



Smithsonian Tropical
Research Institute

GORDON AND BETTY
MOORE
FOUNDATION

UCDAVIS

The formation of the Isthmus of Panama: an unrivalled opportunity to understand drivers, functions and evolution of marine host-associated microbiomes



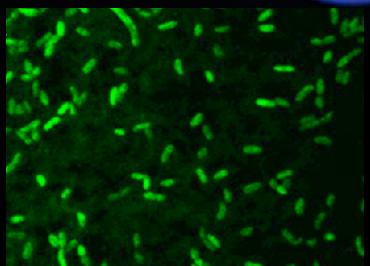
Matthieu Leray, Laetitia Wilkins, Jarrod Scott and the #istmobiome team

Tupper seminar - March 10, 2020

Microbial symbionts fulfill essential functions for hosts

Predator avoidance

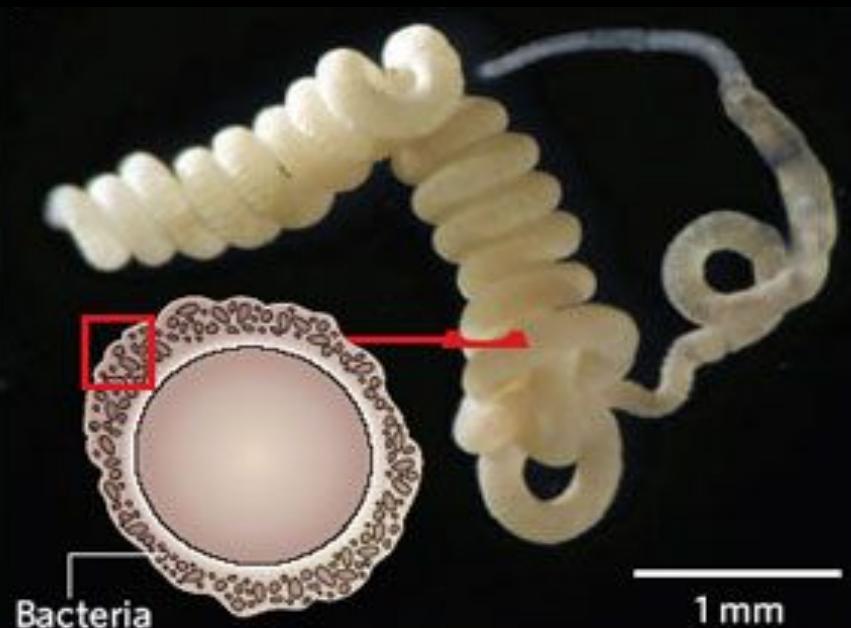
Hawaiian bobtail squid



Vibrio fischeri
Bioluminescent bacteria
for predator avoidance

Nutrition

Gutless marine worm

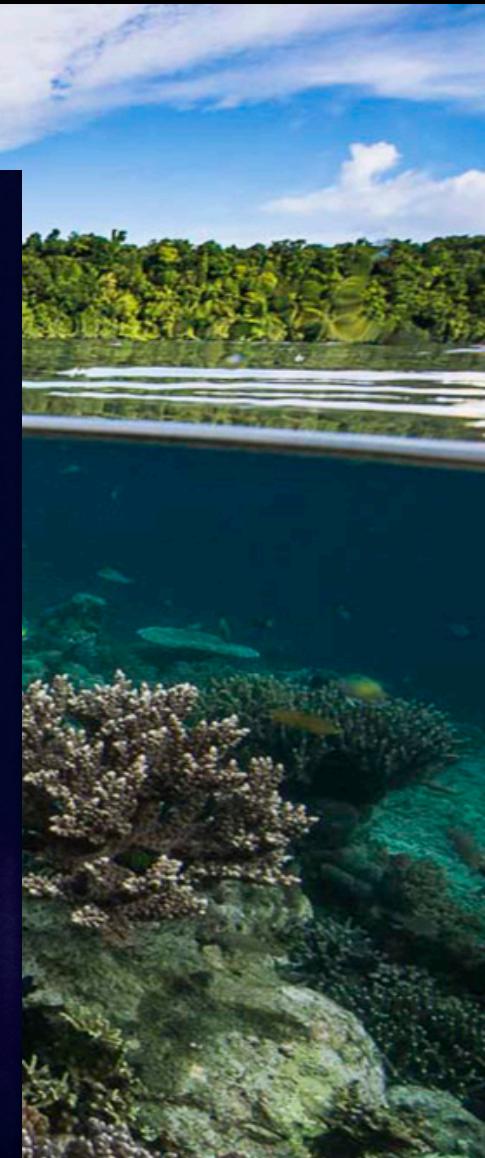
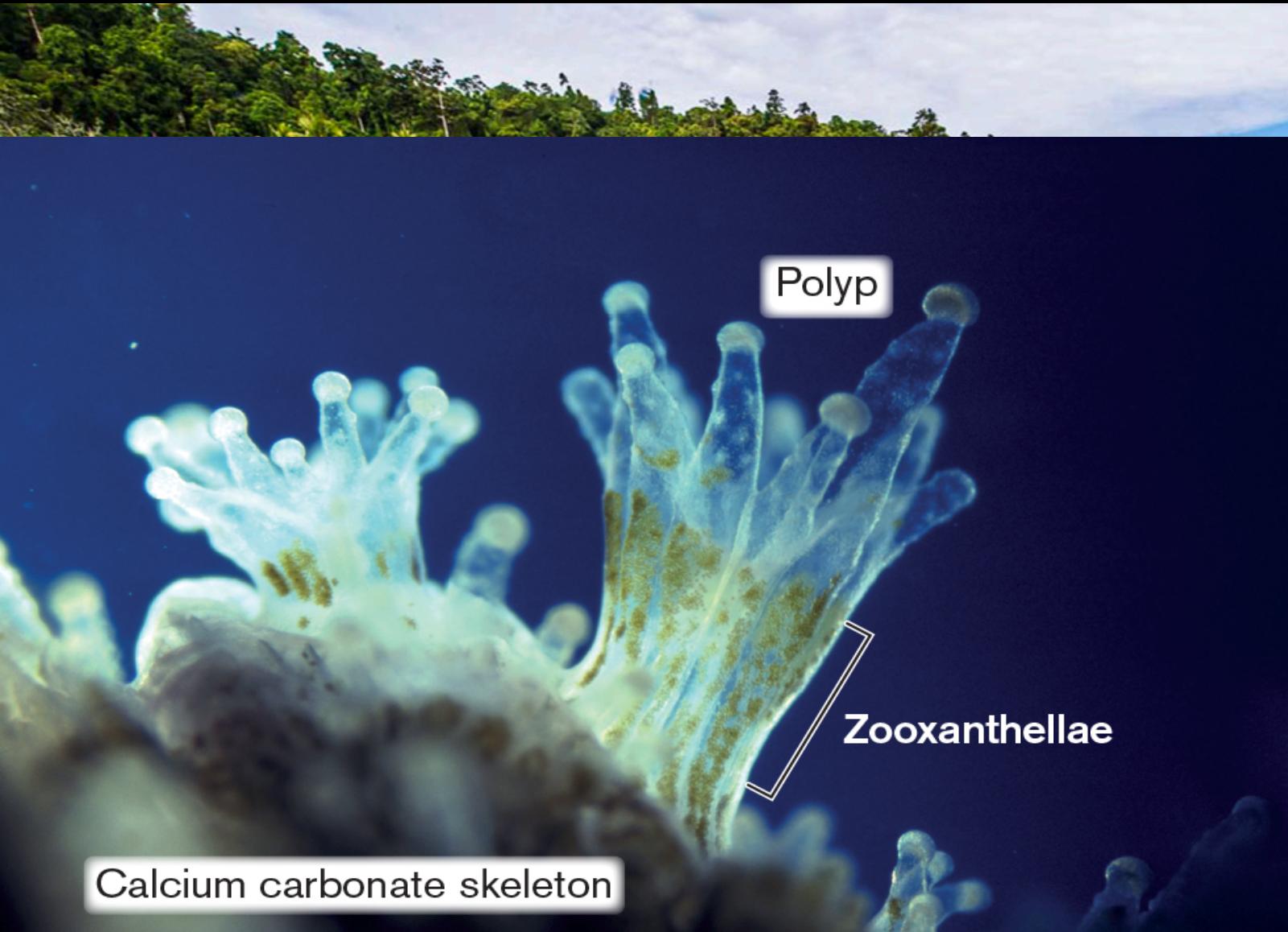


Several chemosynthetic bacteria
They feed the worm

Animal-microbe nutritional symbiosis are the foundation of marine ecosystems

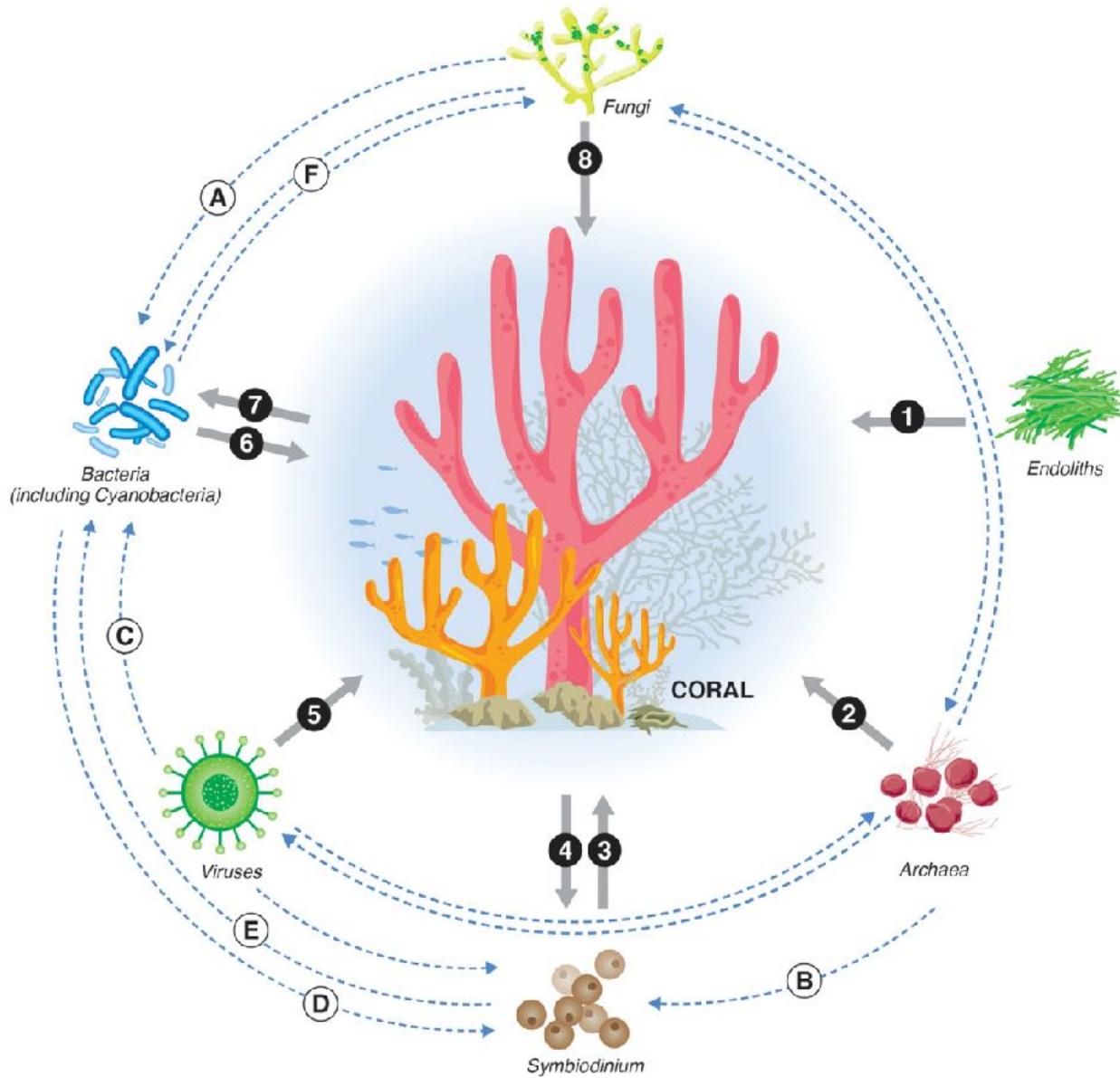


Animal-microbe nutritional symbiosis are the foundation of marine ecosystems



EXAMPLES OF POSSIBLE ROLES AND RELATIONSHIPS BETWEEN CORALS AND THEIR Symbionts

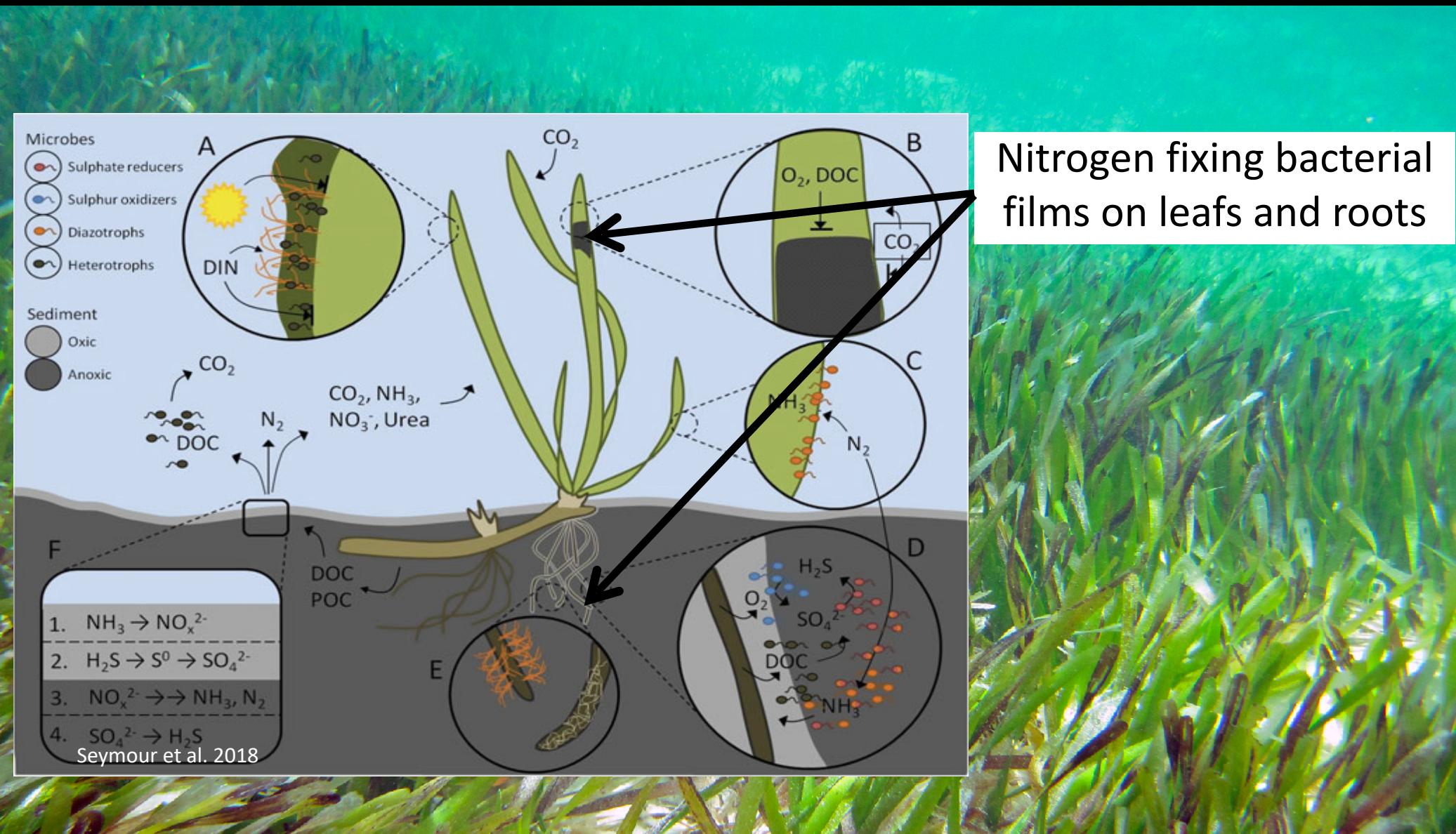
- ① Photosynthate transference.
- ② Nitrogen cycling.
- ③ Main carbon source supplier and production of DMSP that might play a role as antioxidant and on bacterial population control. Protection against UV.
- ④ Provides shelter and protection and role in the nutrient cycles.
- ⑤ Gene transfer. Natural phage therapy by removing bacterial pathogens and controlling algal blooms.
- ⑥ Nutrient cycling, such as S, C and N. Biological control of pathogens. DMSP degradation. Influence settlement and metamorphosis of coral larvae. Modulate coral microbiome?
- ⑦ Shelter, protection, source of nutrients.
- ⑧ Antimicrobial activity, may play a role related to biomineralization, protection of skeletogenic cells and protection against UV. May be involved in C and N cycle.



EXAMPLES OF POSSIBLE RELATIONSHIPS AMONGST CORAL SYMBIONTS

- | | | | | | | | | | | | |
|----------|---|----------|---------------------------|----------|-------------------------------|----------|---------------------------|----------|---|----------|--------------------|
| A | Availability of C and S source through DMSP catabolism. | B | Availability of N source. | C | Transfer of beneficial genes. | D | Availability of N source. | E | Provides C and S source through DMSP production | F | Nutrients exchange |
|----------|---|----------|---------------------------|----------|-------------------------------|----------|---------------------------|----------|---|----------|--------------------|

Animal-microbe nutritional symbiosis are the foundation of marine ecosystems



Microbial symbionts influence biogeochemical cycling within ecosystems



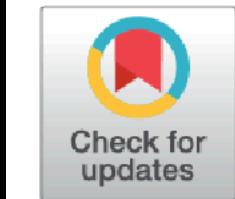
Sponge symbionts play a role in marine phosphorous and nitrogen cycles

PERSPECTIVE

Host-associated microbiomes drive structure and function of marine ecosystems

Laetitia G. E. Wilkins^{1‡*}, Matthieu Leray^{2#}, Aaron O'Dea³, Benedict Yuen³, Raquel S. Peixoto^{1,4,5}, Tiago J. Pereira⁶, Holly M. Bik⁶, David A. Coil¹, J. Emmett Duffy⁷, Edward Allen Herre², Harilaos A. Lessios², Noelle M. Lucey², Luis C. Mejia^{2,8}, Douglas B. Rasher⁹, Koty H. Sharp¹⁰, Emilia M. Sogin¹¹, Robert W. Thacker¹², Rebecca Vega Thurber¹³, William T. Wcislo¹², Elizabeth G. Wilbanks¹⁴, Jonathan A. Eisen^{1,15,16}

1 Genome and Biomedical Sciences Facility, University of California, Davis, Davis, California, United States of America, 2 Smithsonian Tropical Research Institute, Balboa, Ancon, Republic of Panamá, 3 Centre for Microbiology and Environmental Systems Science, Department of Microbial Ecology, University of Vienna, Vienna, Austria, 4 LEMM, Laboratory of Molecular Microbial Ecology, Institute of Microbiology Paulo de Góes, Federal University of Rio de Janeiro (UFRJ), Rio de Janeiro, Brazil, 5 IMAM-AquaRio–Rio de Janeiro Aquarium Research Center, Rio de Janeiro, Brazil, 6 Department of Nematology, University of California, Riverside, Riverside, California, United States of America, 7 Tennenbaum Marine Observatories Network, Smithsonian Environmental Research Center, Edgewater, Maryland, United States of America, 8 Centro de Biodiversidad y Descubrimiento de Drogas, Instituto de Investigaciones Científicas y Servicios de Alta Tecnología (INDICASAT AIP), Panamá, Republic of Panamá, 9 Center for Ocean Health, Bigelow Laboratory for Ocean Sciences, East Boothbay, Maine, United States of America, 10 Department of Biology, Marine Biology, and Environmental Sciences, Roger Williams University, Bristol, Rhode Island, United States of America, 11 Max Planck Institute of Marine Microbiology, Bremen, Germany, 12 Department of Ecology and Evolution, Stony Brook University, Stony Brook, New York, United States of America, 13 Department of Microbiology, Oregon State University, Corvallis, Oregon, United States of America, 14 Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, Santa Barbara, California, United States of America, 15 Department of Evolution and Ecology, University of California, Davis, Davis, California, United States of America, 16 Department of Medical Microbiology and Immunology, University of California, Davis, Davis, California, United States of America

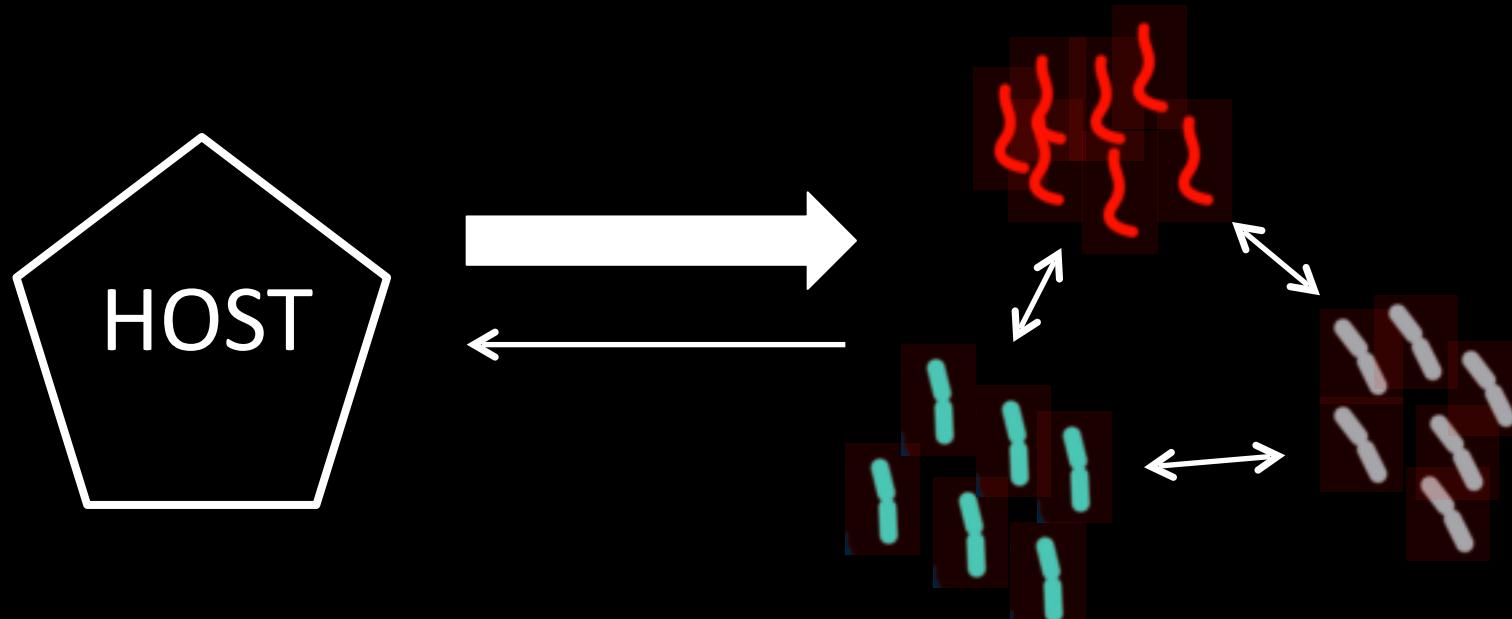


How have interactions between
hosts and microbes/microbiomes evolved?

“The problem of the diverse microbiome”

How have interactions between hosts and microbes/microbiomes evolved?

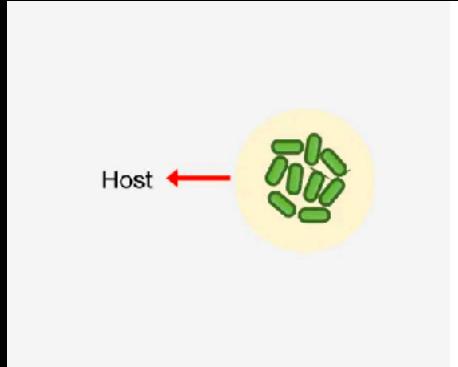
“The problem of the diverse microbiome”



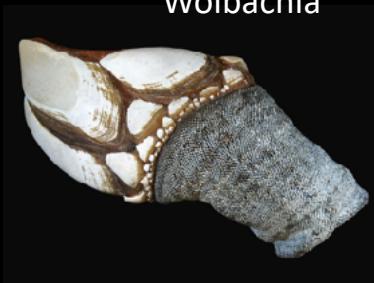
“Evolutionary theory predicts that host-to-microbe effects—rather than the much-studied impacts of microbe on host—**ARE CRITICAL FOR MICROBIOME FORM AND FUNCTION**”

Models of host–microbiome interaction

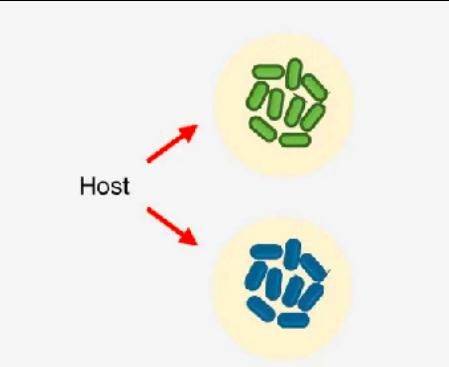
Symbiont control



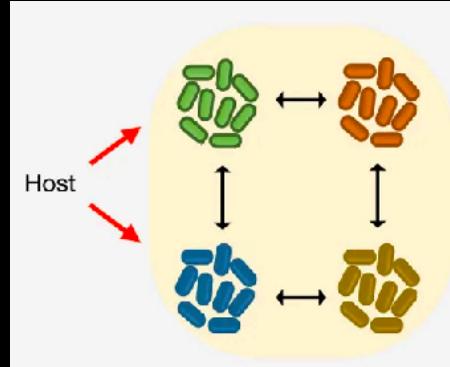
Wolbachia



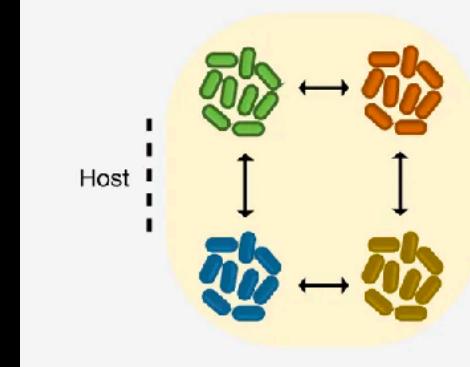
Host control



Microbiome on leash



Open ecosystem



- Each model is consistent with evolutionary theory
- Each model is consistent with real-world examples

Models of host–microbiome interaction

Symbiont controls

Uncommon

Host

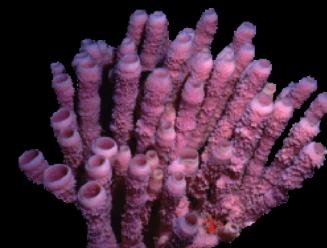
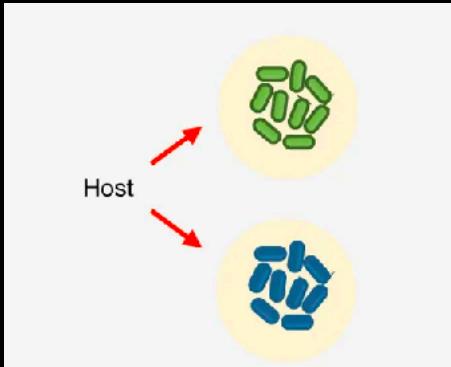
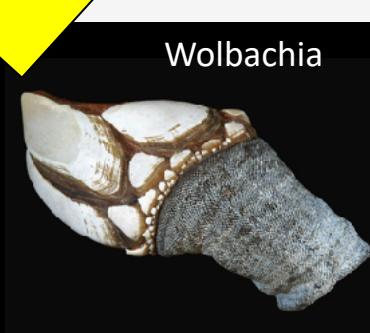
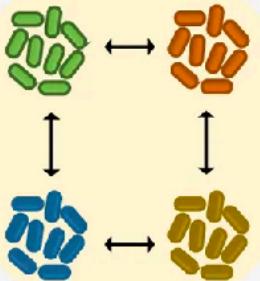
Host control

Host

Microbiome on leash

Open ecosystem

Host



- Each model is consistent with evolutionary theory
- Each model is consistent with real-world examples

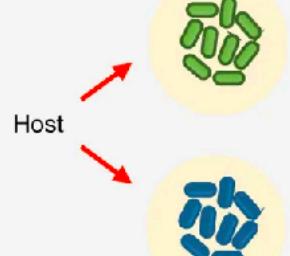
Models of host–microbiome interaction

Symbiont controls

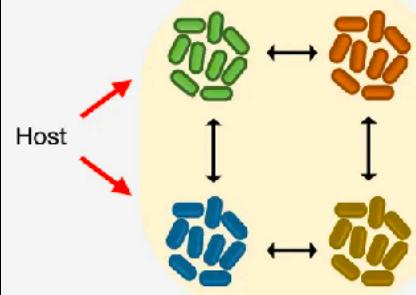
Uncommon

Host

Host control



Microbiome on leash



Open ecosystem

Uncommon

Host



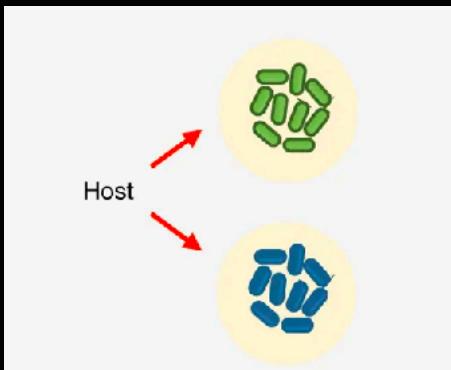
- Each model is consistent with evolutionary theory
- Each model is consistent with real-world examples

Models of host–microbiome interaction

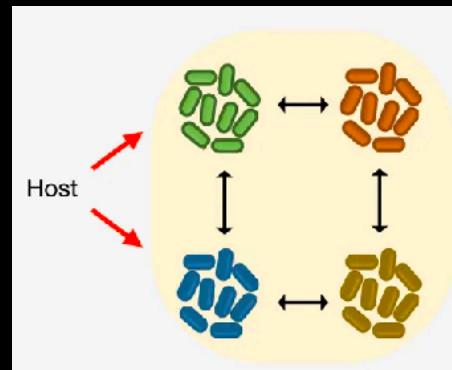
Symbiont controls



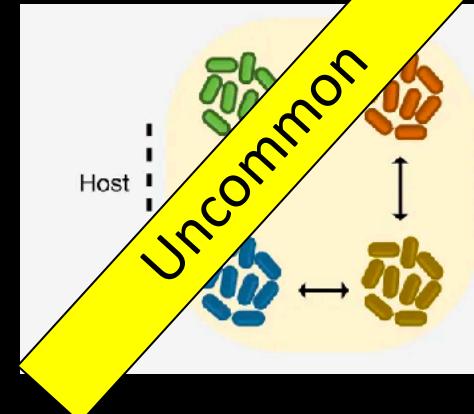
Host control



Microbiome on leash



Open ecosystem



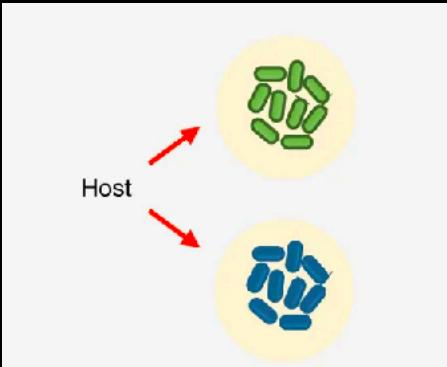
- ◆ Host monitors one or few strains
- ◆ Fine-scale host control mechanisms
- ◆ Possible vertical transmission to increase fitness

Models of host–microbiome interaction

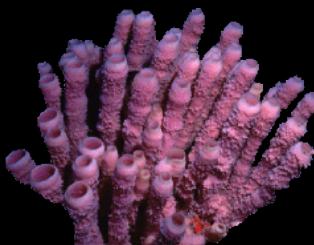
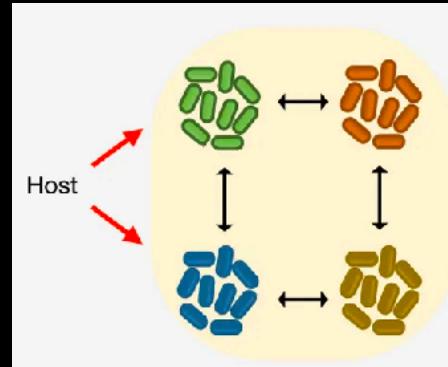
Symbiont controls



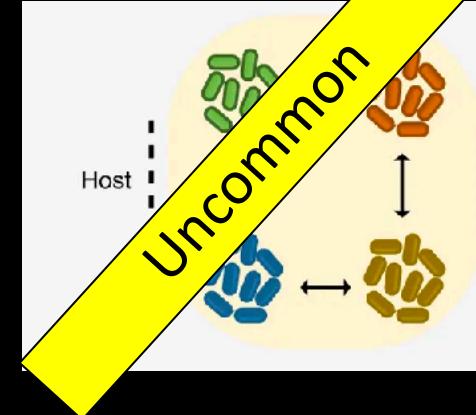
Host control



Microbiome on leash



Open ecosystem



- ◆ Host monitors one or few strains
- ◆ Fine-scale host control mechanisms
- ◆ Possible vertical transmission to increase fitness



- ◆ Many microbial strains co-exists = the “microbiome”
- ◆ Host under selection to foster a beneficial microbiome
- ◆ Primarily horizontal transmission

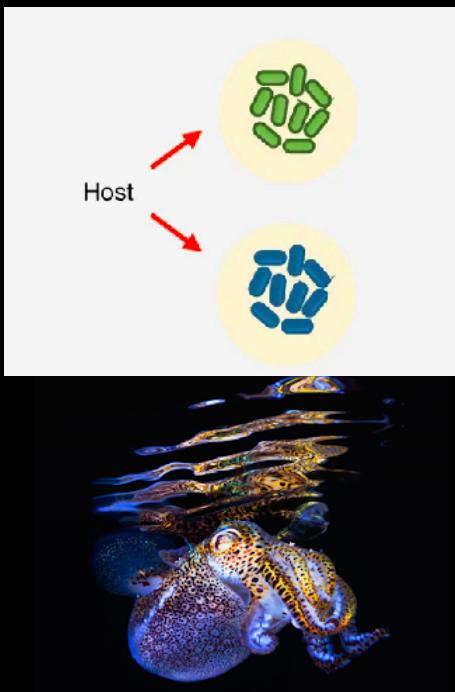


Models of host–microbiome interaction

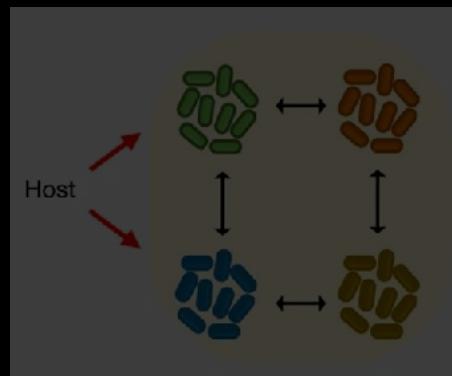
Symbiont control



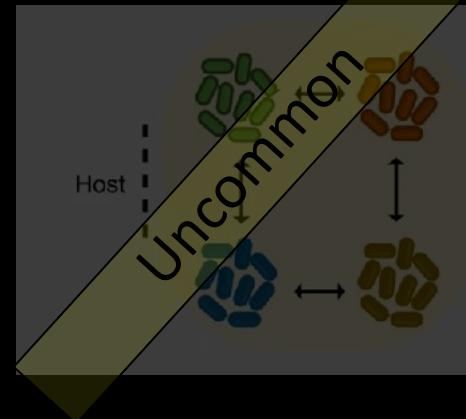
Host control



Microbiome on leash



Open ecosystem



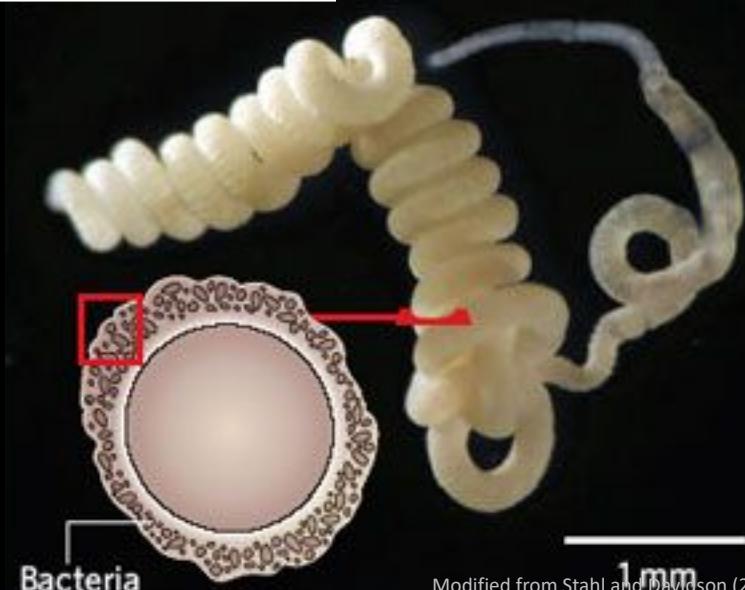
Research is highly biased towards a small number of hosts and microbes

Hawaiian bobtail squid



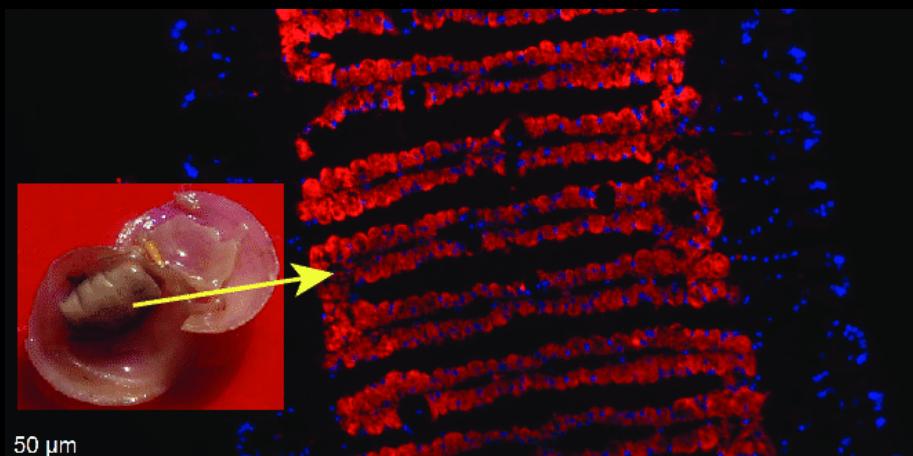
Todd Bretl Underwater Photography

Gutless worm



Modified from Stahl and Davidson (2006)

Lucinid clam



50 µm

Shipworm

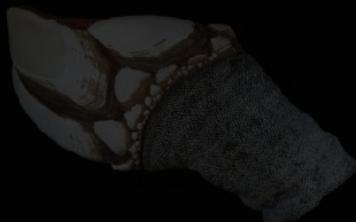


Photo by O'Connor et al. 2014

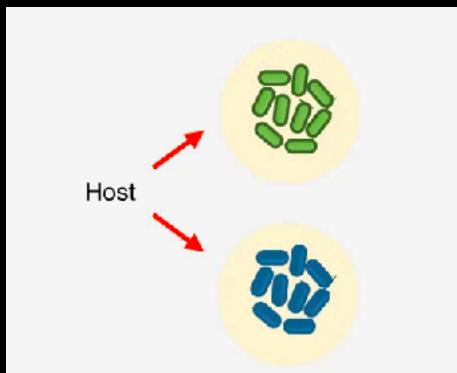
Research is highly biased towards a small number of hosts and microbes

Models of host–microbiome interaction

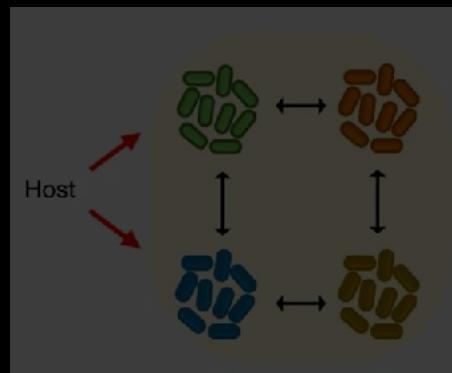
Symbiont control



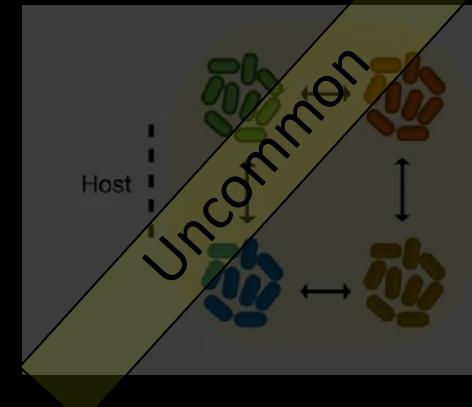
Host control



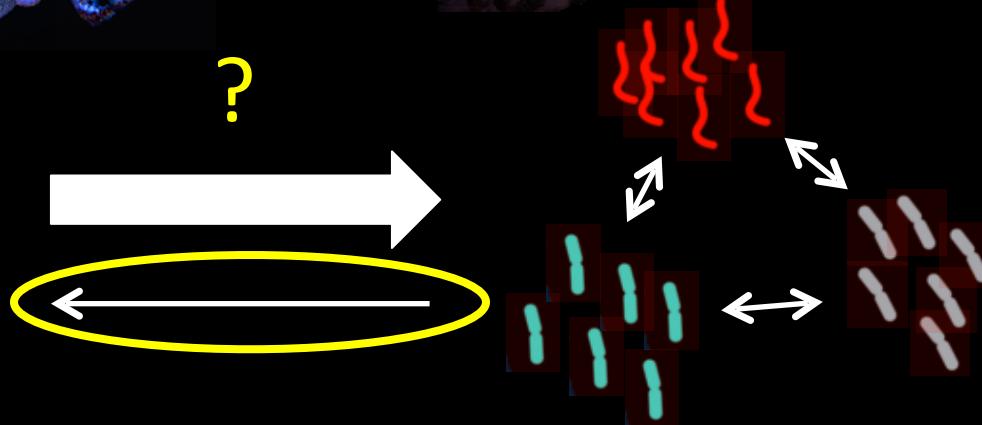
Microbiome on leash



Open ecosystem



?



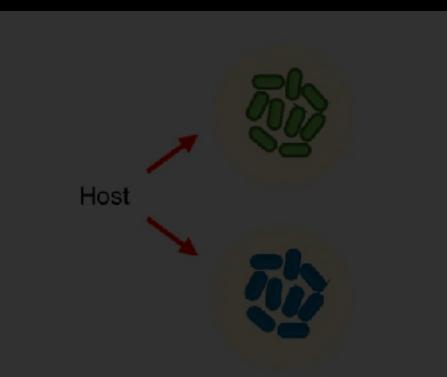
Limited focus on how hosts influence microbiomes

Models of host–microbiome interaction

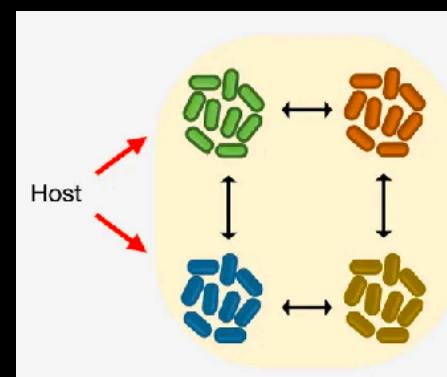
Symbiont control



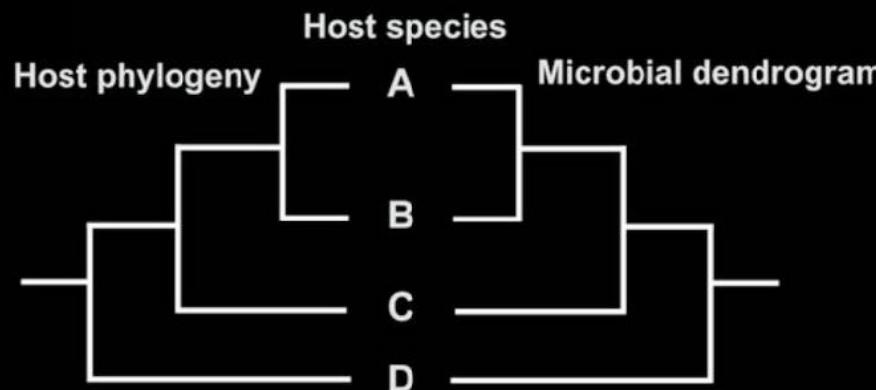
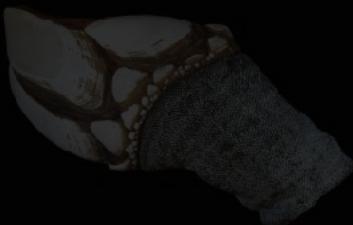
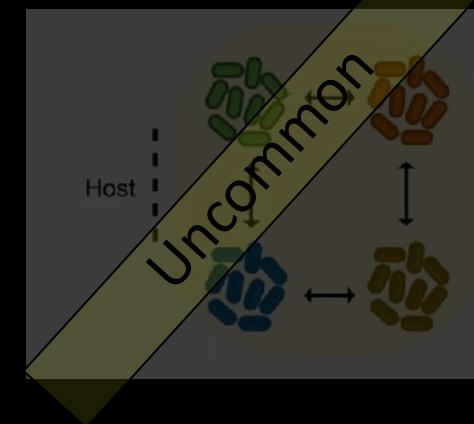
Host control



Microbiome on leash

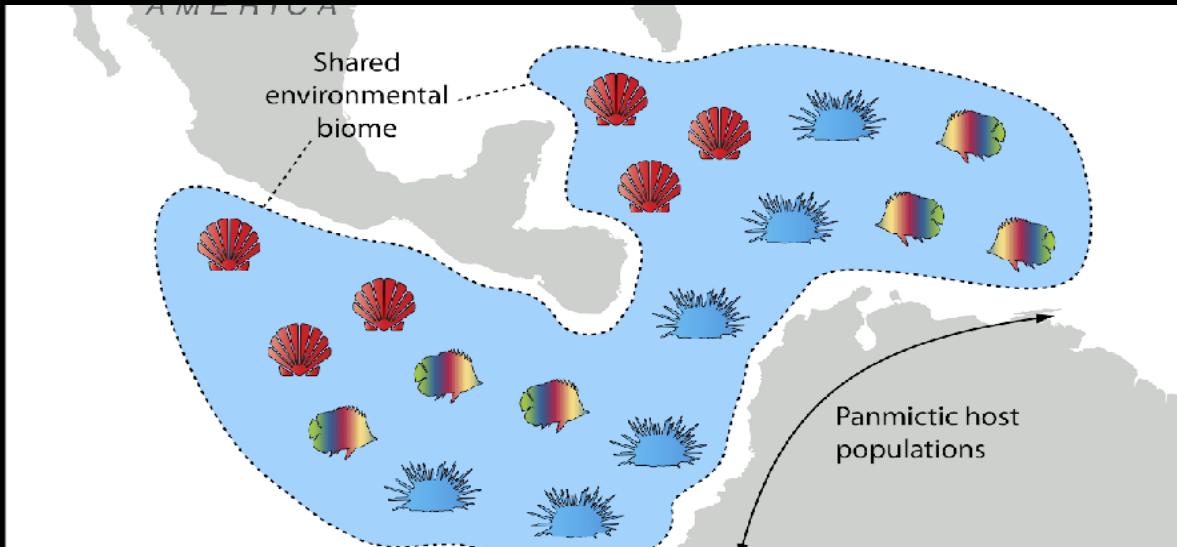


Open ecosystem



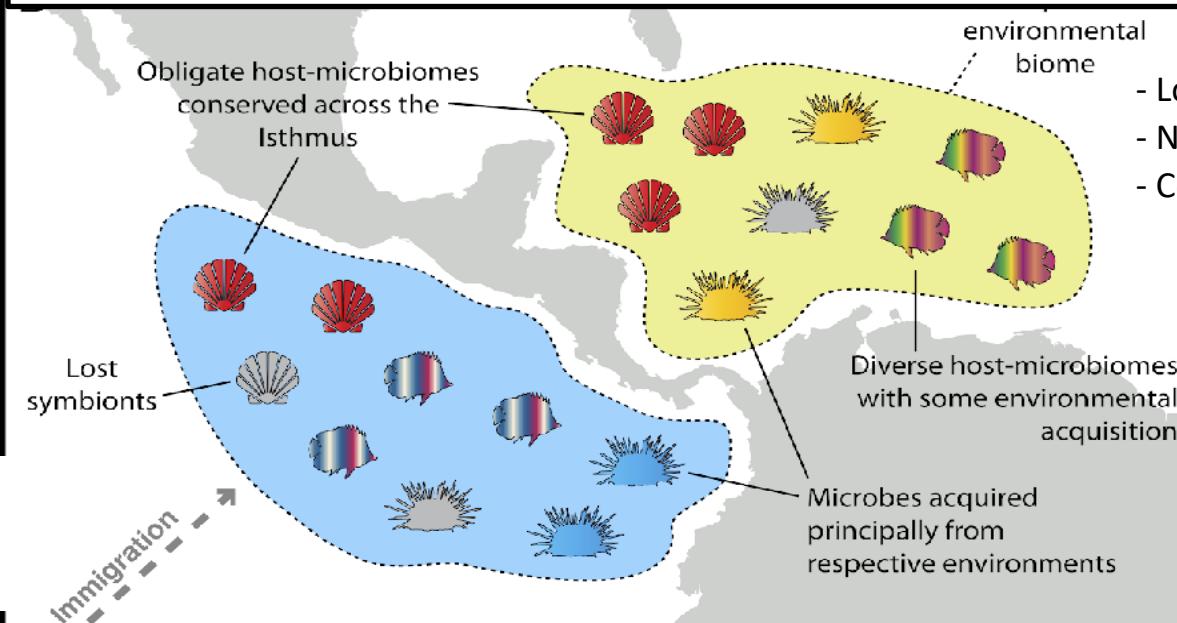
Studies lack evolutionary & ecological contexts

The closure of the isthmus provides the context



3 million years ago

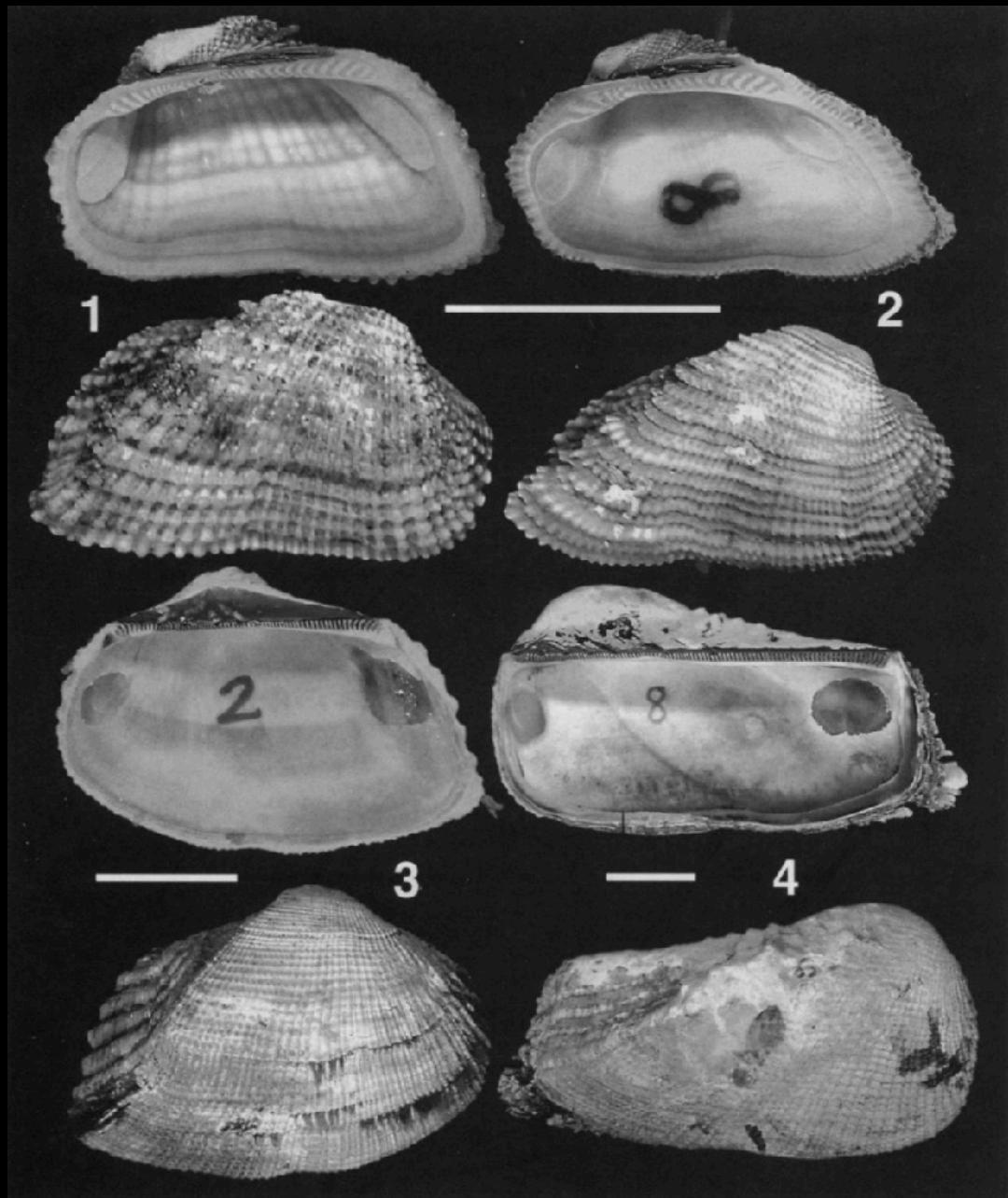
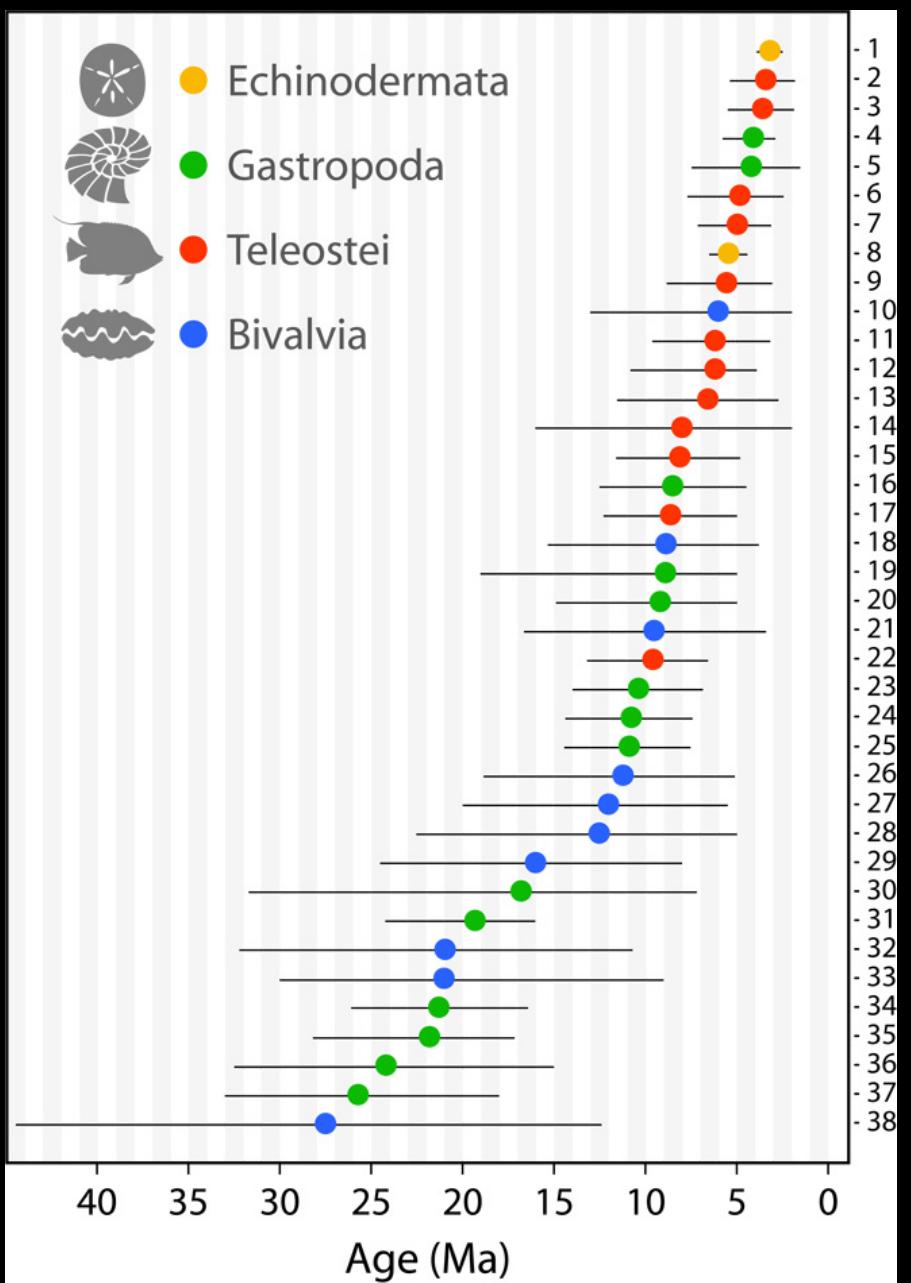
Diversification, adaptation and extinctions
in the last ~3 million years



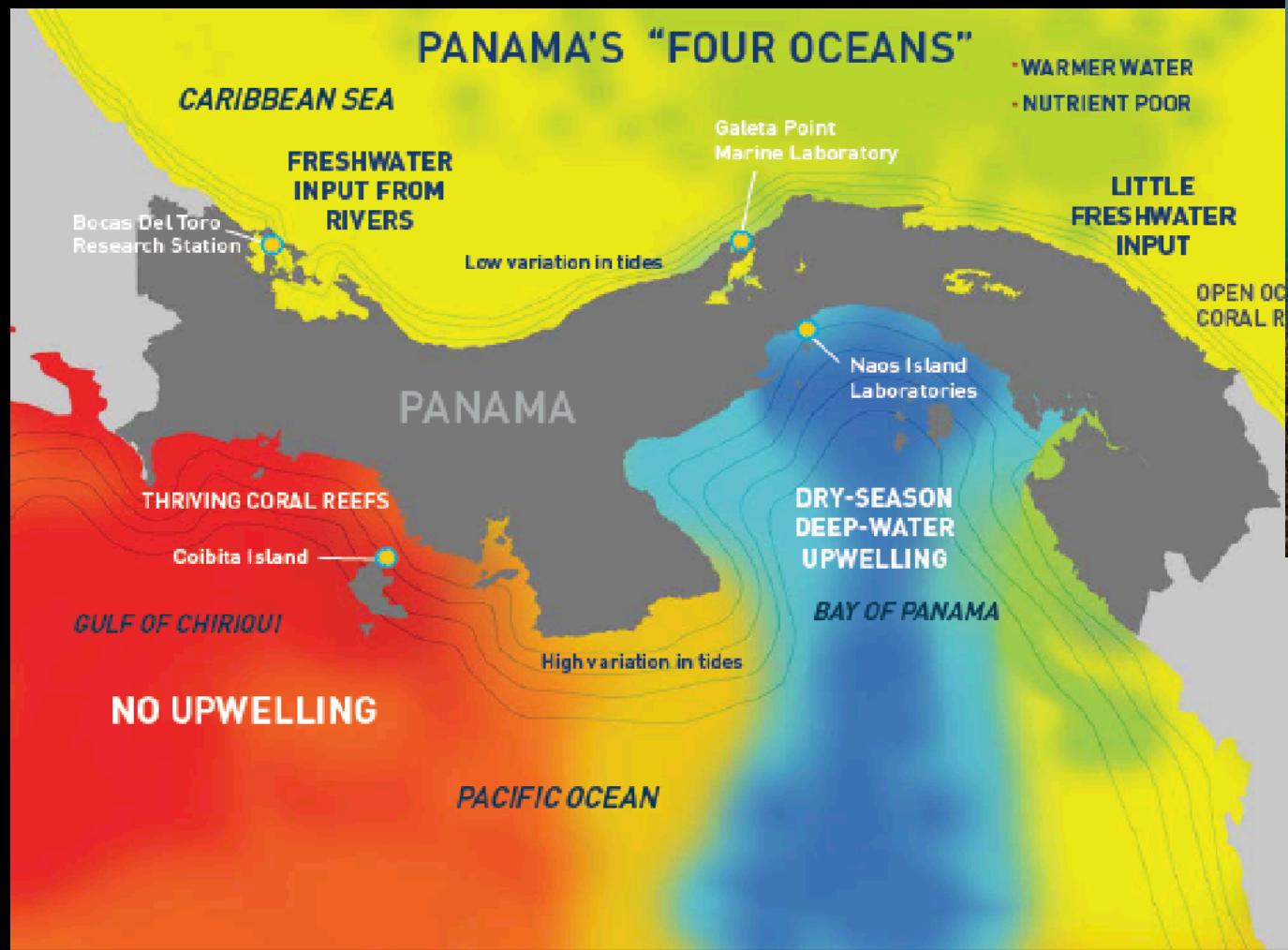
Today

- High nutrient
- Large tides
- Variable temperature

Data: taxonomy, ecology, behavior and evolution of hosts



Physical & Biological monitoring: the environmental context



Historical ecology: fossils & aeDNA



Photo: Sean Mattson



Photo: Estelle Bapst

Focal groups:

Eastern Pacific



Fish
+ microbiome

Caribbean



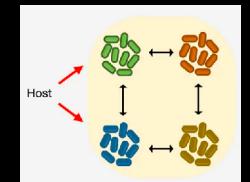
Shrimp
+ microbiome



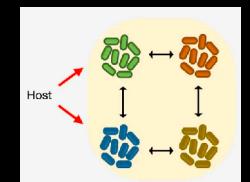
Clam
+ chemosymbiotic
microbe



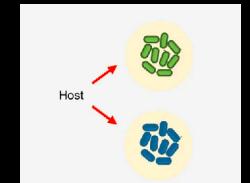
Microbiome on leash



Microbiome on leash

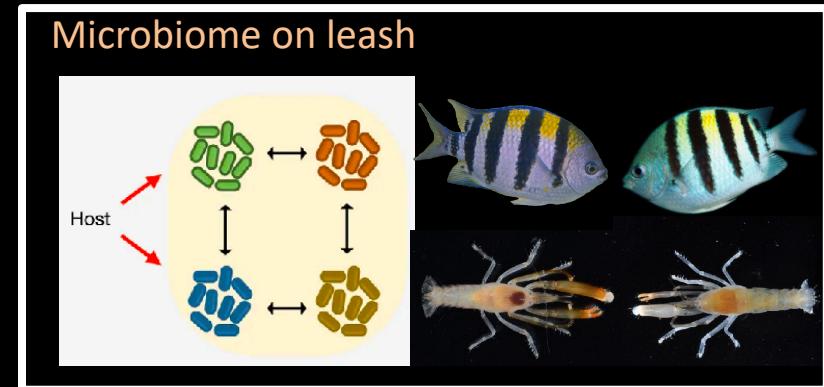
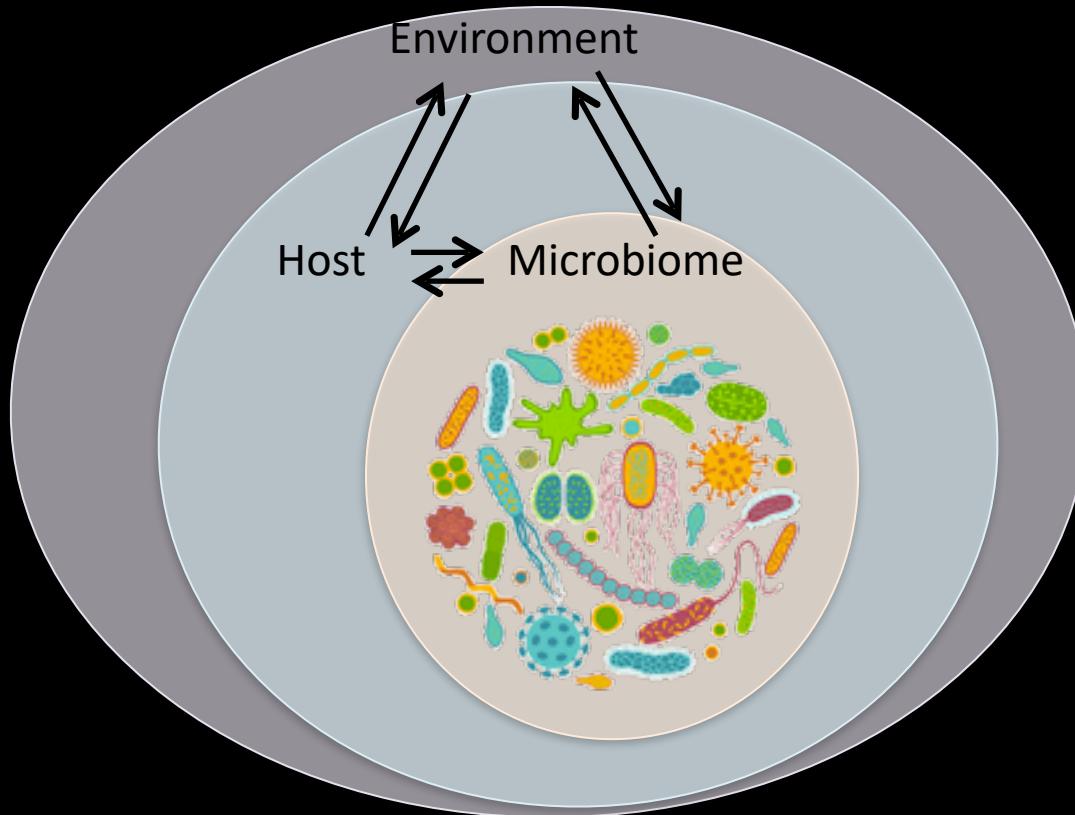


Host control



Research axes

1) Identifying ecological and evolutionary drivers of the microbiome



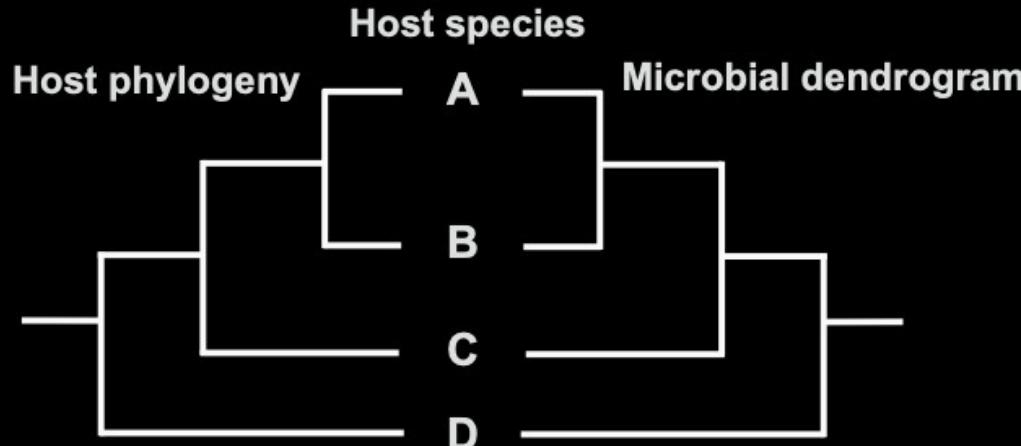
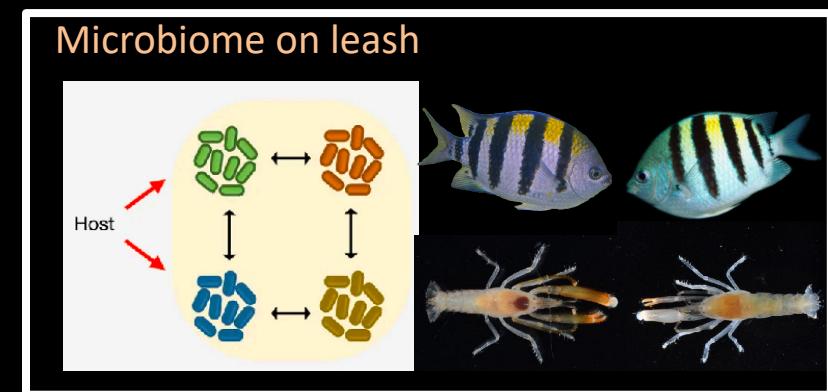
What are the relative contributions of:

- Environment
- Host
- Phylogeny

on community assembly?

Research axes

1) Identifying ecological and evolutionary drivers of the microbiome



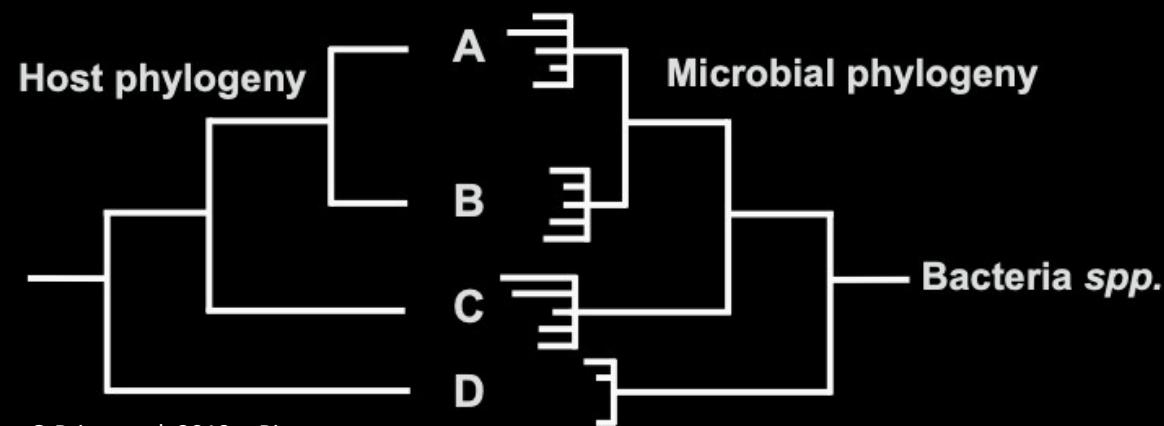
O'Brien et al. 2019 mBio

Are microbiomes structured through phylogenetically related host traits?

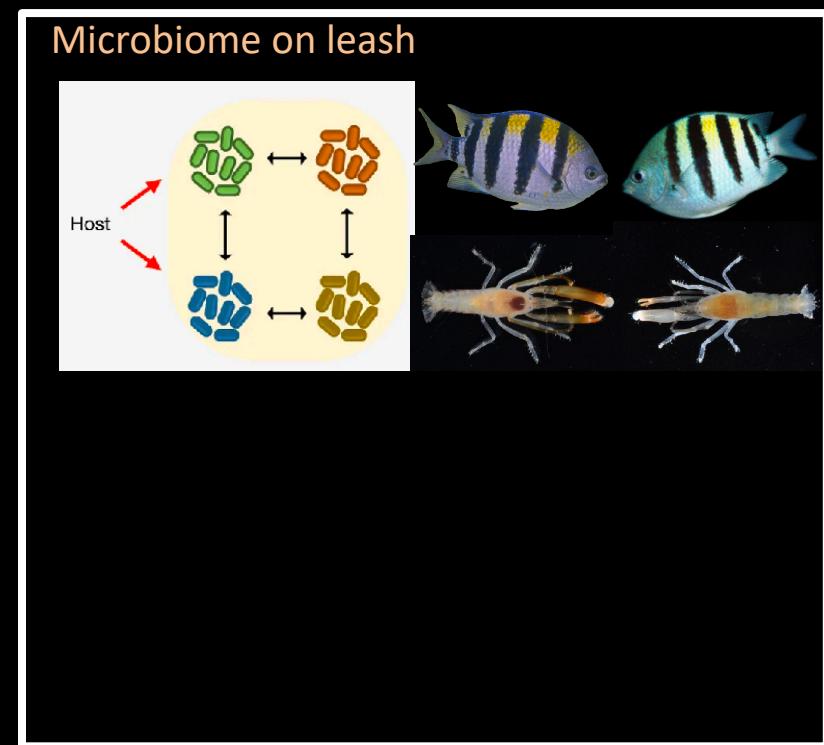
Phylosymbiosis: The ecological relatedness (or similarity) of the microbiome mirrors host phylogeny

Research axes

2) Co-divergence between hosts and microbes



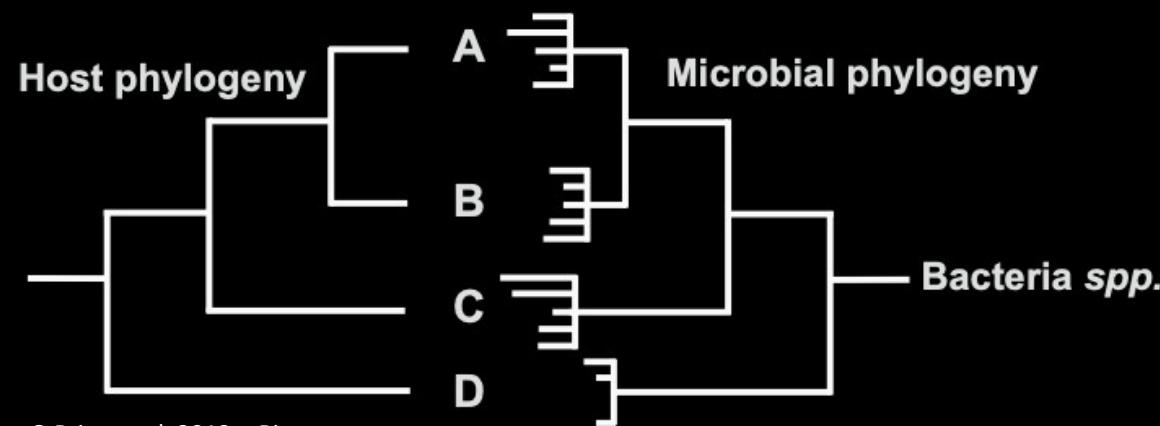
O'Brien et al. 2019 mBio



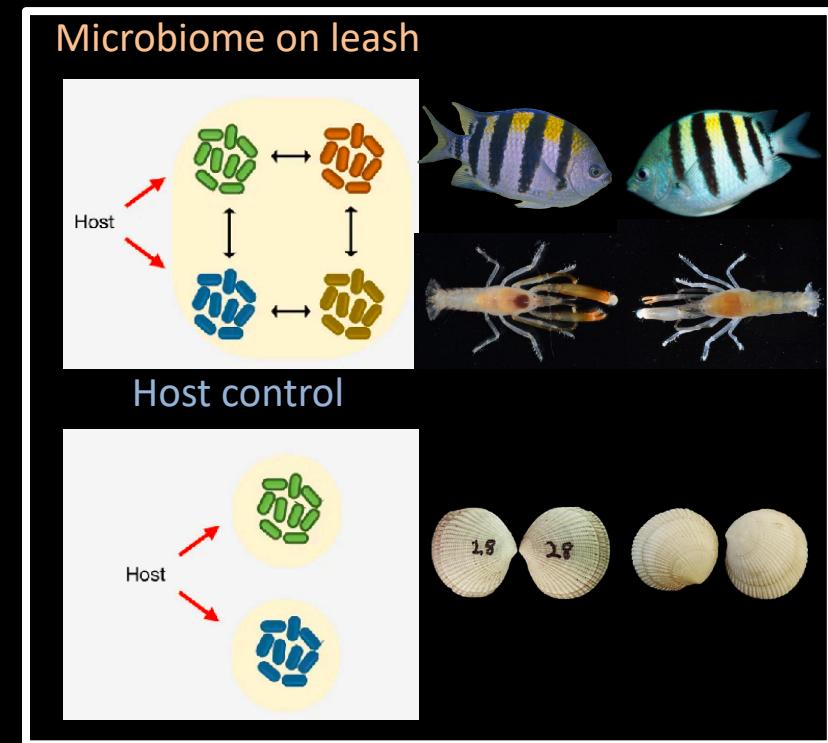
Which microbes have had long-term interactions with hosts? → mutualists? Parasites?

Research axes

2) Co-divergence between hosts and microbes



O'Brien et al. 2019 mBio



Which microbes have had long-term interactions with hosts? → mutualists? Parasites?

How has the gene composition of the microbial genomes changed over time?

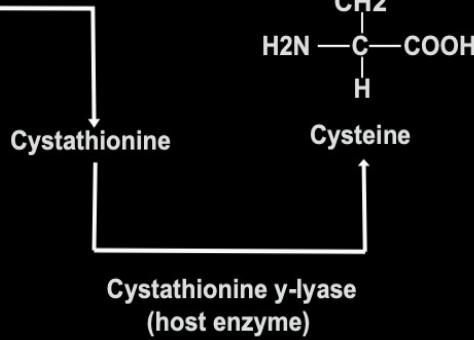
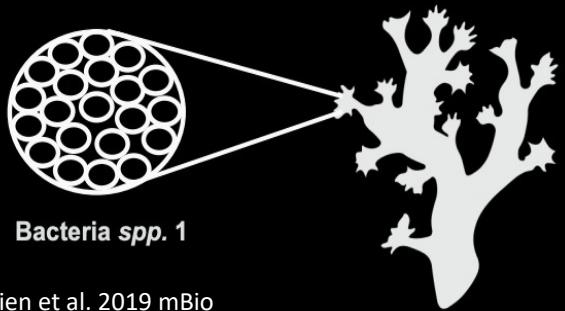
Research axes

3) Adaptation and metabolic cooperation

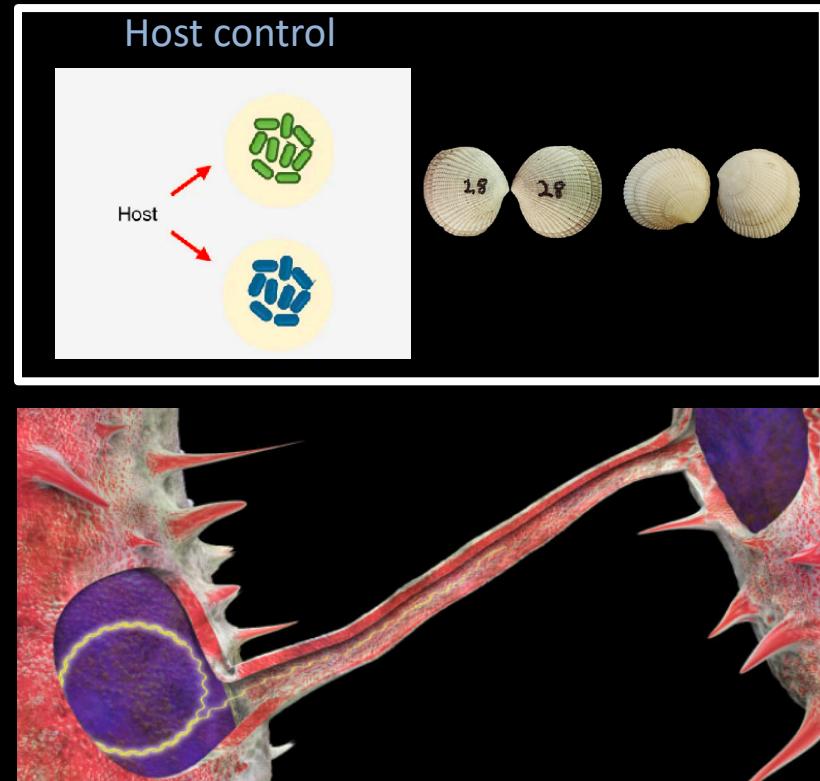
i)

Homocysteine + Serine
(host diet & metabolism)

Cystathionine B-synthase
(symbiont enzyme)



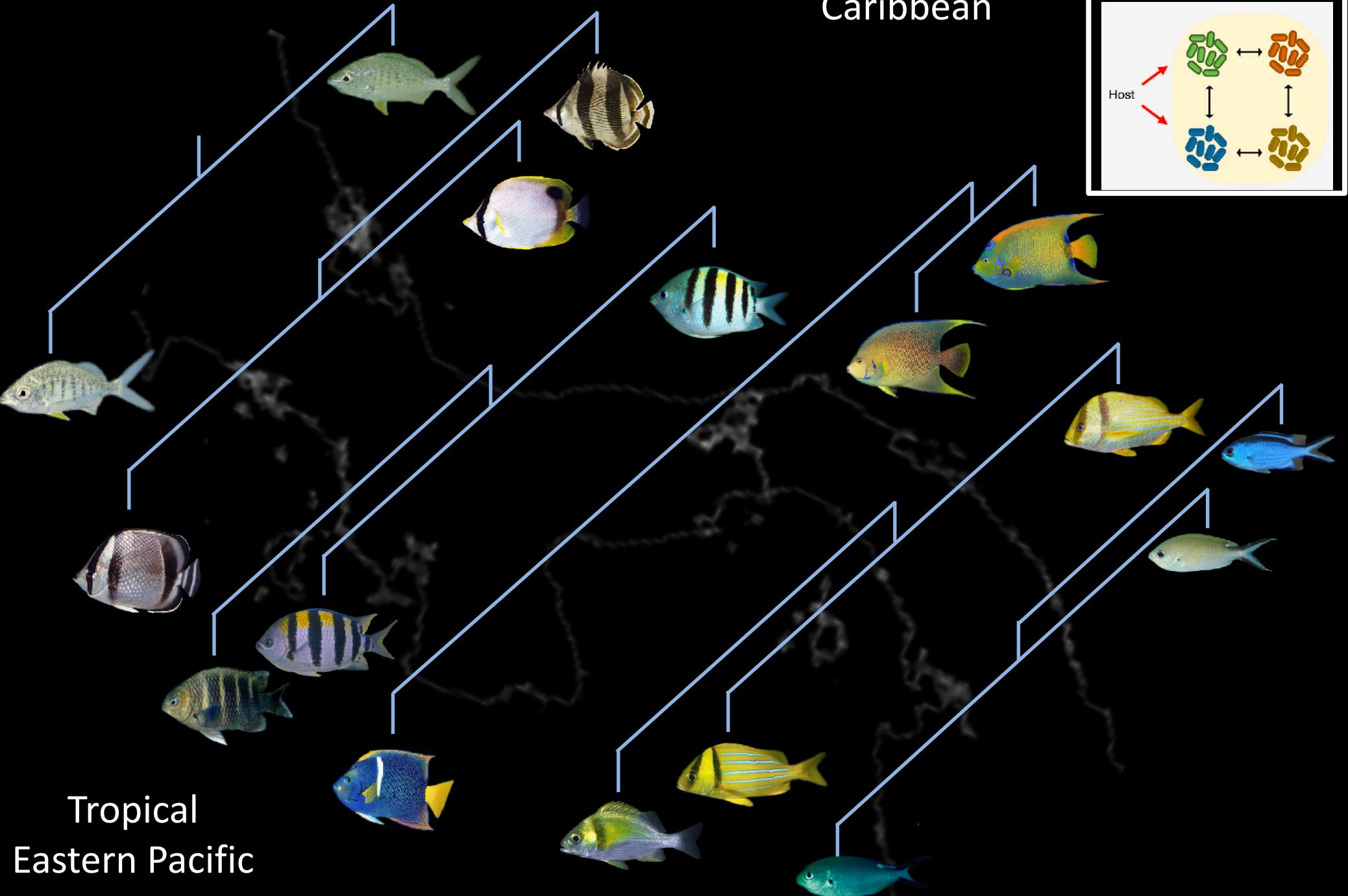
O'Brien et al. 2019 mBio



Do we see evidence of adaptations in microbial genomes?
And to what selective pressures?

Is the metabolic function of the microbe evolving and how?

Caribbean



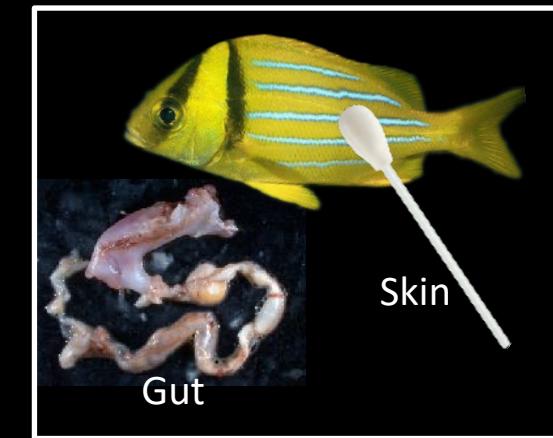
Sampling

Sampling locations



FAMILY	SPECIES	Ocean	NO. SPECIMENS collected to date	TROPHIC GROUP
Blenniidae	<i>Ophioblennius macclurei</i>	Caribbean	11	Herbivore
	<i>Ophioblennius steindachneri</i>	Eastern Pacific	26	
Chaetodontidae	<i>Chaetodon capistratus</i>	Caribbean	21	Omnivore benthic
	<i>Chaetodon ocellatus</i>	Caribbean	21	
	<i>Chaetodon humeralis</i>	Eastern Pacific	32	
	<i>Chaetodon striatus</i>	Caribbean	20	
	<i>Johnrandallia nigrirostris</i>	Eastern Pacific	31	
Gerreidae	<i>Gerres cinereus</i>	Caribbean	20	Carnivore
	<i>Gerres similimus</i>	Eastern Pacific	17	
	<i>Eucinostomus melanopterus</i>	Eastern Pacific	18	
Haemulidae	<i>Anisotremus caesius</i>	Eastern Pacific		Carnivore
	<i>Anisotremus taeniatus</i>	Eastern Pacific	9	
	<i>Anisotremus virginicus</i>	Caribbean	19	
Pomacanthidae	<i>Holacanthus bermudensis</i>	Caribbean		Omnivore benthic
	<i>Holacanthus ciliaris</i>	Caribbean	4	
	<i>Holacanthus passer</i>	Eastern Pacific	26	
	<i>Pomacanthus paru</i>	Caribbean	2	
Pomacentridae	<i>Abudefduf concolor</i>	Eastern Pacific	29	Herbivore
	<i>Abudefduf taurus</i>	Caribbean	8	
	<i>Abudefduf saxatilis</i>	Caribbean	19	
	<i>Abudefduf troschelii</i>	Eastern Pacific	33	Planktivore
	<i>Chromis atrilobata</i>	Eastern Pacific	28	
	<i>Chromis multilineata</i>	Caribbean	4	
	<i>Chromis cyanea</i>	Caribbean		
Serranidae	<i>Cephalopholis colonus</i>	Eastern Pacific	30	Planktivore
	<i>Cephalopholis furcifer</i>	Caribbean		
	<i>Cephalopholis fulva</i>	Caribbean		Carnivore

Sample types



16S rRNA
Earth Microbiome Project
protocols

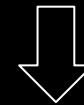
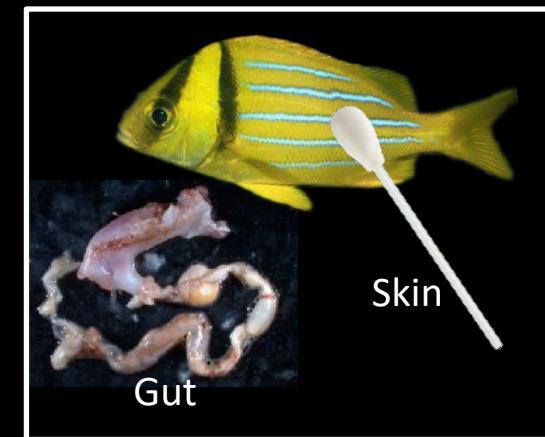
Sampling

Sampling locations

FAMILY	SPECIES	Ocean	NO. SPECIMENS collected to date	TROPHIC GROUP
Blenniidae	<i>Ophioblennius macclurei</i>	Caribbean	11	Herbivore
	<i>Ophioblennius steindachneri</i>	Eastern Pacific	26	
Chaetodontidae	<i>Chaetodon capistratus</i>	Caribbean	21	Omnivore benthic
	<i>Chaetodon ocellatus</i>	Caribbean	21	
	<i>Chaetodon humeralis</i>	Eastern Pacific	32	
	<i>Chaetodon striatus</i>	Caribbean	20	
	<i>Johnrandallia nigrirostris</i>	Eastern Pacific	31	
Gerreidae	<i>Gerres cinereus</i>	Caribbean	20	Carnivore
	<i>Gerres similimus</i>	Eastern Pacific	17	
	<i>Eucinostomus melanopterus</i>	Eastern Pacific	18	
Haemulidae	<i>Anisotremus caesius</i>	Eastern Pacific		Carnivore
	<i>Anisotremus taeniatus</i>	Eastern Pacific	9	
	<i>Anisotremus virginicus</i>	Caribbean	19	
Pomacanthidae	<i>Holacanthus bermudensis</i>	Caribbean		Omnivore benthic
	<i>Holacanthus ciliaris</i>	Caribbean	4	
	<i>Holacanthus passer</i>	Eastern Pacific	26	
	<i>Pomacanthus paru</i>	Caribbean	2	
Pomacentridae	<i>Abudefduf concolor</i>	Eastern Pacific	29	Herbivore
	<i>Abudefduf taurus</i>	Caribbean	8	
	<i>Abudefduf saxatilis</i>	Caribbean	19	
	<i>Abudefduf troschelii</i>	Eastern Pacific	33	Planktivore
	<i>Chromis atrilobata</i>	Eastern Pacific	28	
	<i>Chromis multilineata</i>	Caribbean	4	
	<i>Chromis cyanea</i>	Caribbean		
Serranidae	<i>Cephalopholis colonus</i>	Eastern Pacific	30	Planktivore
	<i>Cephalopholis furcifer</i>	Caribbean		
	<i>Cephalopholis fulva</i>	Caribbean		Carnivore

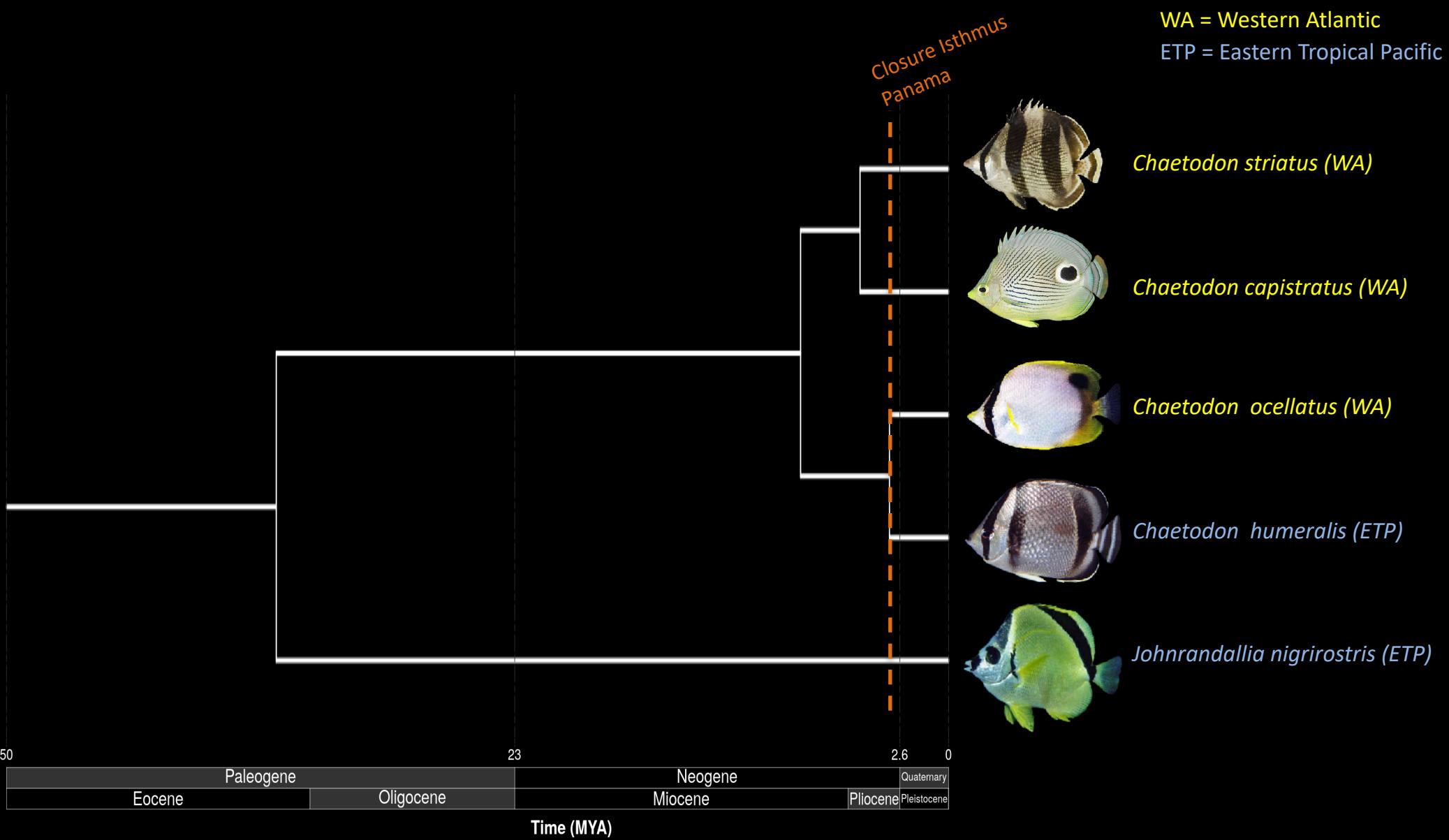


Sample types

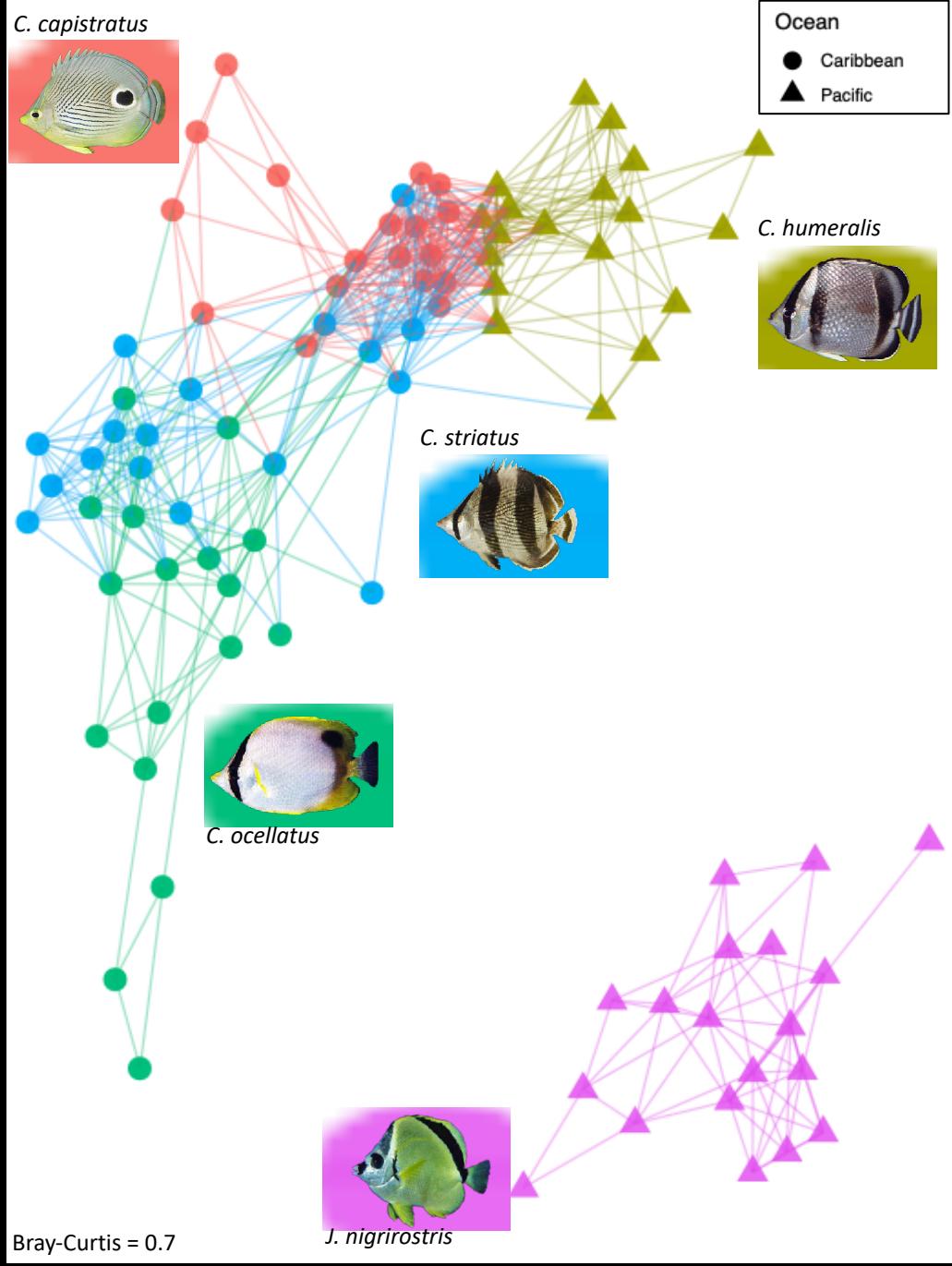


16S rRNA
Earth Microbiome Project
protocols

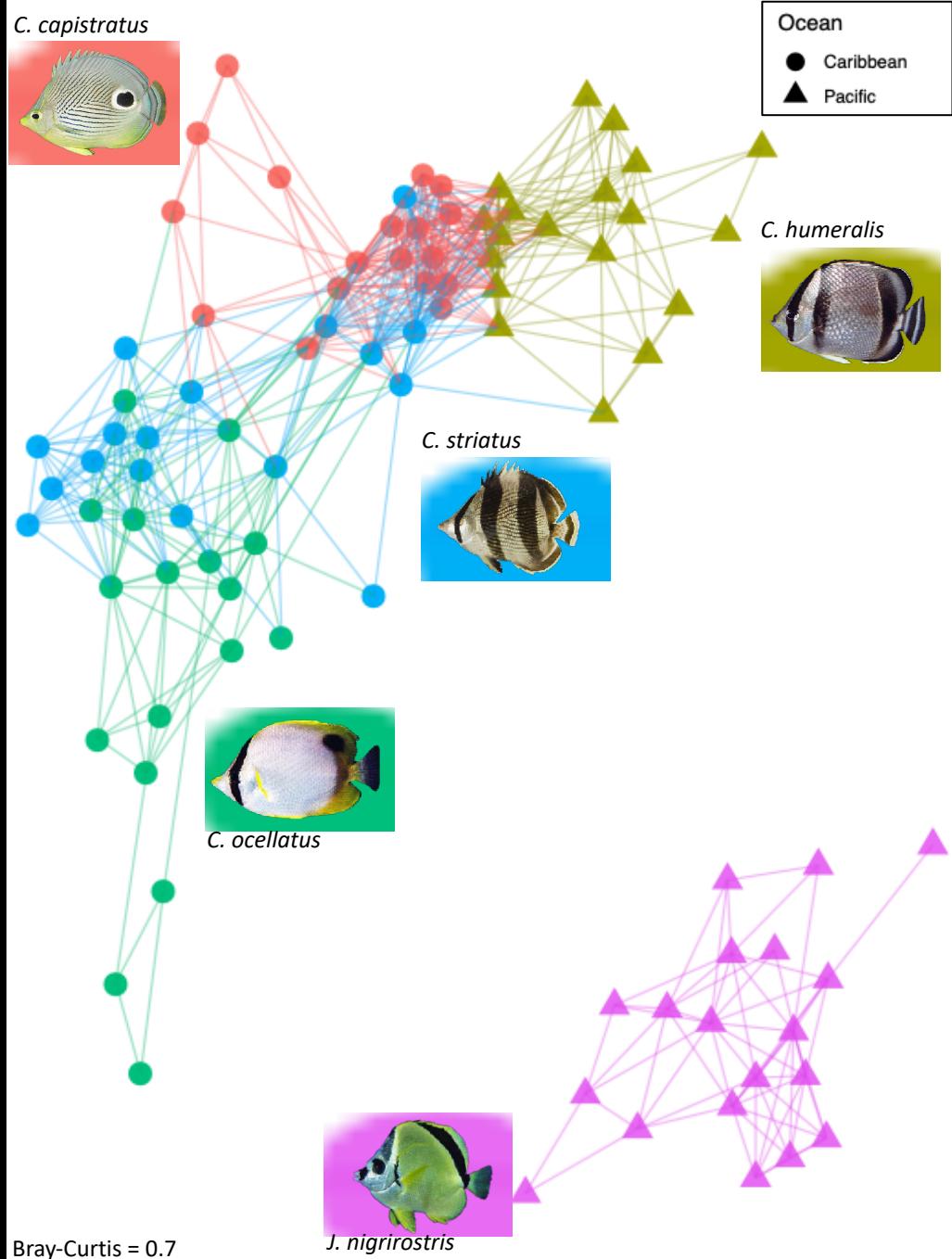
WA = Western Atlantic
ETP = Eastern Tropical Pacific



GUT MICROBIOME



GUT MICROBIOME



PERMANOVA

	Df	SumsSqs	R2	Pr(>F)
Ocean	1	4.207	11%	***
Species	4	8.624	23%	***
Resid.	90	24.781	66%	
Total	94	37.612	100%	

Phylosymbiosis? (=congruence between host phylogeny and microbiome similarity?)

Host tree

(based on molecular markers)

Gut microbiome

(UPGMA tree based on Bray Curtis distances of 16S rRNA ASVs)

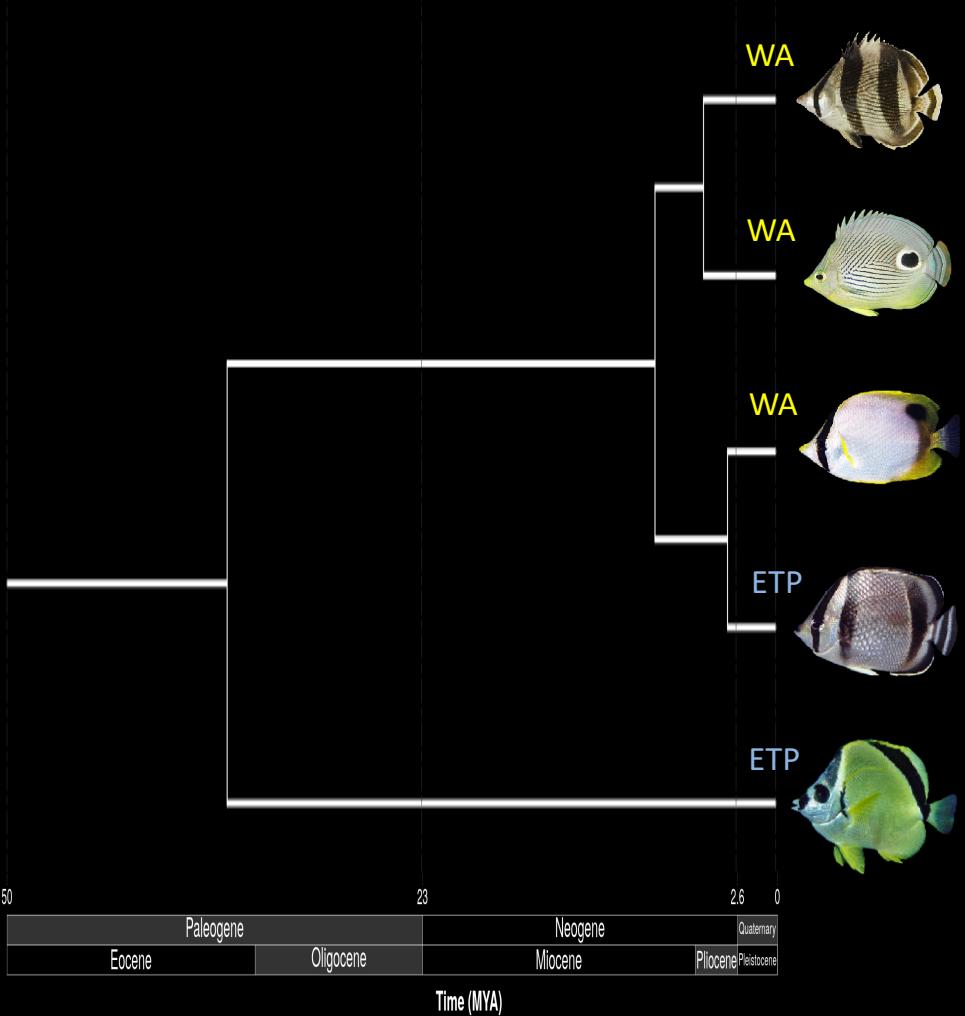
Phylosymbiosis?

WA = Western Atlantic

ETP = Eastern Tropical Pacific

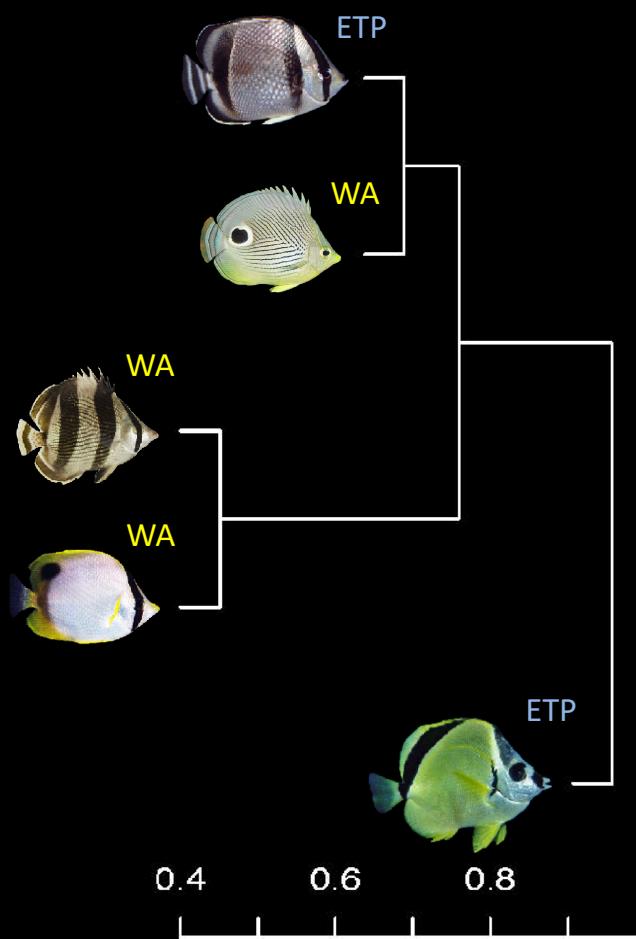
Host tree

(based on molecular markers)



Gut microbiome

(UPGMA tree based on Bray Curtis distances of 16S rRNA ASVs)

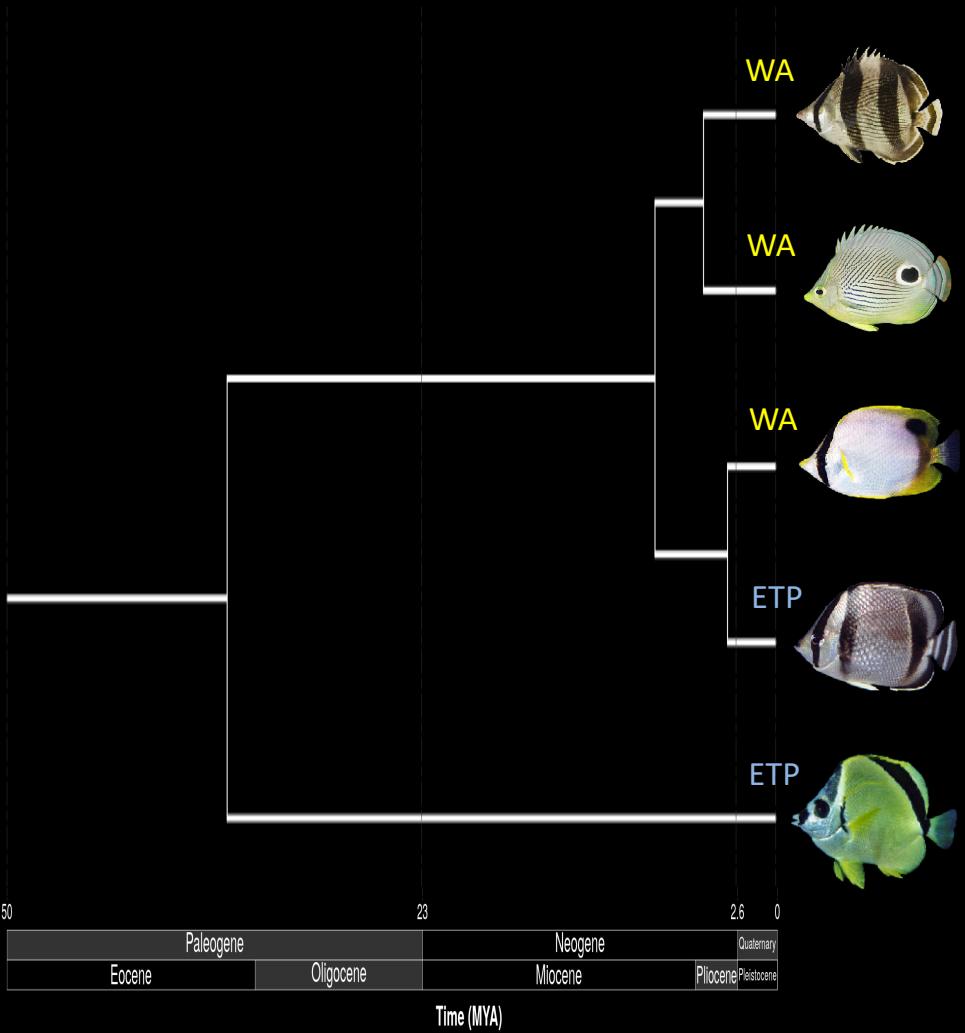


Phylosymbiosis?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

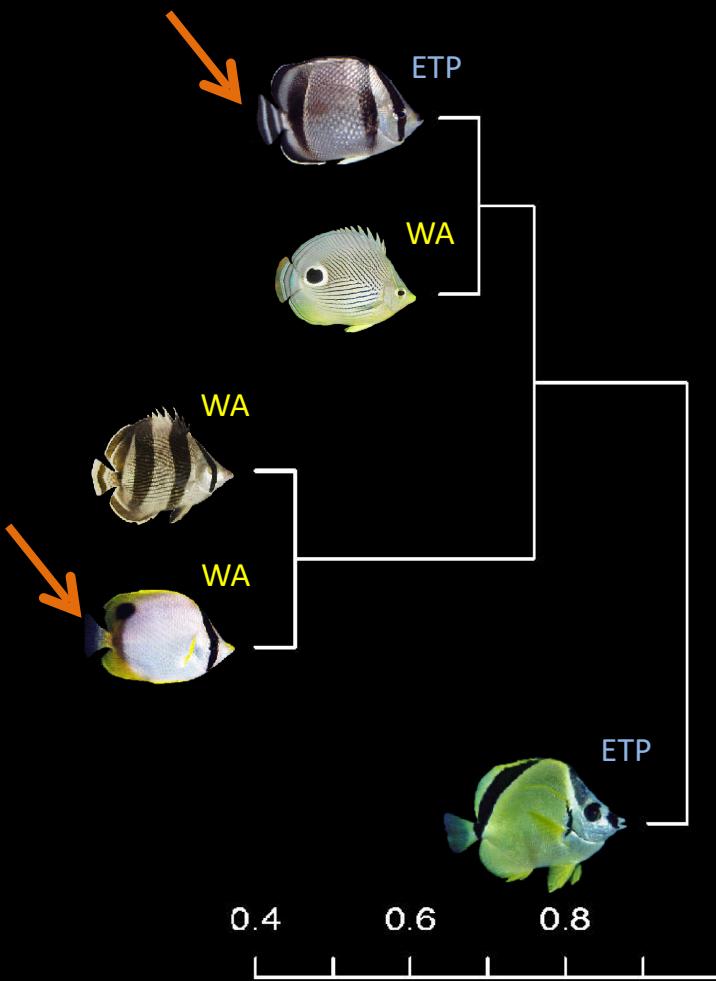
Host tree

(based on molecular markers)



Gut microbiome

(UPGMA tree based on Bray Curtis distances of 16S rRNA ASVs)

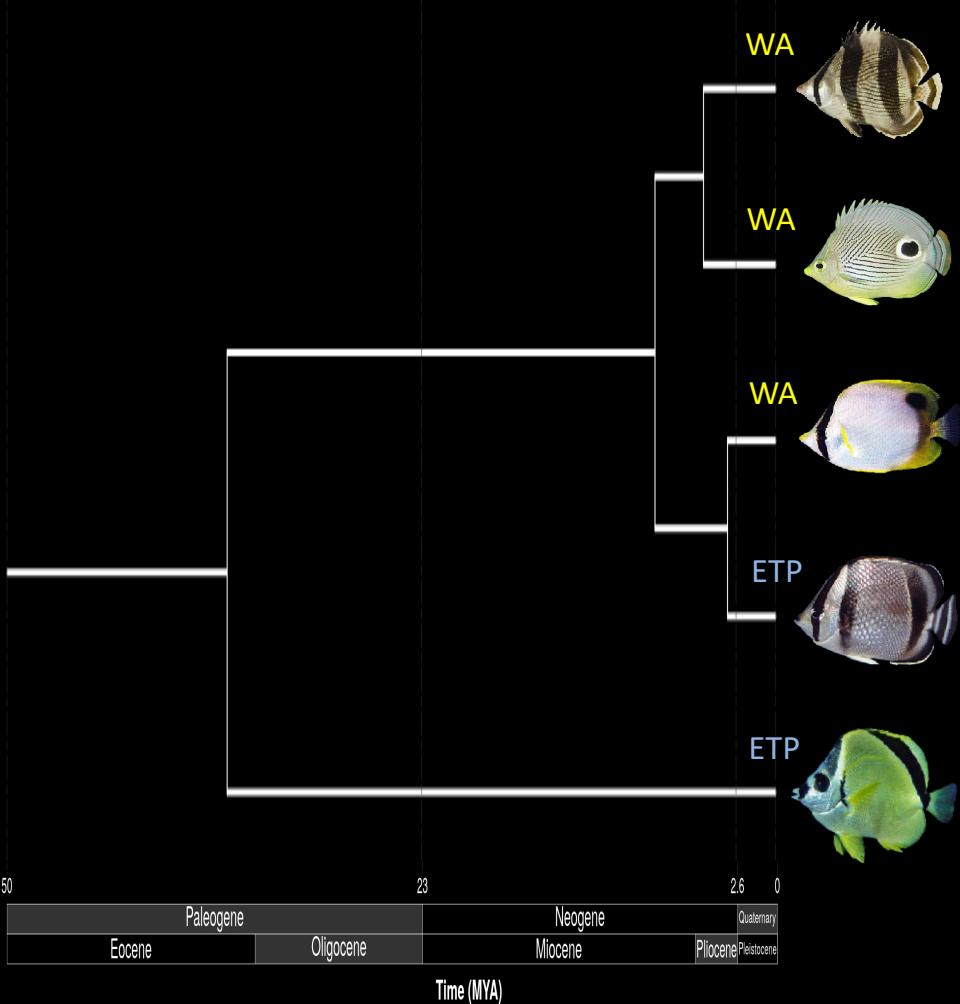


Phylos~~x~~ymbiosis?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

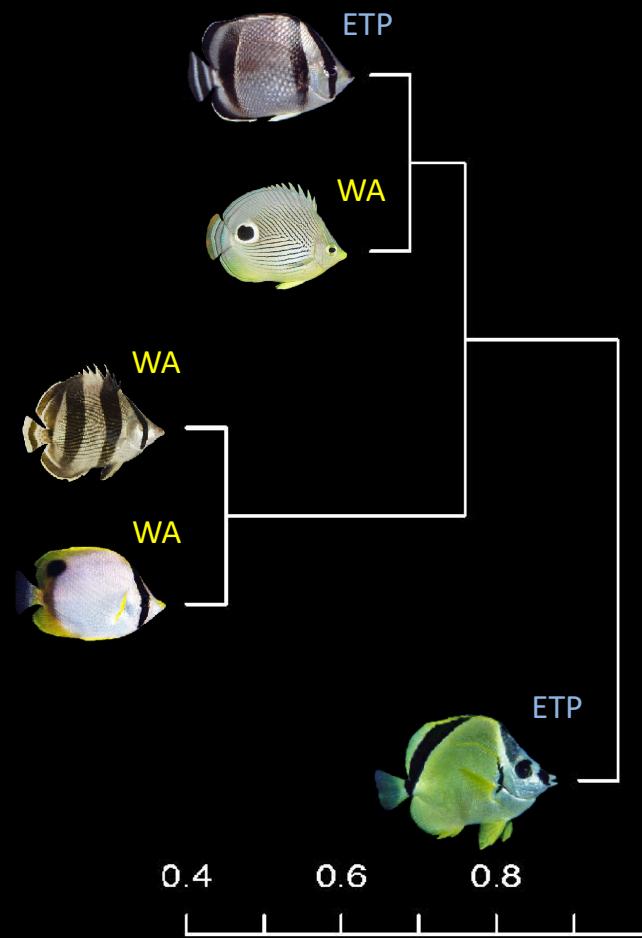
Host tree

(based on molecular markers)



Gut microbiome

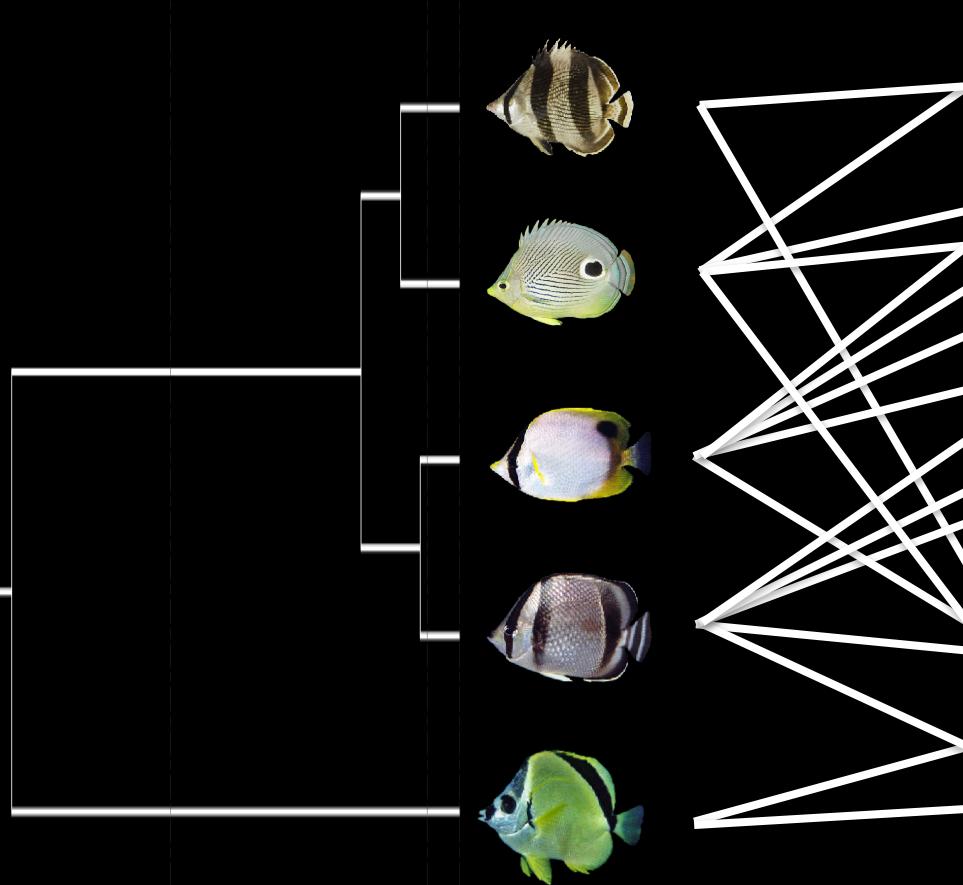
(UPGMA tree based on Bray Curtis distances of 16S rRNA ASVs)



→ Community similarity of gut microbiome does not mirror host phylogeny

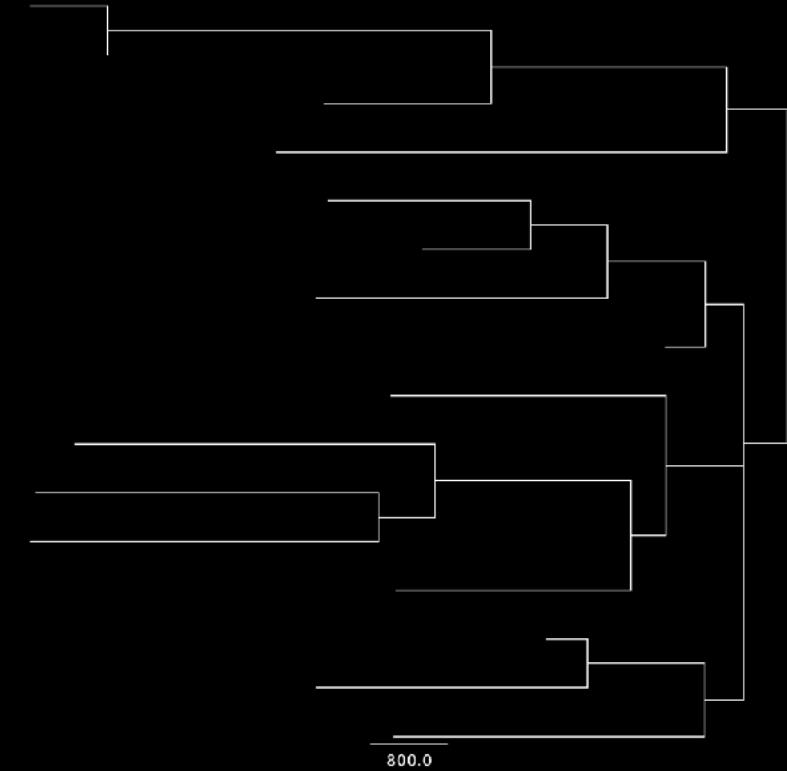
Cophylogeny?

Host tree



Bacterial trees

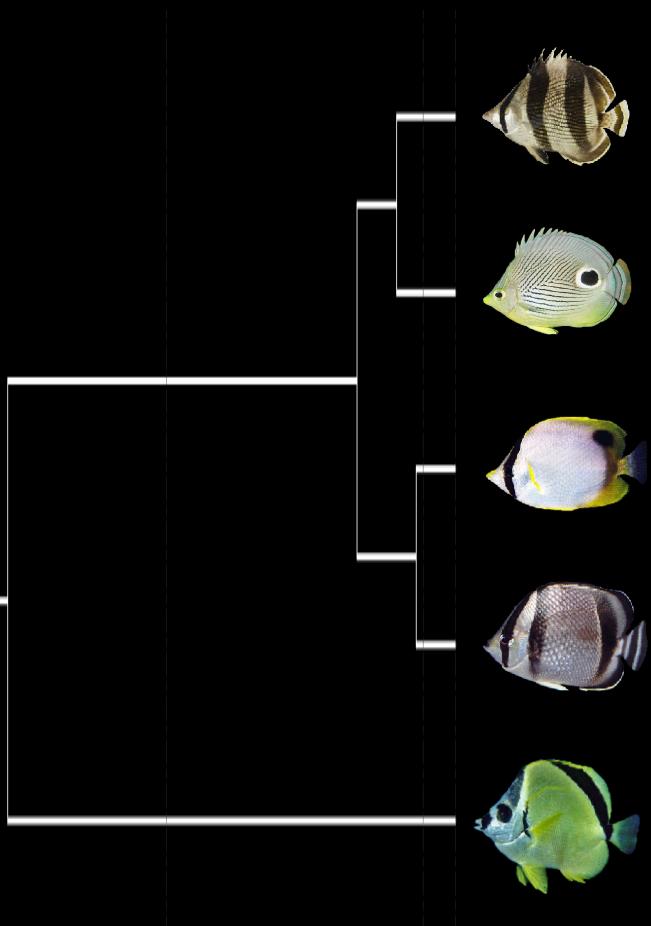
e.g., genus *Coxiella*



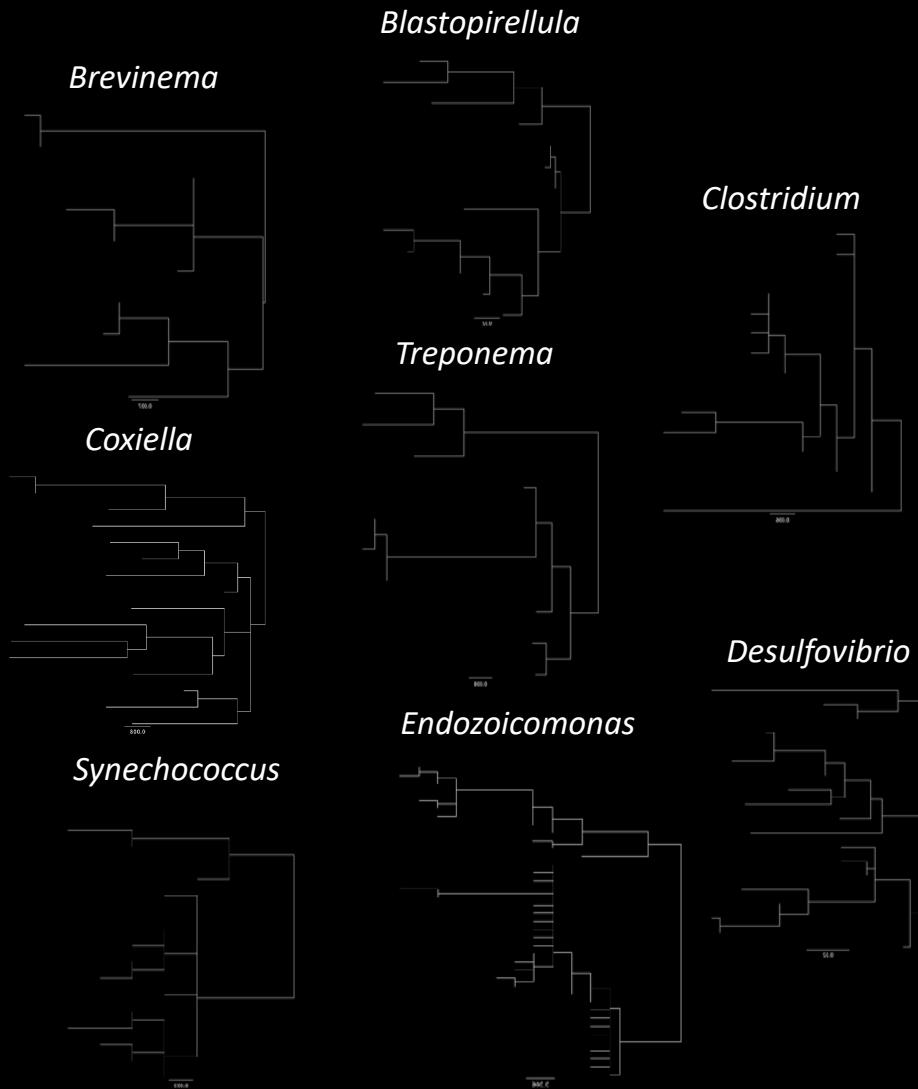
Is at least some part of the bacteria phylogeny
constrained by the one of the host?

Cophylogeny?

Host tree



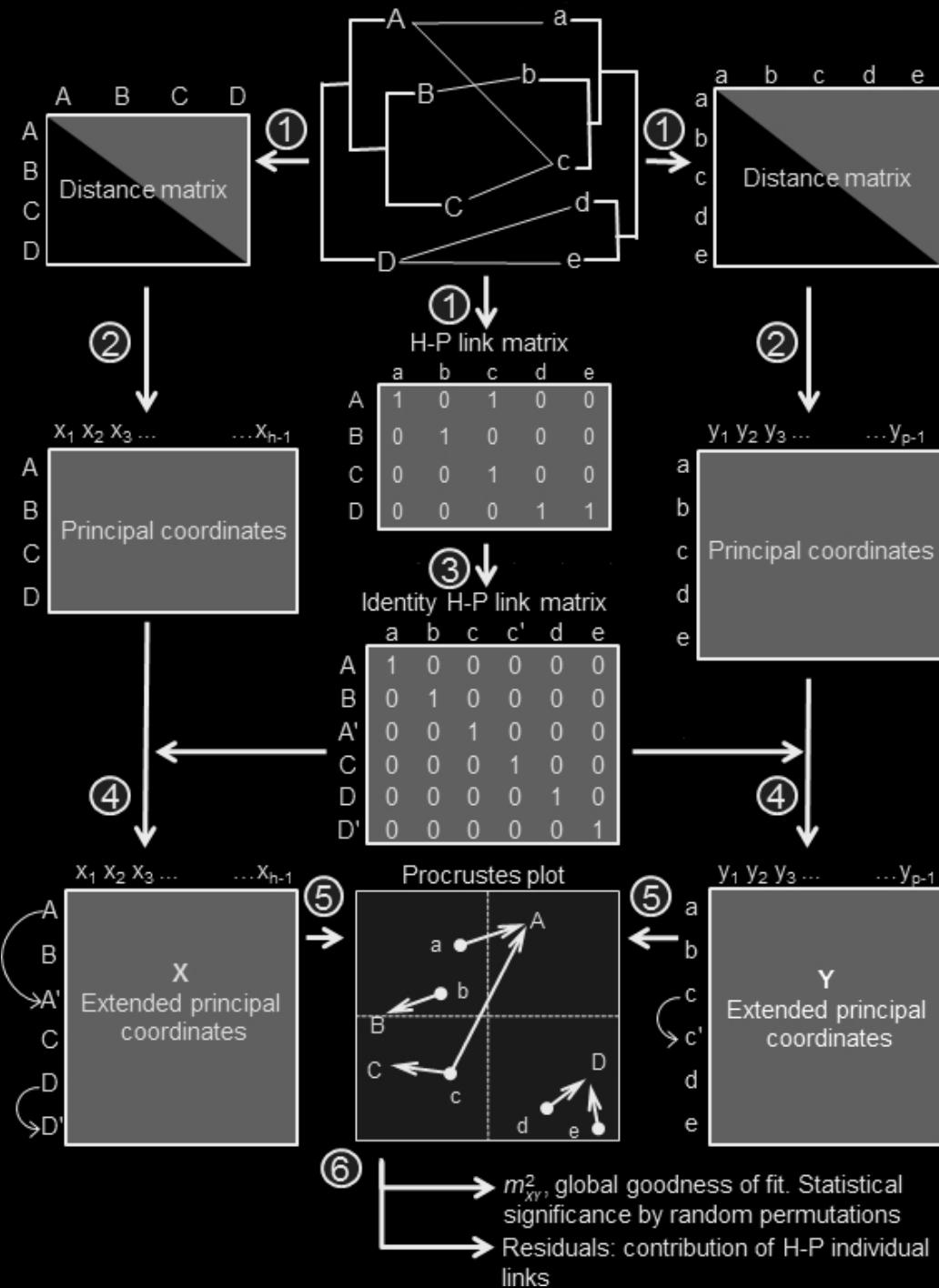
Bacterial trees





Procrustes Approach to Cophylogeny

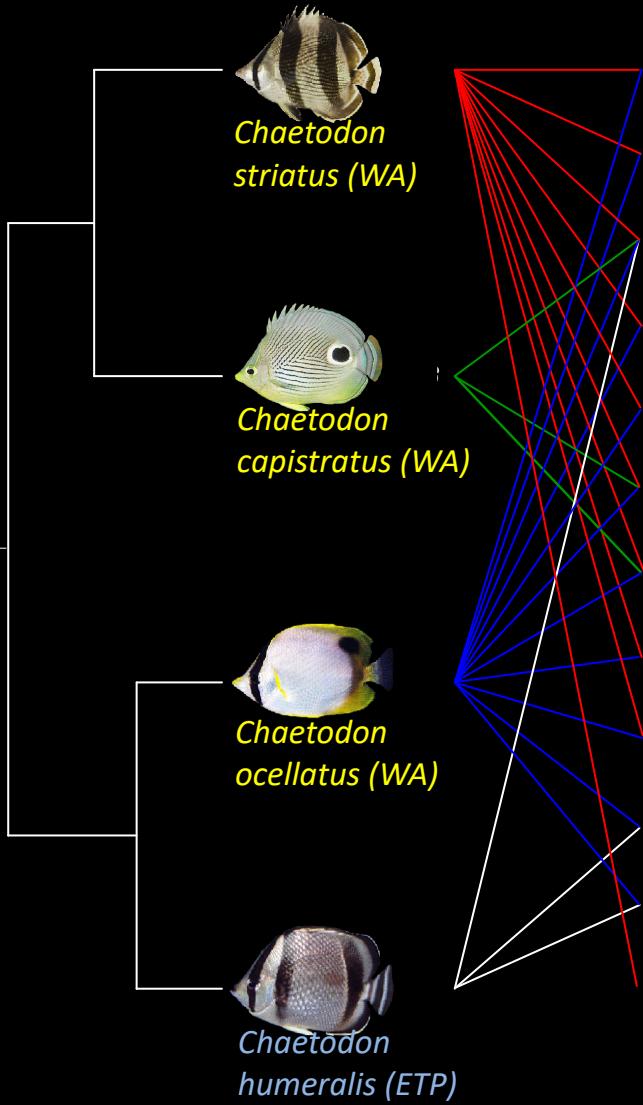
Global-fit method
 quantify the degree of
 agreement between
 the topologies of
 phylogenetic trees



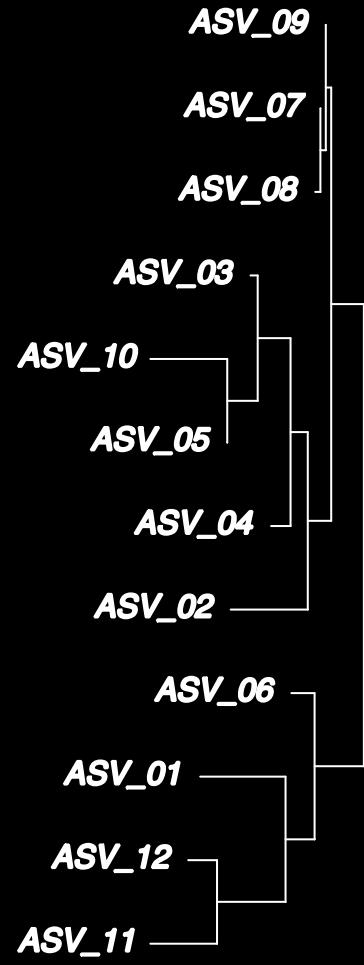
Cophylogeny?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Host tree



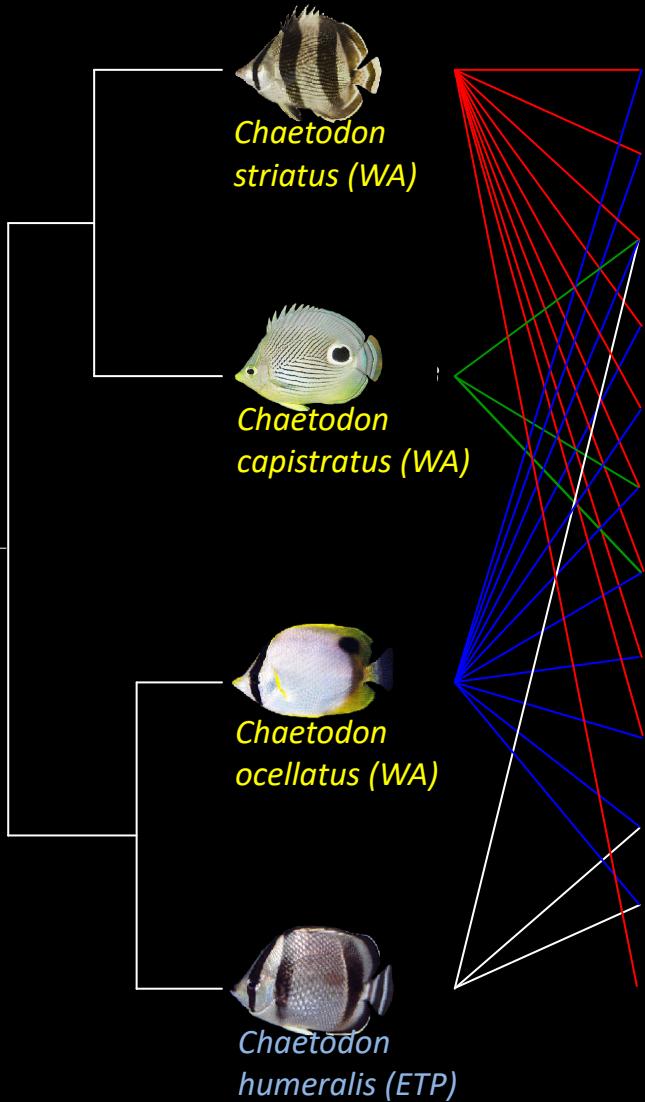
Blastopirellula 16S tree



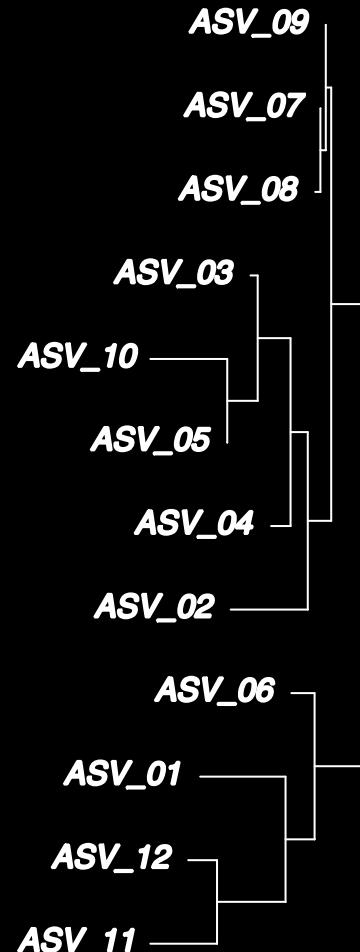
Cophylogeny?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Host tree



Blastopirellula 16S tree



Procrustes analysis

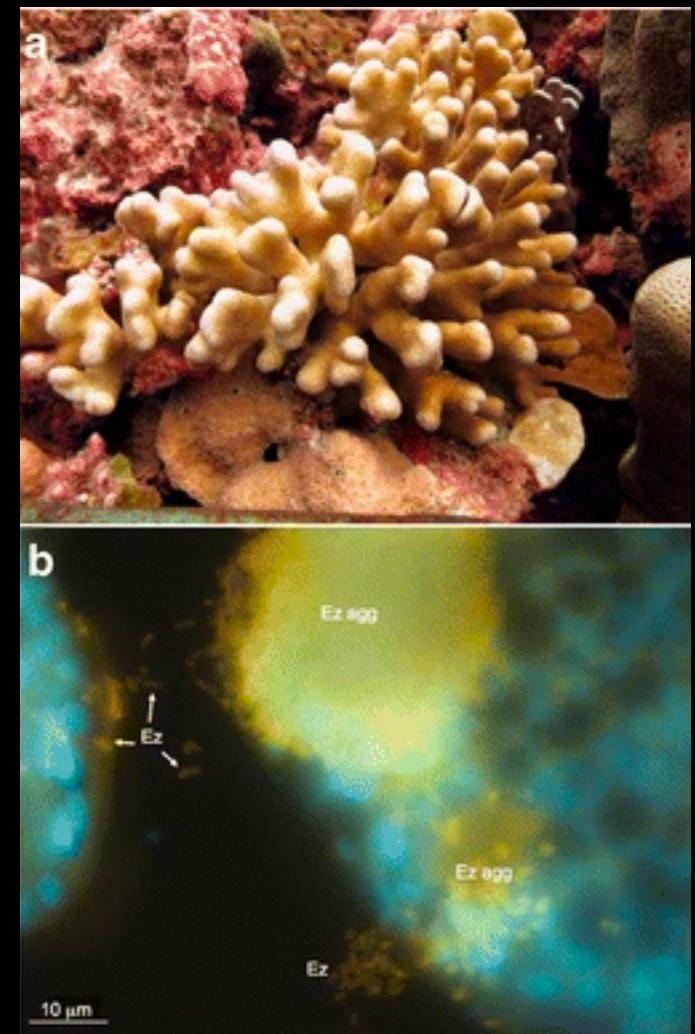
Param	<i>Endozoicomonas</i>
\$p	0.027*
\$ss	5765.733
\$n	1000

Significant co-divergence
between hosts and a
single genus of bacteria

Endozoicomonas -> a prevalent symbiotic marine bacteria

Suggested functions of *Endozoicomonas* bacteria:

Host organism	Suggested function	Reference
Fish	Fish disease	(Mendoza et al. 2013 ; Katharios et al. 2015)
Sponge	Sponge health	(Gardères et al. 2015)
	Bromopyrrole production for feeding deterrence	(Haber and Ilan 2014)
	Carbohydrate fermentation/nitrate reduction	(Nishijima et al. 2013)
	Antibiotic production	(Rua et al. 2014)
Tunicate	Sulphur cycling/nutrient metabolism	(Dishaw et al. 2014)
Hydrothermal vent snail	Host nutrition/sulphur cycling or breakdown of organic compounds	(Beinart et al. 2014)
Hydrothermal polychaete	Methane cycling/food degradation	(Forget and Juniper 2013)
Scleractinian corals	Quorum-sensing molecules	(Bayer et al. 2013b)
	Microbiome structuring	(Jessen et al. 2013)
	Antimicrobial activity/N-acyl homoserine lactones	(Morrow et al. 2015)
	Coral health	(Meyer et al. 2014 ; Roder et al. 2015 ; Webster et al. 2016)
	Coral health and/or disease	(Ziegler et al. 2016)
	Protection from bleaching	(Pantos et al. 2015)
	Dimethylsulfoniopropionate (DMSP) metabolism/sulphur cycling	(Raina et al. 2009 ; Bourne et al. 2013 ; Correa et al. 2013)
	Carbohydrate metabolism/nutrient acquisition	(Correa et al. 2013 ; Morrow et al. 2015)
Octocoral (gorgonians)	Host health	(Vezzulli et al. 2013 ; Ransome et al. 2014)



Endozoicomonas -> a prevalent symbiotic marine bacteria

ARTICLE

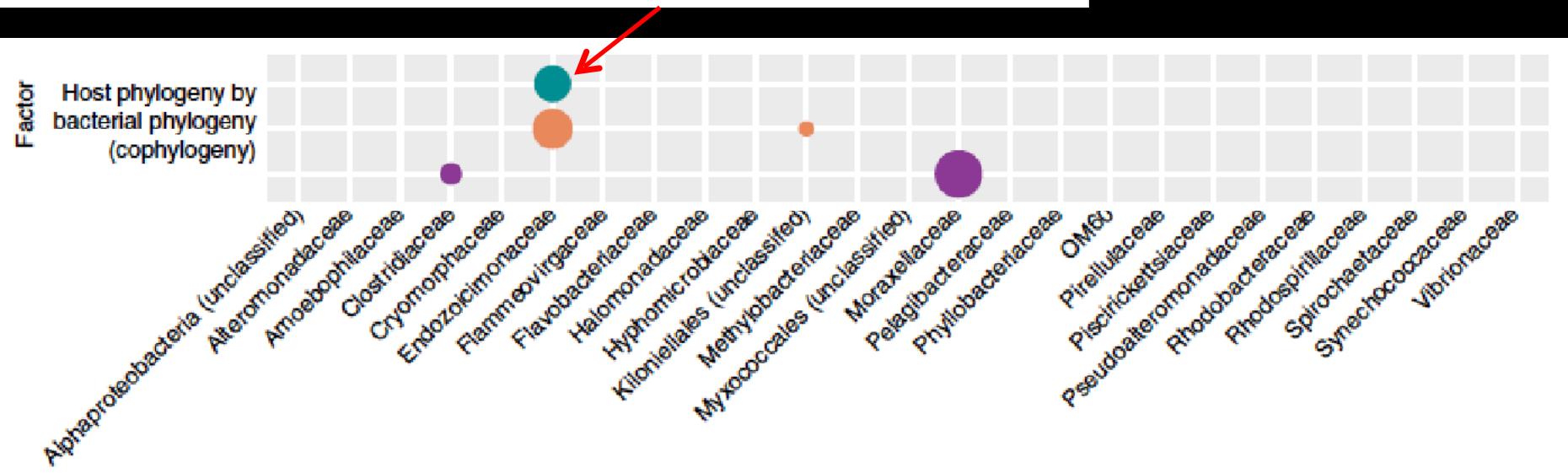
DOI: 10.1038/s41467-018-07275-x

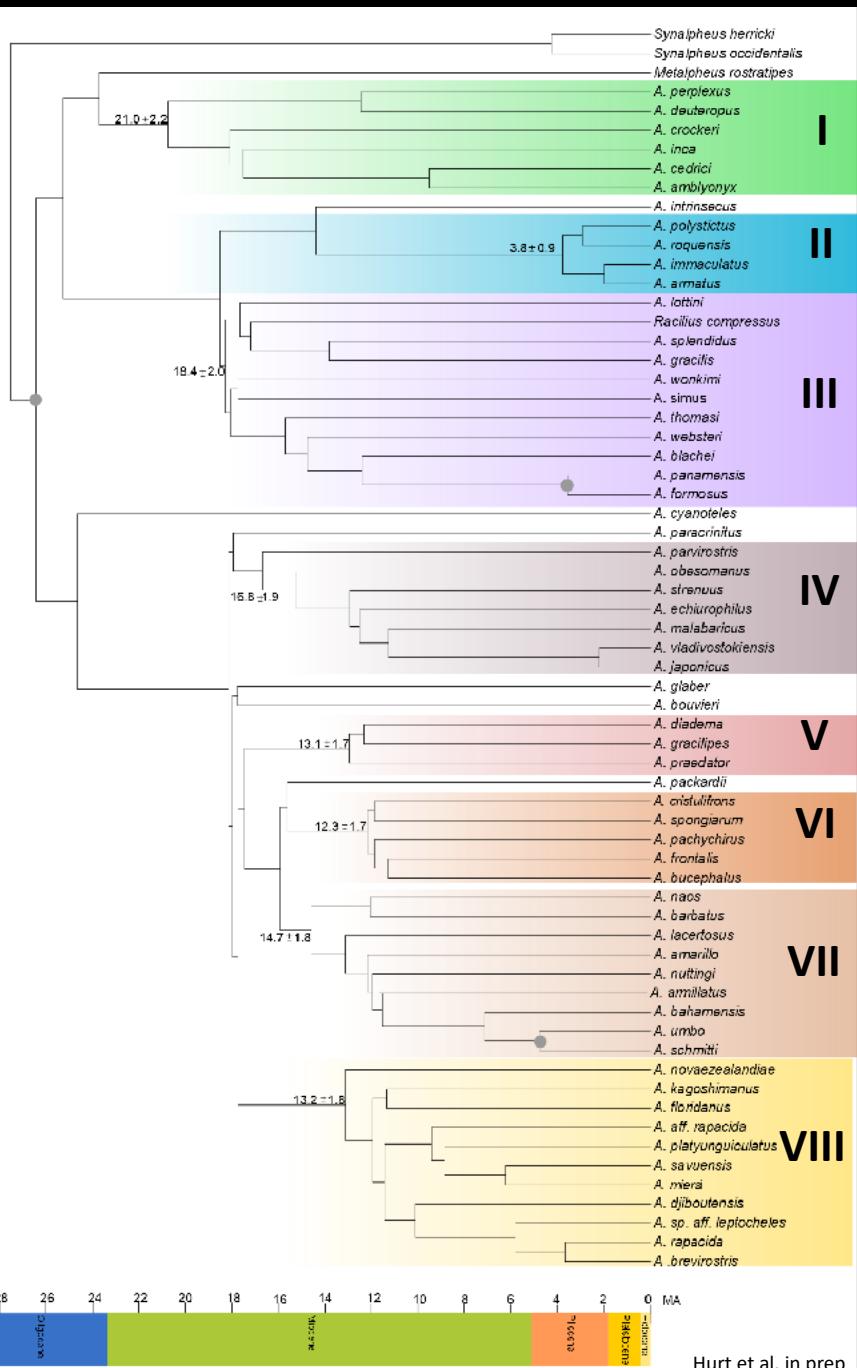
OPEN

Coral-associated bacteria demonstrate phylosymbiosis and cophylogeny

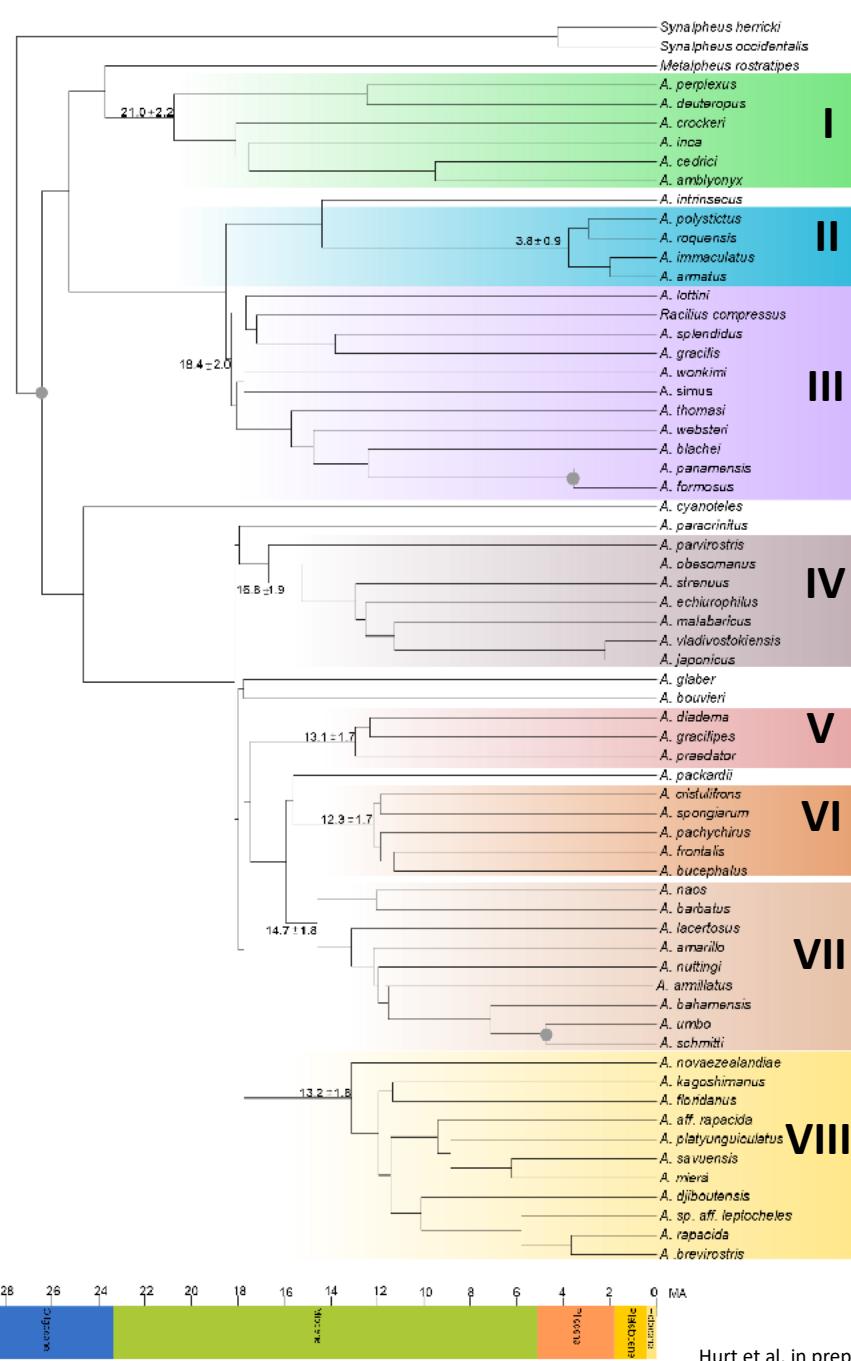
F. Joseph Pollock¹, Ryan McMinds², Styles Smith¹, David G. Bourne^{3,4}, Bette L. Willis^{3,5}, Mónica Medina^{1,6},
Rebecca Vega Thurber² & Jesse R. Zaneveld⁷

13/446 (3%) of genera in coral tissue
were associated with host phylogeny

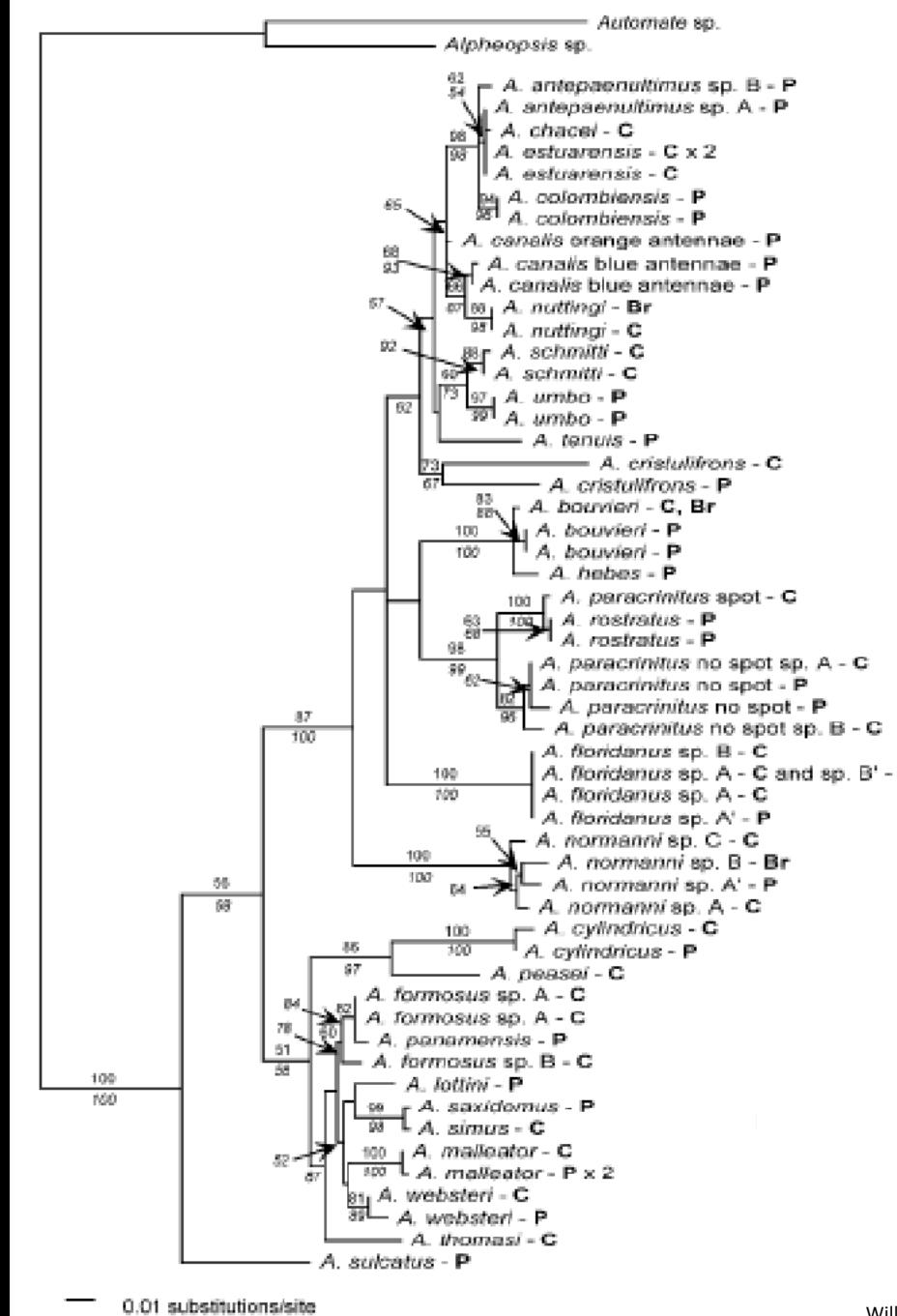




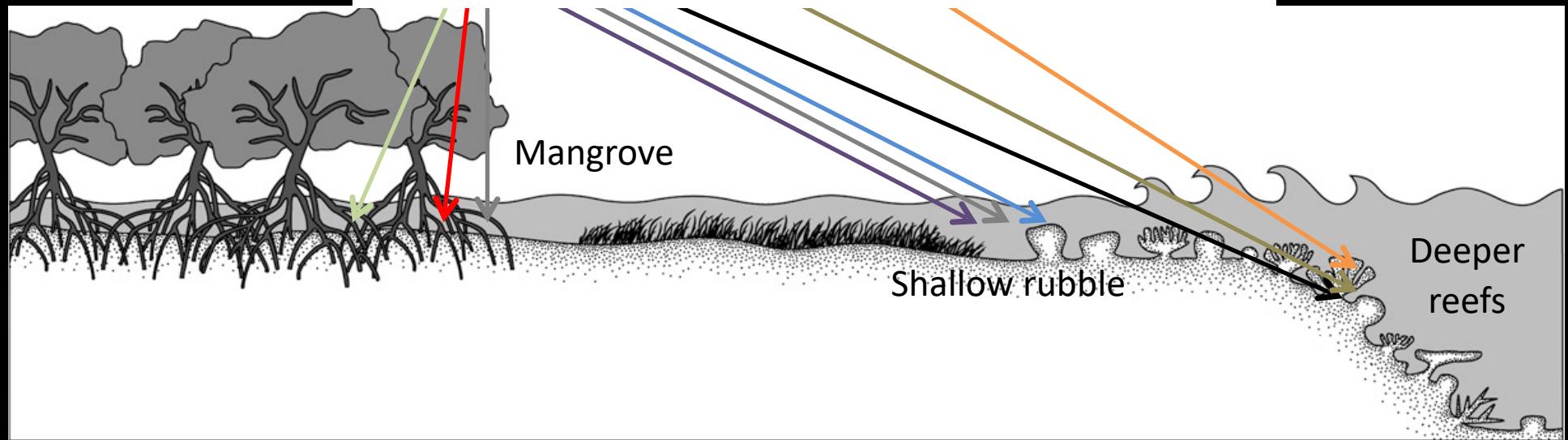
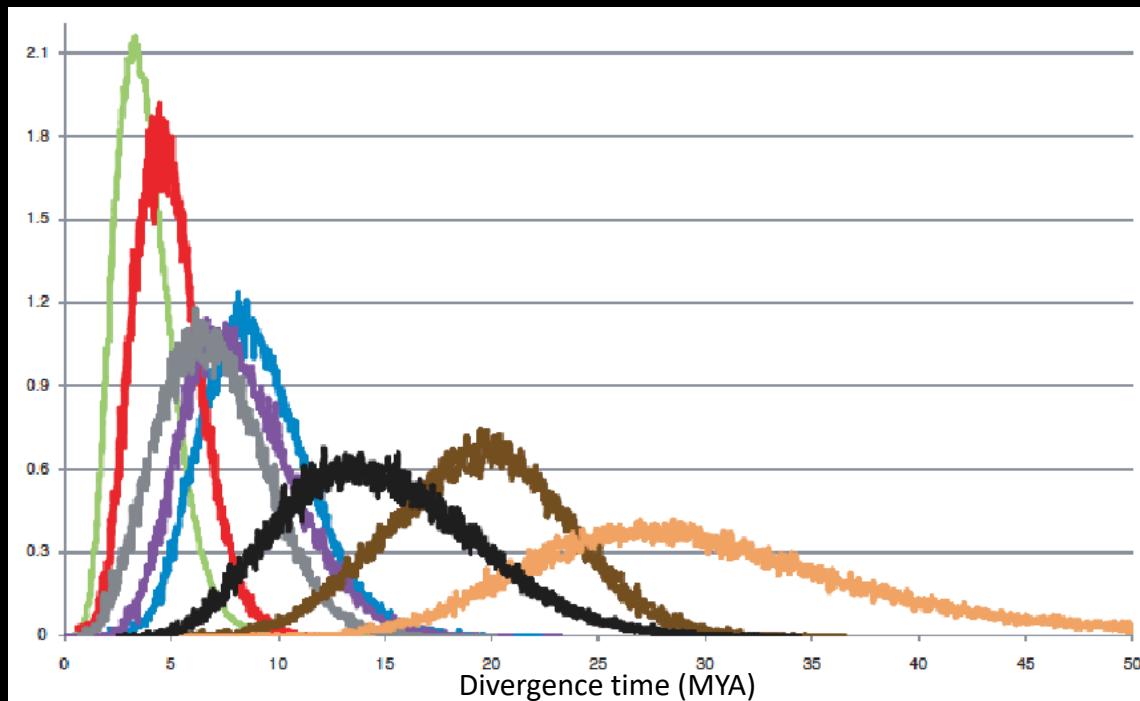
Backbone phylogenomic tree



Gene trees to resolve the tips



“Staggered evolution” Knowlton et al 1993



Species that occur in shallow mangroves diverged last

Collections 2018/2019

Caribbean



Tropical
Eastern Pacific







2 new genera and 8 new species of shrimps



Pachelpheus pachyacanthus

Anker 2020 Zootaxa



Microprosthemella looensis

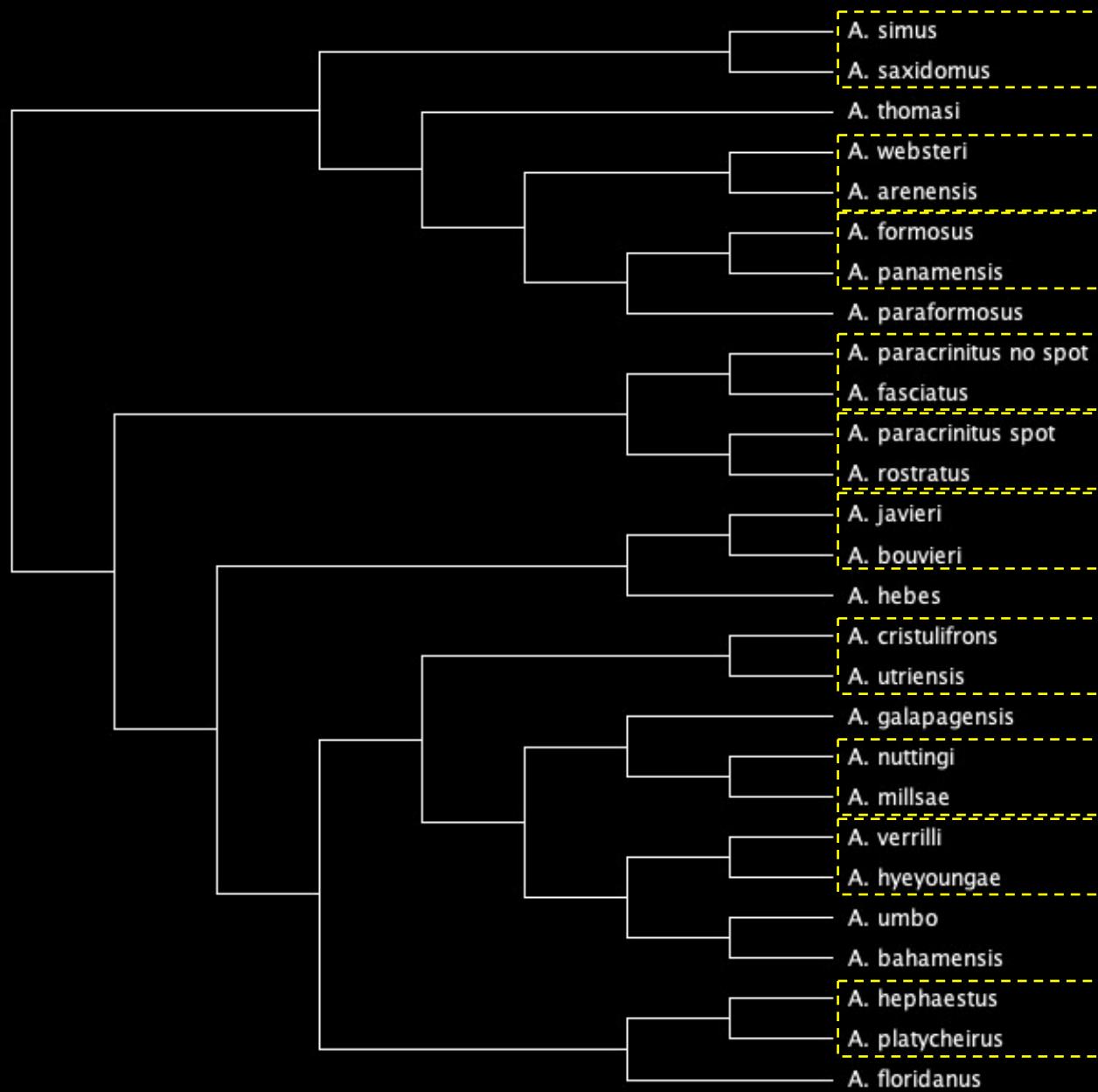
Azevedo Ferreira et al. 2020 Zootaxa



Unesconia coibensis

Anker 2020 Zootaxa

27 species across 6 major clades



Eastern Pacific



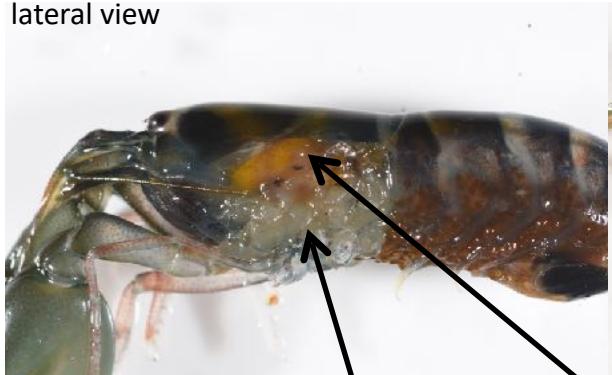
Caribbean



10 transisthmian pairs

Internal anatomy of *Alpheus javieri*

lateral view



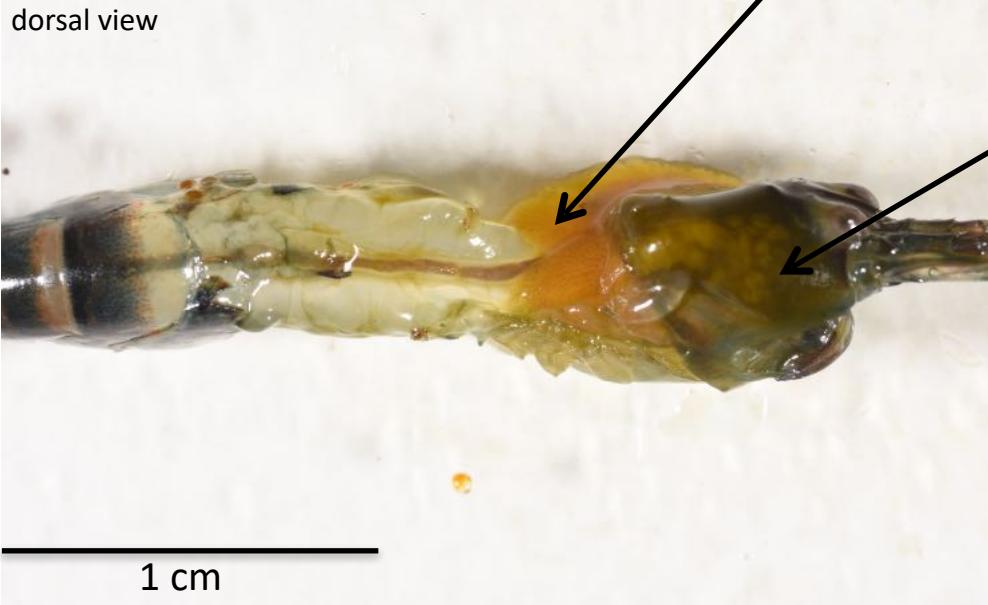
lateral view



dorsal view



dorsal view



dorsal view



Catalina
Rodriguez

Helio
Quintero



426 specimens
1799 tissues



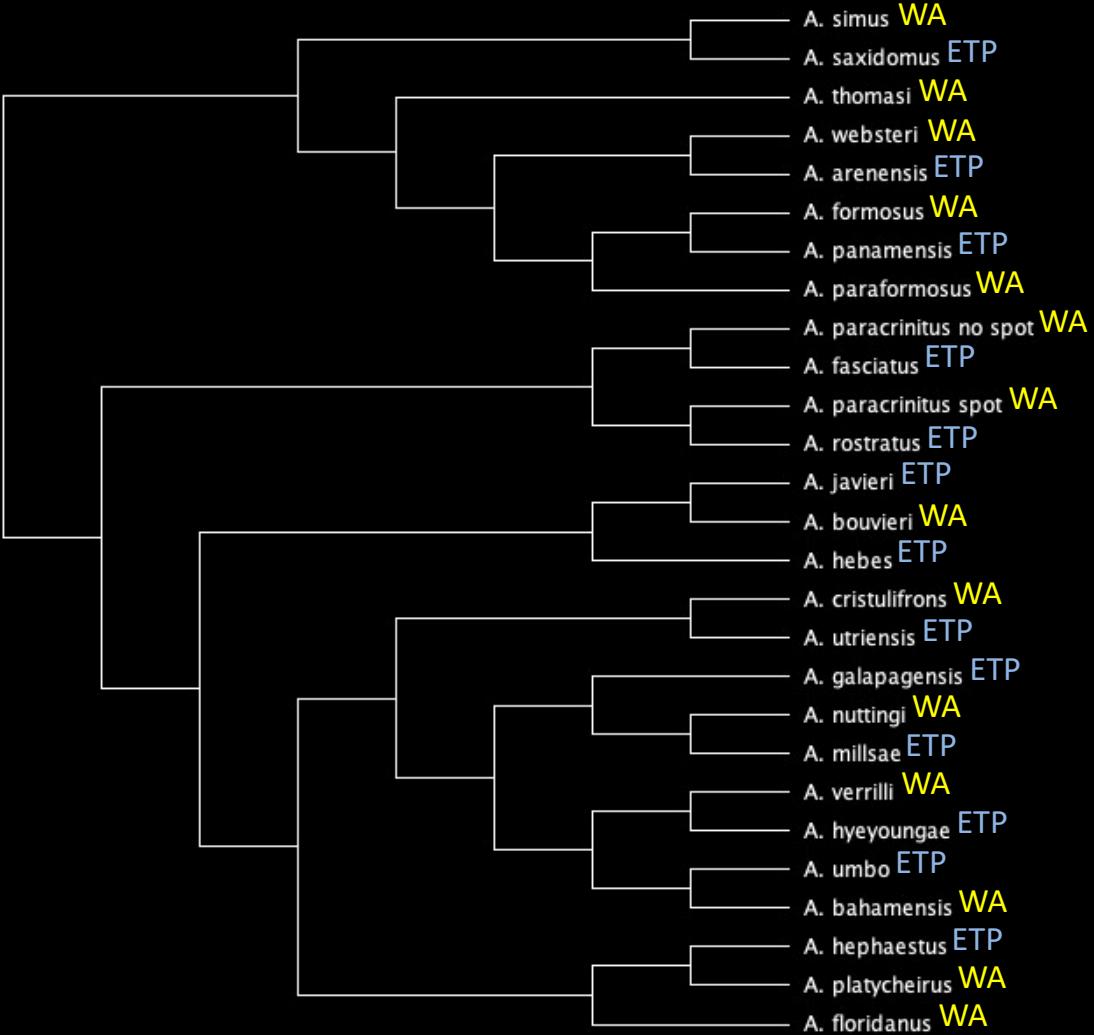
Phylosymbiosis?

WA = Western Atlantic

ETP = Eastern Tropical Pacific

Host tree

(based on molecular markers)



Midgut microbiome

(UPGMA tree based on Bray Curtis distances of 16S rRNA ASVs)

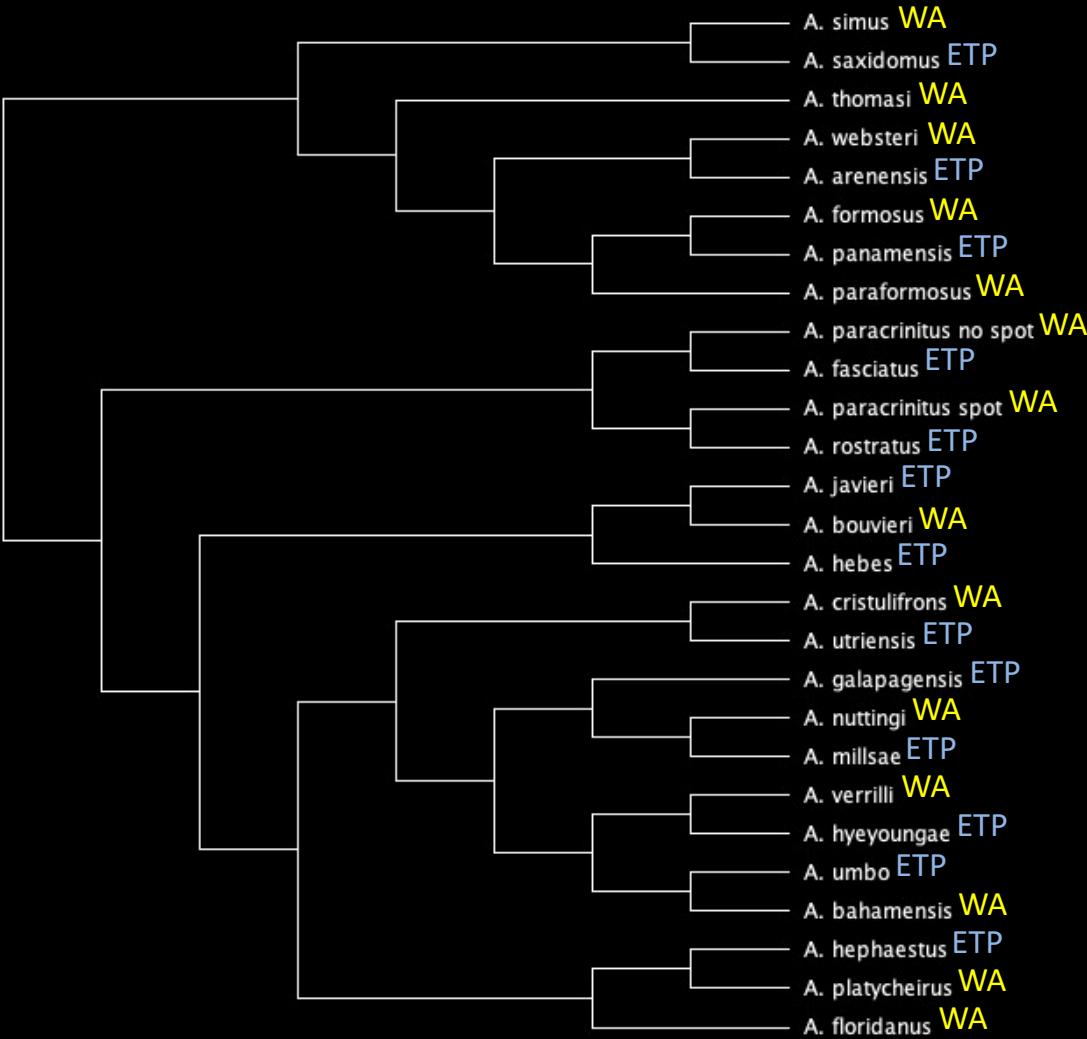


Phylos~~x~~biosis?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Host tree

(based on molecular markers)

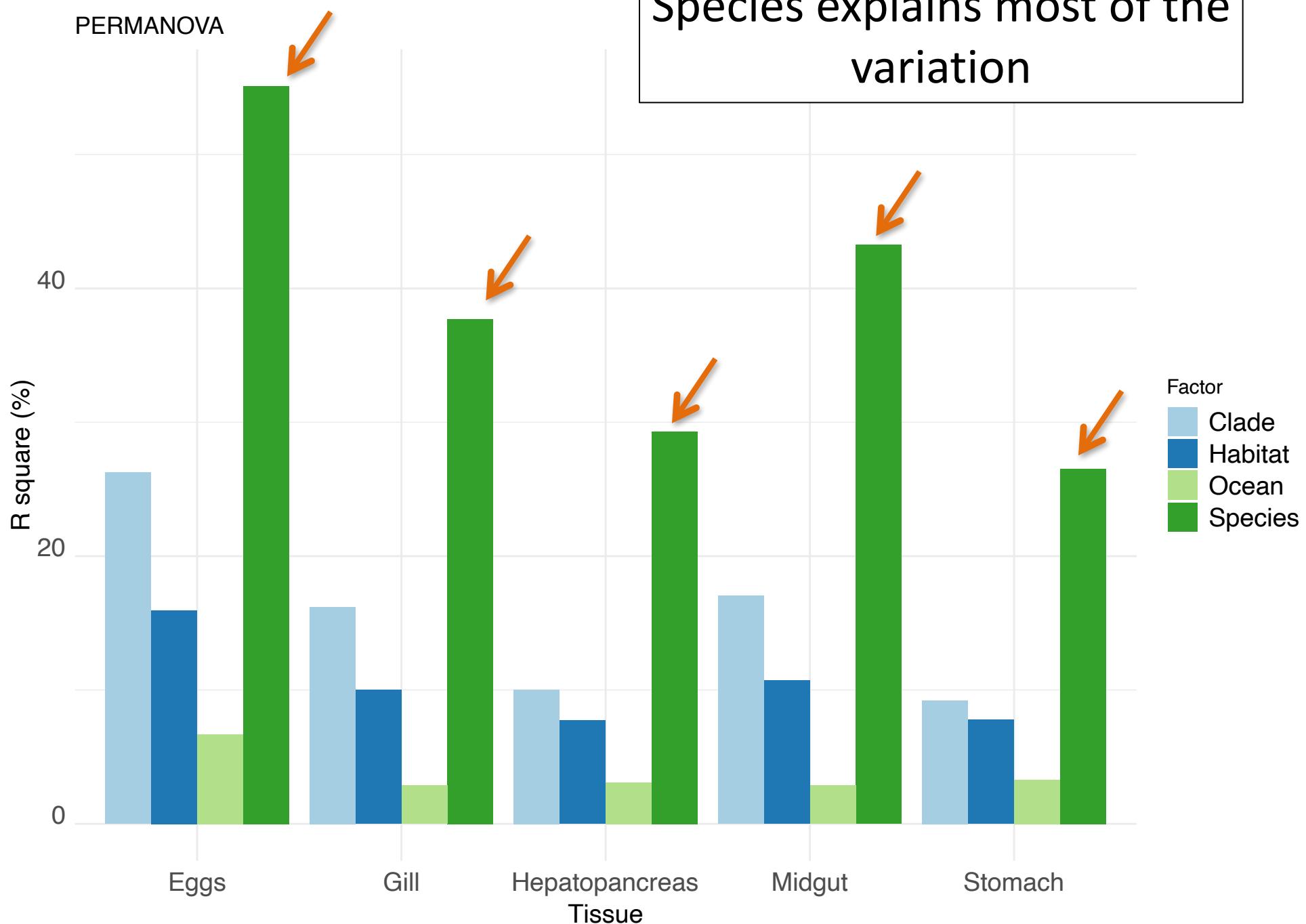


Midgut microbiome

(UPGMA tree based on Bray Curtis distances of 16S rRNA ASVs)



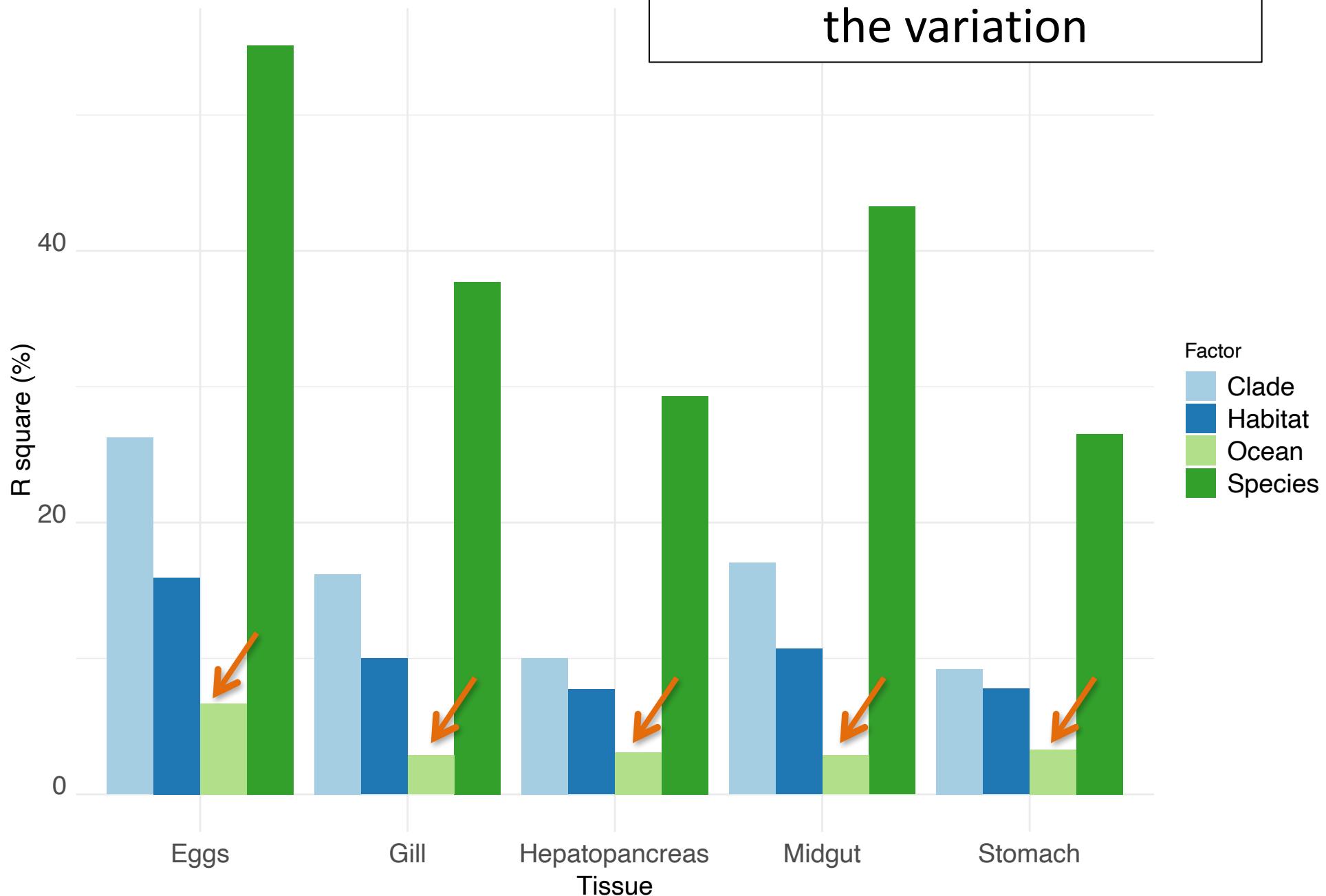
Variance explained



Variance explained

PERMANOVA

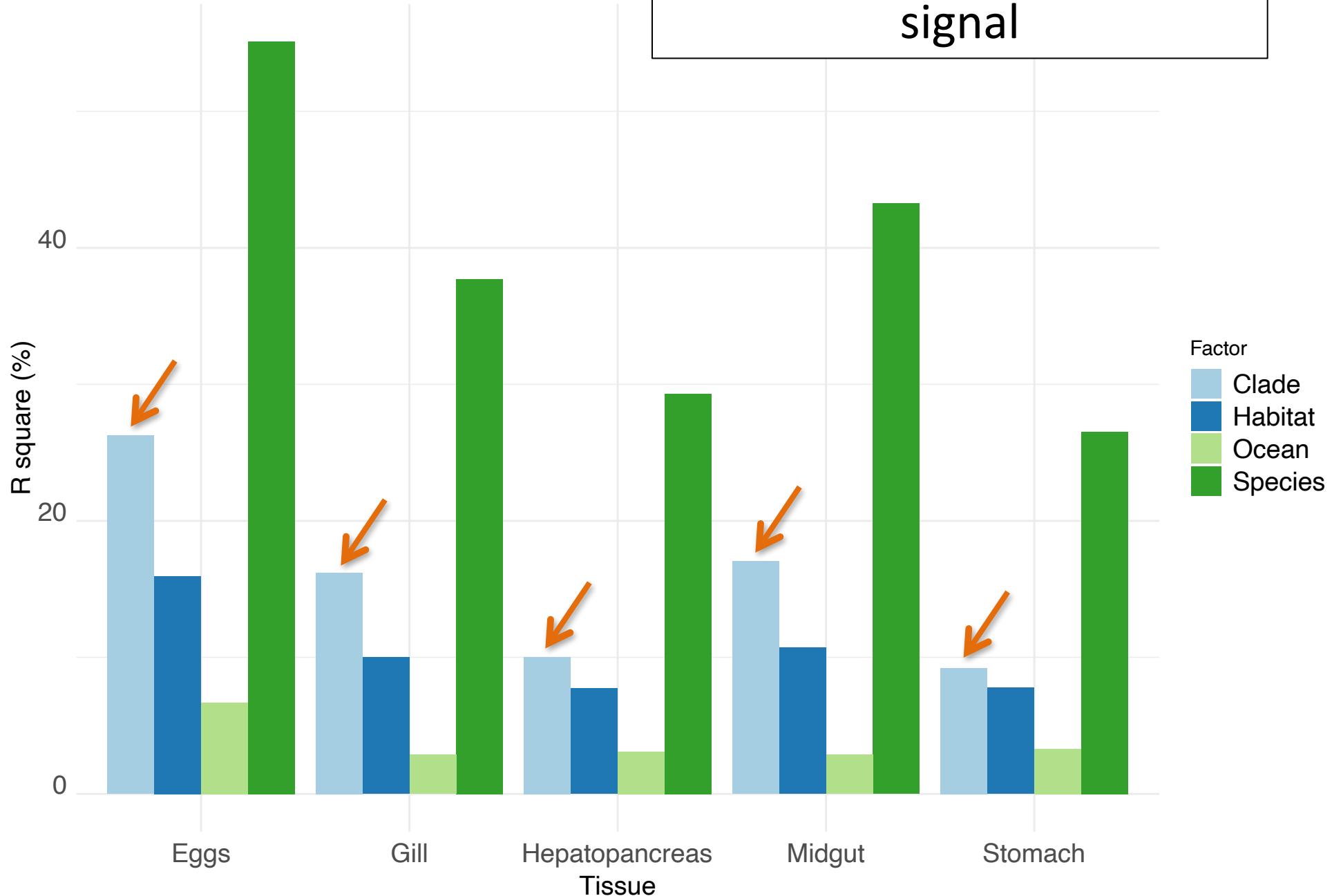
Ocean explains very little of
the variation



Variance explained

PERMANOVA

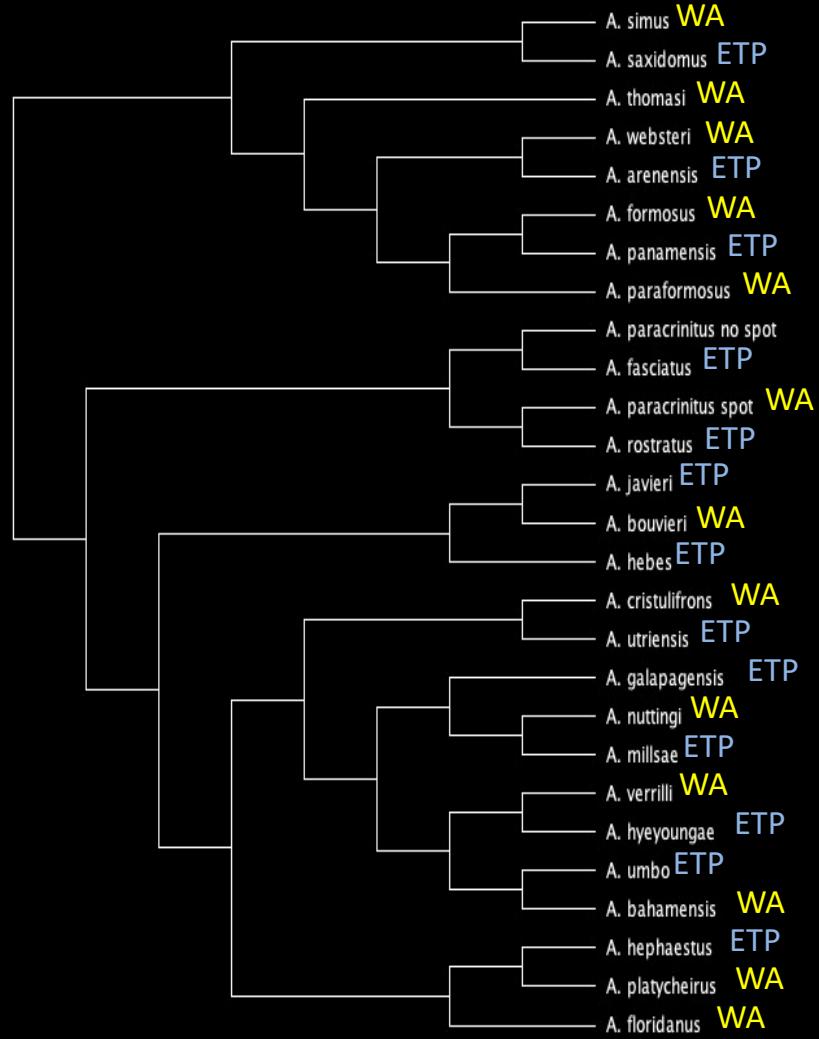
Significant phylogenetic signal



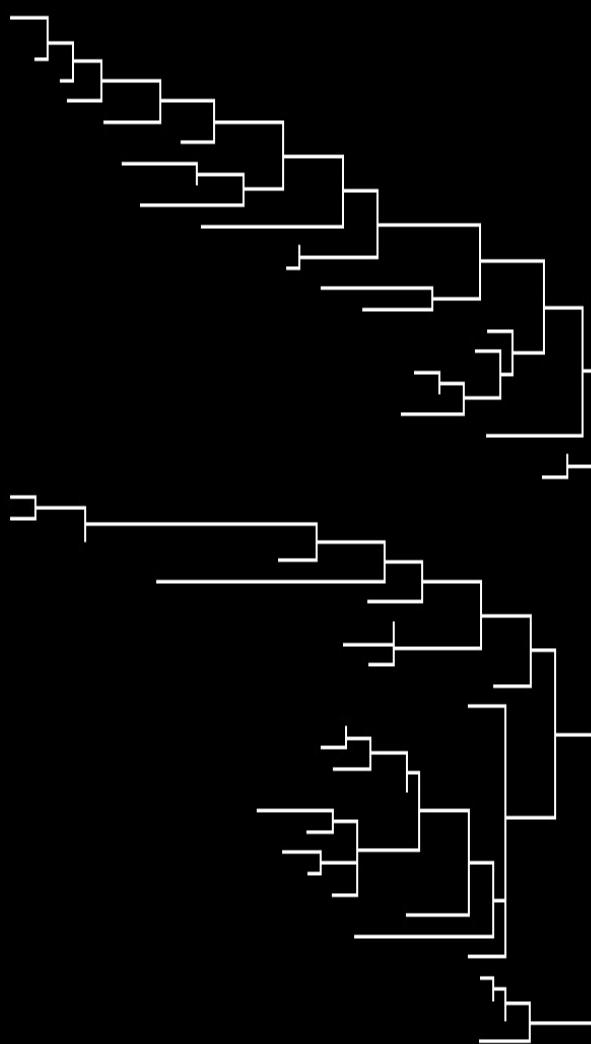
Cophylogeny?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Host tree



e.g., *Blastopirellula* 16S tree

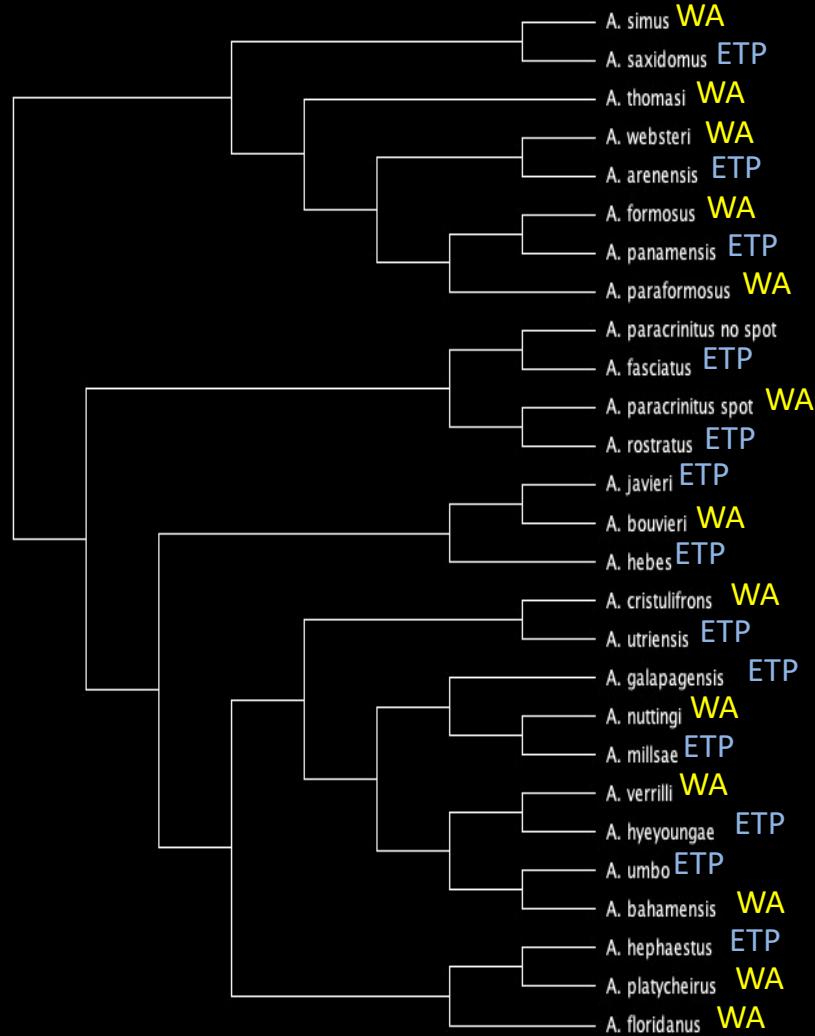


Cophylogeny?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Midgut microbiome

Host tree



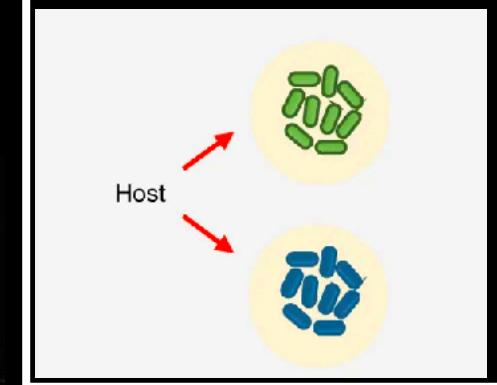
	p-value	sum of squares
Blastopirellula	0.608	0.9937207
Rhodopirellula	0.255	0.9816374
Vibrio	0.019*	0.9860958
Sva0996_marine_group	0.696	0.9810291
Pir4_lineage	0.162	0.9634625

Significant co-divergence
between hosts and a
single genus of bacteria

Lucinid clams



Host control



Laetitia Wilkins,
UC Davis

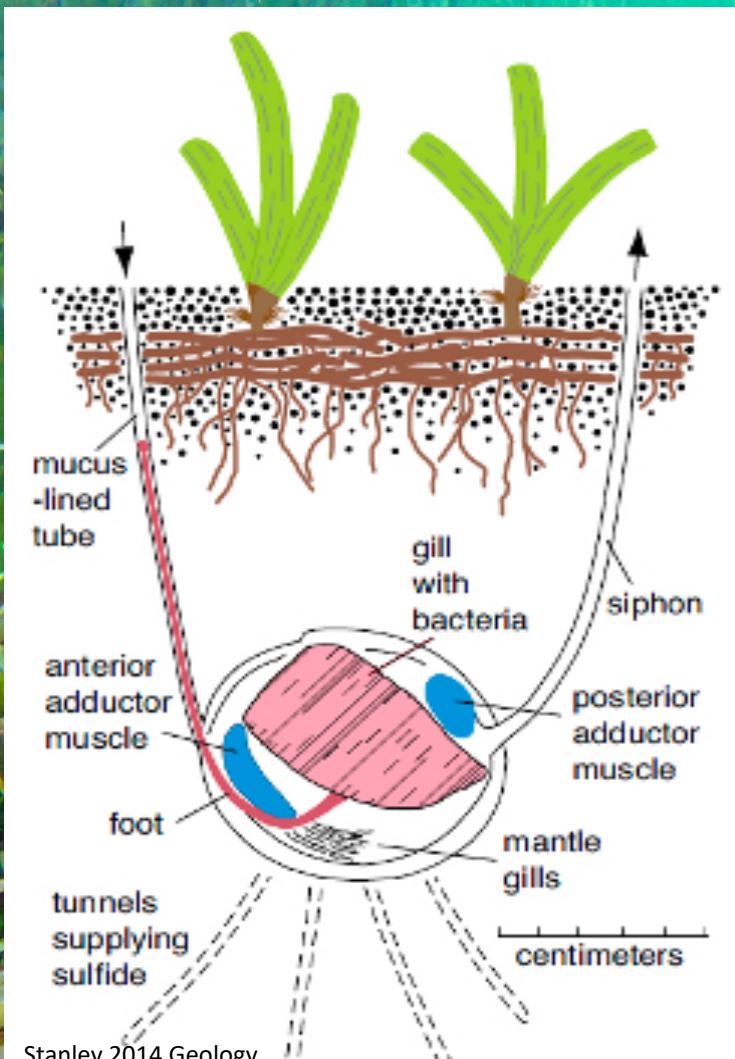
Jillian Petersen,
DOME Uni Vienna

THE SYSTEM

- ONE sulfur oxidizing symbiont per clam (symbiont in gill)
- Found in (sulfide rich) sediments under seagrass
- Symbiont acquired by settling larvae from sediment? Seagrass?



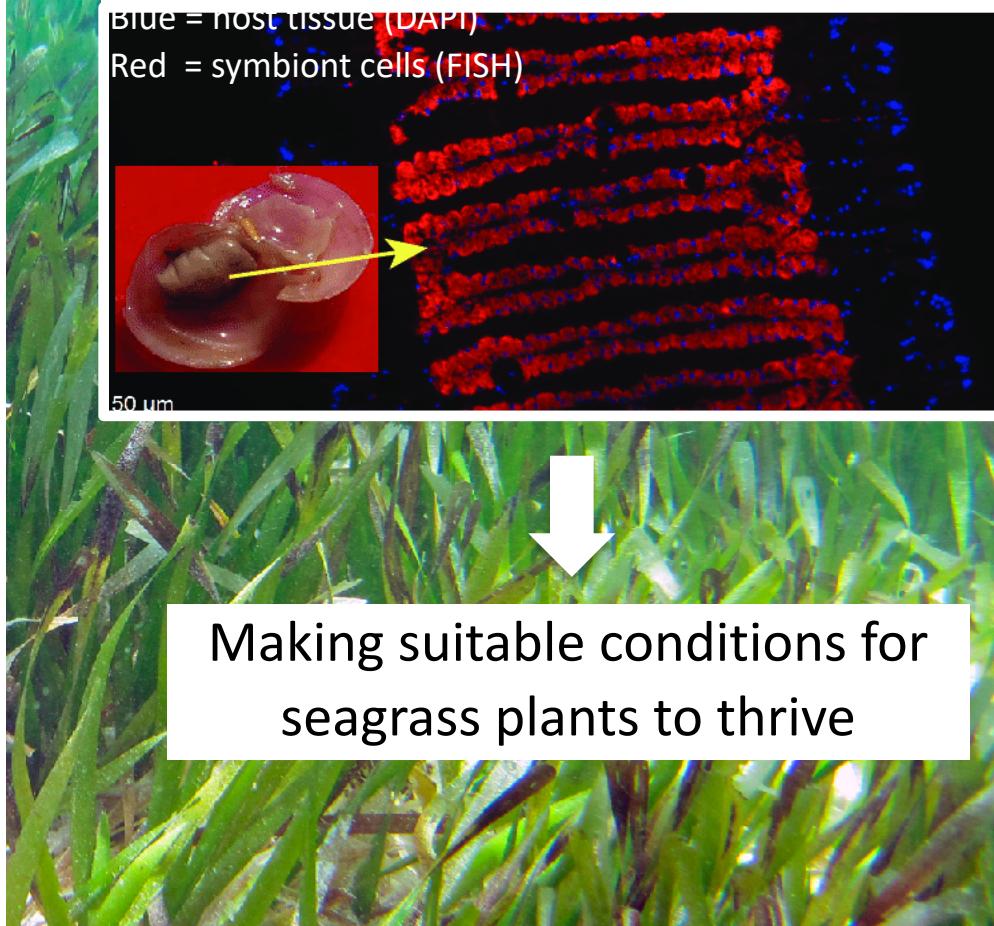
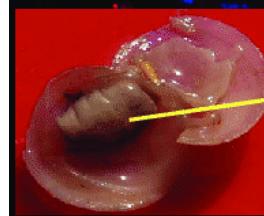
A nutritional symbiosis that is believed to be the foundation of seagrass ecosystems



Lucinid clams and their gill sulfur oxidizing symbionts remove toxic sulfide from the sediment

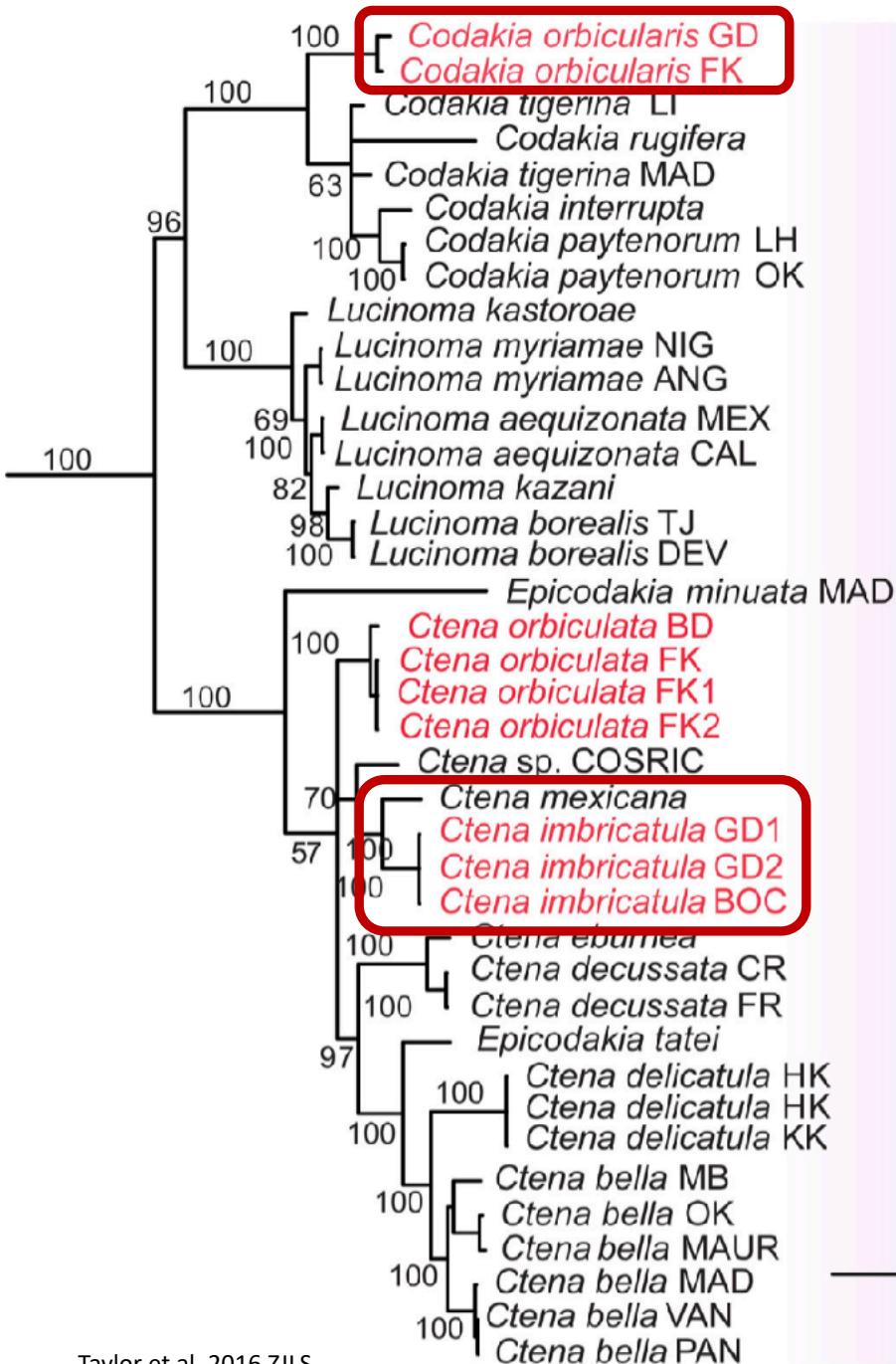
Blue = host tissue (DAPI)

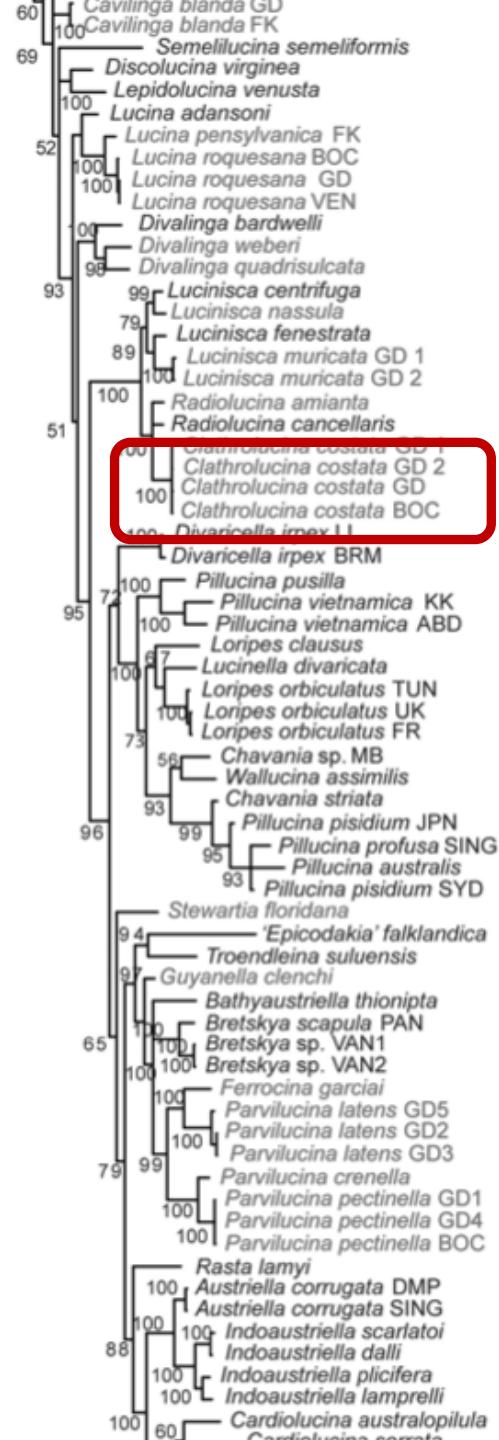
Red = symbiont cells (FISH)



Making suitable conditions for seagrass plants to thrive

CODAKIINAE





LUCININAE

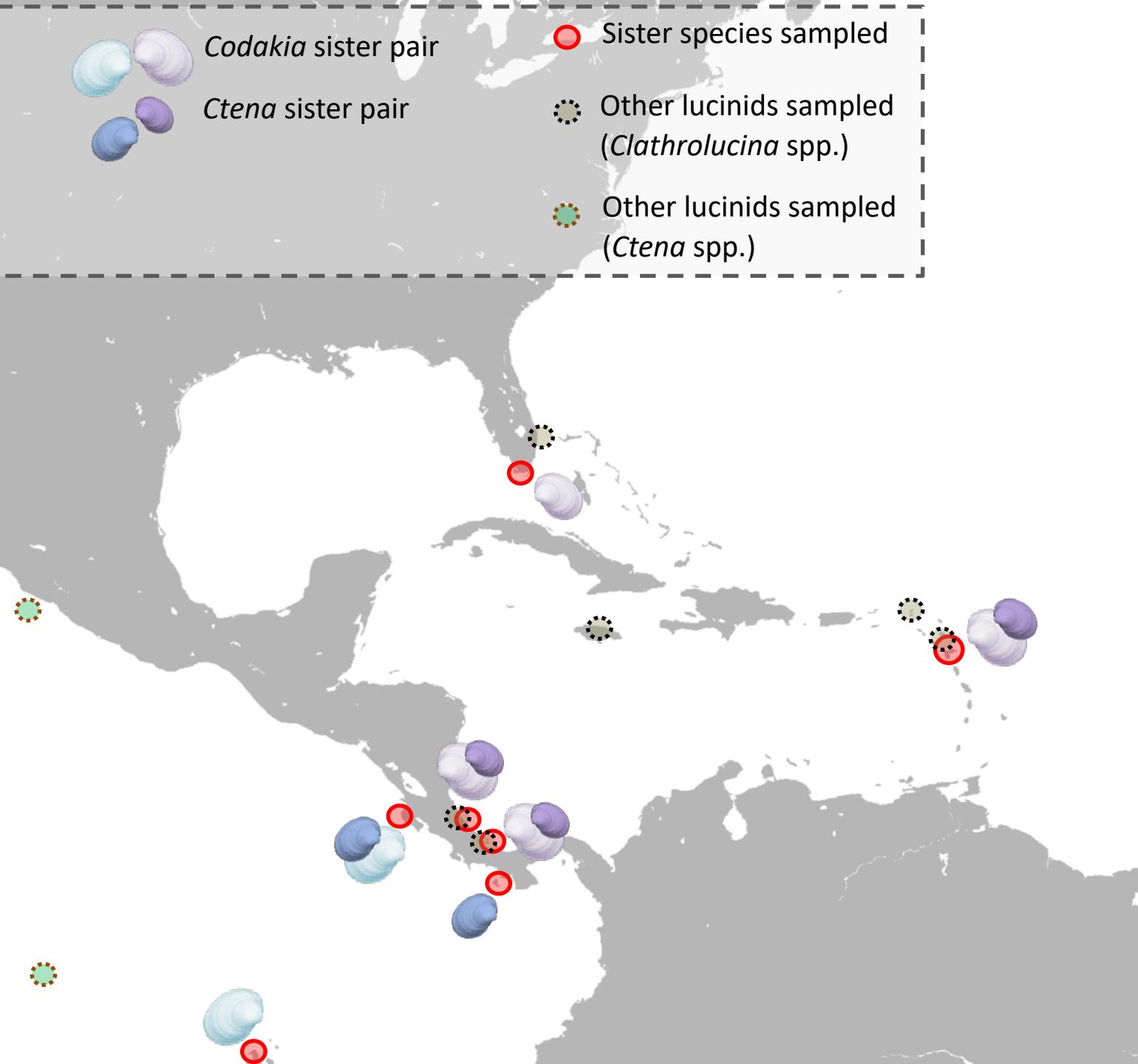
We also included
Clathrolucina costata as an
outgroup

A common species co-
occurring with Ctena and
Codakia in the Caribbean

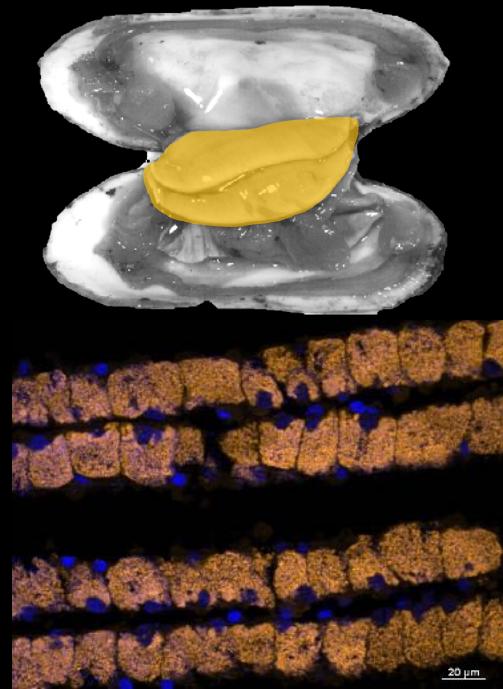
Sampling



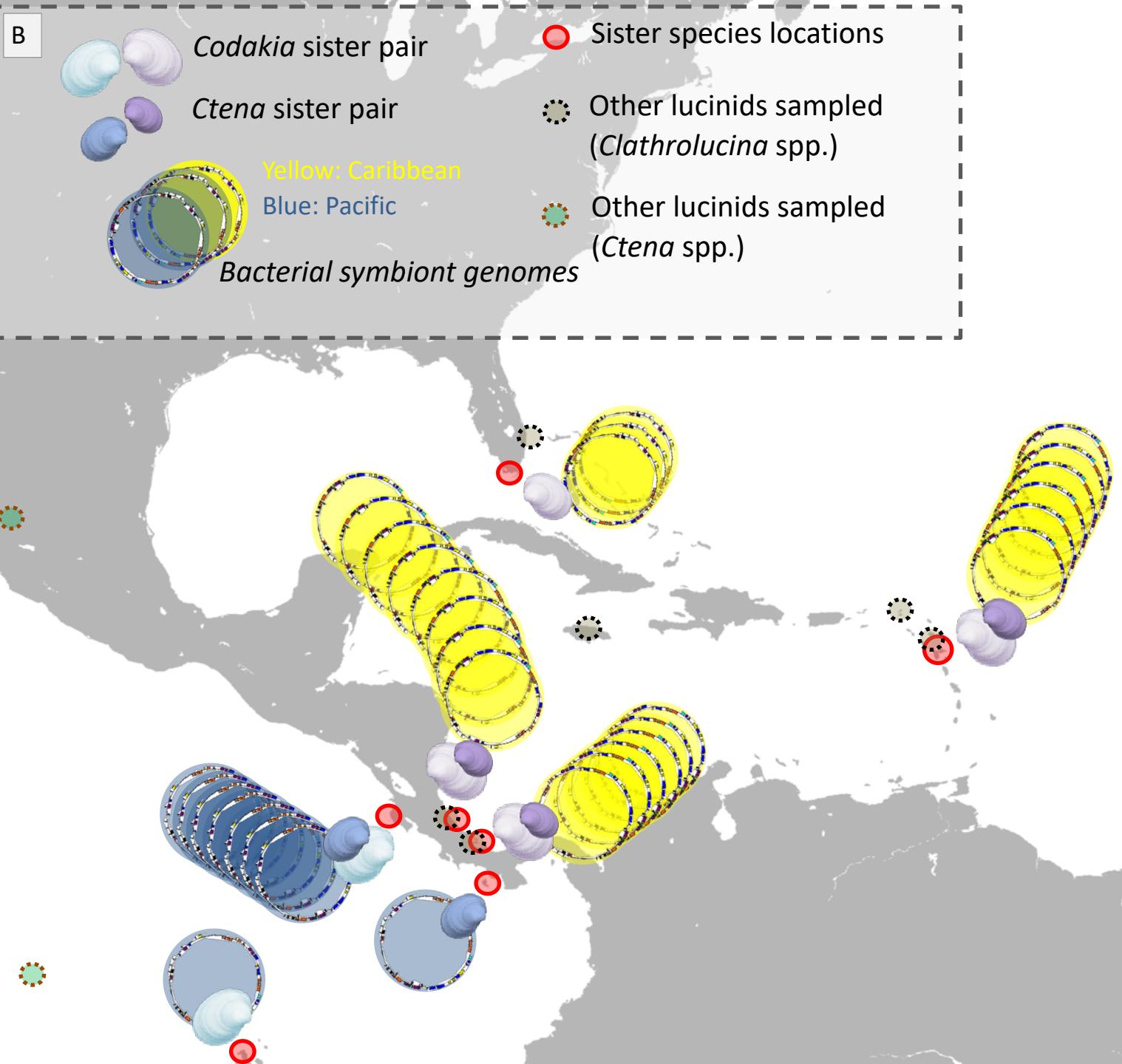
Gustav Paulay,
Florida Museum of Natural History



Symbiont Genome Sequencing



Shotgun metagenomics

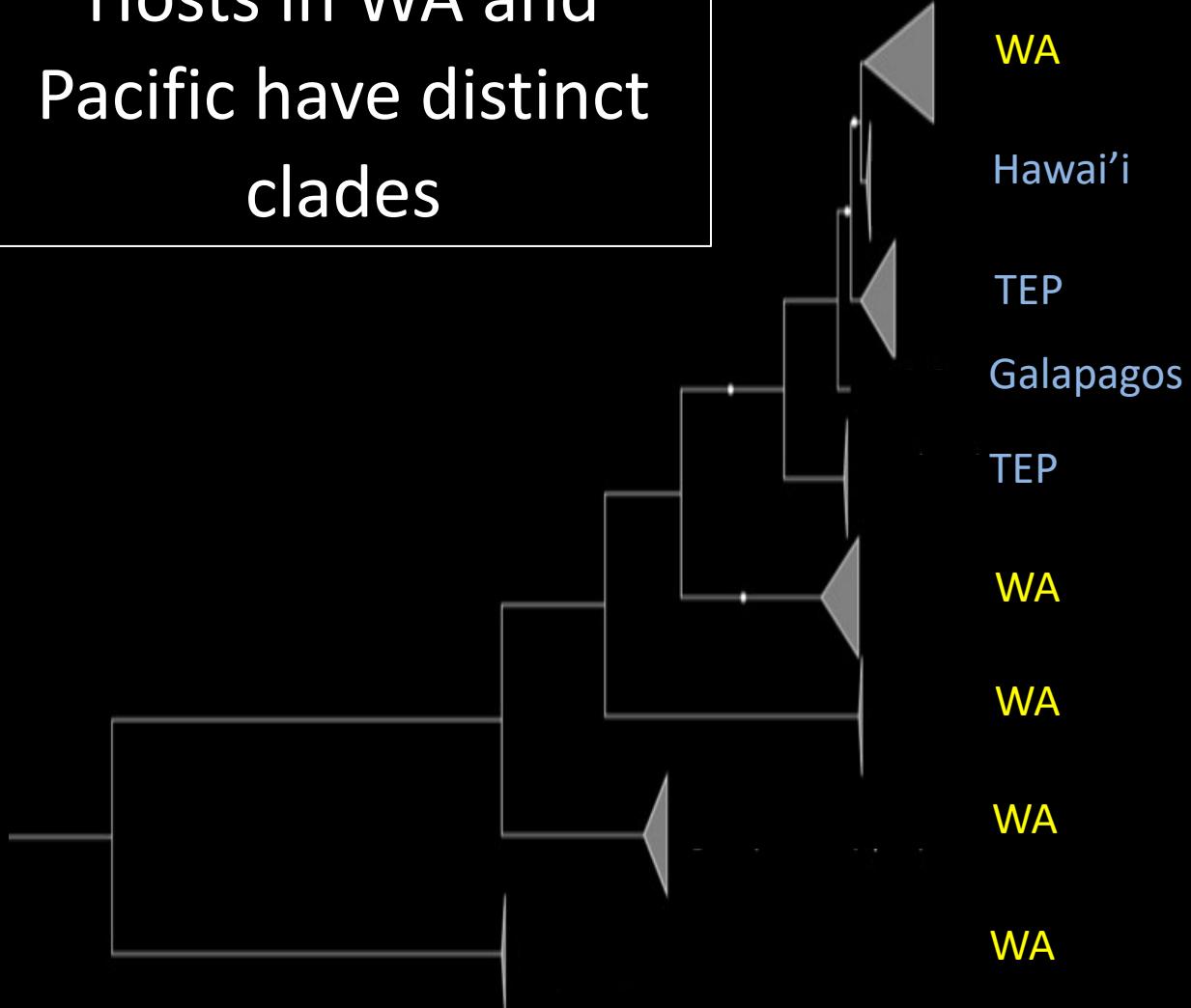


233 high quality genomes clustered into 8 clades

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Hosts in WA and
Pacific have distinct
clades

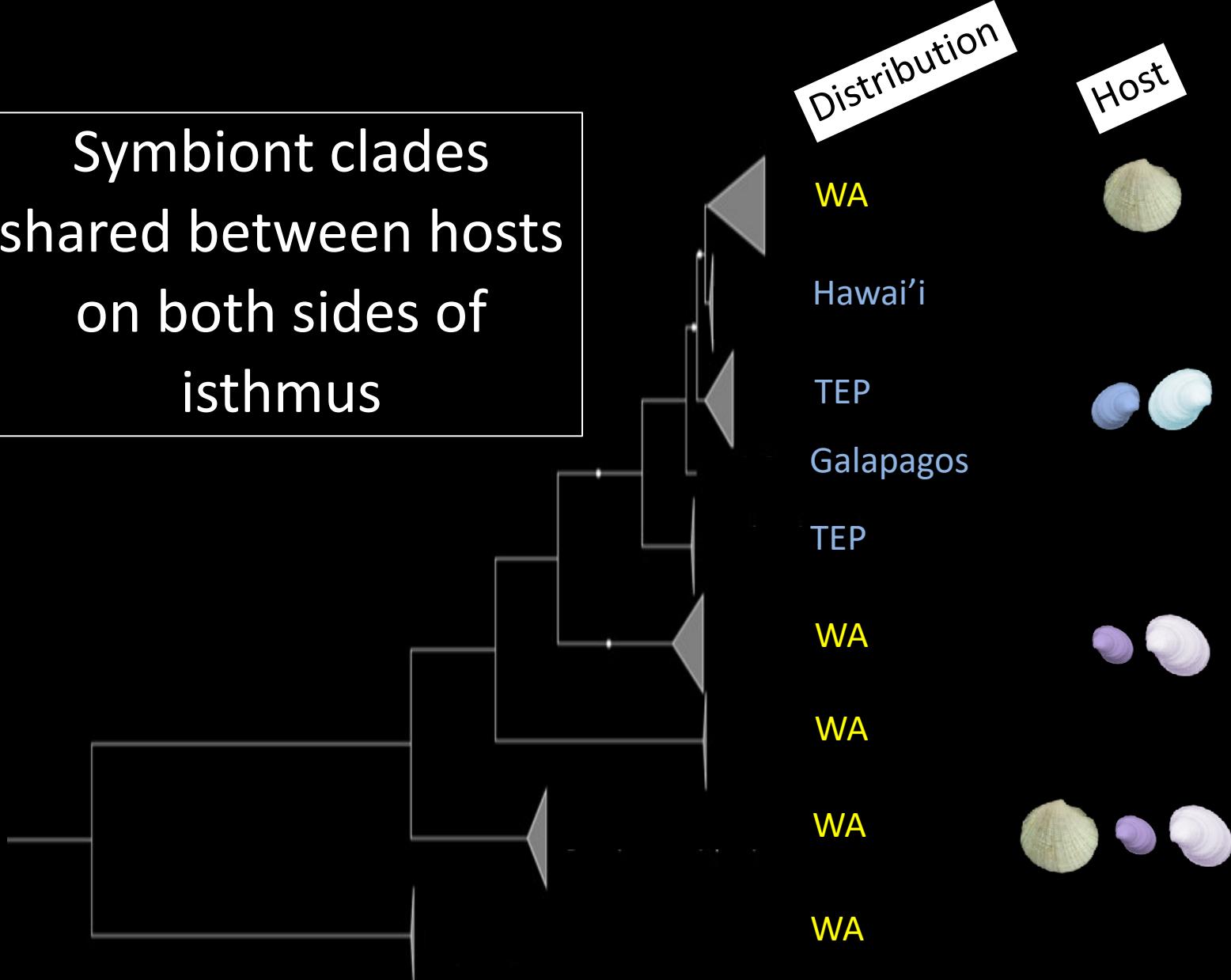
Distribution



233 high quality genomes clustered into 8 clades

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Symbiont clades
shared between hosts
on both sides of
isthmus



Distribution

Host



Clathrolucina costata



Ctena mexicana
Codakia distinguenda



Ctena imbricatula
Codakia orbicularis

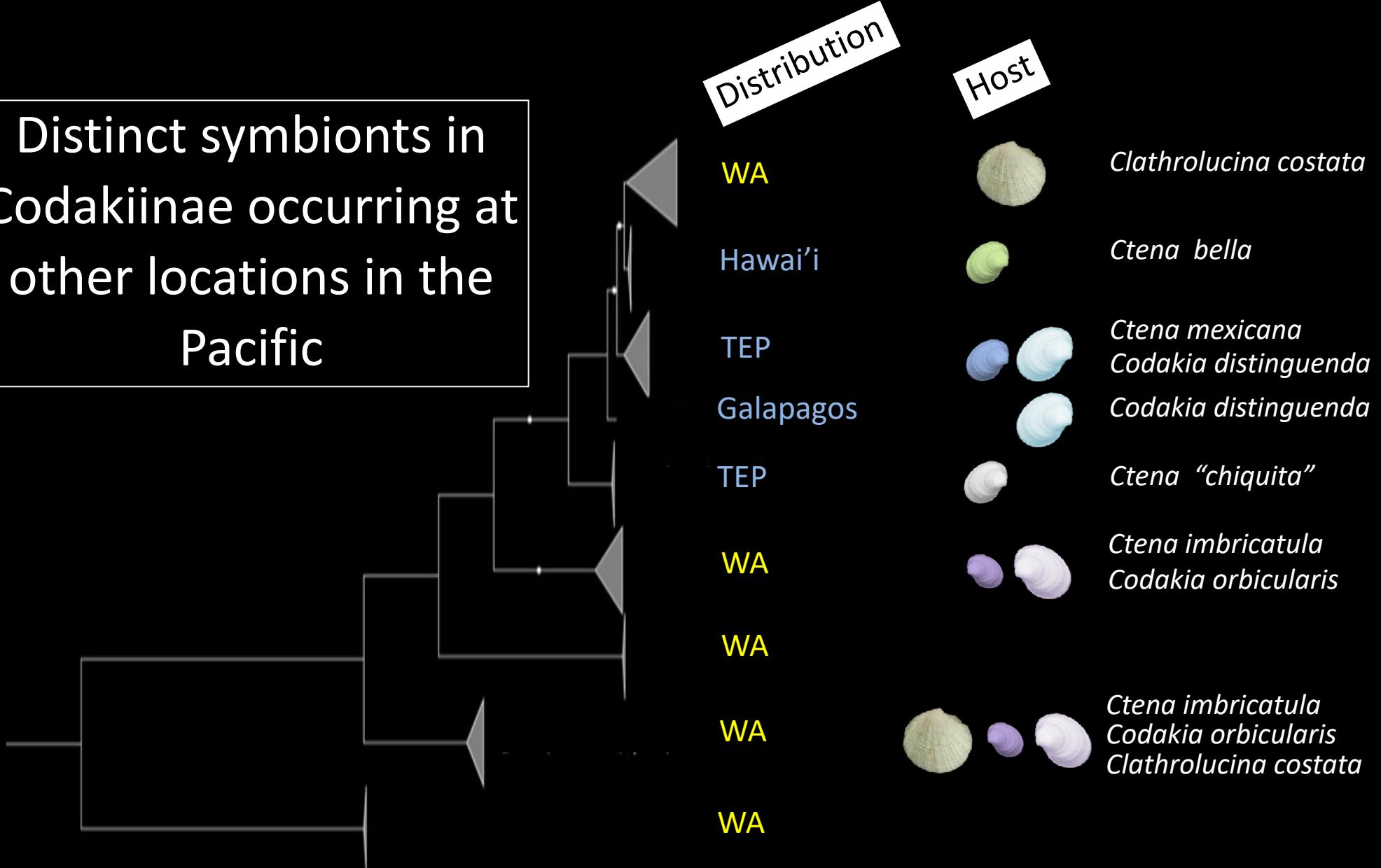


Ctena imbricatula
Codakia orbicularis
Clathrolucina costata

233 high quality genomes clustered into 8 clades

WA = Western Atlantic
ETP = Eastern Tropical Pacific

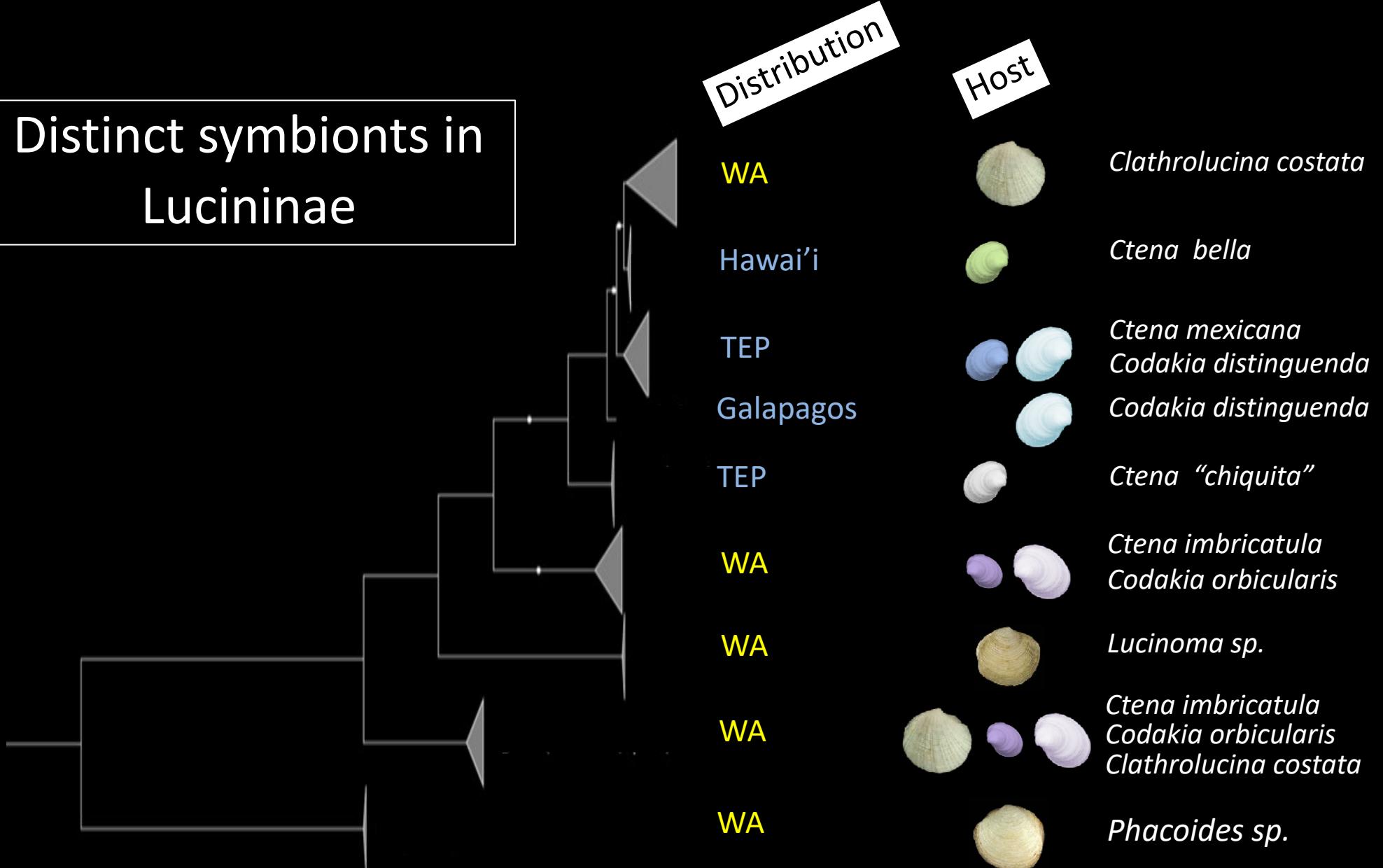
Distinct symbionts in Codakiinae occurring at other locations in the Pacific



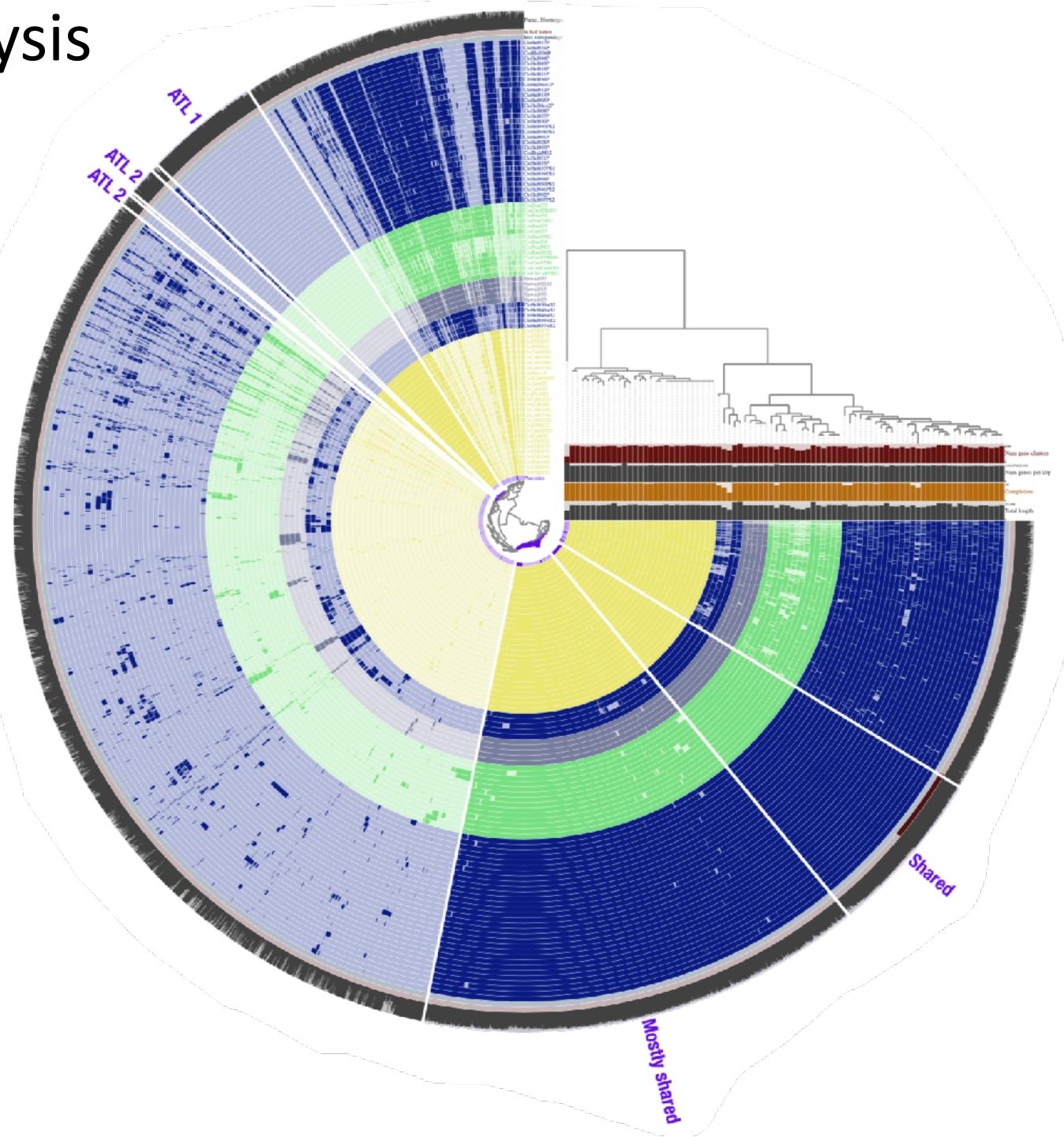
233 high quality genomes clustered into 8 clades

WA = Western Atlantic
ETP = Eastern Tropical Pacific

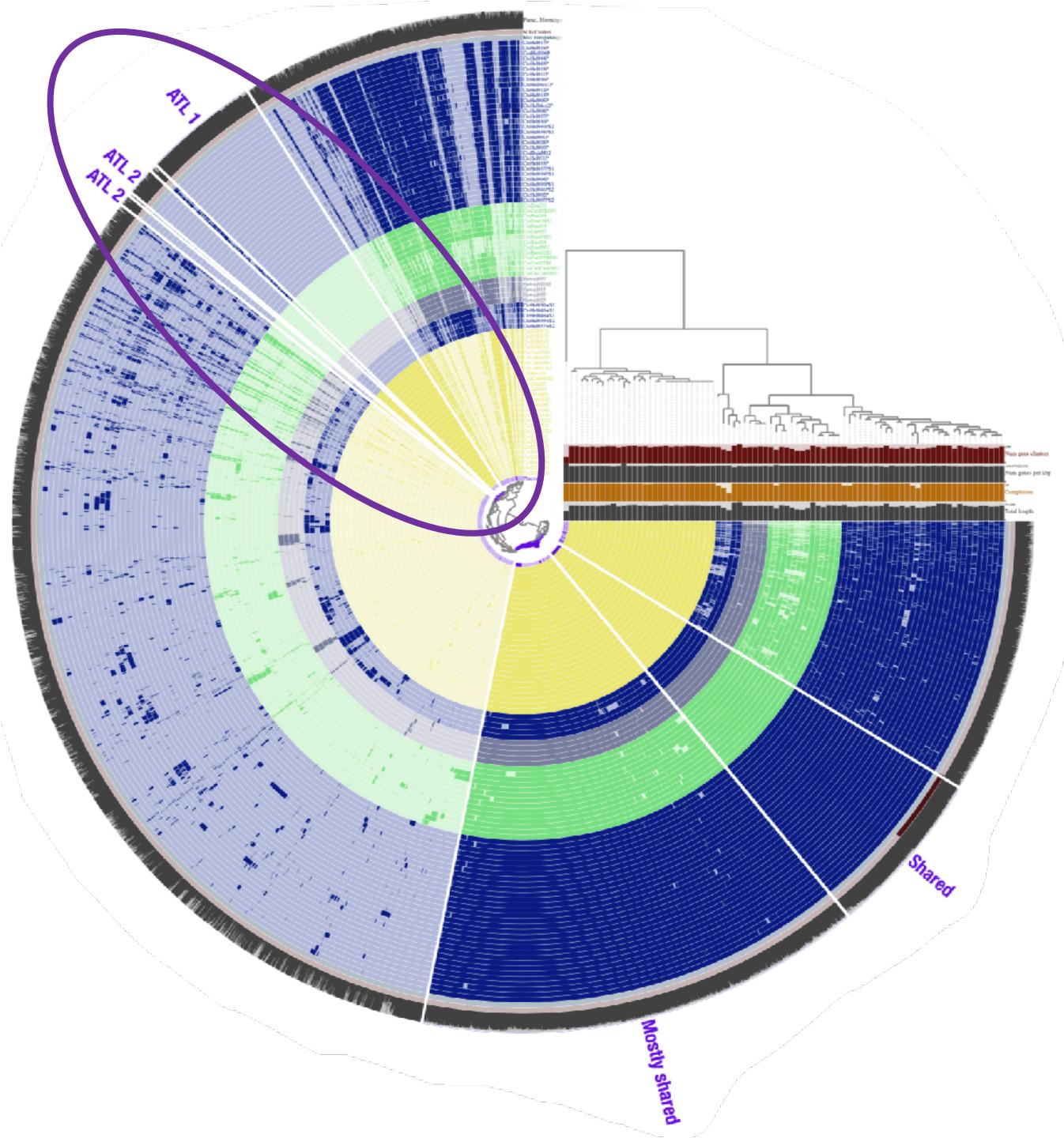
Distinct symbionts in Lucininae



Pangenome analysis

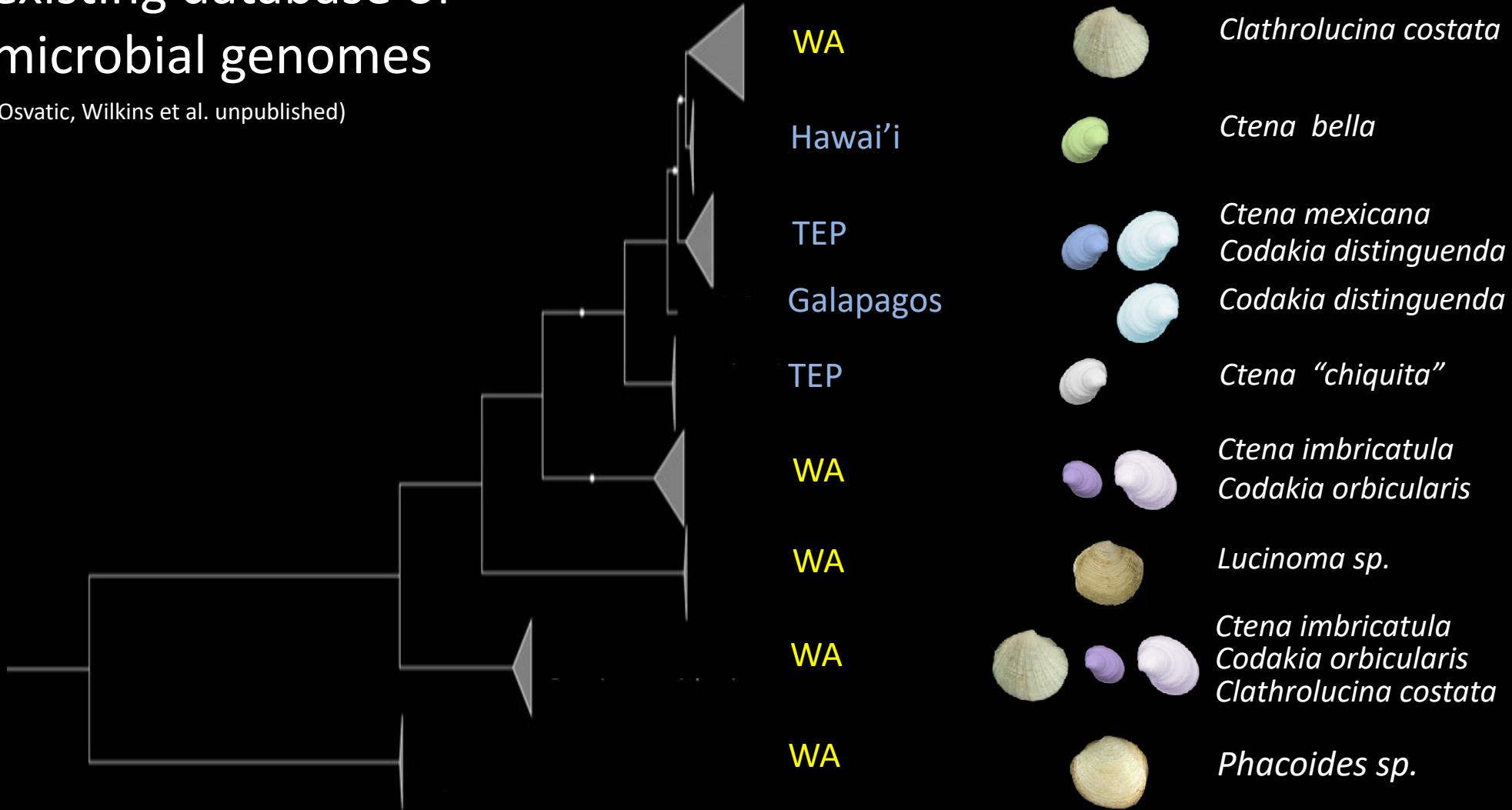


Gene families only found in the Caribbean (Atlantic)



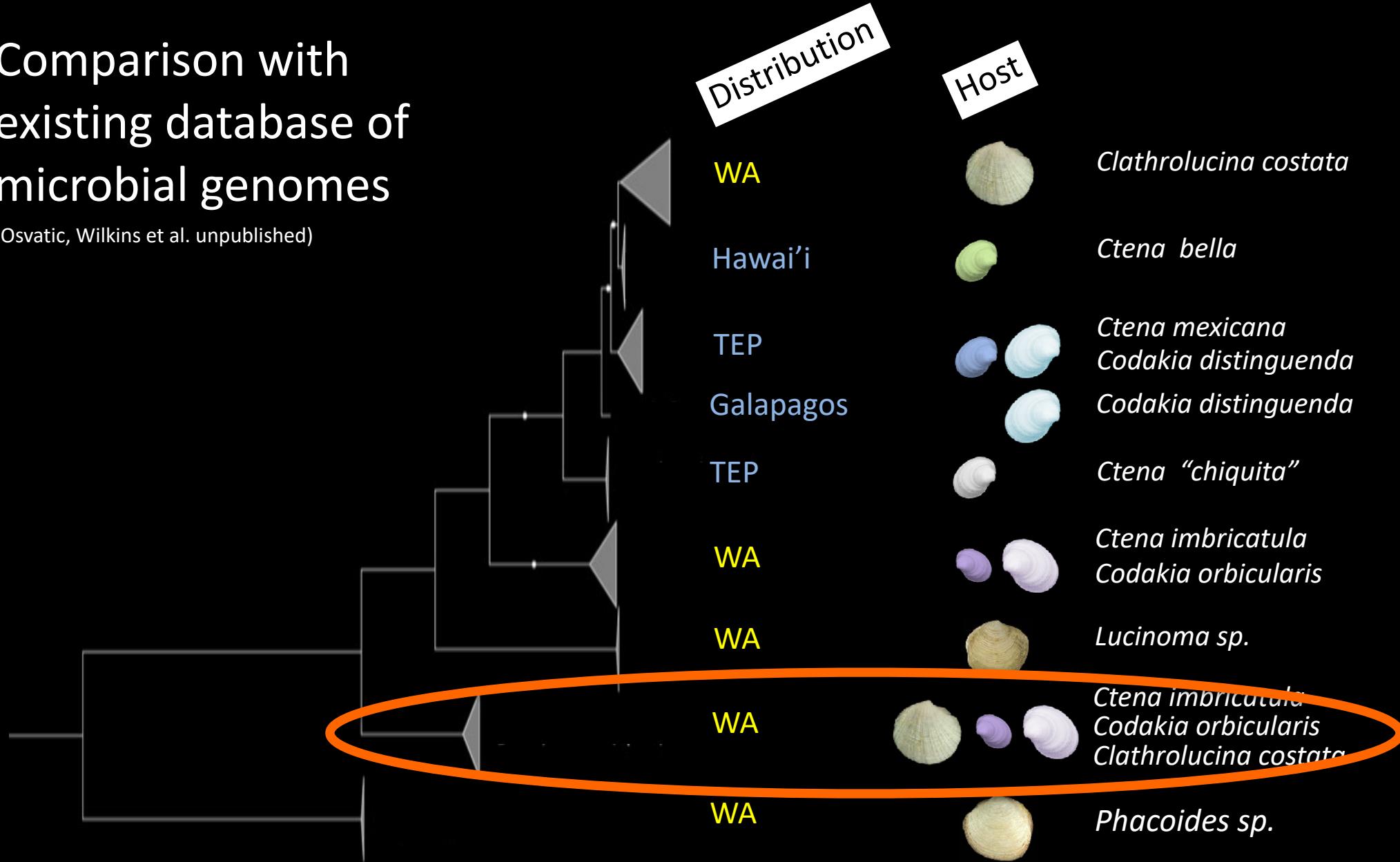
Comparison with existing database of microbial genomes

(Osvatic, Wilkins et al. unpublished)

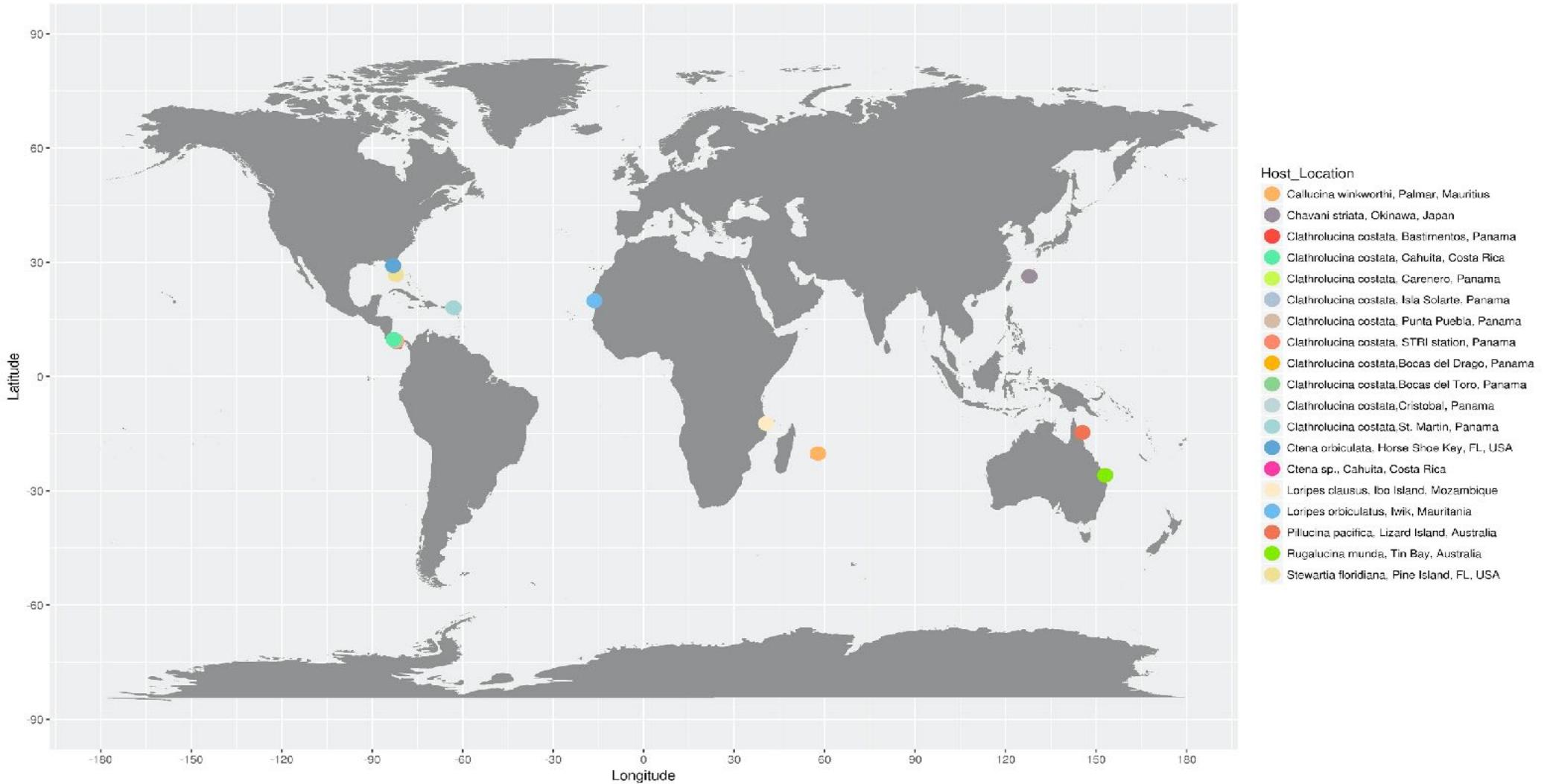


Comparison with existing database of microbial genomes

(Osvatic, Wilkins et al. unpublished)

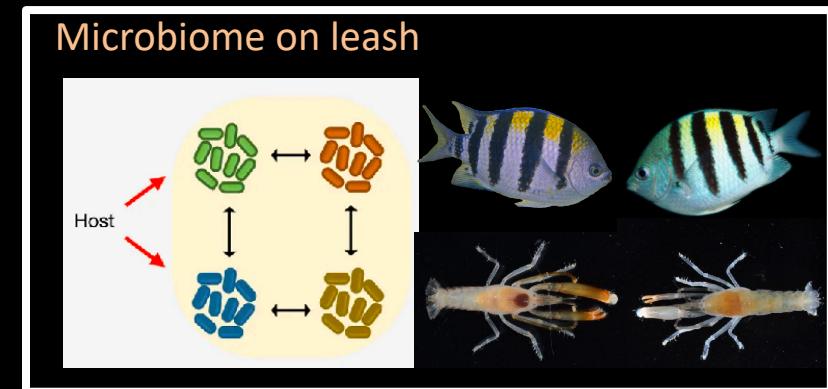
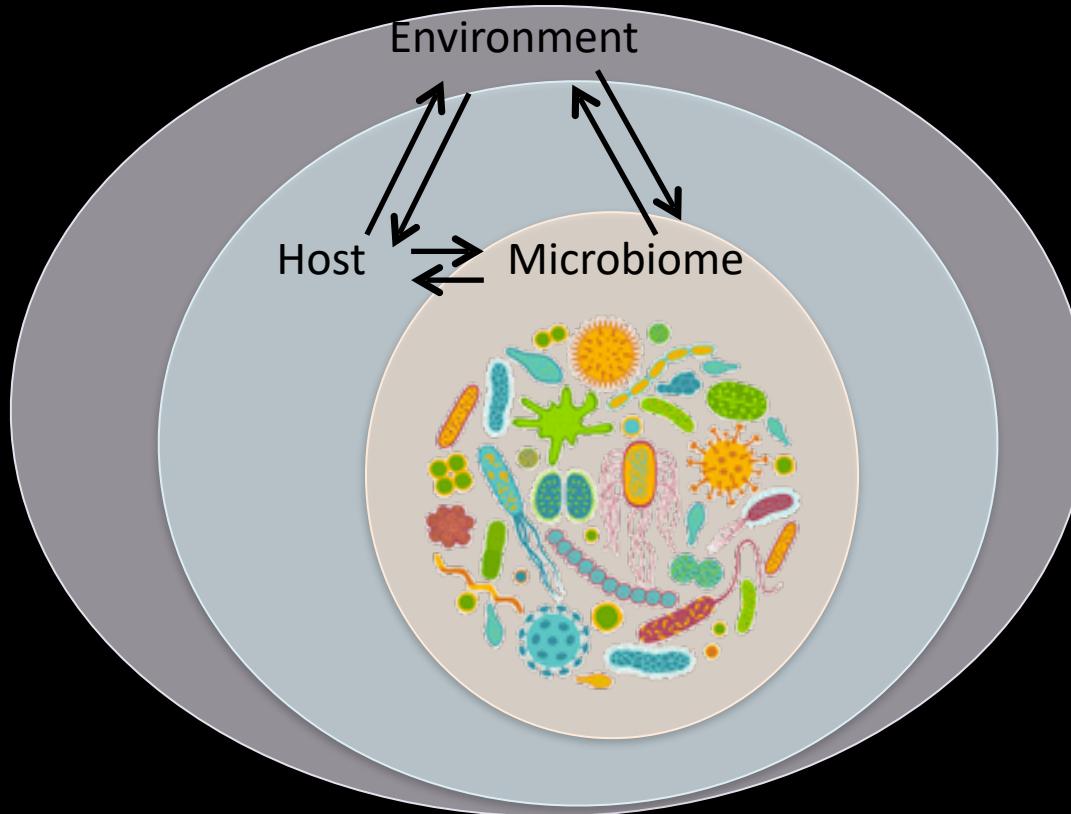


One clade of symbiont is widespread (but absent in TEP)



What have we learned so far?

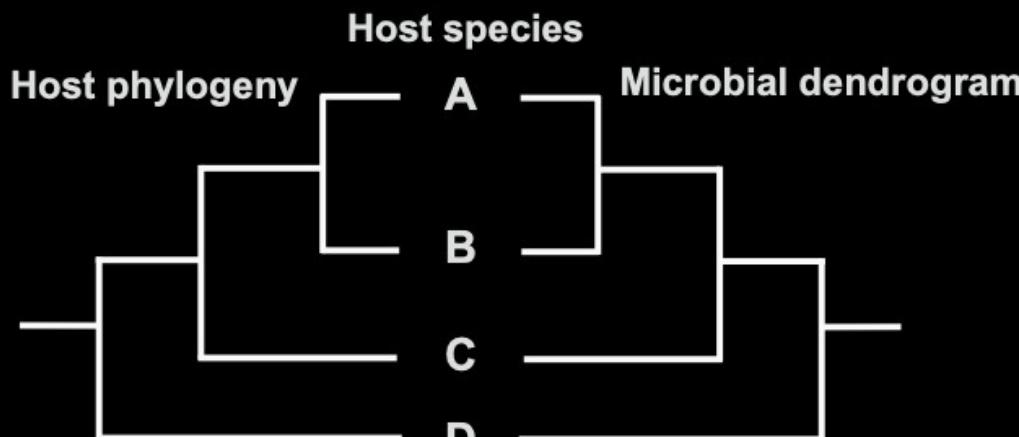
1) Identifying ecological and evolutionary drivers of the microbiome



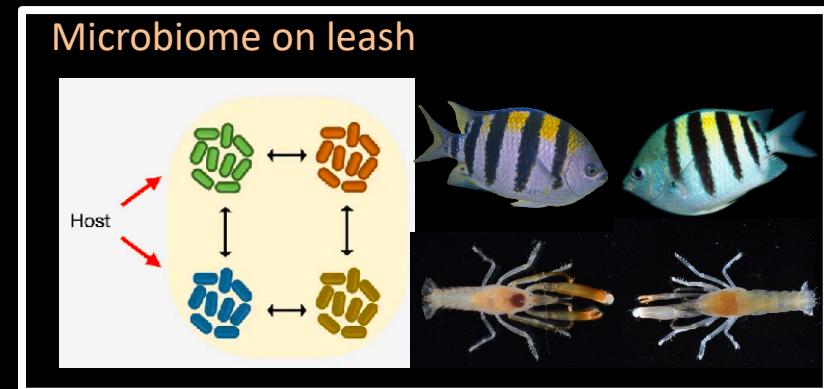
- Species and tissue specific microbiomes
= microbiome on leash
- Limited effect of the “Ocean” on community structure

What have we learned so far?

1) Identifying ecological and evolutionary drivers of the microbiome



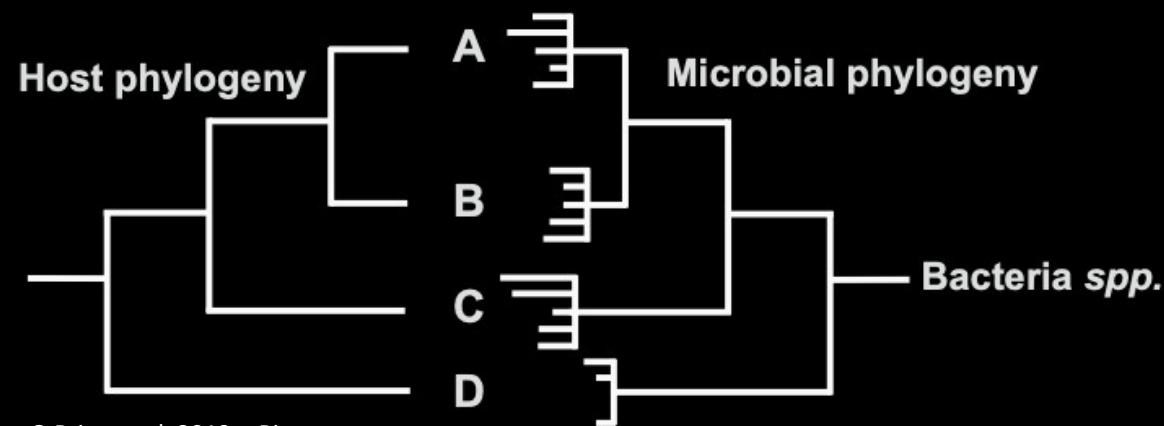
O.Brien et al. 2019 mBio



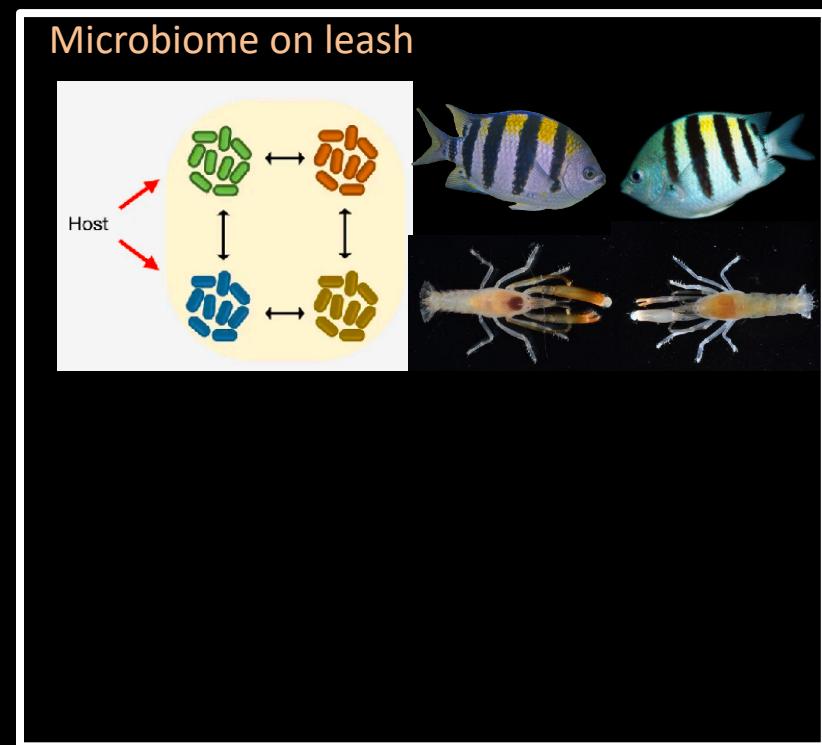
- Species and tissue specific microbiomes
= microbiome on leash
- Limited effect of the “Ocean” on community structure
- Phylogenetic signal

What have we learned so far?

2) Co-divergence between hosts and microbes



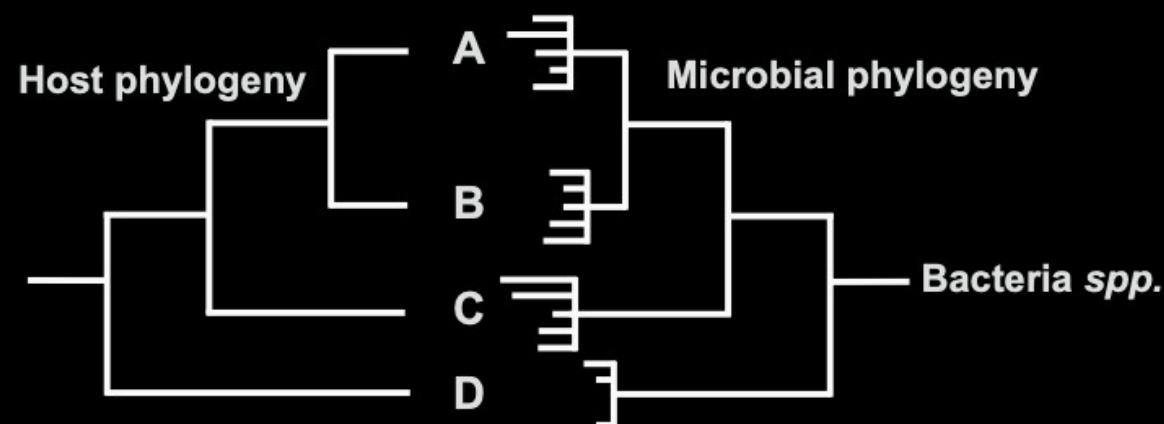
O'Brien et al. 2019 mBio



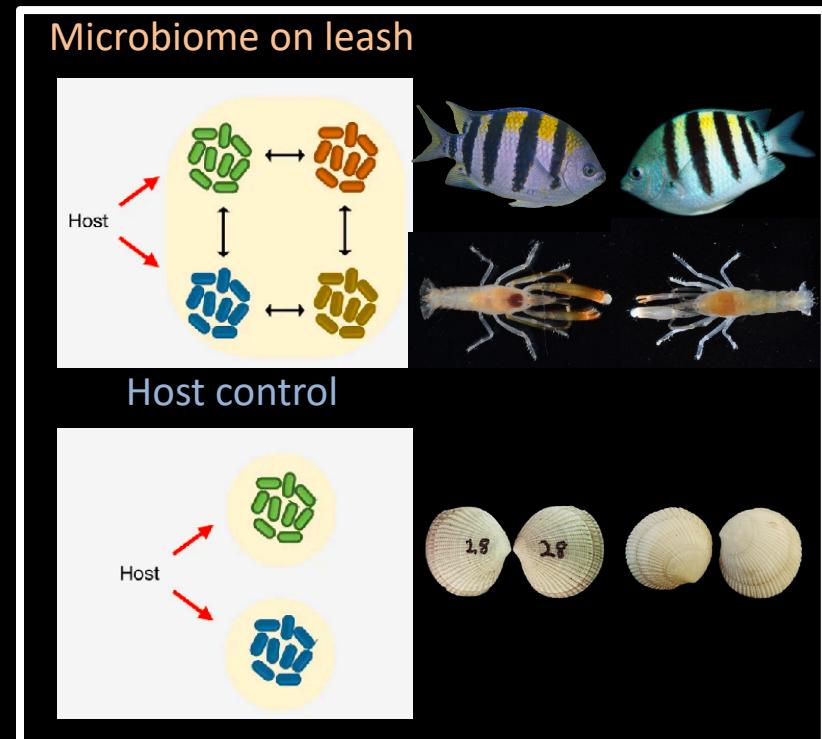
- Evidence of co-divergence between hosts and very few microbes

What have we learned so far?

2) Co-divergence between hosts and microbes



O'Brien et al. 2019 mBio



- Evidence of co-divergence between hosts and very few microbes
- Beneficial microbes are promiscuous (not host specific)
- Beneficial microbe with wide geographical distribution

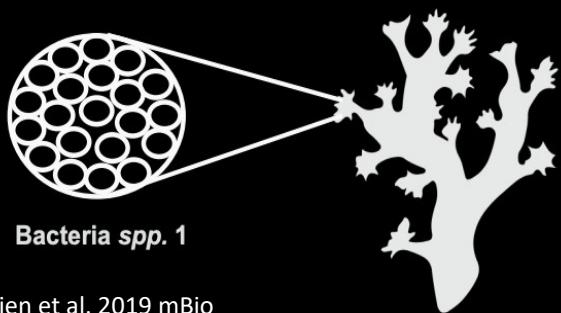
What have we learned so far?

3) Adaptation and metabolic cooperation

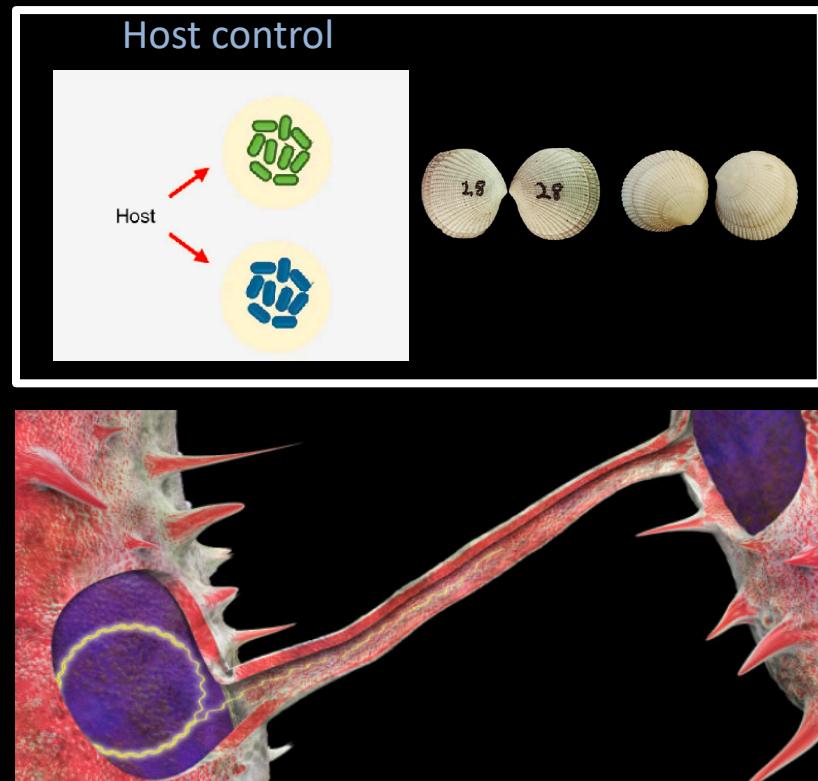
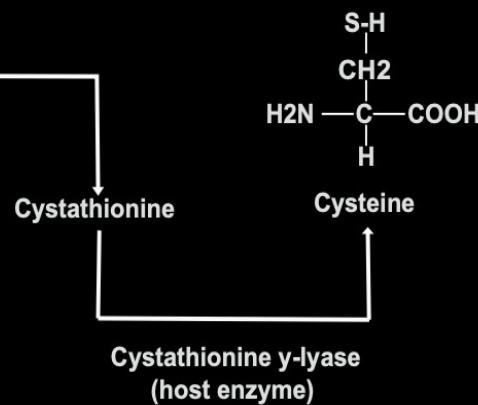
i)

Homocysteine + Serine
(host diet & metabolism)

Cystathione B-synthase
(symbiont enzyme)



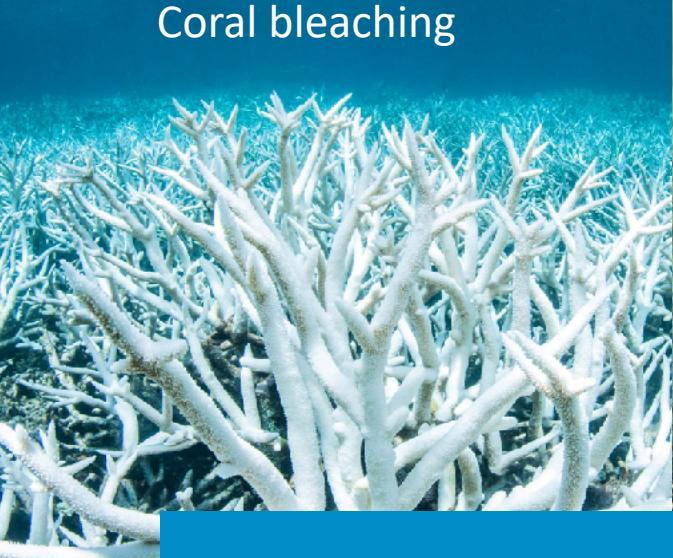
O'Brien et al. 2019 mBio



- Set of genes present only in genome of the Caribbean symbionts

Breakdown of interactions between hosts and microbes/microbiomes

Coral bleaching



Hypoxic events



Disease



EVERY YEAR WE LOSE



2-8%
mangroves



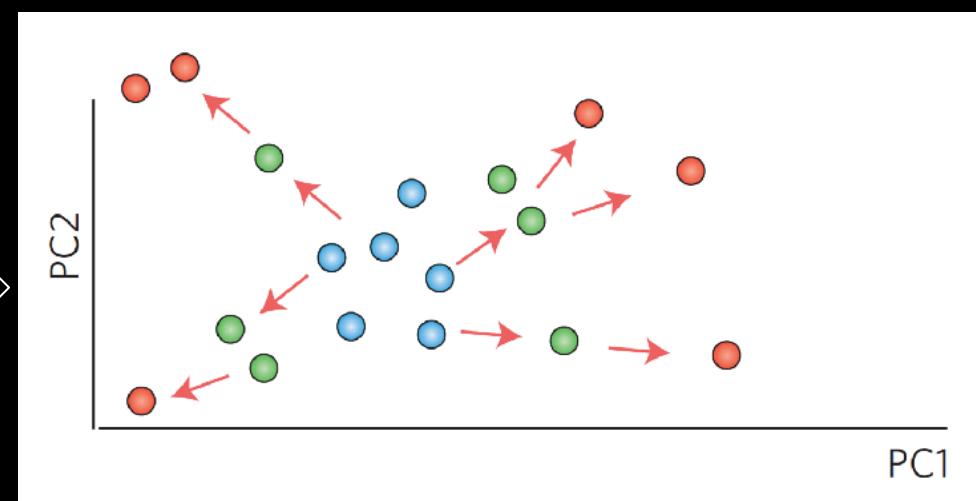
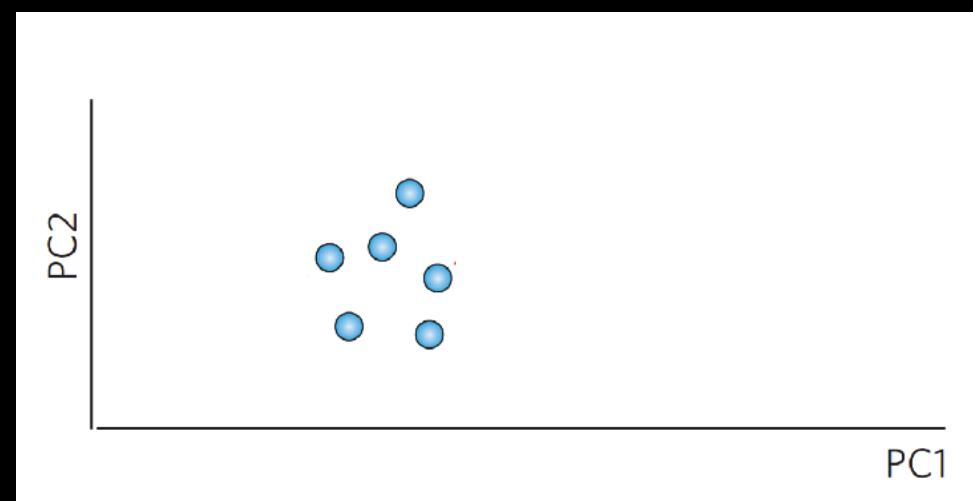
5%
seagrass meadows



5%
coral reefs

Healthy microbiome

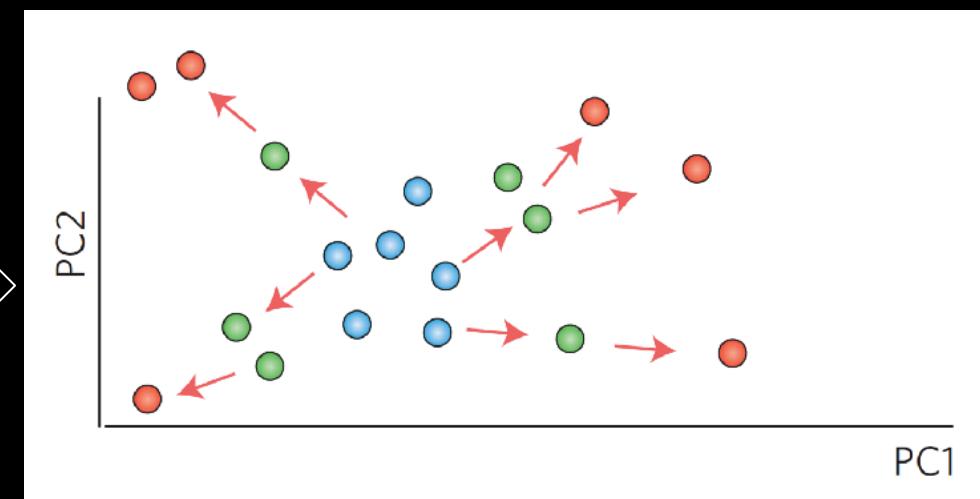
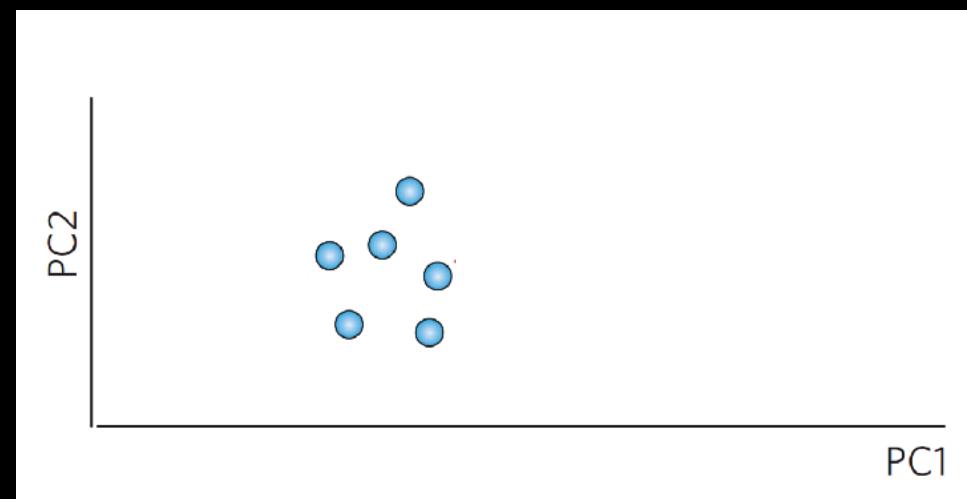
Dysbiotic microbiome



Zaneveld et al. 2017 Nature Microb.

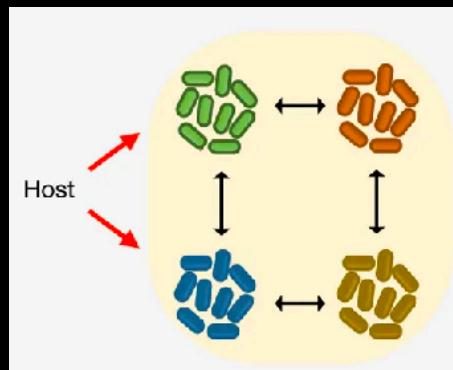
Healthy microbiome

Dysbiotic microbiome

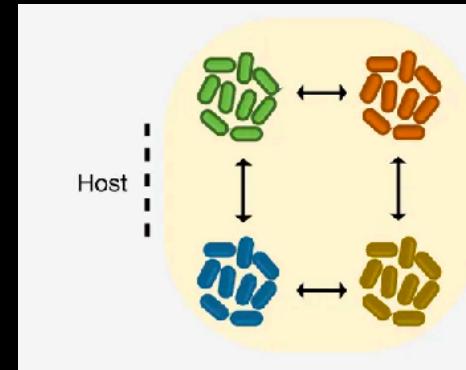


Zaneveld et al. 2017 Nature Microb.

Microbiome on leash



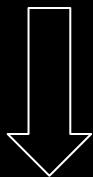
Open ecosystem



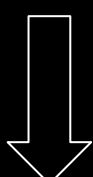
The host can no longer keep its microbiome on a leash

Foster et al. 2017 Nature

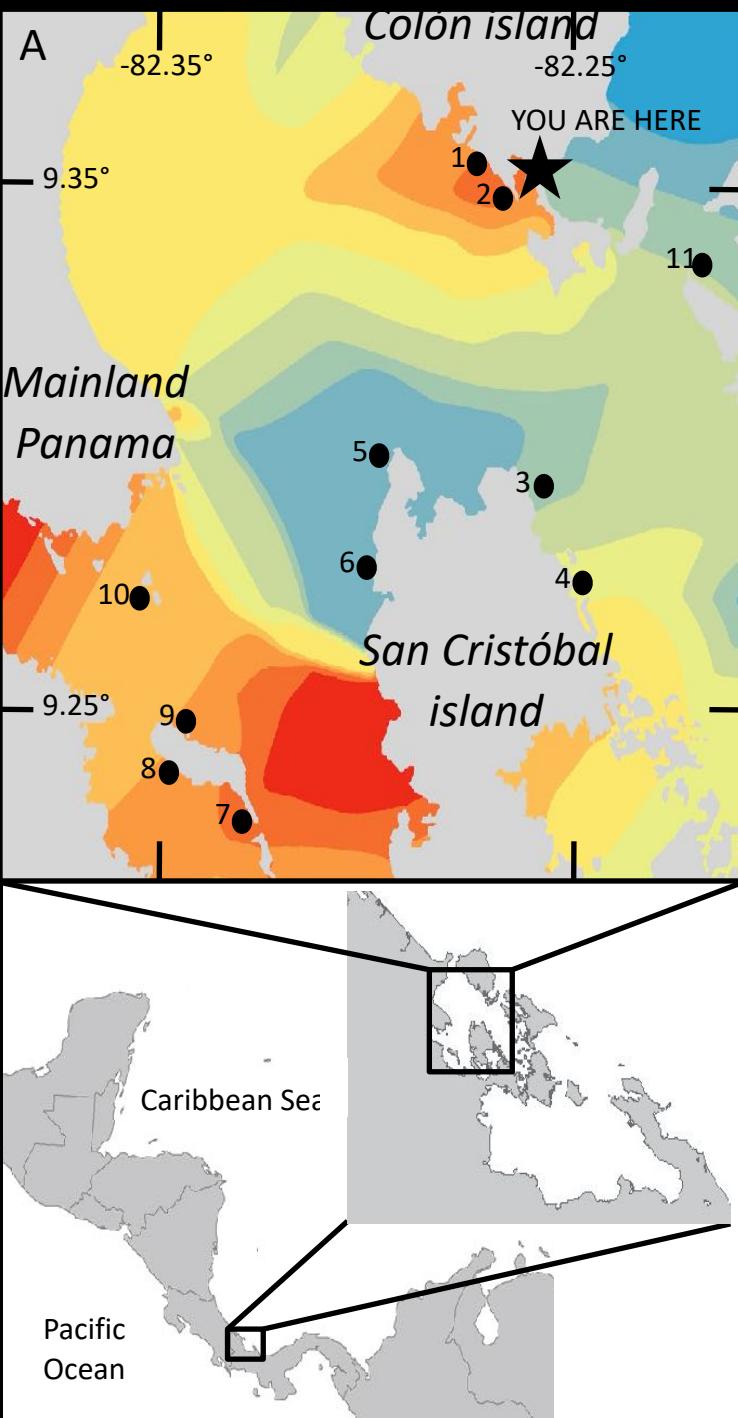
Hypoxia in 2010



Dramatic
reduction in
coral cover



Limited or
no recovery



QUESTION:

Under which conditions do reef associated species show evidence of a dysbiotic microbiome?

HOST:

Foureye butterflyfish
Preferentially feeds on corals

QUESTION:

Under which conditions do reef associated species show evidence of a dysbiotic microbiome?

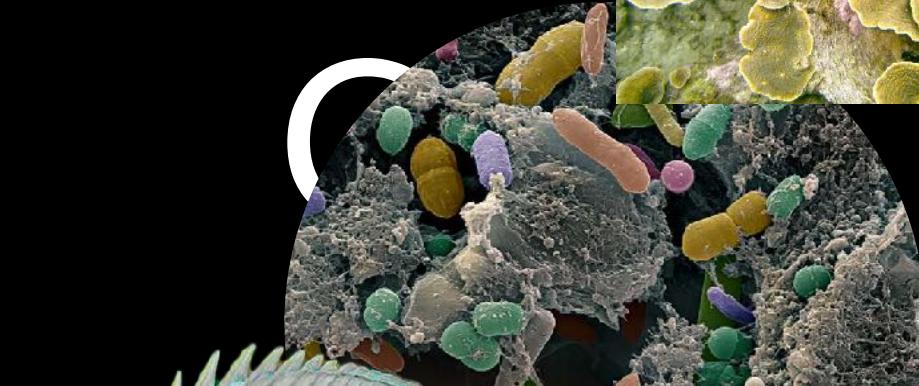
HOST:

Foureye butterflyfish
Preferentially feeds on corals

MICROBIOME:

Gut microbiome
linked to host health, diet & habitat

Habitat

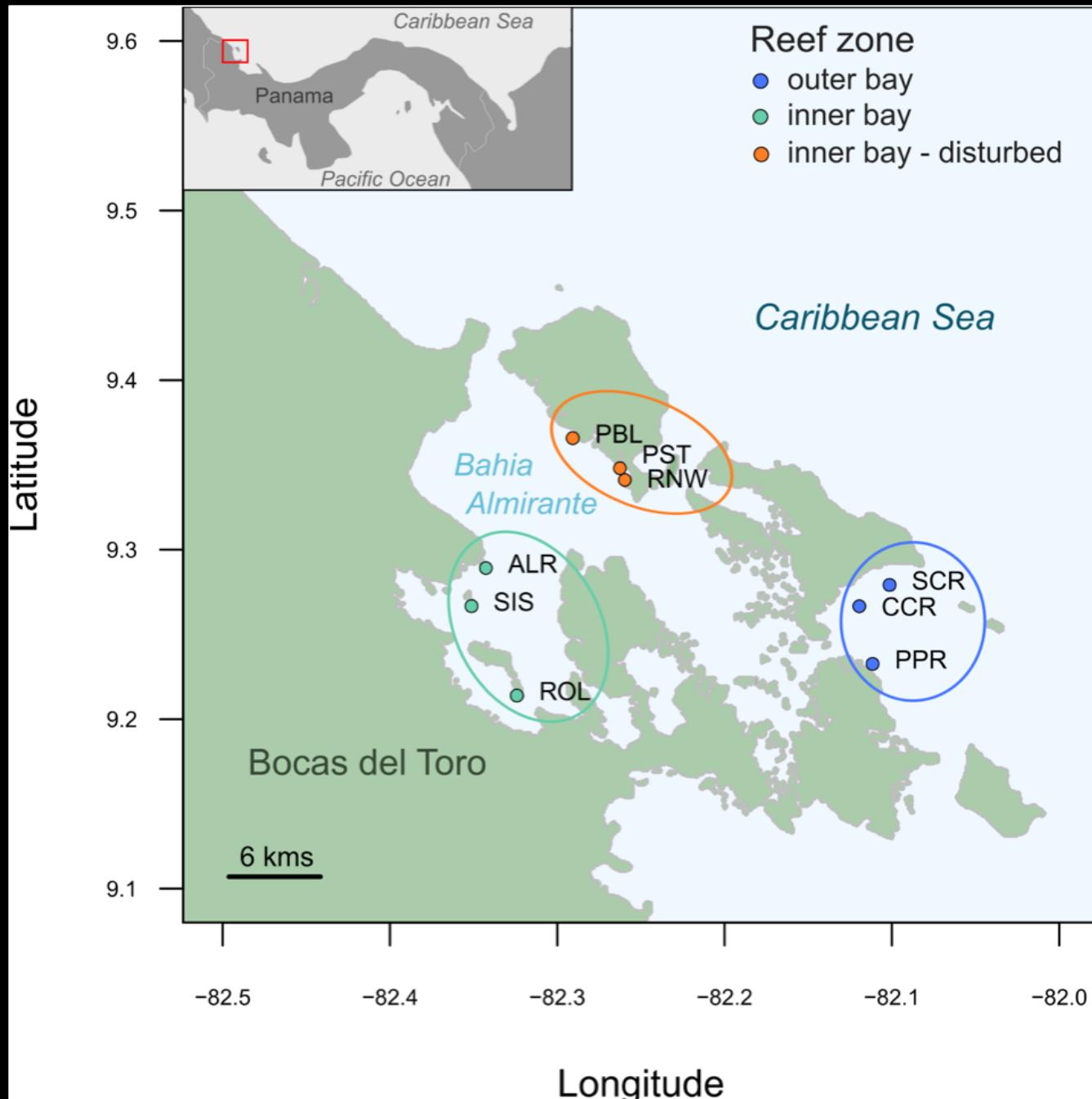


Host health/
genetics



Diet





COLLECTION OF FISH



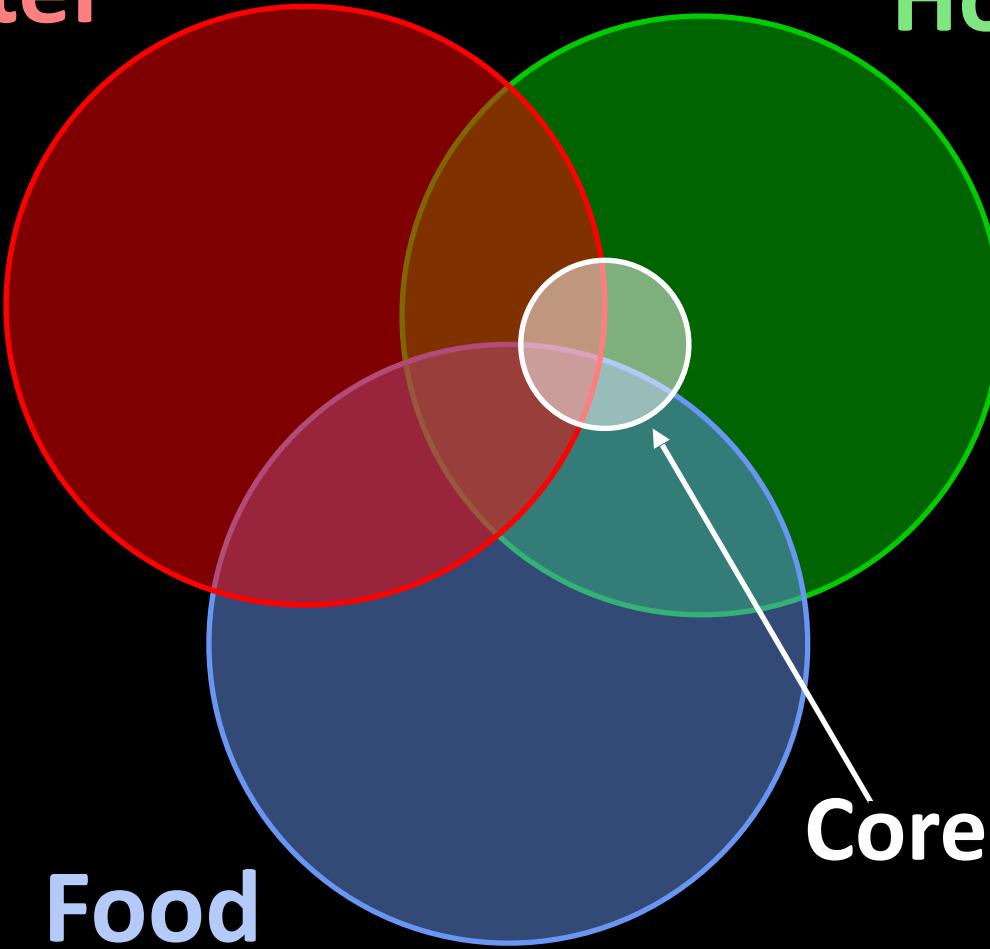
20 specimens per reef
Foureye butterflyfish

COLLECTION IN THE SURROUNDING ENVIR.

- Seawater
 - Algae
 - Sponges
 - Hard corals
 - Soft corals
- Food items

Seawater

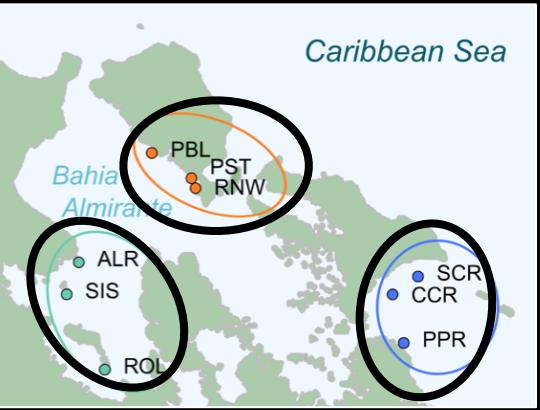
Host



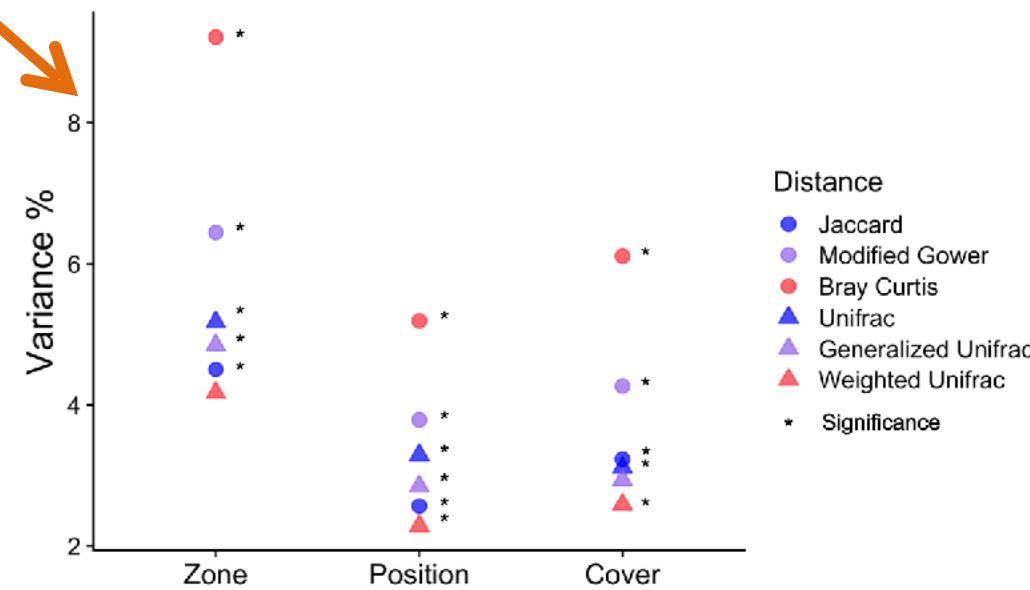
Food

Core microbiome

Zone

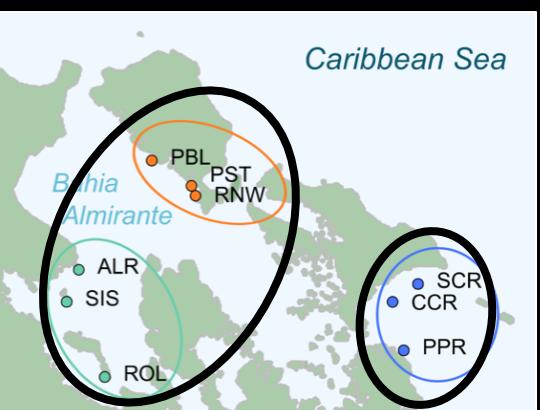


Whole gut microbiome

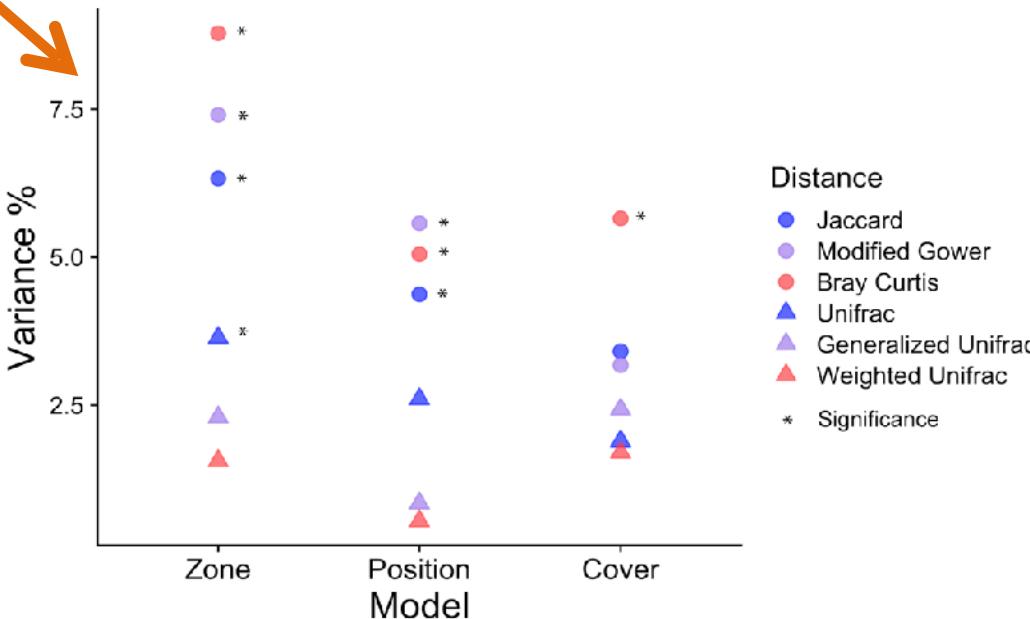


Significant differences in the composition of gut microbiomes across space

BUT



Core gut microbiome

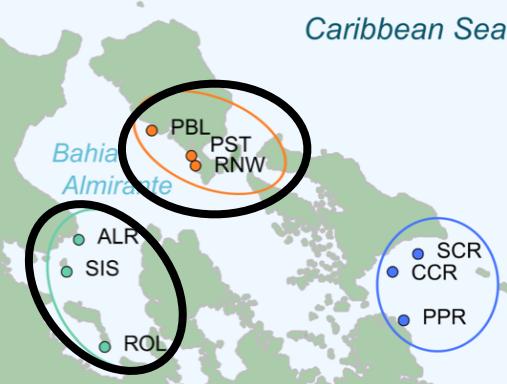


A very small proportion of the variance is explained

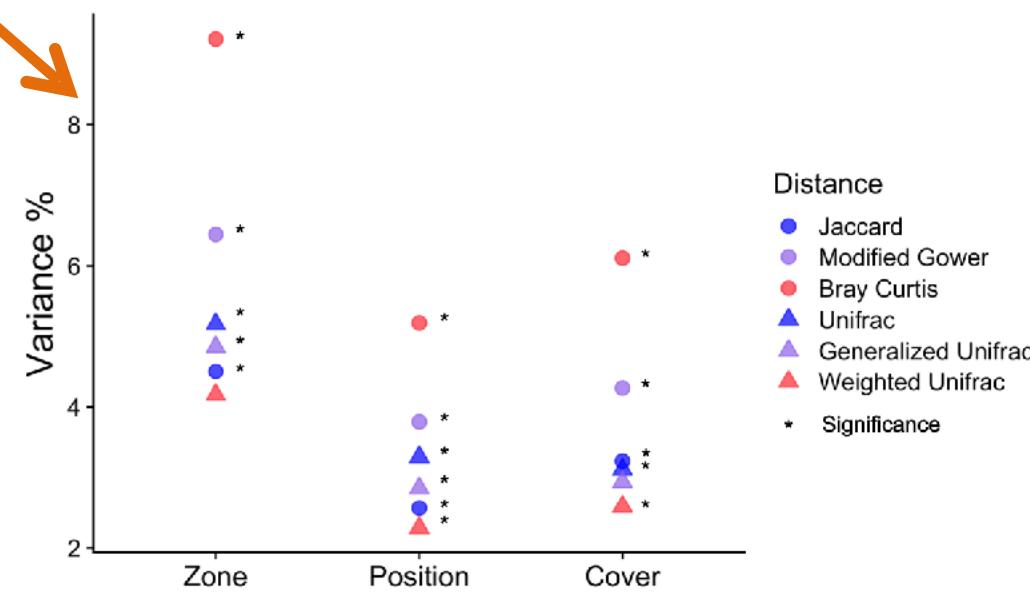
Zone

Position

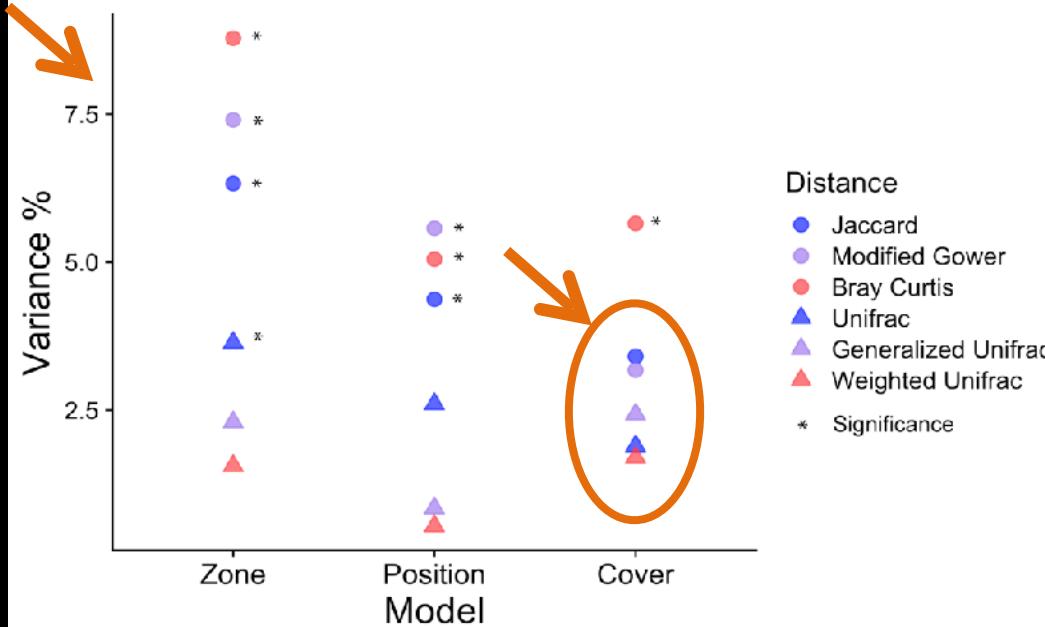
Cover



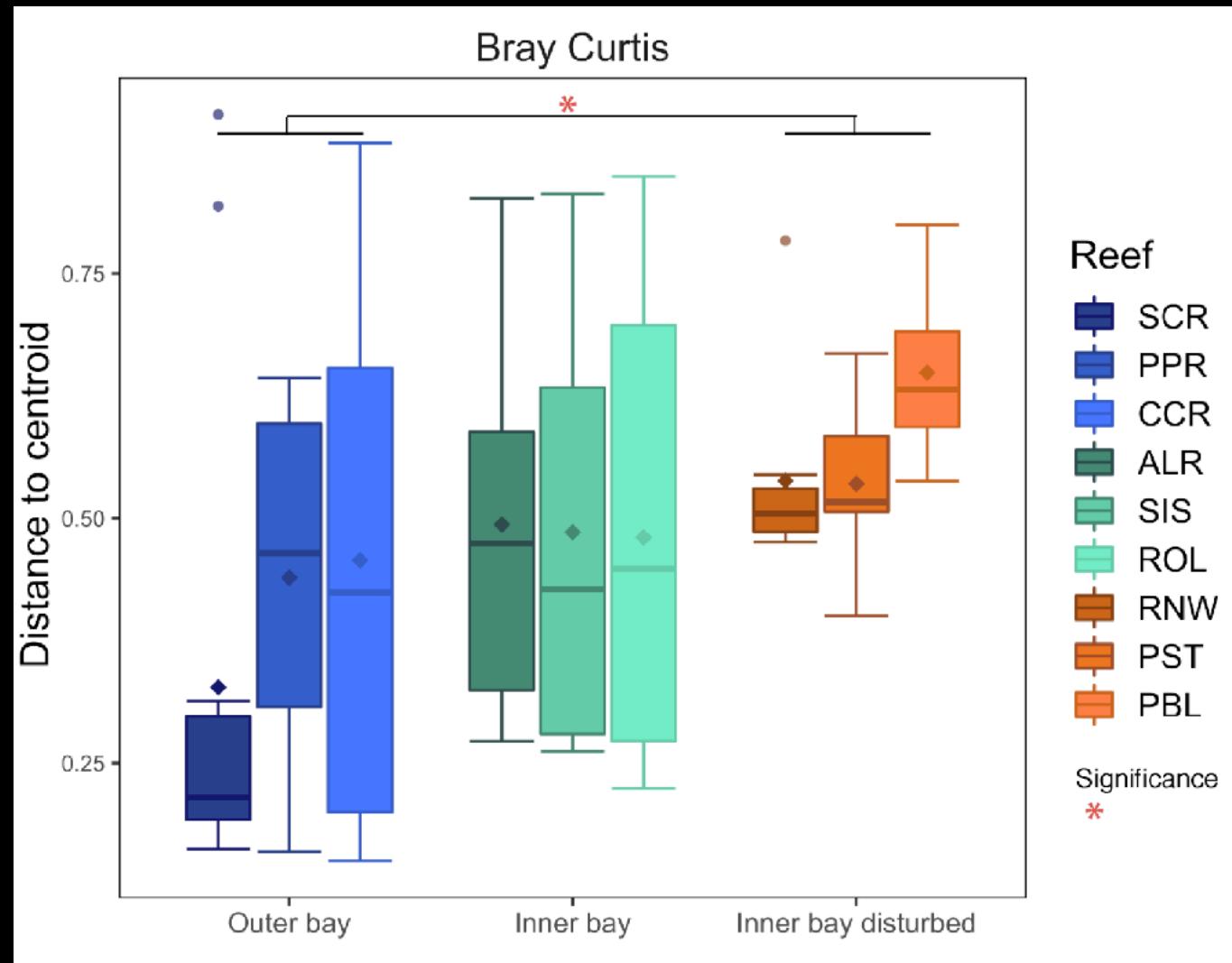
Whole gut microbiome

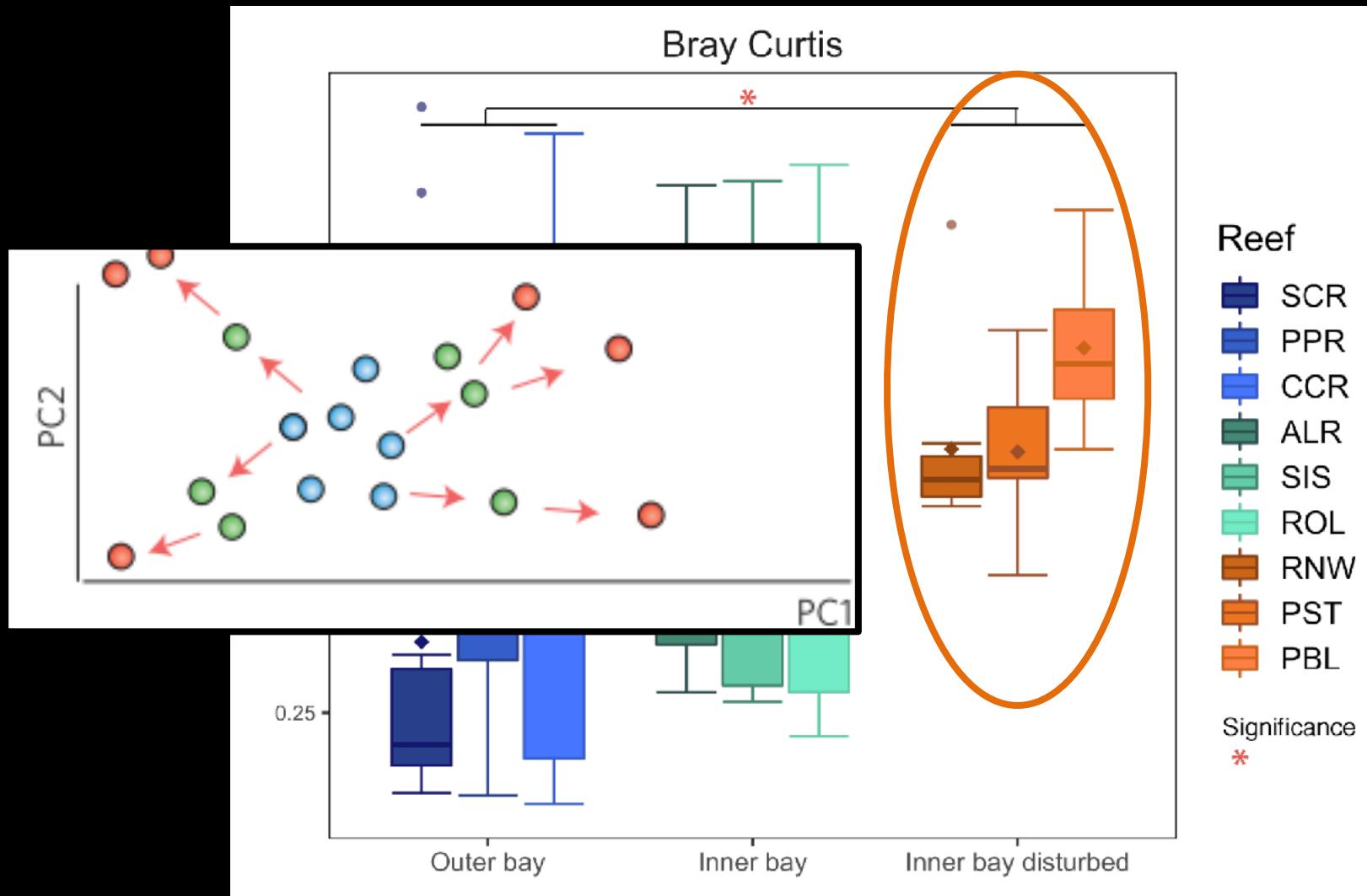


Core gut microbiome



The core
microbiome
is more stable





Dysbiotic gut microbiome on reefs with near absence of corals (no food)



Smithsonian Tropical
Research Institute

GORDON AND BETTY
MOORE
FOUNDATION

UCDAVIS

Acknowledgments (alphabetical order)

FIRST	LAST	INSTITUTION	FIRST	LAST	INSTITUTION
Andrew	Altieri	University of Florida	Owen	McMillan	Smithsonian Tropical Research Institute
Arthur	Anker	Universidade Federal de Goiás	Ipek Yasmin	Meric	University of California, Davis
Fleur	Bruggemann	University of Sorbonne Paris	Bryan	Nguyen	George Washington University
Yolanda	Camacho	University of Costa Rica	Paulo	Pachelle	Universidade Federal do Ceará
Diana	Chin	Stony Brook University	Gustav	Paulay	University of Florida
Friederike	Clever	Manchester Metropolitan University	Tiago	Pereira	University of Georgia
David	Coil	University of California, Davis	Jilian	Petersen	University of Vienna
Nicole	Dubilier	Max Planck Institute, Bremen, Germany	Richard	Preziosi	Manchester Metropolitan University
Jonathan	Eisen	University of California Davis	Helio	Quintero	University of Panama
Olivier	Gros	University of the French Antilles	Kristin	Saltonstall	Smithsonian Tropical Research Institute
Catalina	Guerra	Smithsonian Tropical Research Institute	Jarrod	Scott	Smithsonian Tropical Research Institute
Frederic	Guichard	McGill University	Andrew	Sellers	McGill University
Rhiannon	Harvey	Duke University	Maggie	Sogin	Max Planck Institute, Bremen, Germany
Alexandra	Hiller	Smithsonian Tropical Research Institute	Jade	Sourisse	University of Sorbonne Paris
Kristin	Hultgren	Seattle University	Jonathan	Stillman	University of California, Berkeley
Carla	Hurt	Tennessee Tech University	Amber	Stubler	Occidental College
Jon	Kaye	Gordon and Betty Moore Foundation	John	Taylor	London Natural History Museum
Nicole	Knight	McGill University	Mark	Torchin	Smithsonian Tropical Research Institute
			Marta	Vargas	Smithsonian Tropical Research Institute
			Bill	Wcislo	Smithsonian Tropical Research Institute



Bill Wcislo



Jonathan Eisen



Jon Kaye



The Isthmus of Panama for the study of microbial symbiosis:

WHAT CAN WE LEARN FROM COMPARATIVE
ANALYSIS OF HOST-ASSOCIATED
MICROBIOMES ACROSS TWO OCEANS?

DECEMBER 2019

Smithsonian Tropical Research Institute | Panamá



Workshop funding generously provided, in part,
by the Smithsonian Office of the Provost's One Smithsonian Symposia
Program and the Gordon and Betty Moore Foundation.





Smithsonian Tropical
Research Institute

GORDON AND BETTY
MOORE
FOUNDATION

UCDAVIS

THANK YOU!

