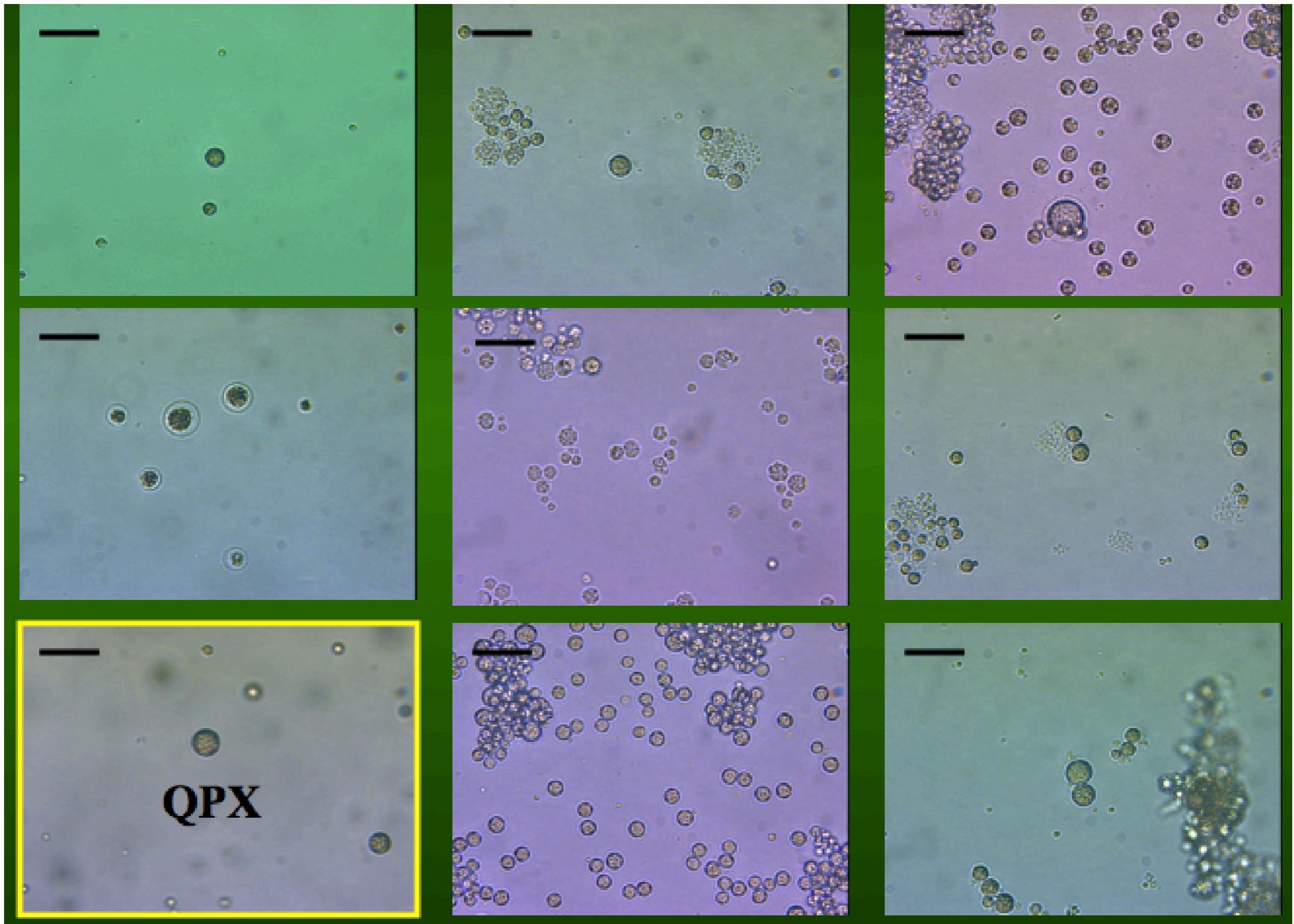


Labyrinthulids





★★★★★

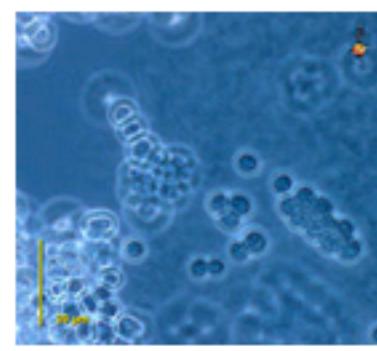
TRUSTED

[add to a collection](#)

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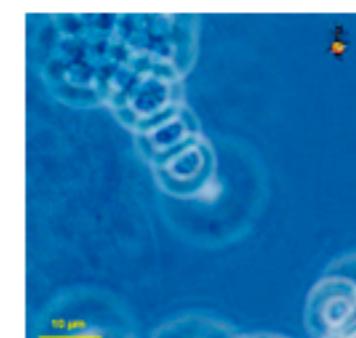
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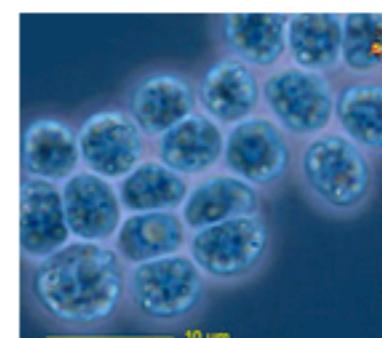
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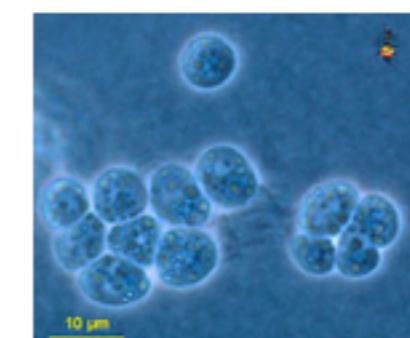
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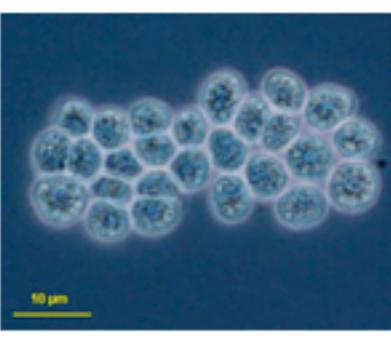
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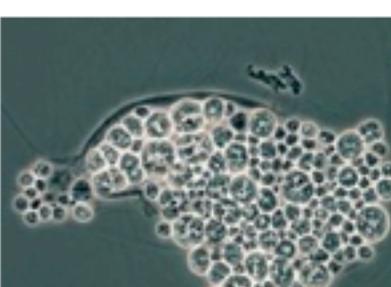
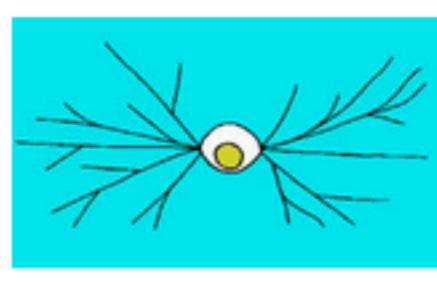
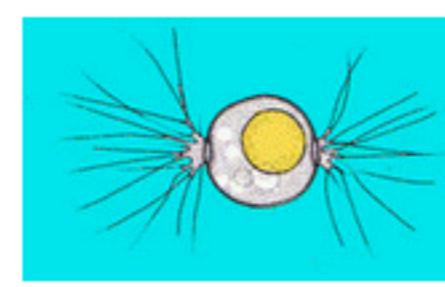
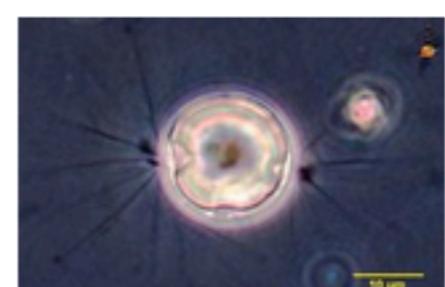
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Labyrinthulids

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

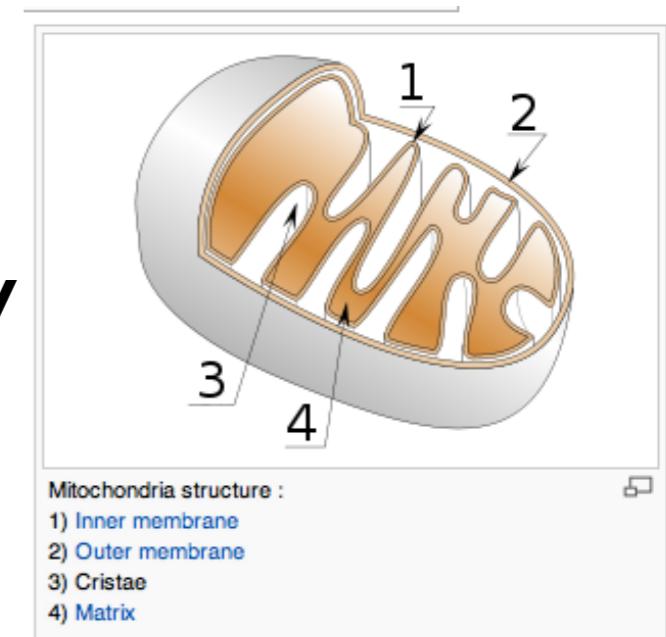
The labyrinthulids are characterized by tubulocristae mitochondria.

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	Taxonomy navigation
Scientific name	Labyrinthulida	 stramenopiles  environmental samples Labyrinthulidae Thraustochytriidae unclassified 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	

Thraustochyrid-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>

Thraustochytrid-like isolates from marine bivalve mollusks

0.036	Batrachochytrium_sp	DQ890358	<i>Crassostrea ariakensis</i>	China	visceral mass <i>T. aureum</i>
	Thraustochytriidae_sp ¹	DQ890359	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. caudivorum</i>
	Oblongospora_sp	DQ890360	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. caudivorum</i>
	Thraustochytrium_multirudimente	DQ890361 ¹	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	Thraustochytrium_striatum	DQ890362 ²	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	Thraustochytrium_kinnei	DQ890363	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	DQ890369	DQ890364 ²	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	DQ890361	DQ890365	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	DQ890362	DQ890366	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum **</i>
	DQ890364	DQ890367	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum **</i>
	DQ890370	DQ890368	<i>Crassostrea virginica</i>	Chesapeake Bay hemolymph	<i>T. aureum **</i>
	DQ890373	DQ890369 ¹	<i>Crassostrea virginica</i>	Chesapeake Bay hemolymph	<i>T. aureum</i>
	DQ890358	DQ890370	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	DQ890377	DQ890371	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	DQ890356	DQ890373	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	DQ890363	DQ890368	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum **</i>
	DQ890376	DQ890367	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum **</i>
	DQ890365	DQ890369 ¹	<i>Crassostrea virginica</i>	Chesapeake Bay hemolymph	<i>T. aureum **</i>
	DQ890371	DQ890370	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	DQ890355	DQ890371	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	DQ890350	DQ890373	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	DQ890354	DQ890374	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>L. haliotidis</i>
	DQ890366	DQ890374	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. caudivorum</i>
	DQ890367	DQ890375	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	DQ890368	DQ890376	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	Thraustochytrium_aureum	DQ890377	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	DQ890357	DQ890378	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	DQ890359	DQ890379	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	DQ890360	DQ890374	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	DQ890375	DQ890375	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
0.031	DQ890379	DQ890373	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. aureum</i>
	Thraustochytrium_caudivorum	DQ890374	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>L. haliotidis</i>
	DQ890374	DQ890375	<i>Mercenaria mercenaria</i>	Virginia	mantle <i>T. caudivorum</i>
	Thraustochytriidae_sp ²	DQ890376	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
0.033	Labyrinthuloides_haliotidis	DQ890377	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	DQ890378	DQ890377	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	QPX ¹	DQ890378	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	QPX ²	DQ890379	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
0.058	DQ890351	DQ890377	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>
	Thraustochytrium_pachydermum	DQ890378	<i>Mya arenaria</i>	Oregon	labial palps and gills <i>T. aureum</i>

Thraustochyrid-like isolates from marine bivalve mollusks



Thraustochyrid-like isolates from marine bivalve mollusks

Maille Lyons, Christopher Dungan, Steven Roberts

INTRODUCTION

Interest in thraustochyrid 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, Bongiorni et al. 2005, Lyons et al. 2007), 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-like protists whose classification is not clear. They may be classified in either the kingdom Stramenopiles (following Dick 2001 and Ragukumar 2002) or Chromista (if following Cavalier-Smith 1994–1998, Cavalier-Smith et al. 1994). The corresponding phylum, class, order, and family designations are different 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

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Roxanna Smolowitz and Kevin R. Uhlinger

Marine Biological Laboratory, 7 MBL St., Woods Hole, Massachusetts 02543

Rebecca J. Gast

Biology Department, Woods Hole Oceanographic Institution, Woods Hole, Massachusetts 02543

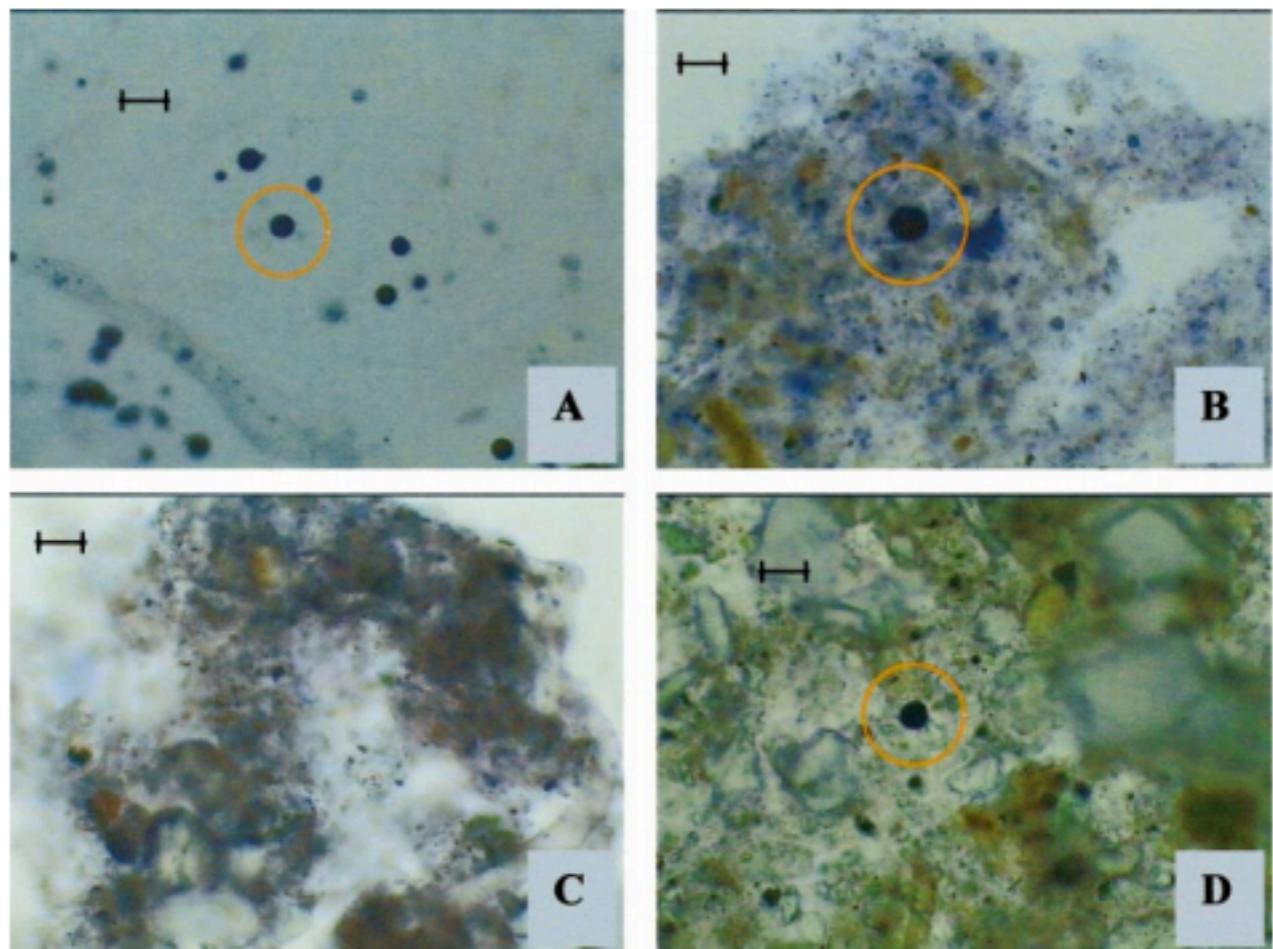
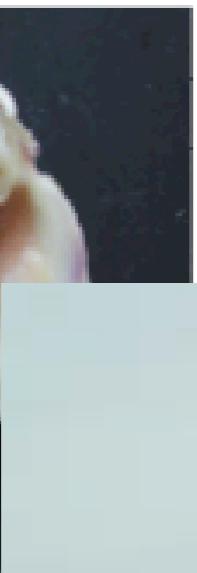
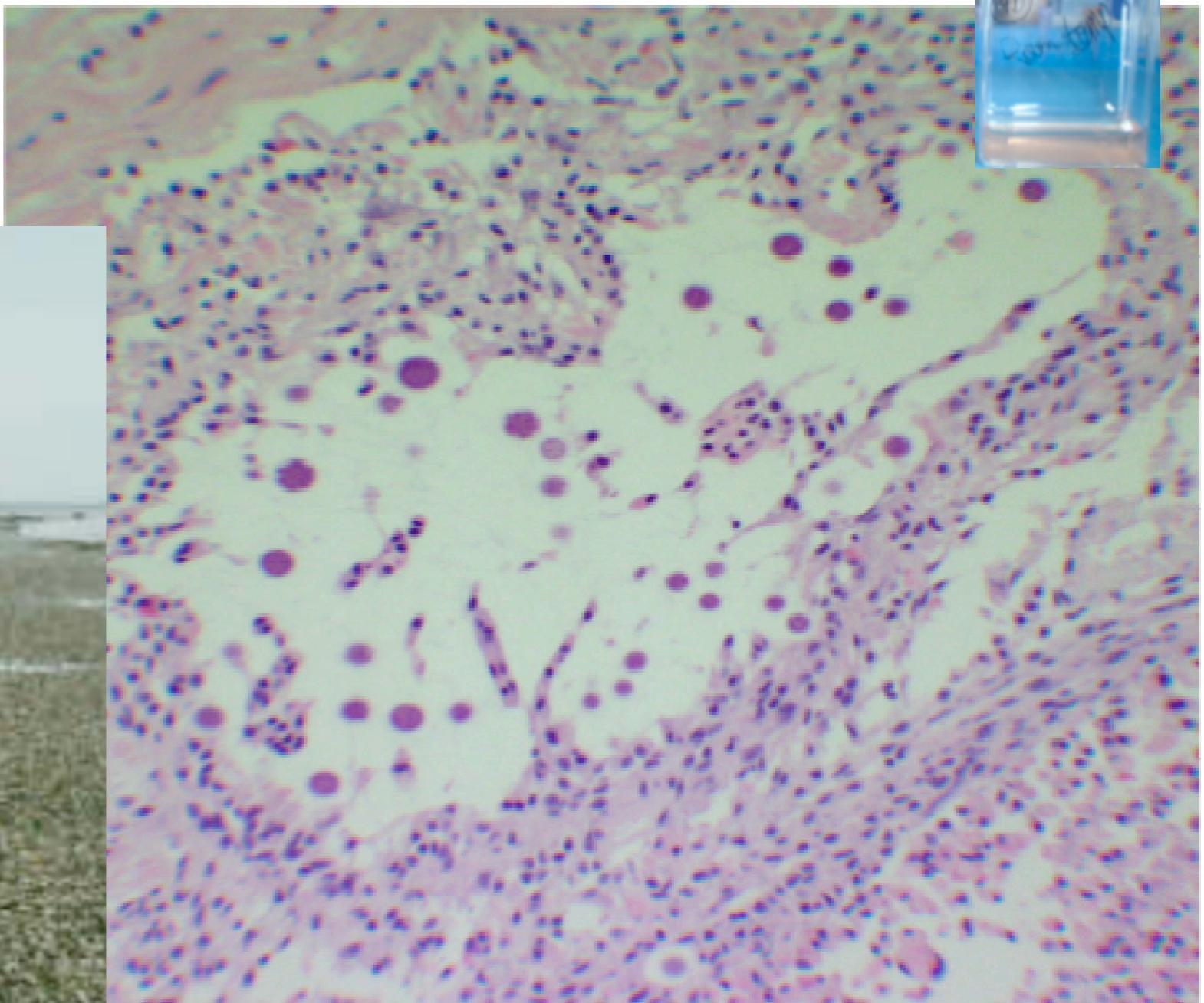


Fig. 2. Examples of in situ hybridization results for Quahog Parasite Unknown (QPX). (A) Positive results for QPX culture. (B) Positive results for laboratory-generated aggregates made with seawater and QPX culture (positive control). (C) Negative results for laboratory-generated aggregates made with 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 μ m.

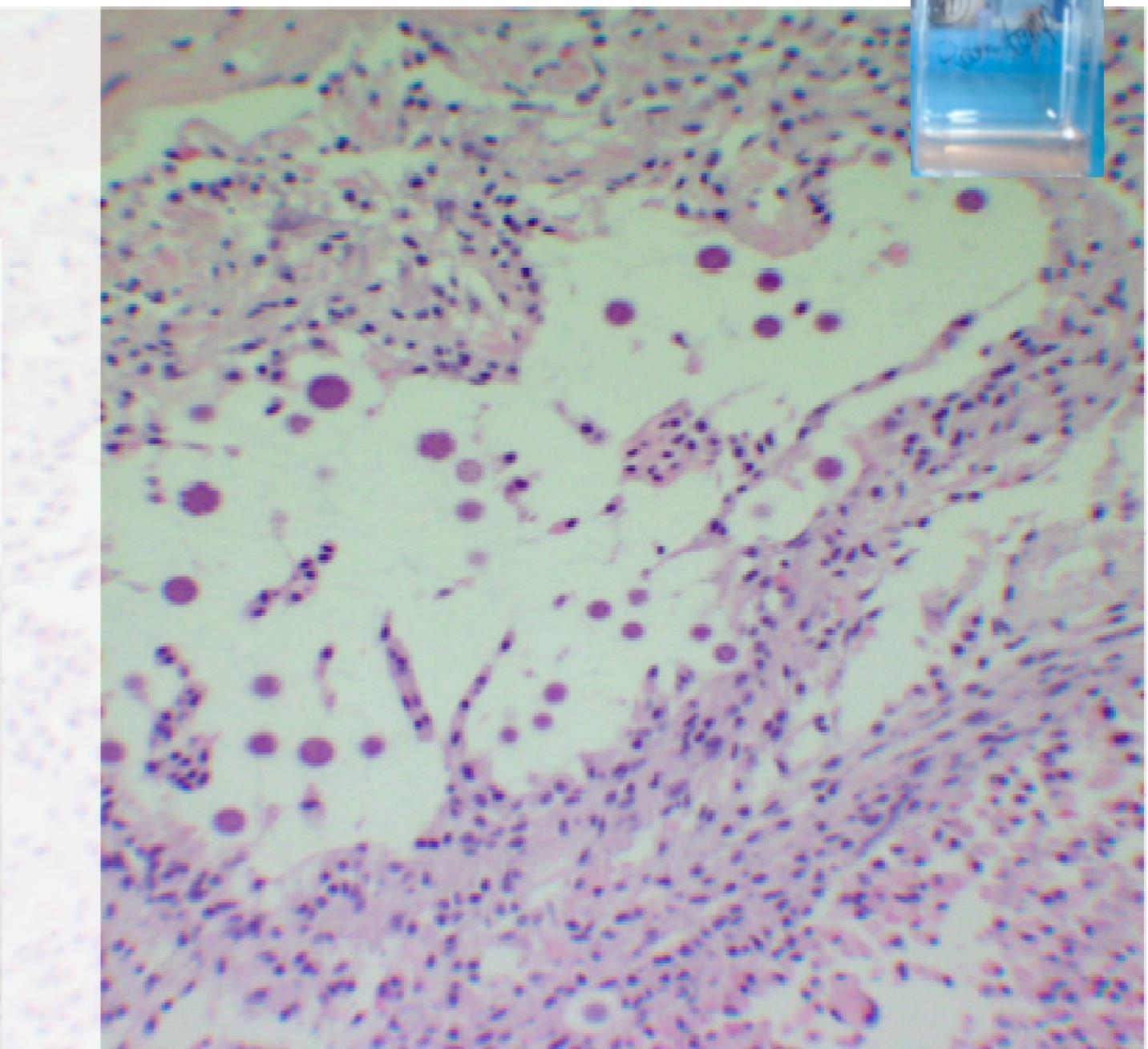
QPX



[METRIC 1]



QPX



Roxanna Smolowitz

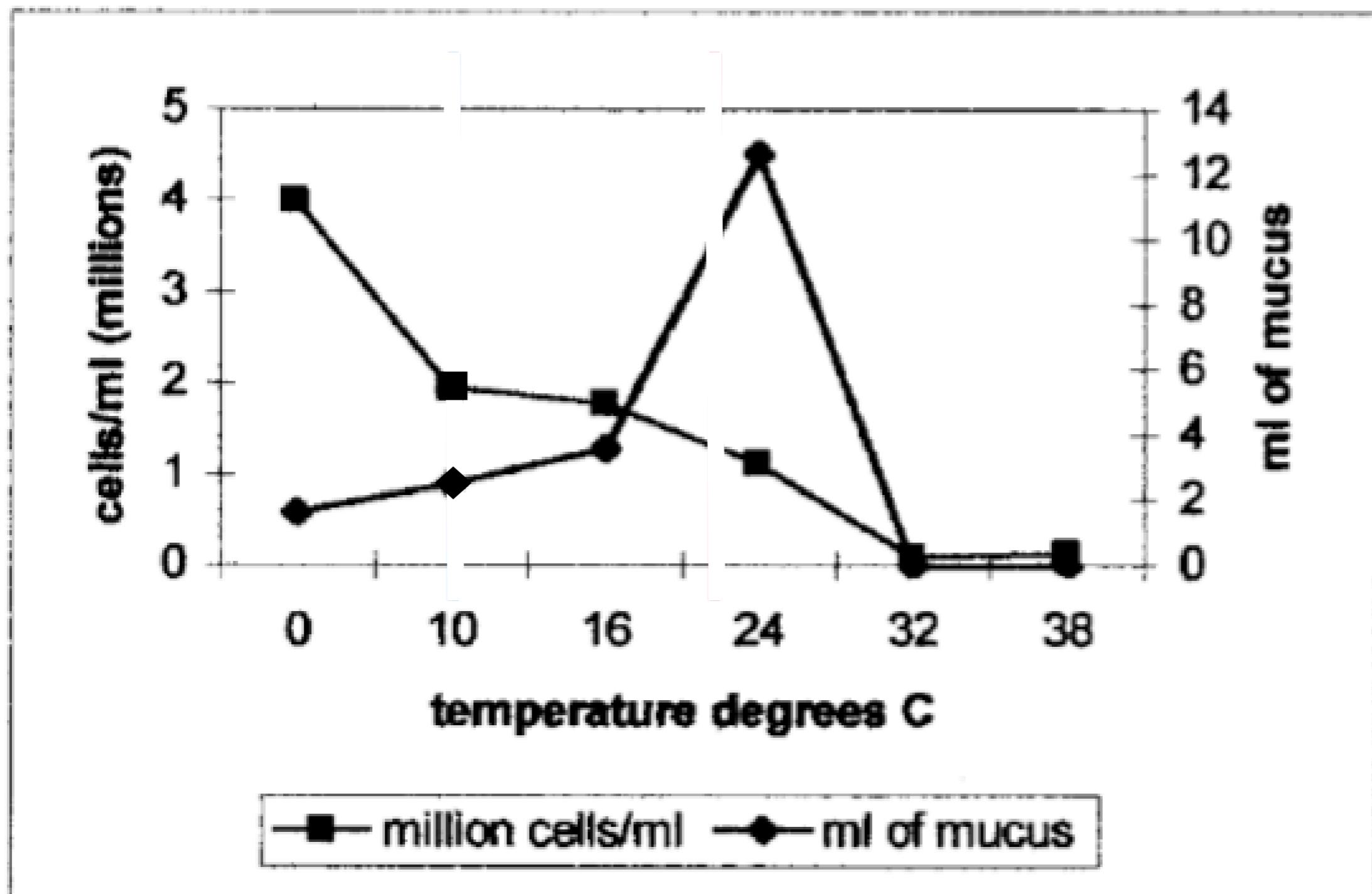
QPX

- 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



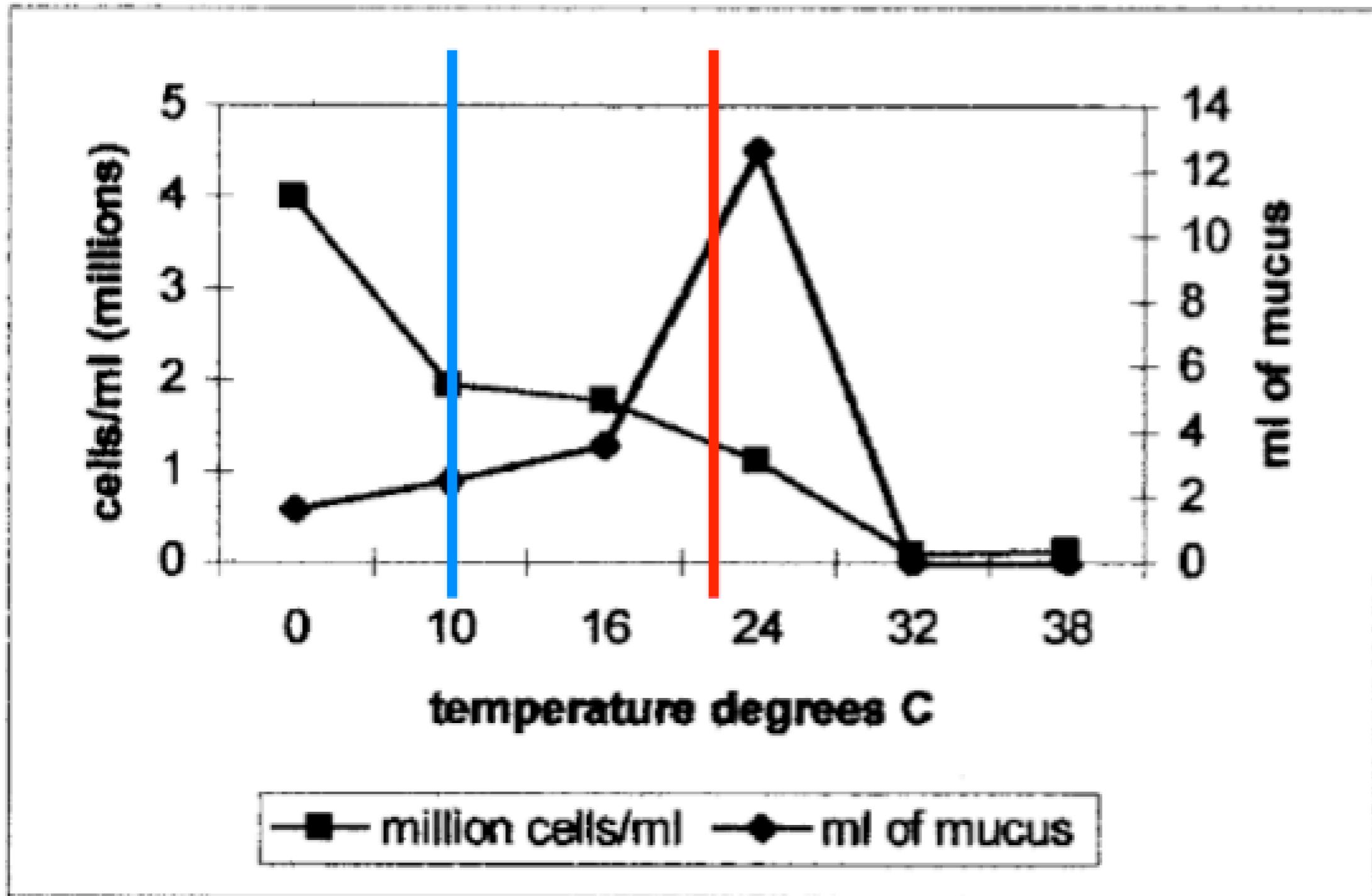
An Experiment

Rationale

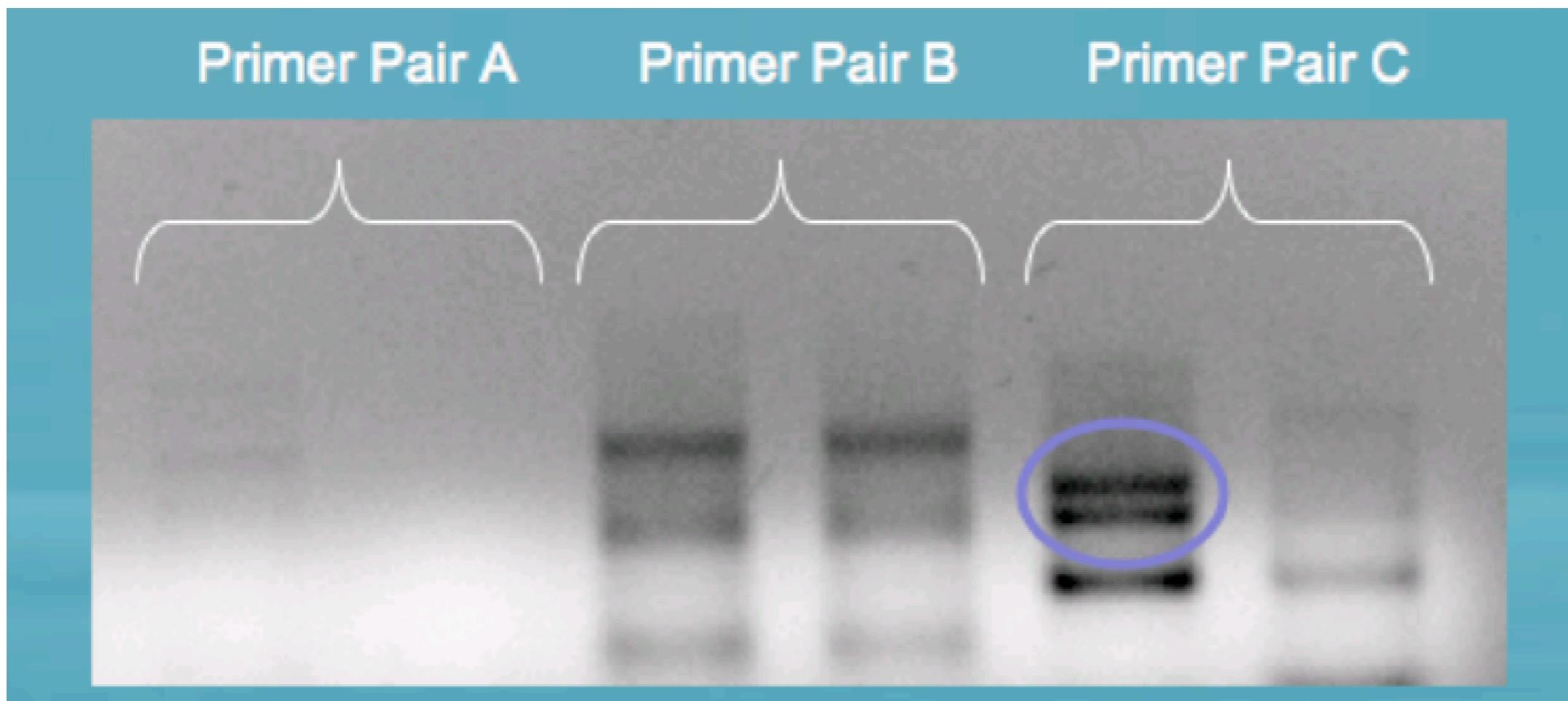
- Understand more concerning **QPX** physiology
 - Environmental influence
 - Differences across strain
 - Pathogenecity

Factors

- Temperature
- Strain



Differential Display



QPX Serine Protease

Top Blastx Hit	Species associated with	e-value	% similar
Glutathione-dependent formaldehyde-activating enzyme	<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 trederiksenii</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
Potassium inwardly-rectifying channel	<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
An International Journal

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

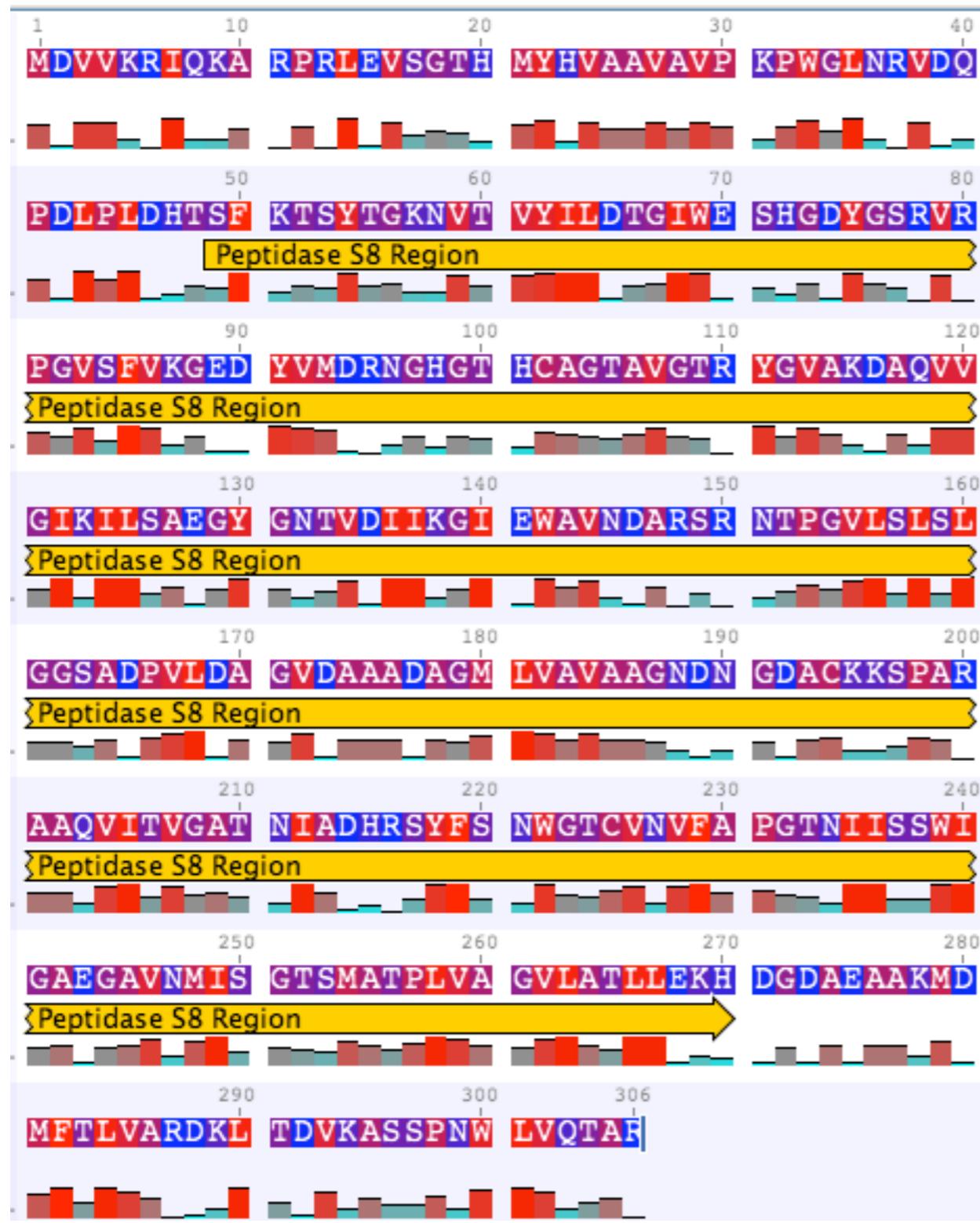
GWYNNE D. BROWN, STEPHEN L. KAATTARI, and KIMBERLY S. REECE*

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 (1.0%)
D:	23 (7.5%)
E:	8 (2.6%)
F:	5 (1.6%)

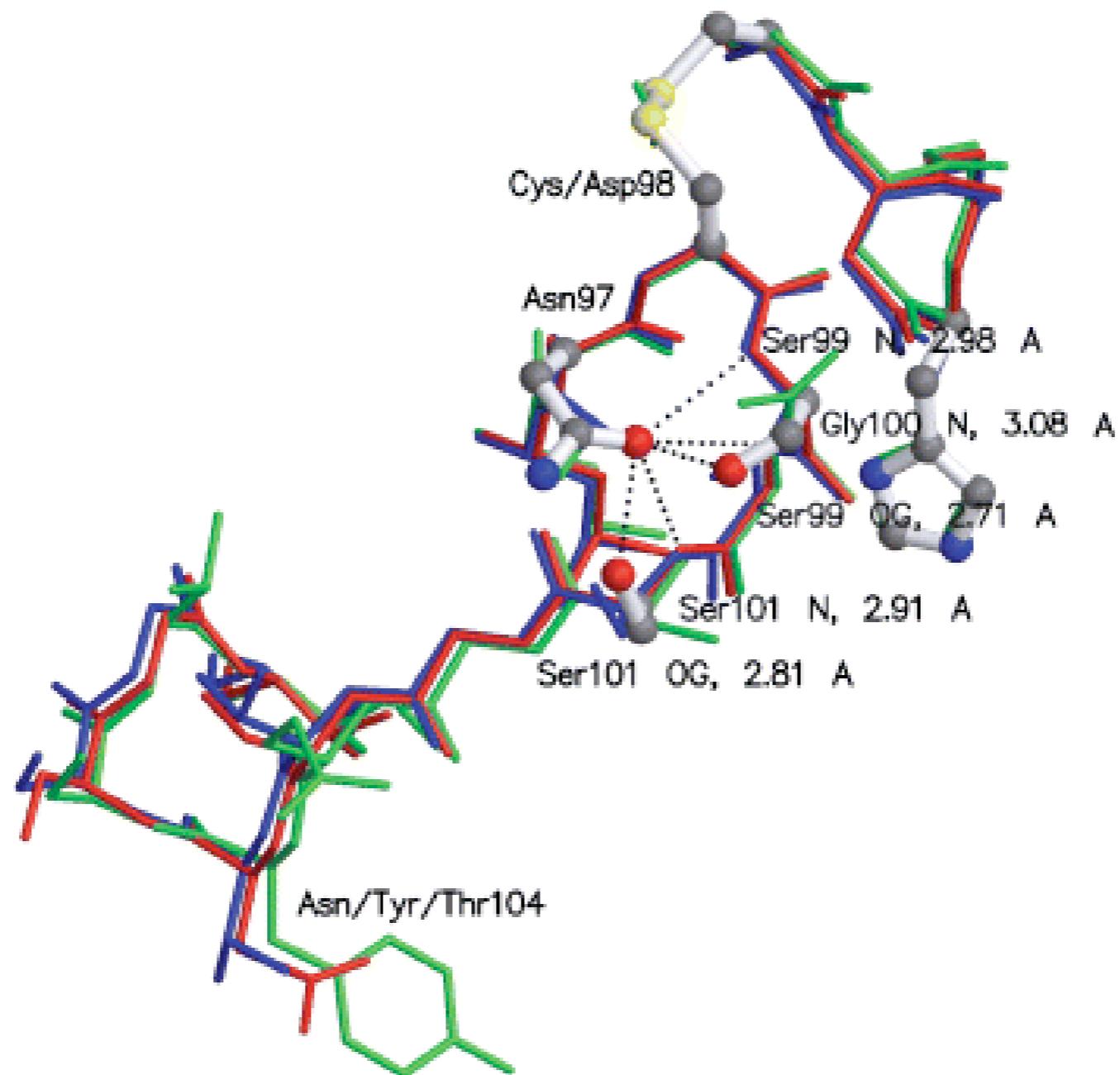
Sequence Analysis



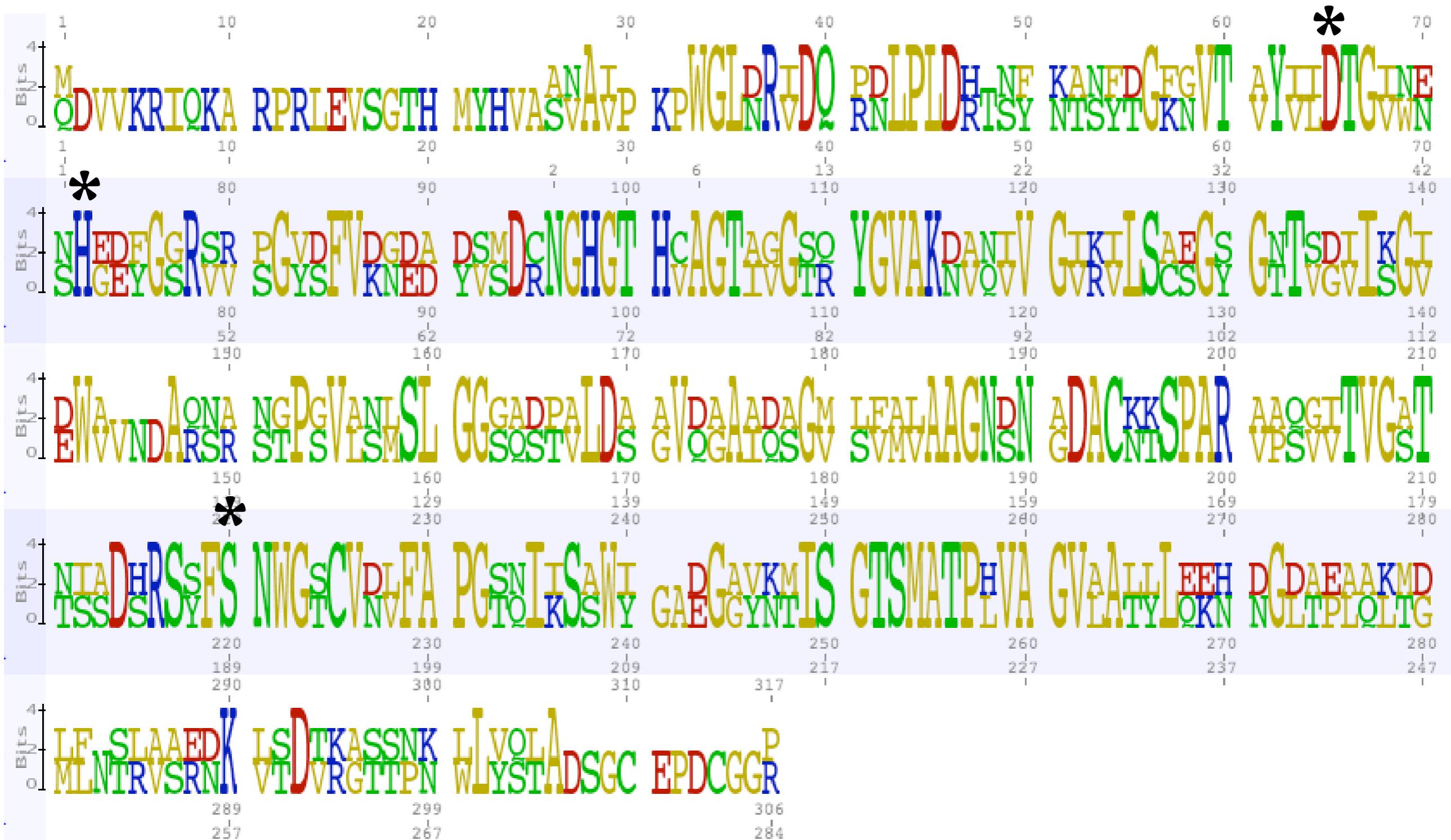
- Subtilase family.
- Subtilases are a family of serine proteases.
- They appear to have independently and convergently evolved a catalytic triad
 - *the three amino acid residues found inside the active site of certain protease enzymes: serine (S), aspartate (D) and histidine (H). They work together 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

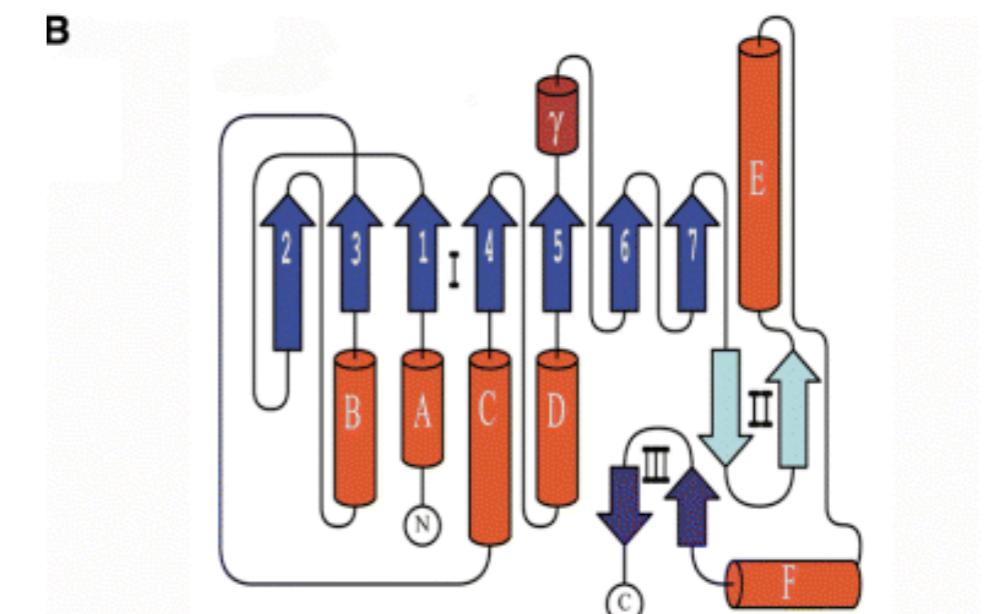
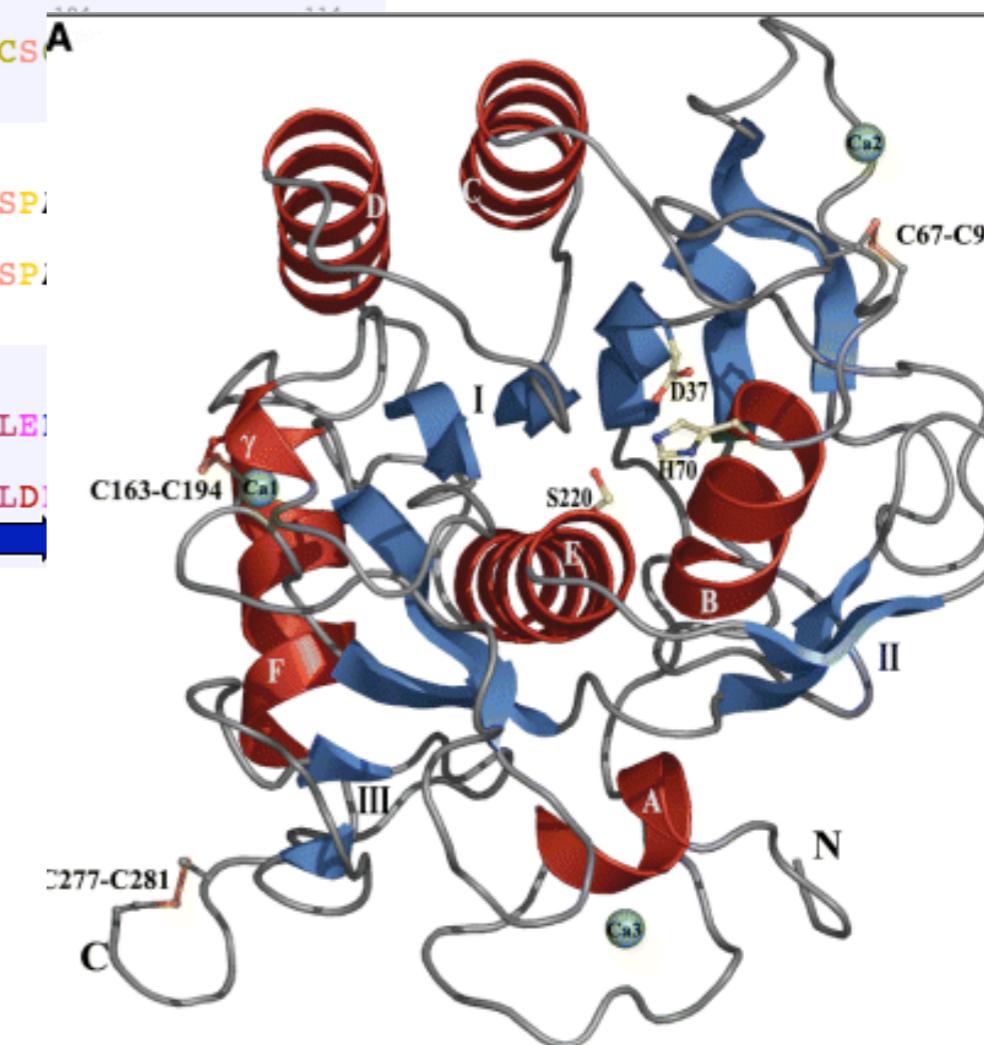
Ronny Helland¹, Atle Noralf Larsen², Arne Oskar Smalås^{1,3} and Nils Peder Willlassen^{1,2}



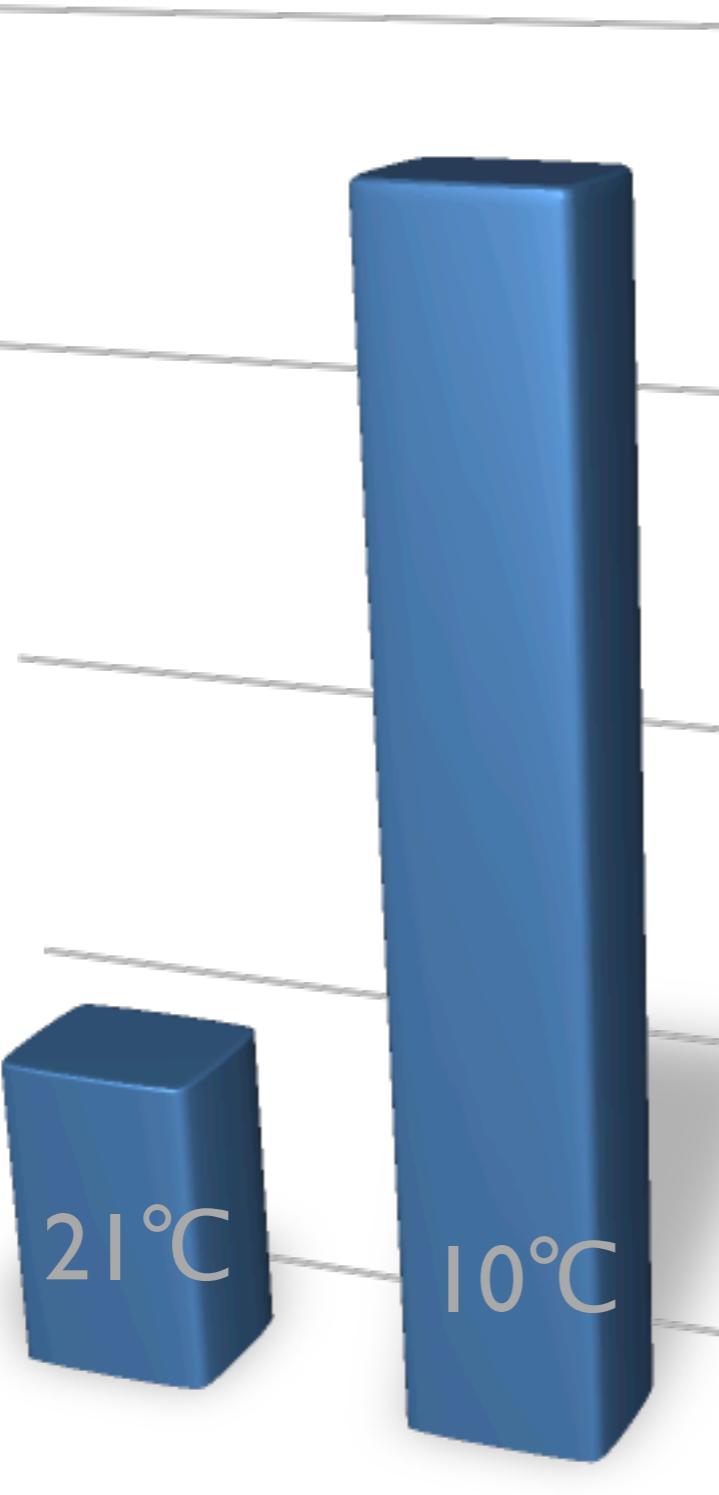
Asp/Ser/His Catalytic Triad



1	10	20	30	40	50	60	70
ABI79453.1	MDVVVKRIQKA	RPRLEVSGTH	MYHVAAVAVP	KPWGLNRVDQ	PDLPLDHTSF	KTSYTGKNVT	VYILDGTGWE
2	3			8	15	24	34
2B6N_A	AD-----	QPSPT-----	-----WGIDRIDQ	RNLPLDN-NY	HTDYDGSGVT	AFVIDTGVLN	
	sheet SecStr						
	80	90	100	110	120	130	140
	80	90	100	110	120	130	140
ABI79453.1	SHGDYGSRVR	PGVSFVKGED	YVMDRNGHGT	HCAGTAVGTR	YGVAKDAQVV	GKILSAEGY	GNTVDIICKGI
2B6N_A	THNEFGGRAS	SGYDFIDNDY	DATDCNGHGT	HVAGTIGGST	YGVAKNVNVV	GVRVLNCS	A
	sheet SecStr		s...	helix SecStr	s...	sh...	sheet Sec...
	150	160	170	180	190		
	150	160	170	180	190		
ABI79453.1	EWAVNDARSR	NTPGVLSLSSL	GGSADPVLD	GVDAAADAGM	LVAVAAGNDN	GDACKKSP	
2B6N_A	NWVKNN---	SGPAVANMSL	GGGASQATDD	AVNAAVAAAGI	TFVVAAGNDN	SNACNYSP	
	{helix...}		sheet ...	helix SecStr	sheet ...		
	220	230	240	250	260		
	220	230	240	250	260		
ABI79453.1	NIADHRSYFS	NWGTCVNVFA	PGTNIISSWI	GAEGAVNMIS	GTSMATPLVA	GVLATLLE	
2B6N_A	TSNDSRSSFS	NYGTCLDIYA	PGSSITSSWY	TSNSATNTIS	GTSMASPHVA	GVAALYLD	
	shee...		sheet ...	shee...	helix SecStr		
	290	300	307				
	289		306				
ABI79453.1	MF-TLVARDK	LTDVKASSPN	WLVQATAR				
2B6N_A	LLKTRATADK	VTDAKTGSPN	KLLFSLA				
	{hel...}						

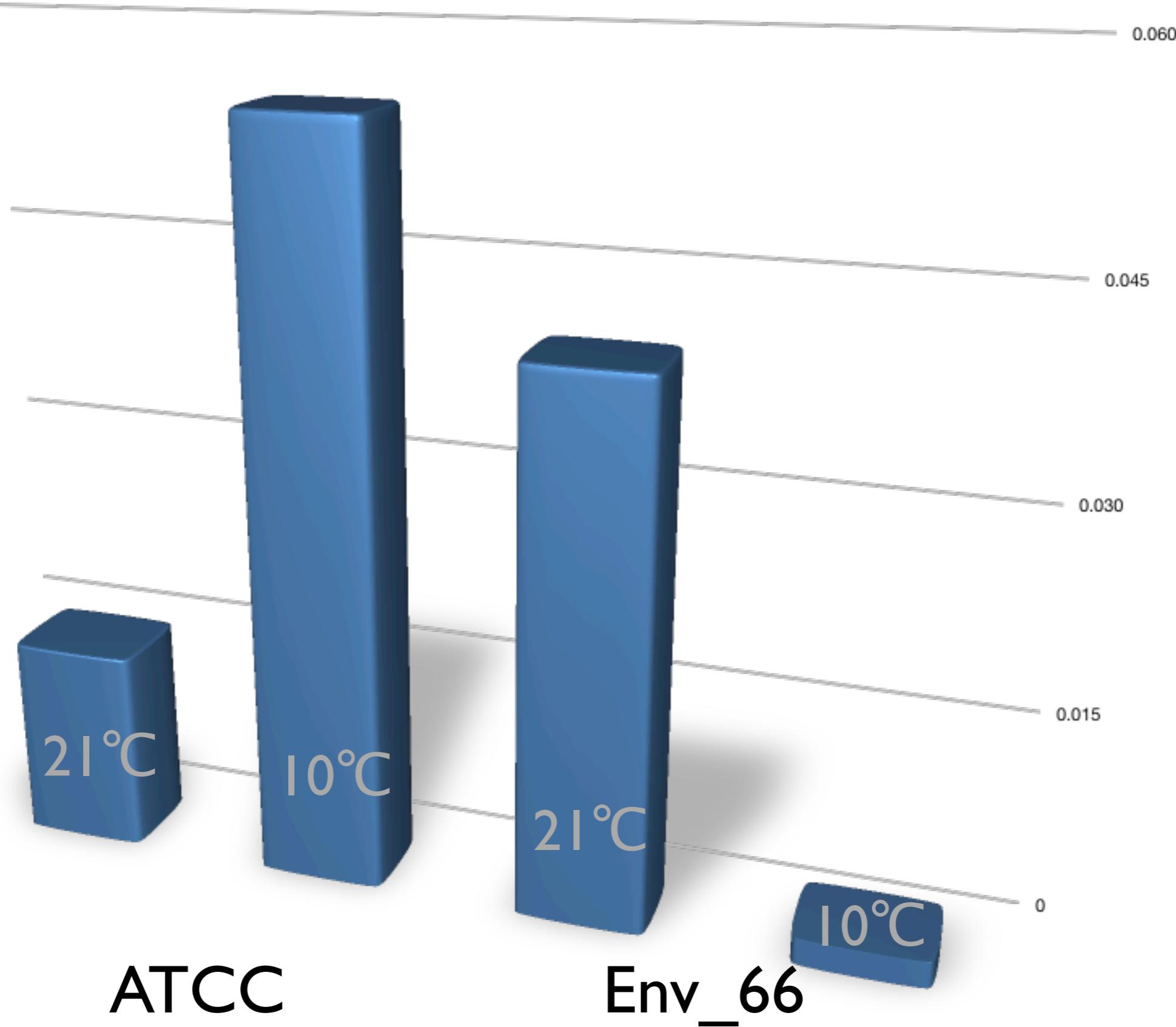


Serine Protease gene expression



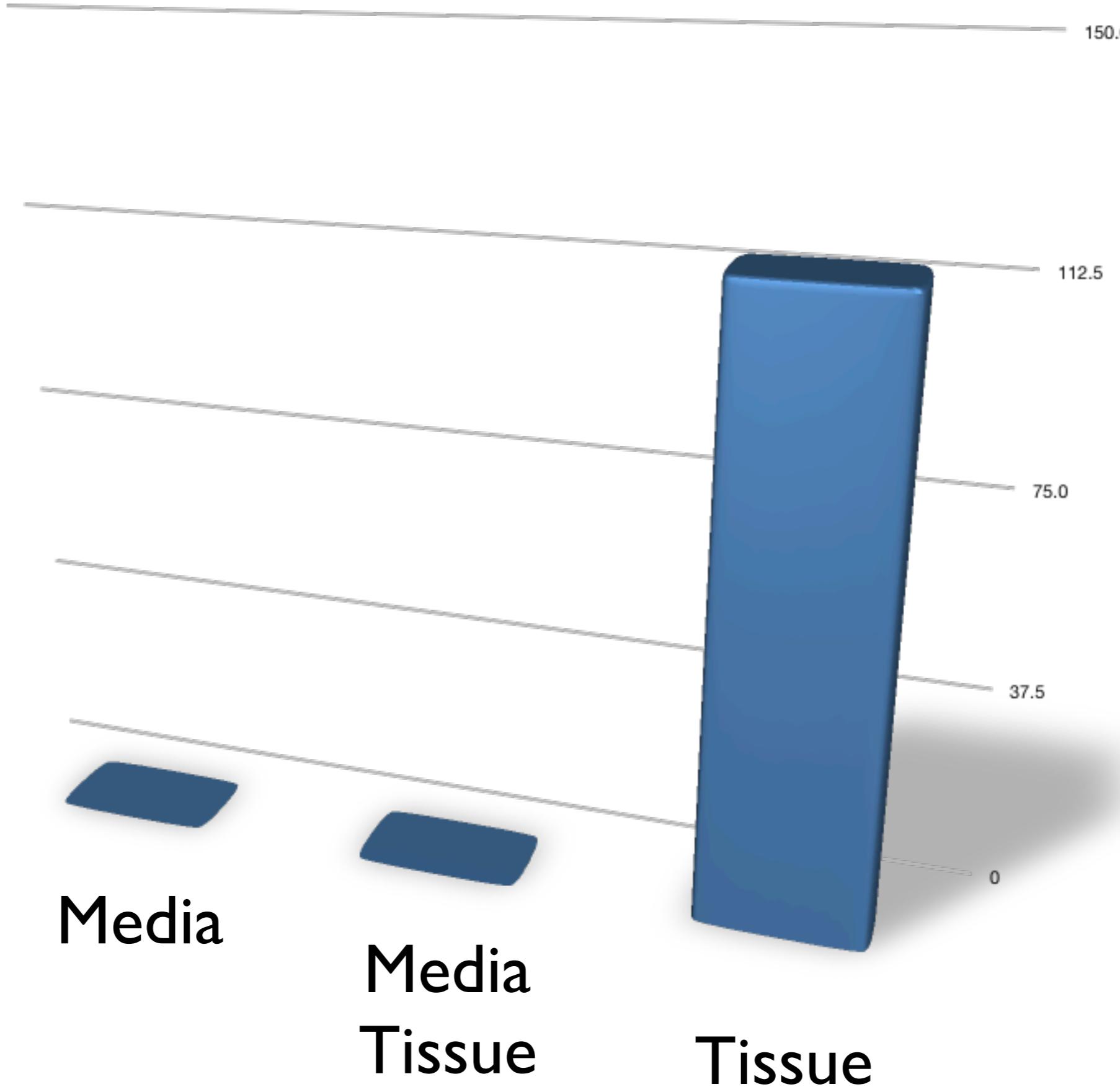
ATCC

Serine Protease gene expression



21°C

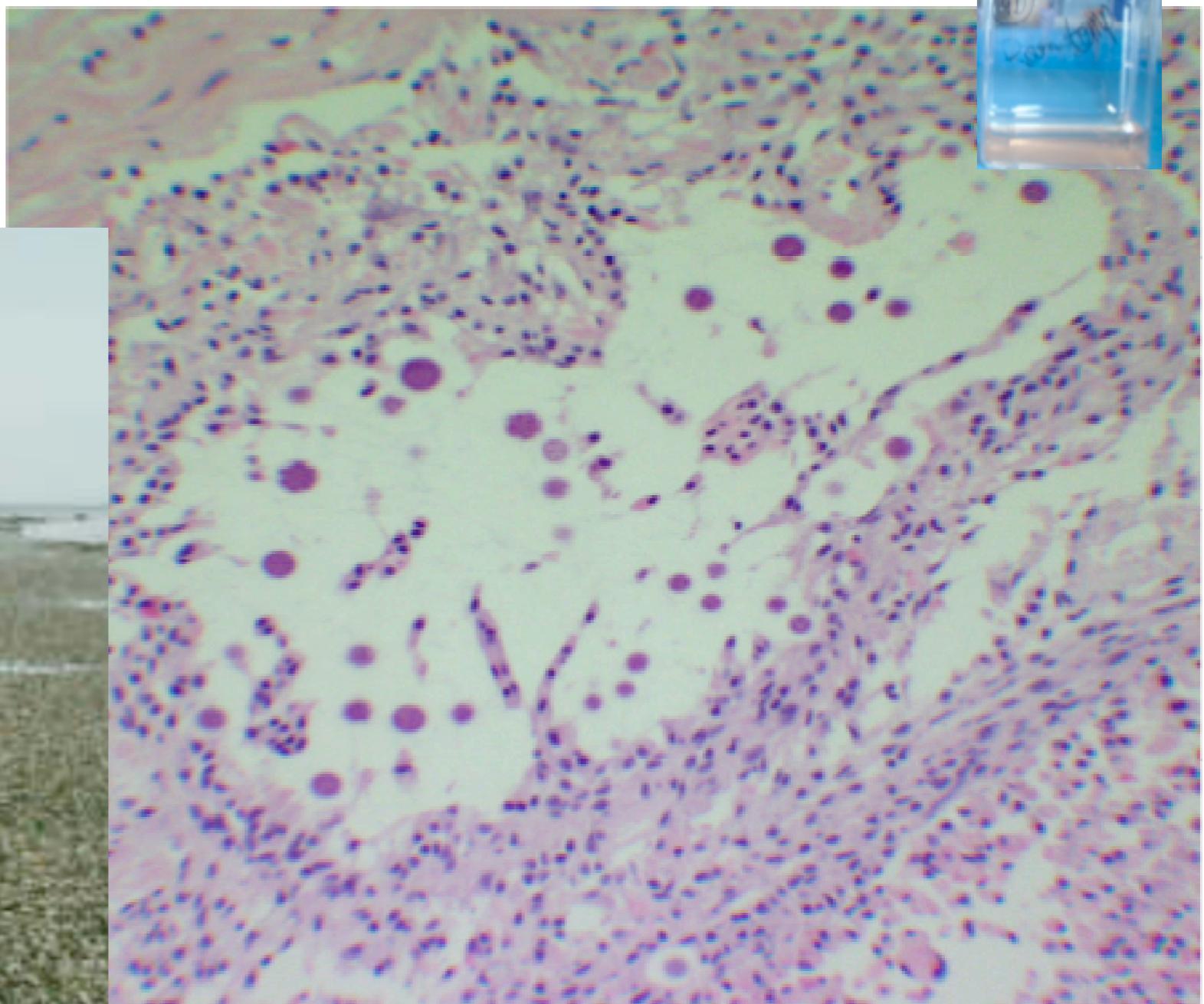
Serine Protease gene expression



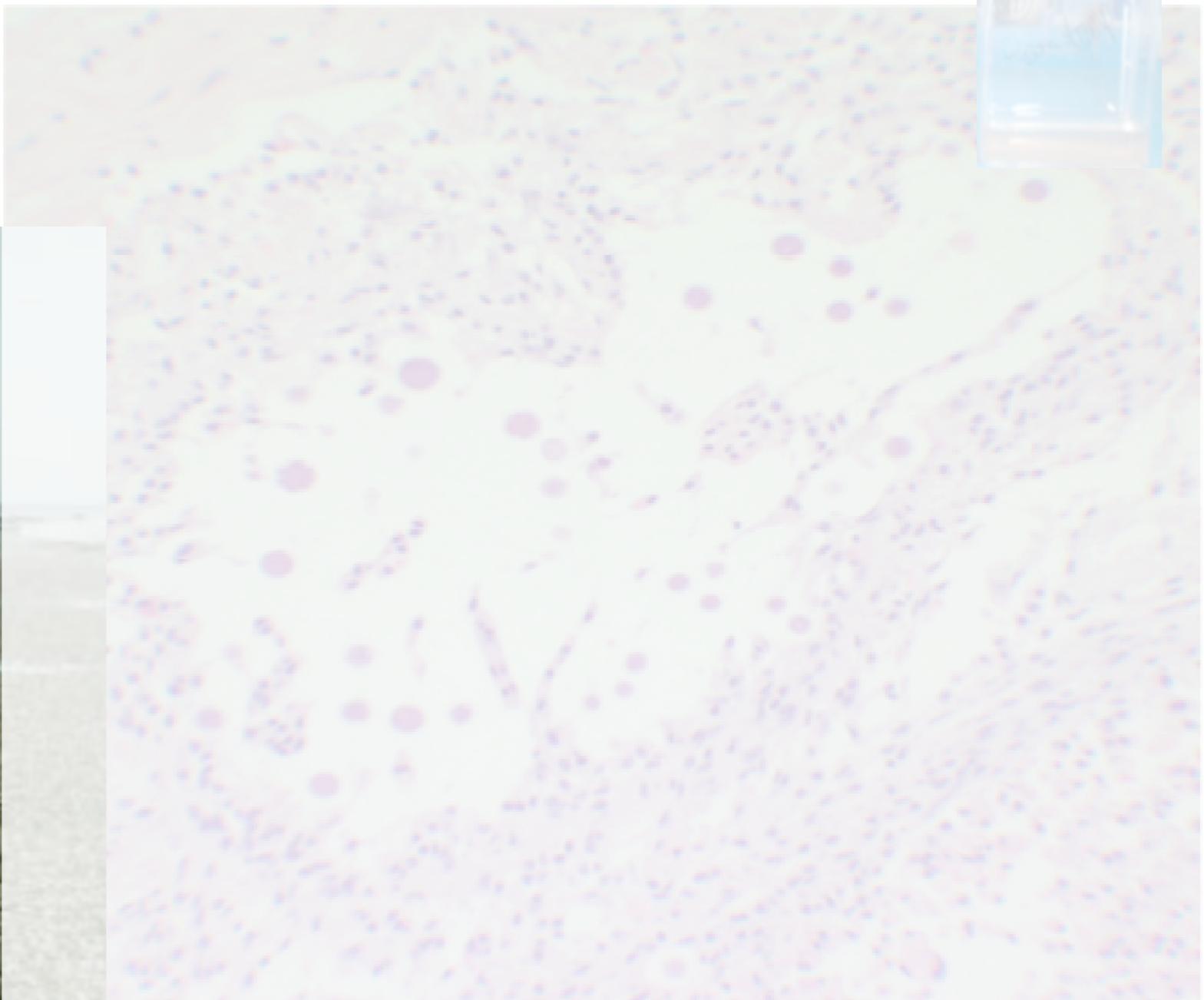
Summary

- 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



Roxanna Smolowitz

Rationale

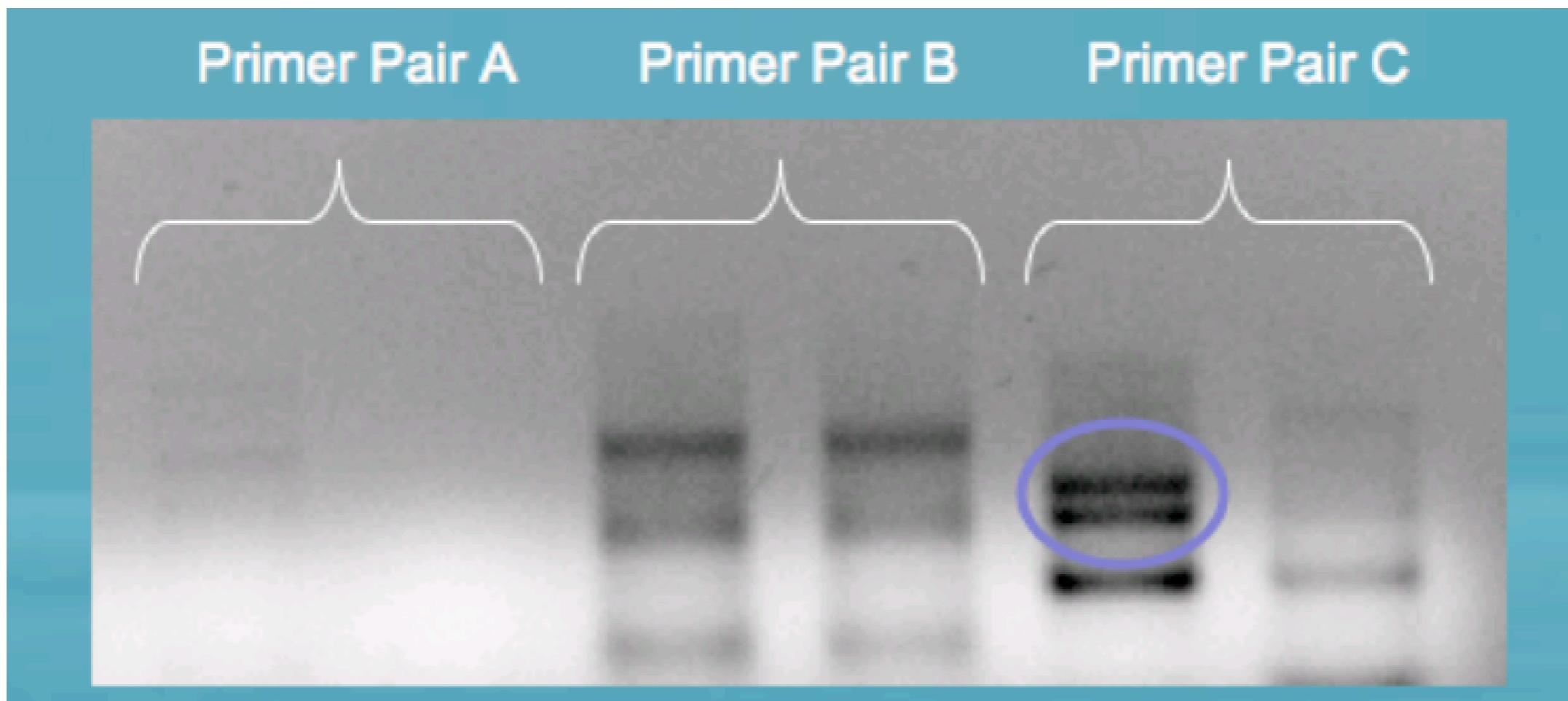
- Understand more concerning **Clam** physiology
 - Environmental Influence
 - Differences in Strain
 - Immune Response



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*

EFFECT OF HOMOGENATE FROM DIFFERENT OYSTER SPECIES ON *PERKINSUS MARINUS* PROLIFERATION AND SUBILISIN 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

Inhibitors of proteases

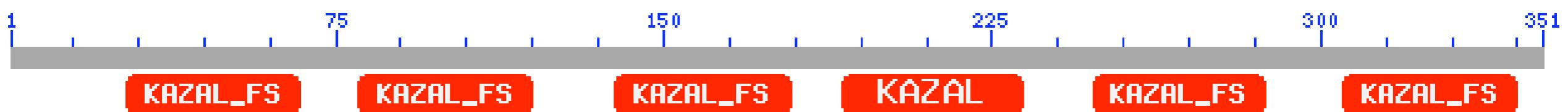
Protease Inhibitory Activity in Selectively Bred Families of Eastern Oysters

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

<u>Dipetalogaster maximus</u> [bugs] taxid 72496		
sp 096790 DPGN_DIPMA Serine protease inhibitor dipetalogast...	83	5e-15
emb CAA10384.1 dipetalogastin [Dipetalogaster maximus]	83	5e-15
<u>Triatoma brasiliensis</u> [bugs] taxid 65344		
qb ABI96910.1 brasiliensin precursor [Triatoma brasiliensis]	82	1e-14
<u>Chlamys farreri</u> [bivalves] taxid 202578		
qb ABB58758.1 serine protease inhibitor-1L [Chlamys farreri]	81	3e-14
qb ABB58759.1 serine protease inhibitor-1S [Chlamys farreri]	80	4e-14
qb ABB89133.1 serine protease inhibitor CFSP13 [Chlamys f...	68	2e-10
qb ABC02759.1 serine protease inhibitor [Chlamys farreri]	65	2e-09

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

CRP-LCACPRIYKPVCGQDGKTYPNQCELNCAGVALFEEGPCIATSPQFDFAPEAPCICT
CRP C CP IY PVCG DGRTY N C C V + C C+CT
CRPEQCVCPSTIYSPVCGYDGKTYSNACSAGCDNVKIRCNRKCPCKG-----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 homologus 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

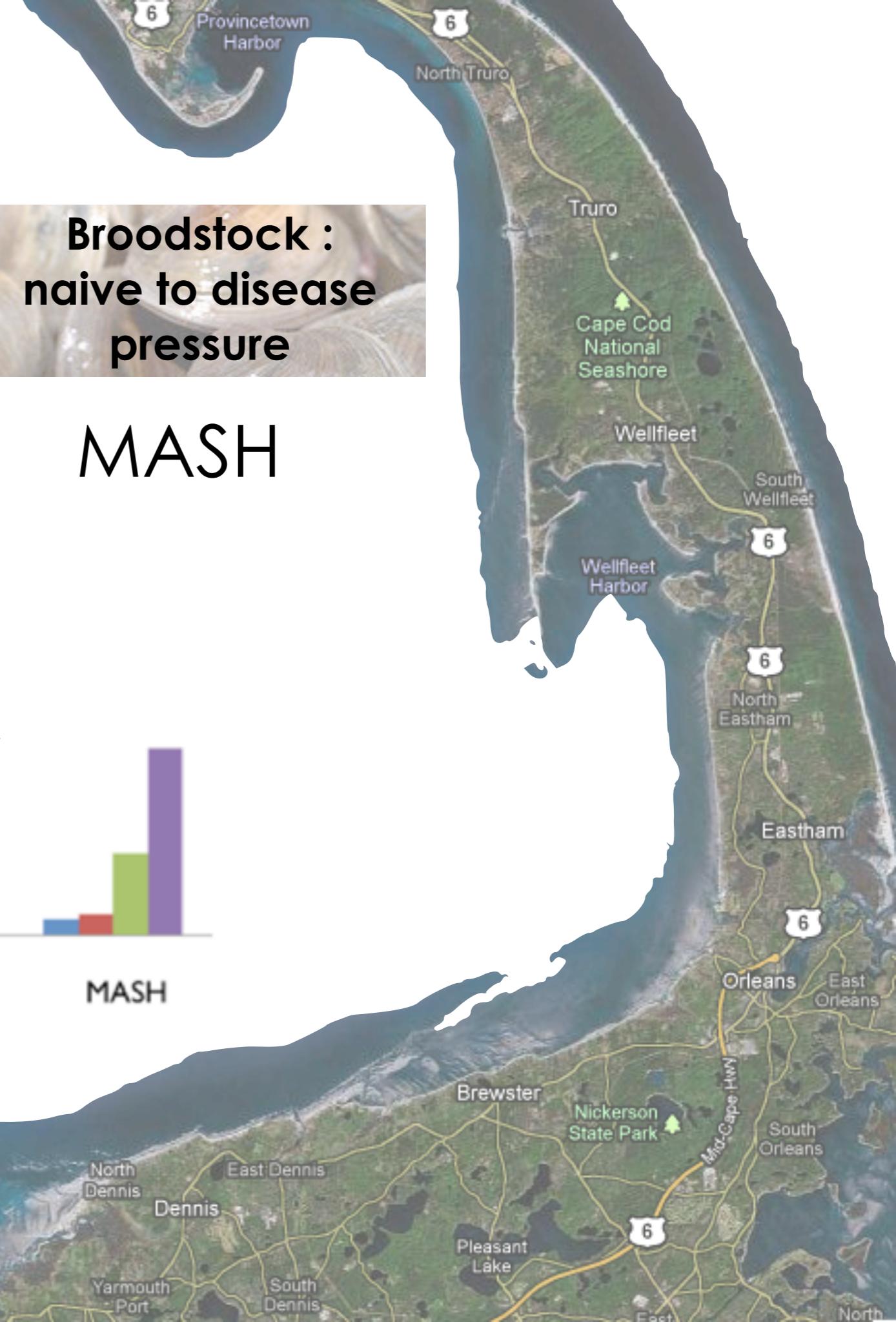
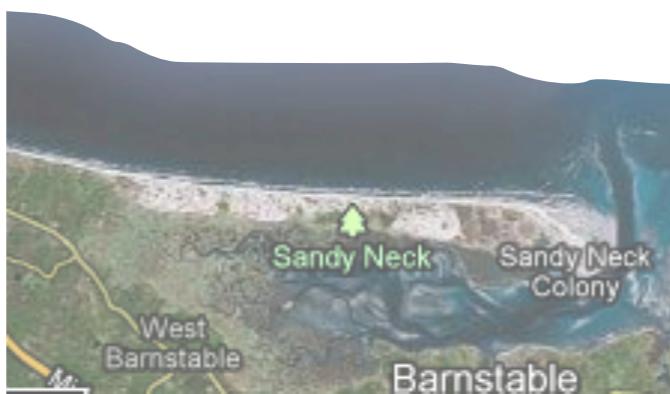
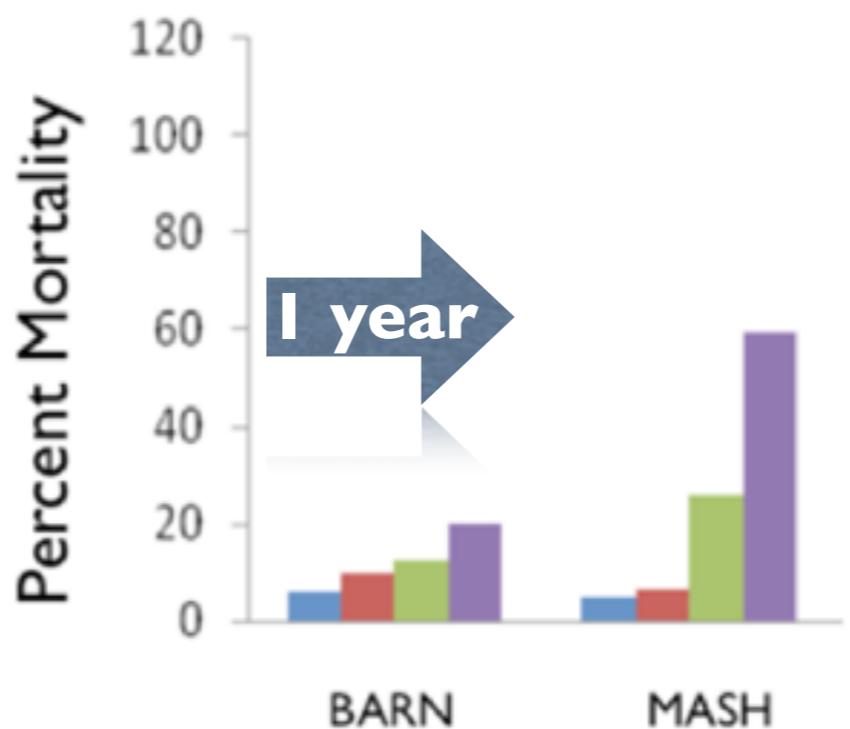


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BARN

MASH

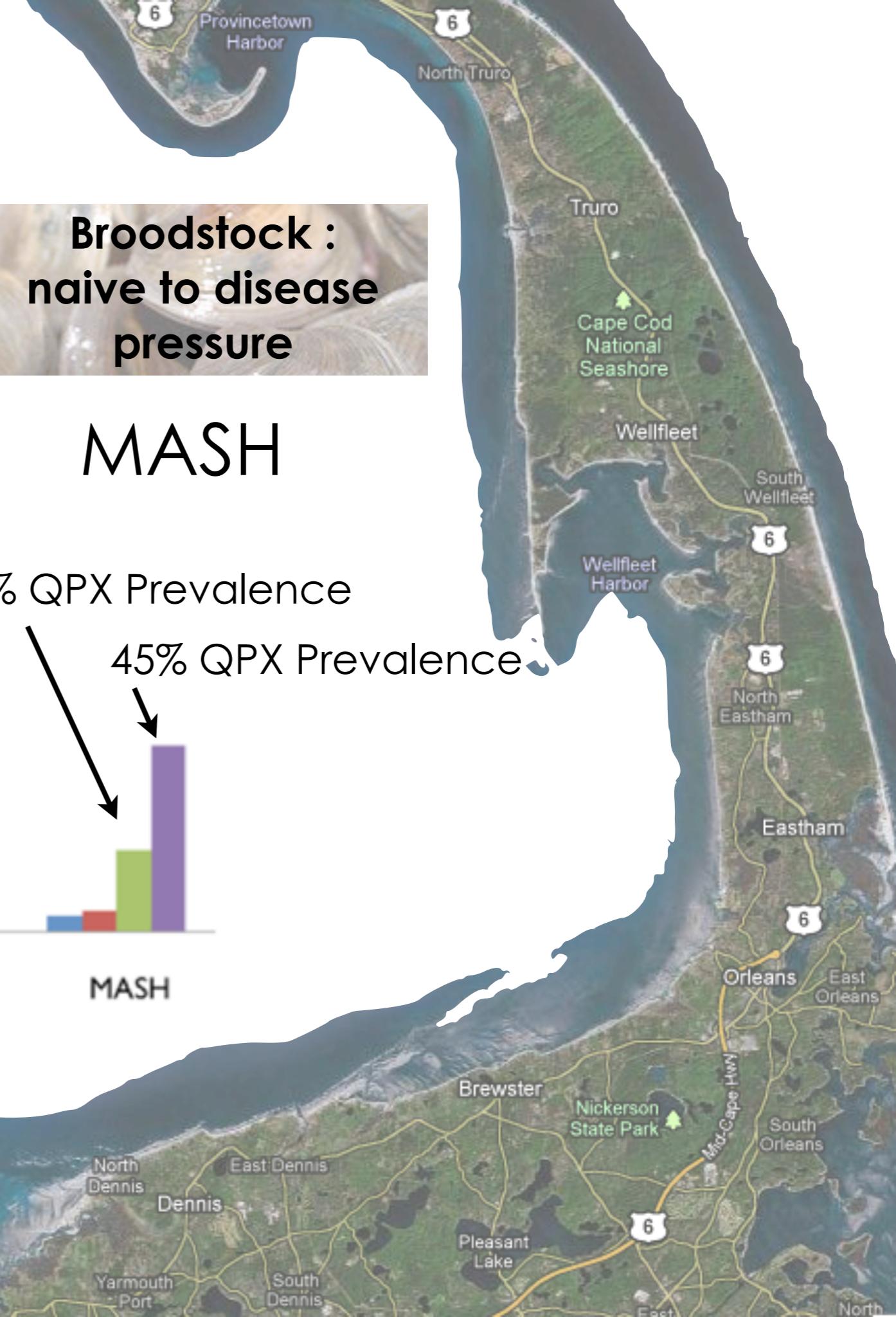
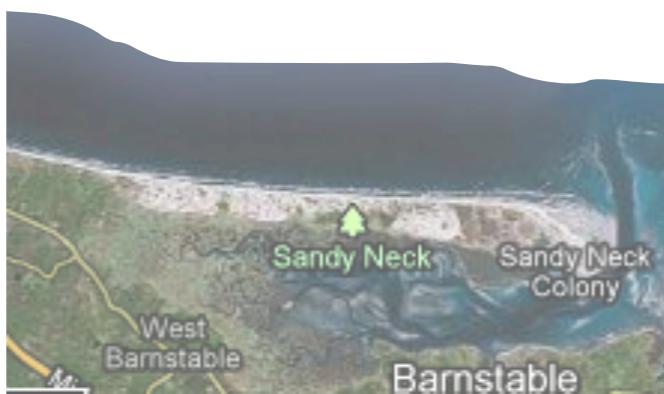
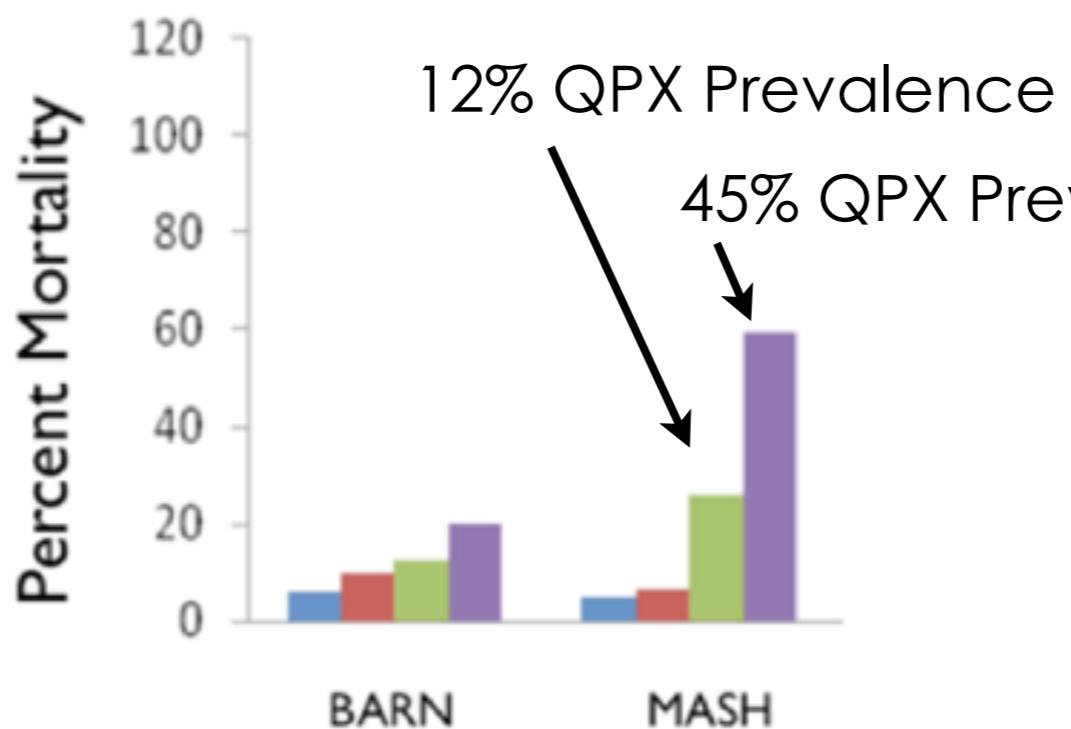


Broodstock :
survived disease
pressure

Broodstock :
naive to disease
pressure

BARN

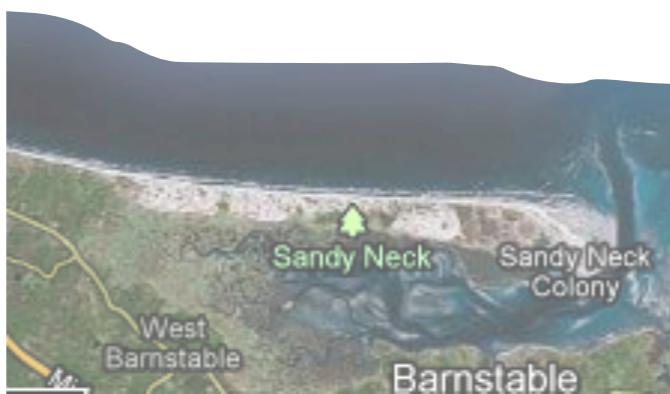
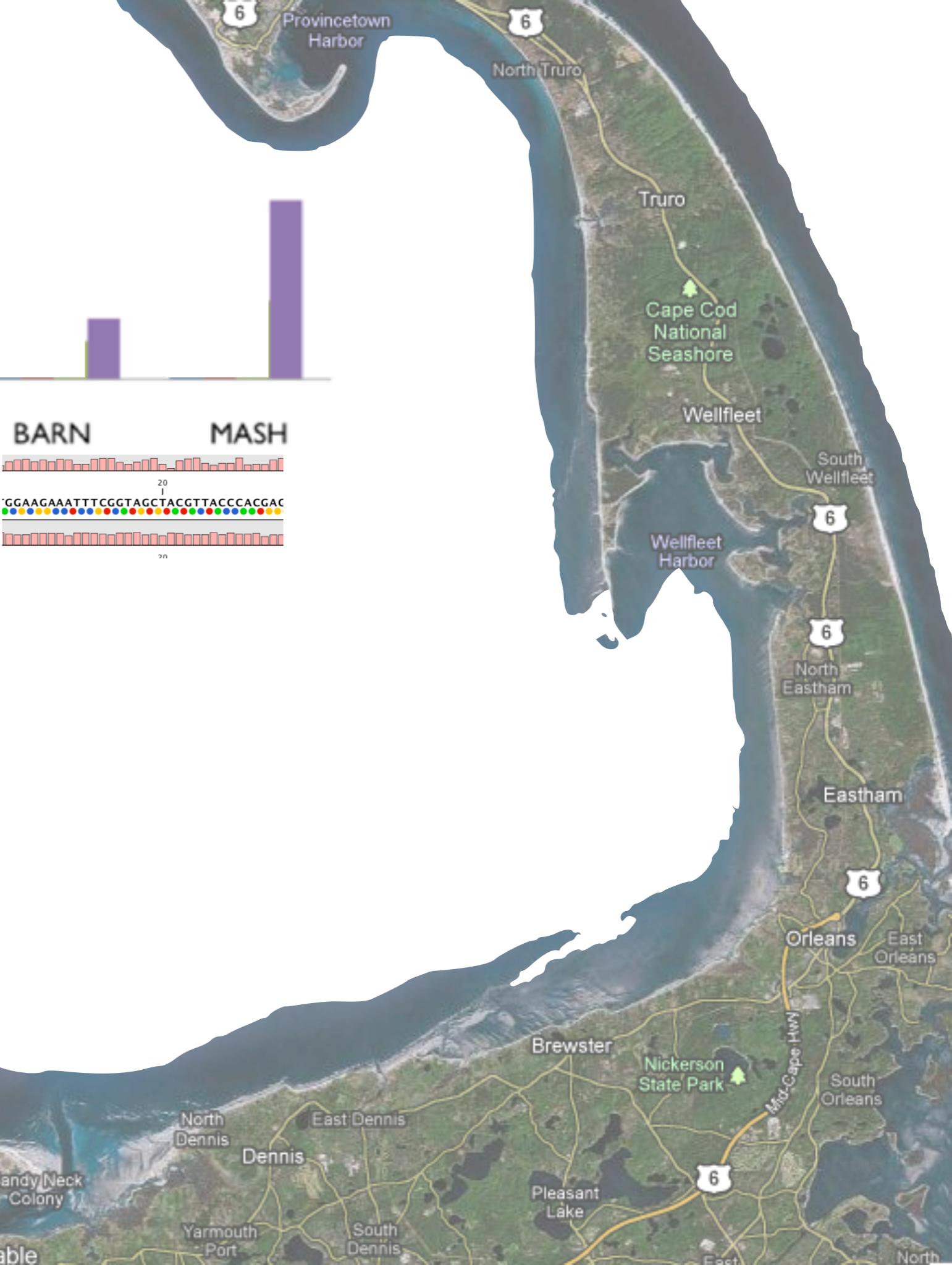
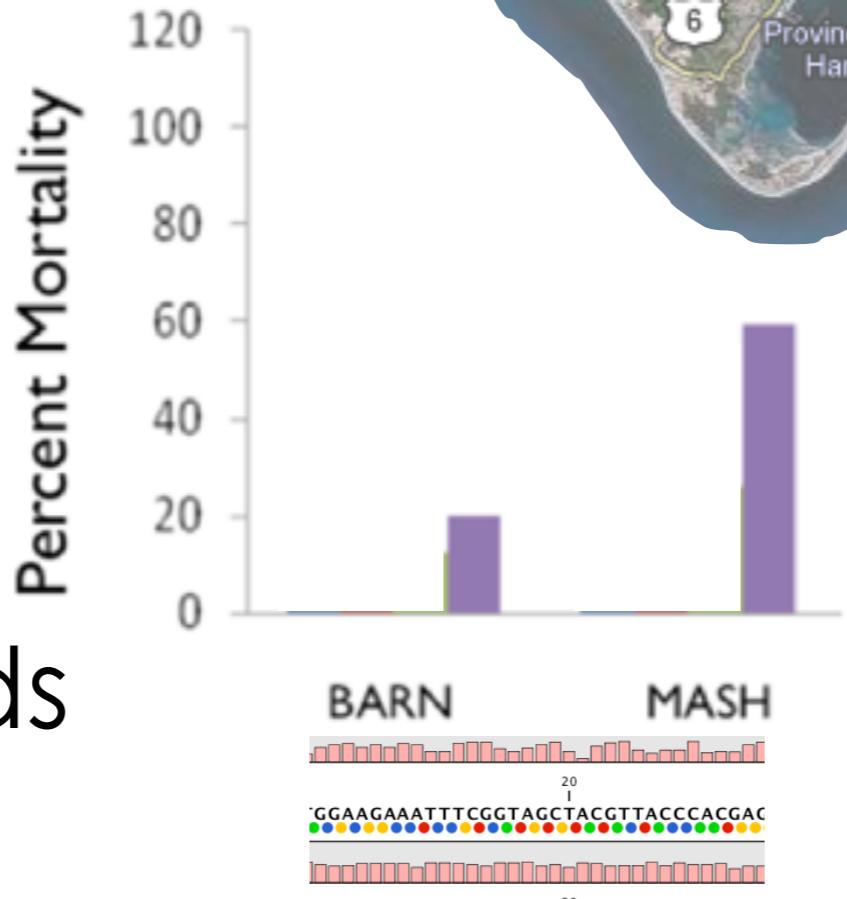
MASH



RNA-Seq

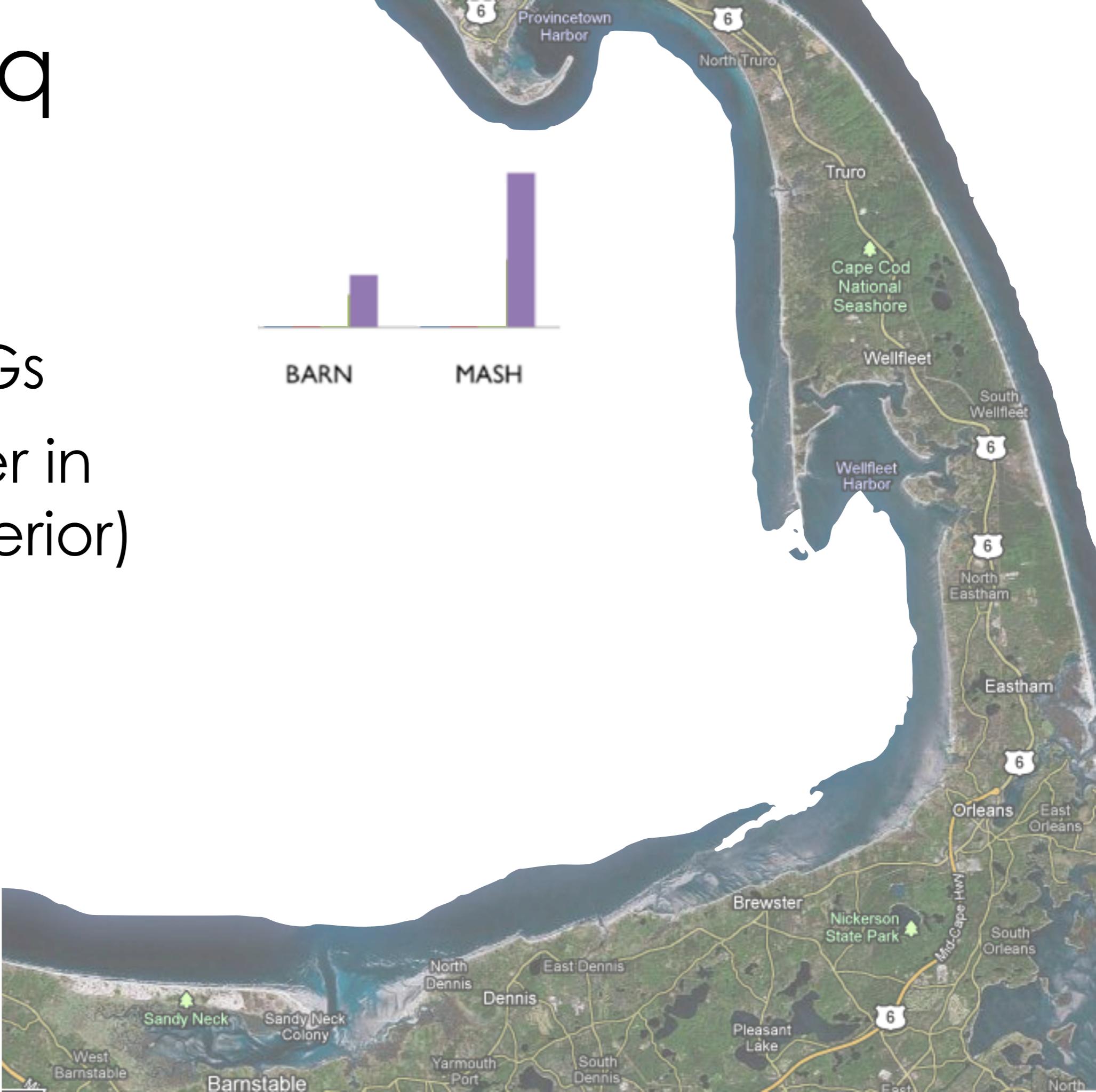
100 million reads

8482 contigs



RNA-Seq

684 DEGs
459 higher in
BARN (superior)



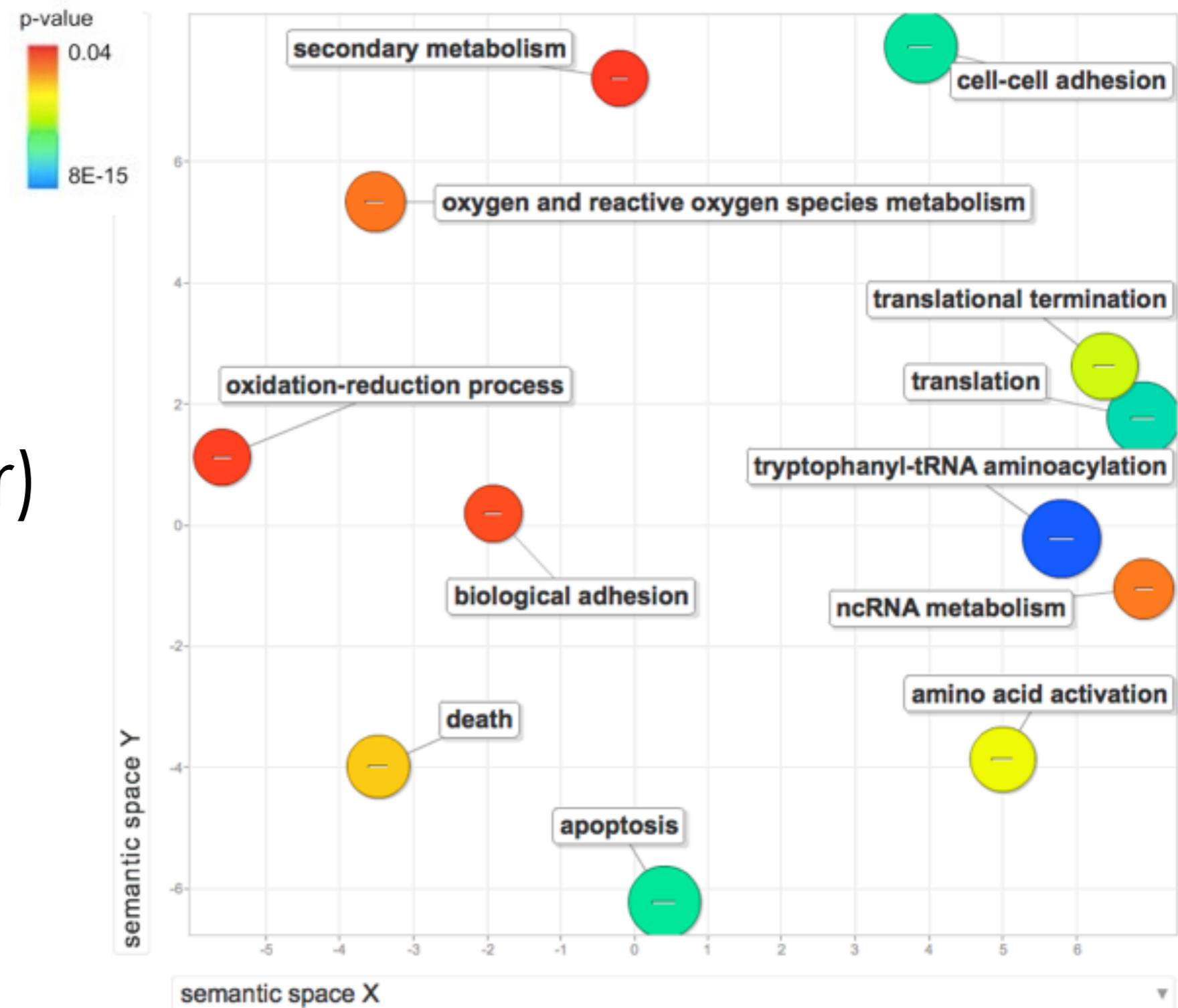
RNA-Seq

684 DEGs

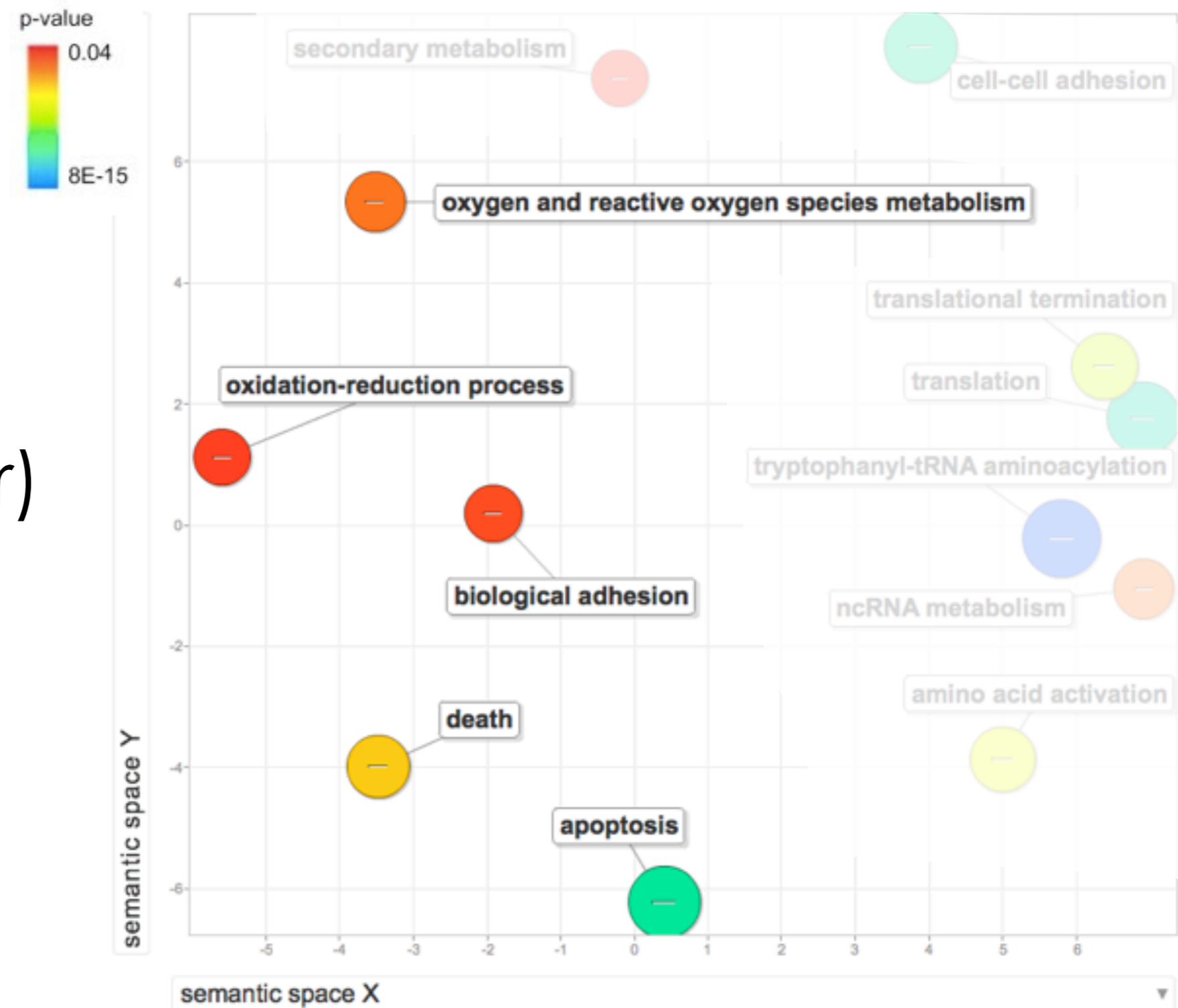
459 higher in
BARN (superior)

33 enriched
biological
processes

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



684 DEGs
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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

peroxidasin, 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

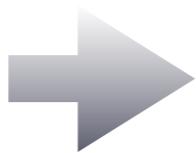
Genotyping



BARN

MASH

Restriction Enzyme



Assisted
Digestion

-
Sequencing

Reduce Representation

Genotyping



BARN

MASH

Restriction Enzyme
Assisted
Digestion

-
Sequencing



Reduce Representation

Sequence multiple individuals

Genotyping



BARN

MASH

Restriction Enzyme
Assisted
Digestion

-
Sequencing



Reduce Representation

Sequence multiple individuals

145 Diagnostic Markers