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Back to the Sea: Seagrass As a Model System for Plant Microbiome Studies

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<https://escholarship.org/uc/item/8wv851r7>

### Author

Eisen, JA

### Publication Date

2018-01-22

Peer reviewed



# **Back to the Sea: Seagrass As a Model System for Plant Microbiome Studies**

**Jonathan A. Eisen  
UC Davis**

**January 22, 2018**

**Bilateral Joint Symposium  
Academia Sinica & UC Davis**

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UC Davis**

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# **Lessons Learned When You Work on Something You Know Nothing About**

**Jonathan A. Eisen  
UC Davis**

**January 22, 2018**

**Bilateral Joint Symposium  
Academia Sinica & UC Davis**

# **Seagrass Microbiome Project**

## **Lesson 1:**

**Good Colleagues Are A Good Thing**



# Sept. 2010: Moore Foundation MMI RFI

## GBMF's Marine Microbiology Initiative (MMI) -- Request for Ideas (RFI)



**Marine Microbiology Request for Ideas** <mmi.rfi@moore.org>

9/21/10



to

The Gordon and Betty Moore Foundation's Marine Microbiology Initiative (MMI) has issued a Request for Ideas (RFI) for marine microbiology and marine microbial ecology research. We are looking to identify the most promising opportunities where a strategic, focused effort over the next five years will help to break open 'black boxes' in the field and take understanding of marine microbial communities to a new level.

More information about the RFI can be found here: <http://www.moore.org/mmi-rfi.aspx>. Researchers interested in contributing an RFI for consideration should submit a two-page idea summary by **November 8, 2010**.

Please forward this to anyone who might be interested. Thank you in advance for helping us spread the word, and our apologies for cross-postings.

– The Marine Microbiology Initiative team

# Sept. 2010: Moore Foundation MMI RFI

GBMF's Marine Microbiology Initiative (MMI) -- Request for Ideas (RFI)



 **Marine Microbiology Request for Ideas** <mmi.rfi@moore.org>

9/21/10



to 

The Gordon and Betty Moore Foundation is a leading supporter of research in marine microbiology, where a strategic understanding of the microbial world is essential for understanding the ocean's role in global climate change.

More information about the initiative is available at [www.moore.org](http://www.moore.org). We encourage you to contribute your ideas and insights to the initiative.

**2 Page Idea Summary  
Due November 8, 2010**

as (RFI) for opportunities to take part in the initiative.

ed in

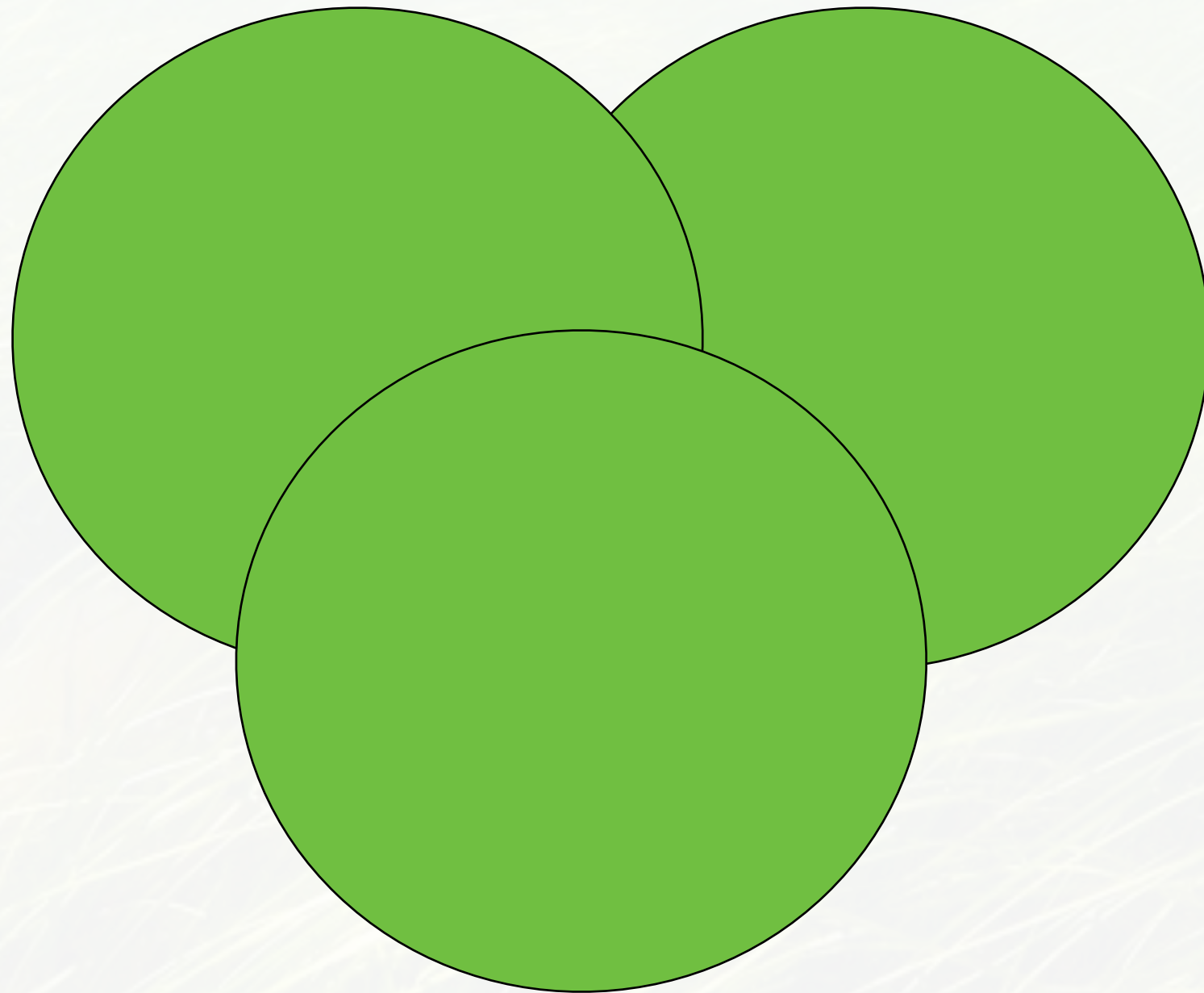
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– The Marine Microbiology Initiative team

# Eisen Lab Microbiome Topics

Ecology

Evolution



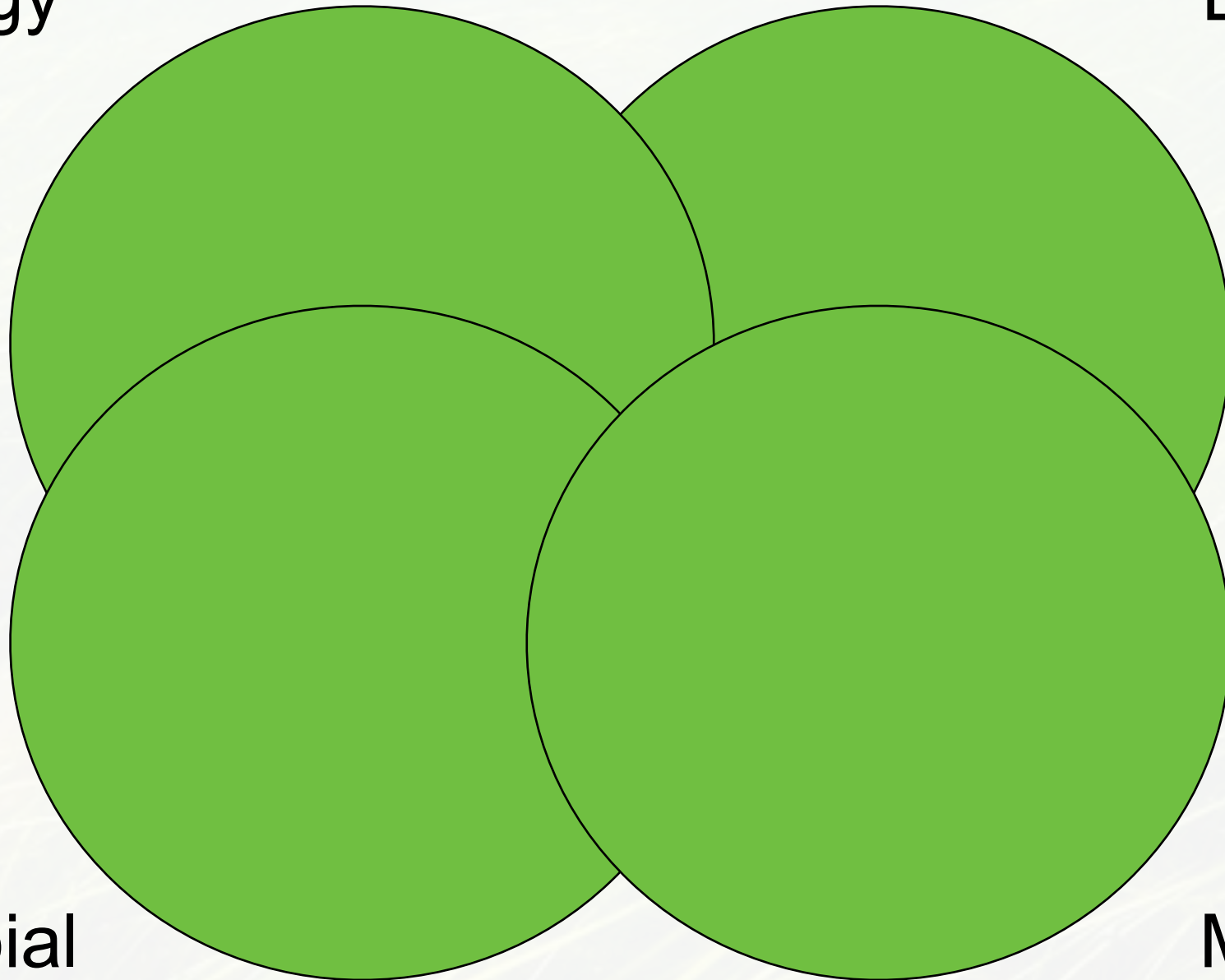
Function



# Eisen Lab Topics

Ecology

Evolution



Microbial  
Communities

Marine  
Biology



# Contacted Colleagues

- **Jessica Green**
- **Katie Pollard**
- **Jenna Lang (in my lab)**
- **Multiple calls, not sure what to propose**
- **Also - extremely busy teaching BIS2C w/ 4 lectures per week and 700 students**



# Oct. 2010 Jim Doyle: Aquatic Monocots





# Oct. 2010 Jim Doyle: Aquatic Monocots

Why monocots lose 2<sup>o</sup> growth?

- probably an adaptation to aquatic habitat
- no need for wood for conduction of support when you live in H<sub>2</sub>O
- supported by fact that basal monocots are aquatic

Aroca

= some even went into ocean

Palm - tree like but  
not secondary  
growth



# Oct. 2010 Jim Doyle: Aquatic Monocots

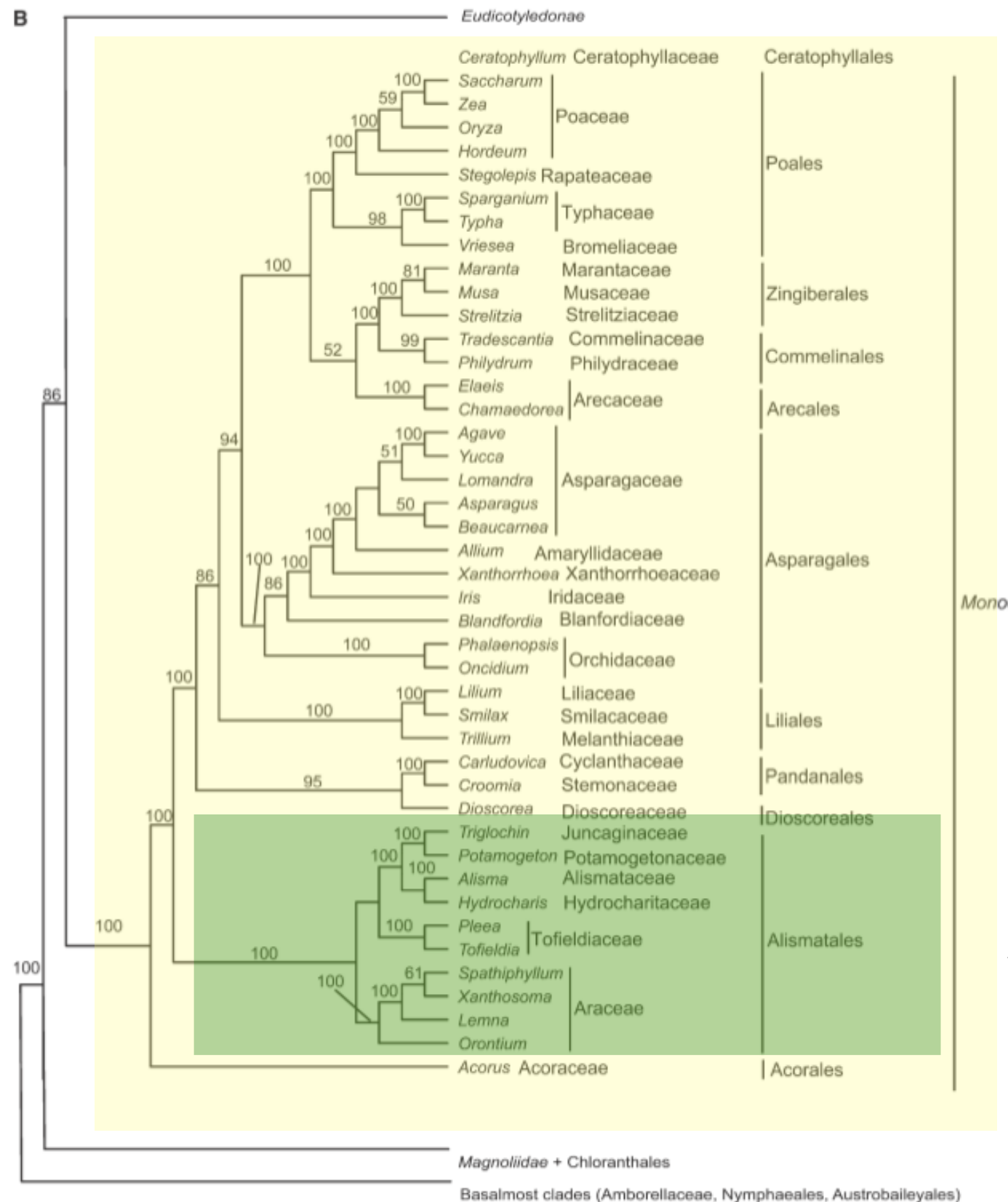
**Alismatales: “sea grasses”: marine monocots**



**Zosteraceae**  
***Zostera* (eelgrass)**



# Seagrass w/in Monocots

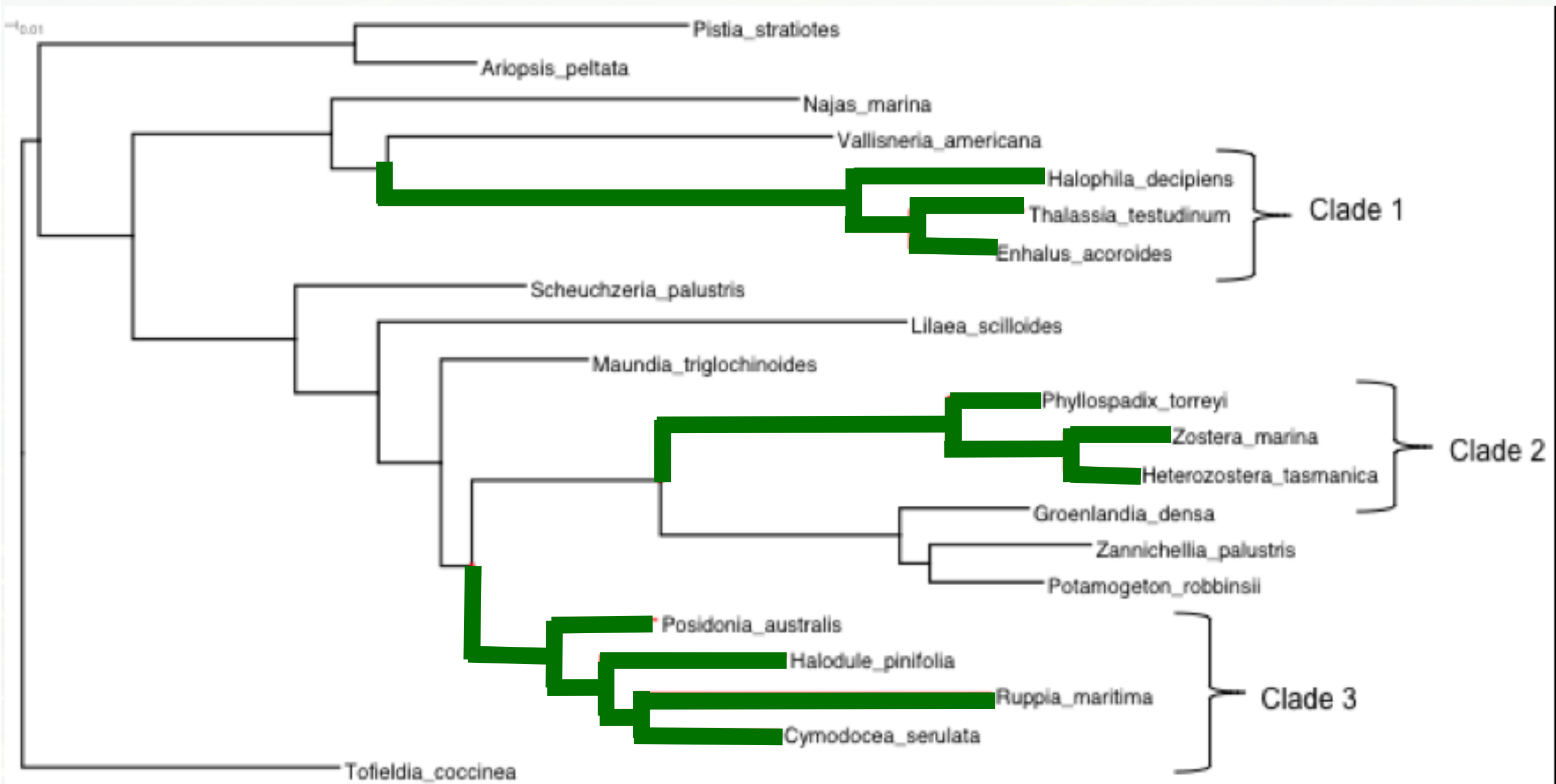


**Dicots**

**Monocots**

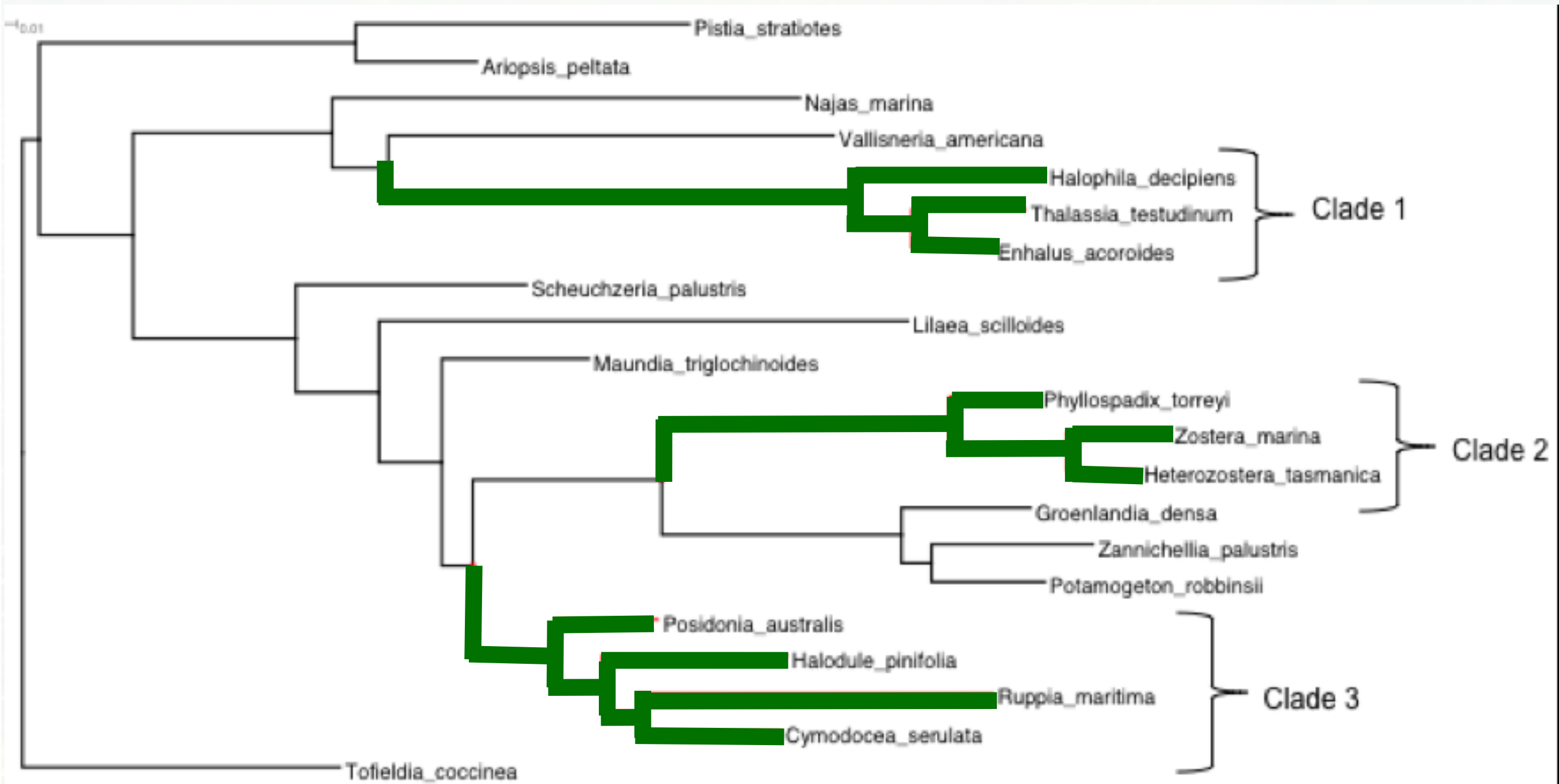
**Alismatales**

# Seagrasses w/in Alismatales



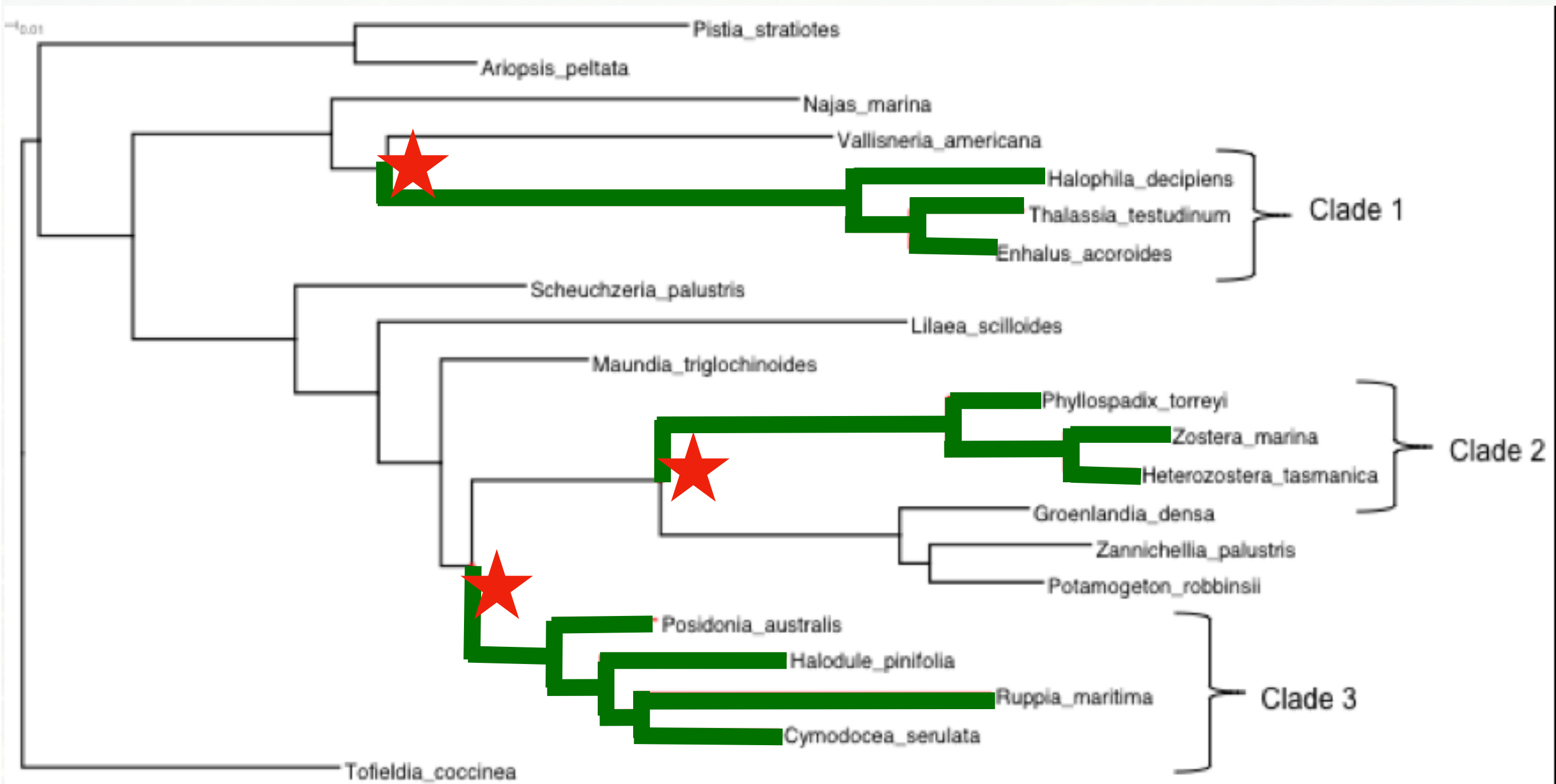
Tree inferred by Jenna Lang based from rbcL sequences using RaxML

# Seagrasses Polyphyletic



Tree inferred by Jenna Lang based from rbcL sequences using RaxML

# Seagrasses: 3 Invasions of Marine



Tree inferred by Jenna Lang based from rbcL sequences using RaxML



# Seagrass Diversity

## Small-bodied

Small, thin leaves  
Small rhizome  
"Guerilla" strategy  
Short-lived with fast turnover  
Low biomass  
Exploits new space  
Abundant flowering  
Many small seeds  
Seed bank

## Large-bodied

Large, thick leaves  
Large rhizome  
"Phalanx" strategy  
Long-lived with slow turnover  
High biomass  
Holds space  
Patchy flowering  
Few larger seeds  
Seeds germinate rapidly



Paddle grass  
*Halophila decipiens*



Star grass  
*Halophila engelmannii*



Widgeon grass  
*Ruppia maritima*



Shoal grass  
*Halodule wrightii*



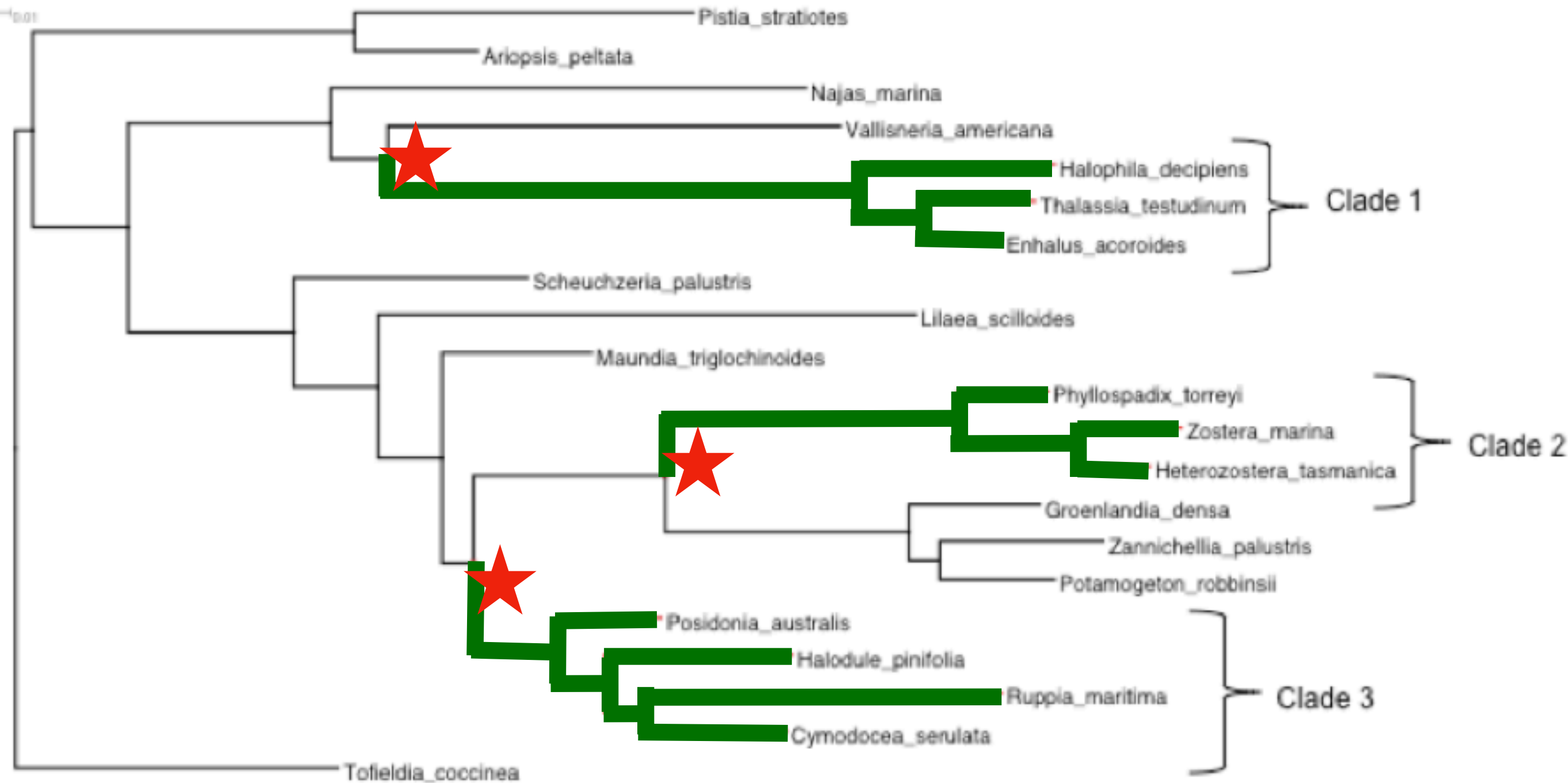
Manatee grass  
*Syringodium filiforme*



Turtle grass  
*Thalassia testudinum*

Image from Reynolds PL. Seagrass and Seagrass Beds  
<http://ocean.si.edu/seagrass-and-seagrass-beds>

# Seagrasses: Significant Convergence



Tree inferred by Jenna Lang based from rbcL sequences using RaxML



# Seagrass Microbiomes?

- **Many reasons for interest**
  - **Convergence of microbiomes?**
  - **Comparison to other monocots**
  - **Adaptations to salt / marine environment**
- **But ...**
  - **No experience in our mega-group working with seagrass ...**
  - **Little literature on seagrass microbiomes**
- **So? ....**

# **Seagrass Microbiome Project**

## **Lesson 1:**

**Good Colleagues Are A Good Thing**



# Jay Stachowicz - Seagrass EcoEvo

## THE STACHOWICZ LAB

[Home](#)[Research](#)[People](#)[Publications](#)[Outreach](#)[Lab Alumni](#)

## Marine Community Ecology





# Letter to Jay Stachowicz

Jay - apologies in advance for a long email ...

I am writing to see if you would have any time in the next week to discuss a somewhat last minute idea I am working on for a two page white paper I want to send to the Moore Foundation.

They have out a call for short idea papers (<http://www.moore.org/mmi-rfi.aspx>) for new research areas in marine microbiology and if they like your white paper might ask for a full proposal. The idea I and a collaborator (actually someone I think you may know - Jessica Green) have is to propose studies of the diversity and function of microbes living in and on marine plants/algae. I think this could be of scientific value and interest both from a comparative point of view as well as in terms of the marine organisms in question. There is some literature on this, as you may be aware, but not an enormous amount. What I have found though suggests that there may be some important and interesting functions yet to be characterized associated with the microbiota living in association with these organisms.

Alas, I know little about the host organisms here - though I have done work on microbes living in and on lots of other species. I know that you have done some work on eelgrass and possibly other marine plants/algae and may even have done some work on microbes with which they are associated (I think a student mentioned this at some point, but not sure anymore what they said).

Anyway - I was wondering if you had any time to talk briefly about this idea in the next week and whether you would be interested in participating in the white paper.



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Anyway - I was wondering if you had any time to talk briefly about this idea in the next week and whether you would be interested in participating in the white paper.



# Jay Stachowicz - Seagrass Guru

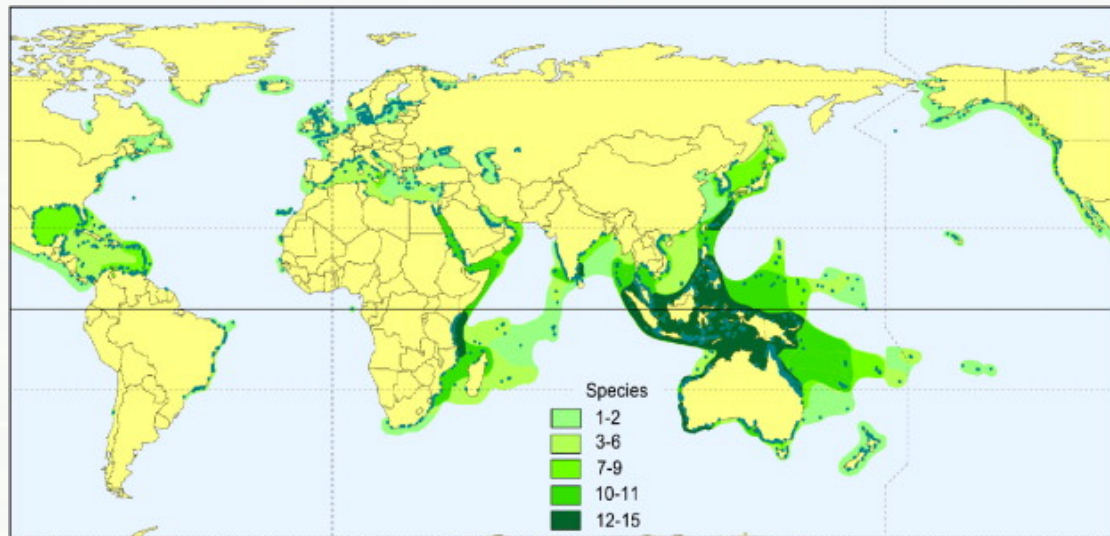


Image from Reynolds PL. Seagrass and Seagrass Beds  
<http://ocean.si.edu/seagrass-and-seagrass-beds>

- **Seagrass Importance**
- **Ecosystem Structure**
- **Living Habitat**
- **Foundation of Food Webs**





*Zostera marina* (eelgrass) is the most abundant seagrass throughout the northern hemisphere





# Eelgrass provides shelter (and food) for many animals



Slide from Jay Stachowicz



# The Seagrass Microbiome Project

- **Aim 1:** How have the microbial communities associated with seagrasses co- evolved with their hosts and what roles in the past and currently do microbes play in adaptations of plants to fresh and marine water life?
- **Aim 2:** What drives the community assembly of the seagrass microbiome, and specifically within the *Zostera marina* model system?
- **Aim 3:** What role does the microbial community play in the functional ecology of the *Zostera marina* (with a specific focus on sulfur and nitrogen metabolism and primary production)?



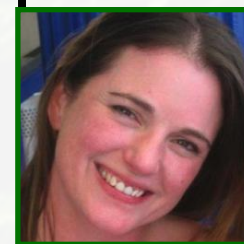
Jonathan Eisen



Jay Stachowicz



Jessica Green



Jenna Lang





# The Seagrass Microbiome Project

- **Aim 1:** How have the microbial communities associated with seagrasses evolved over time and what roles do they play in adaptations of plants to past and current environments? **Evolution** fresh and marine water life?

- **Aim 2:** What is the community assembly of the seagrass microbiome, specifically within the *Zostera marina* model system? **Ecology**

- **Aim 3:** What roles do the microbial community play in the functional ecology of *Zostera marina* (with a specific focus on sulfur and carbon cycling and primary production)? **Function**



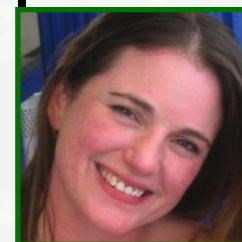
Jonathan Eisen



Jay Stachowicz



Jessica Green



Jenna Lang



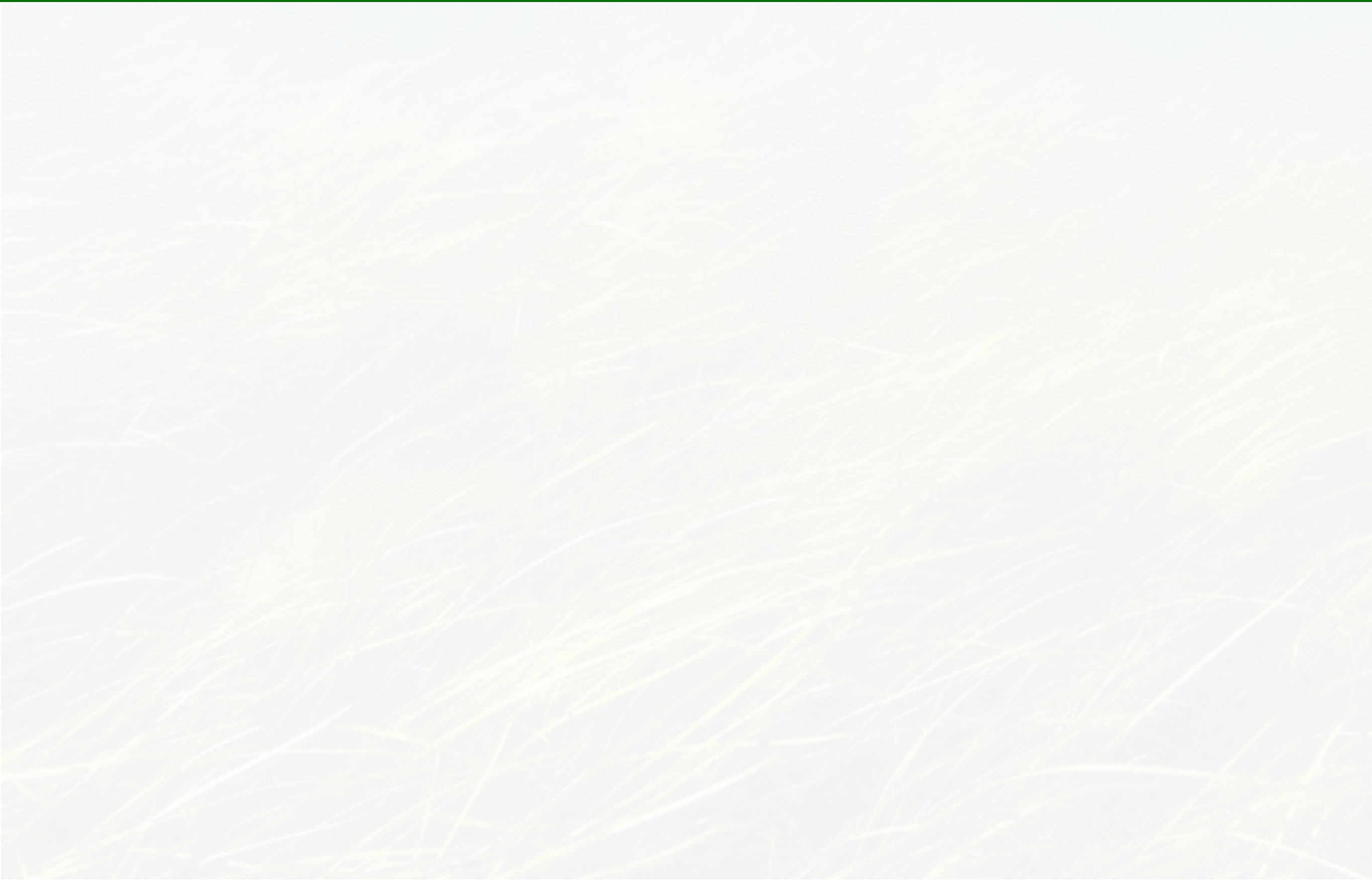


# **Seagrass Microbiome Project**

## **Lesson 2:**

**Location Matters  
Except When it Doesn't**

# Where To Start When You Know Nothing?





# Intraplant Microbiome Biogeography



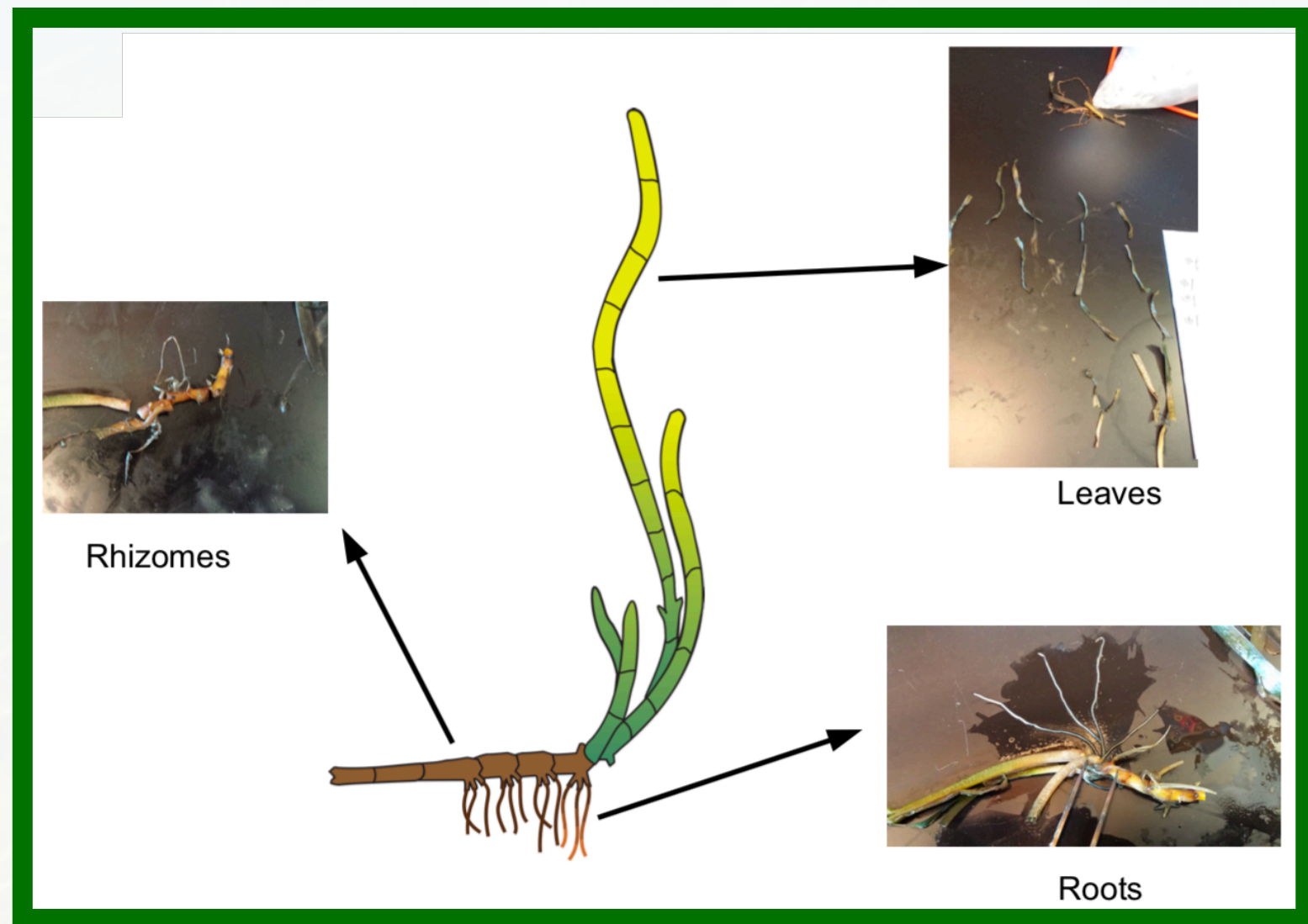
**Hannah  
Holland-Moritz**



**Ruth Lee**

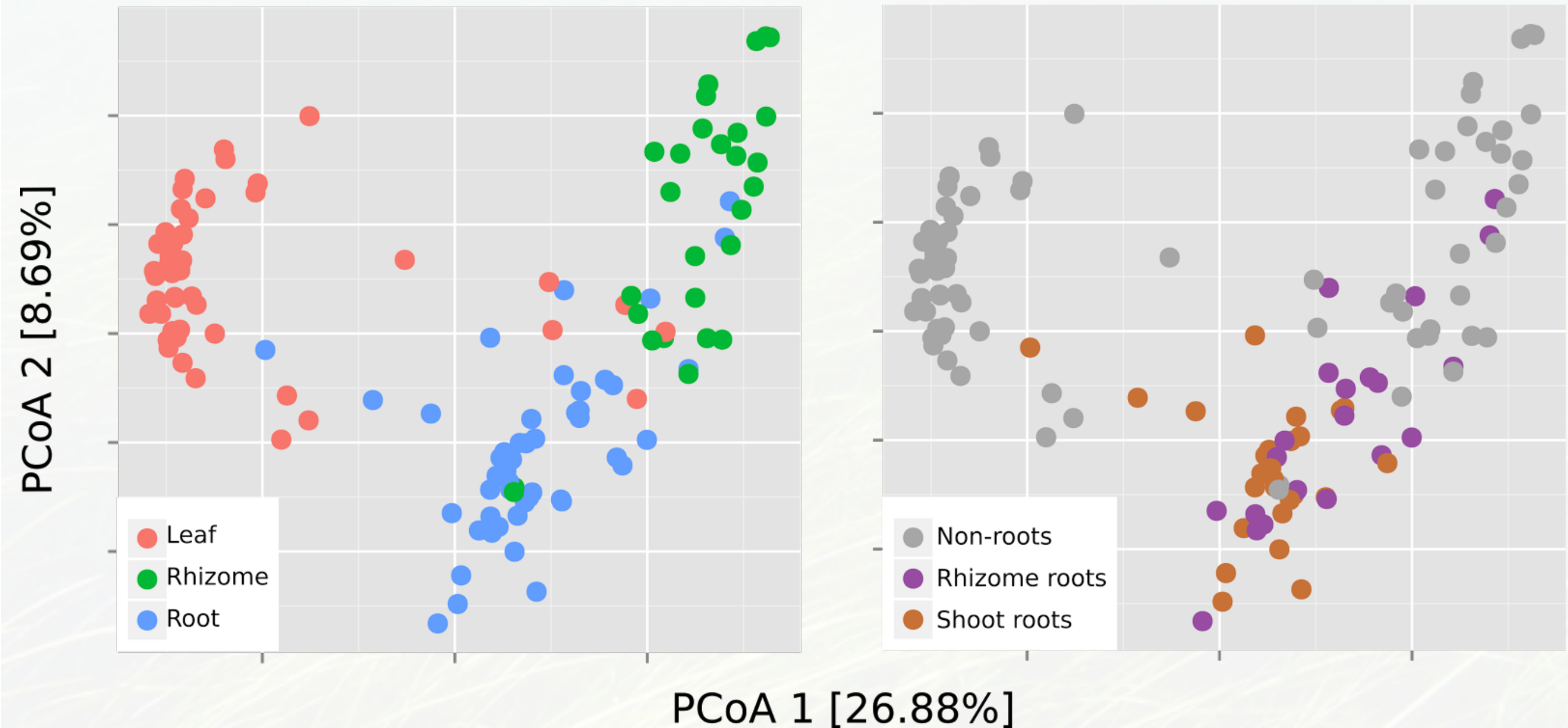


**Jenna Lang**



**rRNA gene PCR, sequencing, informatics**

# Rhizome Roots vs. Shoot Roots vs. Leaf



Variation in microbial community composition in *Z. marina*. PCoA plot of weighted Unifrac distances between samples. Communities cluster by tissue type (PERMANOVA,  $p < 0.001$ ). Within root samples, rhizome roots differ from shoot roots (PERMANOVA,  $p < 0.001$ ).



# Location Matters Except When it Doesn't

- There is more distinct micro-variation below-ground than above
- Proximity to the shoot is an important indicator of community composition (and possibly community function)
- Predicted sulfur cycling microbes dominate all communities regardless of location



# The Seagrass Microbiome Project

- **Aim 1:** How have the microbial communities associated with seagrasses co- evolved with their hosts and what roles in the past and currently do microbes play in adaptations of plants to fresh and marine water life?

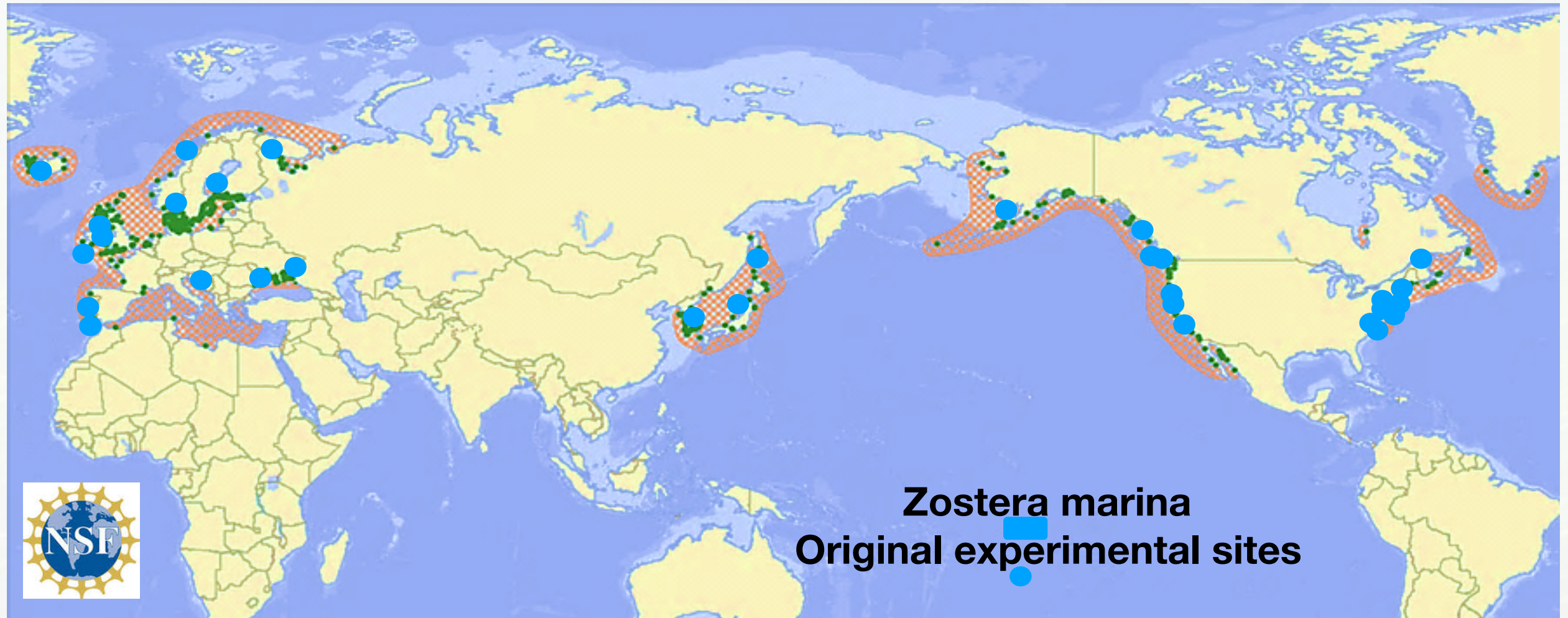
- **Aim 2:** What is the community assembly of the seagrass microbiome specifically within the *Zostera marina* model system:

## Ecology

- **Aim 3:** What role does the microbial community play in the functional ecology of the *Zostera marina* (with a specific focus on sulfur and nitrogen metabolism and primary production)?



# *Zostera* Experimental Network (ZEN)

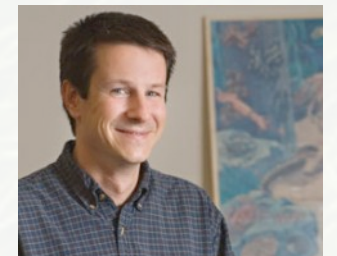


- 40 Sites in 24 countries
- Eelgrass genetic composition
- Eelgrass above and below ground biomass
- Associated epifauna and infauna

<http://zenscience.org>



Emmett Duffy



Jay Stachowicz

Pamela Reynolds

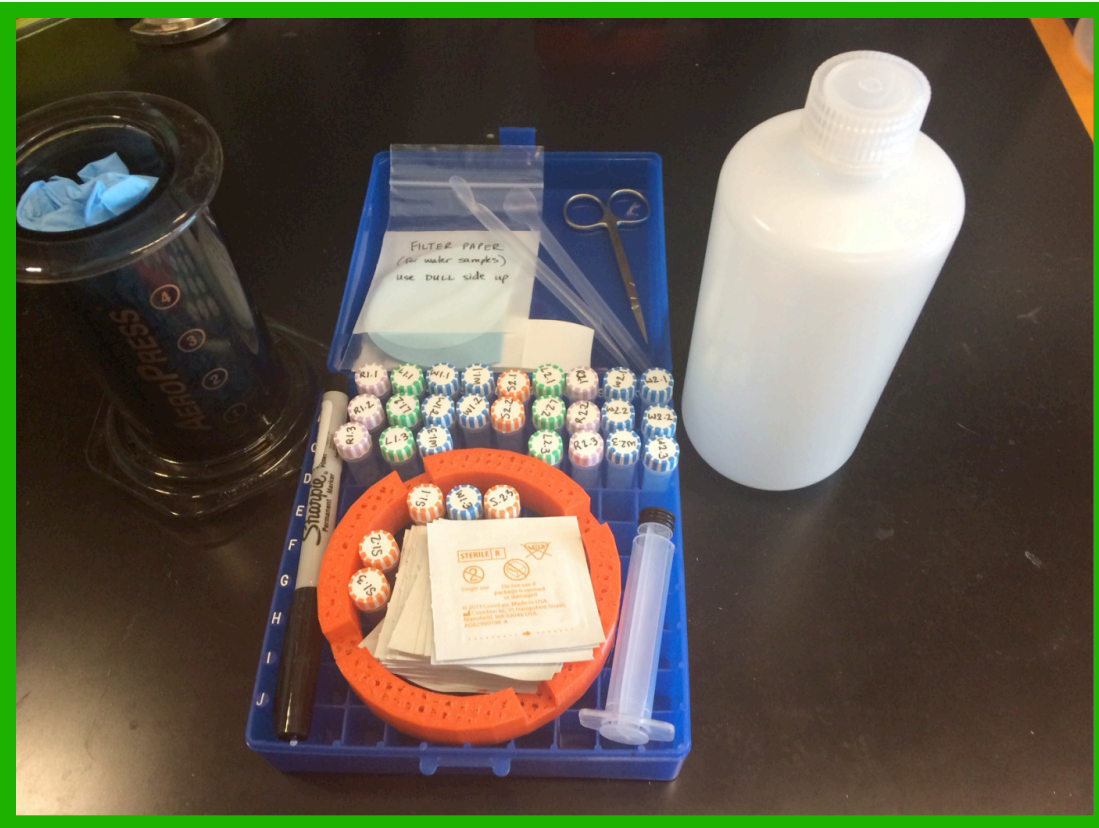


Kevin Hovel





# Seagrass Microbiome ZEN Kit



## Where to sample leaf tissue and the microbiome on a single *Zostera marina* genet

### Plant sampling

☐ Lower leaf area

See photograph of exact area and how to sample the plant tissue

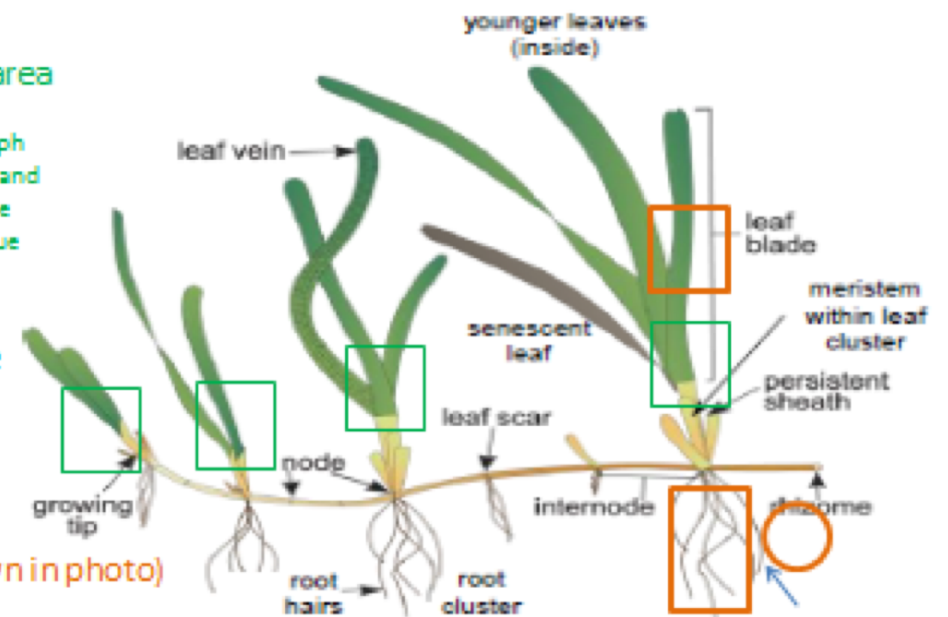
Refer to microbiome kit instructions

### Microbiome sampling

☐ Leaf (as shown in photo)

☐ Root (use up to 5 small roots. However, be sure they are fully submerged in the buffer. Use fewer if too crowded looking. Don't overload)

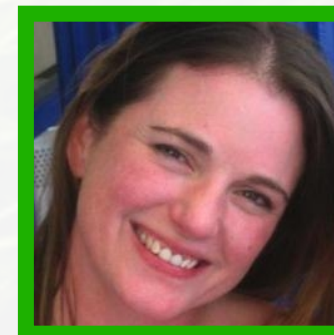
☐ Sediment (take the plug as close to the root you are sampling as possible)



NS: The seagrass shown is *Posidonia* but all seagrasses have this morphological form.



\$25  
custom filters  
3D-printed stand



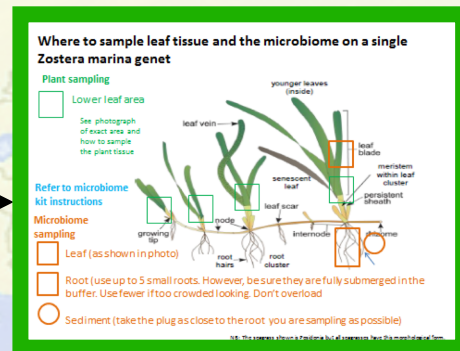
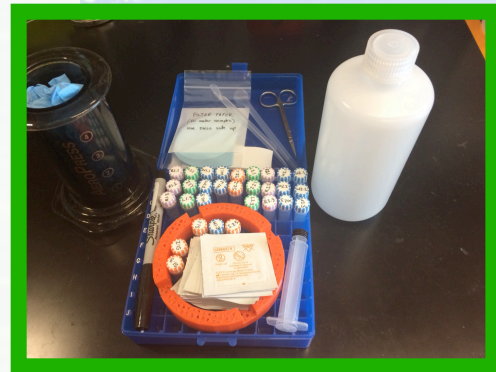
Jenna  
Lang



Russell  
Neches



# ZEN Microbiome Sampling

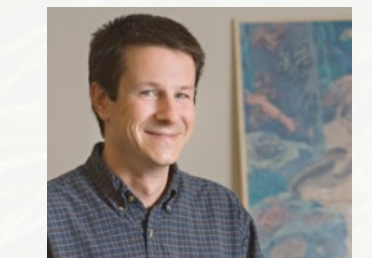


- Sent kits
- Asked to sample leaves, roots, sediment and water

<http://zenscience.org>



Emmett Duffy



Jay Stachowicz

Pamela Reynolds



Kevin Hovel





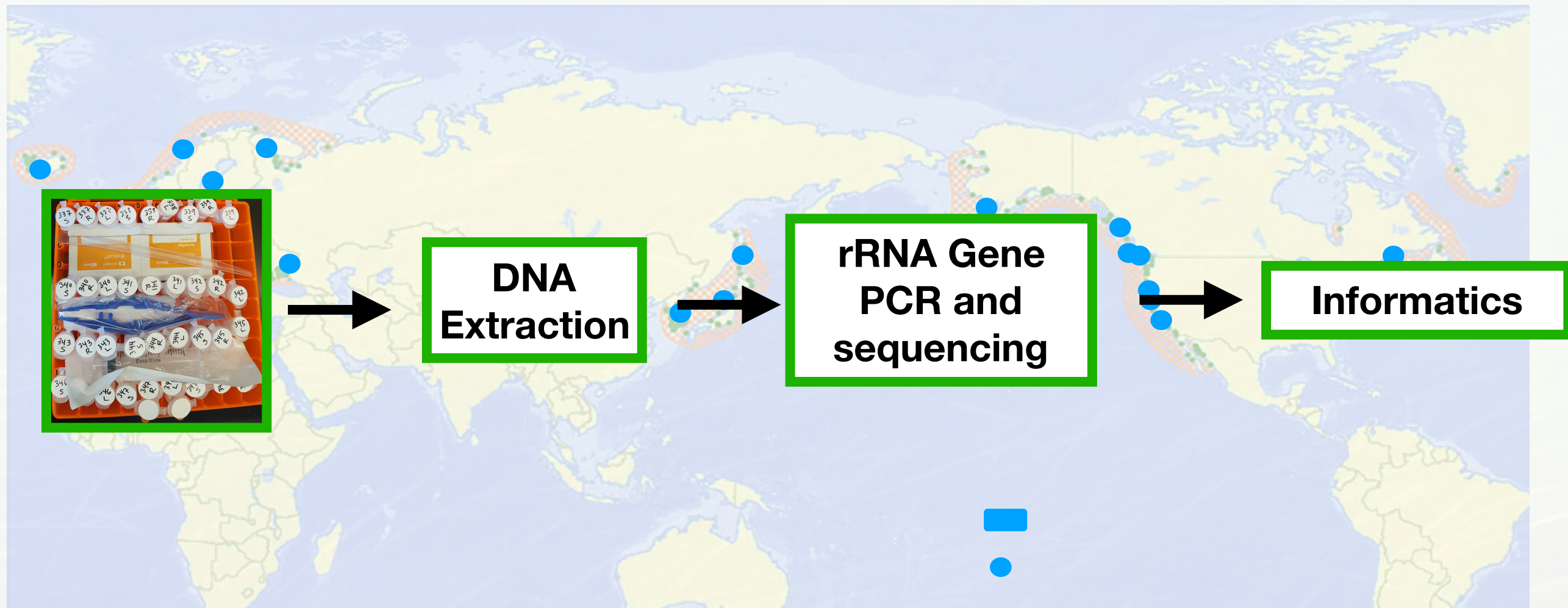
# **Seagrass Microbiome Project**

## **Lesson 3:**

**Good Communities are a Good Thing**



# ZEN Microbiome Sampling



Fahimipour AK, Kardish MR, Lang JM, Green JL, Eisen JA, Stachowicz JJ. 2017. Global-scale structure of the eelgrass microbiome. *Appl Environ Microbiol* 83:e03391-16. <https://doi.org/10.1128/AEM.03391-16>.



Ashkaan  
Fahimipour



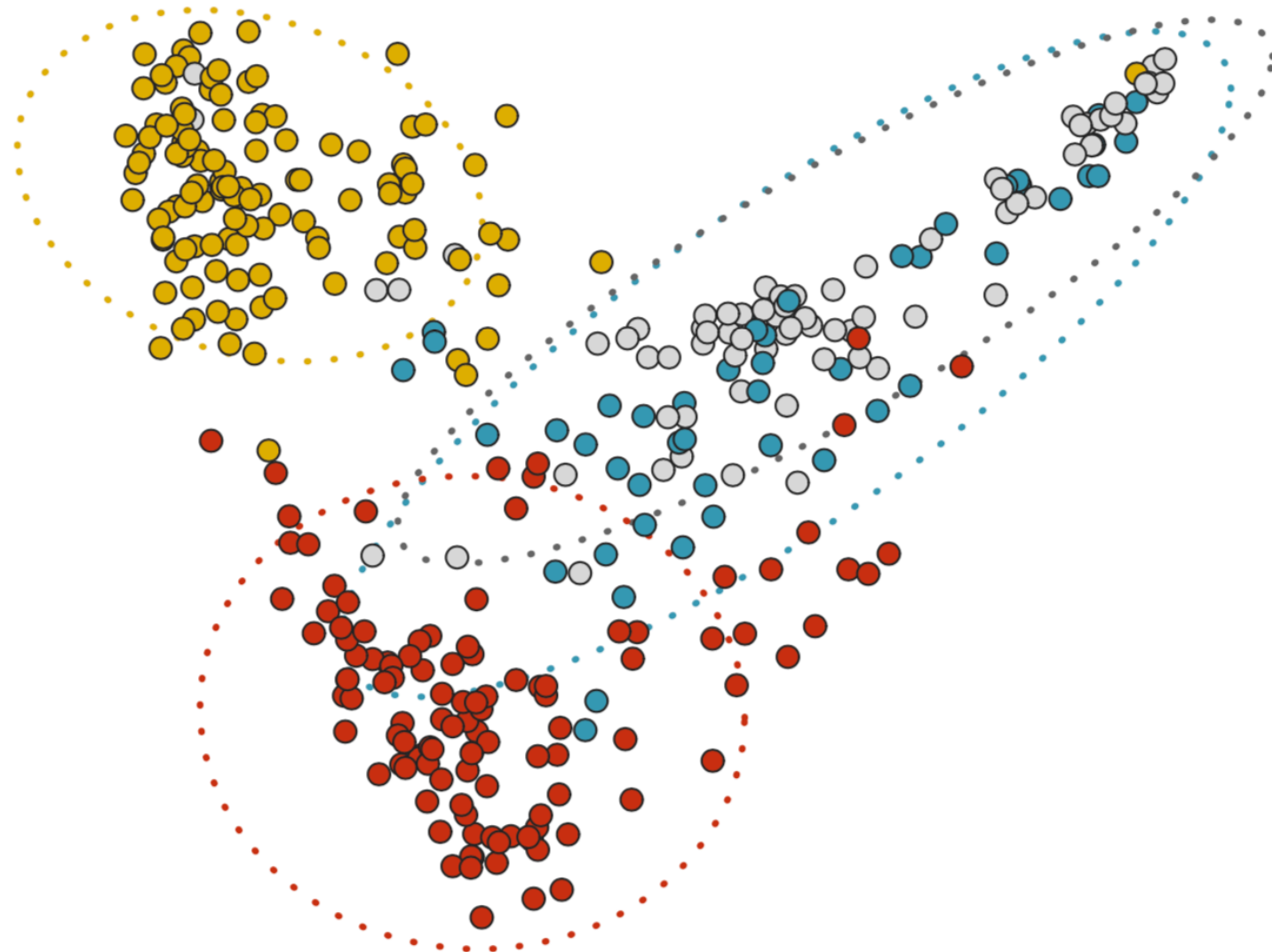
Melissa  
Kardish



Jenna  
Lang

# Global Structure of Eelgrass Microbiome

## PcoA



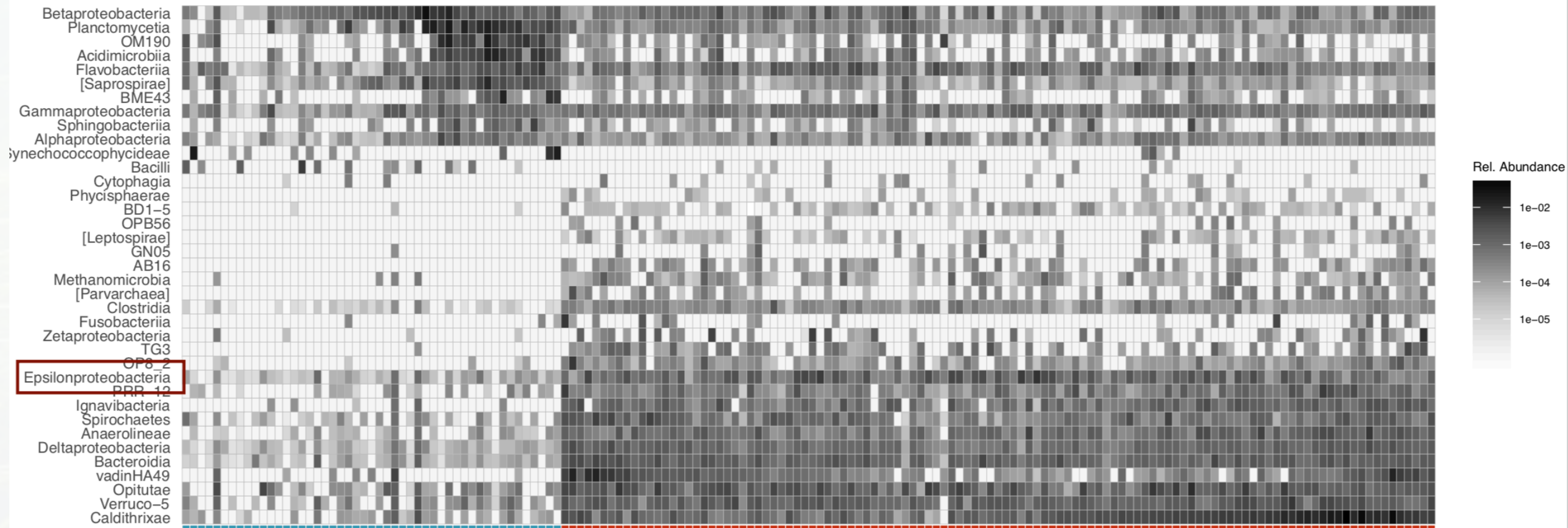
● Leaf ● Water ● Roots ● Sediment

- Leaf, roots and sediment different
- Leaves resemble water
- Leaves more similar to local water

Fahimipour AK, Kardish MR, Lang JM, Green JL, Eisen JA, Stachowicz JJ. 2017. Global-scale structure of the eelgrass microbiome. *Appl Environ Microbiol* 83:e03391-16. <https://doi.org/10.1128/AEM.03391-16>.



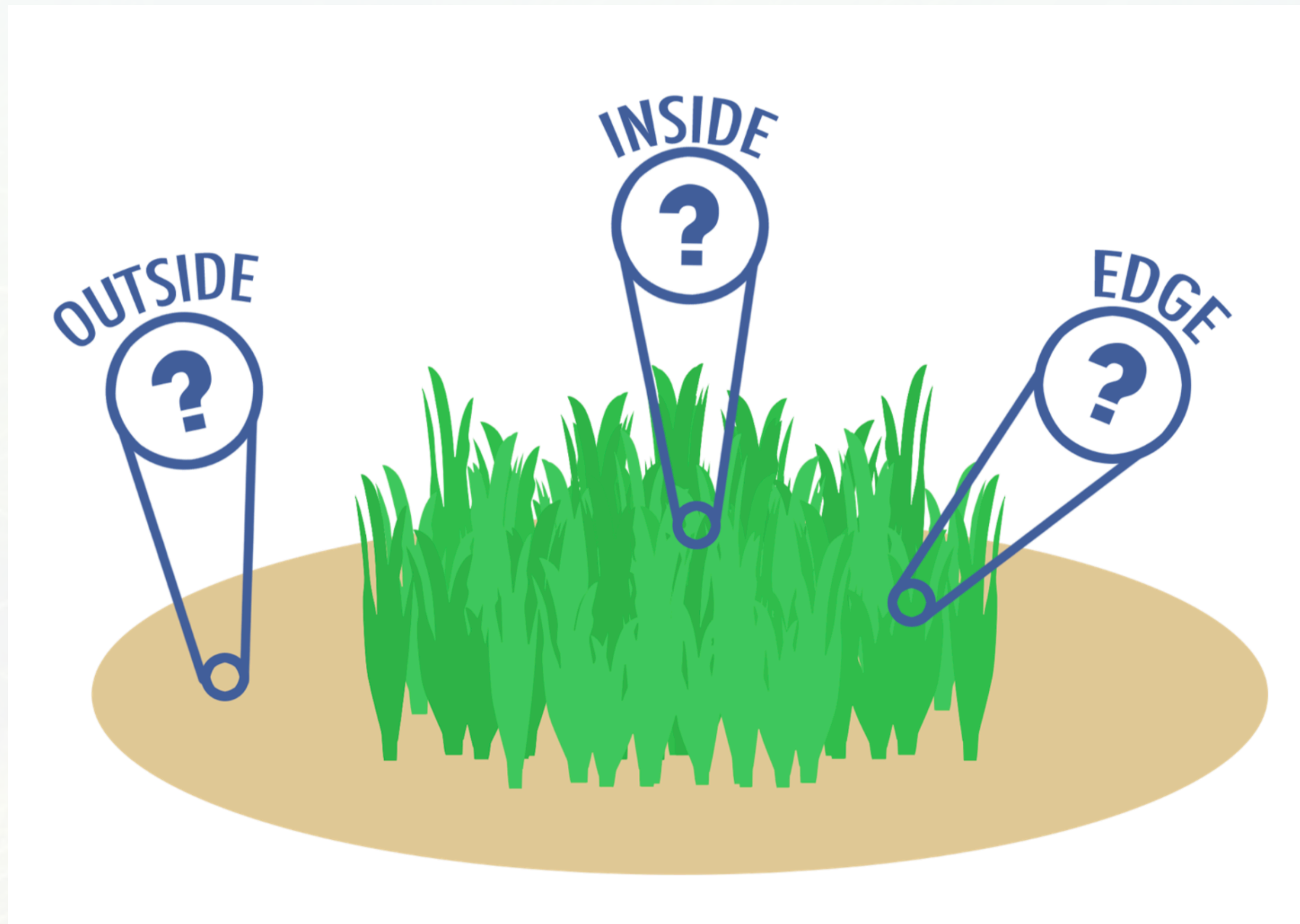
# Sulfur Metabolism Enriched on Roots



*Sulfurimonas* – sulfur oxidizers

Fahimipour AK, Kardish MR, Lang JM, Green JL, Eisen JA, Stachowicz JJ. 2017. Global-scale structure of the eelgrass microbiome. Appl Environ Microbiol 83:e03391-16. <https://doi.org/10.1128/AEM.03391-16>.

# Edge Effects: Does it Matter Where Plants Are?



Ettinger CL, Voerman SE, Lang JM, Stachowicz JJ, Eisen JA. (2017) Microbial communities in sediment from *Zostera marina* patches, but not the *Z. marina* leaf or root microbiomes, vary in relation to distance from patch edge. PeerJ 5:e3246 <https://doi.org/10.7717/peerj.3246>



Cassie  
Ettinger



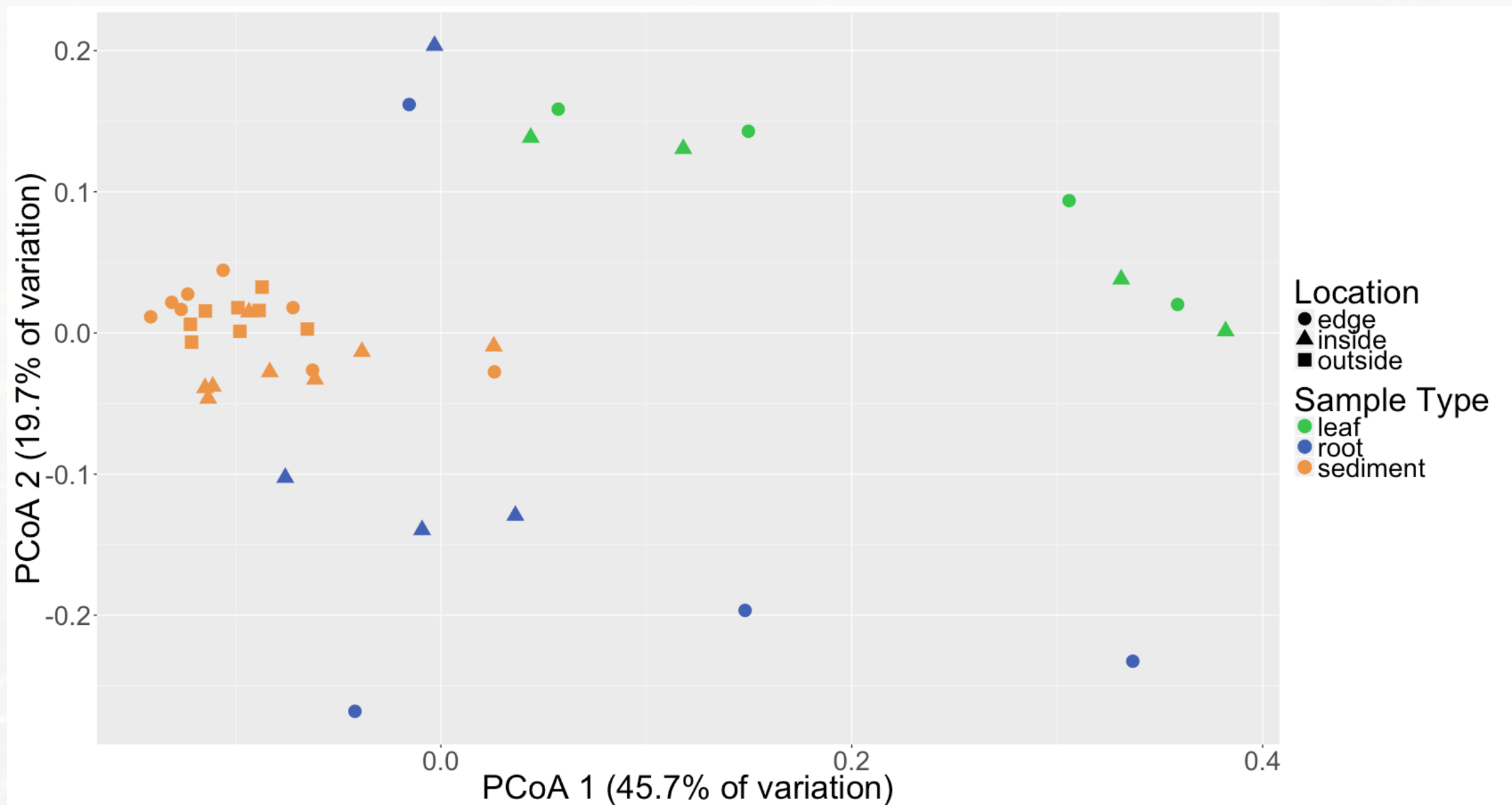
Sofie  
Voerman



Jenna  
Lang



# Edge Effect in Sediment but Not Plant Microbiomes



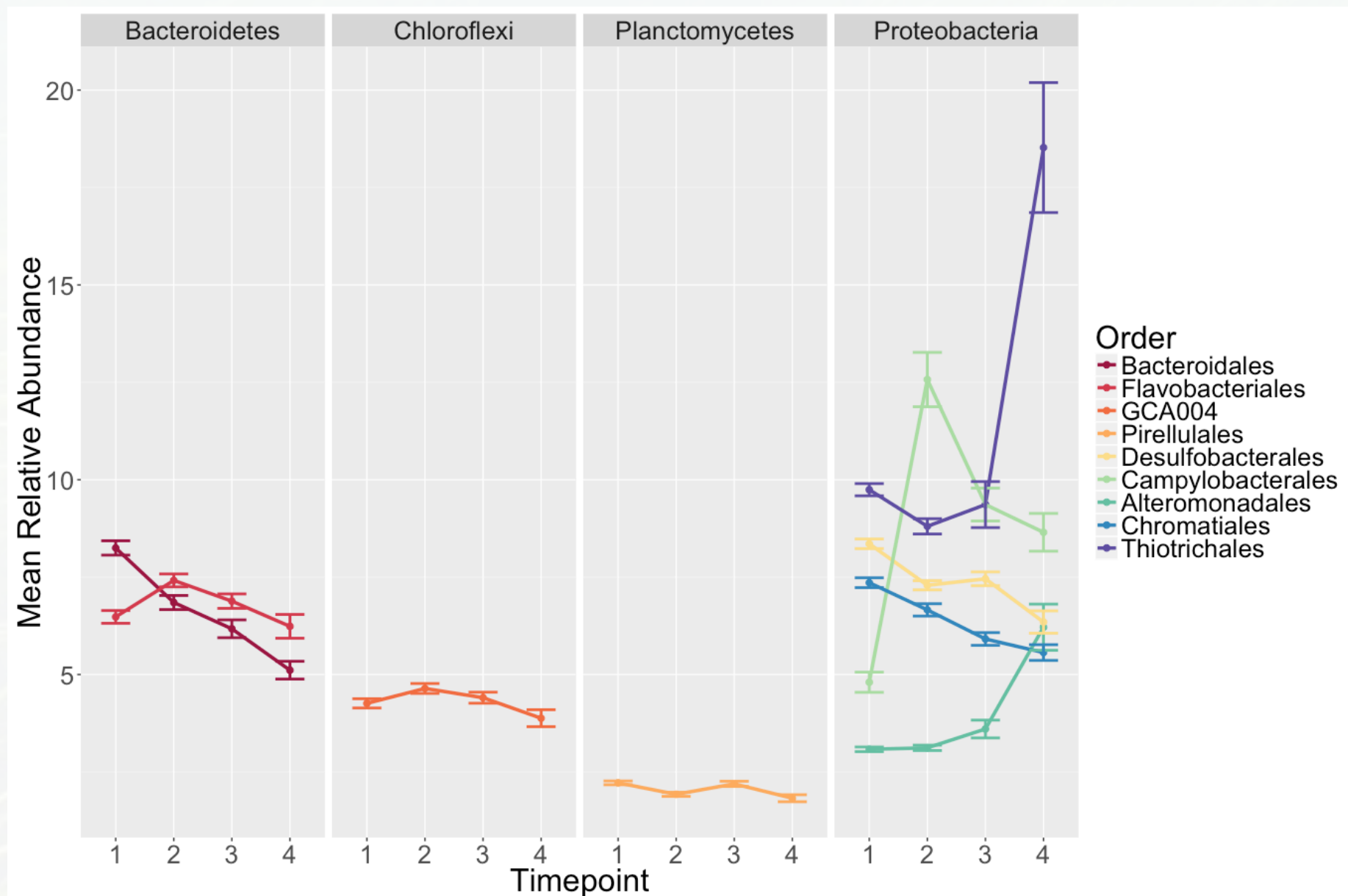
# **Seagrass Microbiome Project**

## **Lesson 4:**

### **Disturbance Can Be Good and Bad**



# Succession During Ammonification



Changes appear driven by sulfur cycling w/ decreases in sulfur reducers (Desulfobacterales) and corresponding increases in sulfide oxidizers (Alteromonadales and Thiotrichales).

Ettinger CL, Williams SL, Abbott JM, Stachowicz JJ, Eisen JA. (2017) Microbiome succession during ammonification in eelgrass bed sediments. PeerJ 5:e3674 <https://doi.org/10.7717/peerj.3674>



Cassie  
Ettinger



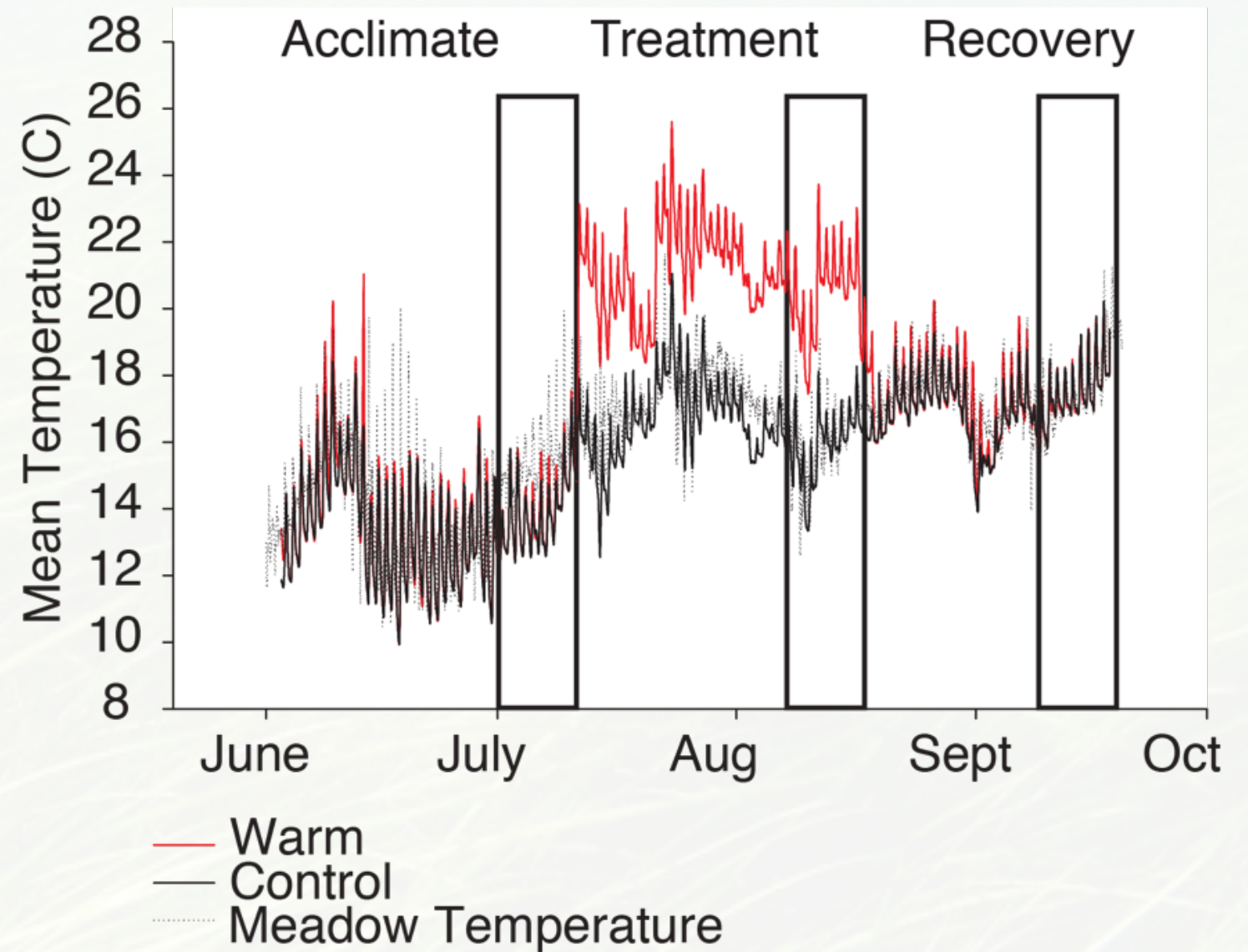
Jessica  
Abbott



Susan  
Williams



# Moderate 4.5° C increase



Alana  
Firl



Laura  
Reynolds



Katie  
DuBois



Jessica  
Abbott



Susan  
Williams



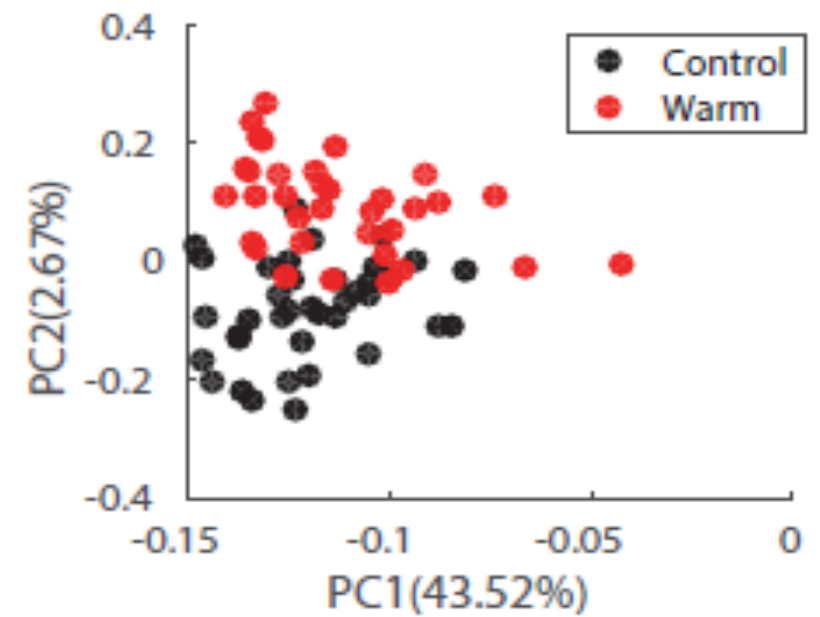
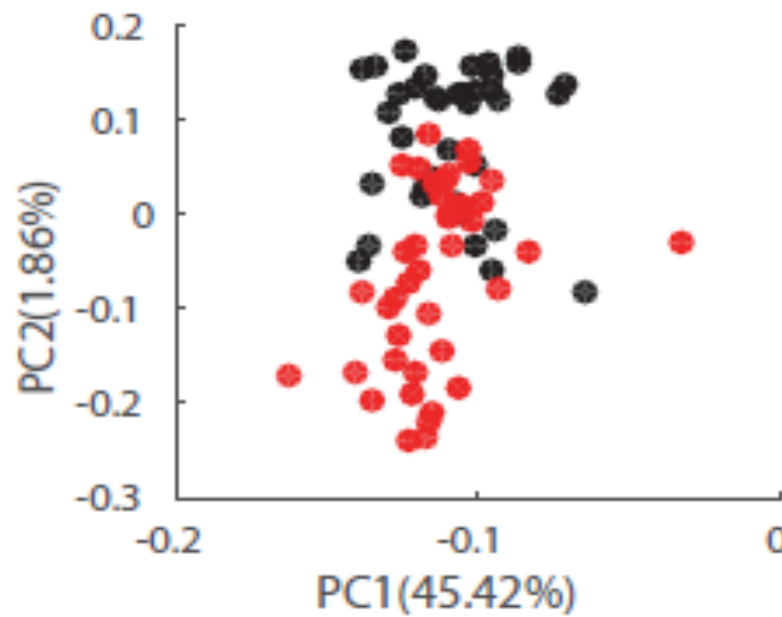
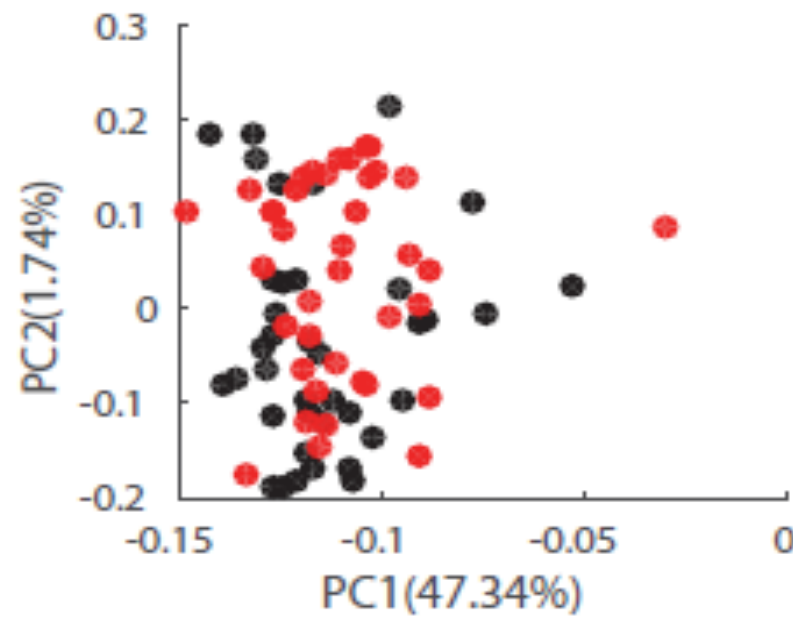
# Leaf microbiomes exhibit T°-related shifts

Acclimation (T1)

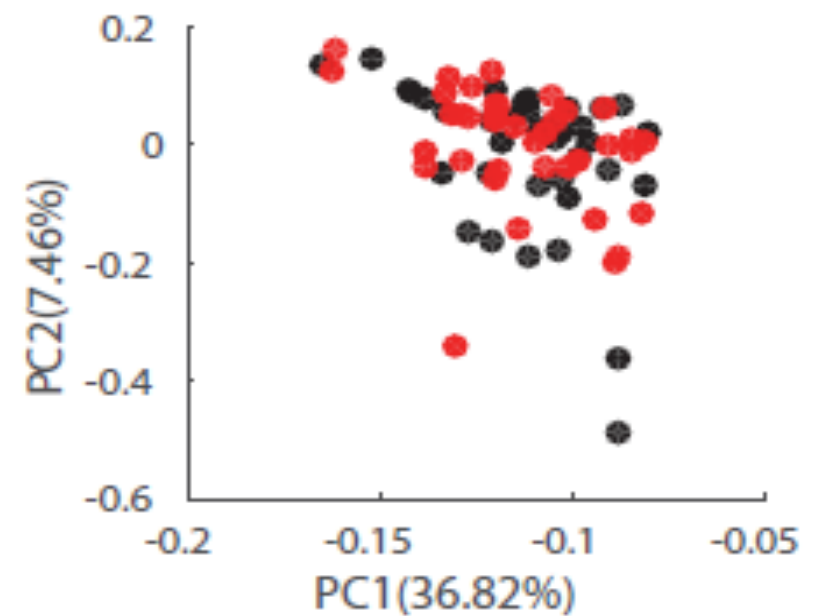
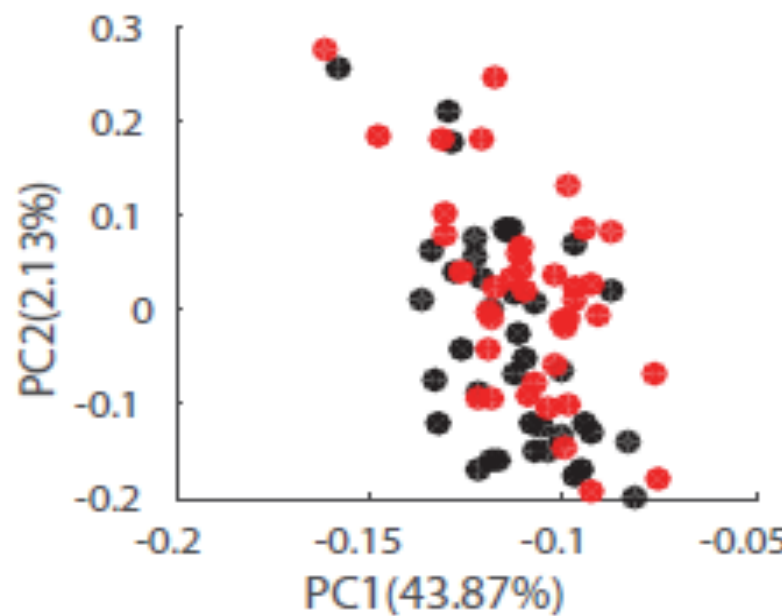
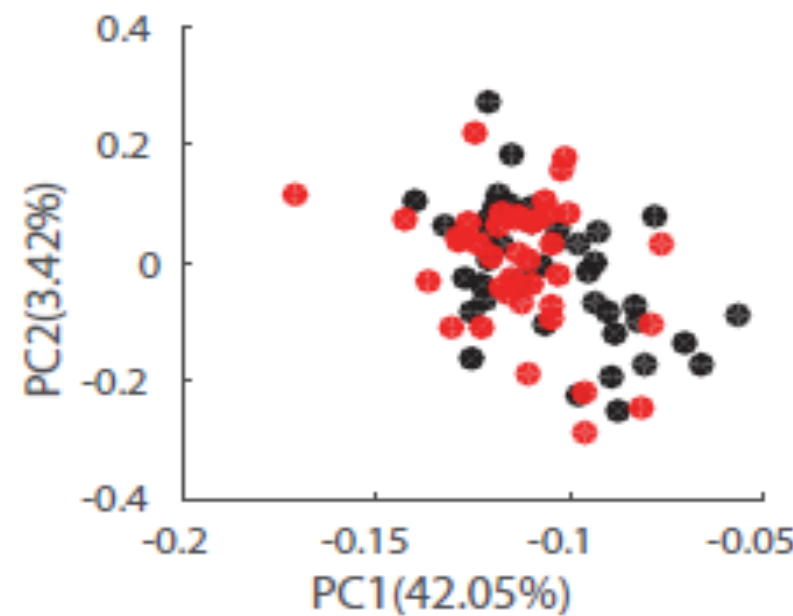
Treatment (T2)

Recovery (T3)

Leaves



Roots



# **Seagrass Microbiome Project**

## **Lesson 5:**

**Don't Forget Your Roots**



# Intraplant Sampling Metagenomics



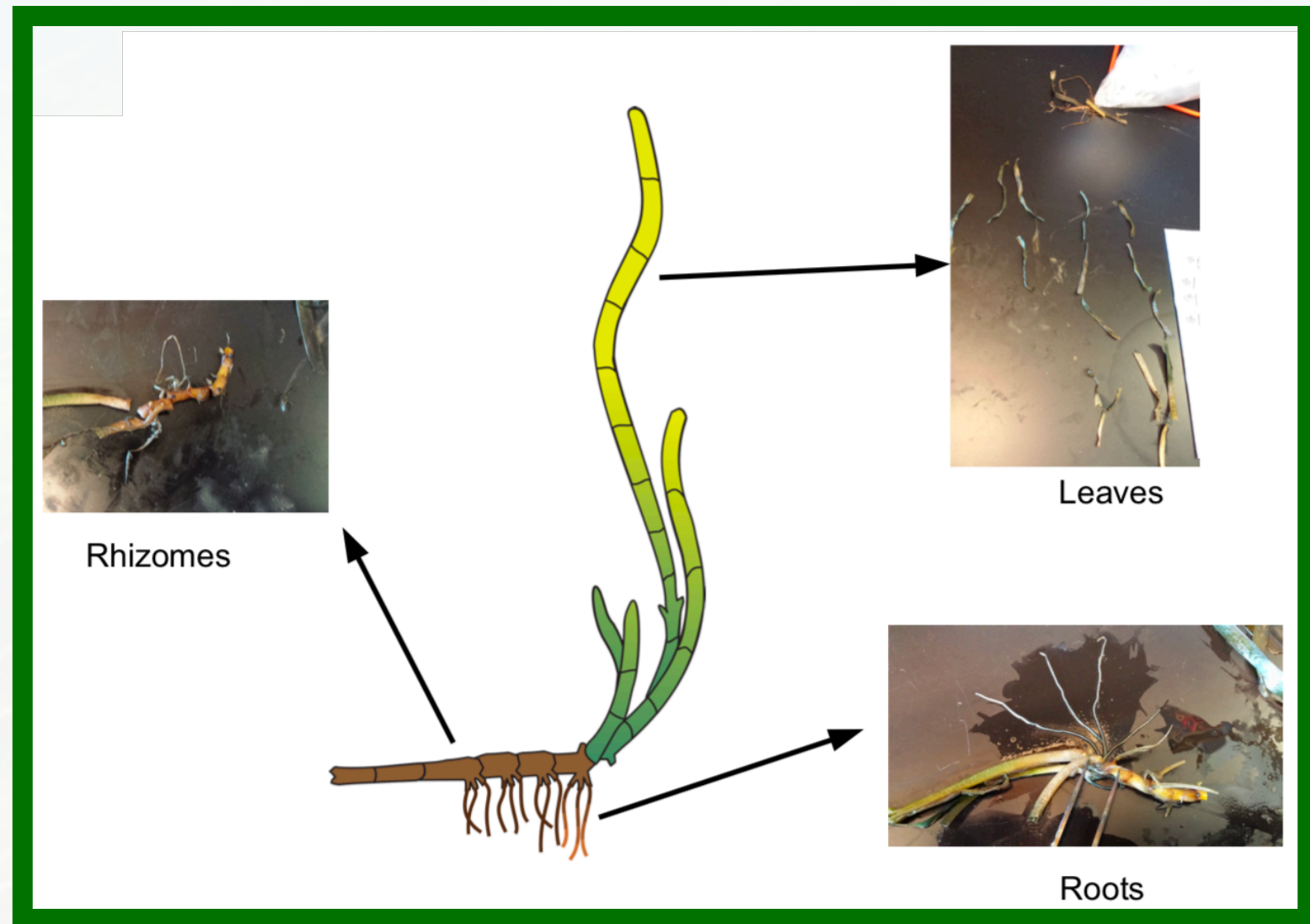
**Laura  
Vann**



**Guillaume  
Jospin**



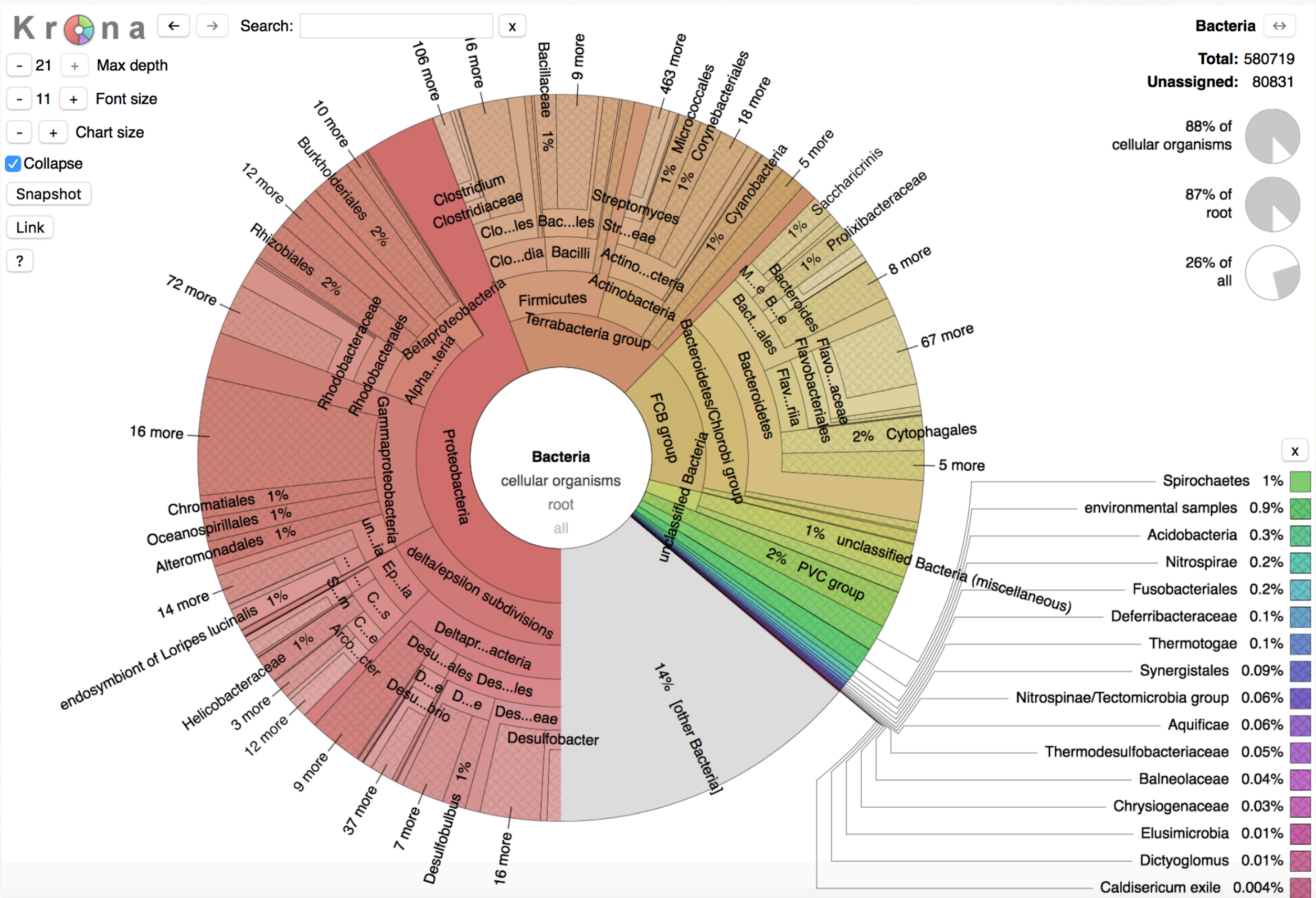
**Melissa  
Kardish**



**Shotgun Metagenomics Sequencing and Informatics**

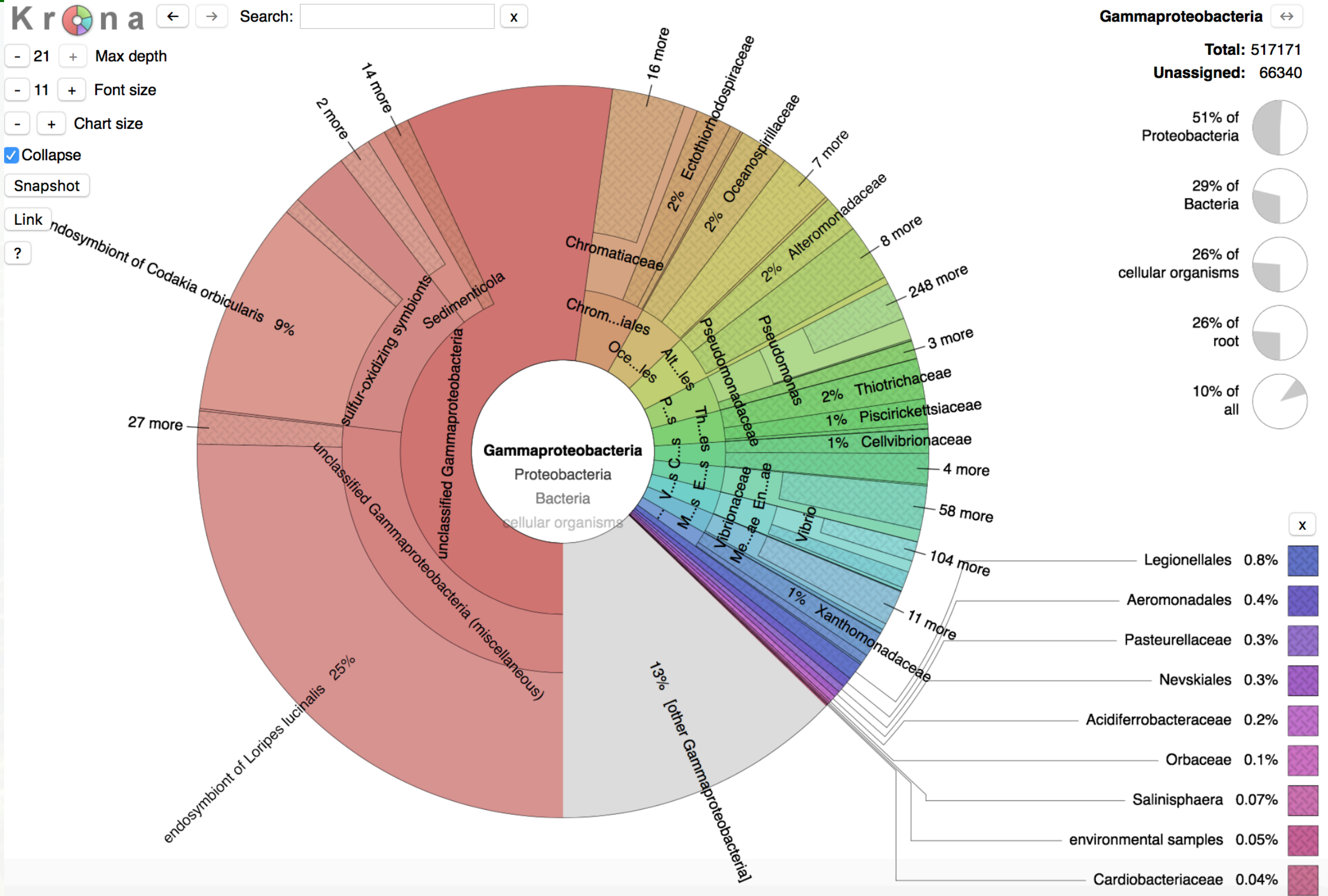


# Kaiju Classification of Reads

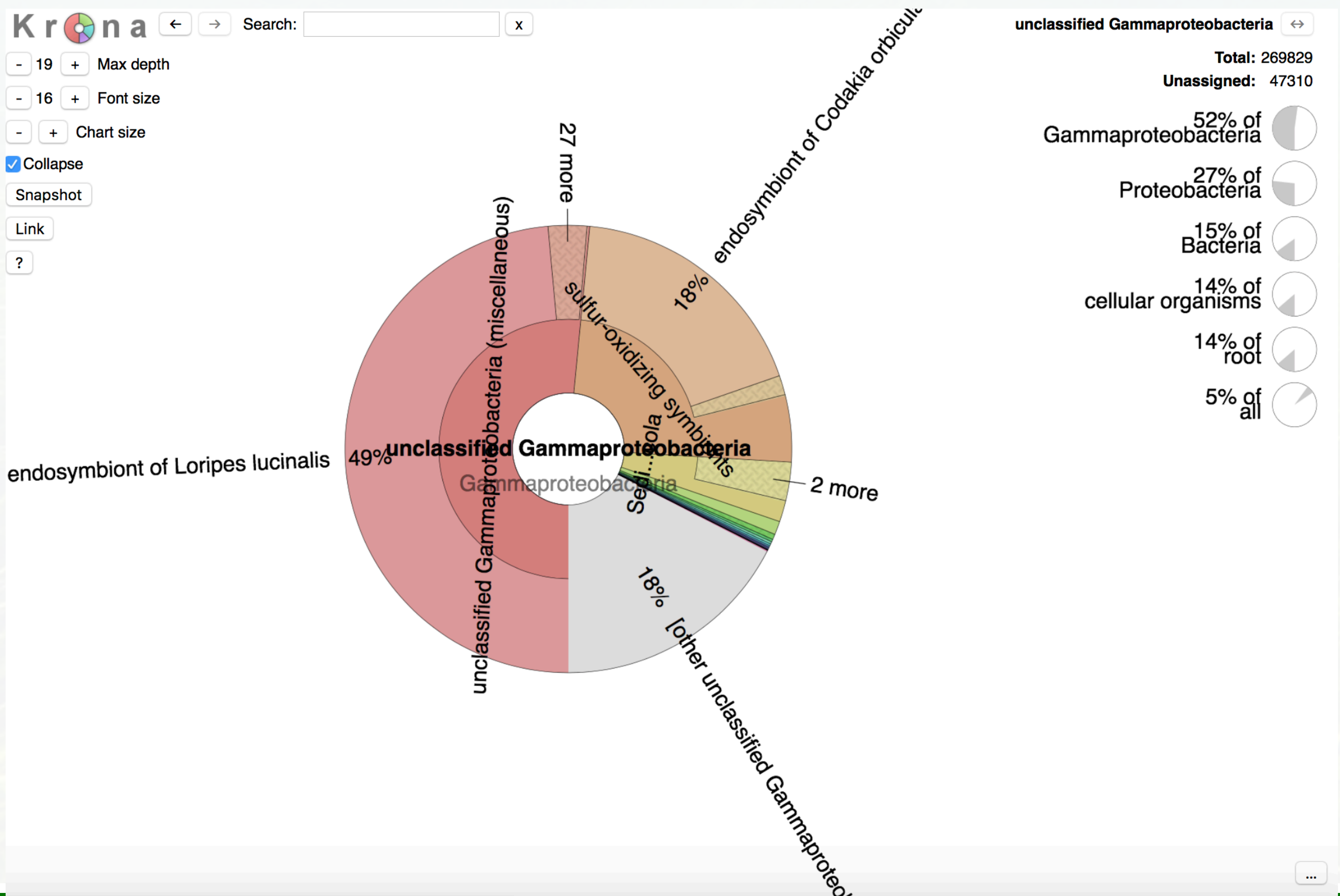




# Zoomed In



# Large #s of “Chemosymbionts” of Clams





# Clams in Seagrass Beds

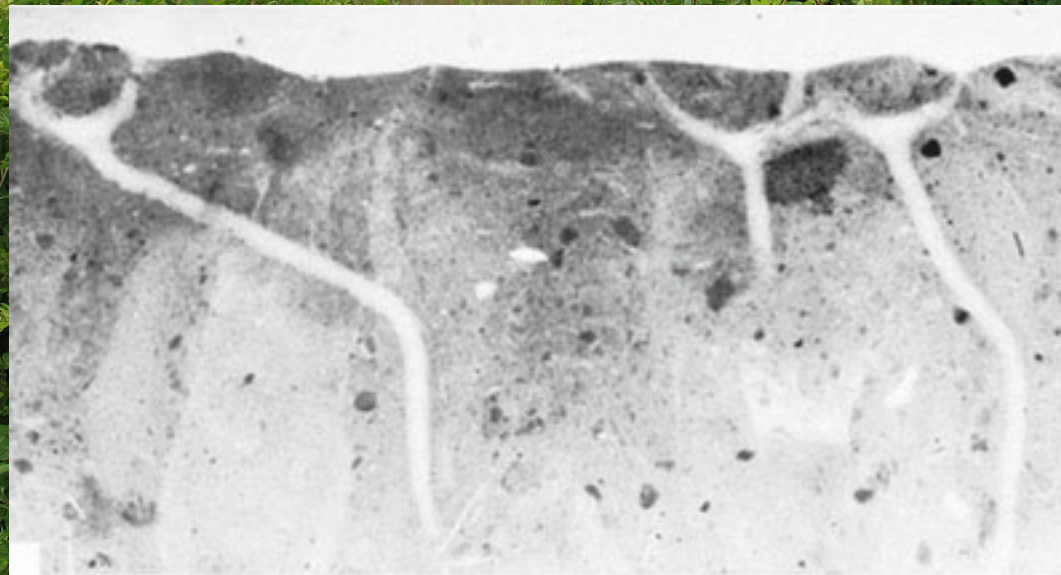


PLATE 3. SOLEMYA





# Chemosymbionts of Bivalves

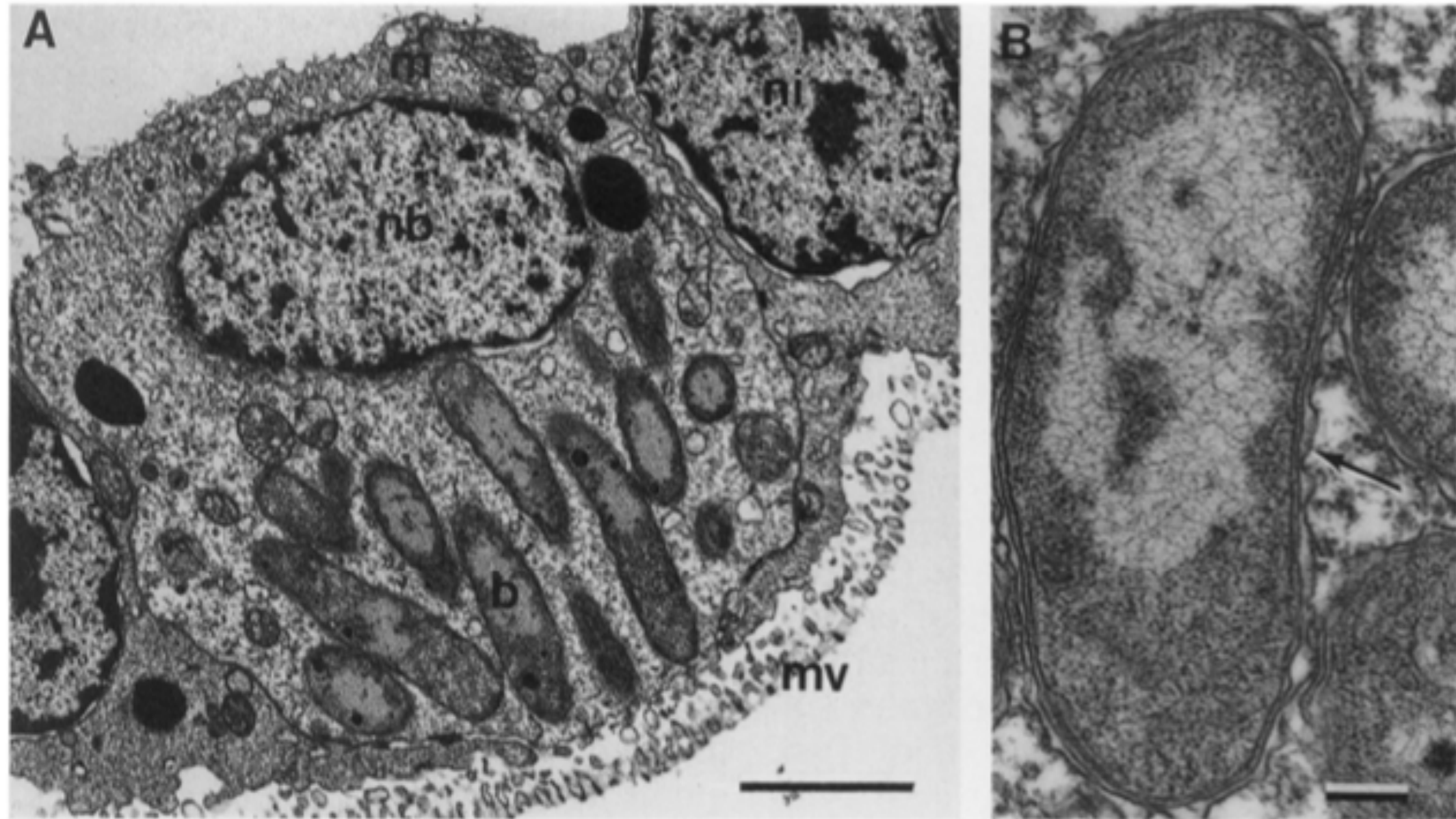
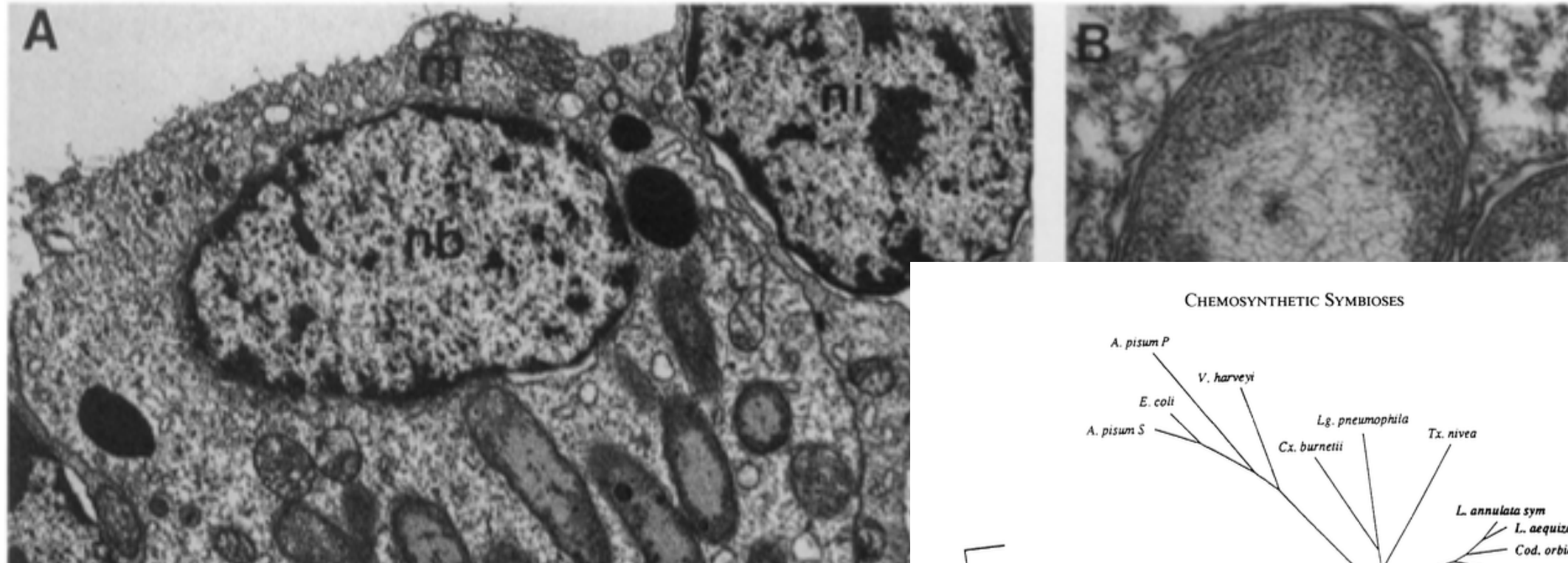


FIG. 2. *Solemya velum*. A. Transmission electron micrograph, transverse section of gill filament, showing rod-shaped bacteria within gill bacteriocyte and intercalary cells lacking symbionts; b: bacteria; mv: microvilli; nb: nucleus of bacteriocyte; ni: nucleus of intercalary cell. B. Same, higher magnification, transverse section of rod-shaped bacterium, showing cell ultrastructure typical of Gram-negative bacteria and peribacterial membrane (arrows). Scale bars, A: 3  $\mu\text{m}$ ; B: 0.2  $\mu\text{m}$ . Reprinted with permission from *Biol. Soc. Wash. Bull.* (Cavanaugh, 1985).



# Chemosymbionts of Bivalves



JOURNAL OF BACTERIOLOGY, May 1992, p. 3416-3421  
0021-9193/92/103416-06\$02.00/0  
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Vol. 174, No. 10

## Phylogenetic Relationships of Chemoautotrophic Bacterial Symbionts of *Solemya velum* Say (Mollusca: Bivalvia) Determined by 16S rRNA Gene Sequence Analysis

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The protobranch bivalve *Solemya velum* Say (Mollusca: Bivalvia) houses chemoautotrophic symbionts intracellularly within its gills. These symbionts were characterized through sequencing of polymerase chain reaction-amplified 16S rRNA coding regions and hybridization of an *Escherichia coli* gene probe to *S. velum* genomic DNA restriction fragments. The symbionts appeared to have only one copy of the 16S rRNA gene. The lack of variability in the 16S sequence and hybridization patterns within and between individual *S. velum* organisms suggested that one species of symbiont is dominant within and specific for this host species. Phylogenetic analysis of the 16S sequences of the symbionts indicates that they lie within the chemoautotrophic cluster of the gamma subdivision of the eubacterial group *Proteobacteria*.

1985).

### CHEMOSYNTHETIC SYMBIOSES

85

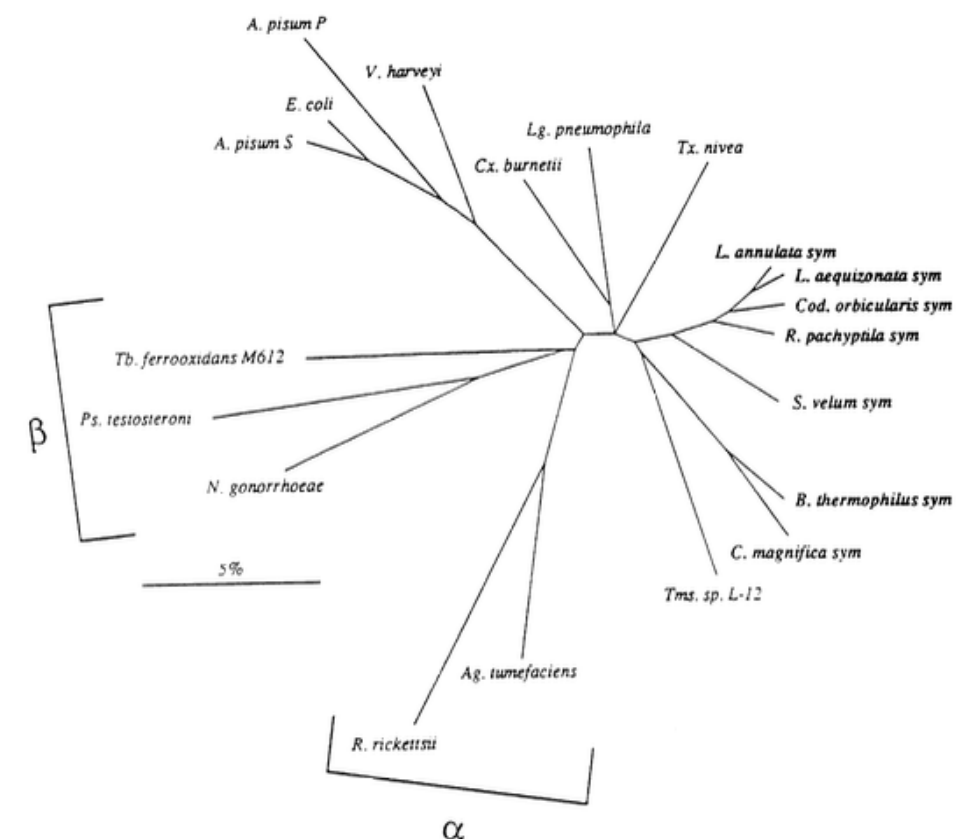


FIG. 4. Unrooted phylogenetic tree, based on evolutionary distances, showing the position of the chemoautotrophic symbionts in relation to that of other Proteobacteria on the basis of 16S rRNA gene sequences. Members of the alpha- (*Rickettsia rickettsii* and *Agrobacterium tumefaciens*) and beta-subclasses (*Thiobacillus ferrooxidans* M612, *Pseudomonas testosteroni*, and *Neisseria gonorrhoeae*) of the Proteobacteria are bracketed; all others are of the gamma subclass. These include chemoautotrophic symbionts (listed in bold type) of bivalves (*Lucinoma aequizonata* sym, *L. annulata* sym, *Codakia orbicularis* sym, *Solemya velum* sym, *Bathymodiolus thermophilus* sym, *Calymene magnifica* sym) and the vent tubeworm (*Riftia pachyptila* sym), free-living species (*Thiomicrospira* sp. L-12, *Thiothrix nivea*, *Legionella pneumophila*, *Coxiella burnetii*, *Escherichia coli*, and *Vibrio harveyi*), and aphid symbionts, *Acyrtosiphon pisum* S and *Acyrtosiphon pisum* P. Sym = symbiont. Reprinted (with modifications) from *Journal of Bacteriology* (Eisen et al., 1992).

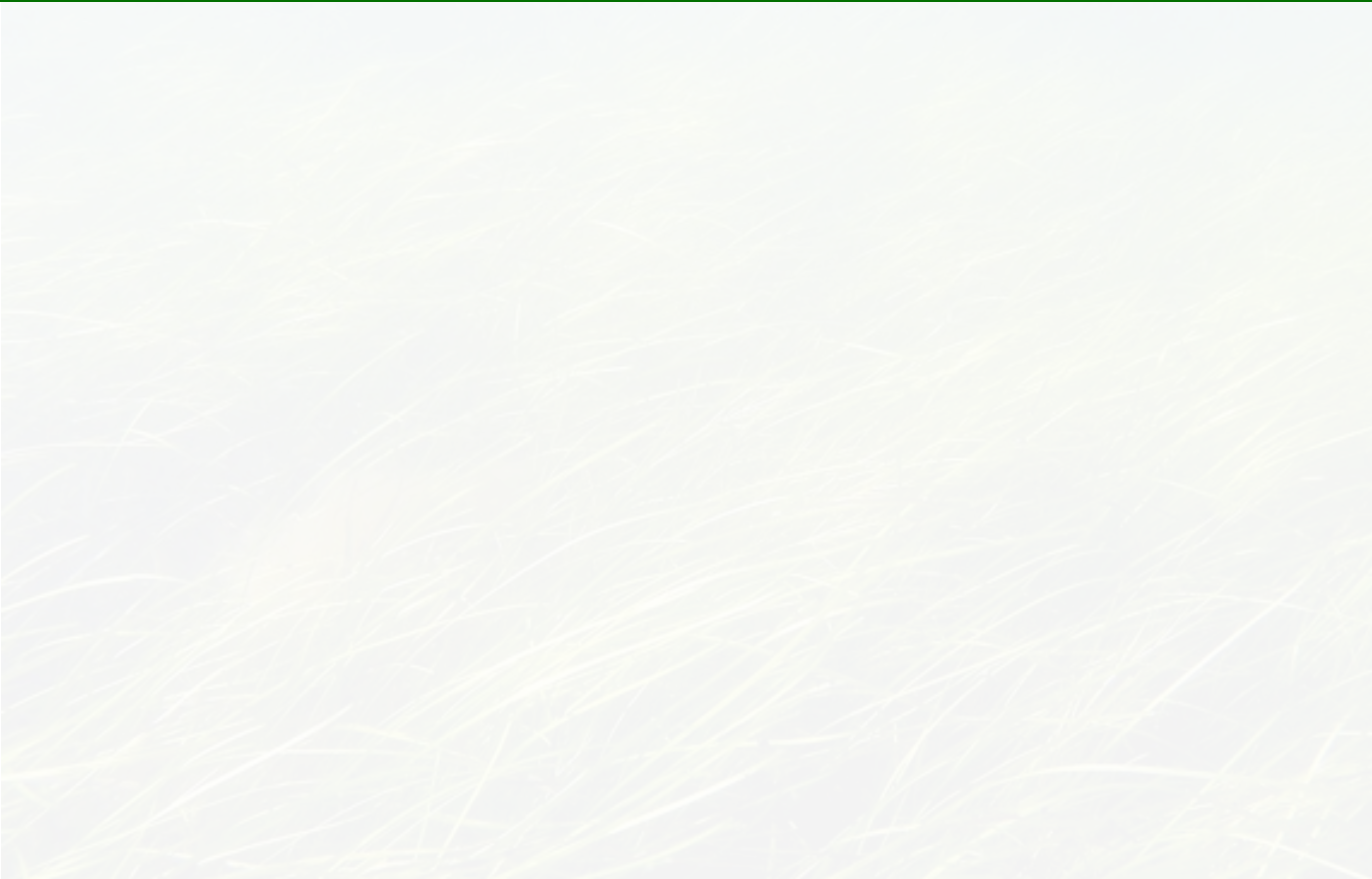
# Chemosymbionts



Lucinoma\_annulata\_symbiont.1  
833692  
Lucinoma\_aequizonata\_gill\_symbiont  
**16S\_hit\_from\_Zostera**  
686128  
Loripes\_lacteus\_gill\_symbiont\_clone\_2B  
Loripes\_lacteus\_gill\_symbiont\_clone\_2C  
Loripes\_lacteus\_gill\_symbiont\_clone\_1B.1  
Loripes\_lacteus\_gill\_symbiont\_clone\_1C  
Loripes\_lacteus\_gill\_symbiont\_clone\_1A.1  
Loripes\_lacteus\_gill\_symbiont\_clone\_2A  
Codakia\_costata\_gill\_symbiont\_partial

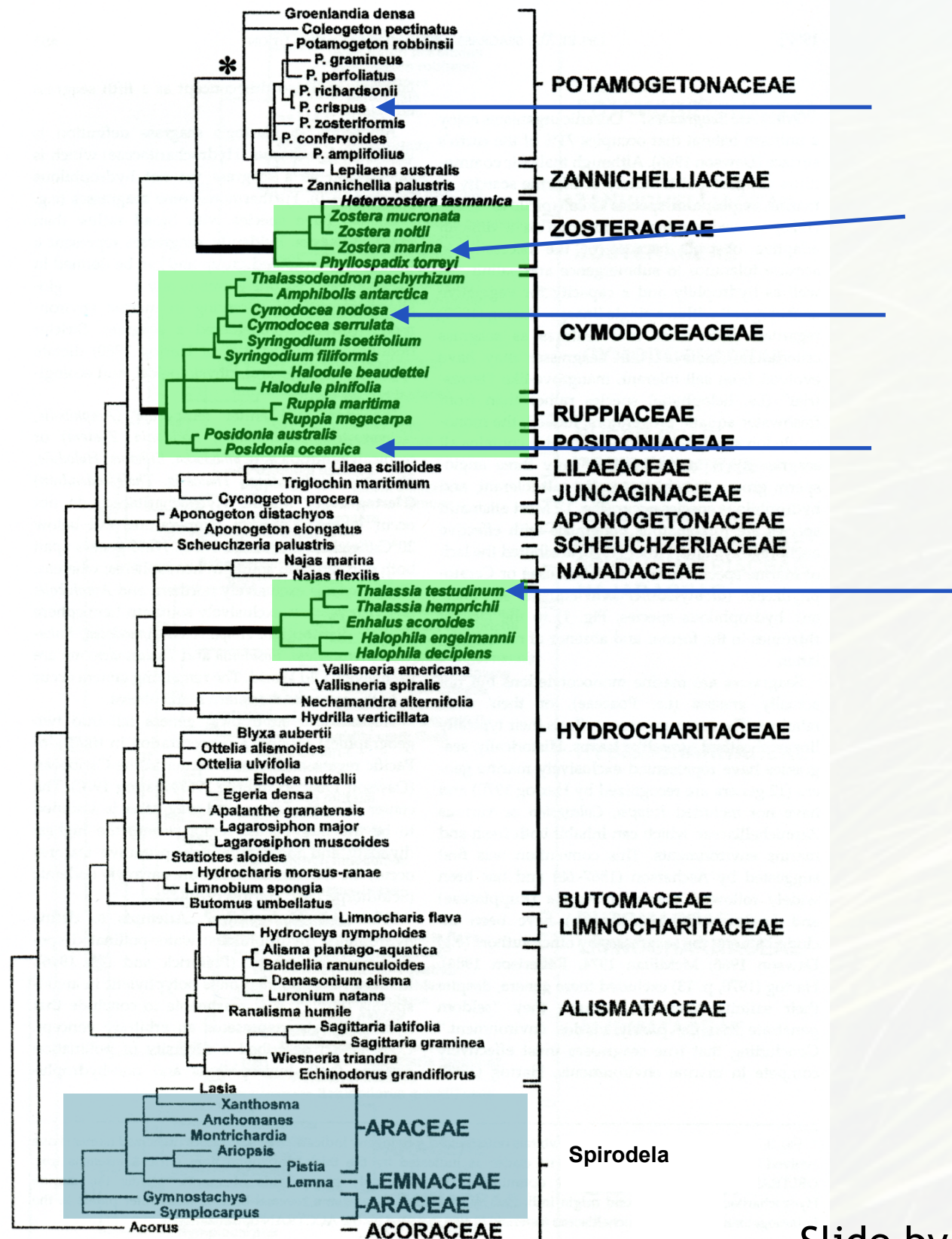


# Future Plans





# JGI Seagrass Pop Geno/Microbiomics



*Potamogeton crispus*

216 *Zostera marina*

*Cymodocea nodosa*

*Posidonia oceanica*

*Thalassia testudinum*



Jay  
Stachowicz



Jeanine  
Olsen

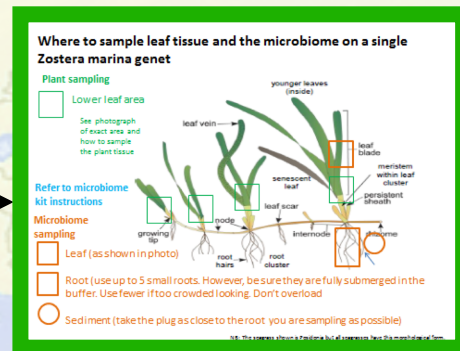
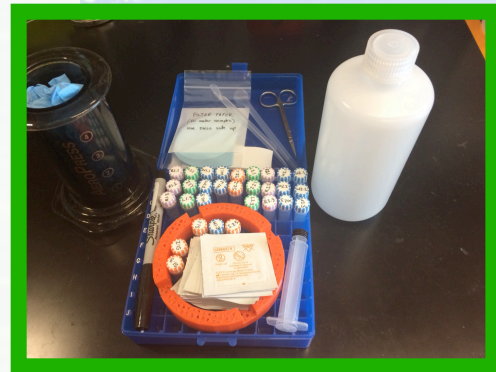


Yves van  
De Peer

Slide by Laura Vann from Tree from Les et al., Syst. Bot. 1997



# JGI Seagrass Population Sampling



- Sent kits
- Sampled microbiomes of leaves, roots, sediment
- Sampled leaves for genomes

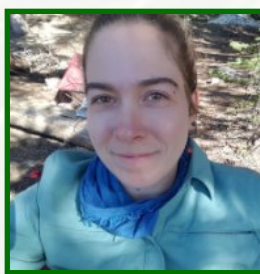
<http://zenscience.org>



Jay  
Stachowicz



Jeanine  
Olsen



Laura  
Vann



# Microbial Manipulation of Seagrass?



**Raquel  
Peixoto**



# Microbial Manipulation of Mangroves



**Raquel  
Peixoto**



**Before... no plants even after  
revegetation**



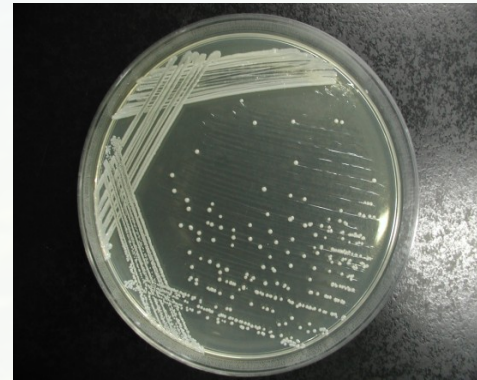
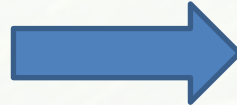
**3 years after PGPR oil degrading +  
biostimulation treatment**

Taketani et al., 2009 (Journal of Microbiology), 2010 (Antonie); Santos et al., 2010 (PLOS One), Santos et al., 2011 (PLOS One); Santos et al 2010 WASP; Peixoto et al., 2011 (Antonie) Carmo et al., 2011 TJOM; Peixoto et al., *in preparation*; Carmo, Santos, Peixoto, Rosado, patent 2016

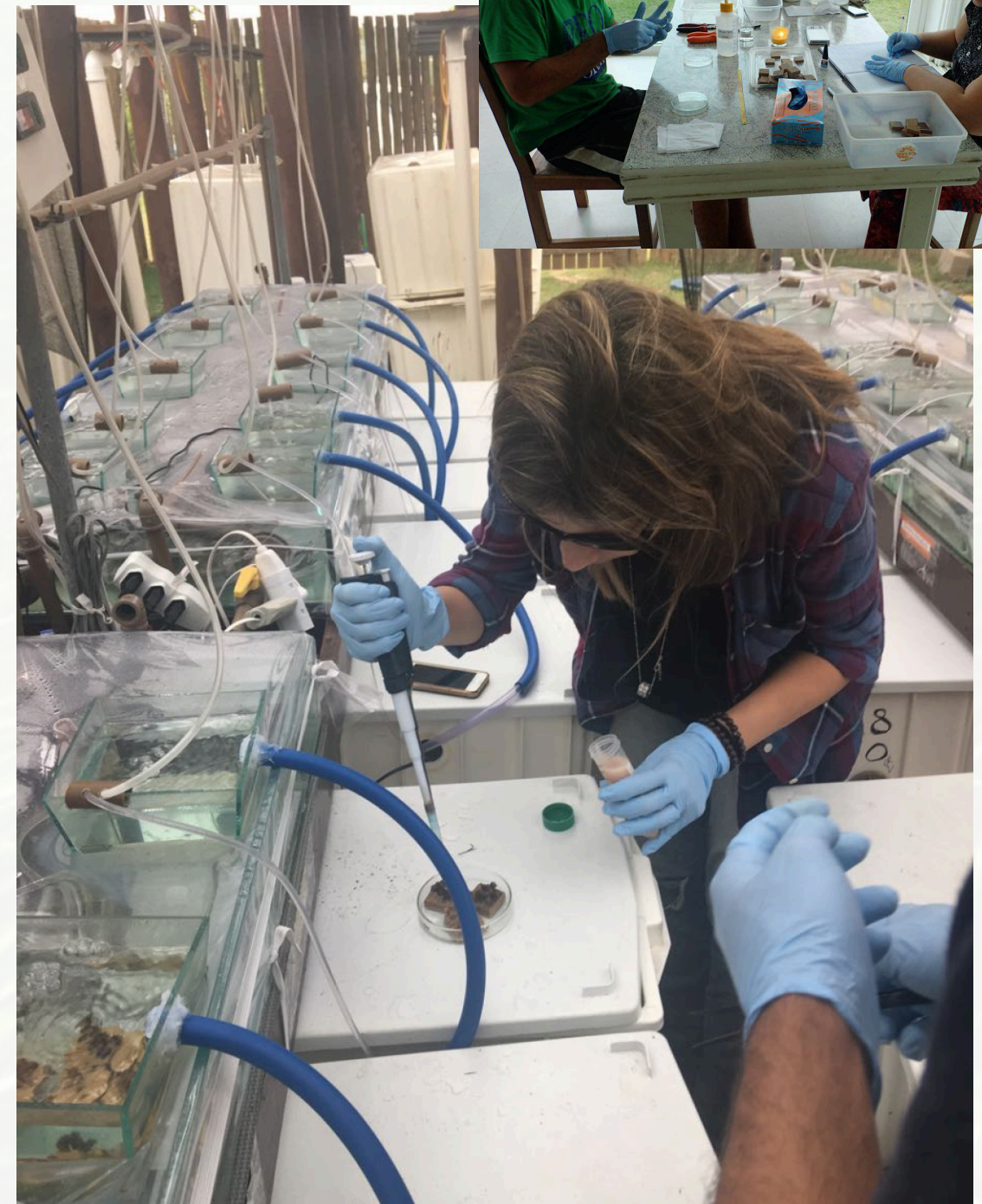
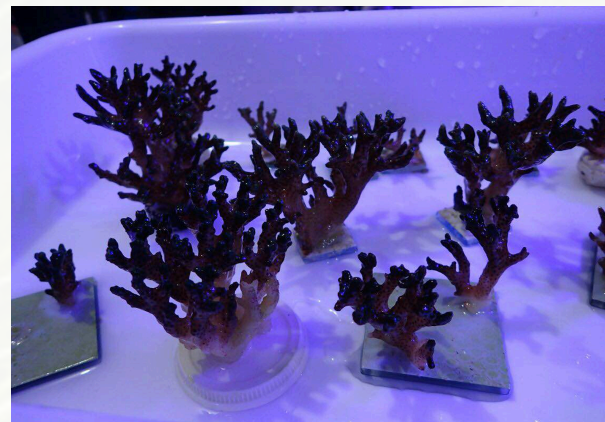


# Microbial Manipulation of Coral

Probiotic consortium from *Pocillopora damicornis*

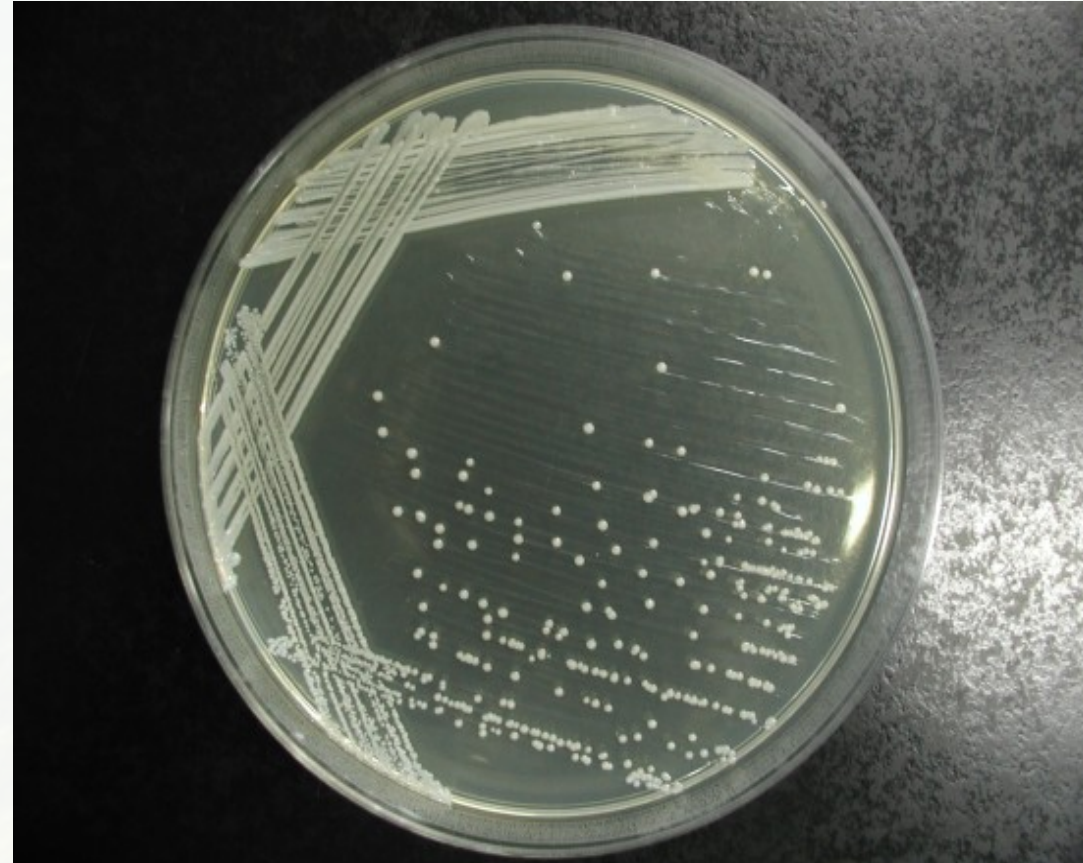


BMC screening  
7 strains





# Microbial Manipulation of Seagrass?



Jay Stachowicz



Melissa Kardish



Raquel Peixoto



# Massively Parallel Undergraduates

- Karley Lujan
- Marcus Cohen
- Katie Somers
- Taylor Tucker
- Hoon San Ong
- Neil Brambhatt
- Hena Hundal
- Daniel Oberbauer
- Briana Pompa-Hogan
- Alex Alexiev
- Ruth Lee

Pic of Karley Lujan



David Coil



# **Seagrass Microbiome Project**

## **Key Lesson:**

**Good People Are A Good Thing**





Guillaume  
Jospin

Alana  
Firl

Laura  
Reynolds

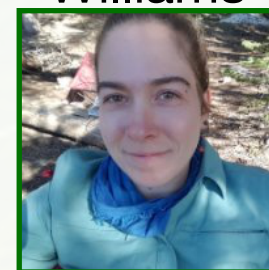
Katie  
DuBois

Jessica  
Abbott

Susan  
Williams

James  
Doyle

Russell  
Neches



Melissa  
Kardish

Cassie  
Ettinger

Sofie  
Voerman

Yves van  
De Peer

Jeanine  
Olsen

Laura  
Vann

Ashkaan  
Fahimipour



Ruth  
Lee

Hannah  
Holland-Moritz

Pamela  
Reynolds

- Karley Lujan
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- Katie Somers
- Taylor Tucker
- Hoon San Ong
- Neil Brambhatt
- Hena Hundal
- Daniel Oberbauer
- Briana Pompa-Hogan
- Alex Alexiev
- Ruth Lee



Jay Stachowicz

Jessica Green

Jenna Lang

David Coil

GORDON AND BETTY  
**MOORE**  
FOUNDATION