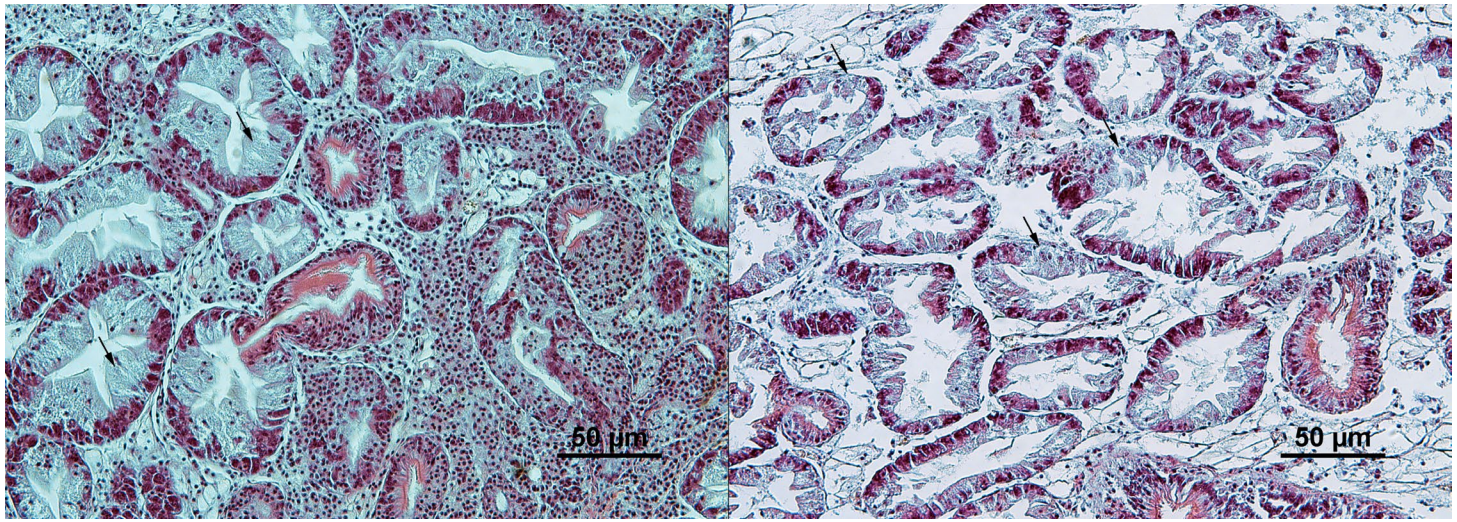


What we know about oyster mortality in NC

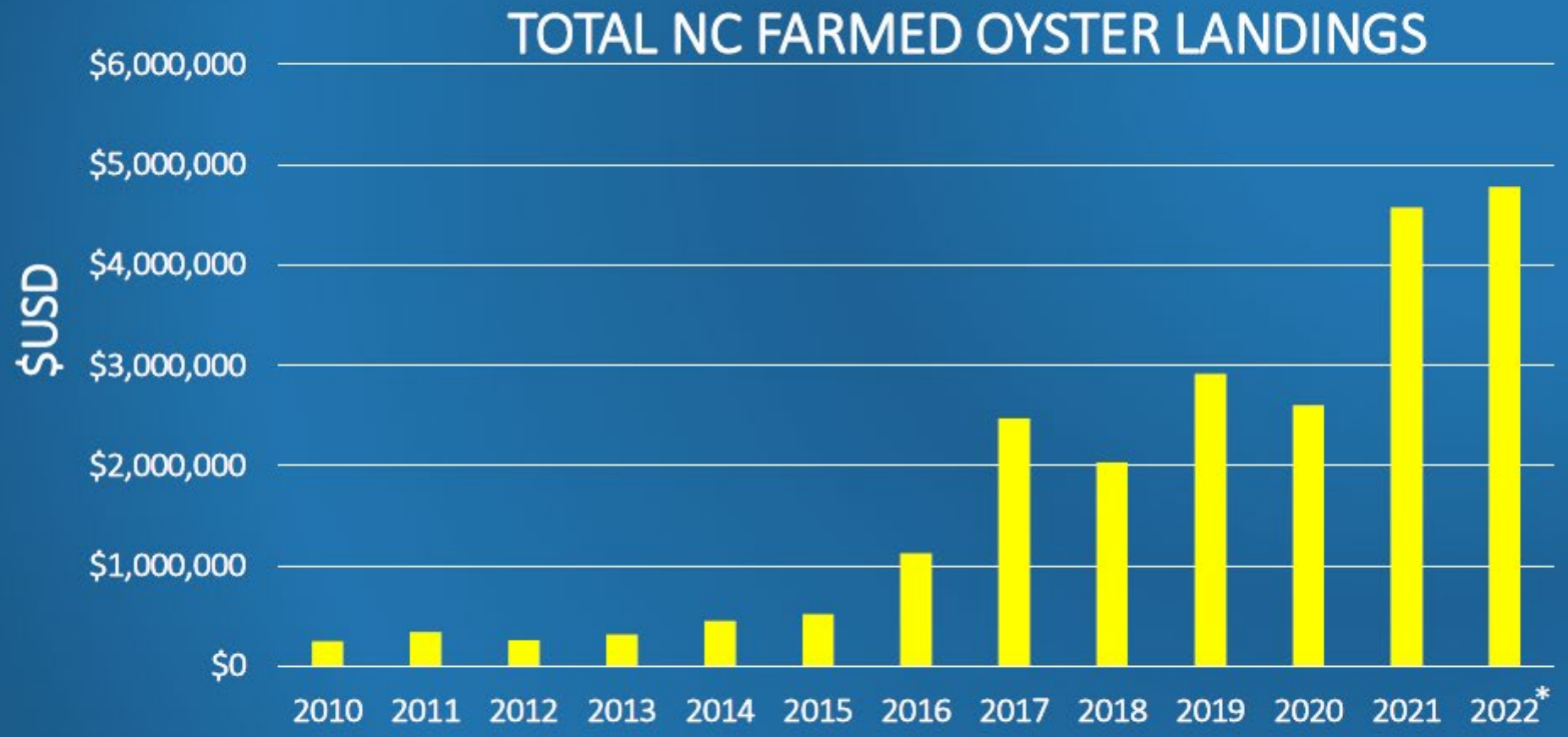
TAL BEN-HORIN

TUESDAY NOV 7TH 2023

NC STATE UNIVERSITY CMAST
The Center for Marine Sciences and Technology

Shellfish Pathology Laboratory

North Carolina Farmed Oyster Production



*2022 Data is preliminary

Sea Grant North Carolina

2022 Farmed Oysters: $4.78M (+5% from 2021) | Highest Ever

Oyster aquaculture in the Southeast frequently faces dramatic mortality events during warmer months

Brutal season for farmed oyster mortality along North Carolina coast

LENA BECK COASTAL REVIEW ONLINE Jun 24, 2022 Updated Jun 24, 2022 6

Mark Ciesielski, a doctoral candidate in the Noble Lab in the University of North Carolina Institute of Marine Sciences, checks a shellfish growing study site. Photo: Alyssa LaFaro/UNC

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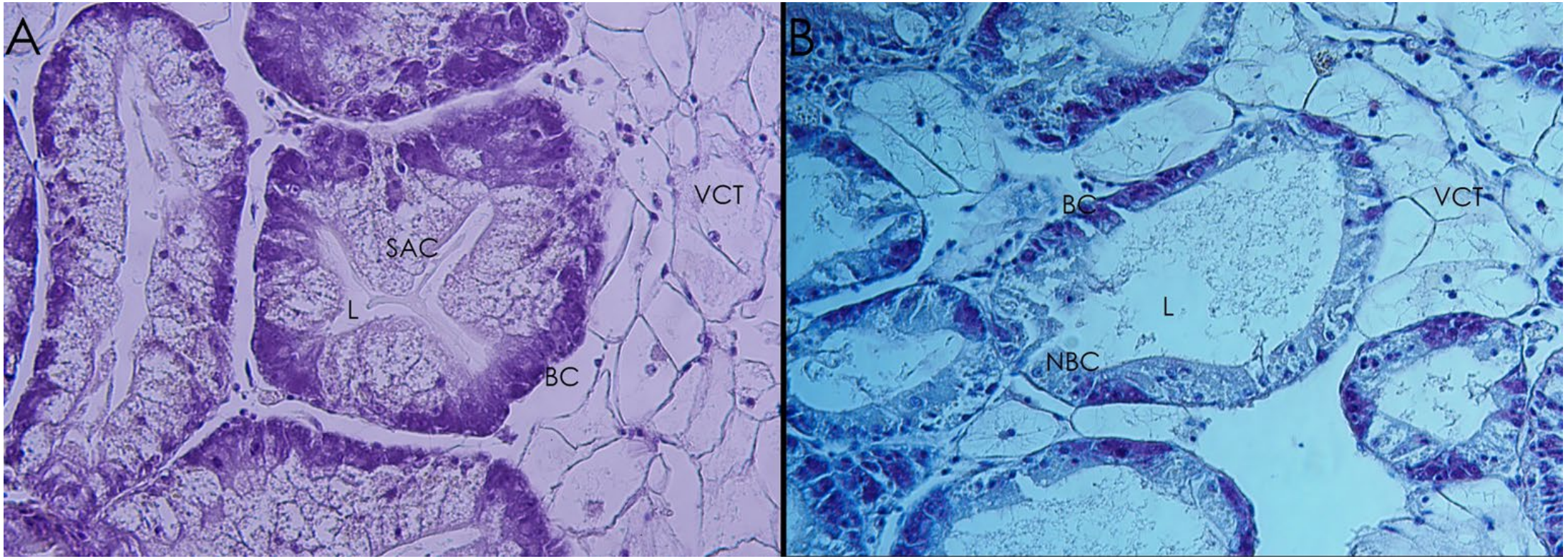
What's killing North Carolina's oysters?

05:11

August 02, 2022 By Zachary Turner, WUNC

Researchers count and measure oyster shells to determine their health. (Zachary Turner/WUNC)

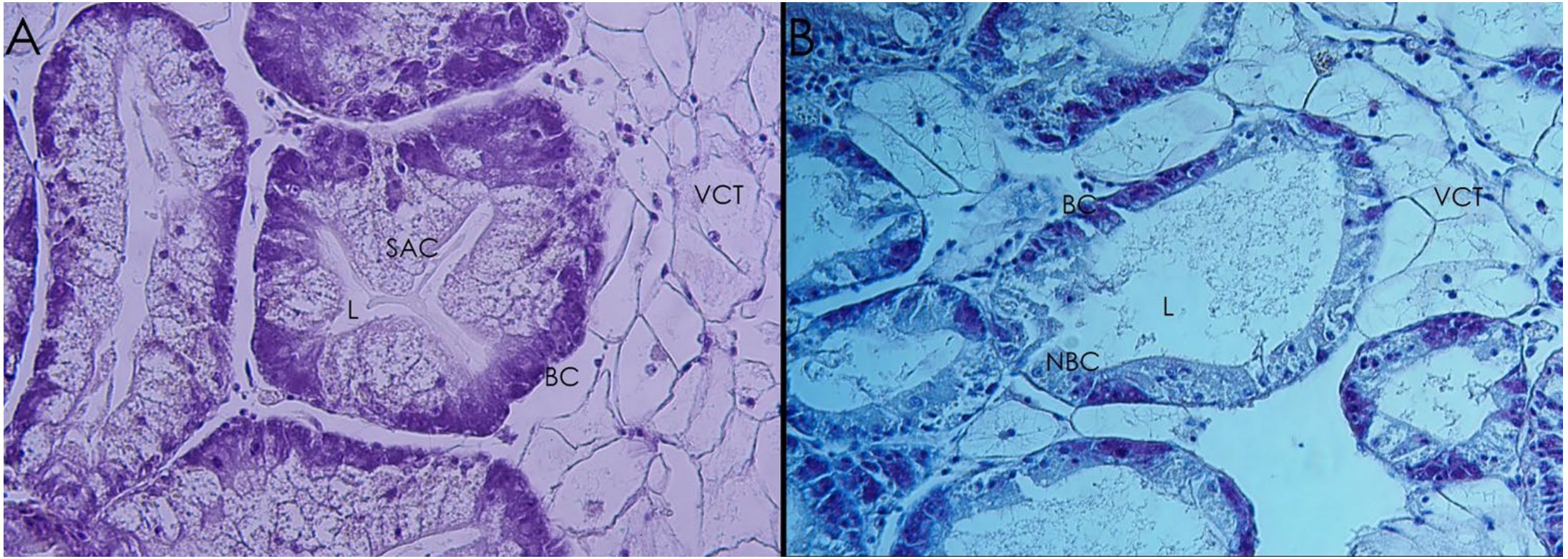
Oyster farming is an up-and-coming industry in North Carolina. But something is killing the oysters. Researchers are working with oyster farmers to uncover the cause.



The typical pathology indicates oysters are starving

Widespread sloughing of **secretory absorptive cells** (**SAC**) within digestive diverticula, cellular debris and expanded **lumen** (**L**) area, condensed cytoplasm and flattening of **basophilic epithelial cells** (**BC**), **necrotic basophilic cells** (**NBC**) show nuclear dissolution (220x)

Left = Healthy digestive tubules; Right = Tubules typically seen through mortality events



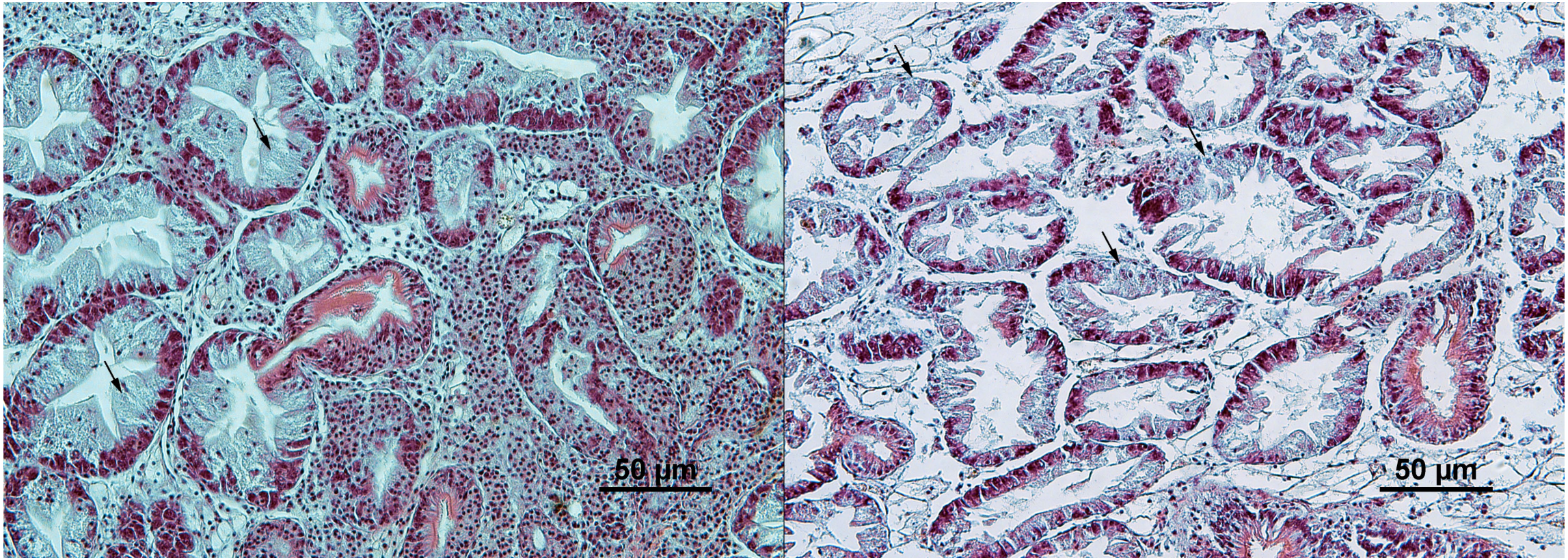
SACs are the site of intracellular digestion (proteins, fats, sugars, electrolytes, vitamins, etc.)

Analogous disorders in humans include:

- Conditions such as lactose intolerance and celiac disease
- Bacterial infection such as cholera
- Several viruses including rotavirus

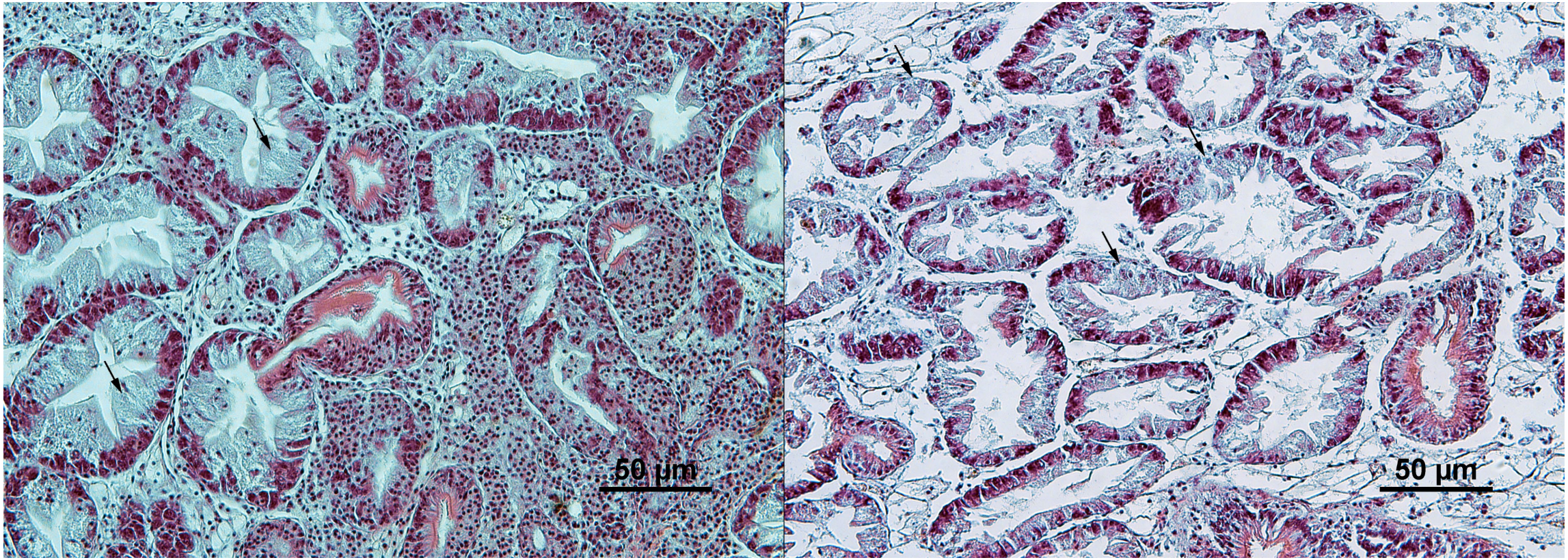
Persistent digestive tubule pathology precedes observed oyster mortality by 3-4 weeks

Summer mortality chronology

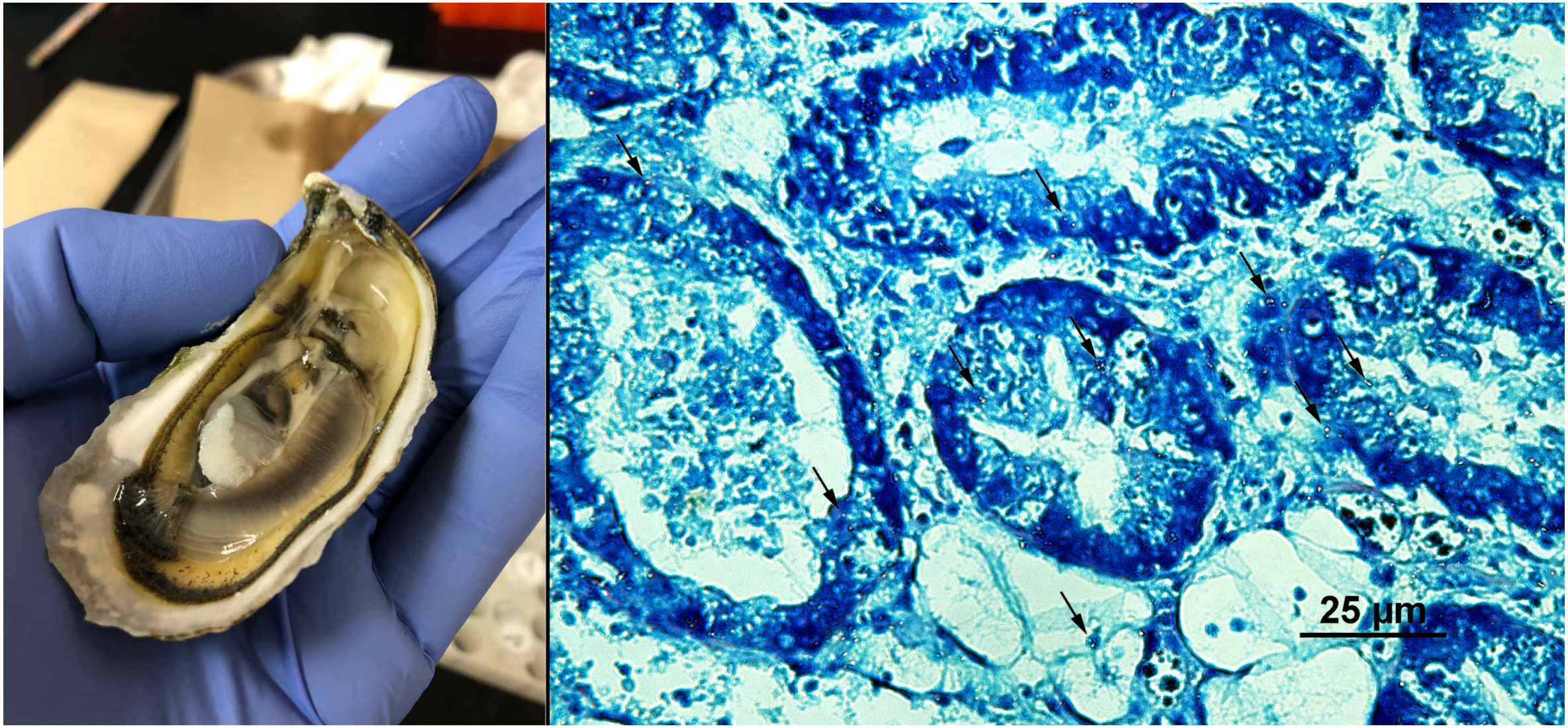


(*left*) massive hemocyte infiltration throughout digestive tubules and vesicular connective tissue. Tubule architecture relatively intact.

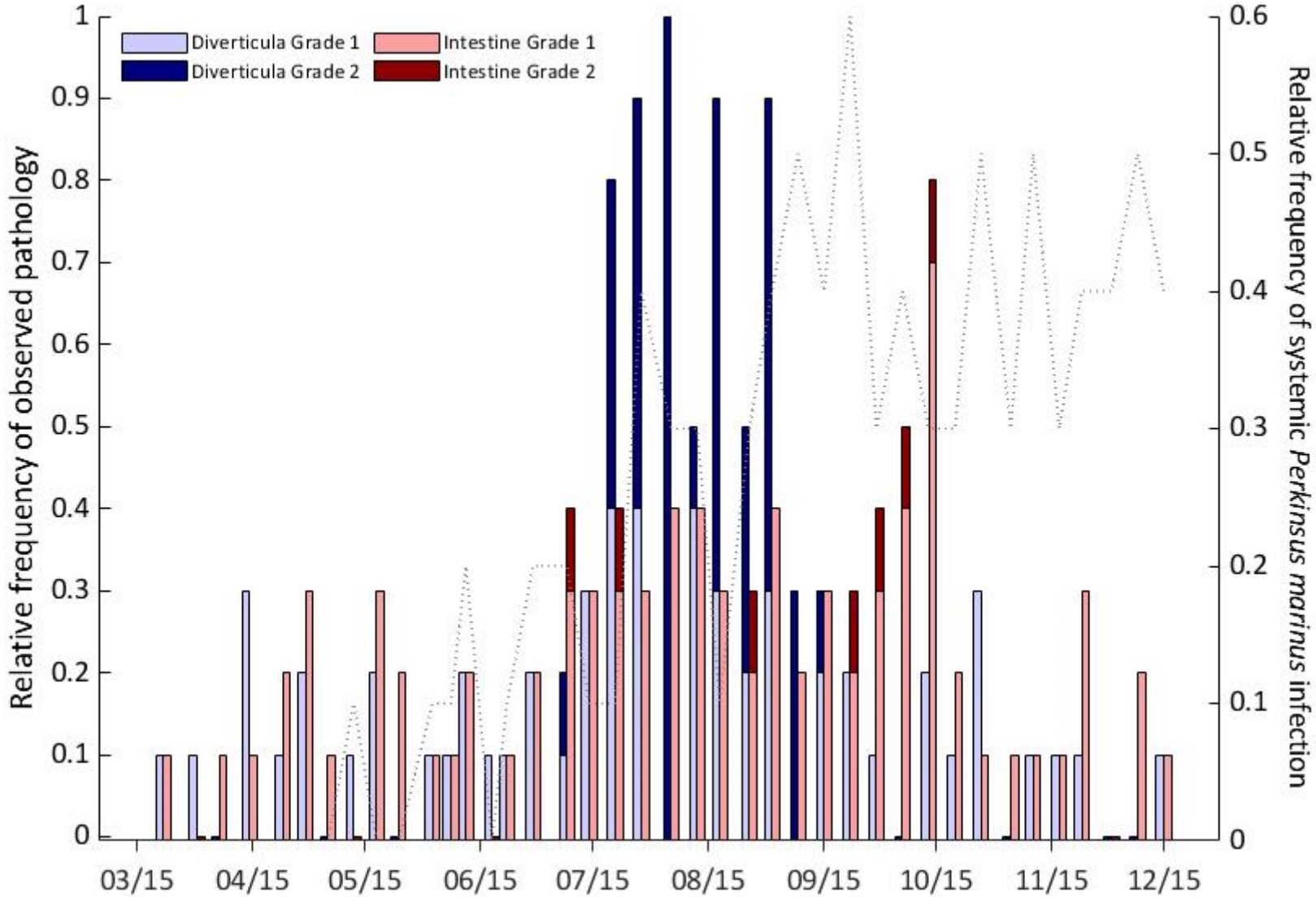
Summer mortality chronology



(*right*) persistent sloughing and necrosis of secretory absorptive cells through the following weeks

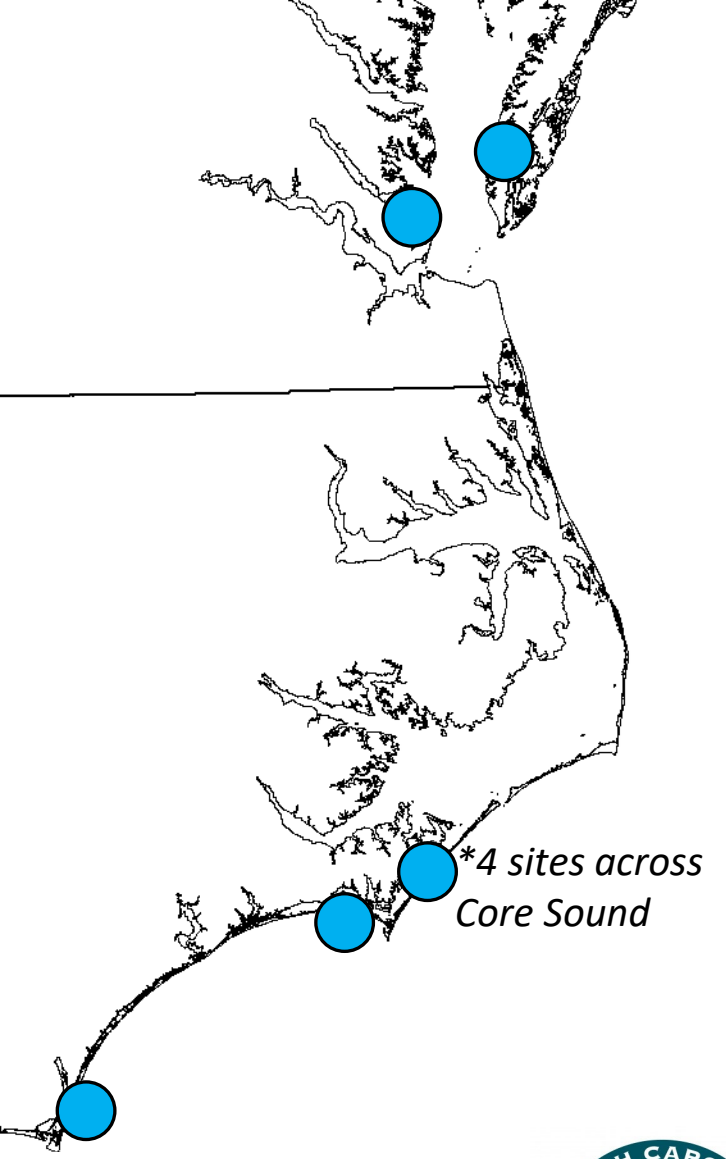


Animals are healthy otherwise. Numerous coccoid and rod-shaped bacteria associated with digestive tubules



Grade 1: Sloughing absorptive cells and reduced/condensed cytoplasm in epithelial cells observed in < 10% of tubules

Grade 2: As above but in > 10% of tubules, nuclear dissolution and exposed basement membrane in epithelial cells, and occasional observed colliquative necrosis



Reciprocal Transplant Experiment (Spring-Fall 2022)

VIMS

HNRY 2N + HNRY 2N (HNRY 2N)

HNRY 2N + GNL 4N (HNRY 3N)

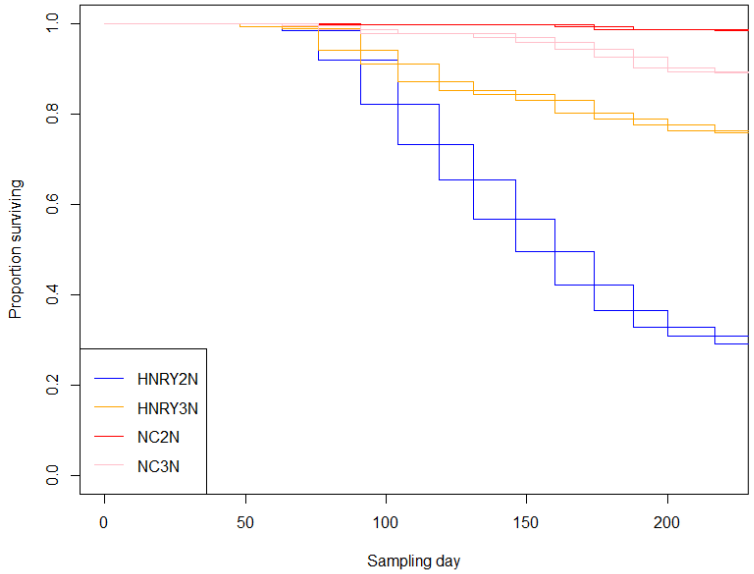
UNCW

Hewlett's Creek 2N + HNRY 2N (NC 2N)

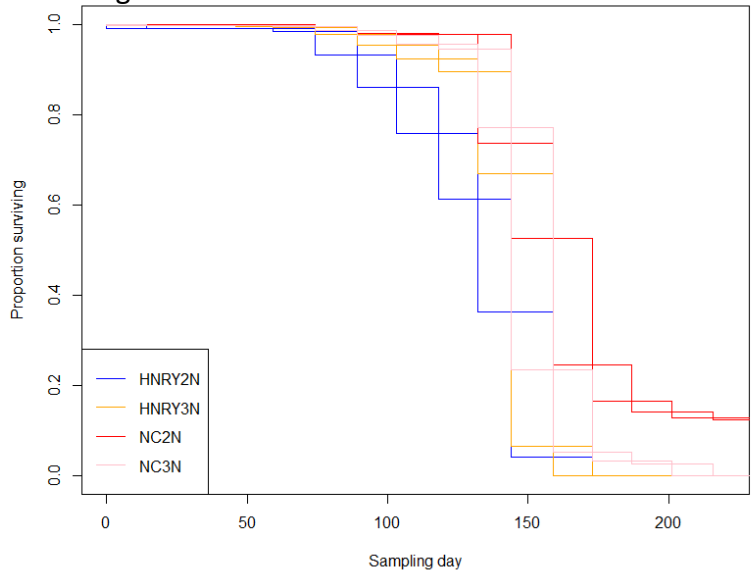
Hewlett's Creek 2N + GNL 4N (NC 3N)

NORTH CAROLINA
Department of Environmental Quality

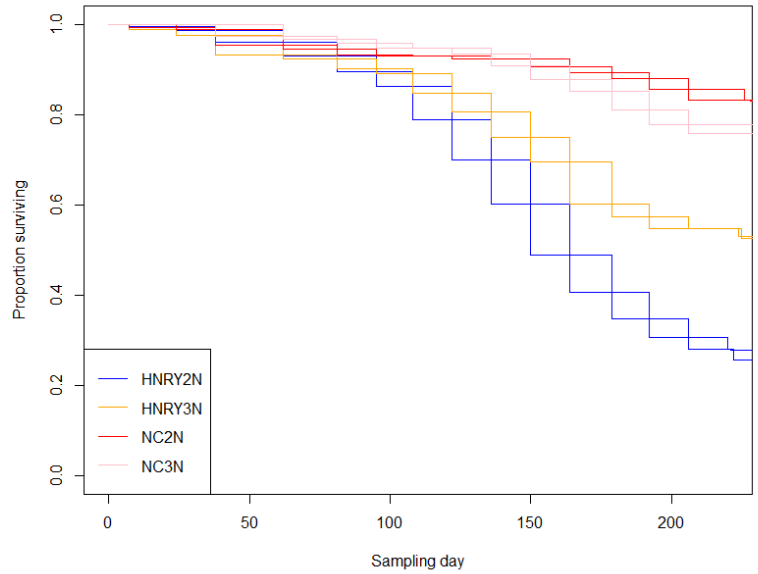
Core Sound 1



Bogue Sound

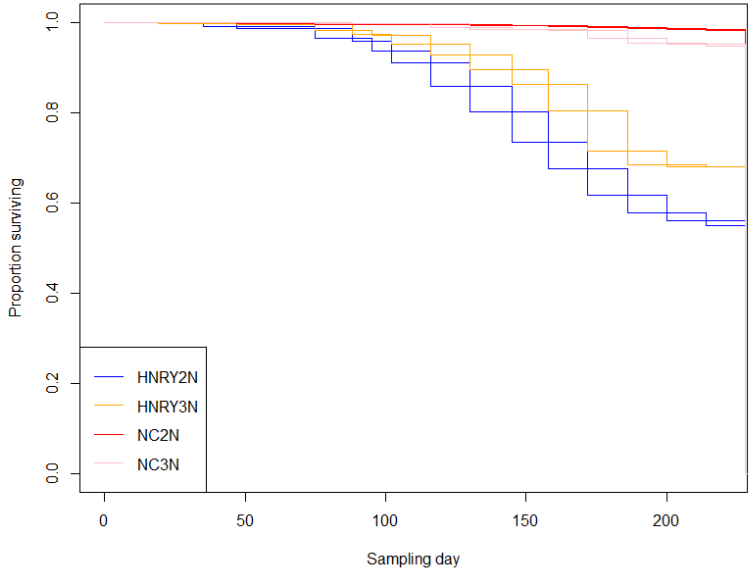


Masonboro Sound

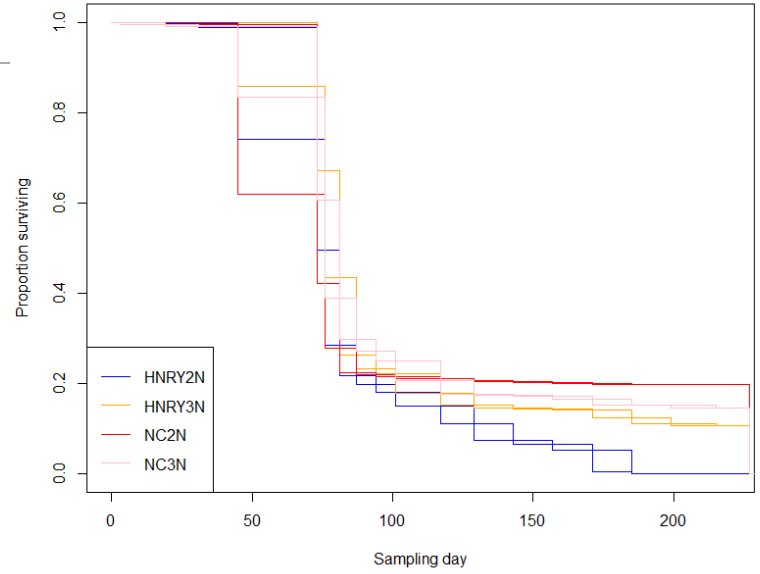


We saw near complete mortality at two sites, high mortality at a third site, in line with observations from regional growers. Our NC lines generally performed best, but when mortality hit all lines were equally susceptible. Very little evidence for increased susceptibility in 3Ns.

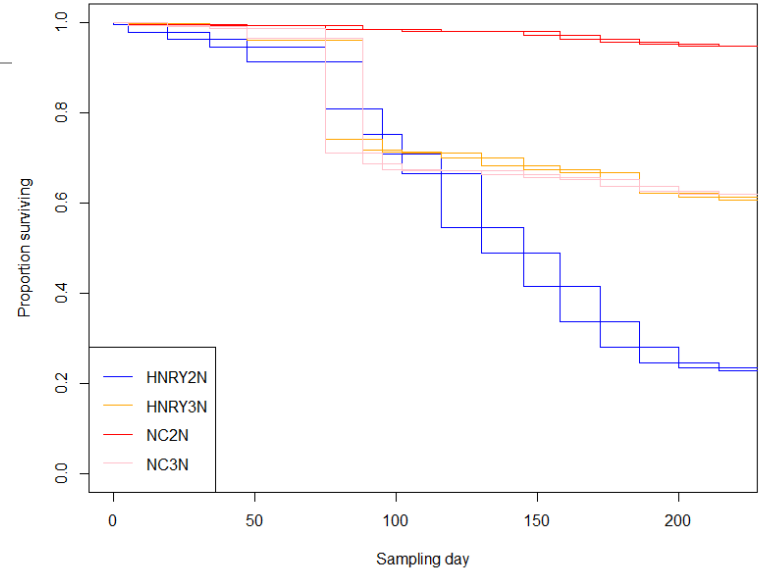
Core Sound 2

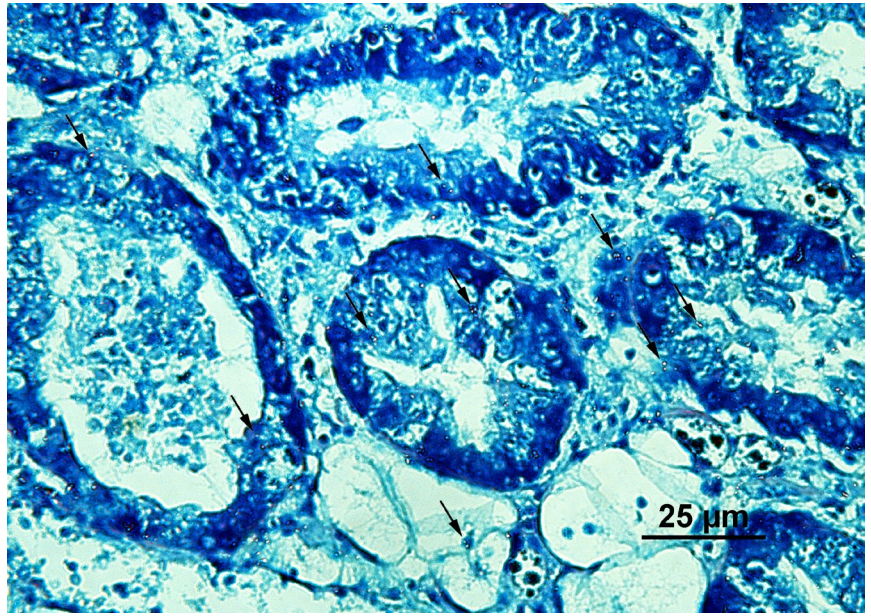


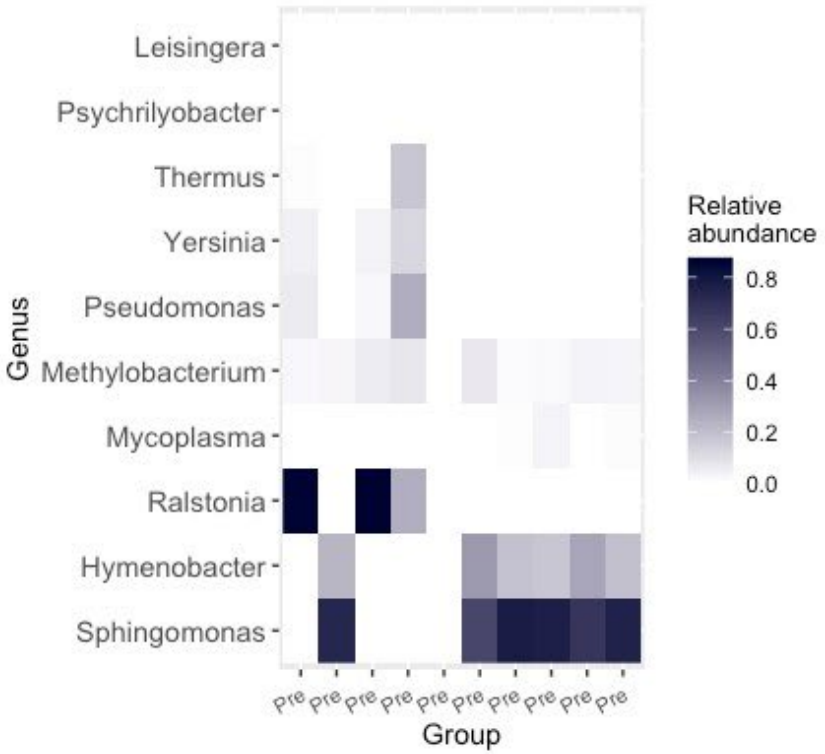
Core Sound 3

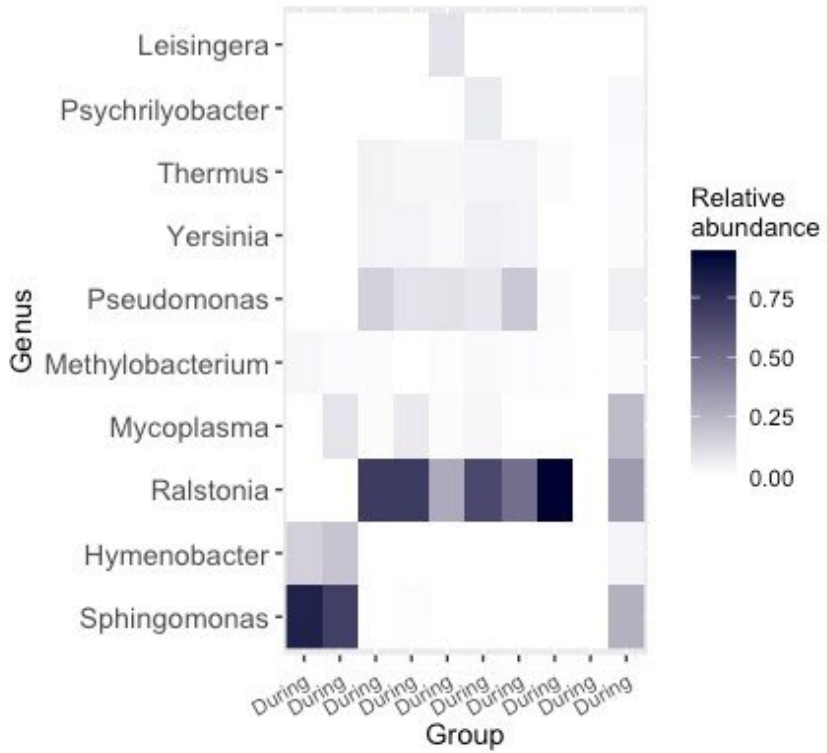


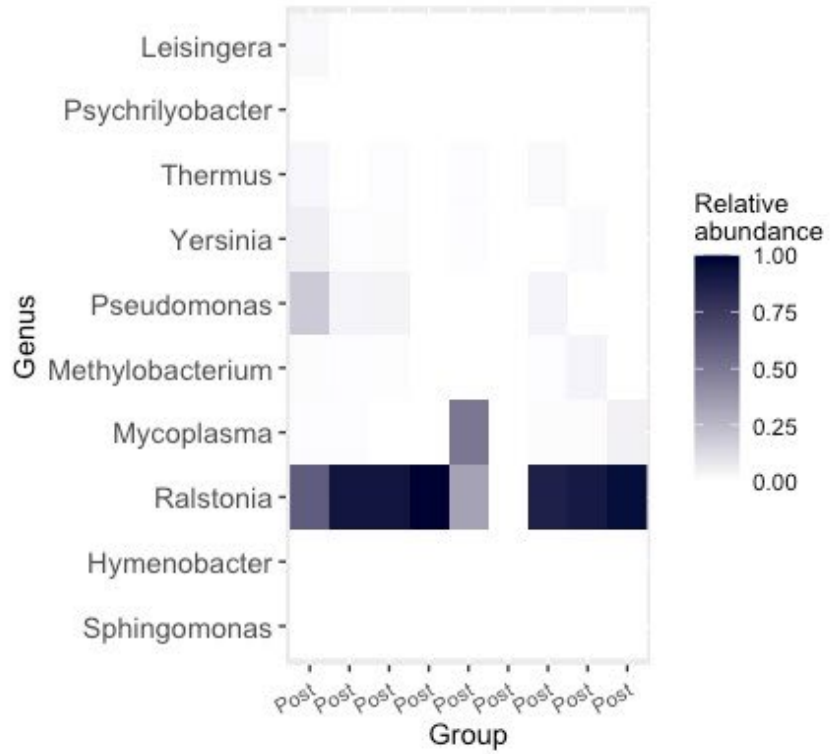
Core Sound 4




25 μm


Leisingera
Psychrilyobacter
Thermus
Yersinia
Pseudomonas
Methylobacterium
Mycoplasma
Ralstonia
Hymenobacter
Sphingomonas
Genus
Pre Pre Pre Pre Pre Pre Pre Pre Pre Pre
Group
Relative abundance
0.8
0.6
0.4
0.2
0.0


Leisingera
Psychrilyobacter
Thermus
Yersinia
Pseudomonas
Methylobacterium
Mycoplasma
Ralstonia
Hymenobacter
Sphingomonas
Genus
During During During During During During During During During
Group
Relative abundance
0.75
0.50
0.25
0.00


Leisingera
Psychrilyobacter
Thermus
Yersinia
Pseudomonas
Methylobacterium
Mycoplasma
Ralstonia
Hymenobacter
Sphingomonas
Genus
Post Post Post Post Post Post Post Post Post
Group
Relative abundance
1.00
0.75
0.50
0.25
0.00

What do we know?

Mortality is isolated to *high salinity sites*

Shifts toward increased dominance by Pseudomonas/Ralstonia in diverticula-associated microbes

All deployed lines appear susceptible, geographic origin seems a better predictor than ploidy

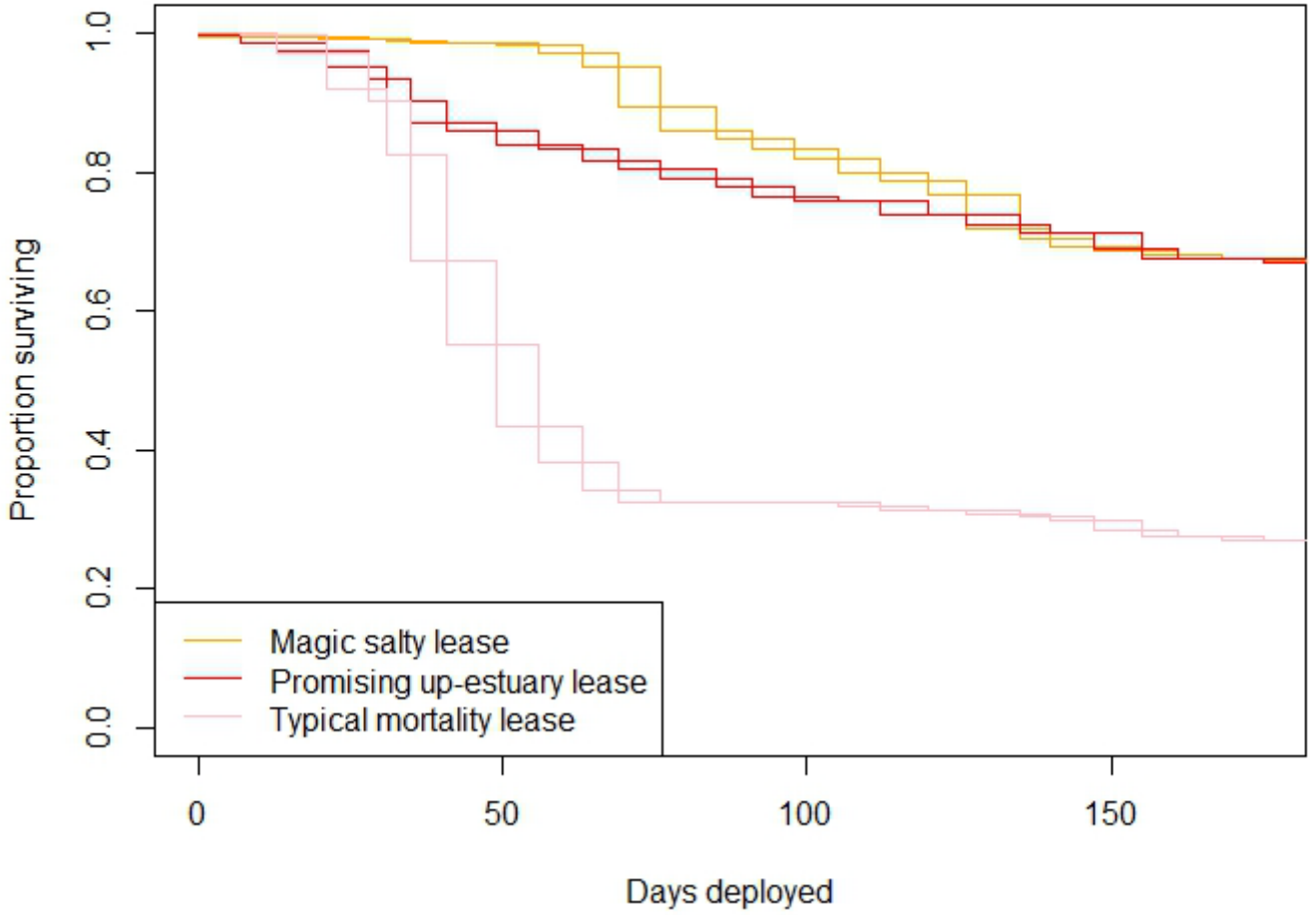
Where are we going next?

Further characterizing microbial community shifts, especially how this varies across field sites and by genetic lines

Are wild NC oysters more resilient & can we selectively breed for resistance?

collaboratory
science. policy. solutions.

Where oysters are grown matters (and it's not just salinity)

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