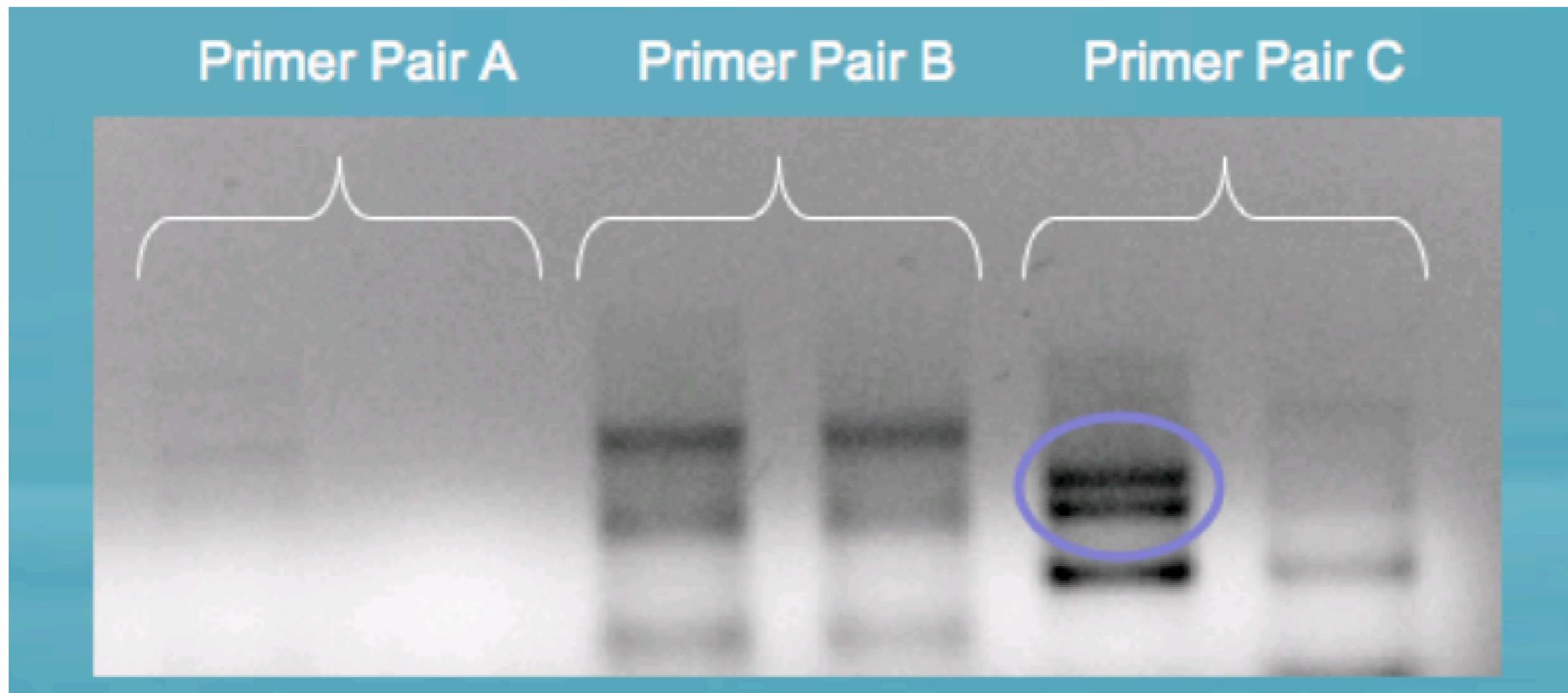
Factors

- Temperature
- Strain



■ million cells/ml ◆ ml of mucus

Differential Display



QPX Serine Protease

Top Blastx Hit	Species associated with	e-value	% similar
Glutathione-dependent formaldehyde-activating	<i>Ralstonia metallidurans</i>	1.00E-04	45
Subtilisin-like serine protease pepC precursor	<i>Aspergillus niger</i>	2.00E-16	63
Permeases of the major facilitator superfamily	<i>Yersinia frederiksenii</i>	0.66	47
40s ribosomal protein s23	<i>Theileria annulata</i>	9.00E-38	96
ATP-binding cassette / transporter, sub-family G,	<i>Toxoplasma gondii</i>	4.00E-25	60
mitogen-activated protein kinase	<i>Pan troglodytes</i>	3.30E+00	46
Multidrug Resistance Protein family member (mrp)	<i>Caenorhabditis elegans</i>	3.00E-14	66
mitogen-activated protein kinase 2	<i>Toxoplasma gondii</i>	1.00E-12	84
haemagglutinin repeat protein	<i>Pseudomonas fluorescens</i>	2.70E+00	52
polysaccharide biosynthesis protein	<i>Methylococcus capsulatus</i>	4.30E+00	47
<u>Potassium inwardly-rectifying channel</u>	<i>Homo sapiens</i>	1.00E-07	55

Proteases

- Critical factor in disease pathogenesis
- Serine proteases produced by pathogen
 - Facilitate penetration
 - Stimulate degradation of host proteins involved in immune defense

Current
Microbiology

Alkaline Serine Protease Is an Exotoxin of *Vibrio alginolyticus* in Kuruma Prawn, *Penaeus japonicus*

EFFECT OF HOMOGENATE FROM DIFFERENT OYSTER SPECIES ON [PERKINSUS MARINUS](#) PROLIFERATION AND SUBTILISIN GENE TRANSCRIPTION

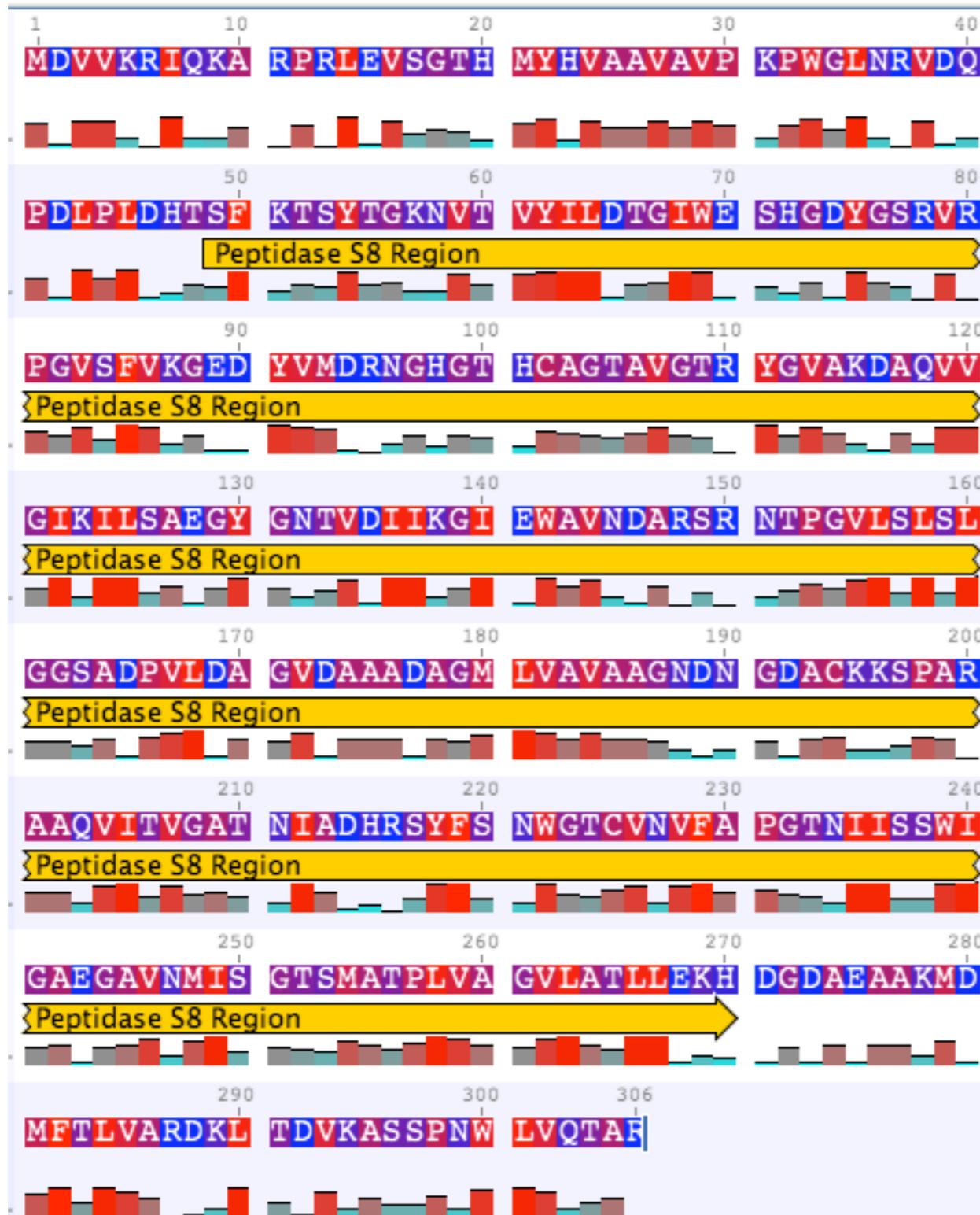
GWYNNE D. BROWN, STEPHEN L. KAATTARI, and KIMBERLY S. REECE*

Production of proteinase during experimental infection of *Ostrea edulis* L. larvae with *Vibrio alginolyticus* NCMB 1339 and the antigenic relationship between proteinases produced by marine vibrios pathogenic for fish and shellfish

A. S. NOTTAGE¹ T. H. BIRKBECK¹

¹Department of Microbiology, University of Glasgow, Scotland

Complete Protein



Length: 306

Frequencies:

A:	38	(12.4%)
C:	3	(01.0%)
D:	23	(07.5%)
E:	8	(02.6%)
F:	5	(01.6%)
G:	32	(10.5%)
H:	8	(02.6%)
I:	14	(04.6%)
K:	15	(04.9%)
L:	18	(05.9%)
M:	8	(02.6%)
N:	14	(04.6%)
P:	12	(03.9%)
Q:	5	(01.6%)
R:	14	(04.6%)
S:	20	(06.5%)
T:	21	(06.9%)
V:	34	(11.1%)
W:	6	(02.0%)
Y:	8	(02.6%)

Sequence Analysis

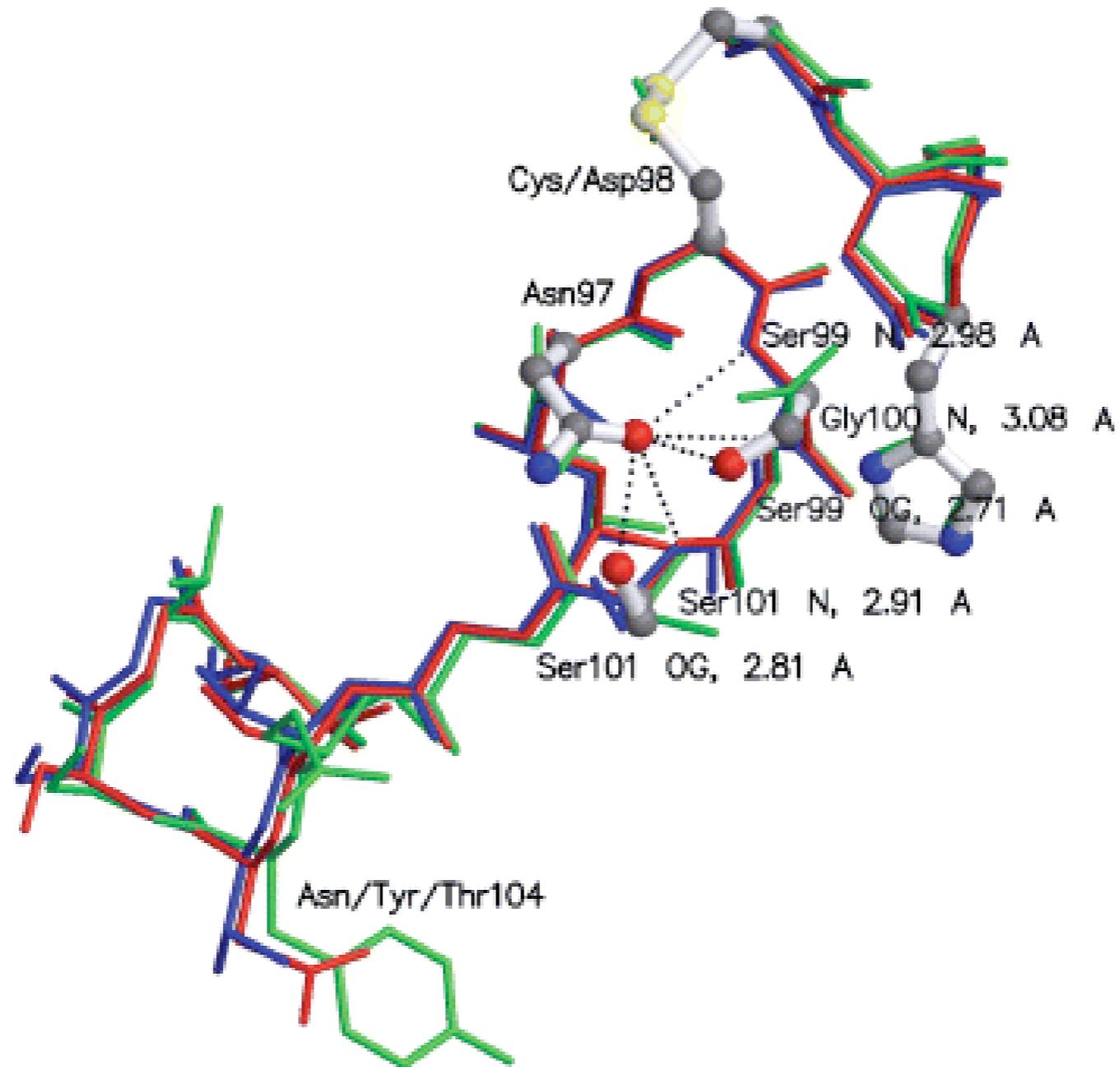
Putative conserved domains have been detected, click on the image below for detailed results.



- Subtilase family.
- Subtilases are a family of serine proteases.
- They appear to have independently and convergently evolved a catalytic triad
 - *the three amino acid residues found inside the active site of certain protease enzymes: serine (S), aspartate (D) and histidine (H). They work together to break peptide bonds on polypeptides.*
- Structure is an alpha/beta fold containing a 7-stranded parallel beta sheet.

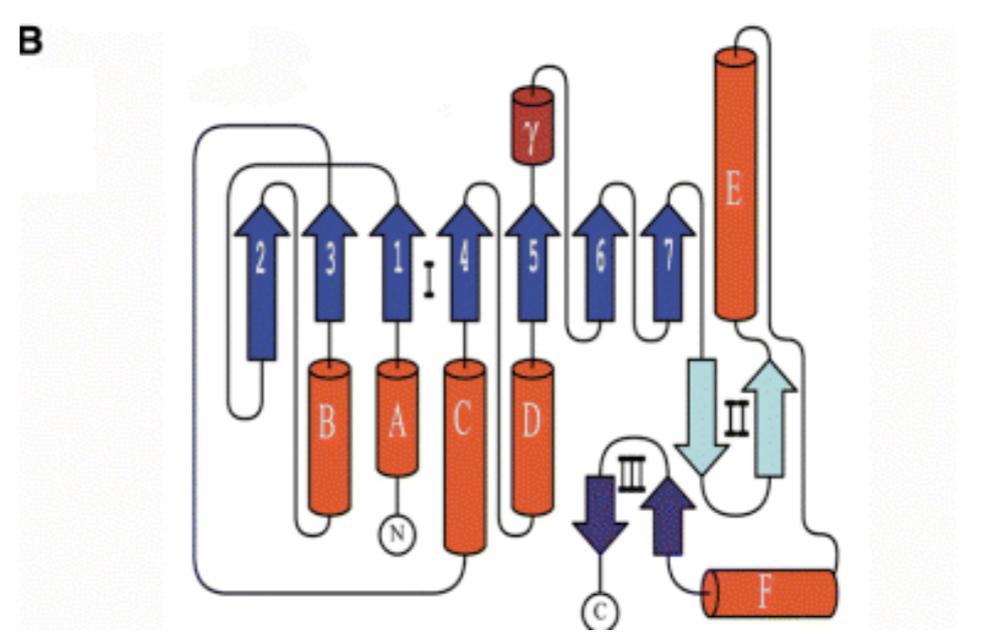
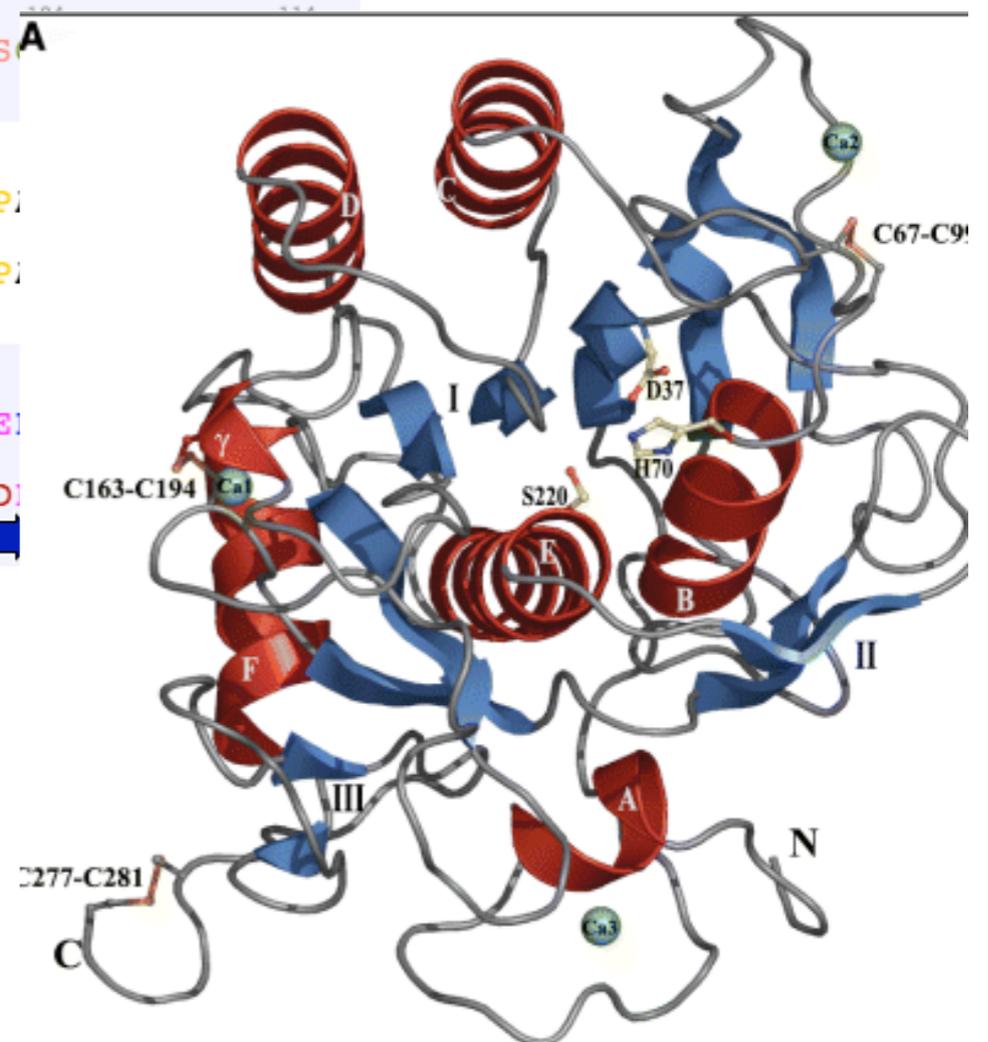
The 1.8 Å crystal structure of a proteinase K-like enzyme from a psychrotroph *Serratia* species

Ronny Helland¹, Atle Noralf Larsen², Arne Oskar Smalås^{1,3} and Nils Peder Willassen^{1,2}

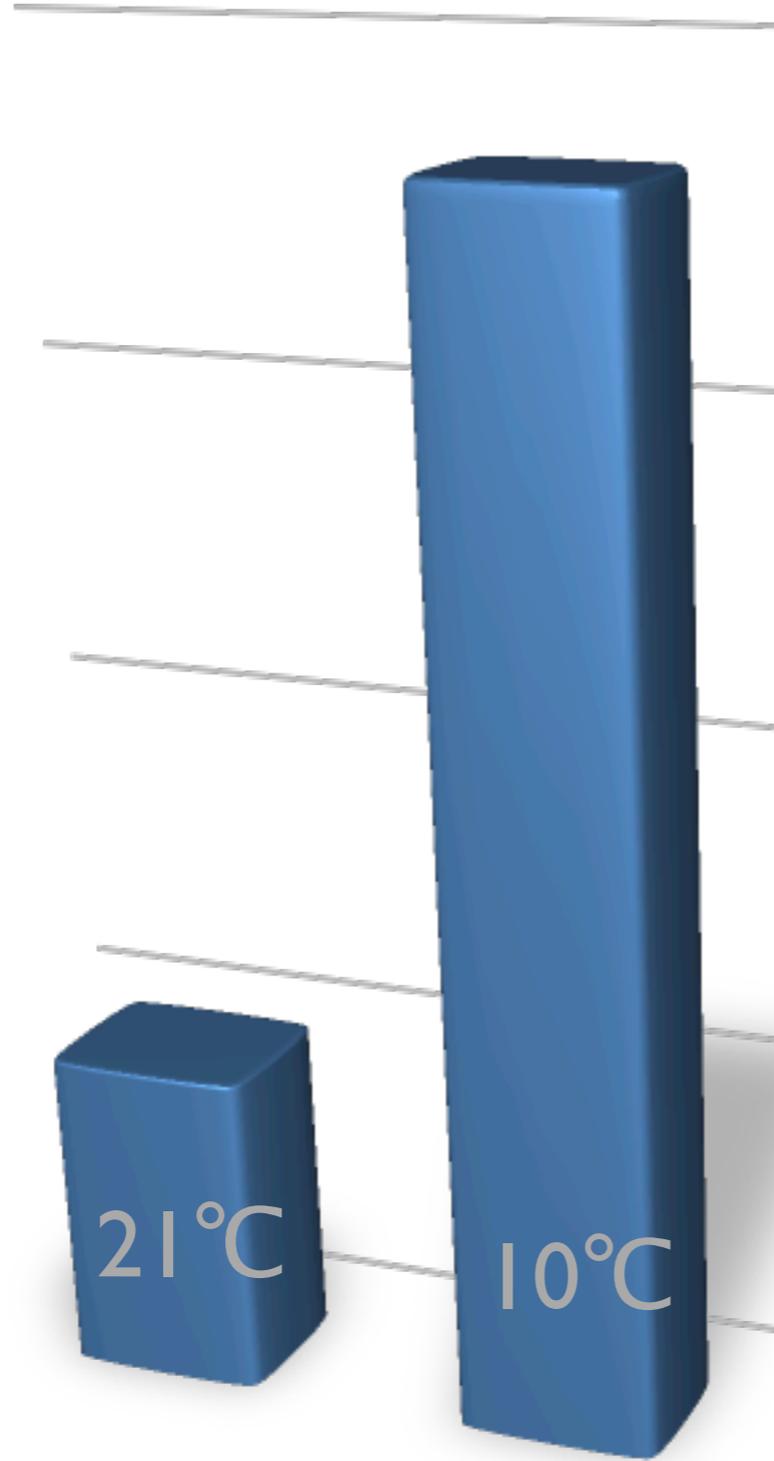


Asp/Ser/His Catalytic Triad



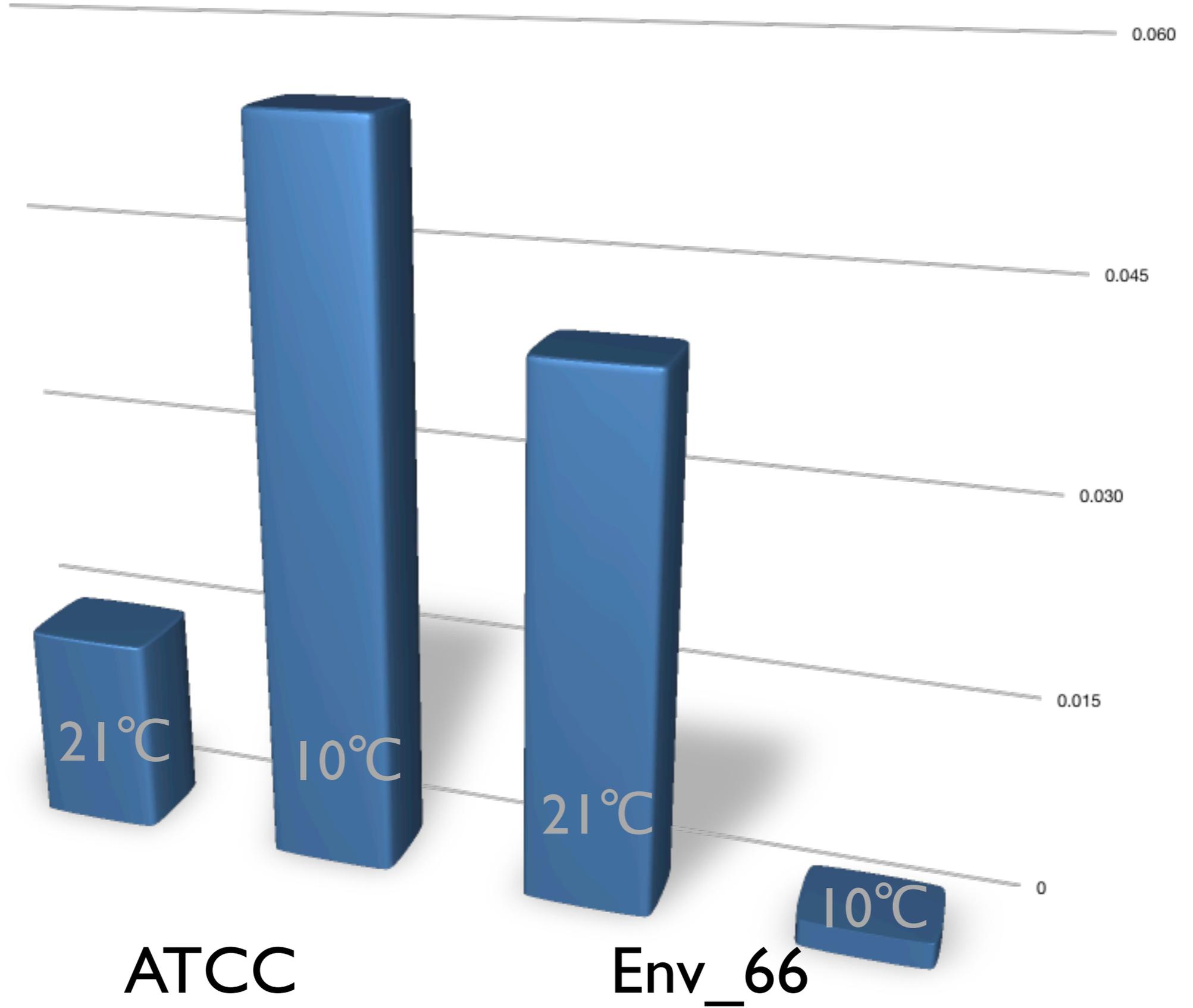


Serine Protease gene expression



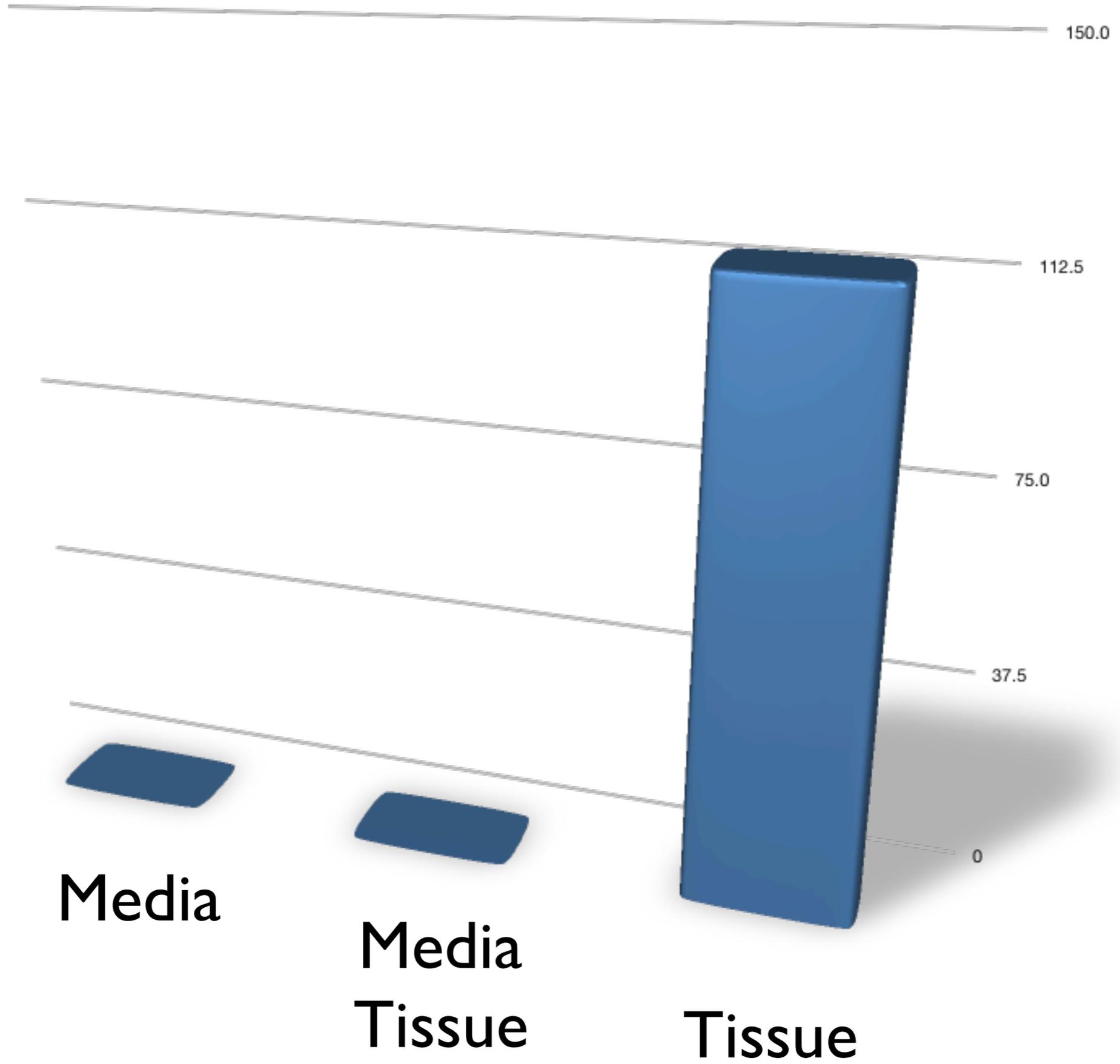
ATCC

Serine Protease gene expression



Serine Protease gene expression

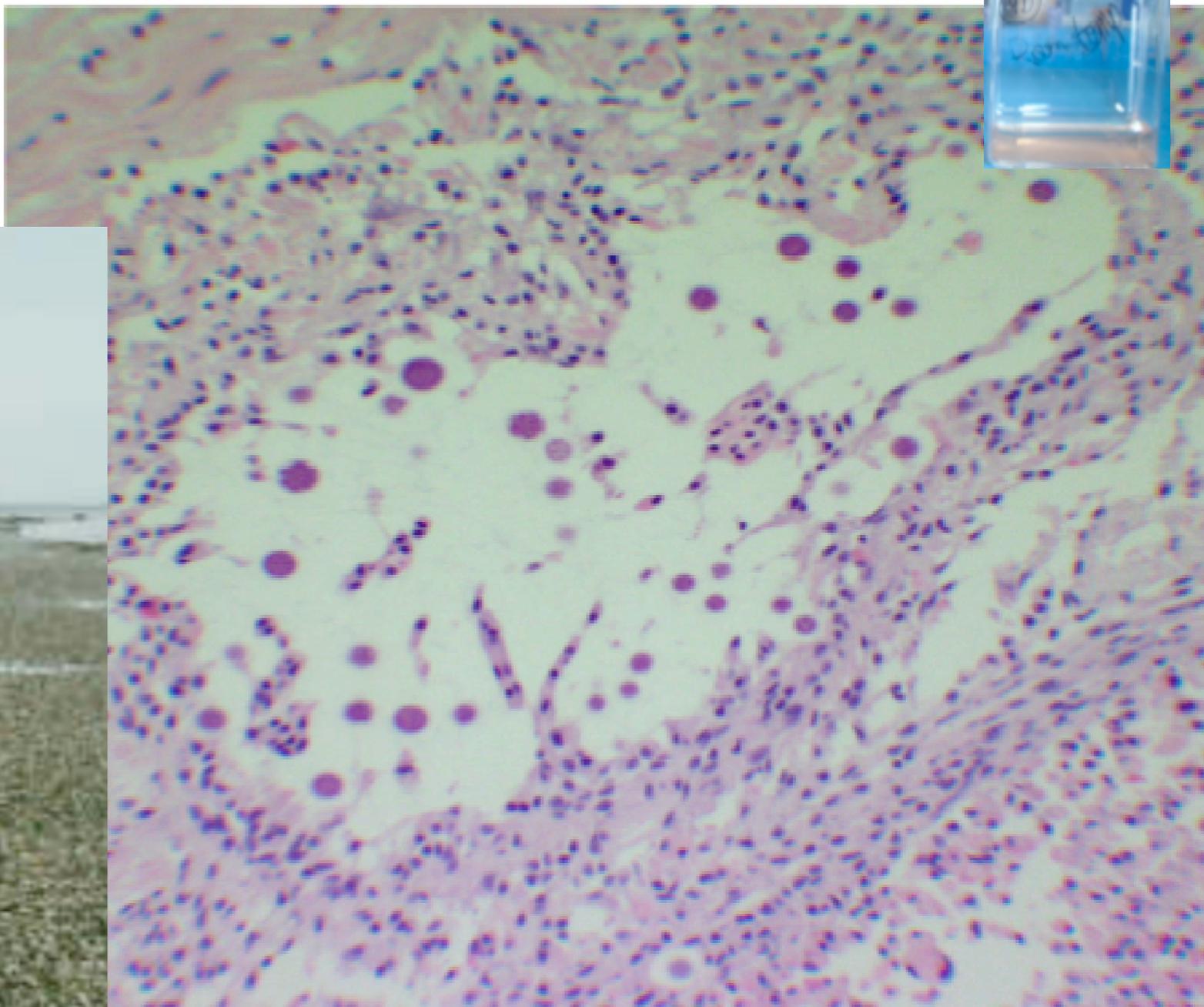
21°C



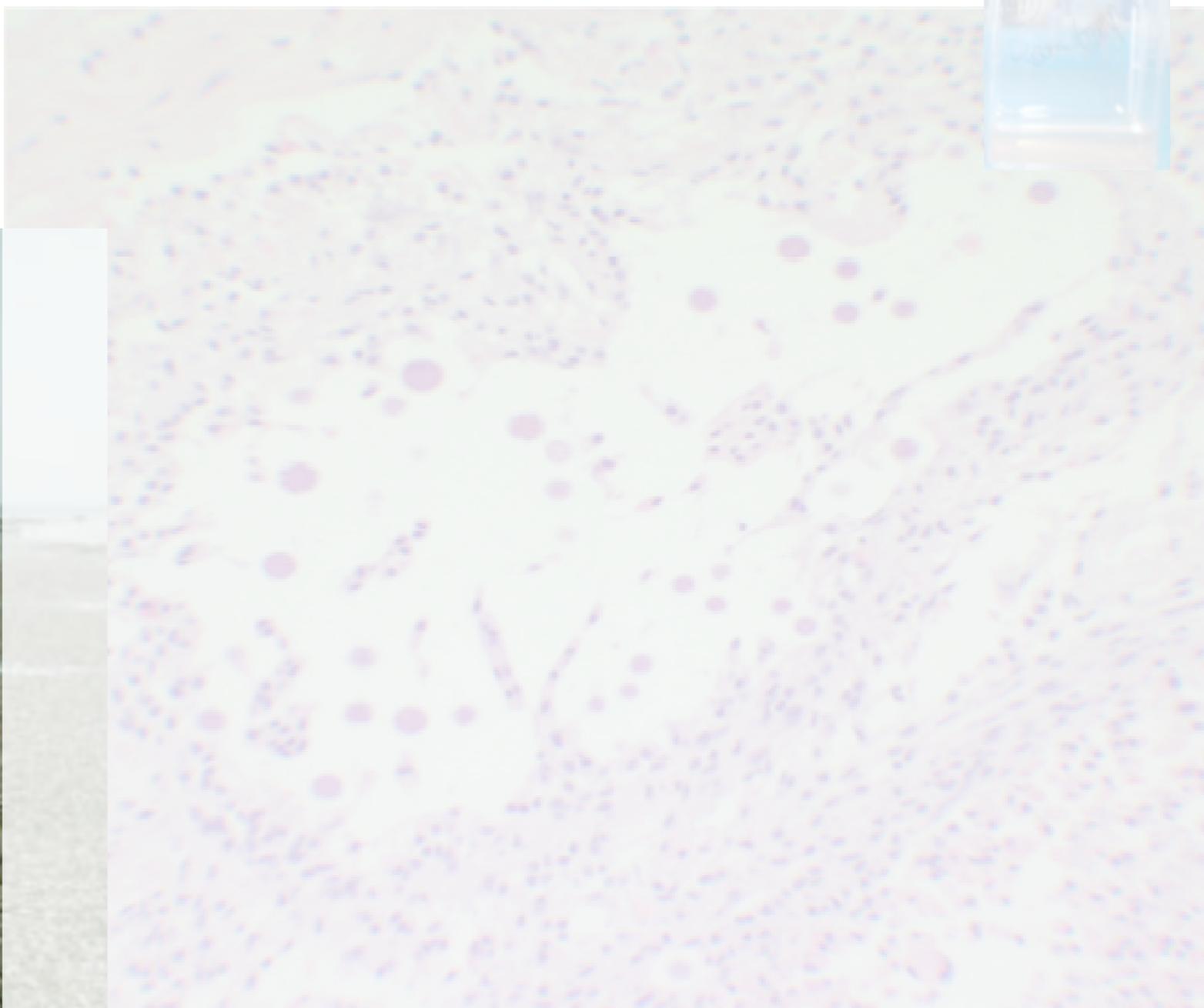
Summary

- Complete CDS of Subtilisin-like serine protease
 - Catalytic Triad
- Expression varies across strains
 - temperature dependent
- Significantly upregulated when in contact with host tissue

Another experiment



Roxanna Smolowitz



Rationale

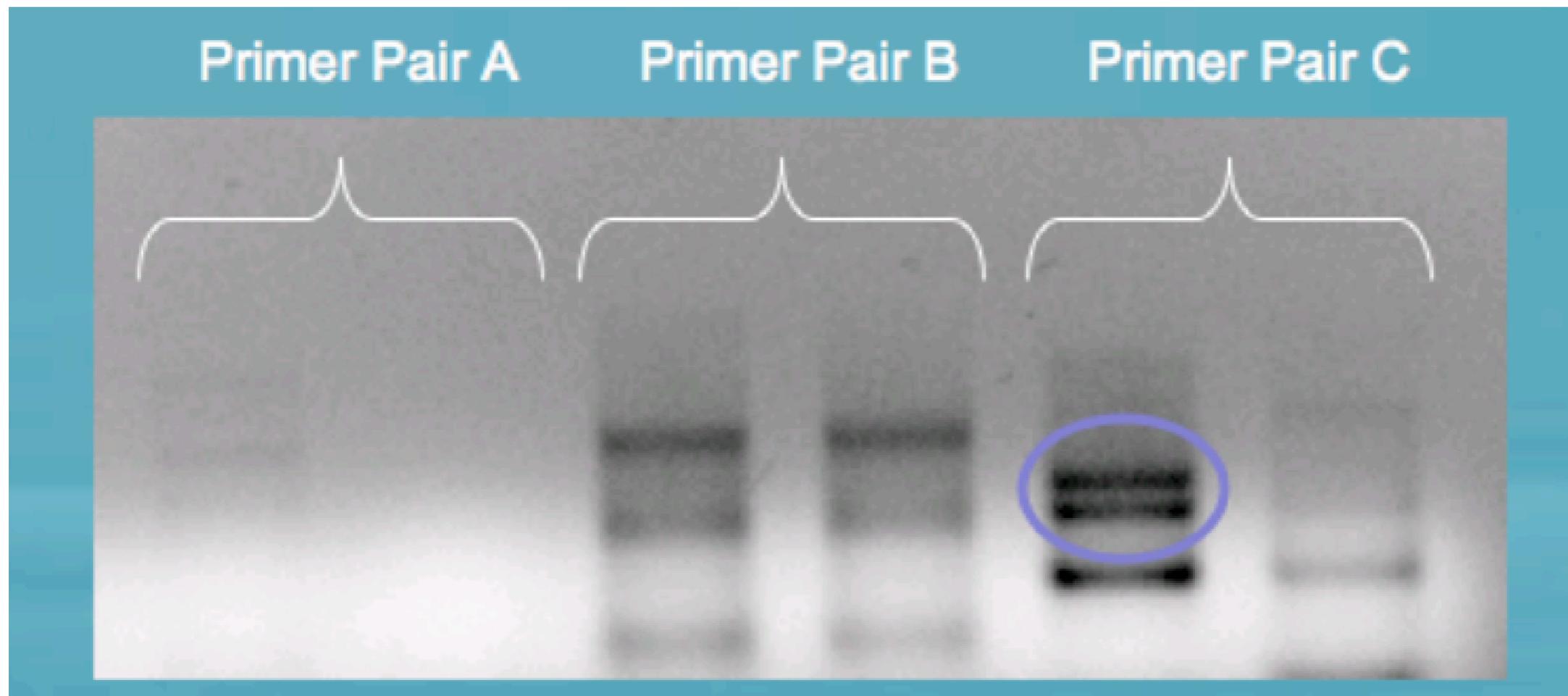
- Understand more concerning **Clam** physiology
 - Environmental Influence
 - Differences in Strain
 - Immune Response



Approach

- **Differential Display Analysis**
- Construction of cDNA library from hemocytes
- Gene Discovery

Differential Display



Differential Expression

- Infected versus uninfected
 - 7 upregulated
 - 6 downregulated
- Comparison across strains
 - 10 upregulated FL (June 7:Aug 3)
 - 8 upregulated NJ (June 2:Aug 6)
 - 1 upregulated MA (June)

Results

- Few ribosomal proteins
- Hemocyte receptors
 - Important signaling cascade
- Unexpected difficulty identifying products
 - ????
- Serine Protease Inhibitor

Serine Protease Inhibitor

- Critical factor in disease pathogenesis
- Serine proteases produced by pathogen
 - Facilitate penetration
 - Stimulate degradation of host proteins involved in immune defense

Proteases

Current
Microbiology
An International Journal

Alkaline Serine Protease Is an Exotoxin of *Vibrio alginolyticus* in Kuruma Prawn, *Penaeus japonicus*

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A. S. NOTTAGE¹, T. H. BIRKBECK¹

¹Department of Microbiology, University of Glasgow, Scotland

Inhibitors of proteases

Protease Inhibitory Activity in Selectively Bred Families of Eastern Oysters

J. L. Oliver^a, P. M. Gaffney^b, S. K. Allen, Jr^c, M. Faisal^d, and S. L. Kaattari^d

Hard Clam

Serine Protease Inhibitor

Putative conserved domains have been detected, click on the image below for detailed results.



Organism Report

Dipetalogaster maximus [bugs] taxid 72496

sp O96790 DPGN_DIPMA Serine protease inhibitor dipetalogas...	<u>83</u>	5e-15
emb CAA10384.1 dipetalogastin [Dipetalogaster maximus]	<u>83</u>	5e-15

Triatoma brasiliensis [bugs] taxid 65344

qb ABI96910.1 brasiliensin precursor [Triatoma brasiliensis]	<u>82</u>	1e-14
--	-----------	-------

Chlamys farreri [bivalves] taxid 202578

qb ABB58758.1 serine protease inhibitor-1L [Chlamys farreri]	<u>81</u>	3e-14
qb ABB58759.1 serine protease inhibitor-1S [Chlamys farreri]	<u>80</u>	4e-14
qb ABB89133.1 serine protease inhibitor CFSP13 [Chlamys f...]	<u>68</u>	2e-10
qb ABC02759.1 serine protease inhibitor [Chlamys farreri]	<u>65</u>	2e-09

Domain indicating that protein is able to inhibit subtilisin-like serine protease

CRP-LCACPRIYKPVCGQDGKTYPNQCELNCAGVALFEEGPCIATSPQFDFAPEAPCICT
CRP C CP IY PVCG DGKTY N C C V + C C+CT
CRPEQCVCPSTIYSPVCGYDGKTYSNACSAAGCDNVKIRCNRKCPCKG-----IGCVCT
* * * * * * *

Contains cysteine residues necessary for tertiary structure

Inhibitor Expression

- Currently do not have a complete picture
 - Different across strains
- Is it induced upon recognition of QPX?
 - Upon QPX expression of protease?
- Difference in sequence?
- What is the role temperature?

Summary

- Difficulty in identifying homologous sequences
- Serine Protease Inhibitor is highly regulated and likely associated with proper immune function
- Expression pattern could be developed as a marker

Disease tolerance

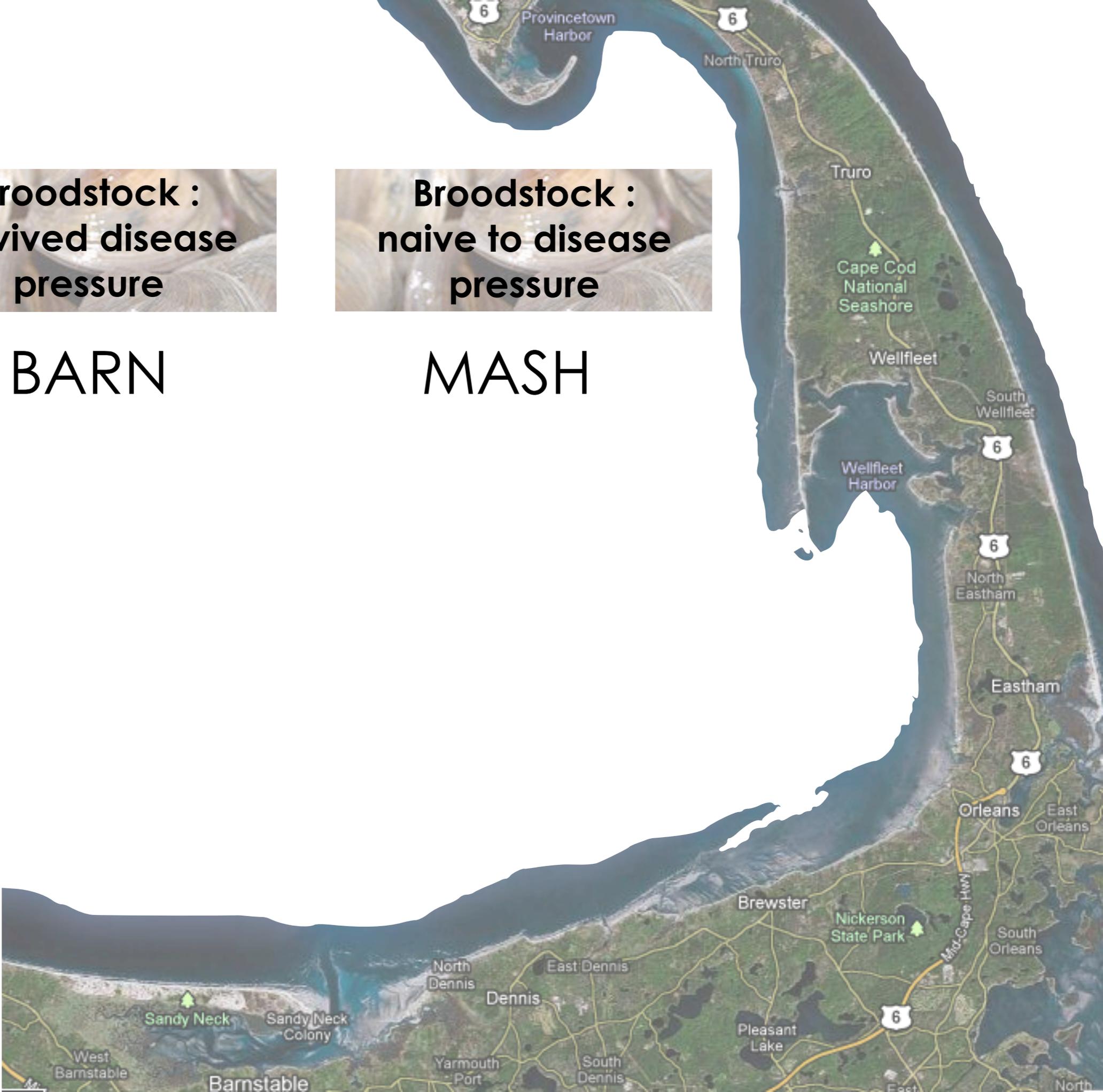
QPX and *Mercenaria mercenaria*

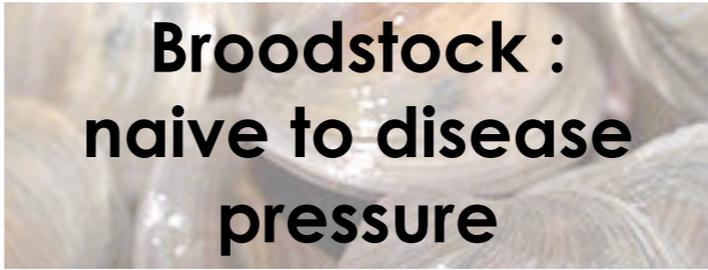
**Broodstock :
survived disease
pressure**

BARN

**Broodstock :
naive to disease
pressure**

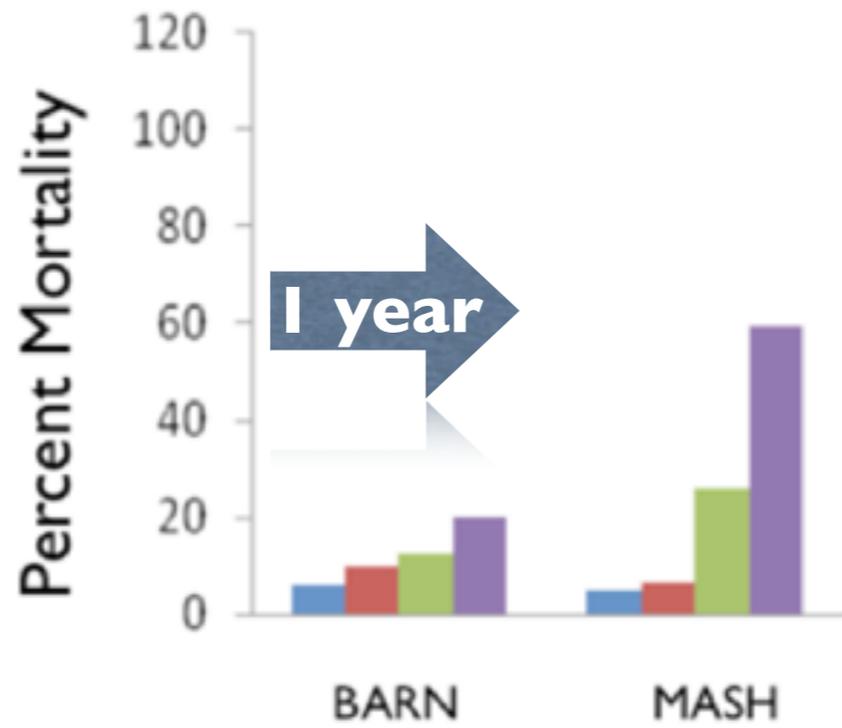
MASH





BARN

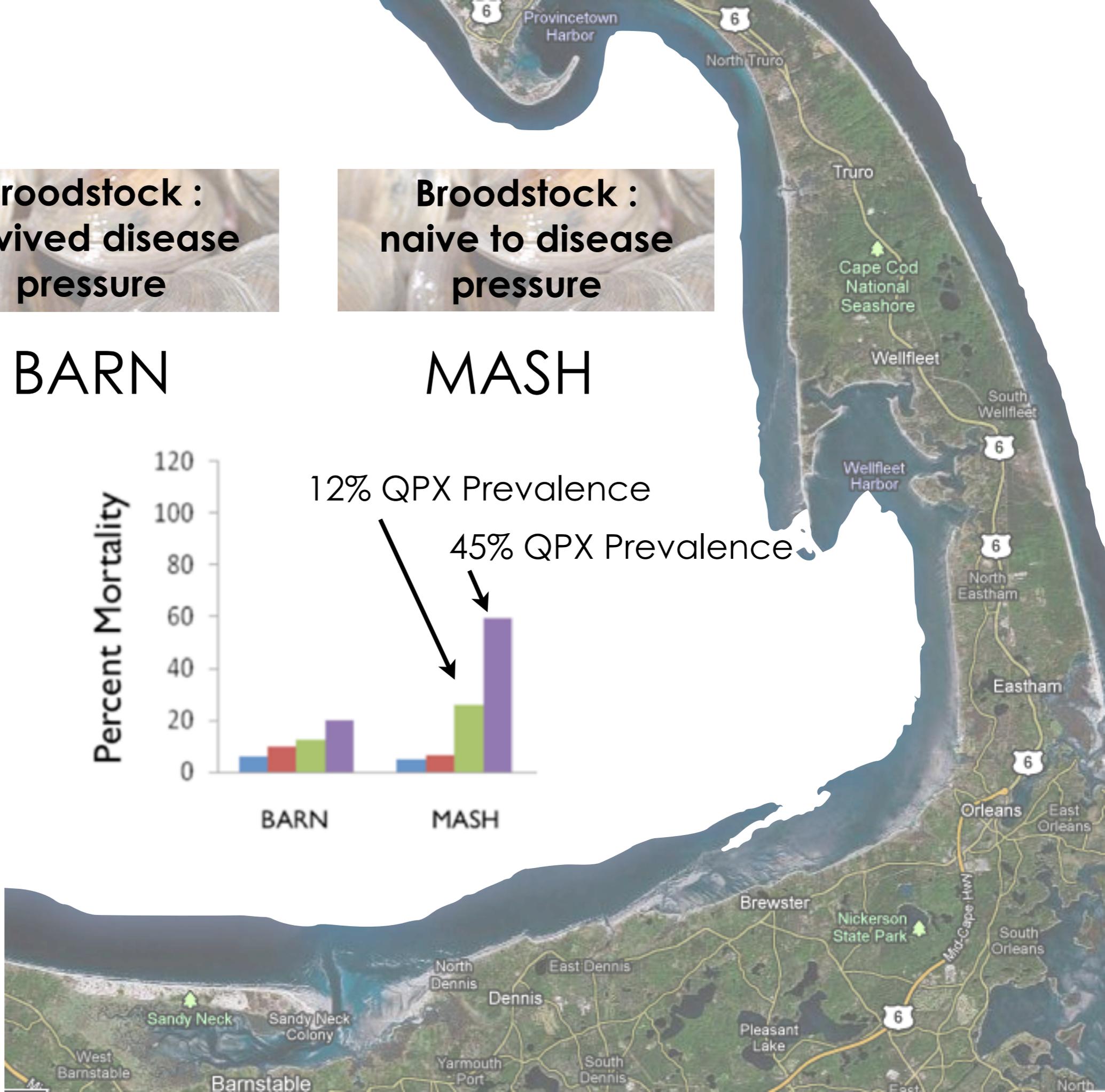
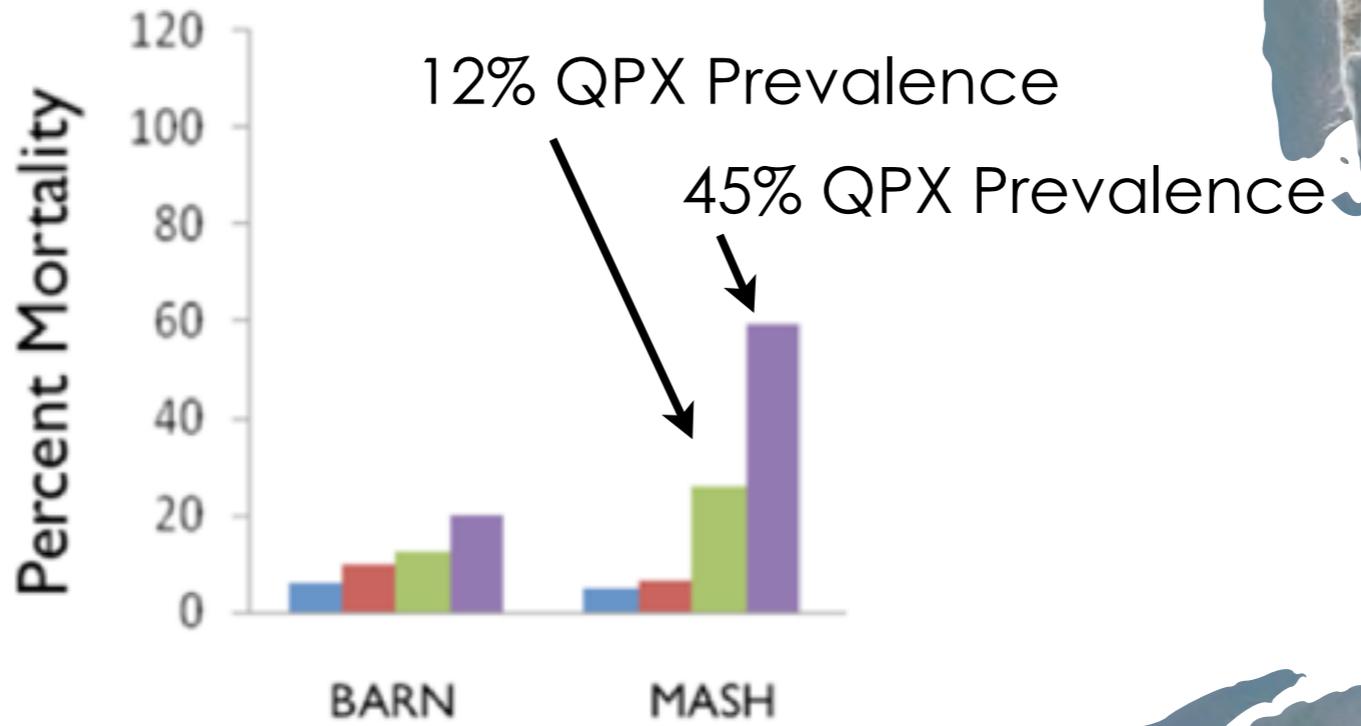
MASH





BARN

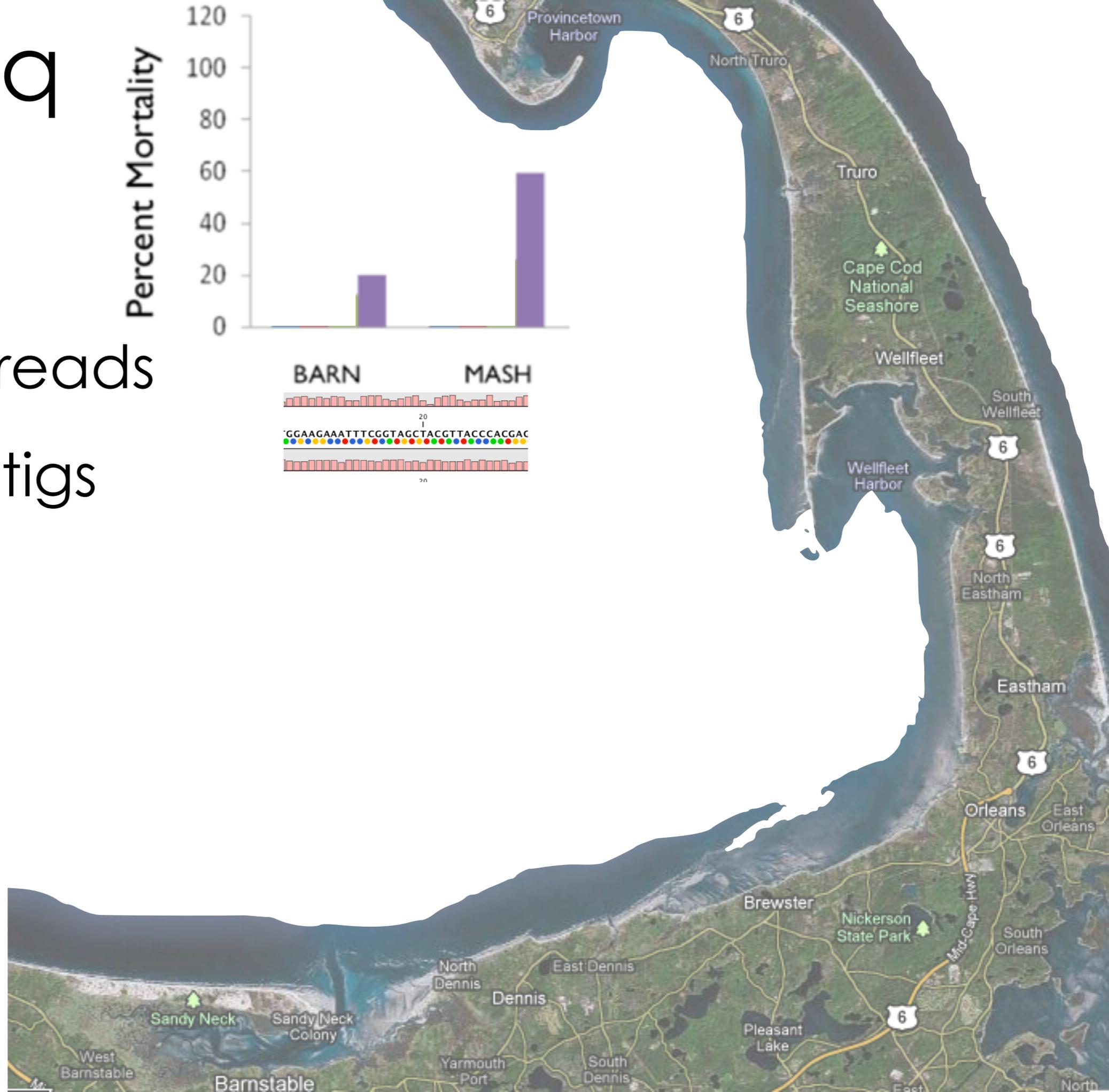
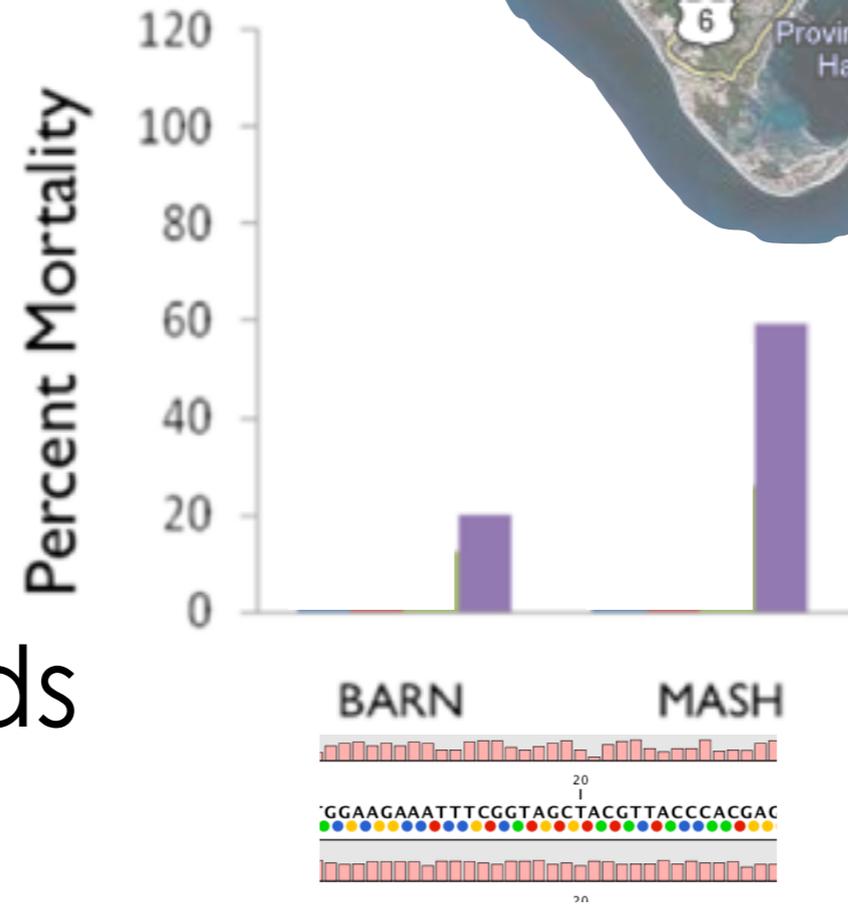
MASH



RNA-Seq

100 million reads

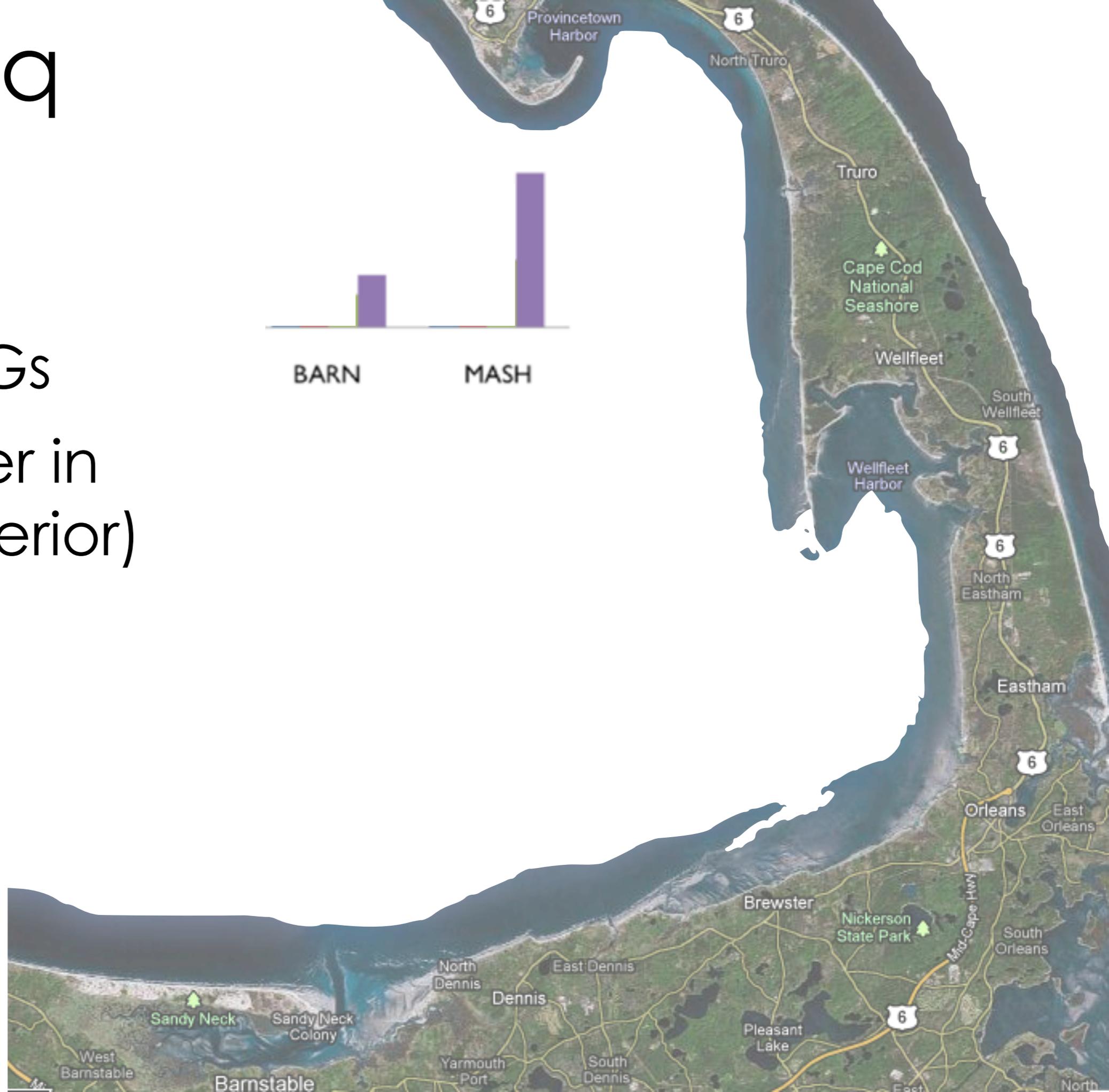
8482 contigs



RNA-Seq

684 DEGs

459 higher in
BARN (superior)



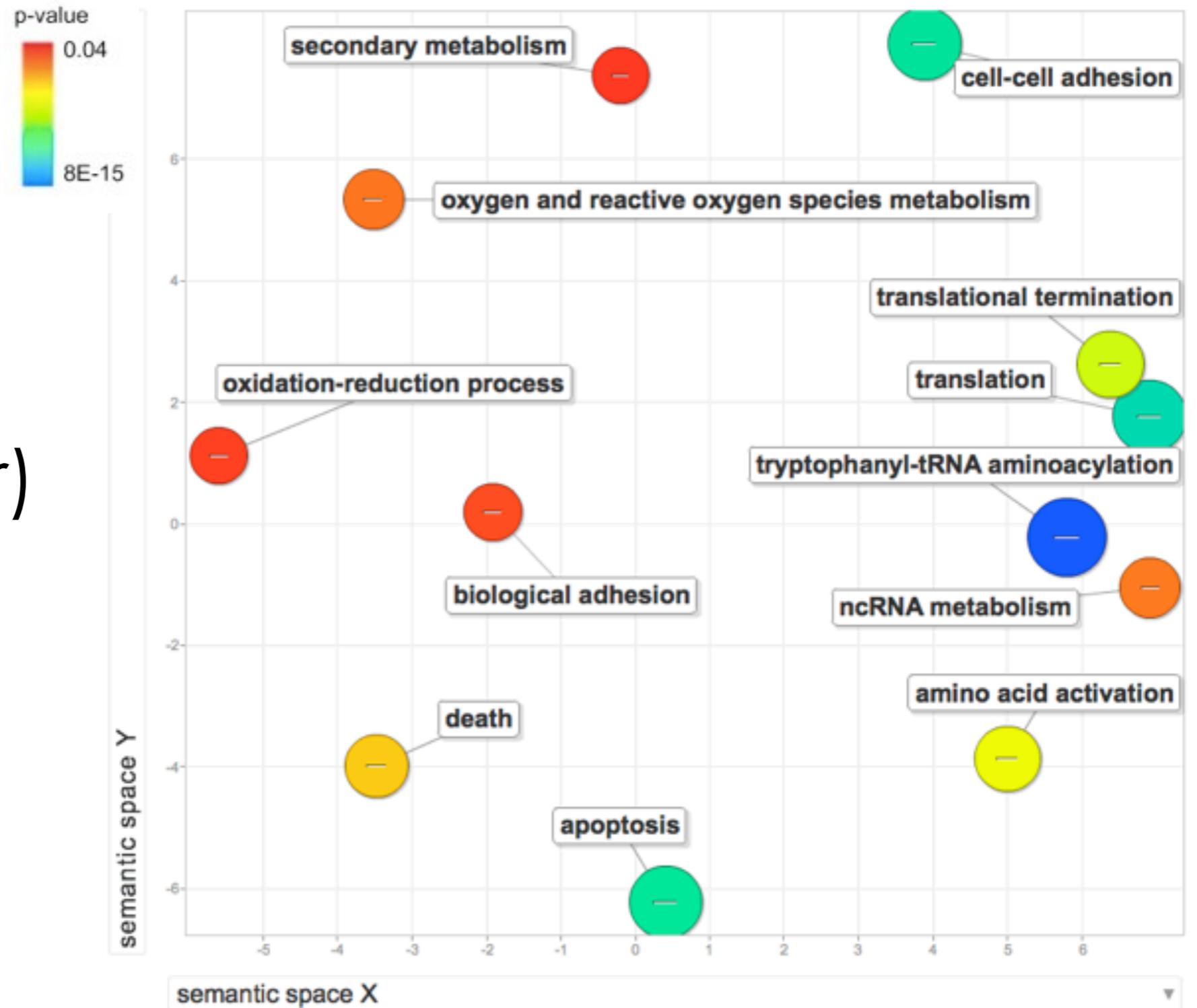
RNA-Seq

684 DEGs

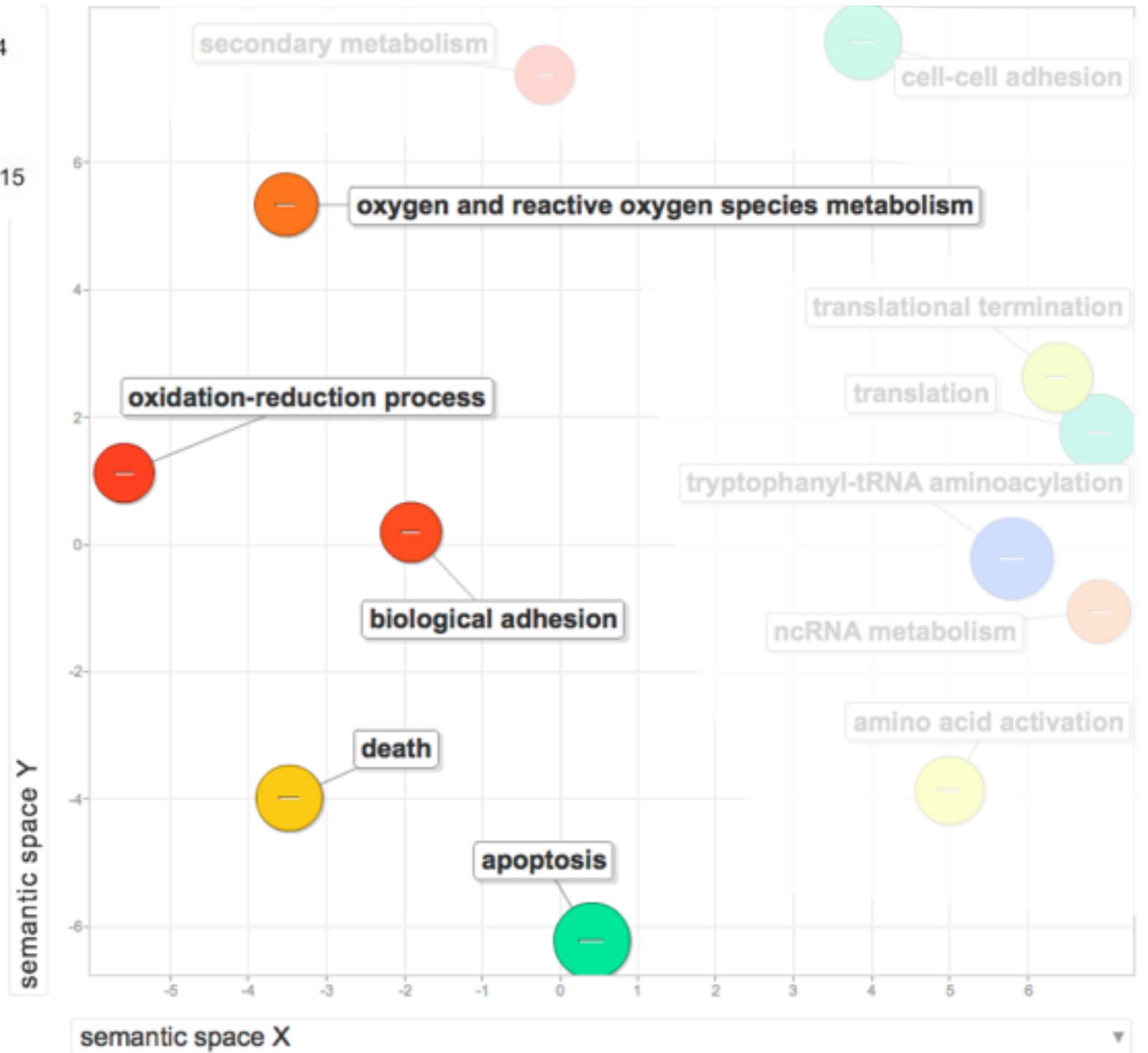
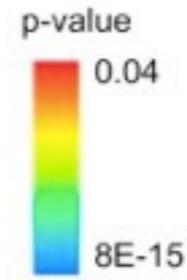
459 higher in
BARN (superior)

33 enriched
biological
processes

684 DEGs
459 higher in
BARN (superior)
33 enriched
biological
processes



684 DEGs
459 higher in
BARN (superior)
33 enriched
biological
processes



684 DEGs
459 higher in
BARN (superior)
33 enriched
biological
processes

apoptosis

baculoviral IAP repeat-containing protein,
apoptosis 1 inhibitor, TNF receptor-
associated factor 3, protein FADD

adhesion

neuroglian, protocadherin

oxidation reduction processes

peroxidase, thyroid peroxidase,
epidermis-type lipoxygenase,
hydroxysteroid 11-beta-dehydrogenase,
carbonyl reductase, cytochrome P450,
superoxide dismutase, sorbitol
dehydrogenase

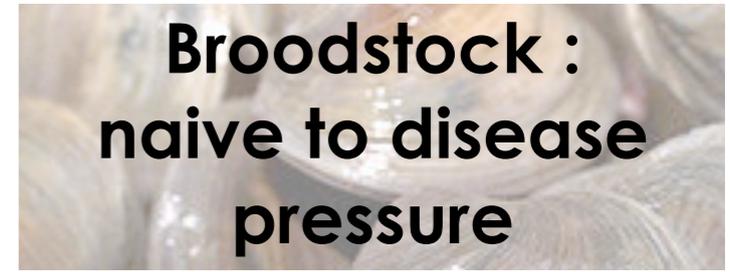
translation

asparaginyl-tRNA synthetase, eukaryotic
initiation factor, tryptophanyl-tRNA
synthetase, eukaryotic peptide chain
release factor subunit

Genotyping



BARN



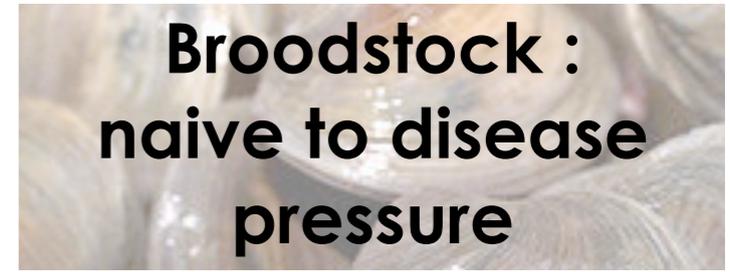
MASH

Restriction Enzyme
Assisted
Digestion
-
Sequencing

Genotyping

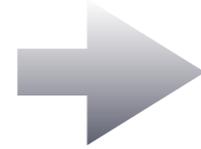


BARN



MASH

Restriction Enzyme
Assisted
Digestion
-
Sequencing



Reduce Representation

Genotyping

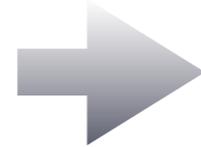


BARN



MASH

Restriction Enzyme
Assisted
Digestion



Reduce Representation

-
Sequencing

Sequence multiple individuals

Genotyping

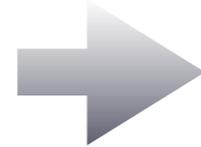


BARN



MASH

Restriction Enzyme
Assisted
Digestion



Reduce Representation

-
Sequencing

Sequence multiple individuals

145 Diagnostic Markers