Oyster Microbiome and its potential role in Sydney Rock Oyster and Pacific Oyster diseases

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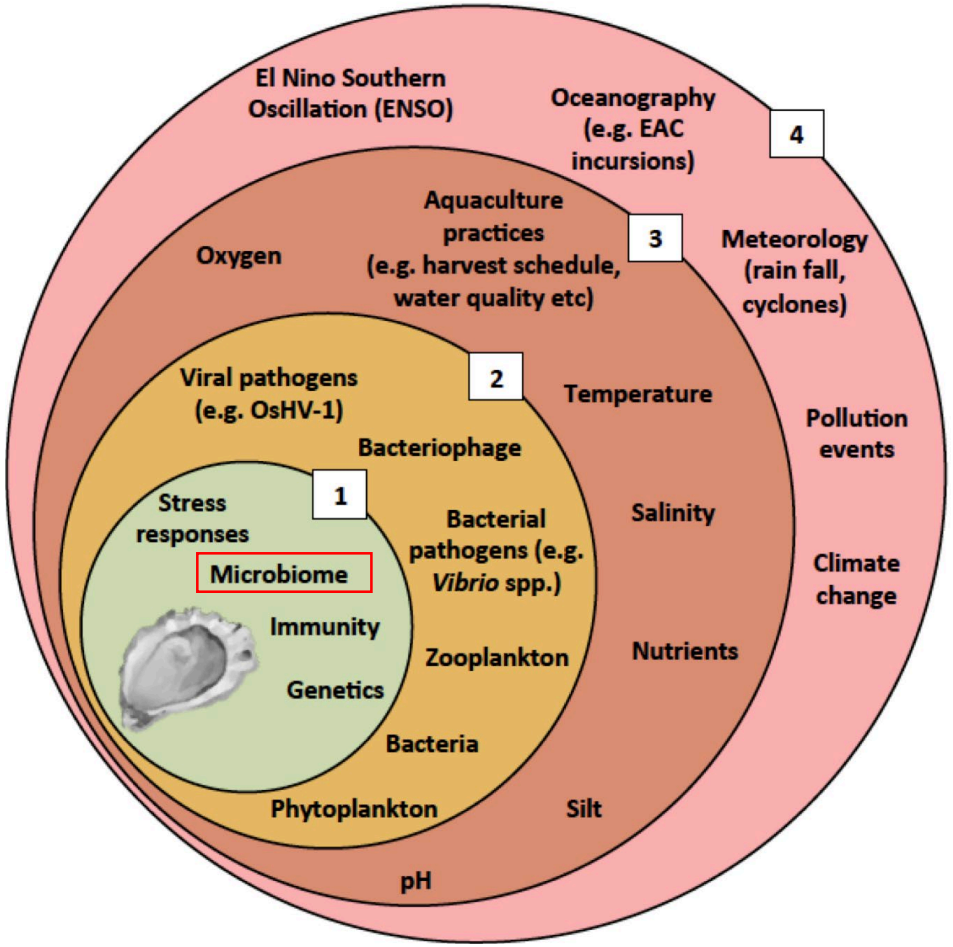
NSW GOVERNMENT Department of Primary Industries

QX-disease

The Sydney Morning Herald

NATIONAL

Sydney rock oysters face wipe-out from parasite



POMS – OsHV-1

Hawkesbury River oyster farming industry under threat from Pacific Oyster Mortality Syndrome

By Mohamed Taha

Updated Mon 28 Jul 2014, 3:15pm

Oyster farmers on the Hawkesbury River on the NSW Central Coast are fighting to save the crippled industry as an outbreak of disease destroys oysters.

Pacific Oyster Mortality Syndrome disease found in Tasmania for first time

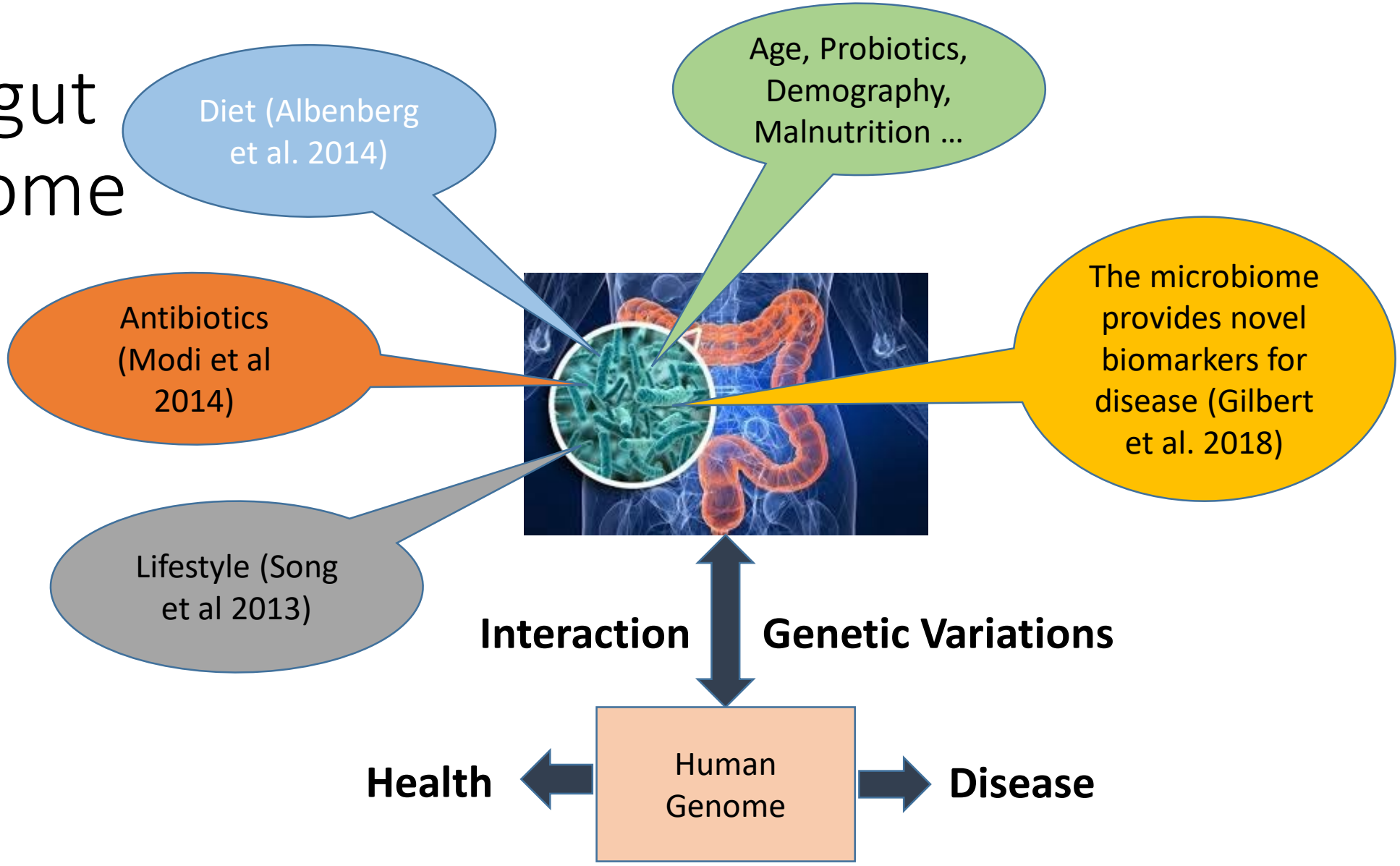
By Alex Blucher

Updated Tue 2 Feb 2016, 7:41pm

An oyster disease capable of wiping out the Tasmanian industry has been found in the state for the first time.


Microbiome

Human gut microbiome



Oyster Microbiome – what was known in relate to QX and POMS

SRO; Saccostrea glomerata

PO; *Crassostrea gigas*

- SRO digestive gland microbiota is changed following infection by spore forming protozoan parasite, *Marteilia sydneyi* (Green and Barnes 2010).
- Mortalities are reduced when oysters infected with OsHV-1 are treated with antibiotics (Petton et al. 2015)
- OsHV-1 infection leads to immune-suppression allowing bacteria to cause disease (De longeril et al. 2018)

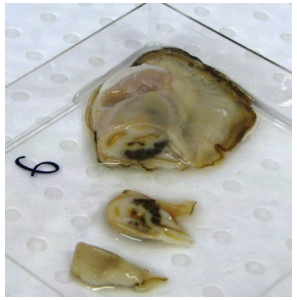
Hypotheses

Oyster Microbiome is involved in disease. Understanding the process that change oyster microbiome can help us to identified important triggers for those diseases.

Aims

- Characterise SRO and PO microbiome composition across family lines with different level of QX and OsHV-1 disease resistance
- Characterise SRO and PO microbiome composition before and during QX and OsHV-1 disease event
- Identified bacterial groups that can act as a potential marker for disease onset

Methods



Dissecting: Adductor, Mantle, gills, digestive gland

Extracting DNA

DNA sequencing (16S rRNA gene) to view the microbiome

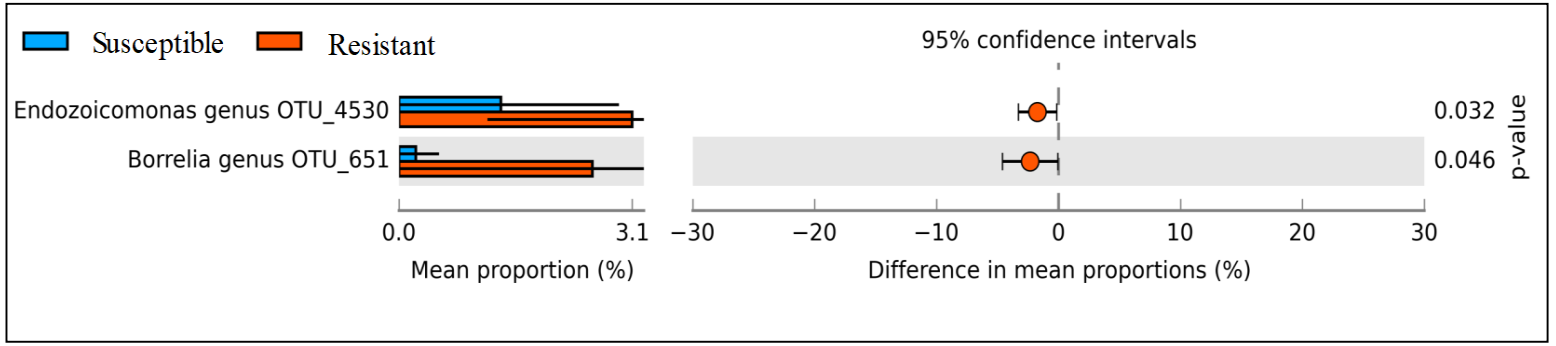
data analysis

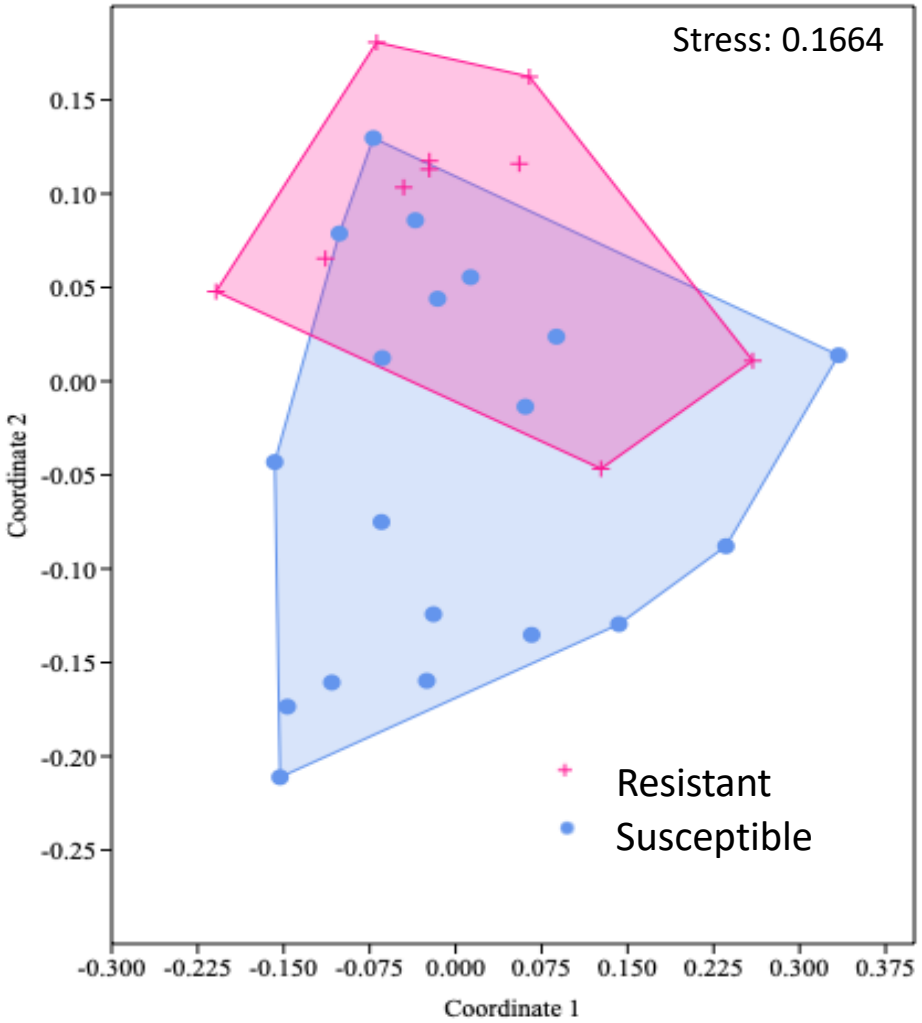
SRO-microbiomes separation according to QX resistance

NMDS - Non-metric multidimensional scaling

Wallis Lake: 6 family lines

- 4 susceptible (≤ 50% survival)
- 2 resistant (>50% survival)
- 5 oysters/family line/sampling time





PERMANOVA: F = 1.663, p = 0.0215

STAMP analysis – Wallis Lake

PO - Microbiome composition differs according to disease-resistance family line

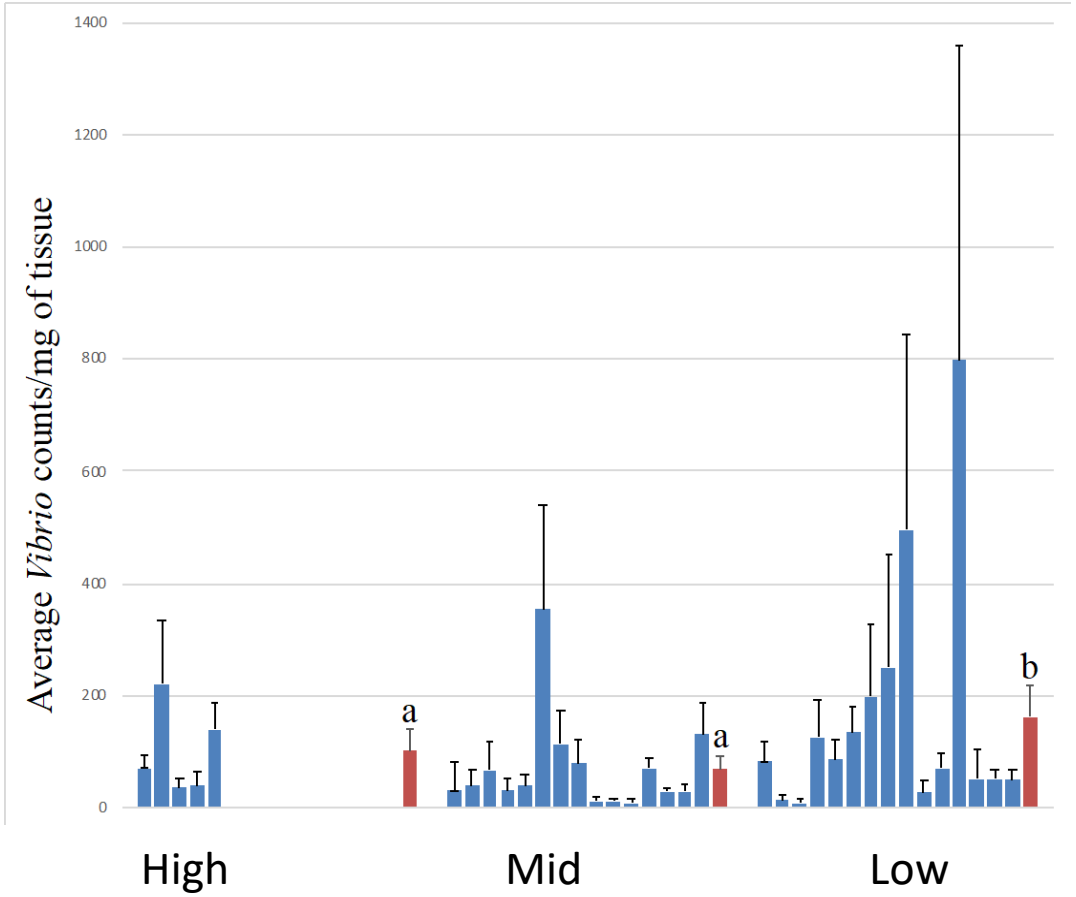
George river: 35 family lines

- 15 susceptible = low resistance (≤ 30% survival)
- 15 mid resistant (30% < survival < 60%)
- 5 high resistant (60% ≤ survival)
- 5 oysters/family line/sampling time

For example

Family line	POMS survival (%)	Resistance group (RG)	Association analysis
F_66	82.6	High	*Tenacibaculum* sp.
F_84	39.1	Med	
F_86	5.2	Low	*Vibio* sp.

High vs. Low - p = 0.0281; F = 1.47
Med vs. Low - p = 0.0001; F = 2.93



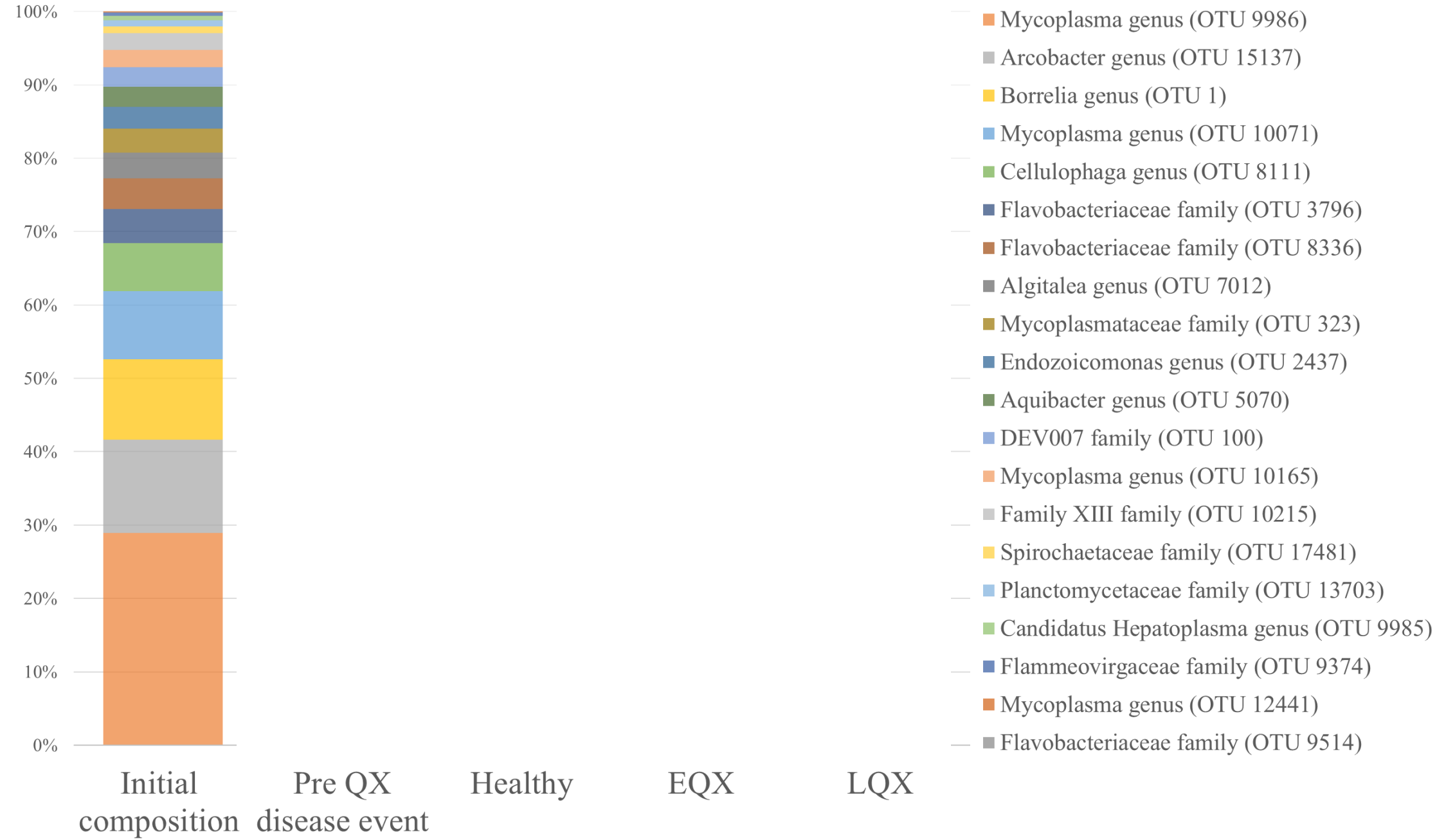
Microbiome shift during QX outbreak in George river

- 3 mid resistance family lines ~ 50% survival rate
- Pre – QX disease event: 5 oysters/family line/fortnight
- During QX disease event: 10 oysters/family line/fortnight

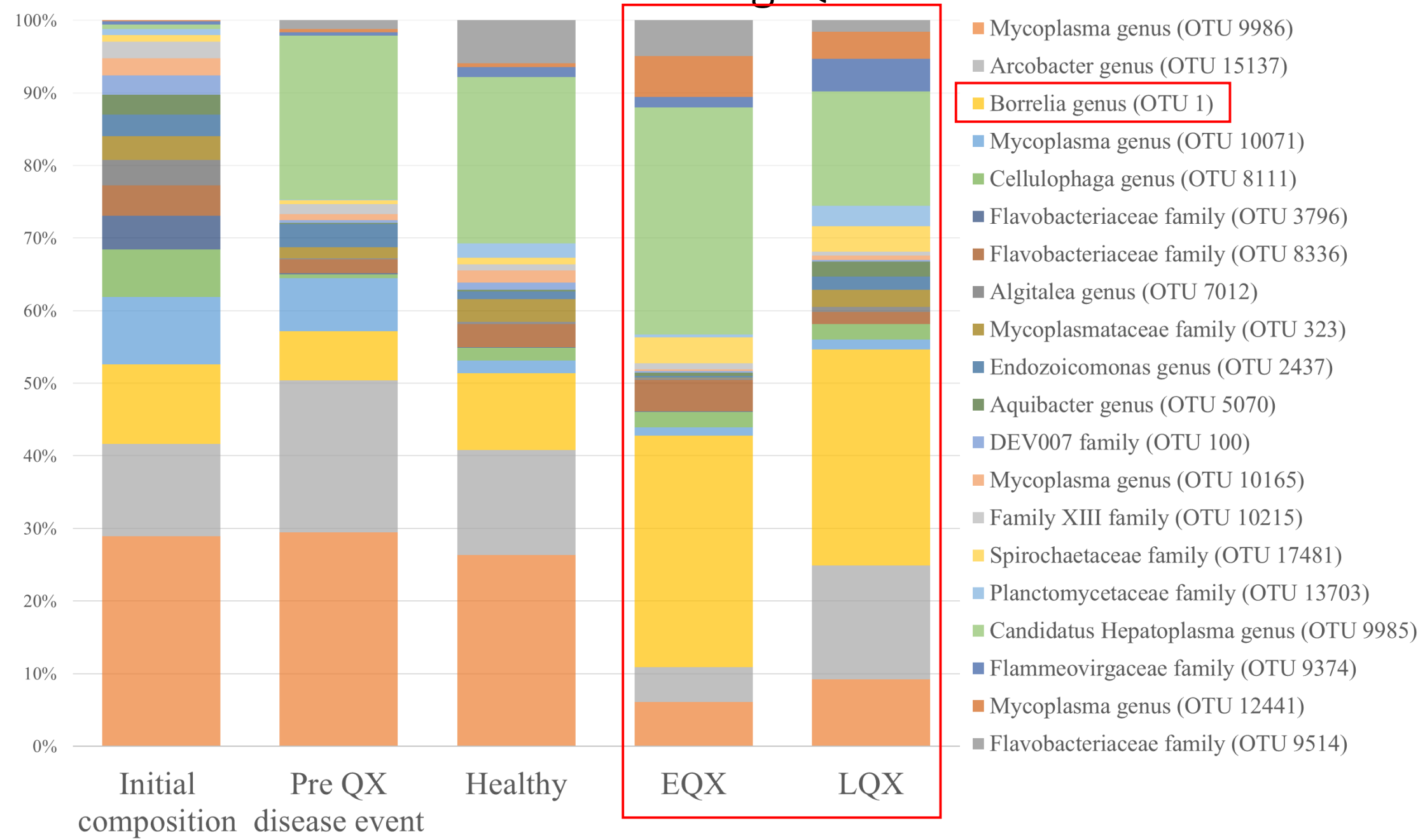
⬇

Samples were tested for QX using Cytology and PCR on the ITS1 region

PRO - Microbiome shifts during QX diseases

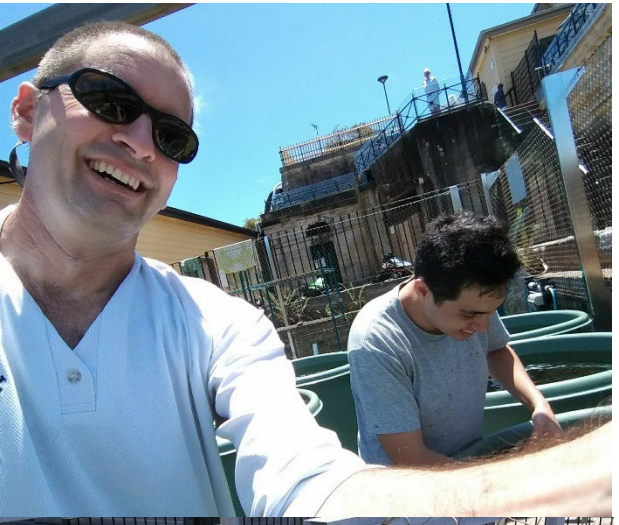


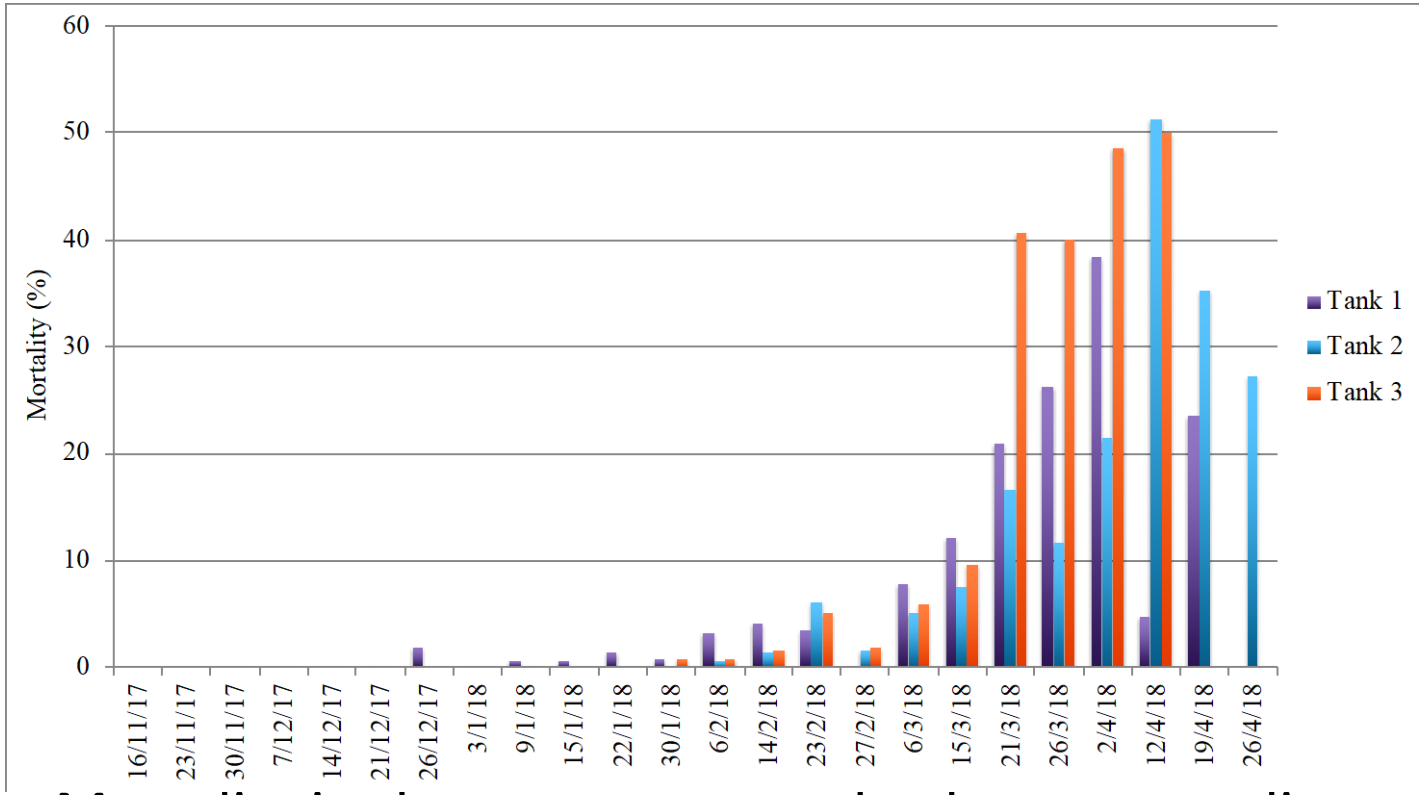
PRO - Microbiome shifts during QX diseases



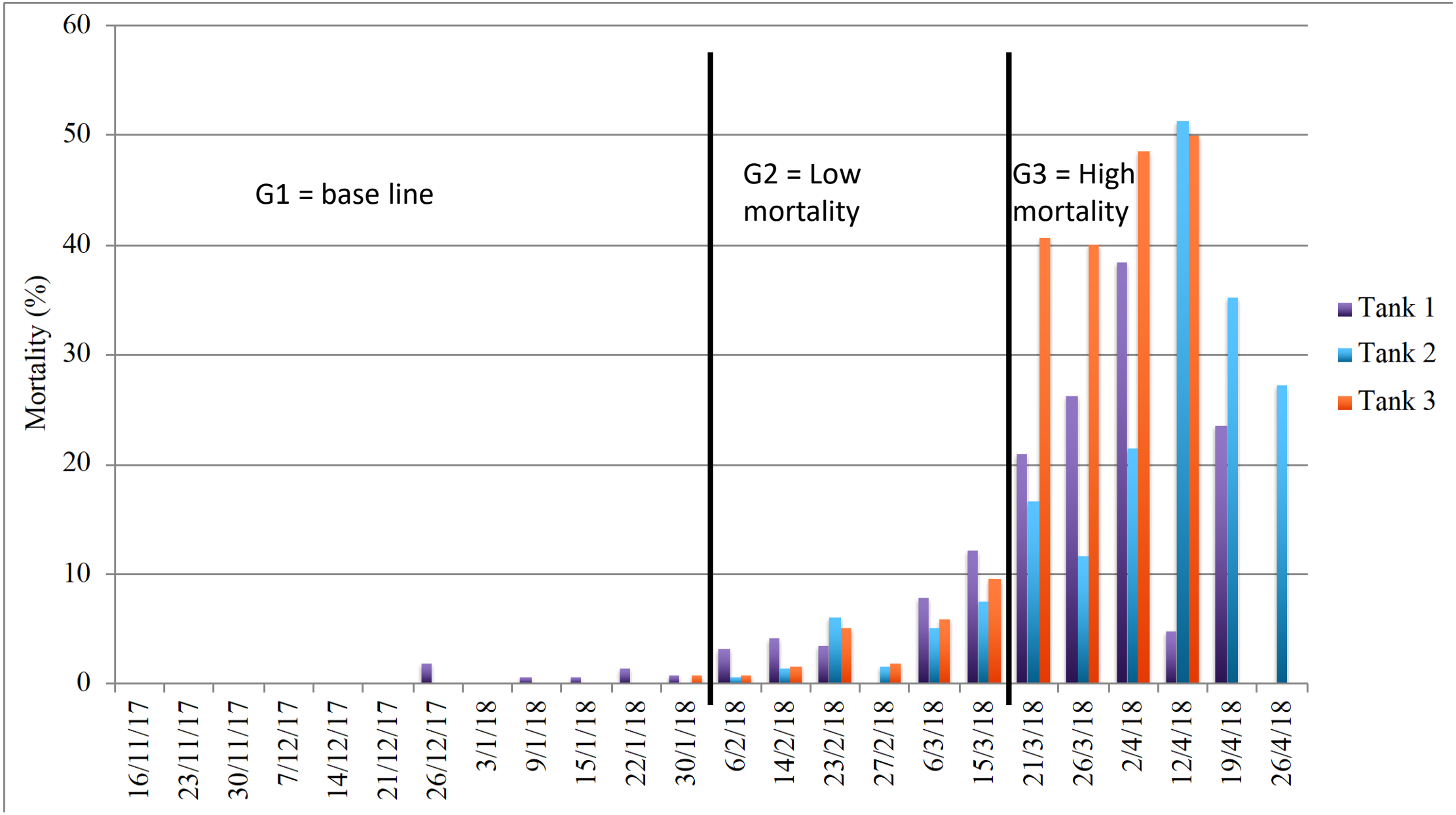
PO - Longitudinal study:

- 28 weeks of weekly sampling
- 424 oysters sampled
- 283 dead oysters



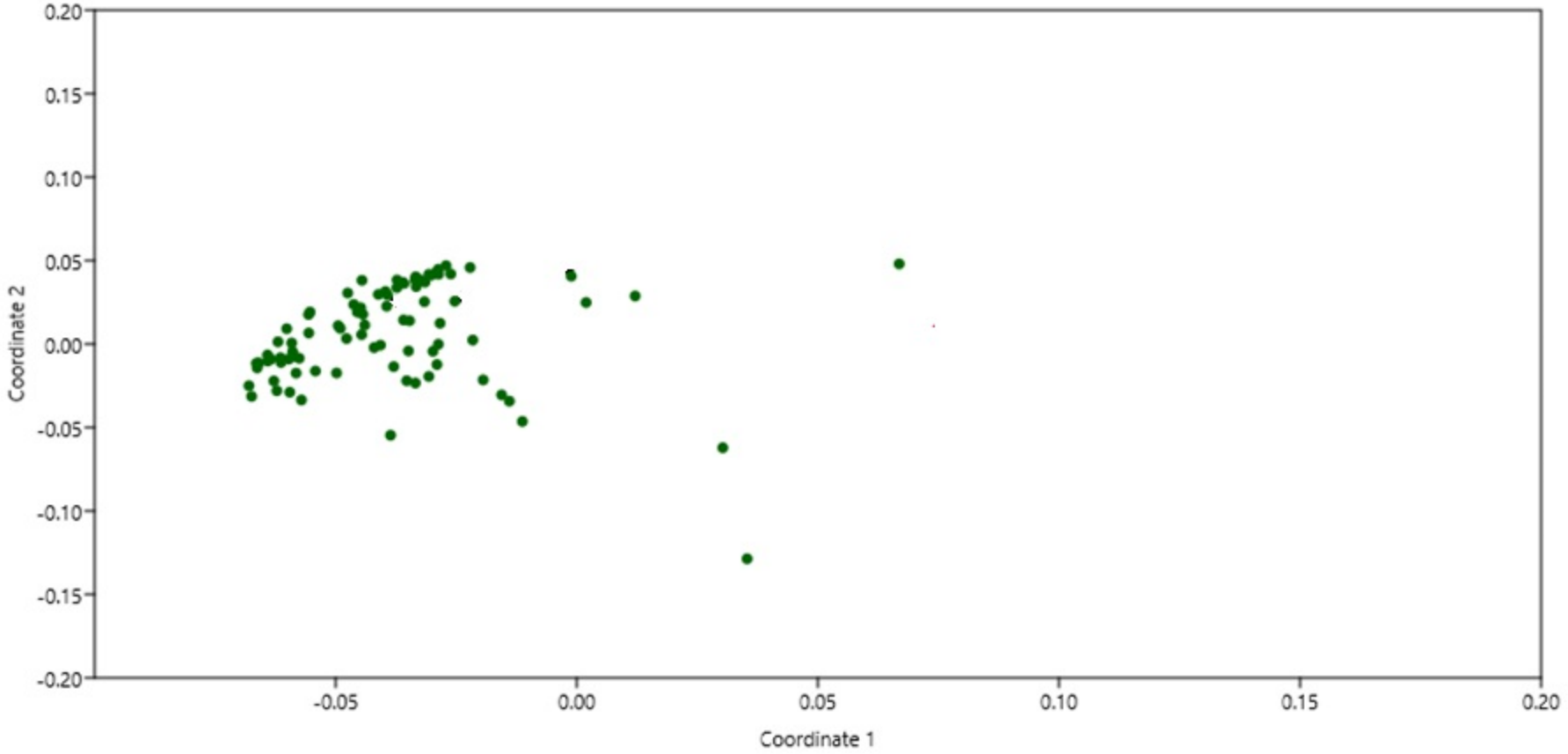


Mortality in three separate tanks shown mortality as a proportion of the previous week



For comparisons between different mortality thresholds, samples were split into three groups.
G2 begins when all three tanks have a mortality. G3 starts when all three tanks are >10% mortality

PO – Oyster microbiome changes during mortality event



nMDS with 95% ellipses at the zOTU level for: baseline (G1; green), low mortality (G2; red) and high mortality (G3; black). Stress = 0.26

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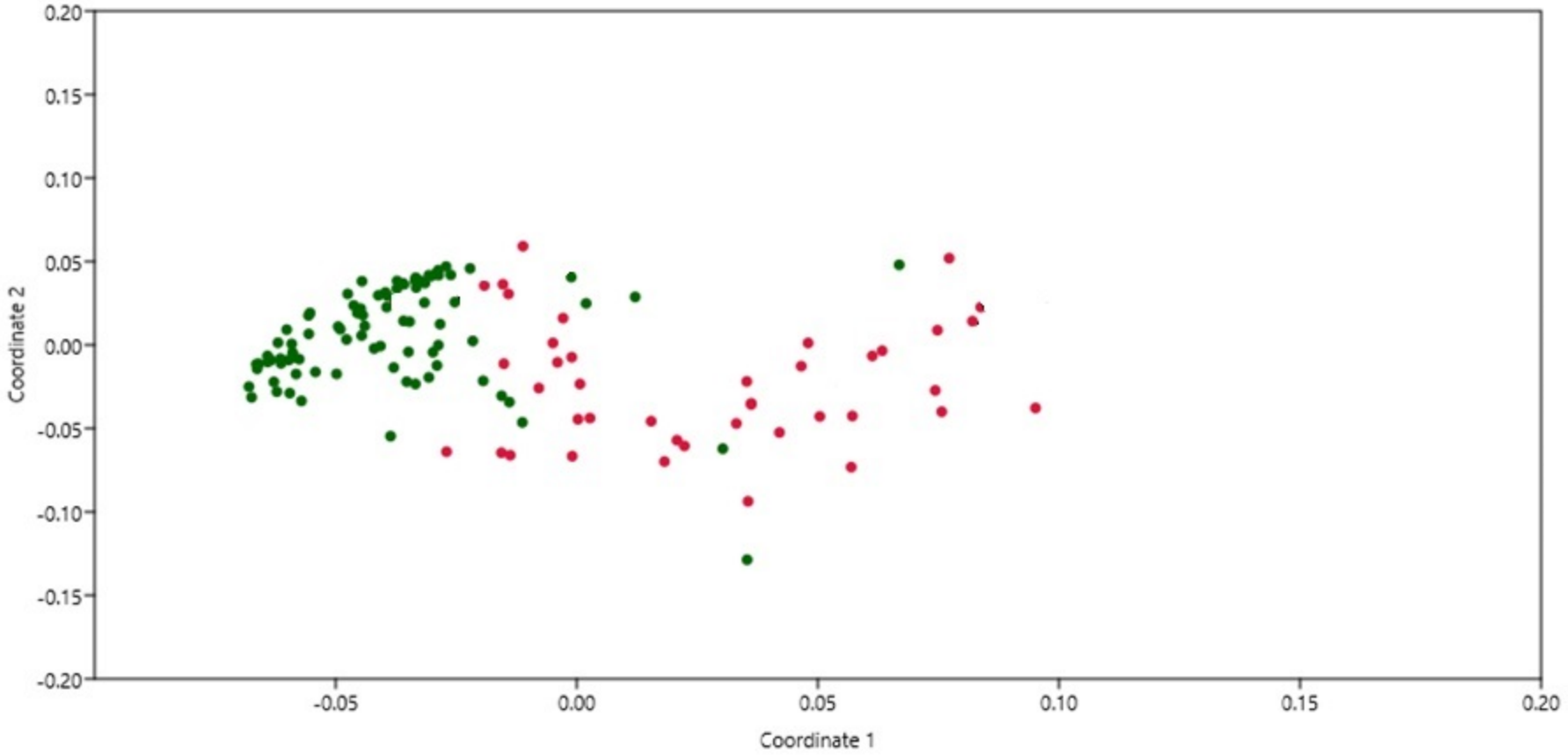

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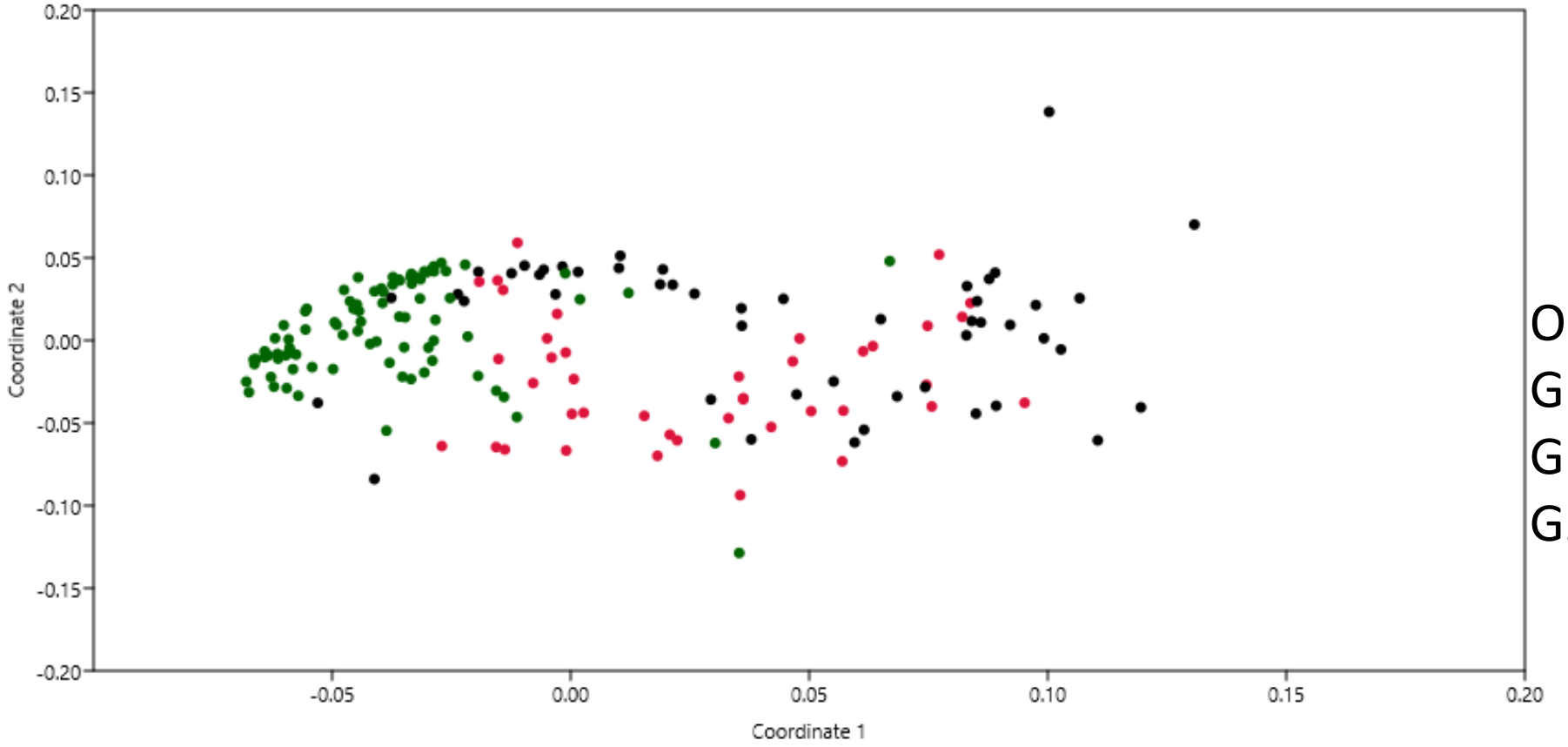

One-way PERMANOVA:
G1vG2; p = 0.0001 F = 10
G1vG3; p = 0.0001 F = 12
G2vG3; p = 0.0001 F = 4

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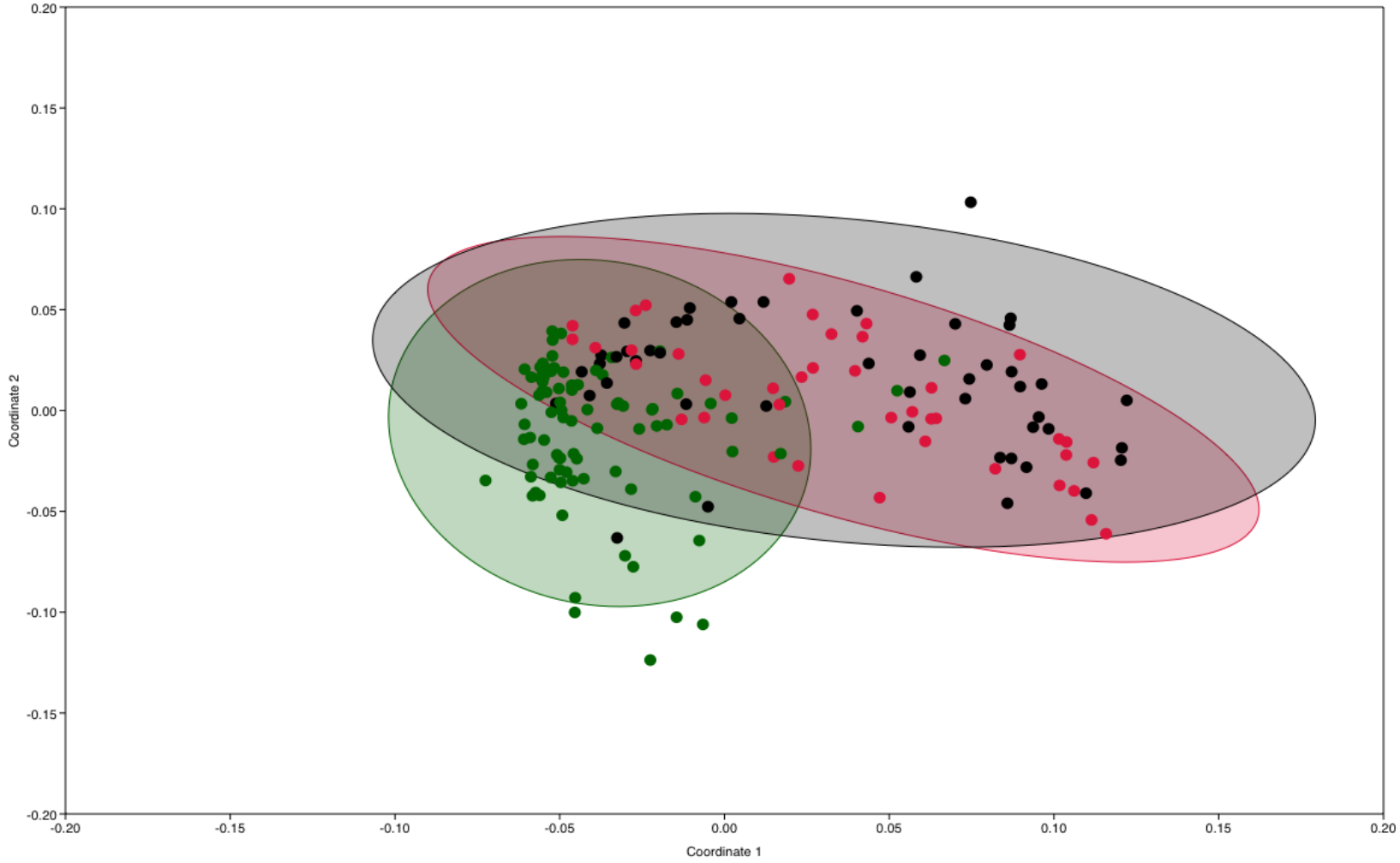

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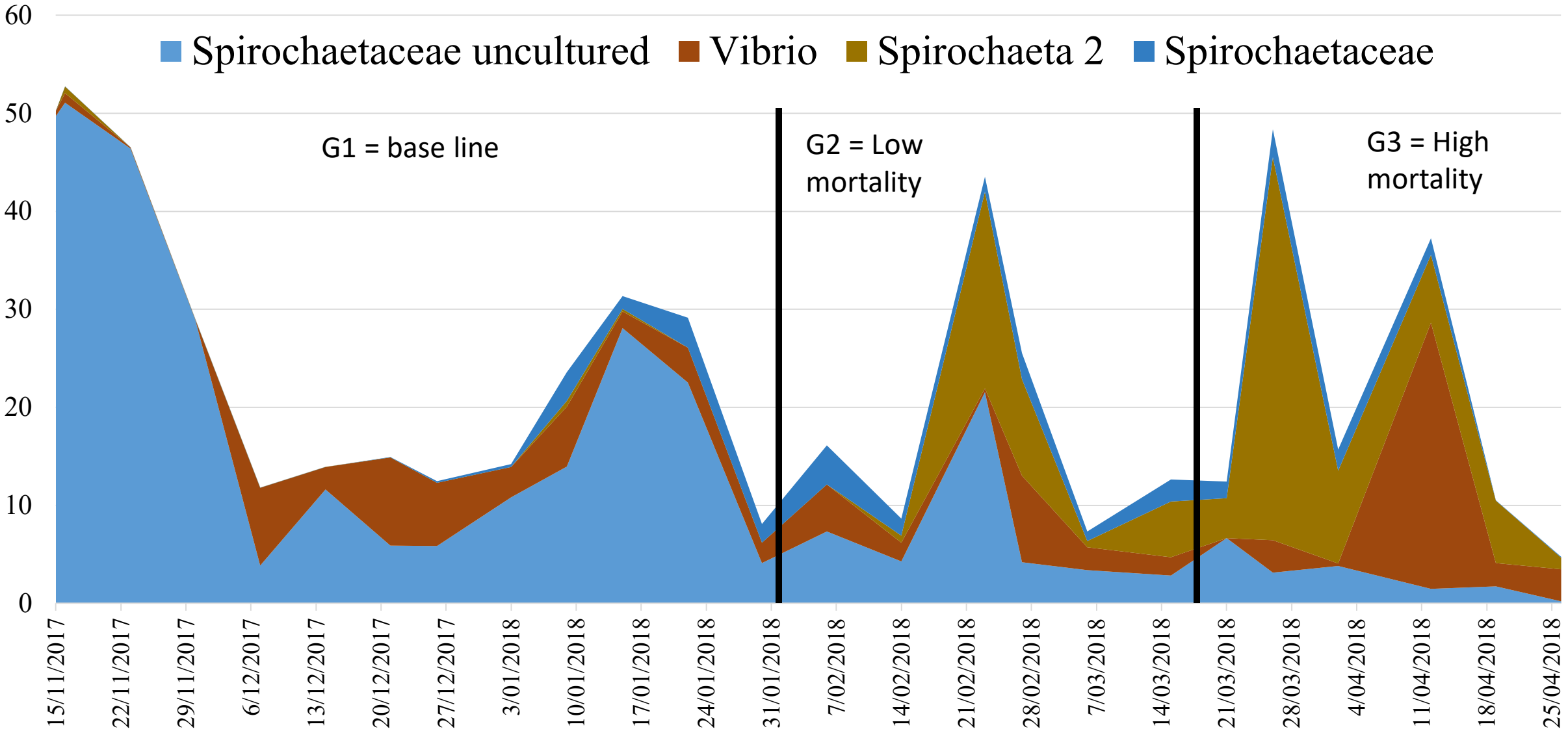
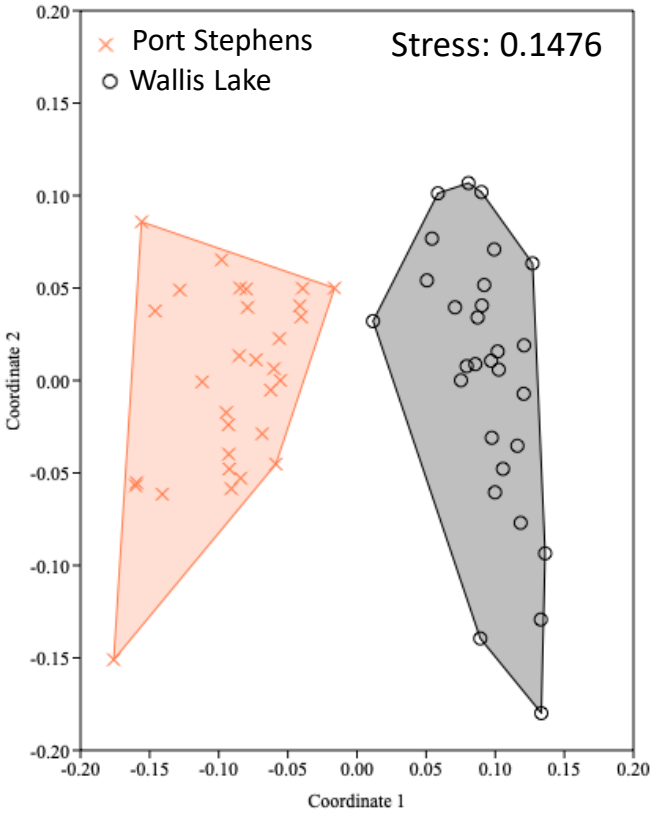
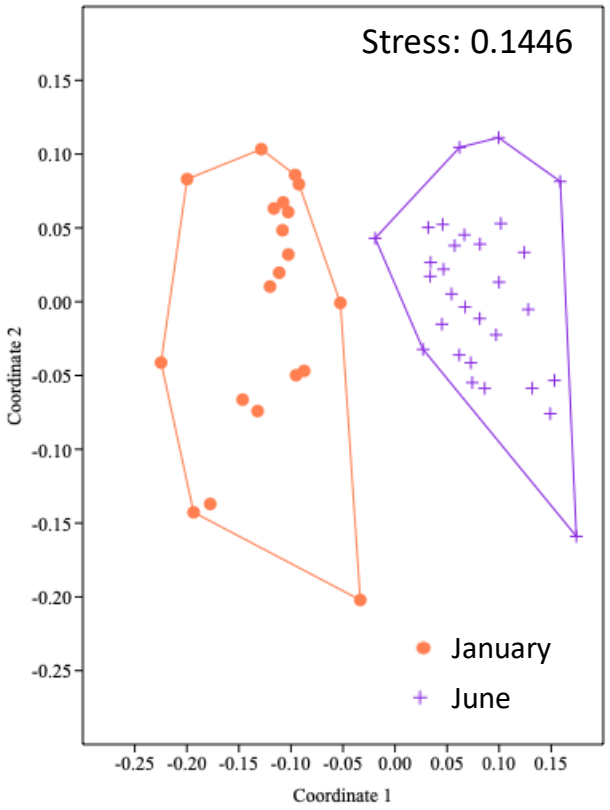
Beta diversity shifts at the genus level for Tanks 2



SRO microbiomes separate according to geographic location and season



PERMANOVA: F = 12.69, *p* = 0.0001



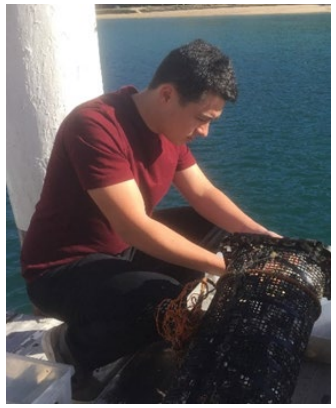
Port Stephens
PERMANOVA: F = 11.36, *p* = 0.0001
SIMPER: 88.58% dissimilarity

Summary

- Disease resistance (genetics) influences microbiome composition
  - Vibrio abundance higher in disease susceptible oysters
- Potential to use the microbiome as a marker for disease onset
  - Shift in the spirochete community
- Microbiome is dynamic, shifts in response to:
  - Location
  - Season
  - Oyster tissue type

Acknowledgements

Viet Khue Nguyen



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