

Cameron Brown*, Alex Rosa-Calix, Dr. Andrei L. Barkovskii



Climate Change

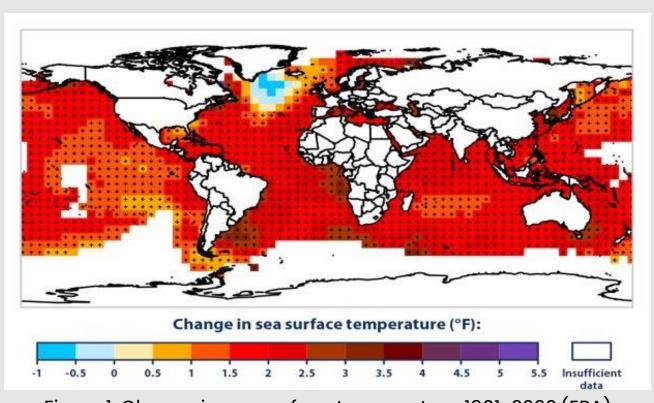


Figure 1. Change in sea surface temperature, 1901-2020 (EPA)

Climate Change

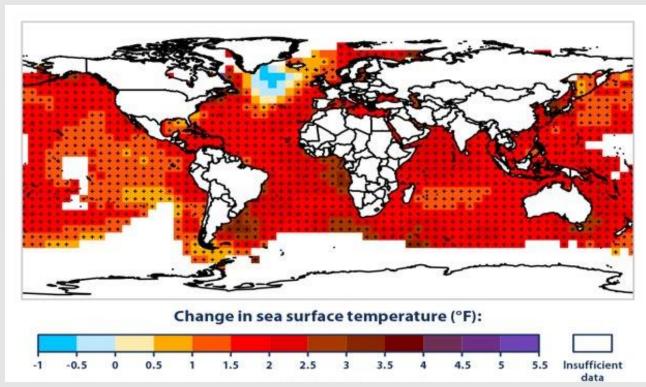


Figure 1. Change in sea surface temperature, 1901-2020 (EPA)

Scientists' warning to humanity: microorganisms and climate change

ylis, Michael J. Behrenfeld, Antje Boetlus, Philip W. Boyd, Almée T. Classen, Thomas W. Crowther berto Danovaro, Christine M. Foreman, Jef Huisman, David A. Hutchins, Janet K. Jansson, David M. Karl, Britt Koskella, David B. Mark Welch, Jennifer B. H. Martiny, Mary Ann Moran, Victoria J. Orphan, David S. Reay, Justin V. Remais, - Nicole S. Webster + Show authors

Nature Reviews Microbiology 17, 569-586 (2019) Cite this article 310k Accesses | 720 Citations | 2028 Altmetric | Metrics

Abstract

In the Anthropocene, in which we now live, climate change is impacting most life Microorganisms support the existence of all high opnic life forms. To understand how

humans and other life forms on Earth (Jen. The role of changing temperature in microbial metabolic anthropogenic climate change, it is vita processes during permafrost thaw

majority'. We must learn not just how micro production and consumption of greenhous Published April 1 climate change and other human activities. Asses role and global importance of microorgani humanity on notice that the impact of climmicroorganisms, which are essential for acl Atomor

ned online 2021 Dec 30, doi: 10.2147/IDR.S305077

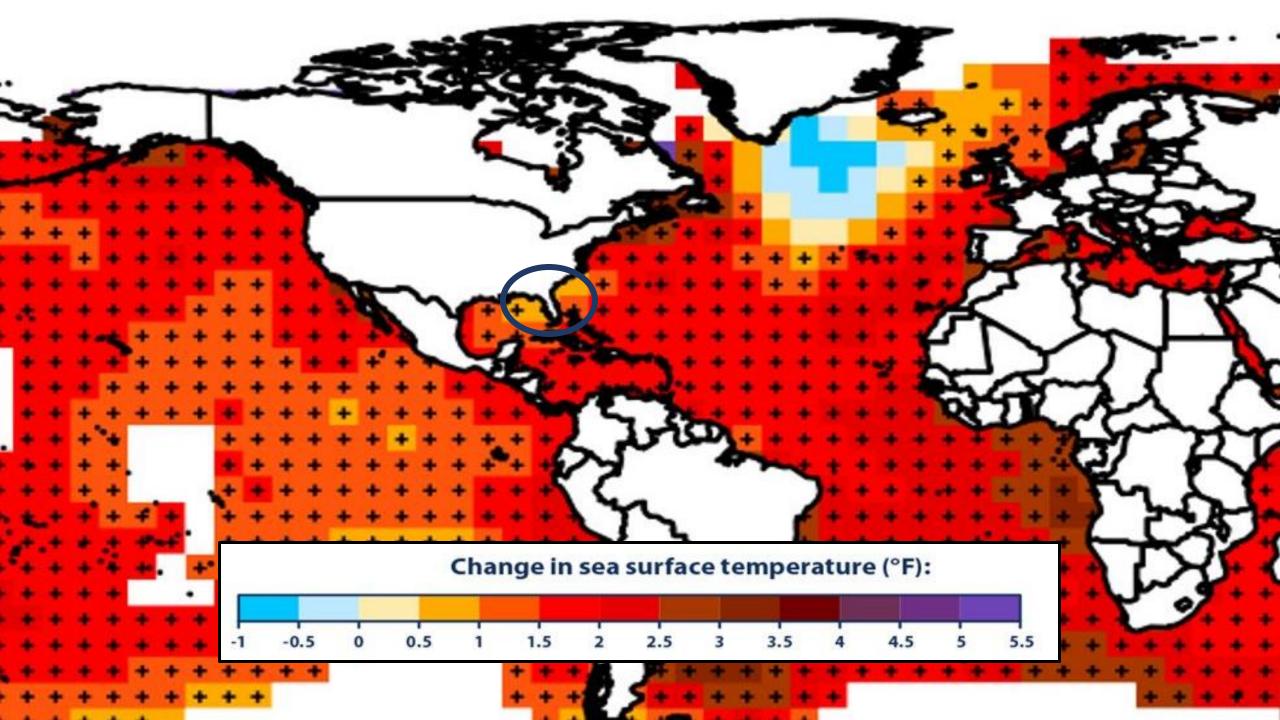
Accomplished one fourth of the Earth's Northern Remogners is underlain by permahost, earth materials (soil, organic matter, or bedrock), that has been continuously frozen for at least two consecutive years. Numerous studies point to evidence of accelerated climate warming in the processes may ortically impact ecosystem processes at the landscape scale. Here, we sought to understand how the permatroid metabolome responds to thaw and how this response differs based on location (i.e. chronosequence of permahout formation constituting diverse permahout Overall, permetrost thaw induced a shift in microbial metabolic processes. Of note were the dissimilarities in biochemical structure between frozen and threed samples. The threed permatical metabolismes from different locations were highly similar. In the intact permatics several metabolites with antagonist properties were identified. Elustrating the competitive riagonistic metabolites decreased with warmer temperature, indicating a shift in ecological strategies in theward permatroet. These findings illustrate the impact of change in temperature ndergoes than, knowledge that will become crucial for PMCID: PMC8722568 dynamics as the Arctic and Antercic landscapes

Climate Change and Infections on the Move in North America

er, 1, 2 Kathryn C Conlon, 2, 3, 4 Angel Desai, 1 and Leda N Kob

Author Information + Article notes + Copyright and License information Discigimen

Climate change is increasingly recognized for its impacts on human health, including how biotic and abiotic factors are driving shifts in infectious disease. Changes in ecological conditions and processes due to temperature and precipitation fluctuations and intensified disturbance regimes are affecting infectious pathogen transmission, habitat, hosts, and the characteristics of pathogens themselves. Understanding the relationships between climate change and infectious diseases can help clinicians broaden the scope of differential diagnoses when interviewing, diagnosing, and treating patients presenting with infections lacking obvious agents or transmission pathways. Here, we highlight key examples of how the mechanisms of climate change affect infectious diseases associated with water, fire, land, insects, and human transmission pathways in the hope of expanding the analytical framework for infectious disease diagnoses. Increased awareness of these relationships can help prepare both clinical physicians and epidemiologists for continued impacts of climate change on infectious disease in the









Oysters, clams, shrimp, red drum, almaco jack, spotted seatrout, summer flounder, snook, pompano, black seabass, and algae¹

Vibrio harveyi and Vibrio campbellii

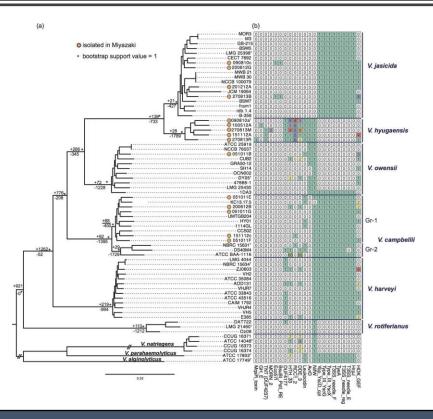


Figure 5. Phylogenetic tree of Harveyi clade (Ke *et al.*)





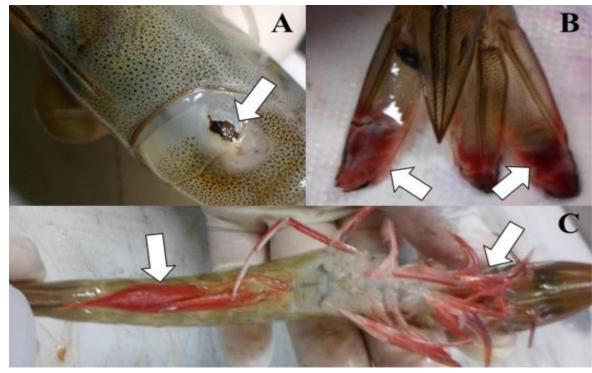
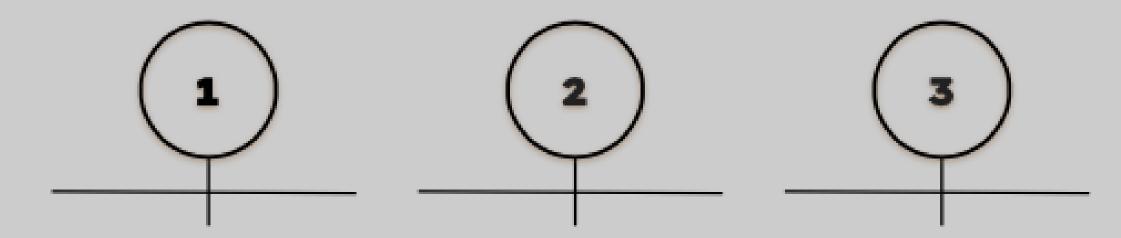


Figure 6. Muscle necrosis with *V. harveyi* infection

Figure 7. *V. harveyi* infection in shrimp (CDN)

Vibrio harveyi & Vibrio campbellii Acute Hepatopancreatic Necrosis Disease (AHPND) and Early Mortality Syndrome (EMS)²

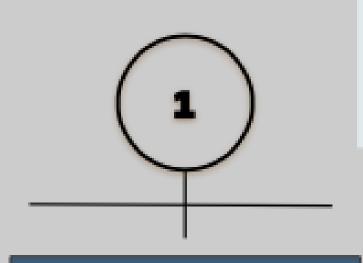
Blindness, Gastroenteritis, Vasculitis, Scale Ioss, Muscle necrosis, Tail rot, Anorexia, Lethargy, Kidney damage, and Brain swelling



DEVELOPMENT

Develop molecular tools to screen for environmental Vibrio harveyi/campbellii

Haemolysin regulation



Exotoxin formation & excretion, adhesion factors, quorum sensing

Mobility & biofilm formation

Vhp

activity

Vhha

Srp

DEVELOPMENT

Develop molecular tools to screen for environmental Vibrio harveyi/campbellii

Haemolysin regulation Vhh

ToxR

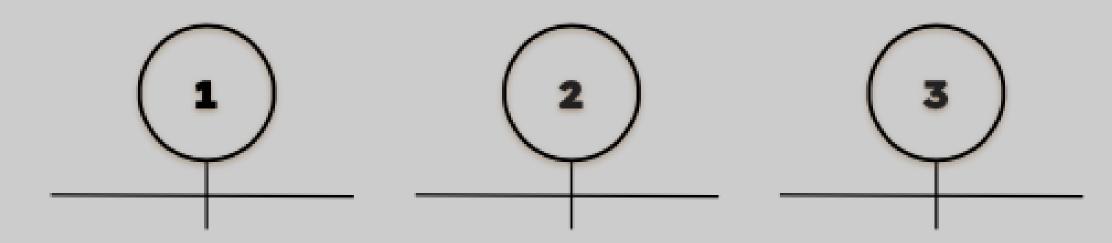
LuxR

Virulence expressionrelated factors Stressresponse regulation

Serine

protease

RpoA



DEVELOPMENT

to screen for environmental Vibrio harveyi/campbellii

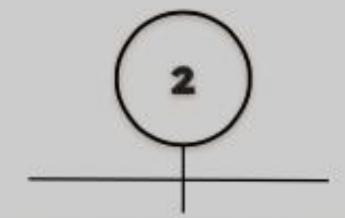
DETECTION

of Vibrio harveyi and
Vibrio campbellii in
environmental water and
sediment samples from
Townsend, GA



Figure 8. Horiba water parameter meter (Horiba)





DETECTION

of Vibrio harveyi and Vibrio campbellii in environmental water and sediment samples from Townsend, GA

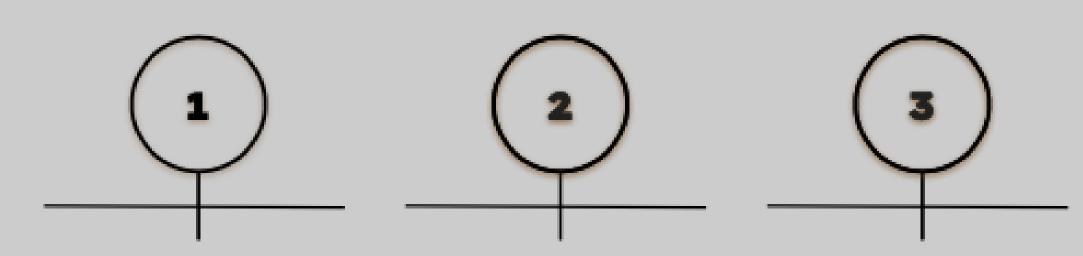


Figure 9. Map of Townsend and Sapelo Island, GA (Etsy)





Figure 11. Thermocycler (Bio-rad)



DEVELOPMENT

to screen for environmental Vibrio harveyi/campbellii

DETECTION

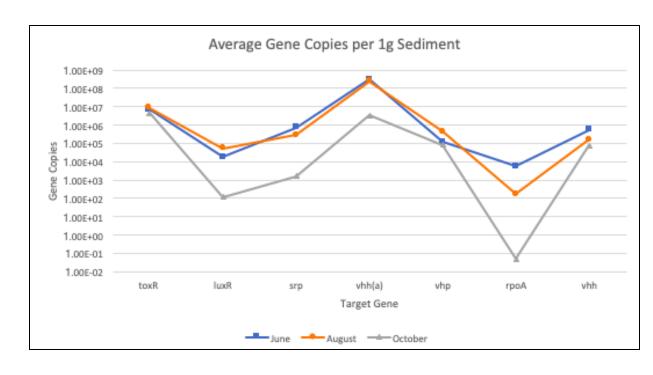
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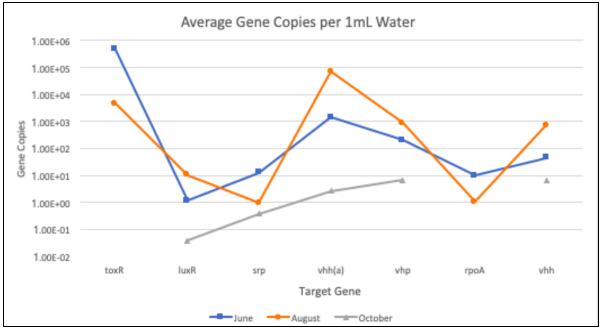
PREVALENCE

Report the dynamics in distribution and concentration of 7 virulence genes in environmental samples over time

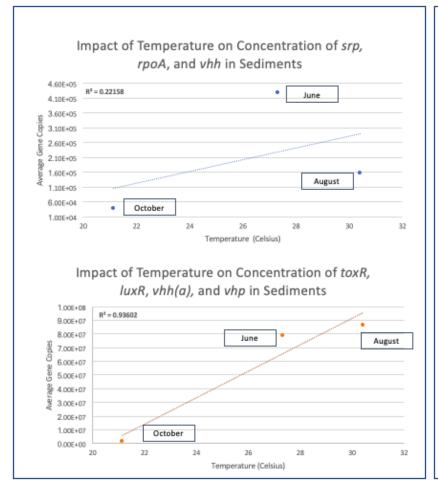
Results & Conclusions

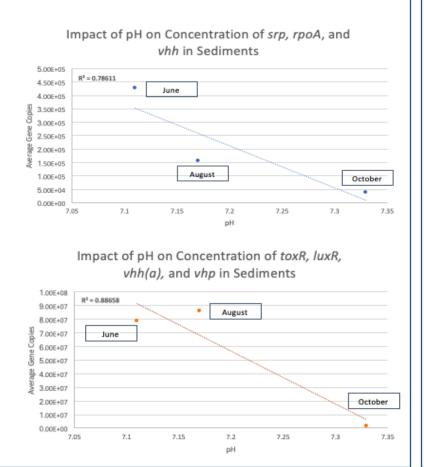
- Average gene copy number ranged from 0 to 10⁵ in water samples and 10⁻² to 10⁸ in sediment samples
- toxR and rpoA were not detected in water samples in October
- luxR, srp, and vhp occurred in the highest concentrations in both water and sediment in August

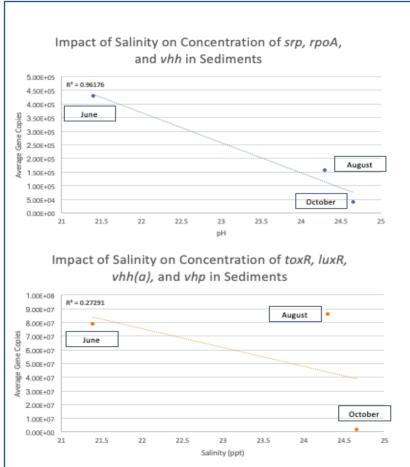




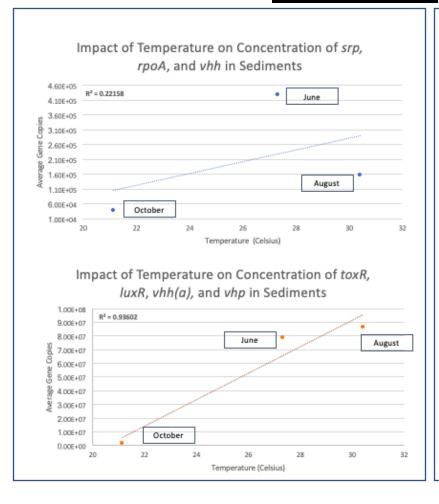
Gene/Parameter	pН	Temperature (Celsius)	Salinity (ppt)	Turbidity (NTU)	Dissolved Oxygen (mg/L)	Conductivity (mS/cm)	TDS (g/L)	Potential Water Density
toxR	-0.758719	0.994005	-0.182694	-0.434791	-0.892259	-0.074187	-0.314036	-0.598426
luxR	-0.567118	0.933085	0.074547	-0.650428	-0.747295	0.183049	-0.061060	-0.373884
srp	-0.933443	0.567939	-0.952115	0.586352	-0.820860	-0.913013	-0.984726	-0.989201
vhh(a)	-0.997854	0.860594	-0.736341	0.192898	-0.984648	-0.658012	-0.821115	-0.959566
vhp	-0.341404	0.812427	0.323294	-0.820760	-0.555853	0.424744	0.192289	-0.128246
rpoA	-0.729208	0.215565	-0.997112	0.848571	-0.544829	-0.999440	-0.977669	-0.860868
vhh	-0.822943	0.358516	-0.997308	0.760362	-0.663579	-0.983327	-0.998059	-0.927018
All gene averages	-0.931753	0.974051	-0.498261	-0.111706	-0.991483	-0.400554	-0.610987	-0.830164

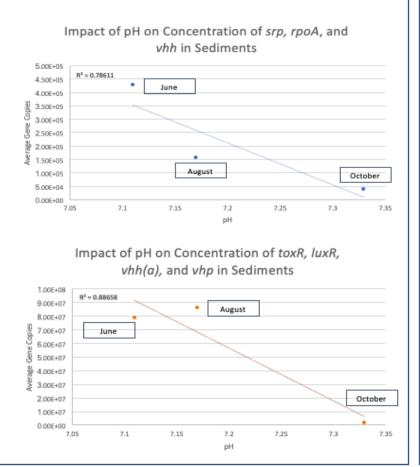


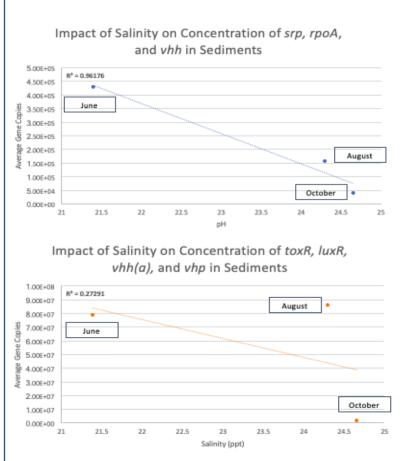




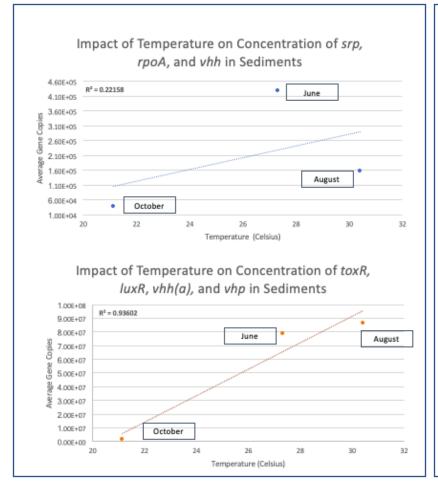
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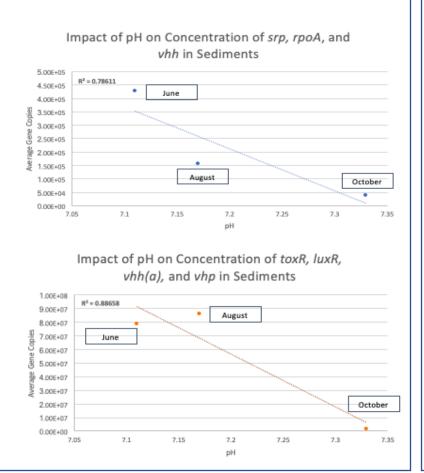


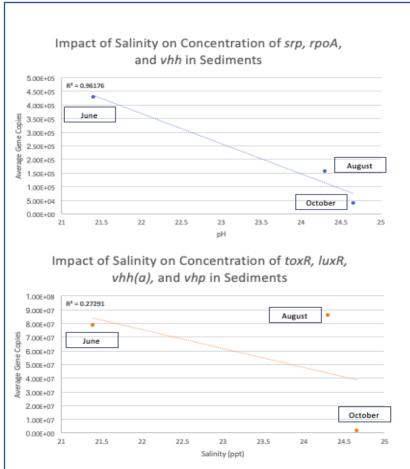




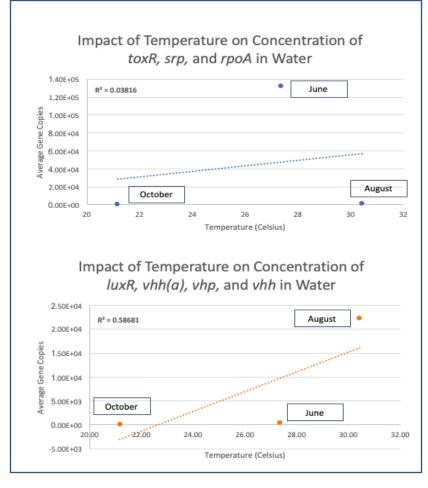
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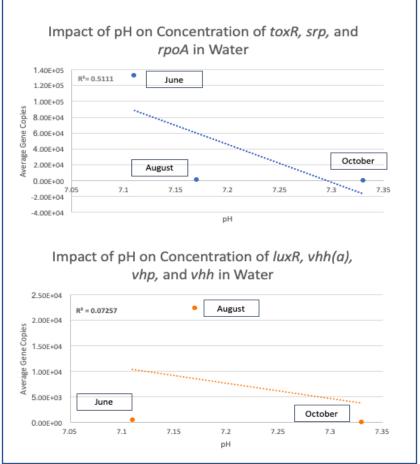


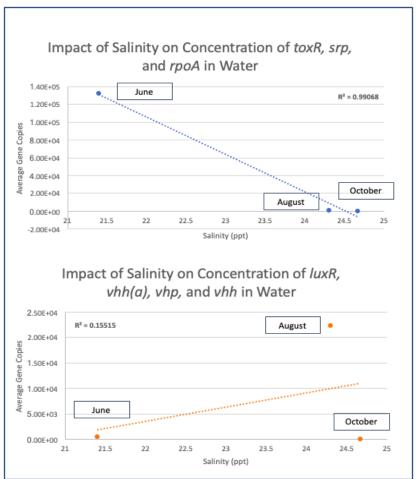




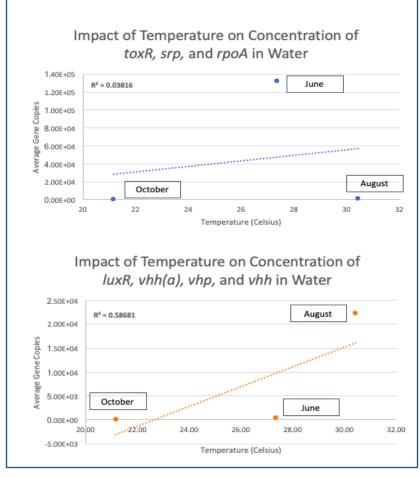
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toxR	-0.716556	0.197649	-0.995555	0.858116	-0.529383	-0.999885	-0.973657	-0.851407
luxR	-0.348787	0.816989	0.315840	-0.816241	-0.562375	0.417609	0.184563	-0.136044
srp	-0.738192	0.228456	-0.998029	0.841502	-0.555868	-0.998911	-0.980362	-0.867520
vhh(a)	-0.271061	0.767152	0.392293	-0.860706	-0.492948	0.490440	0.264233	-0.054659
vhp	-0.452515	0.876950	0.206537	-0.745688	-0.652261	0.312198	0.072257	-0.247186
rpoA	-0.774680	0.282419	-0.999976	0.810048	-0.601382	-0.994751	-0.989838	-0.893921
vhh	-0.300860	0.786726	0.363502	-0.844460	-0.519763	0.463105	0.234117	-0.085680
All gene averages	-0.948251	0.603424	-0.937819	0.550331	-0.845074	-0.894281	-0.976161	-0.994669

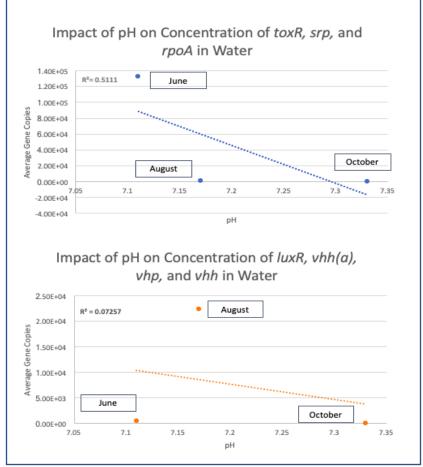


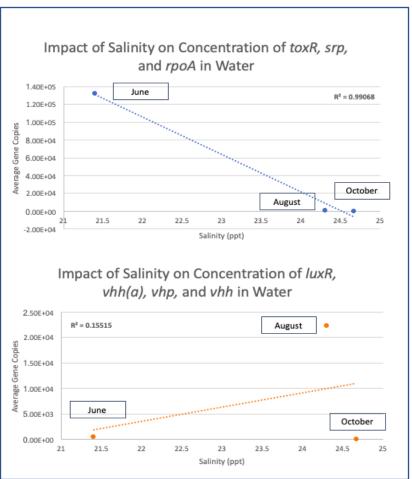




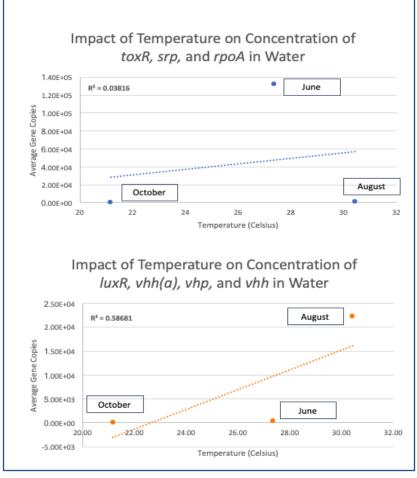
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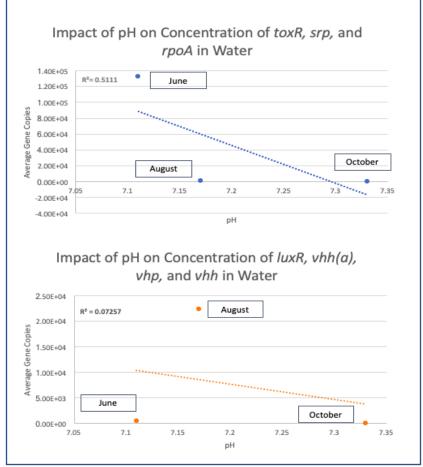


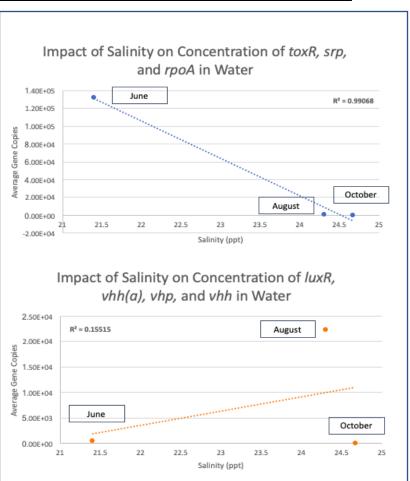




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Summary





- Our findings indicate the presence of Vibrio harveyi/campbellii in Coastal Georgia waters for the first time
- All 7 genes were detected in each sampling event in high concentrations
- In general, there is a
 positive correlation
 between temperature and
 gene copy number
- Supplementary data in our lab has evidenced the presence of V. harveyi/campbellii in clams and oysters

Acknowledgements

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- Thank you to Mr. Charles Phillips, the owner of Sapelo Sea Farms, for providing the sampling sites and boats
- Additional thanks to Mr. Charles Phillips and my peers Ella
 Velimirovich and Sydney Brown for help with sample collection
- A huge thank you to Dr. Andrei L. Barkovskii for entrusting, guiding, and supporting me throughout the course of this project



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- 7. Figure 8. https://www.horiba.com/int/products/detail/action/show/Product/u-50-434/
- 8. Figure 9. https://www.etsy.com/market/sapelo_island_map
- 9. Figure 10. Produced by Cameron Brown
- 10. Figure 11. https://www.bio-rad.com/en-us/product/c1000-touch-thermal-cycler-for-classroom?ID=dcdab038-4e77-49a8-bcaa-f67e8648550d