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(Seattle, Wash.)

Apr 6th, 10:30 AM - 10:45 AM

The microbiome of the canopy-forming kelps, *Nereocystis* and *Macrocystis*, from the outer Olympic Coast to the Puget Sound

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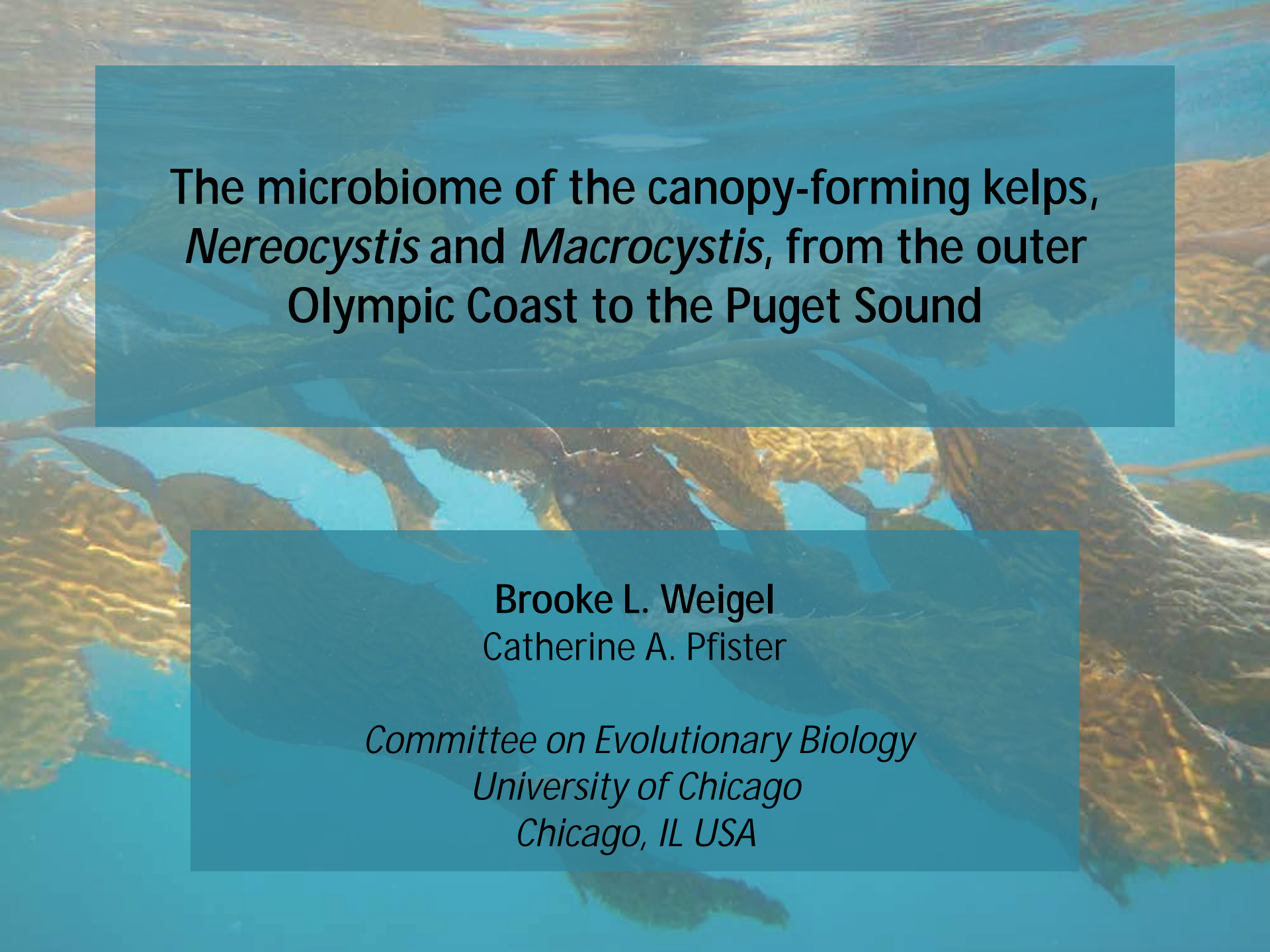


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The microbiome of the canopy-forming kelps,
Nereocystis and *Macrocystis*, from the outer
Olympic Coast to the Puget Sound

Brooke L. Weigel
Catherine A. Pfister

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Canopy-forming kelps in the Salish Sea

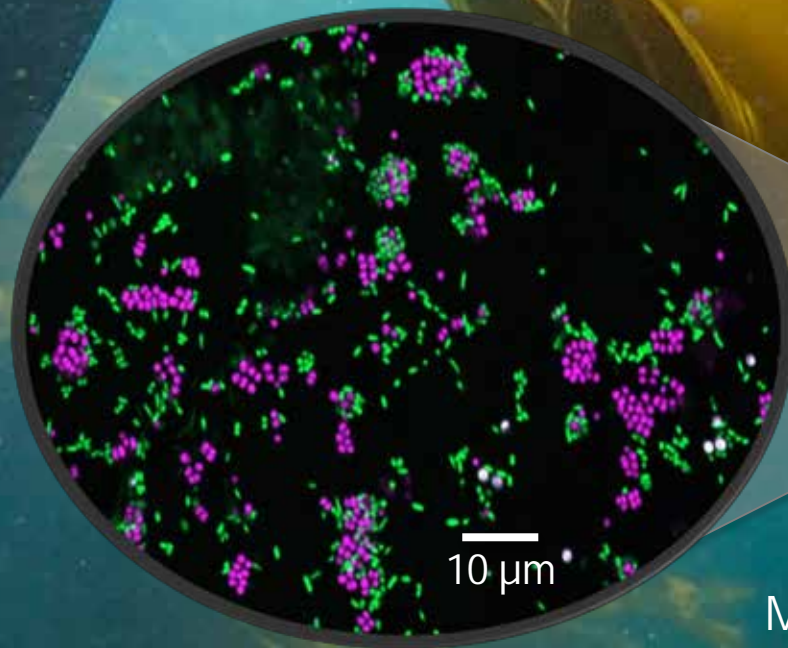


Macrocystis pyrifera
(Perennial)



Nereocystis luetkeana
(Annual)

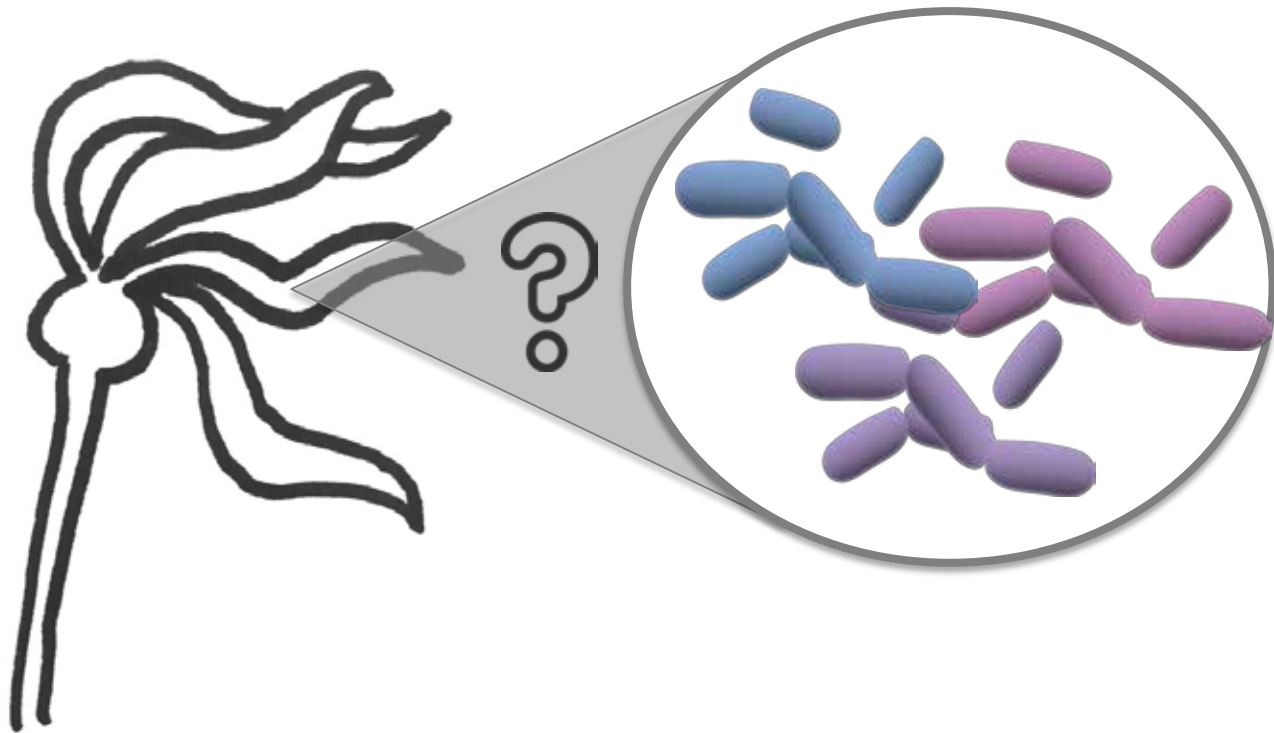
Epiphytic microbial communities on *Nereocystis* kelp blades



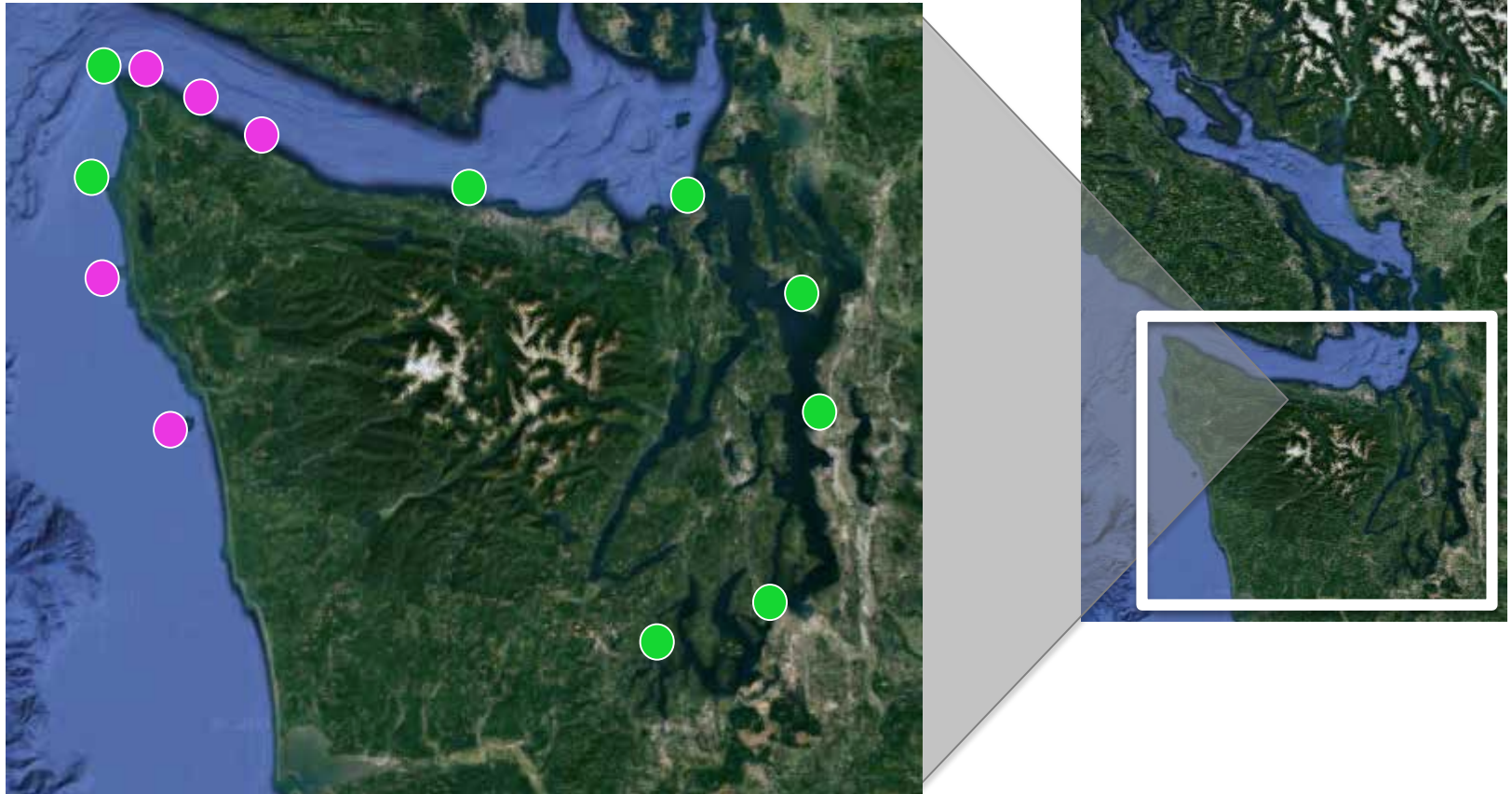
Alphaproteobacteria
Gammaproteobacteria

Microscopy Image Credit:
Jessica Mark Welch

Part I: Which microbes live on the blade surfaces of the canopy forming kelps *Nereocystis* and *Macrocystis*, and do they vary across a large spatial gradient?



Kelp forest spatial sampling

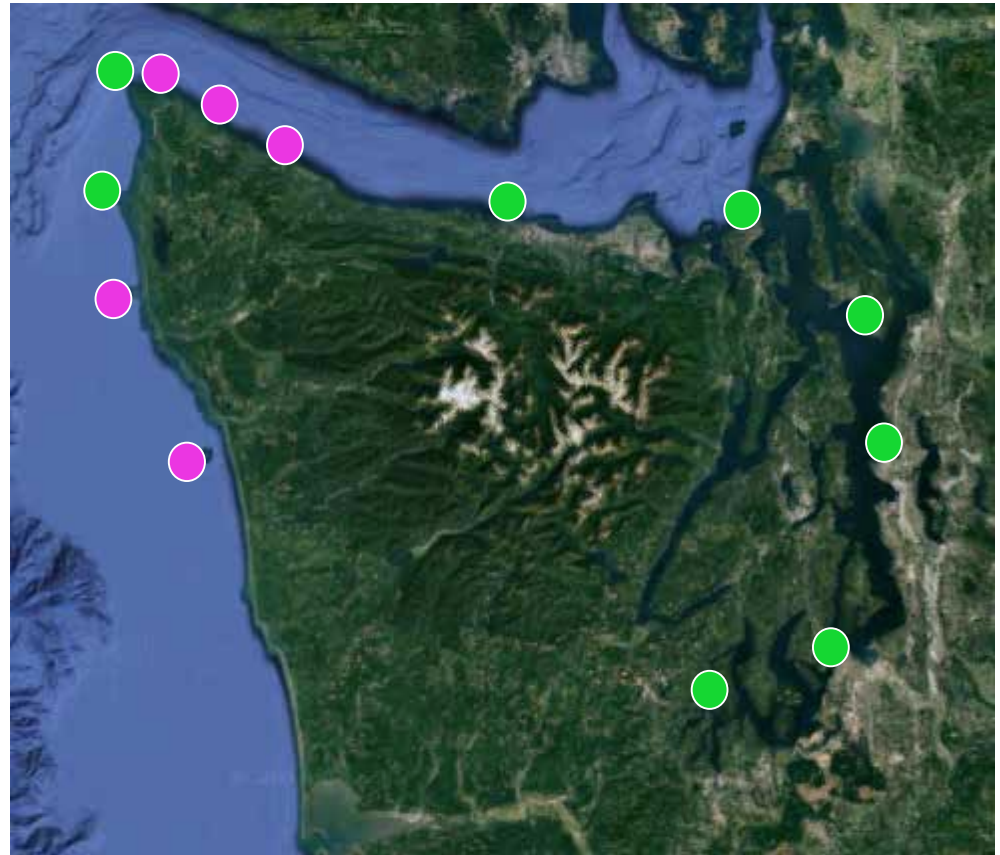


Green = *Nereocystis* only
Pink = *Nereocystis* + *Macrocystis*

Kelp forest spatial sampling

At each of the 13 sites:

- Sampled *Nereocystis* ($n = 6$) and *Macrocystis* ($n = 6$) blade tissues
- Sampled seawater ($n = 3$) microbial communities: filtered 1.0 L through a $0.22 \mu\text{m}$ filter to collect microbes
- Collected environmental data (water temperature, salinity, etc.)

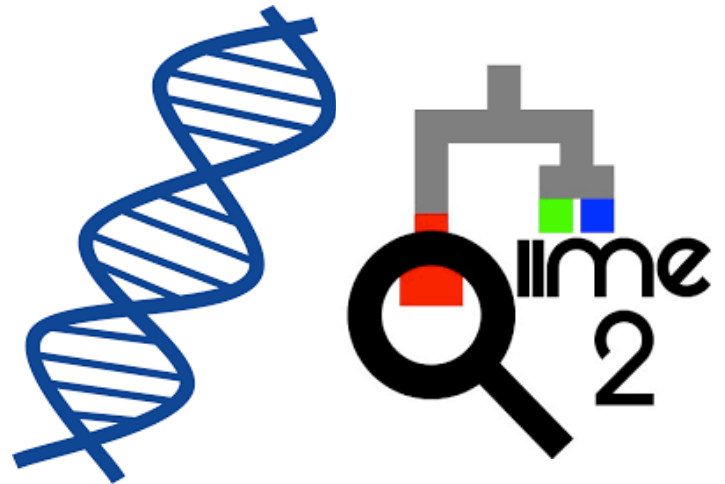


Green = *Nereocystis* only
Pink = *Nereocystis* + *Macrocystis*

Characterizing kelp and seawater microbial communities

Next-generation DNA sequencing:

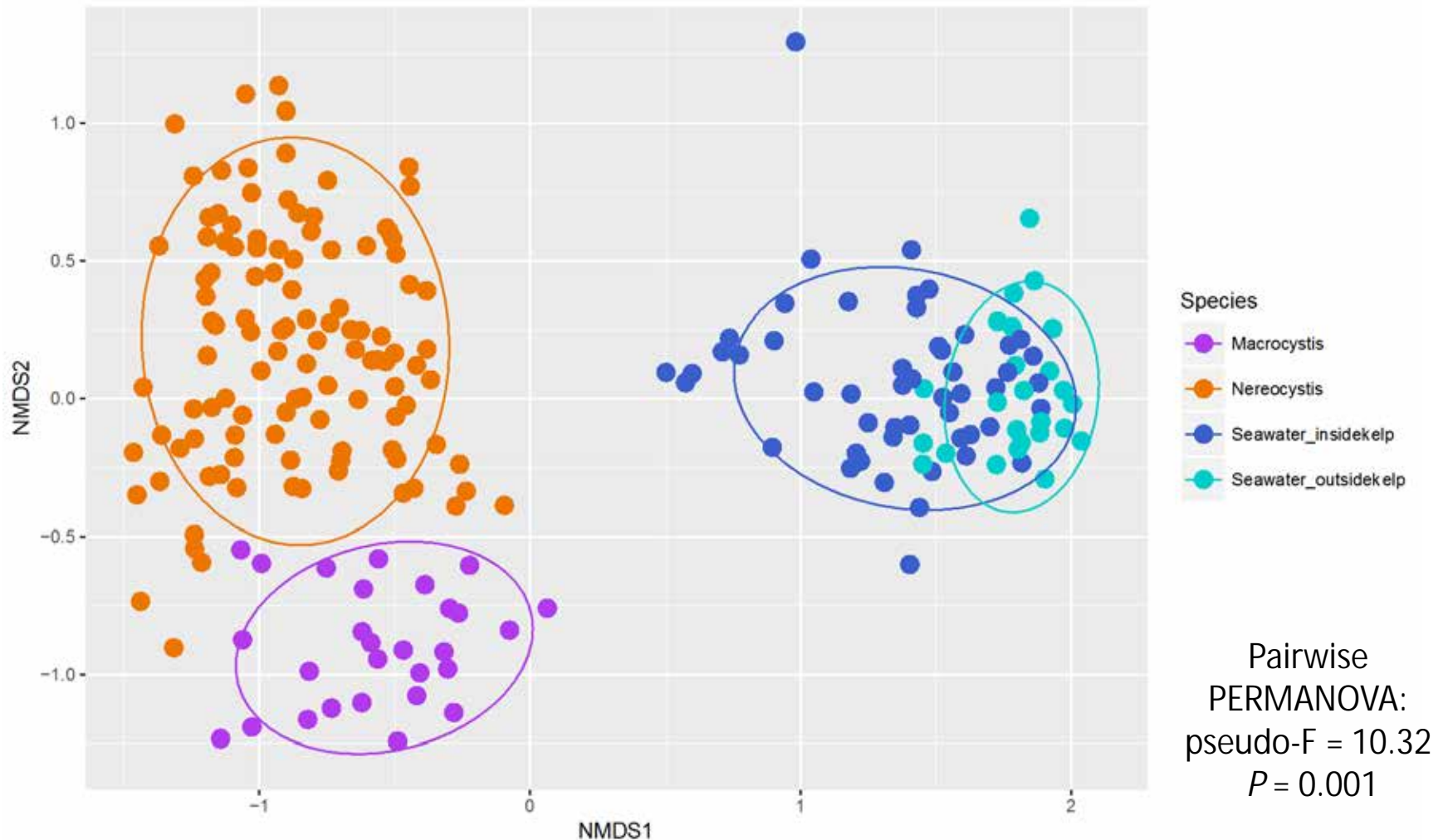
- 16S rRNA gene
- bacterial/archaeal primers (515 F - 806 R)
- Average # of bacterial sequences per sample = 28,000
- Classified as different microbial taxa with the Green Genes database, and clustered into bacterial species with QIIME2



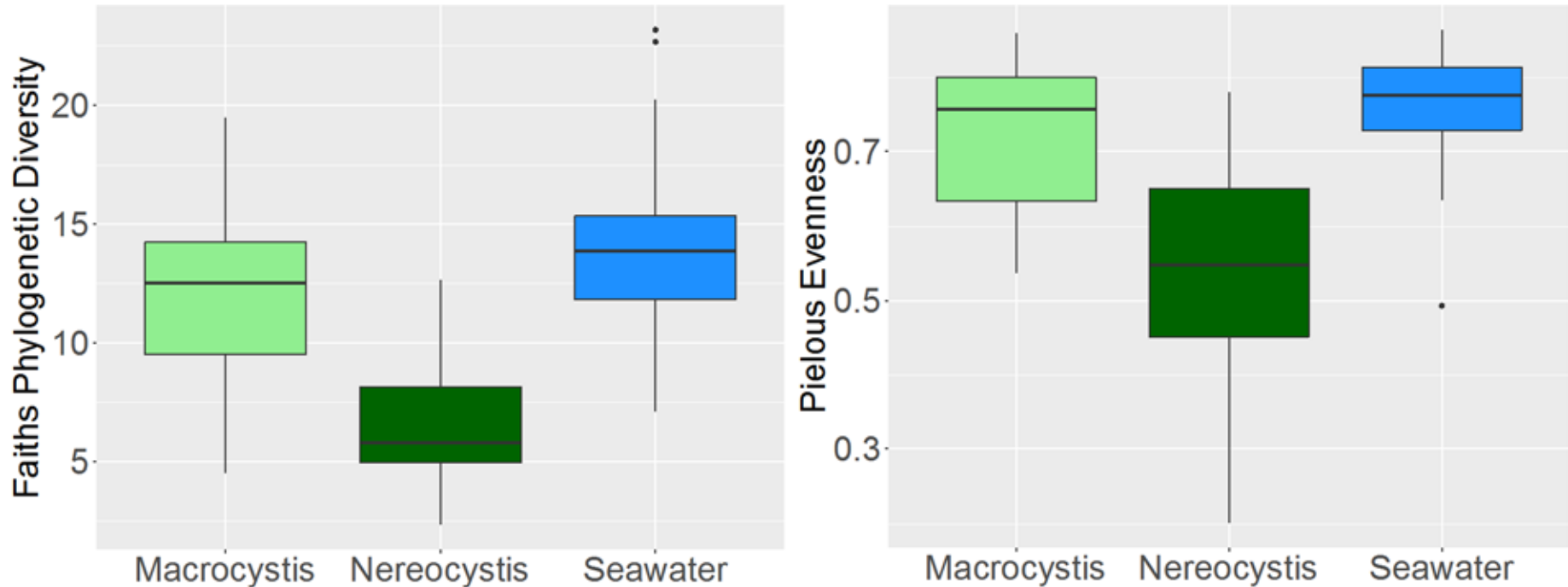
Results



Nereocystis and *Macrocystis* host significantly different microbial communities



Macrocystis microbiome has greater bacterial diversity & evenness of taxa



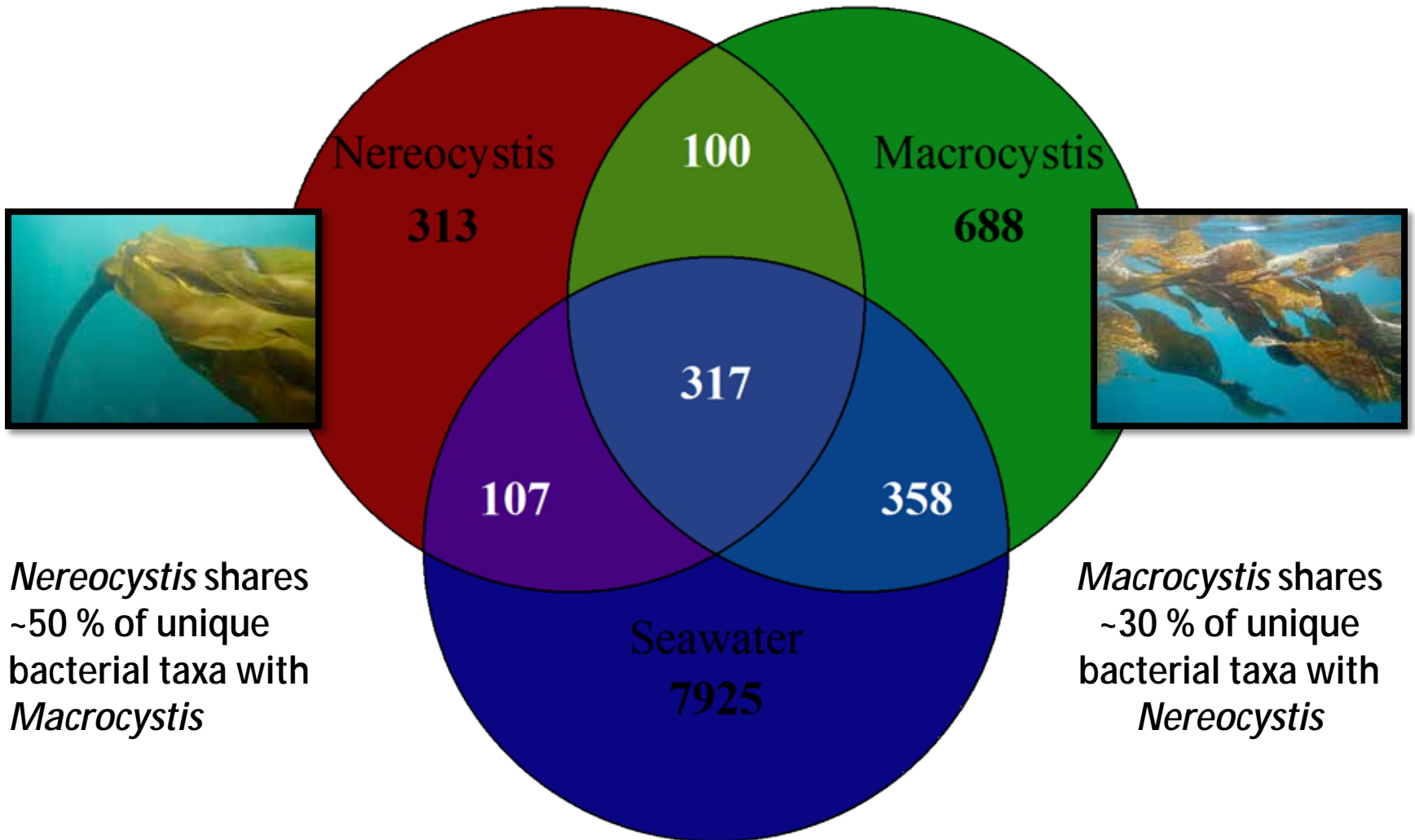
Average # bacterial species per sample

Macrocystis = 164

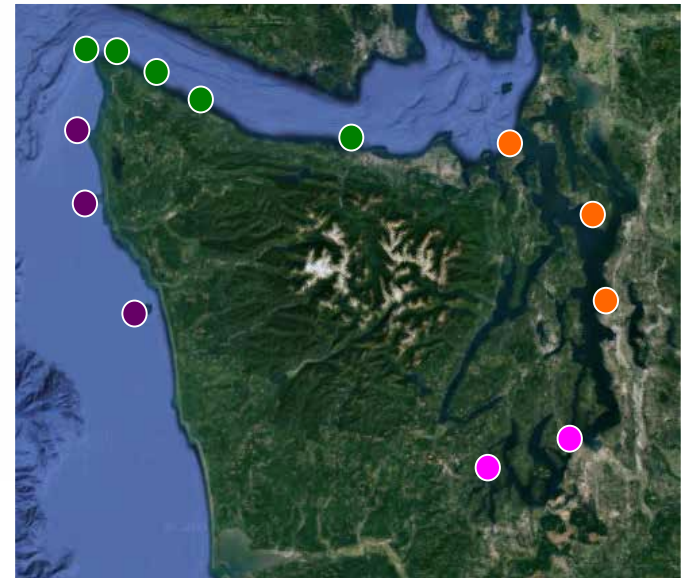
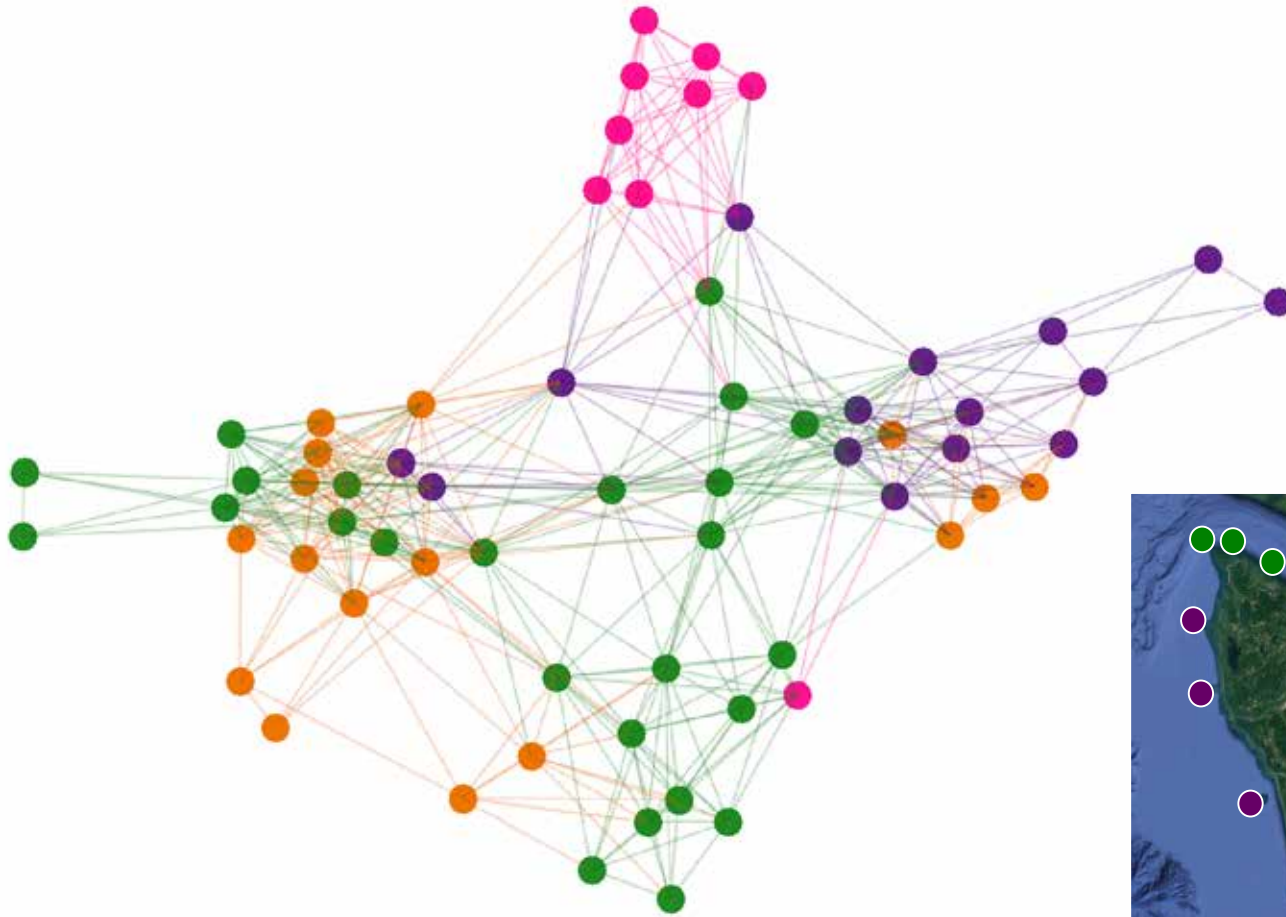
Nereocystis = 62

Seawater = 321

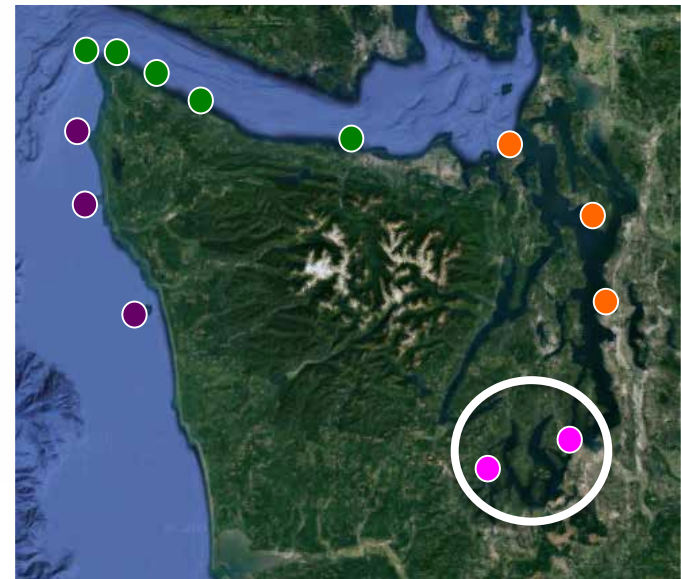
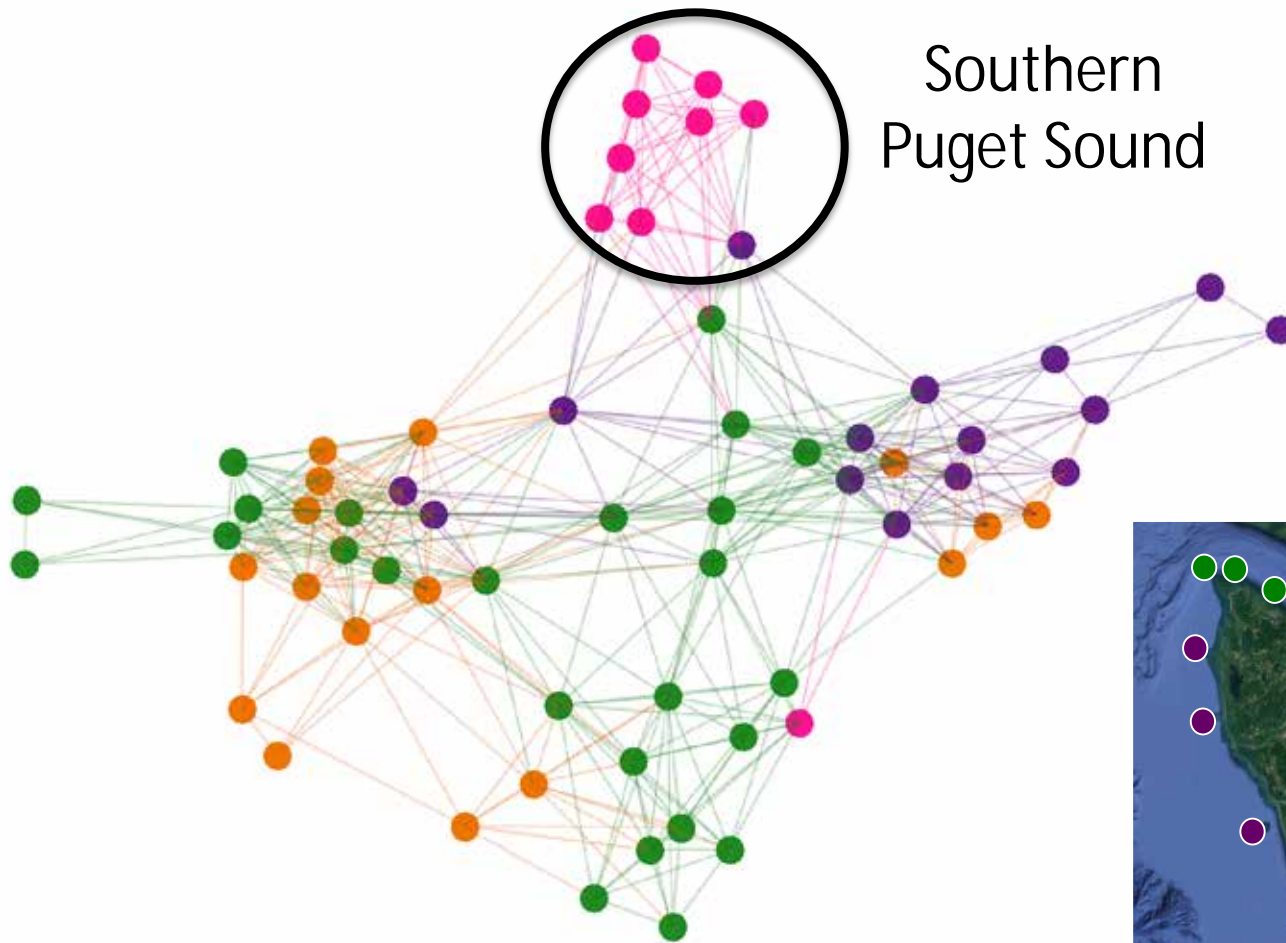
Nereocystis and *Macrocystis* host some distinct microbes, share others



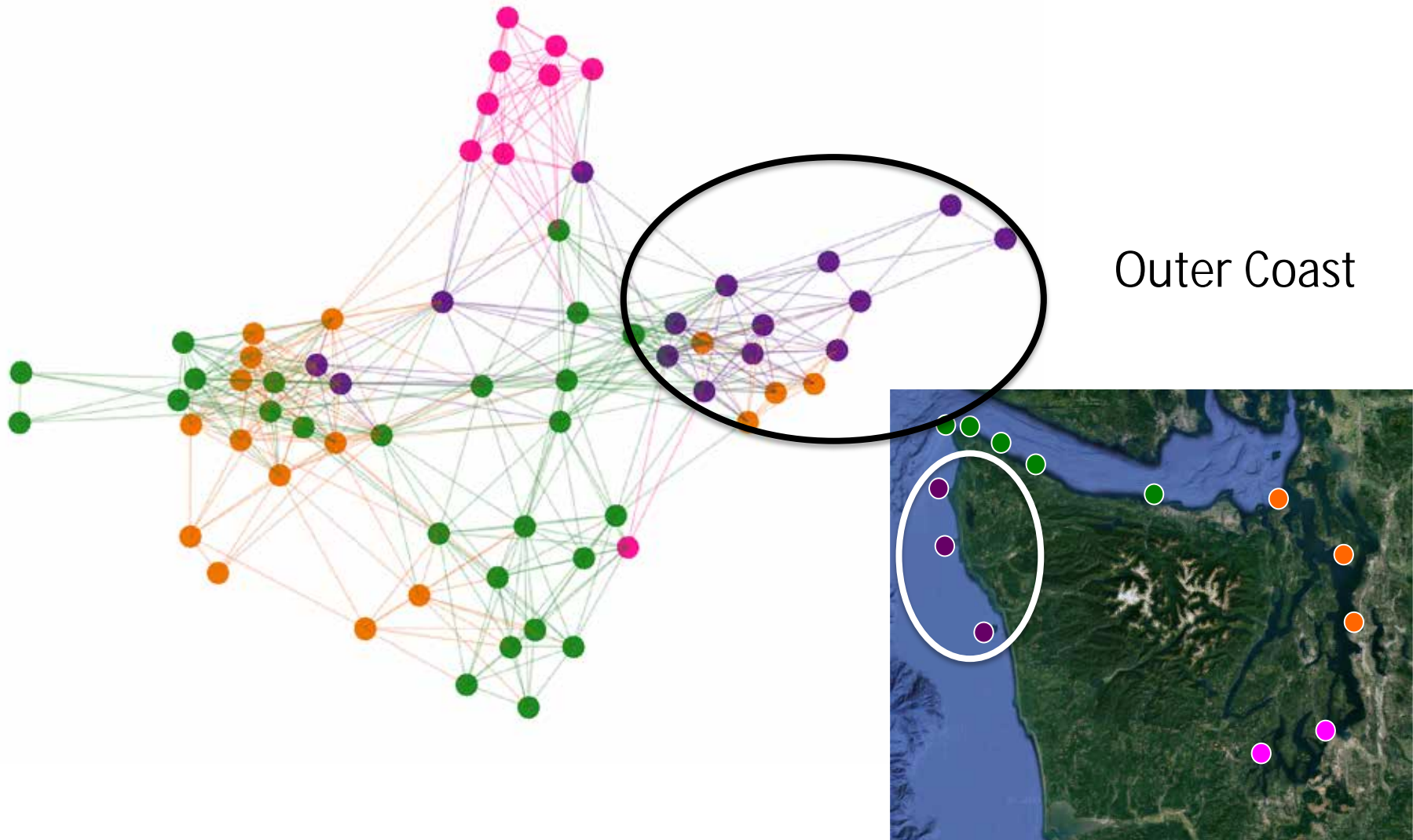
Nereocystis microbial communities have a unique composition at certain sites



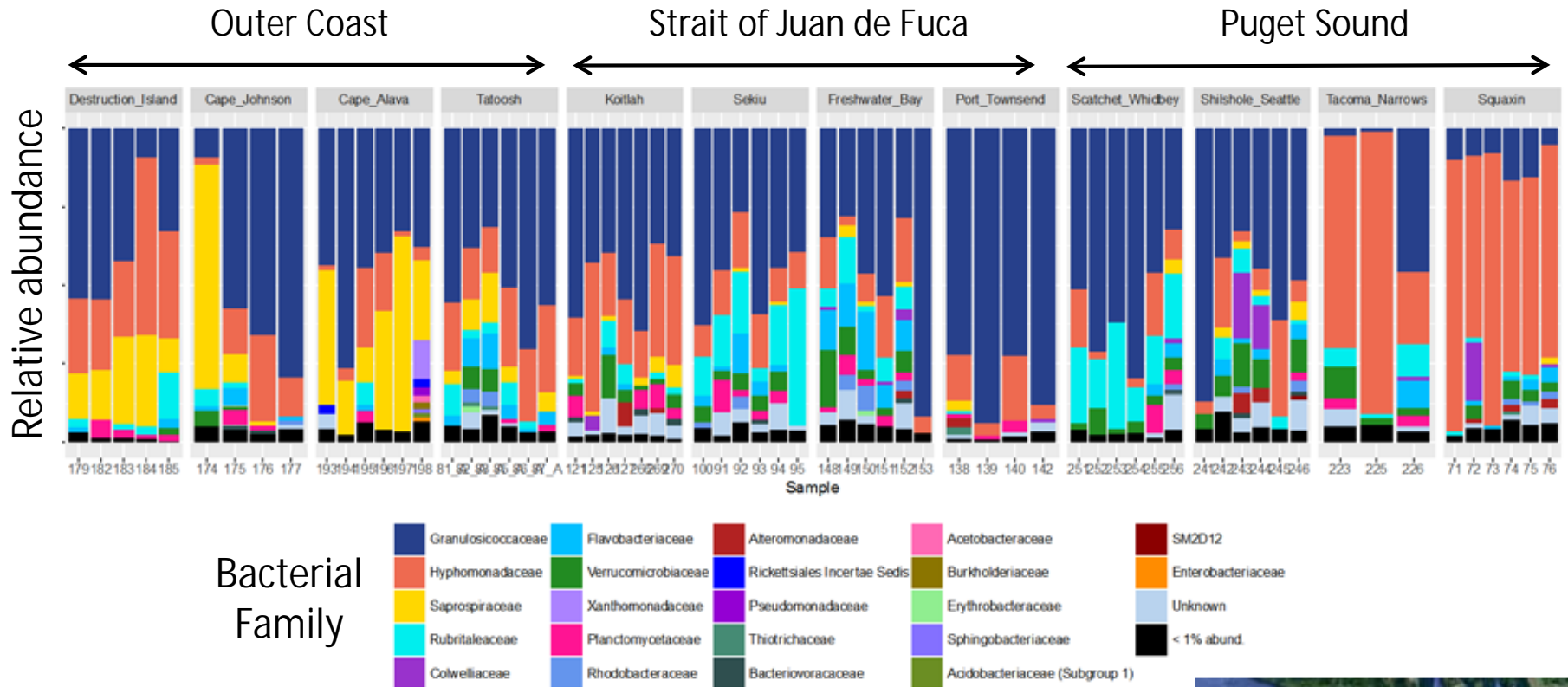
Nereocystis microbial communities have a unique composition at certain sites



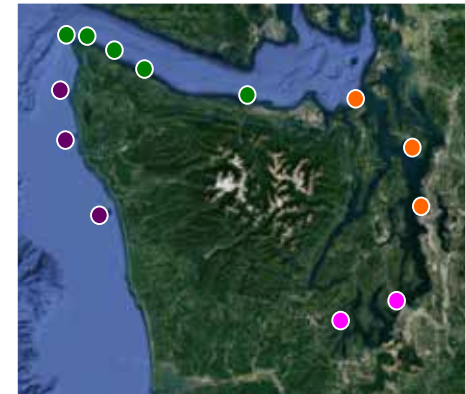
Nereocystis microbial communities have a unique composition at certain sites



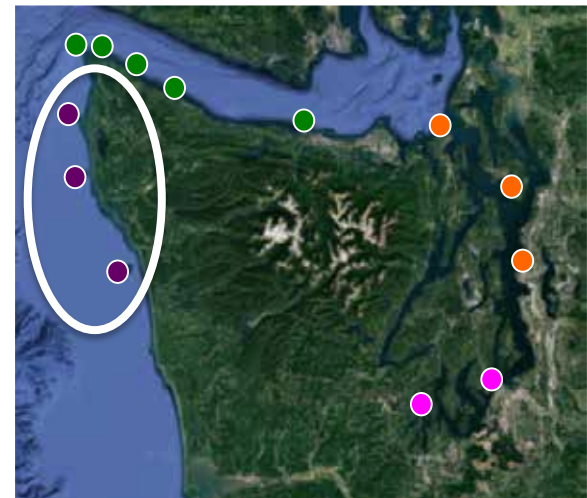
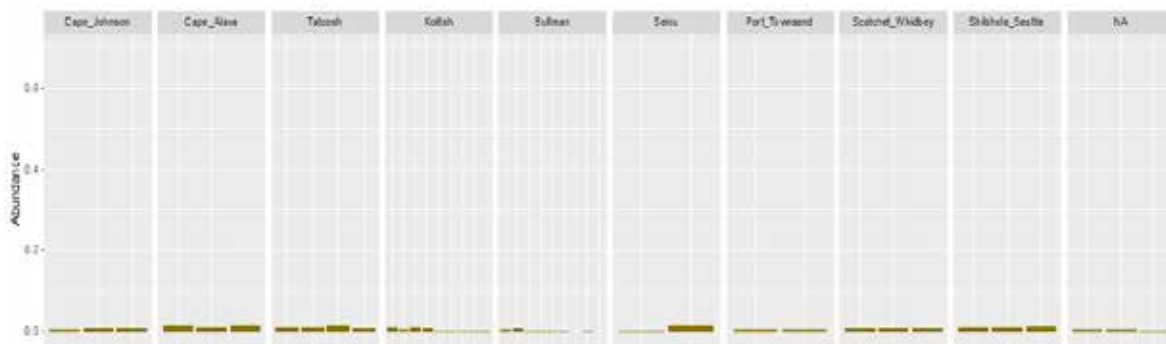
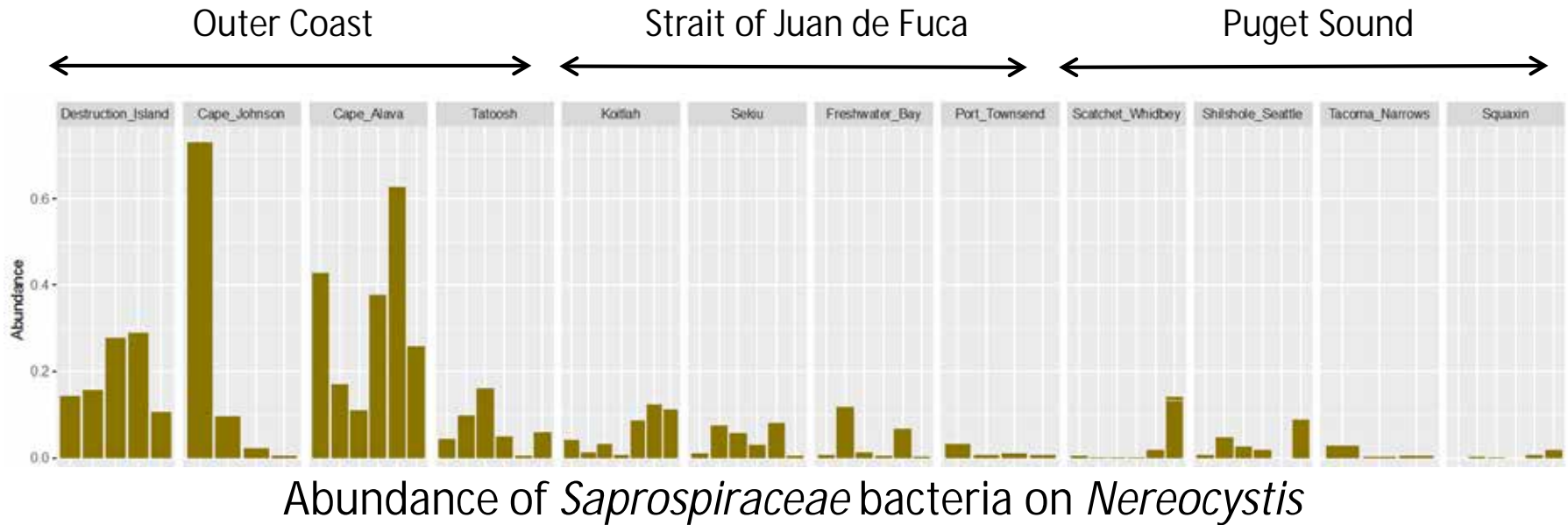
Spatial variation in the *Nereocystis* microbiome



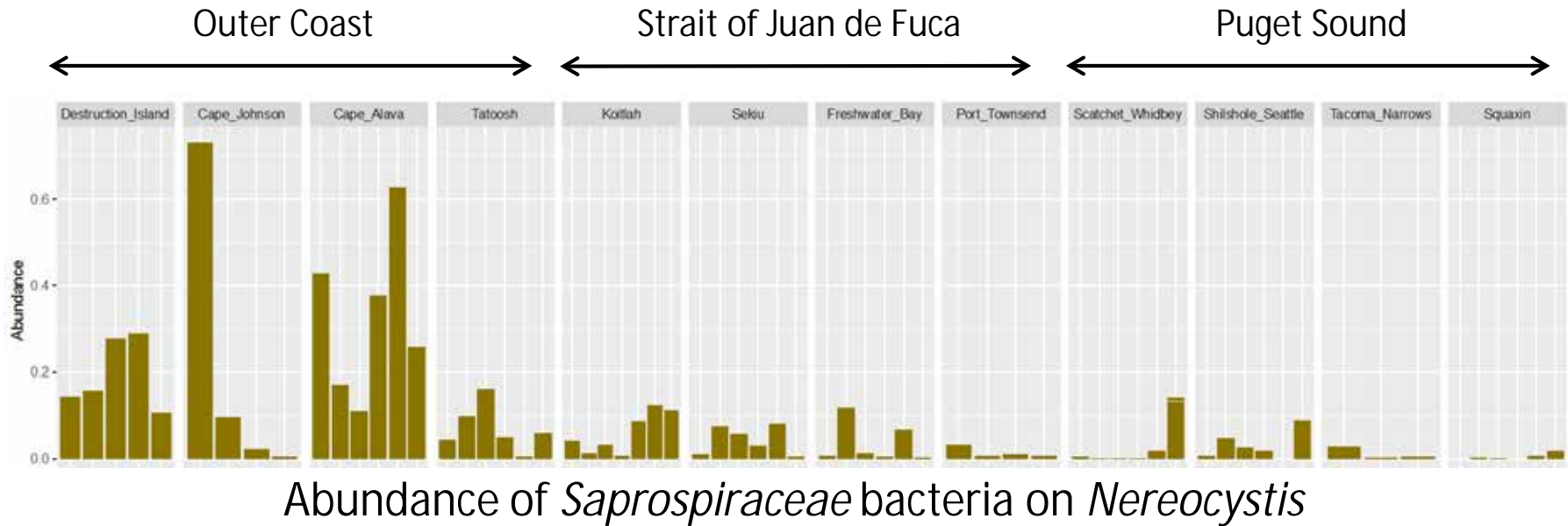
Significant spatial variation among sites
(PERMANOVA, pseudo-F = 2.40, $P = 0.001$)



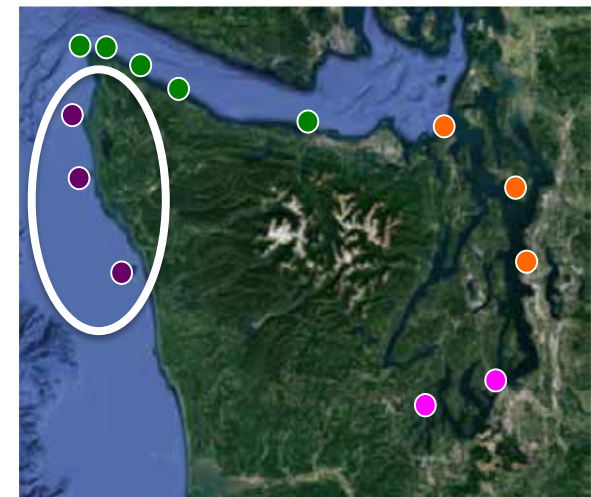
Spatial variation in the *Nereocystis* microbiome



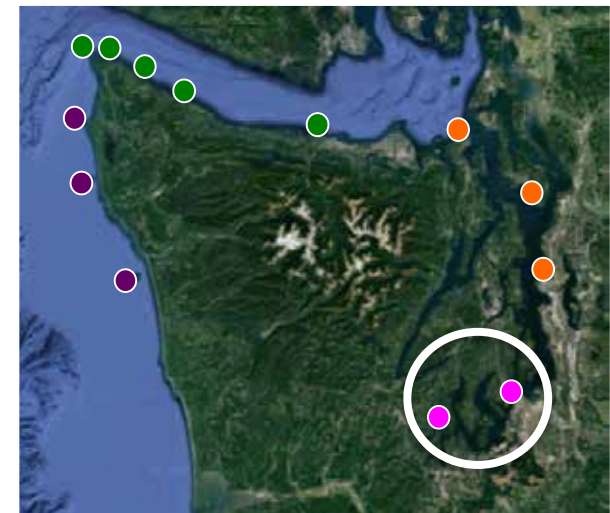
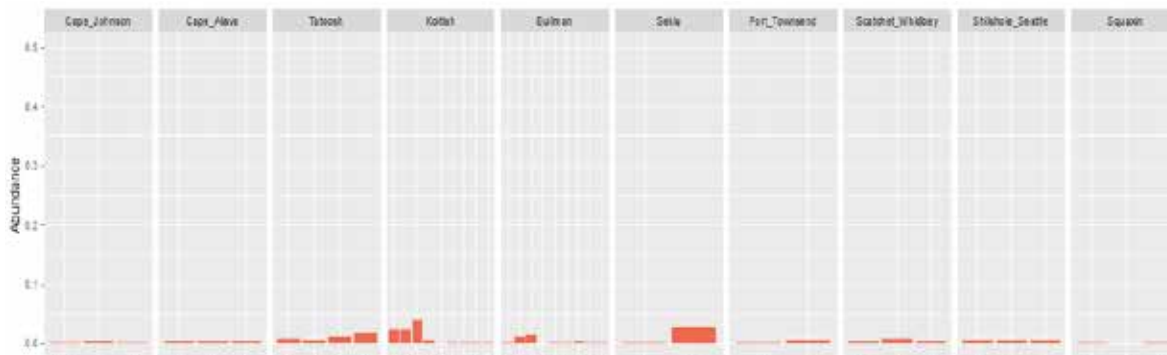
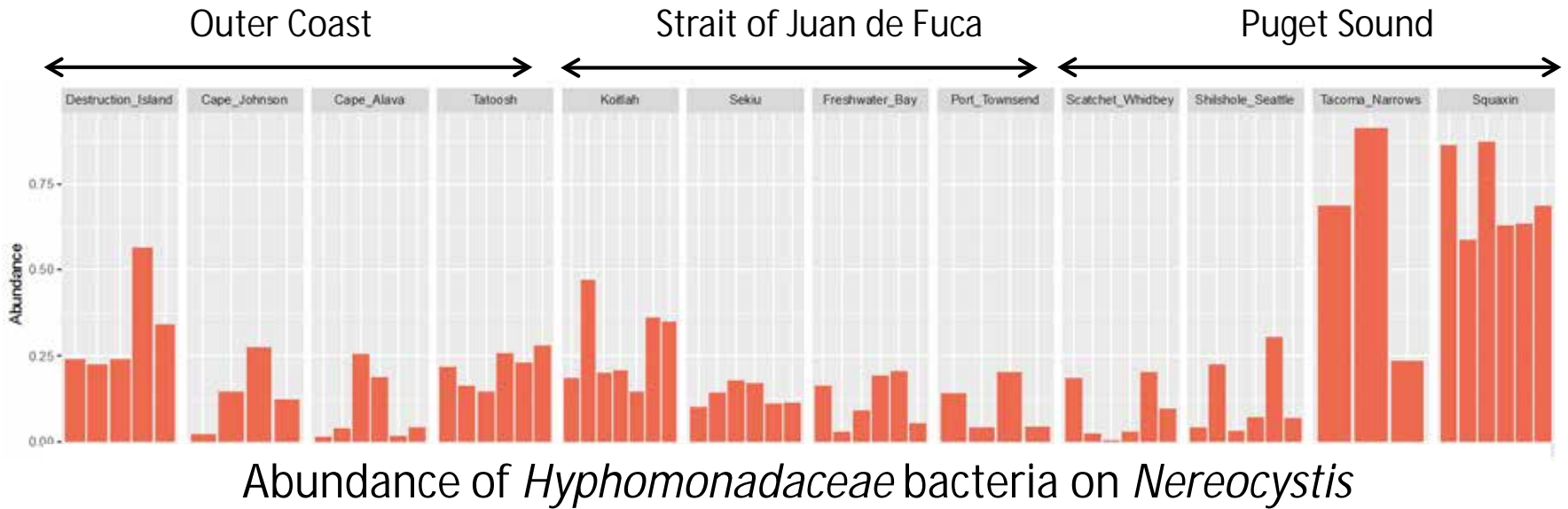
Spatial variation in the *Nereocystis* microbiome



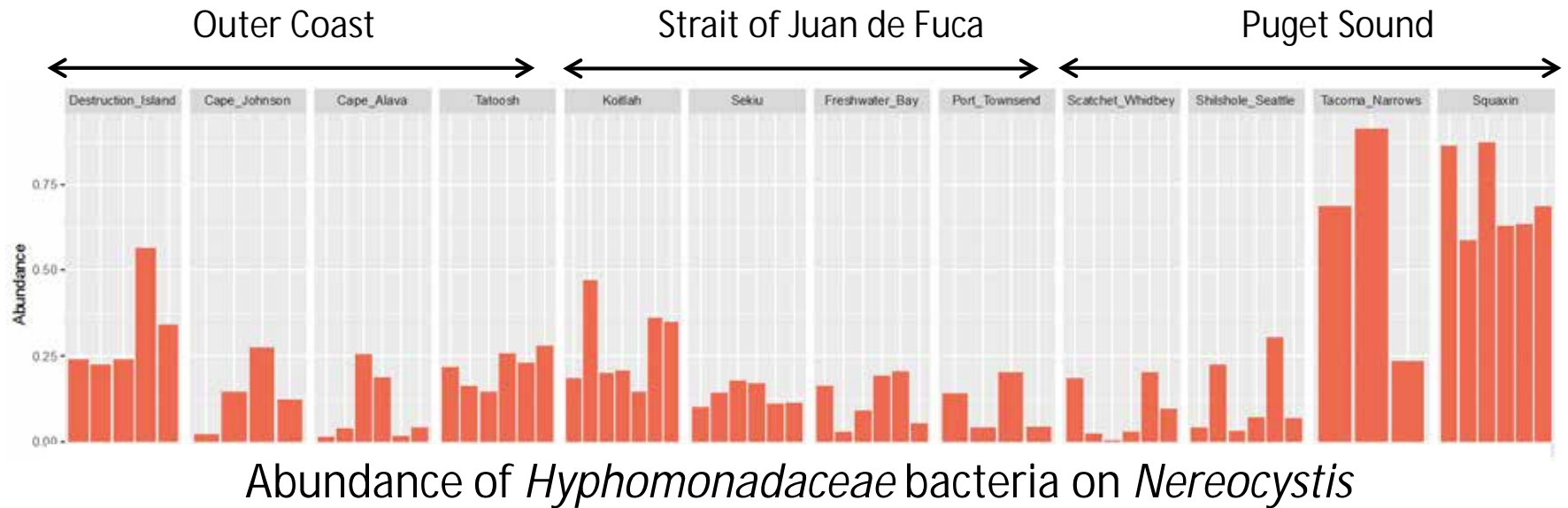
- *Saprospiraceae* (phylum *Bacteroidetes*) are significantly more abundant on the outer coast of WA
- *Saprospiraceae* are known to degrade complex carbon substrates in marine environments (McIlroy and Nielsen 2014)



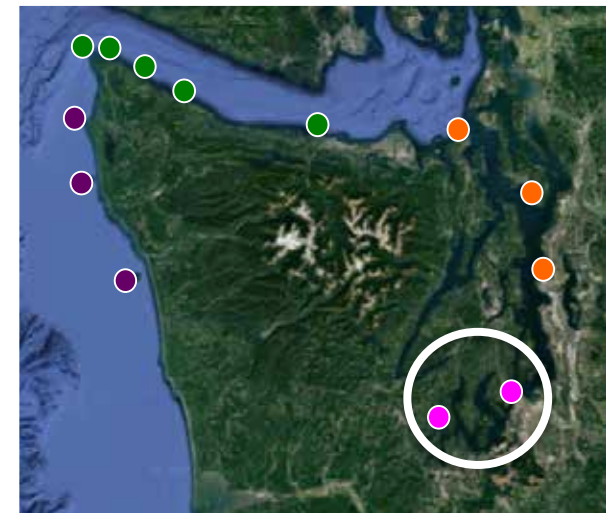
Spatial variation in the *Nereocystis* microbiome



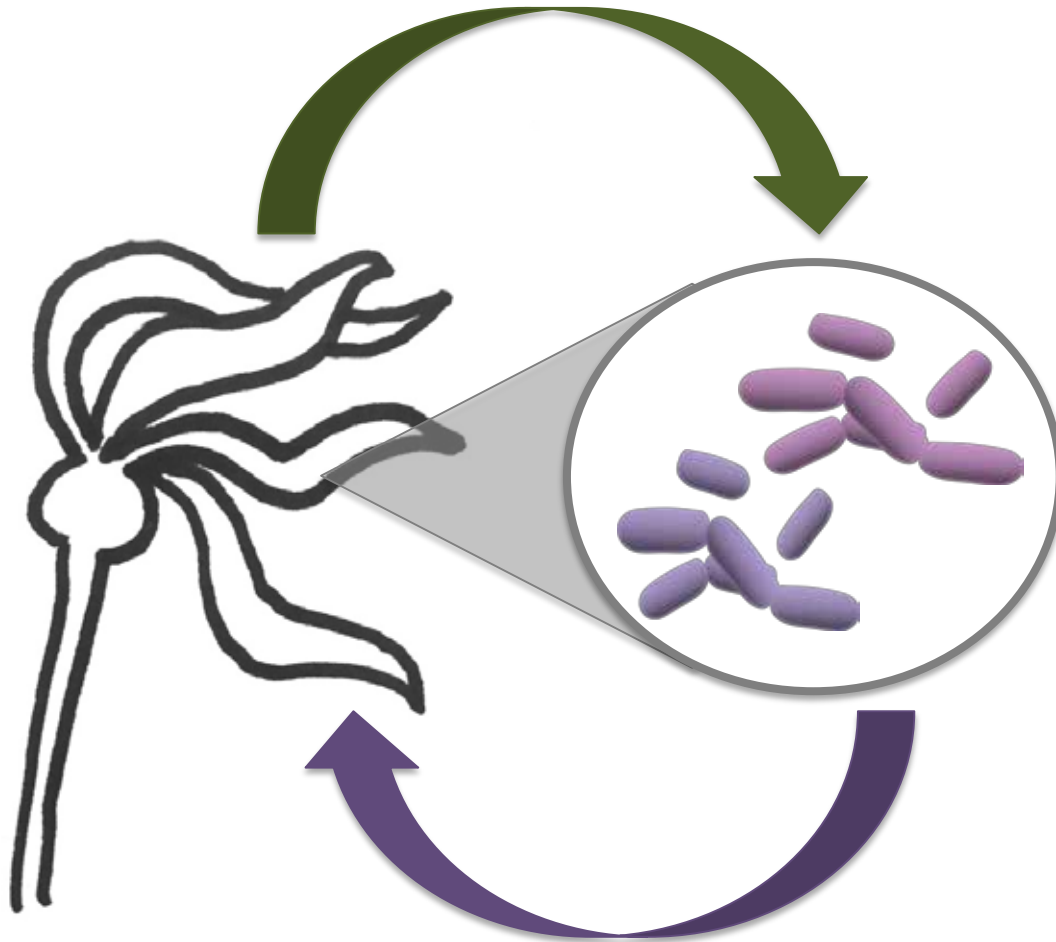
Spatial variation in the *Nereocystis* microbiome



- Family *Hyphomonadaceae* (class *Alphaproteobacteria*) are more abundant in southern Puget Sound
- *Hyphomonadaceae* are aerobic, heterotrophic, stalked bacteria that often live in oligotrophic waters (Abraham and Rohde 2014)

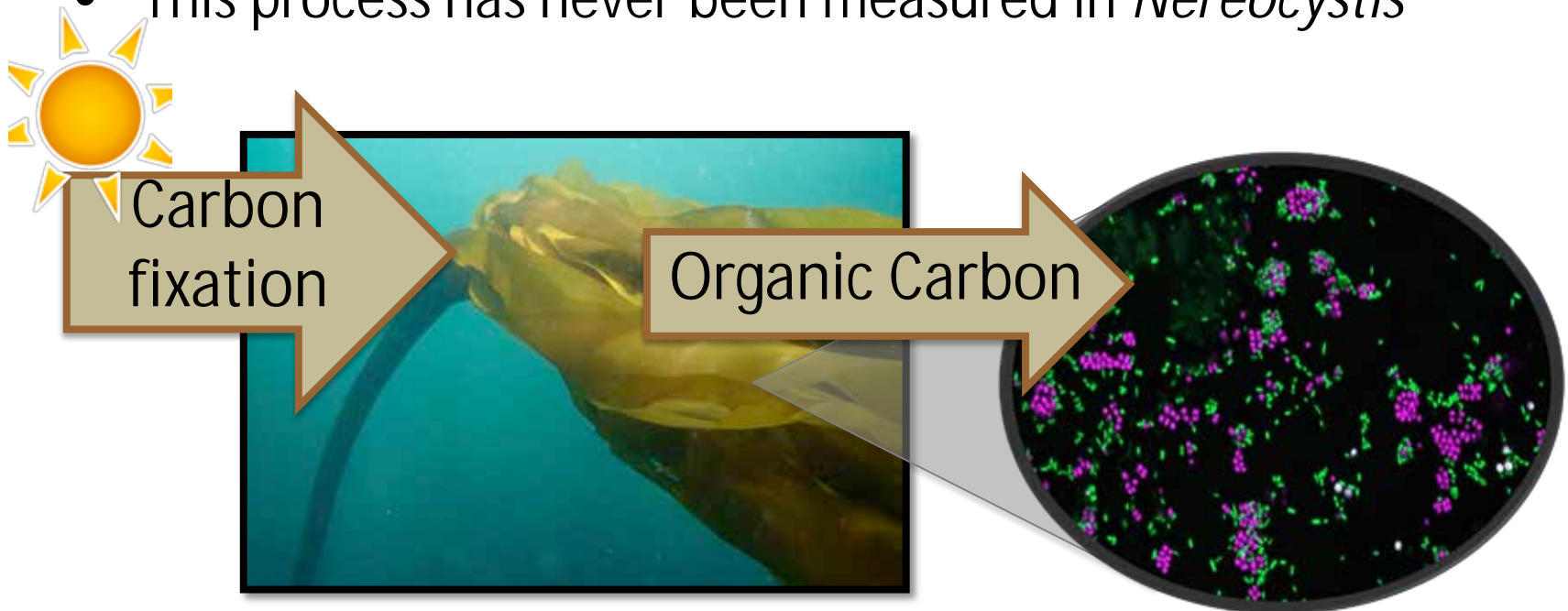


Part II: how do kelp and their microbes interact, and why should we care?

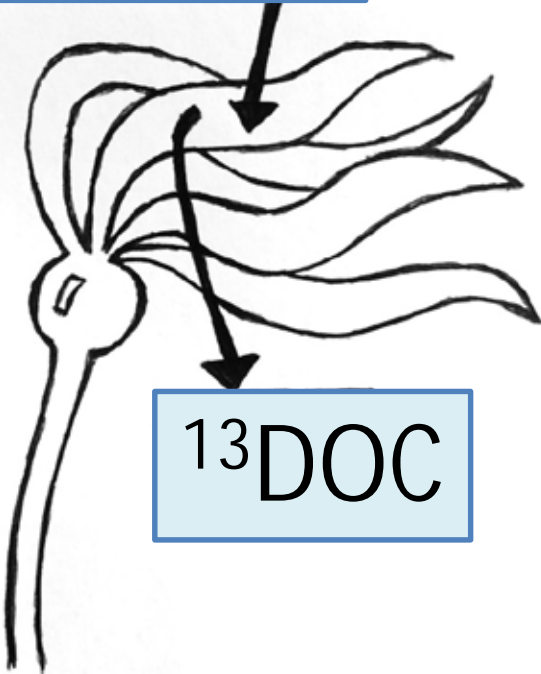
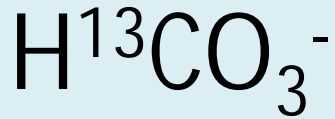


Kelp provide an abundant carbon resource for microbes

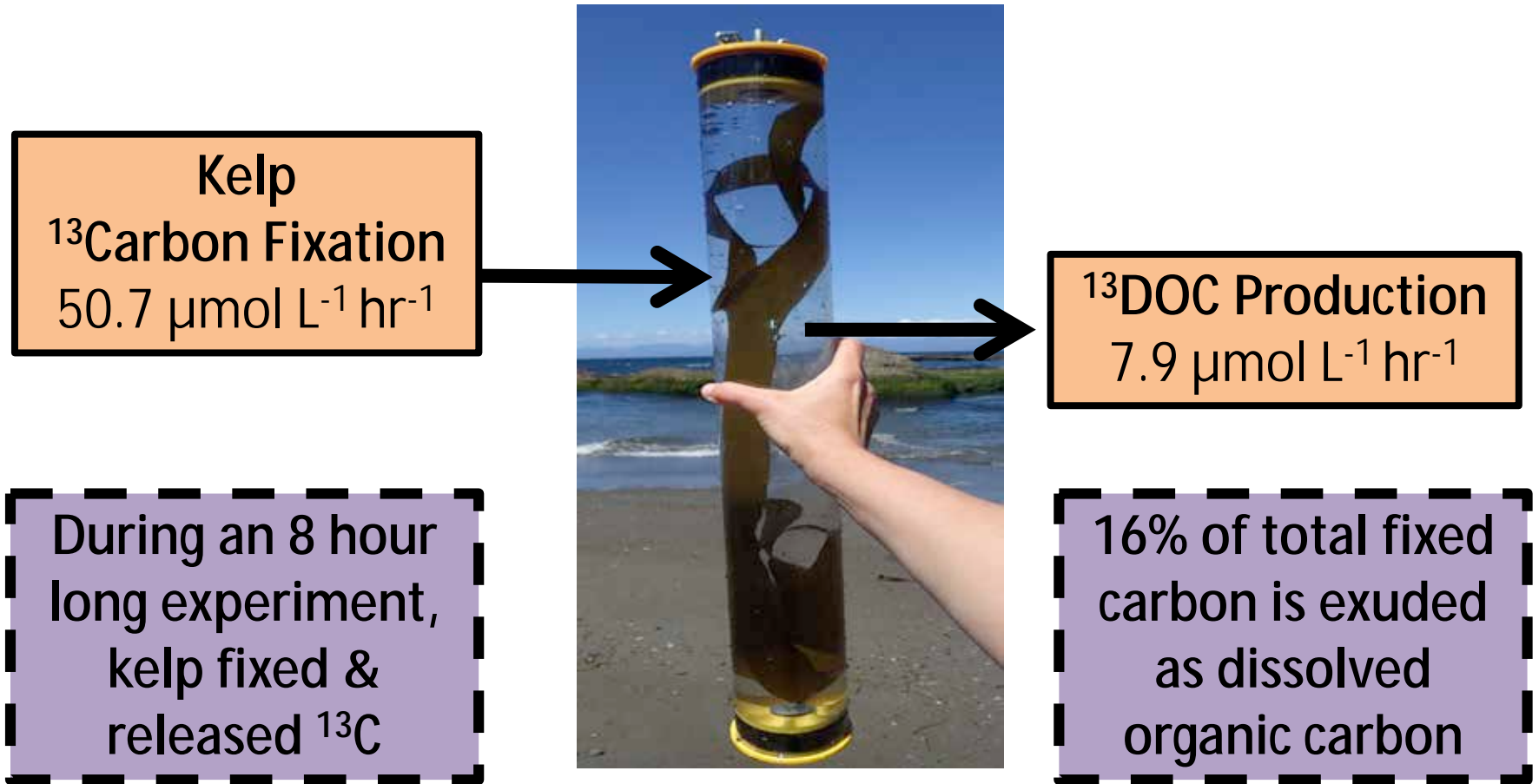
- On average, 14 – 40% of the carbon fixed by kelp is leaked into the surrounding seawater as dissolved organic carbon (Abdullah and Fredriksen 2004, Wada et al. 2007, Reed et al. 2015)
- This process has never been measured in *Nereocystis*



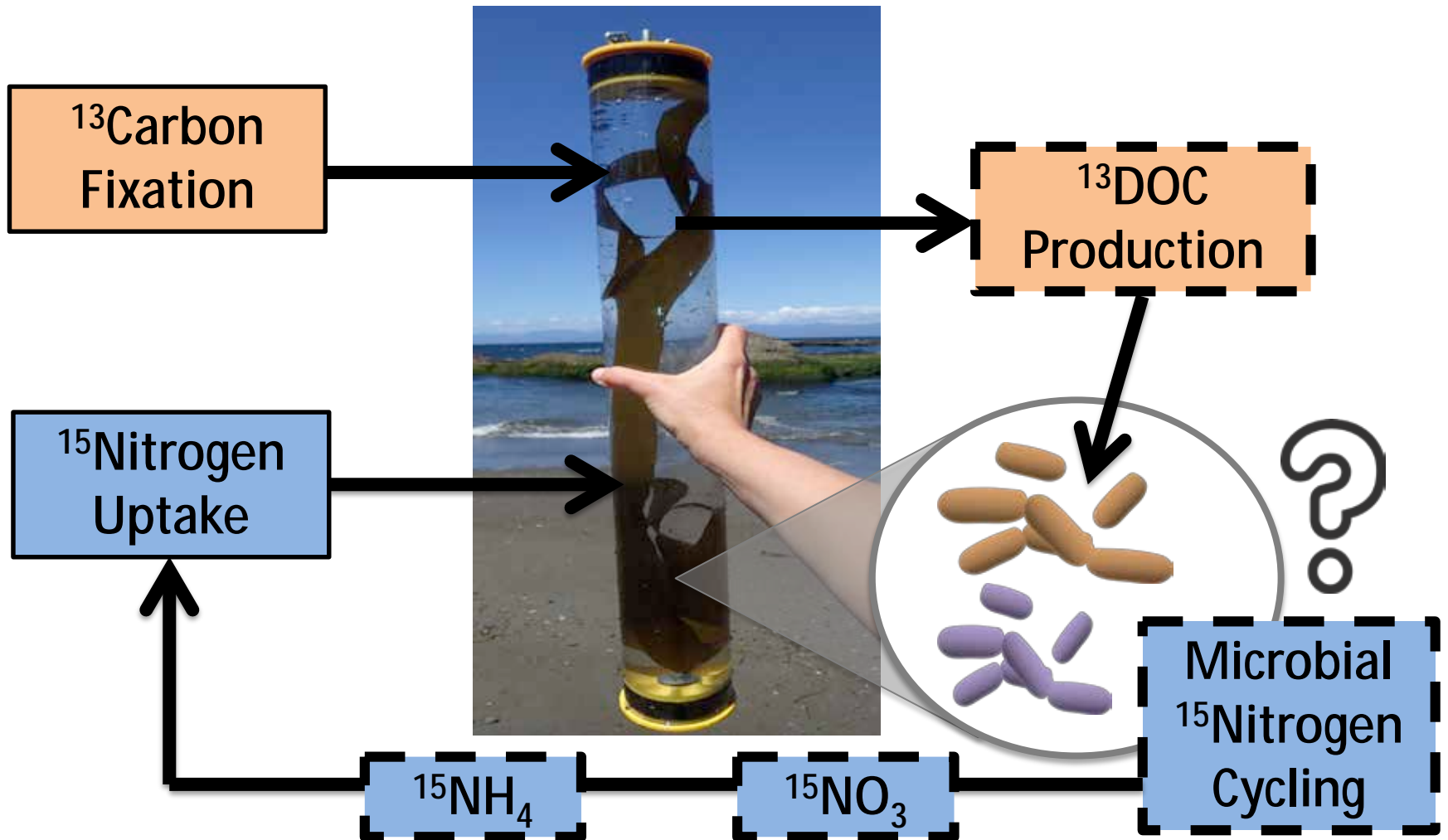
Nereocystis blade dissolved organic carbon (DOC) production using ^{13}C Bicarbonate



Nereocystis blades exude 16% of total fixed carbon as dissolved organic carbon



Future directions: understand the links between the kelp microbiome, dissolved carbon exudation & nutrient cycling in kelp forests



Acknowledgements

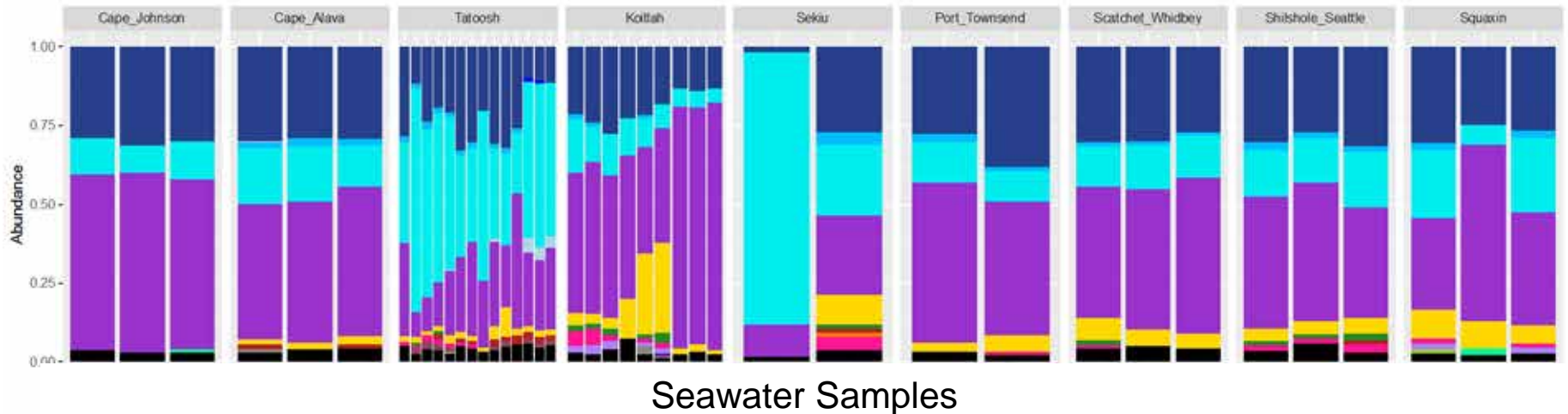
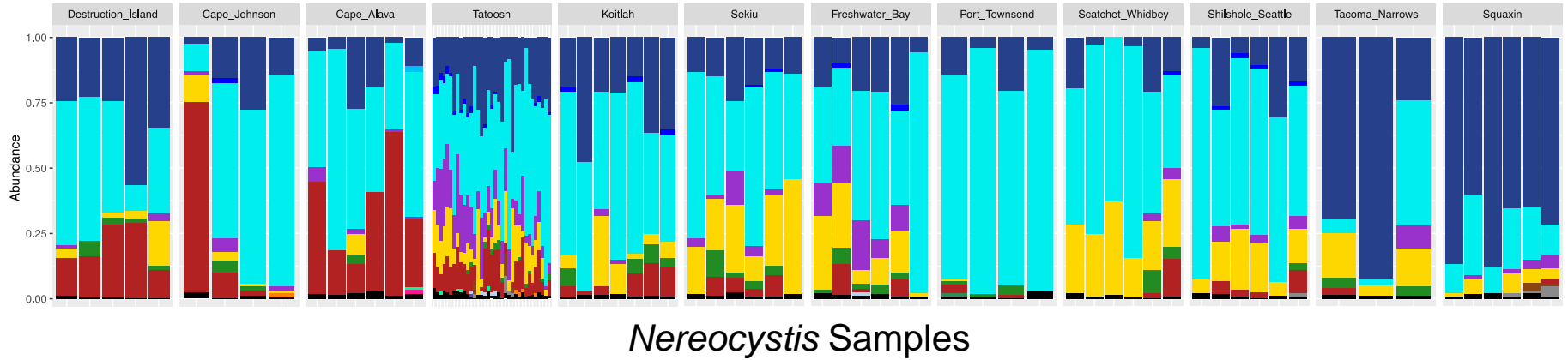


- Cathy Pfister (UChicago), PhD thesis advisor
- Jessica Mark-Welch (MBL), microscopy imaging of kelp bacteria
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 - National Geographic Early Career Grant
 - University of Chicago Committee on Evolutionary Biology



EXTRA SLIDES...
(for questions)

Nereocystis vs. Seawater Spatial Variation

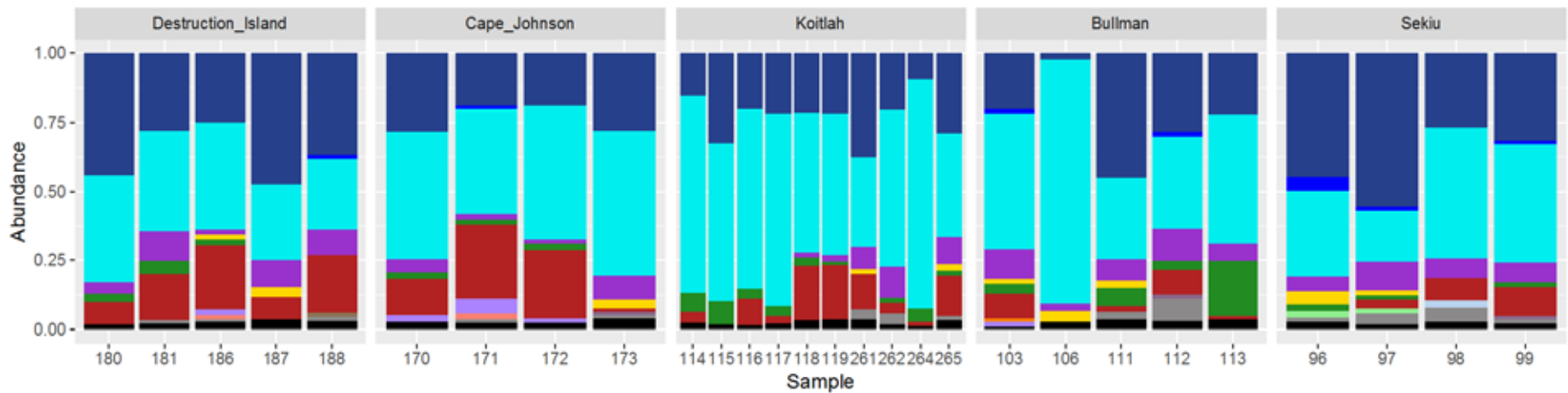
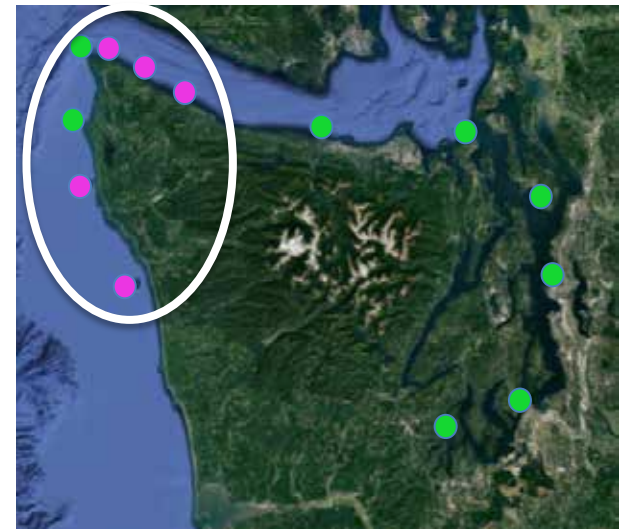


Bacterial
Class

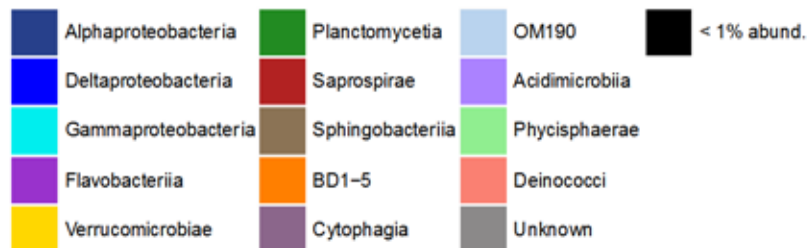


Spatial variation in the *Macrocystis* microbiome

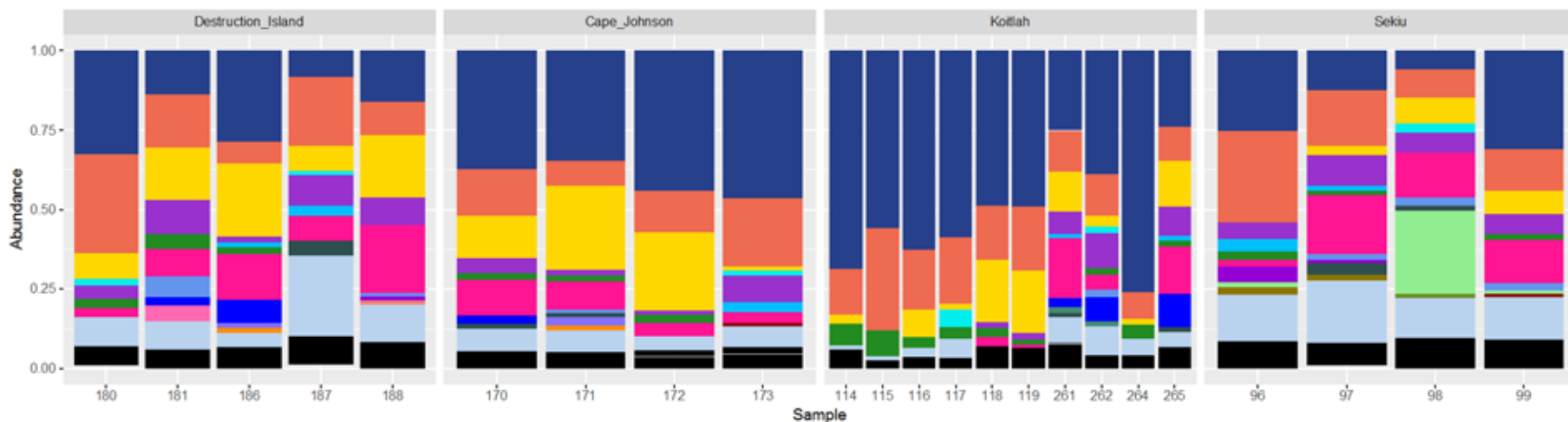
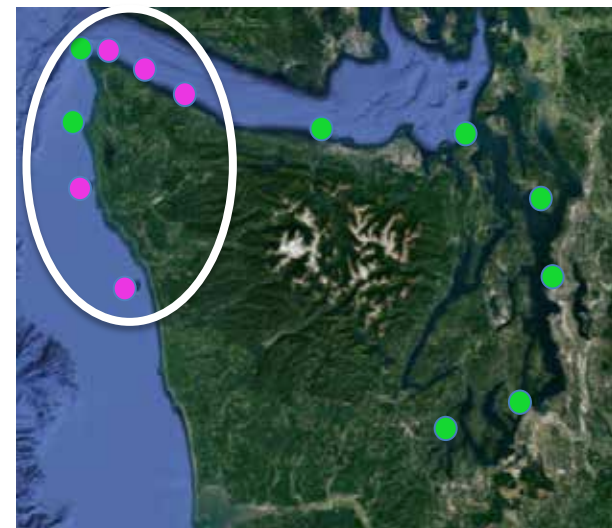
Significant spatial variation among sites
(PERMANOVA, pseudo-F = 1.98, $P = 0.001$)



Bacterial
class



PERMANOVA:
 Cape Johnson and
 Destruction Island
 microbial communities
 are the same ($P = 0.16$), all other sites are
 significantly different
 ($P \leq 0.05$)



Bacterial
 family

