



Smithsonian Tropical
Research Institute

GORDON AND BETTY
MOORE
FOUNDATION

UC DAVIS

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



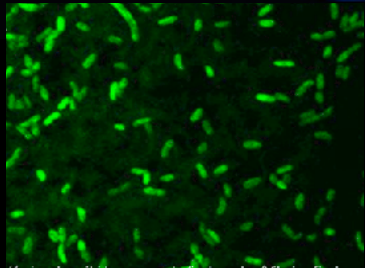
Matthieu Leray, Laetitia Wilkins, Jarrod Scott and the #istmob biome team

Tupper seminar - March 10, 2020

Microbial symbionts fulfill essential functions for hosts

Predator avoidance

Hawaiian bobtail squid

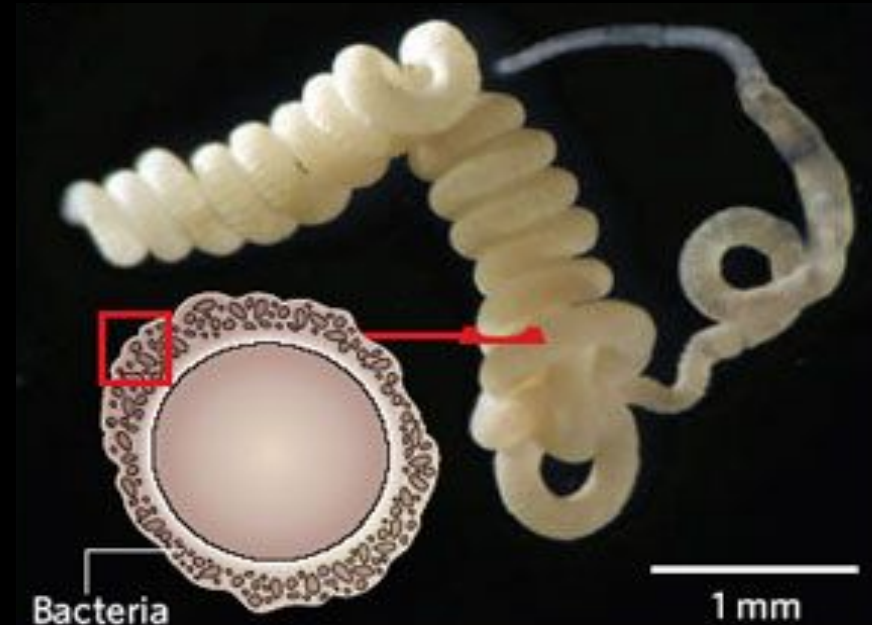


Vibrio fischeri

Bioluminescent bacteria
for predator avoidance

Nutrition

Gutless marine worm



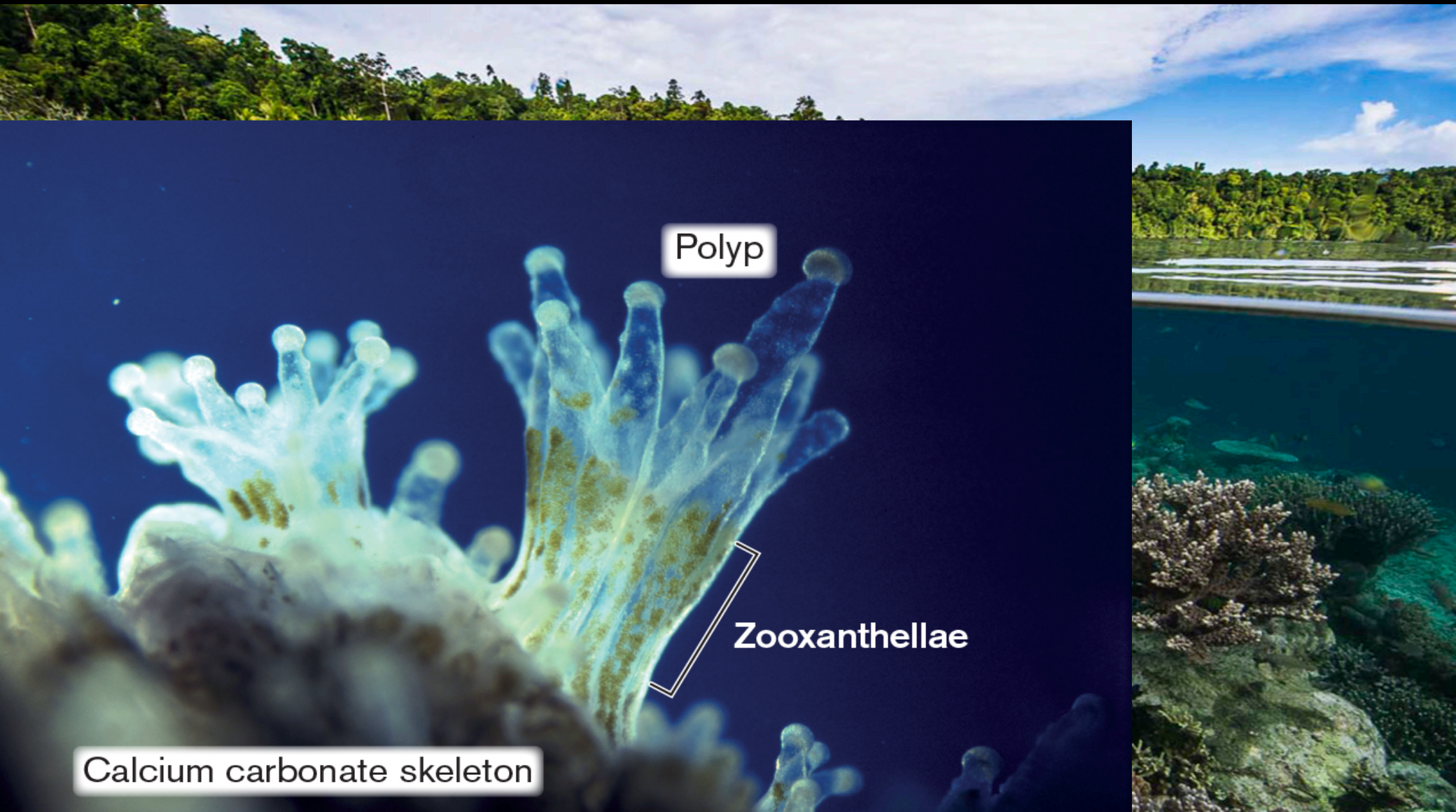
Several chemosynthetic bacteria

They feed the worm

Animal-microbe nutritional symbiosis are the foundation of marine ecosystems

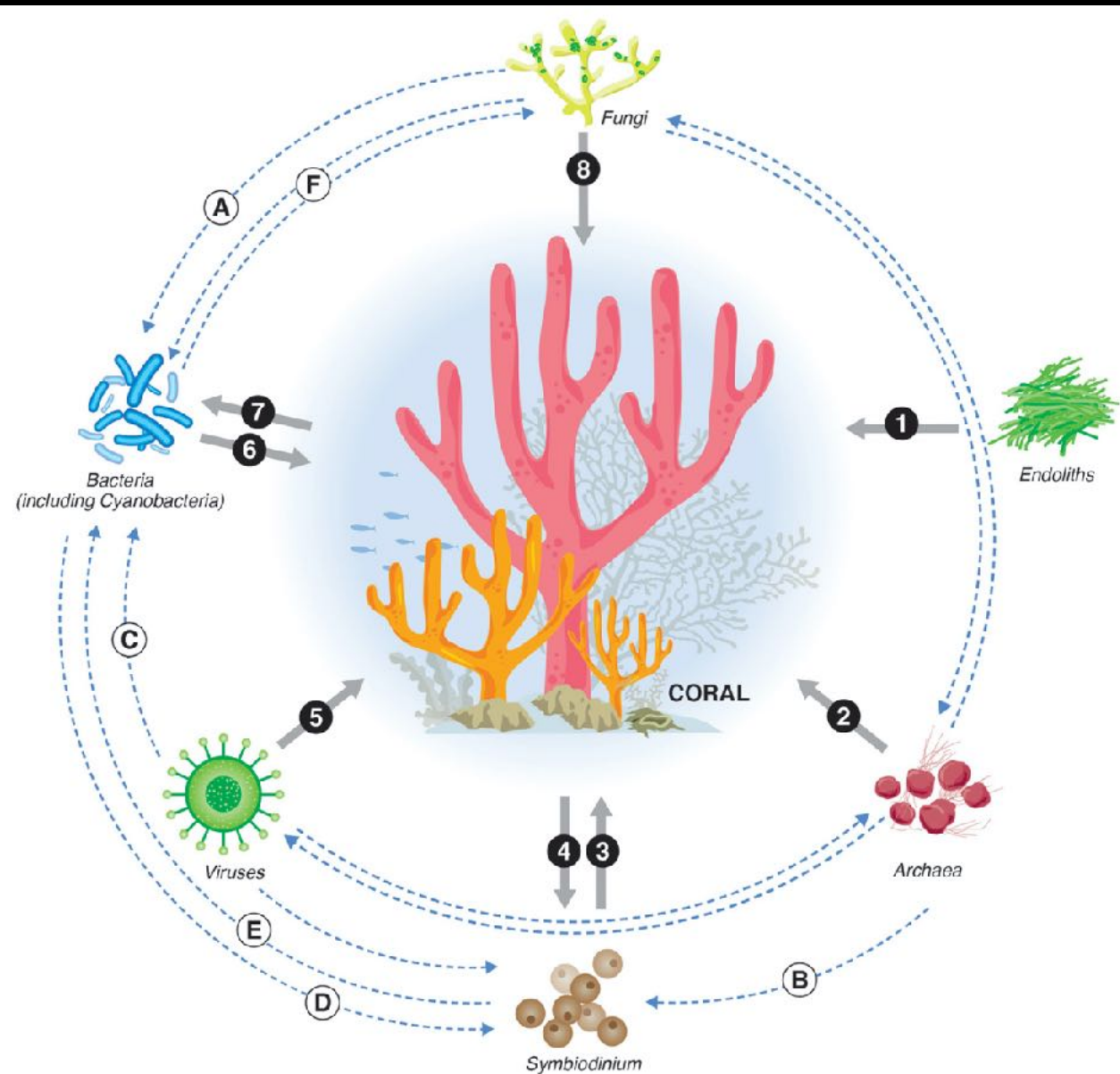


Animal-microbe nutritional symbiosis are the foundation of marine ecosystems



EXAMPLES OF POSSIBLE ROLES AND RELATIONSHIPS BETWEEN CORALS AND THEIR SYMBIONTS

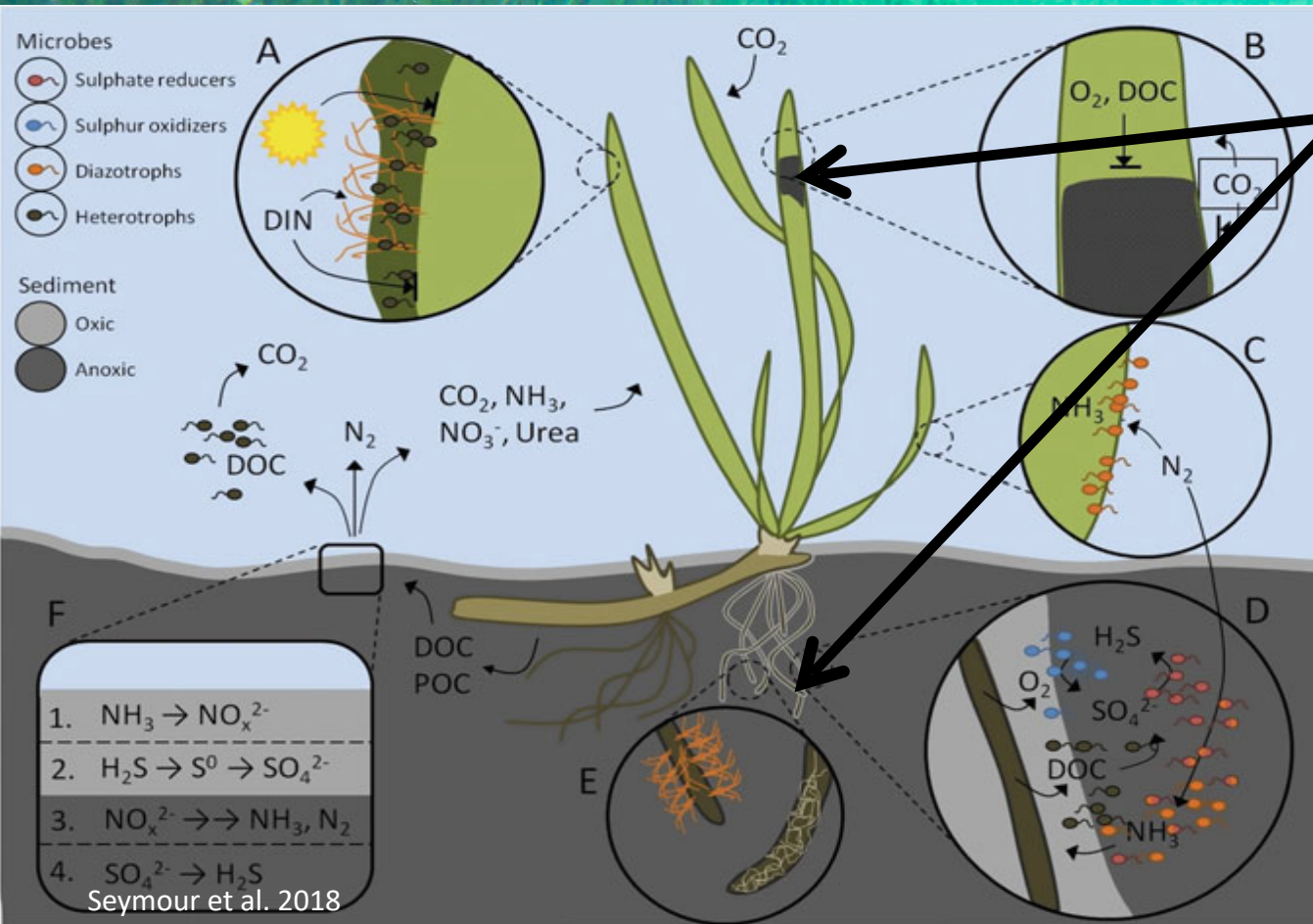
- 1 Photosynthate transference.
- 2 Nitrogen cycling.
- 3 Main carbon source supplier and production of DMSP that might play a role as antioxidant and on bacterial population control. Protection against UV.
- 4 Provides shelter and protection and role in the nutrient cycles.
- 5 Gene transfer. Natural 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



Nitrogen fixing bacterial films on leafs and roots

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'Dea², 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. Thacker^{12,12}, Rebecca Vega Thurber¹³, William T. Wcislo², Elizabeth G. Wilbanks¹⁴, Jonathan A. Eisen^{1,15,16}

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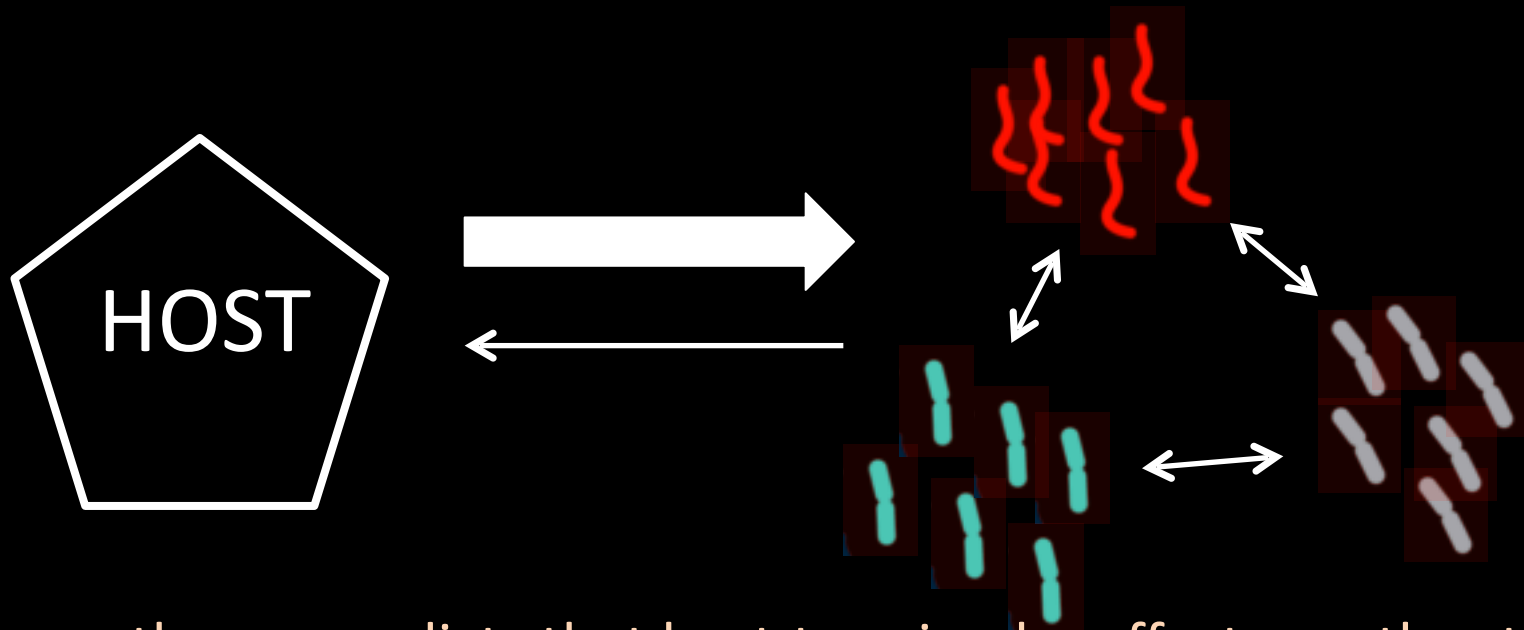


How have interactions between
hosts and microbes/microbiomes evolved?

“The problem of the diverse microbiome”

How have interactions between hosts and microbes/microbiomes evolved?

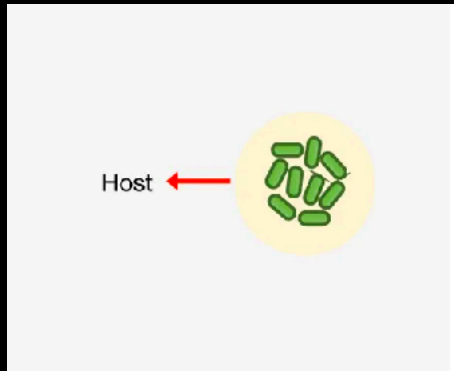
“The problem of the diverse microbiome”



“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

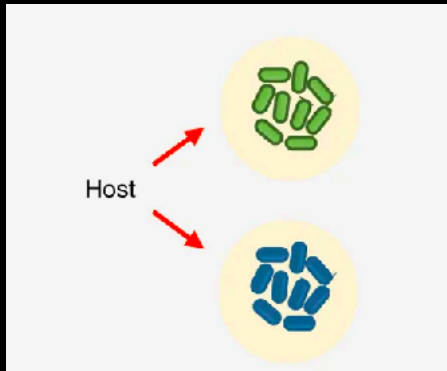
Symbiont control



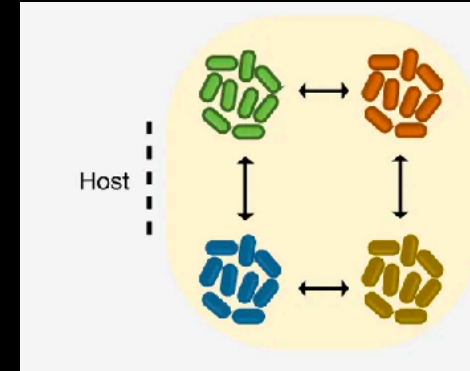
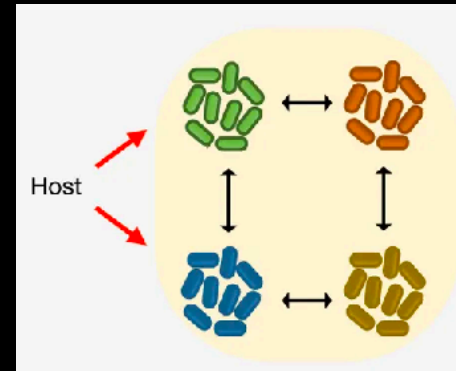
Wolbachia



Host control



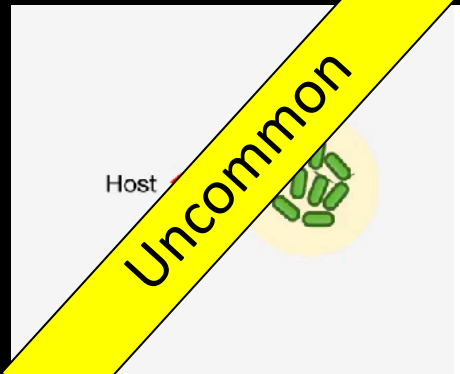
Microbiome on leash



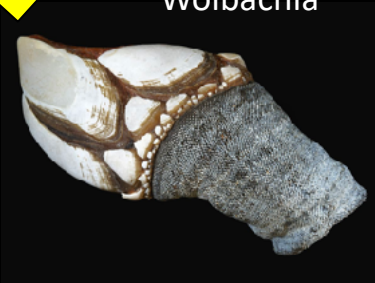
- Each model is consistent with evolutionary theory
- Each model is consistent with real-world examples

Models of host–microbiome interaction

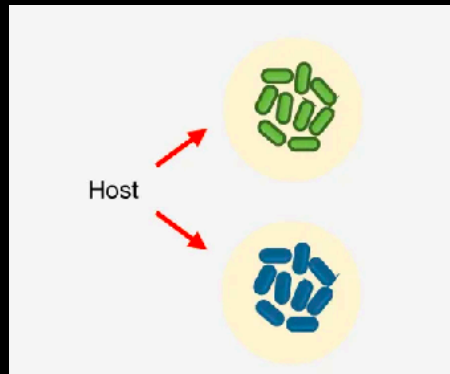
Symbiont control



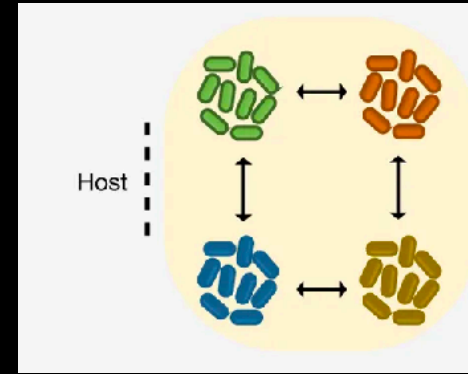
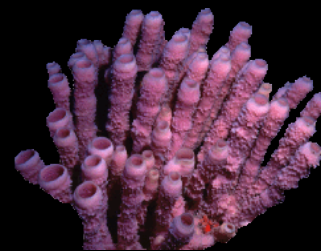
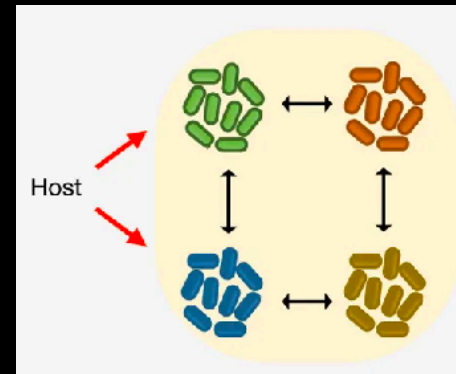
Wolbachia



Host control



Microbiome on leash



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Models of host–microbiome interaction

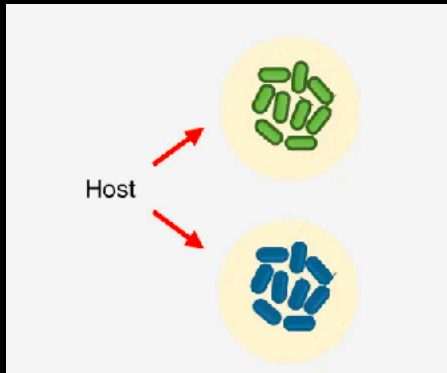
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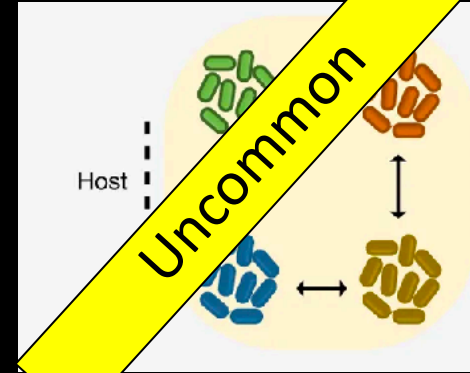
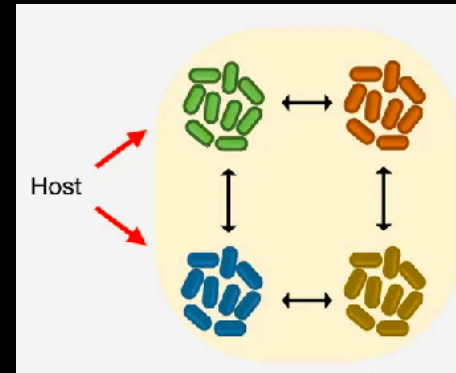
Wolbachia



Host control



Microbiome on leash



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Models of host–microbiome interaction

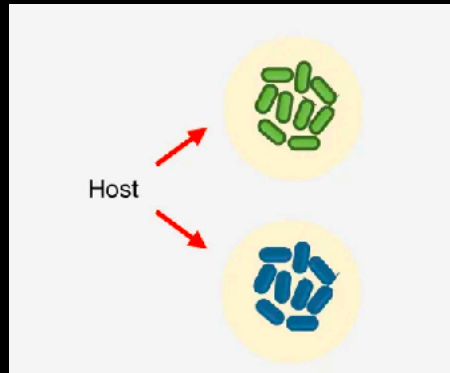
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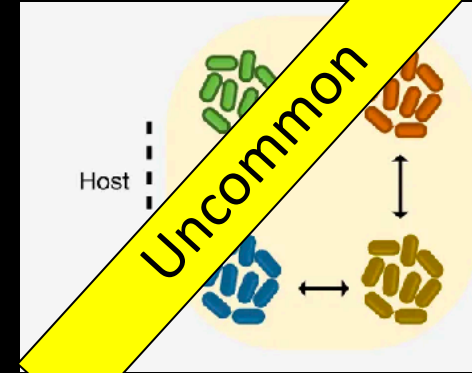
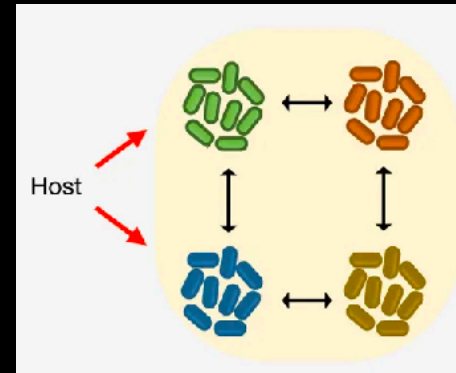
Wolbachia



Host control



Microbiome on leash



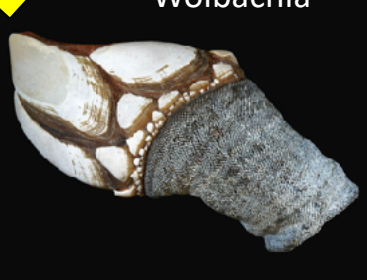
- ◆ Host monitors one or few strains
- ◆ Fine-scale host control mechanisms
- ◆ Possible vertical transmission to increase fitness

Models of host–microbiome interaction

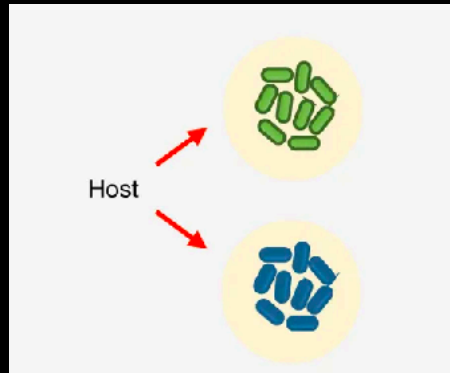
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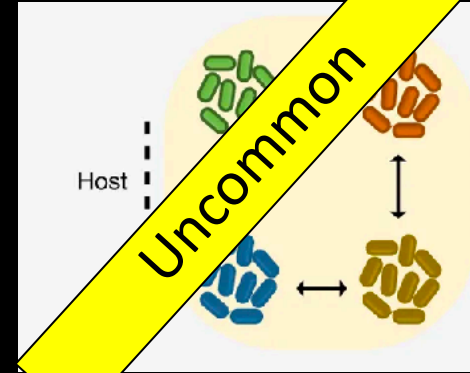
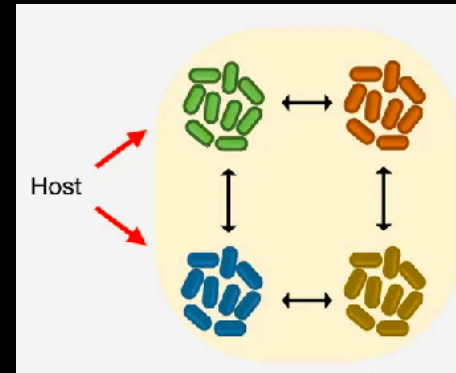
Wolbachia



Host control



Microbiome on leash Open ecosystem



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

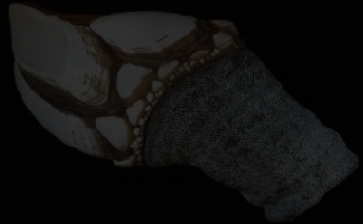
- ◆ Many microbial strains co-exists = the “microbiome”
- ◆ Host under selection to foster a beneficial microbiome
- ◆ Primarily horizontal transmission

Models of host–microbiome interaction

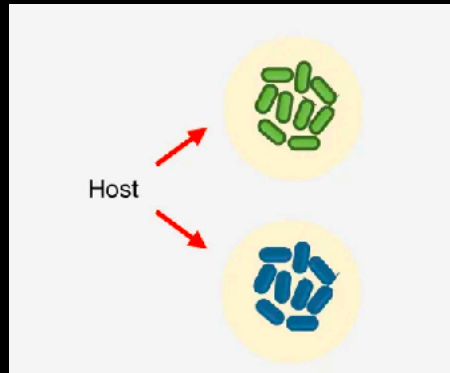
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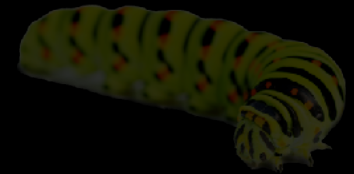
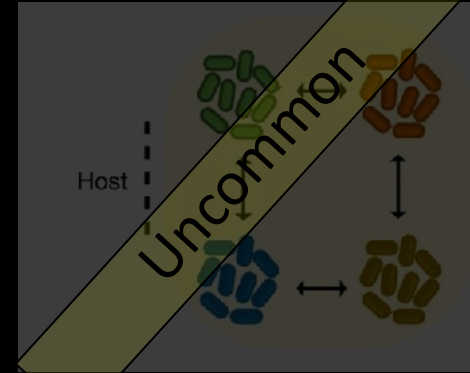
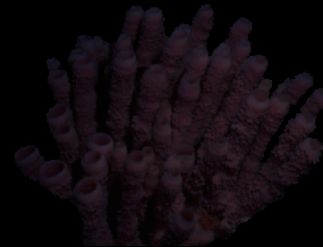
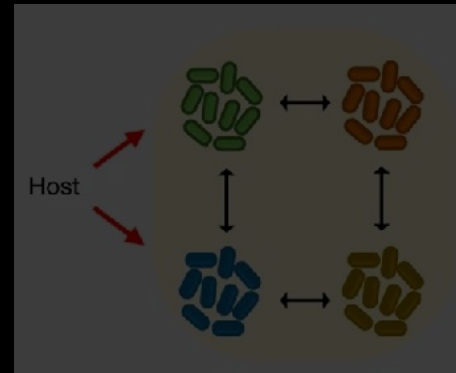
Wolbachia



Host control



Microbiome on leash Open ecosystem



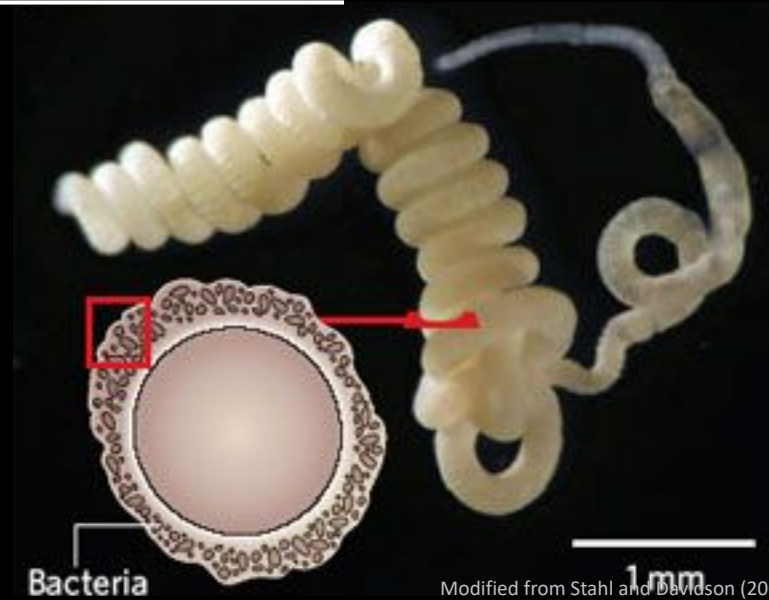
Research is highly biased towards a small number of hosts and microbes

Hawaiian bobtail squid



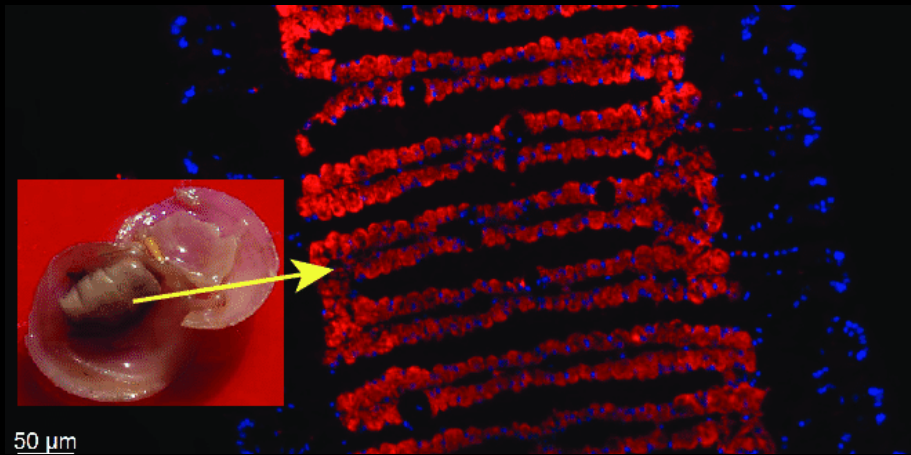
Todd Bretl Underwater Photography

Gutless worm



Modified from Stahl and Davidson (2006)

Lucinid clam



Shipworm



Photo by O'Connor et al. 2014

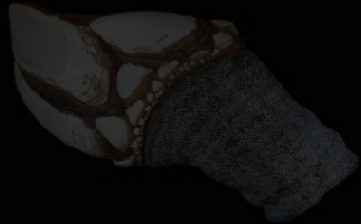
Research is highly biased towards a small number of hosts
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Models of host–microbiome interaction

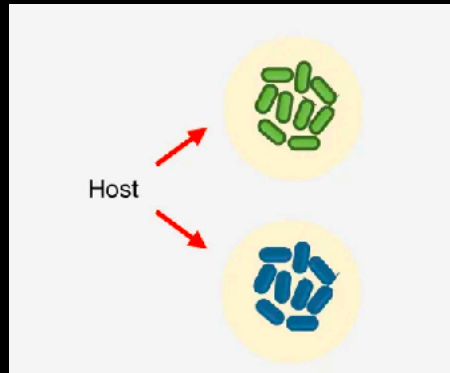
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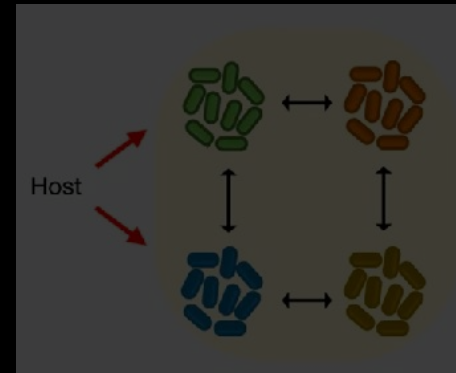
Wolbachia



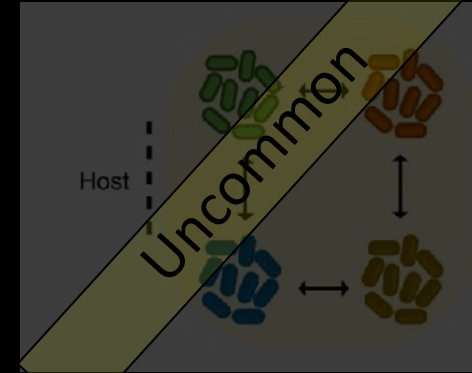
Host control



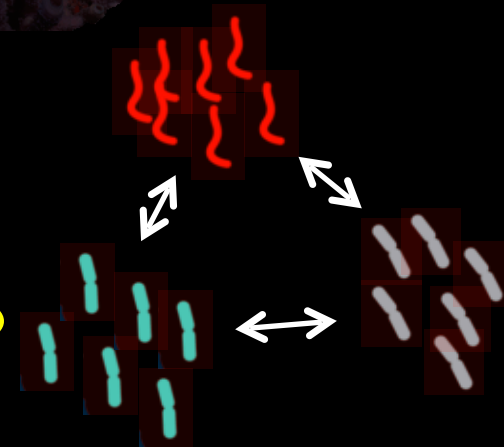
Microbiome on leash



Open ecosystem



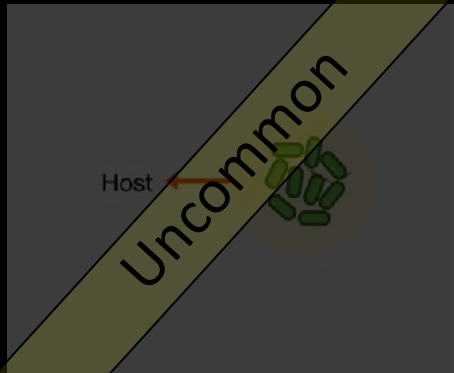
?



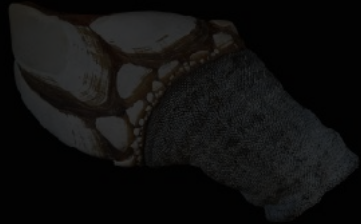
Limited focus on how hosts influence microbiomes

Models of host–microbiome interaction

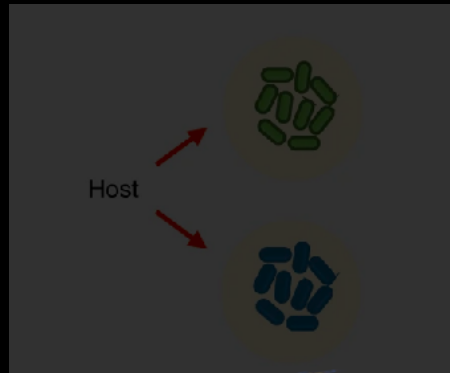
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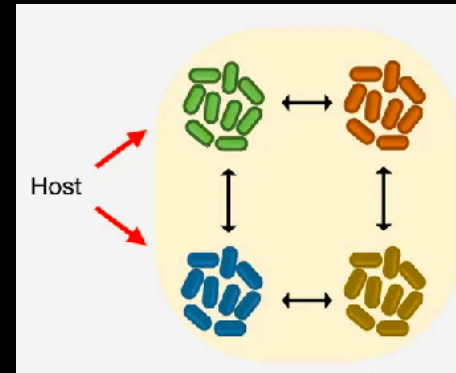
Wolbachia



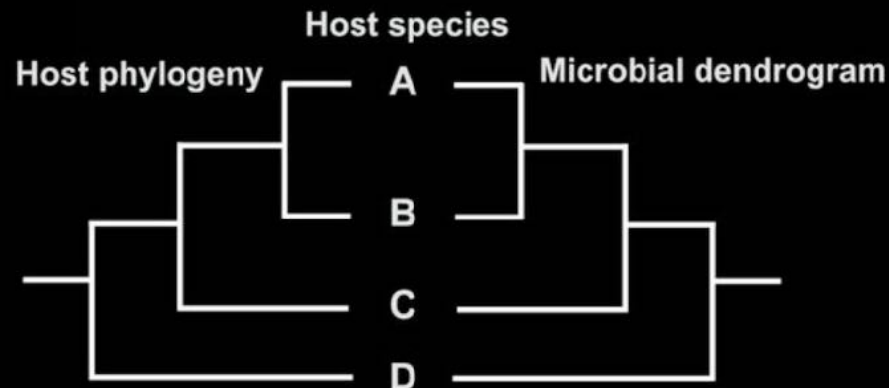
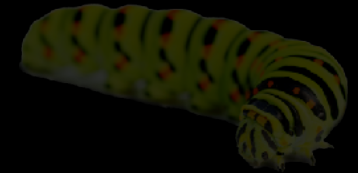
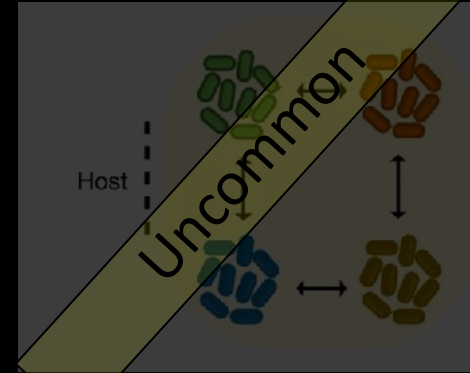
Host control



Microbiome on leash

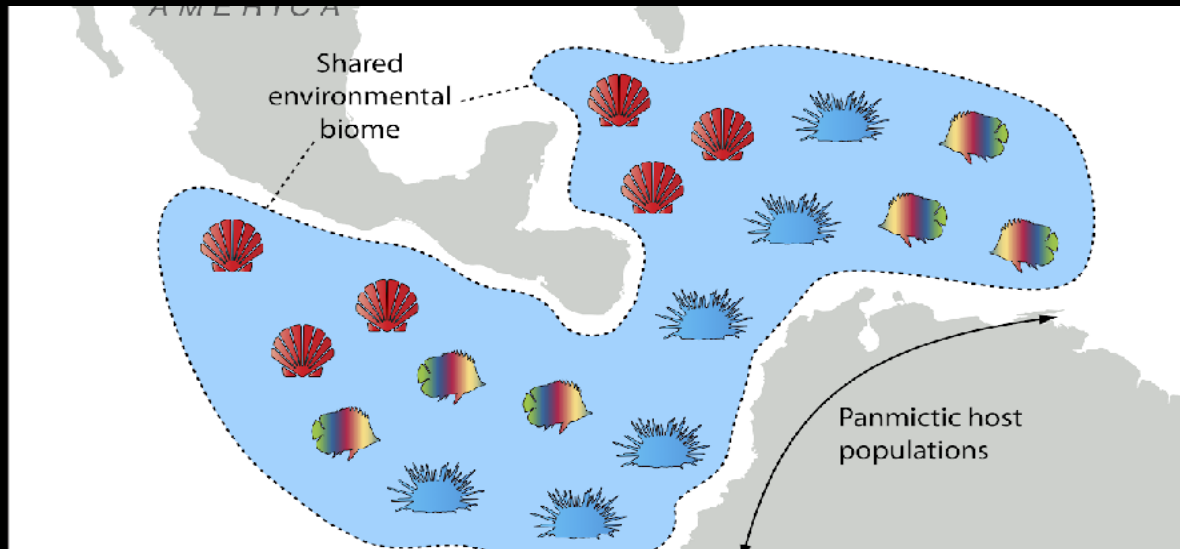


Open ecosystem



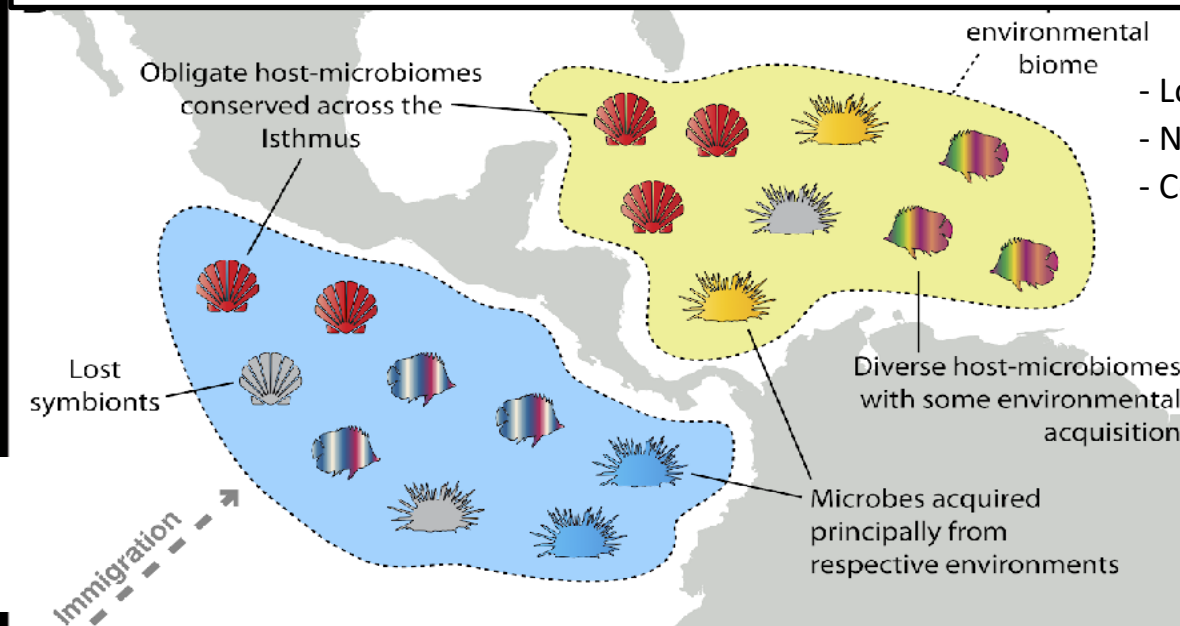
Studies lack evolutionary & ecological contexts

The closure of the isthmus provides the context



3 million years ago

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

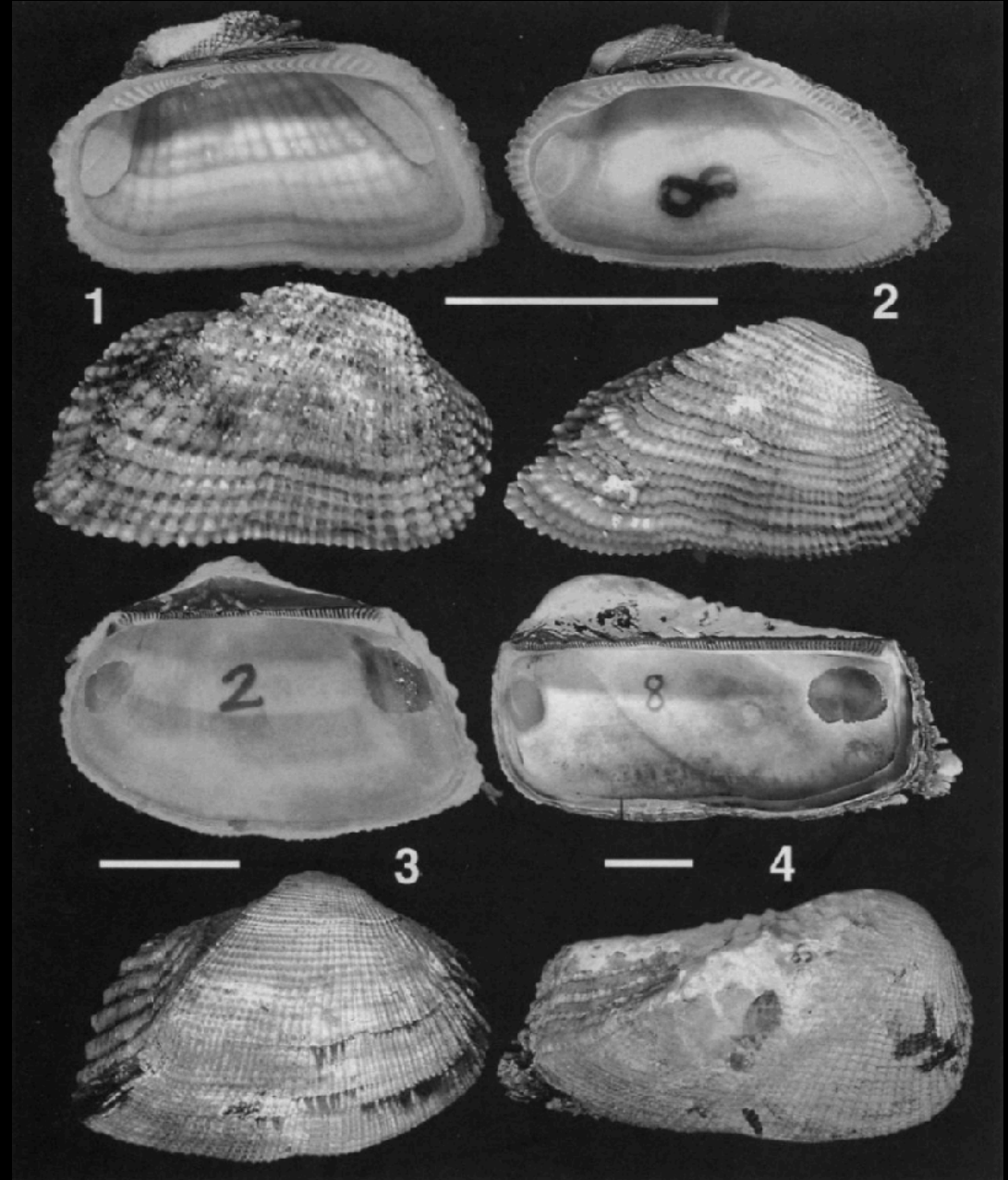
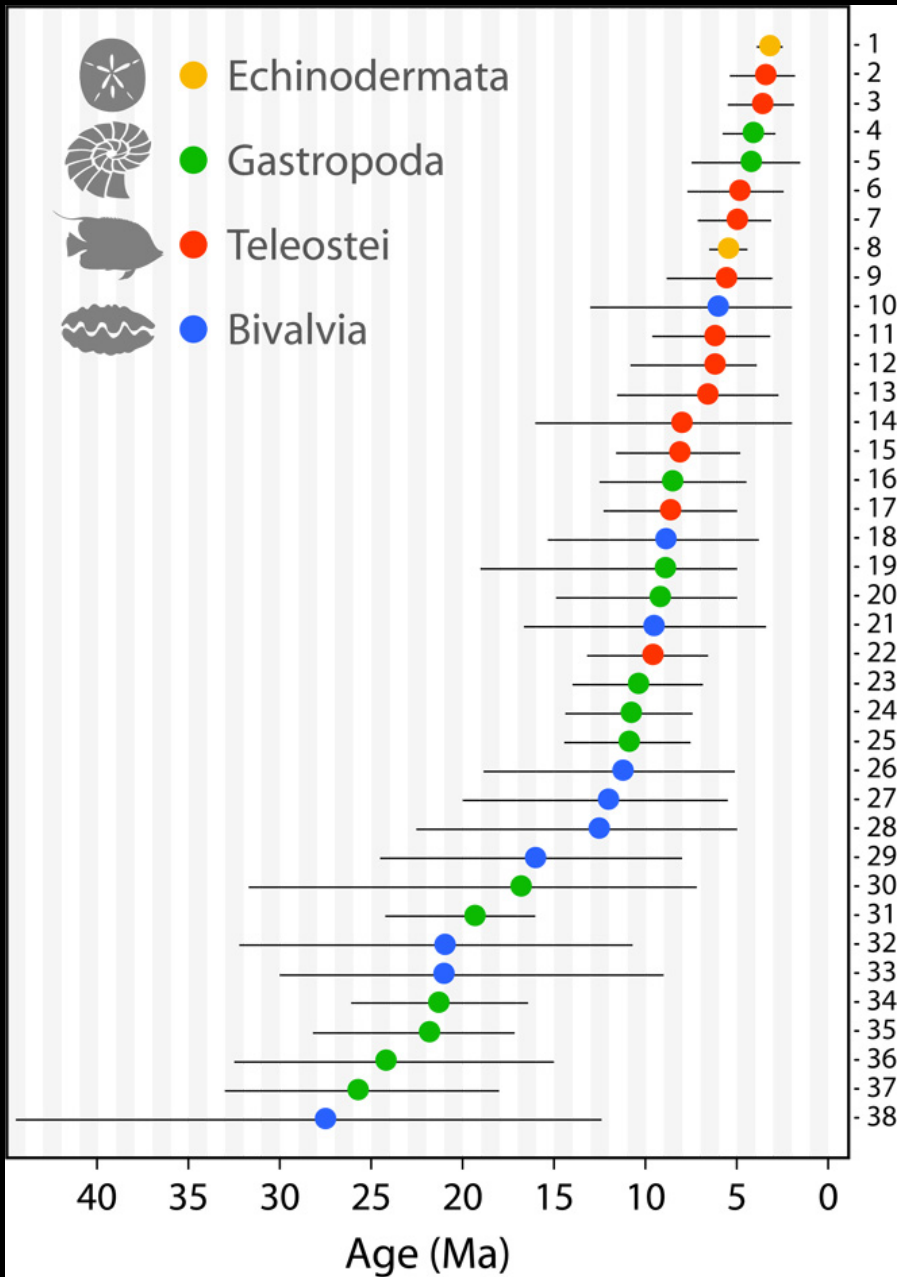


- Low nutrient
- No tides
- Constant temperature

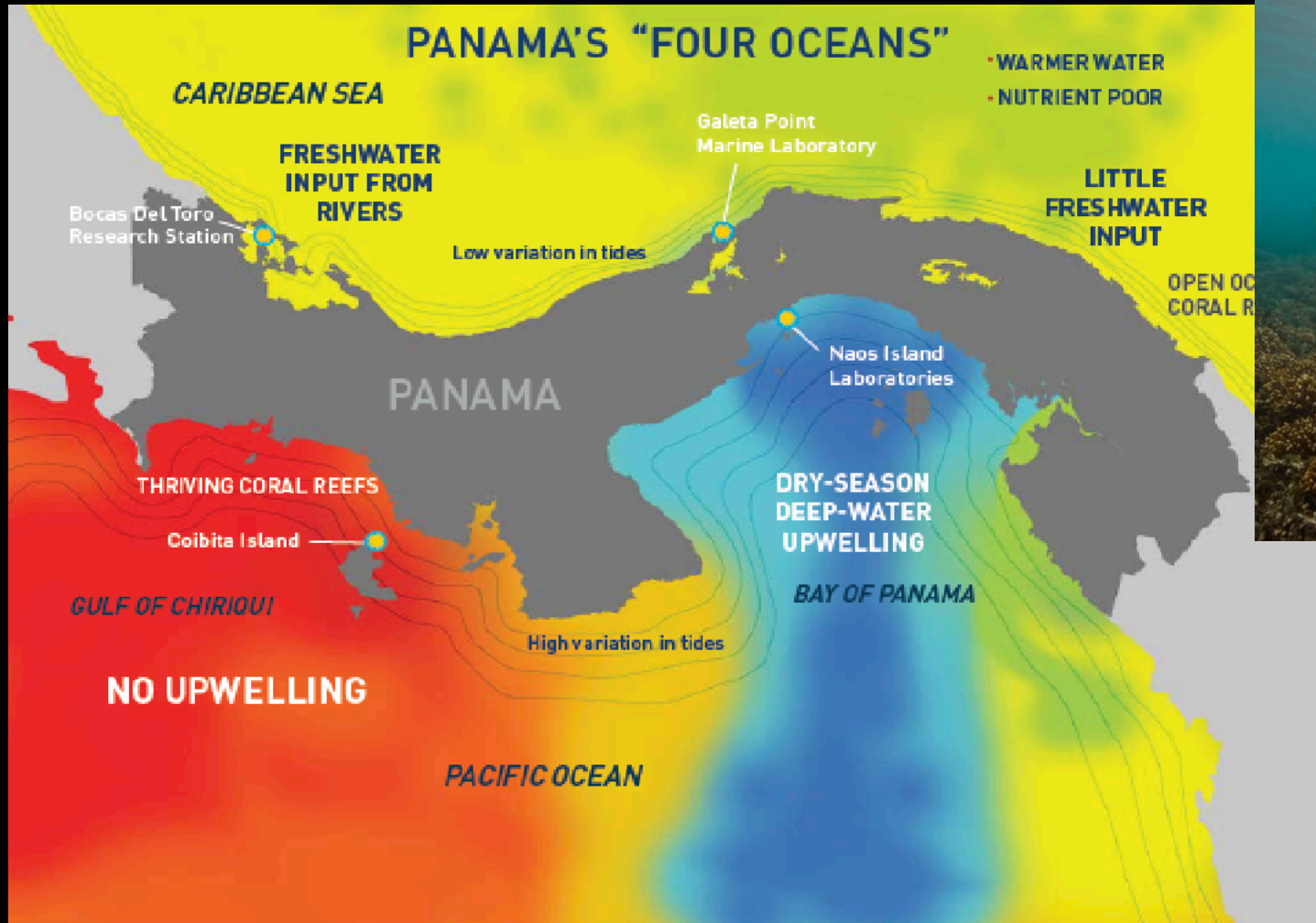
Today

- 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

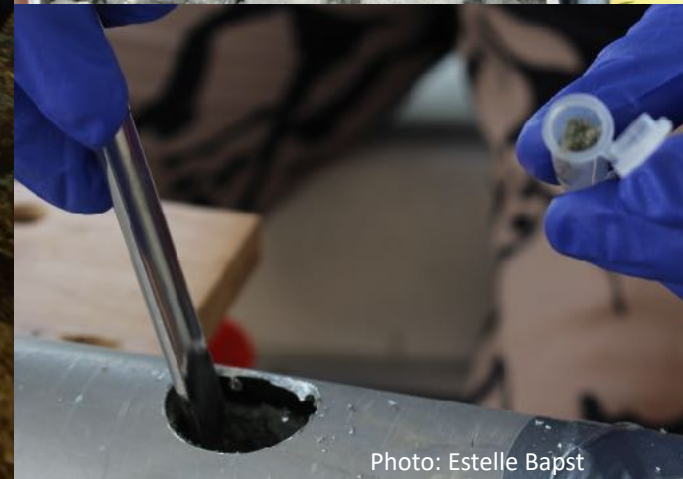


Photo: Estelle Bapst

Focal groups:

Eastern Pacific

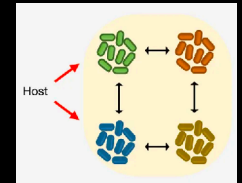
Caribbean

Fish

+ microbiome



Microbiome on leash

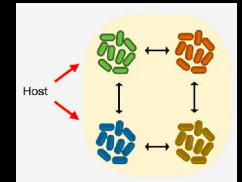


Shrimp

+ microbiome



Microbiome on leash

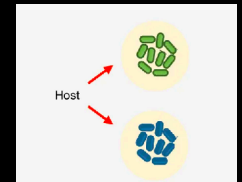


Clam

+ chemosymbiotic
microbe

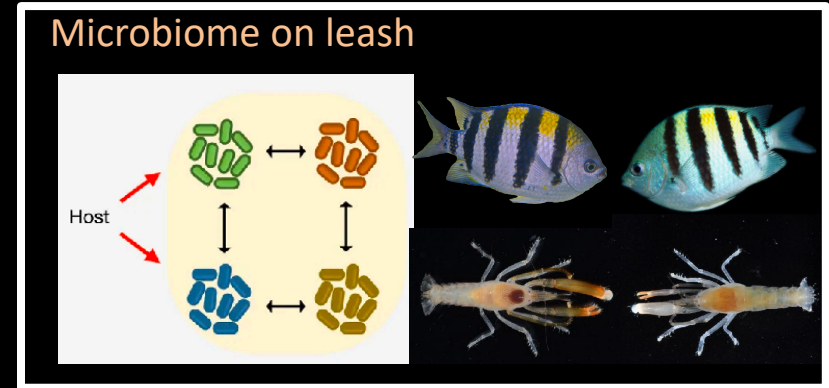
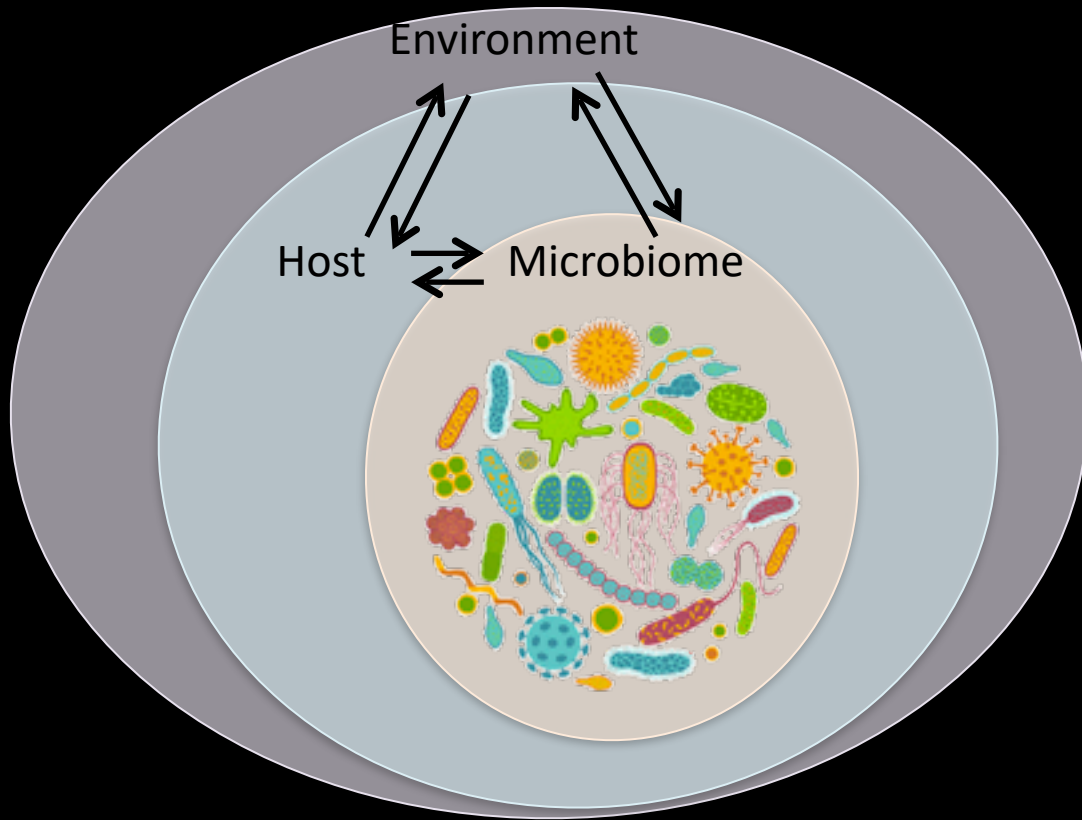


Host control



Research axes

1) Identifying ecological and evolutionary drivers of the microbiome

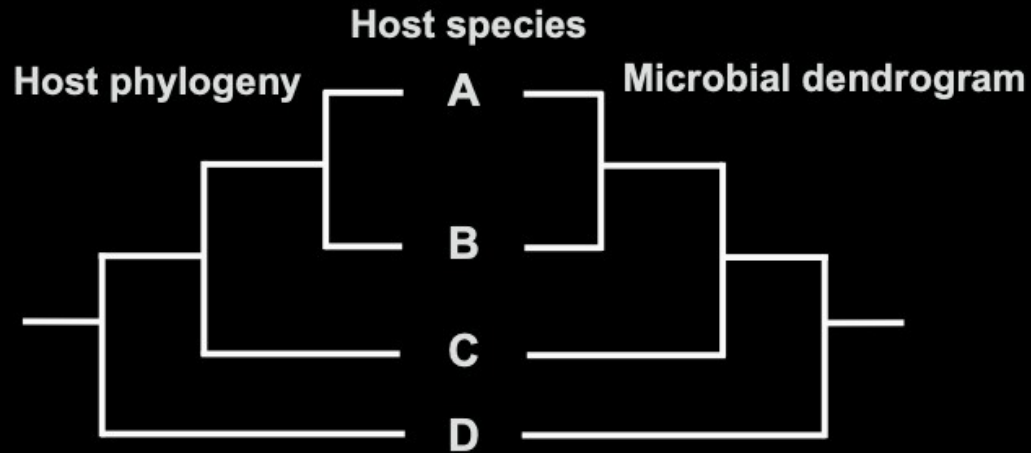
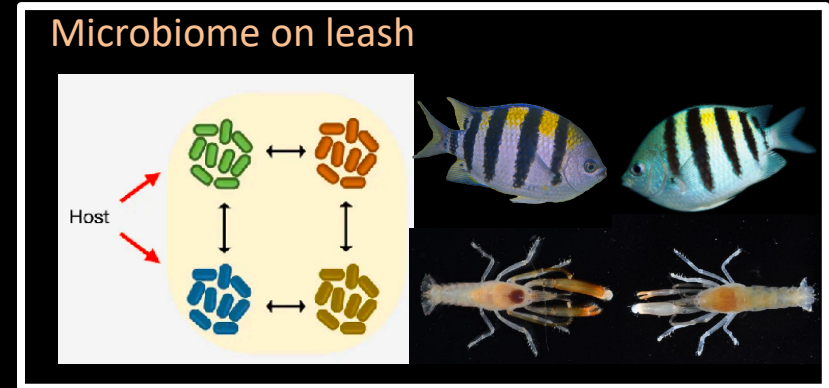


What are the relative contributions of:

- Environment
 - Host
 - Phylogeny
- on community assembly?

Research axes

1) Identifying ecological and evolutionary drivers of the microbiome



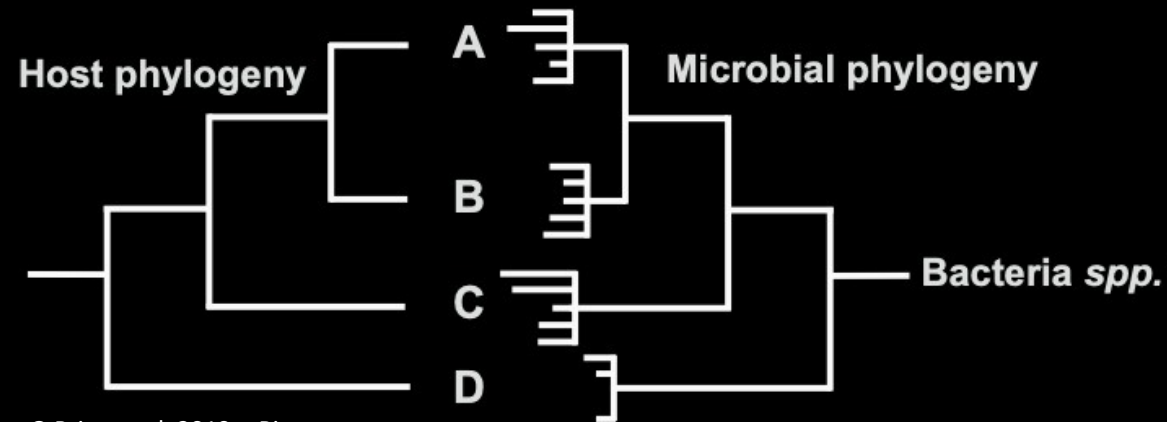
O.Brien et al. 2019 mBio

Are microbiomes structured through phylogenetically related host traits?

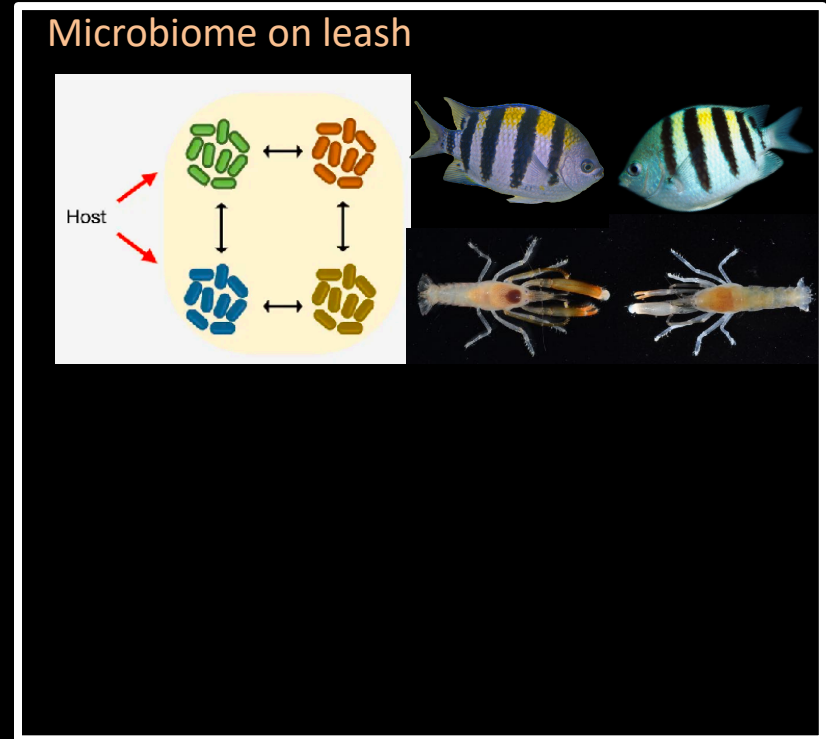
Phylosymbiosis: The ecological relatedness (or similarity) of the microbiome mirrors host phylogeny

Research axes

2) Co-divergence between hosts and microbes



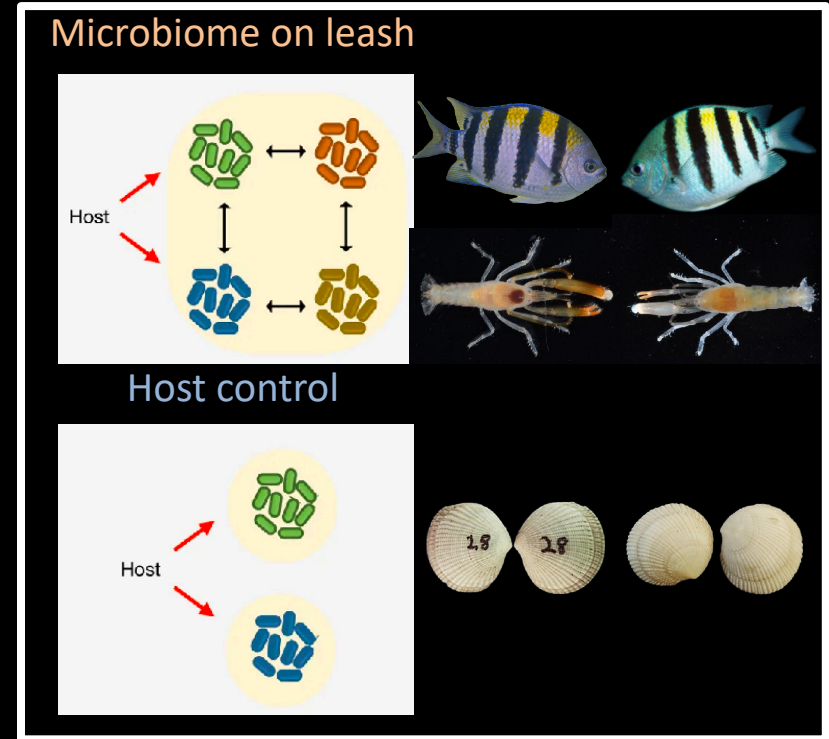
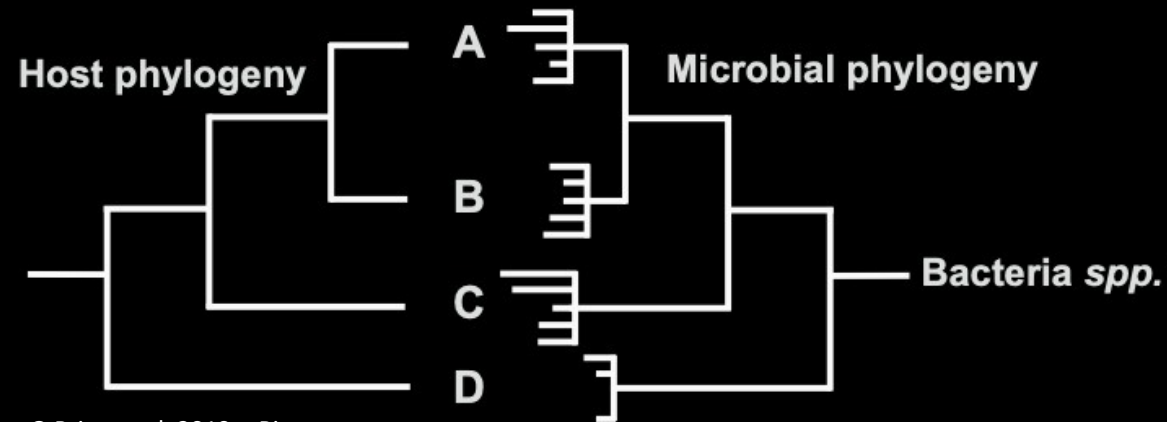
O'Brien et al. 2019 mBio



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

Research axes

2) Co-divergence between hosts and microbes

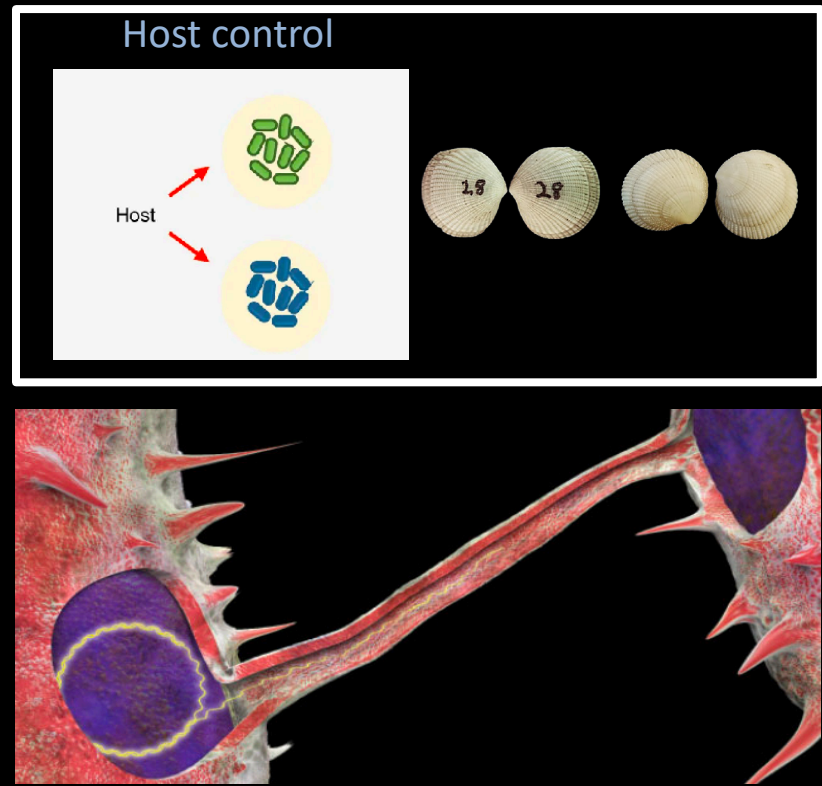
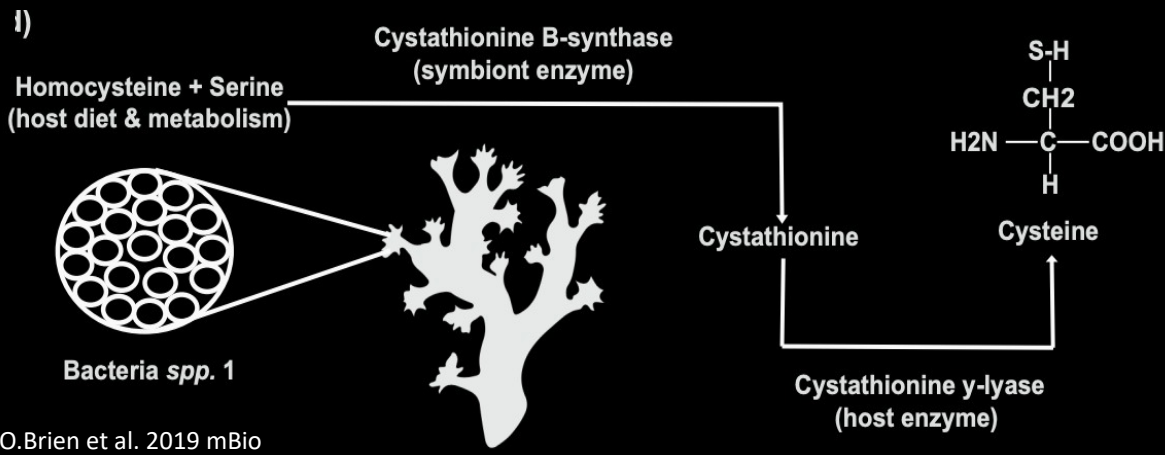


Which microbes have had long-term interactions with hosts? \Rightarrow mutualists? Parasites?

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

Research axes

3) Adaptation and metabolic cooperation

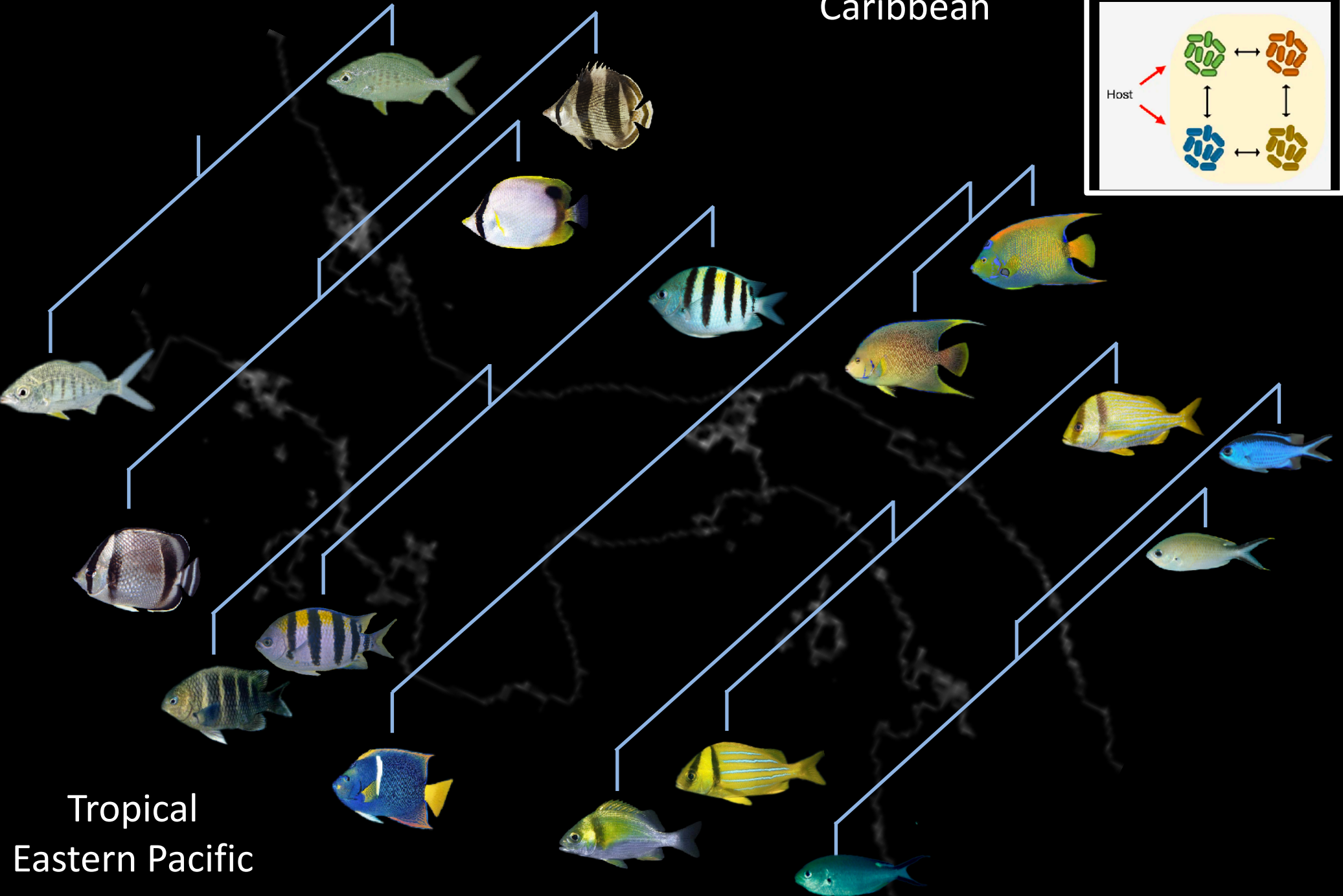
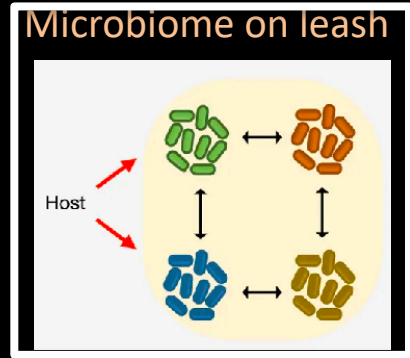


Do we see evidence of adaptations in microbial genomes?

And to what selective pressures?

Is the metabolic function of the microbe evolving and how?

Caribbean



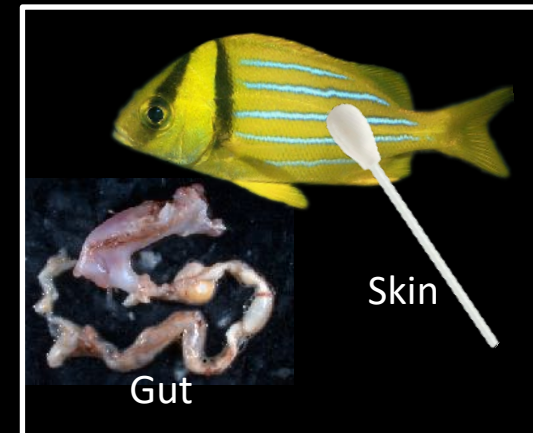
Sampling

	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	Planktivore
		<i>Abudefduf saxatilis</i>	Caribbean	19	
		<i>Abudefduf troschelii</i>	Eastern Pacific	33	
		<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 fuscifer</i>	Caribbean		Carnivore
		<i>Cephalopholis fulva</i>	Caribbean		

Sampling locations










Sample types



16S rRNA
Earth Microbiome Project
protocols

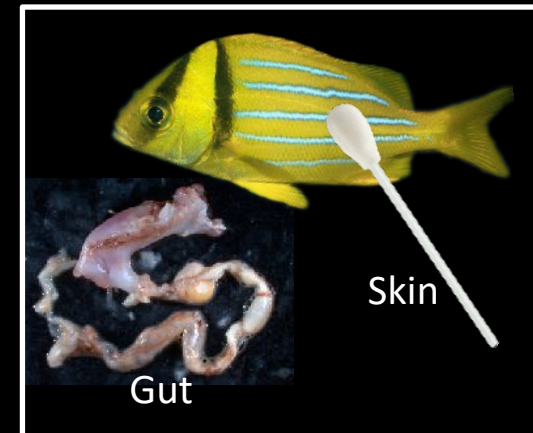
Sampling

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

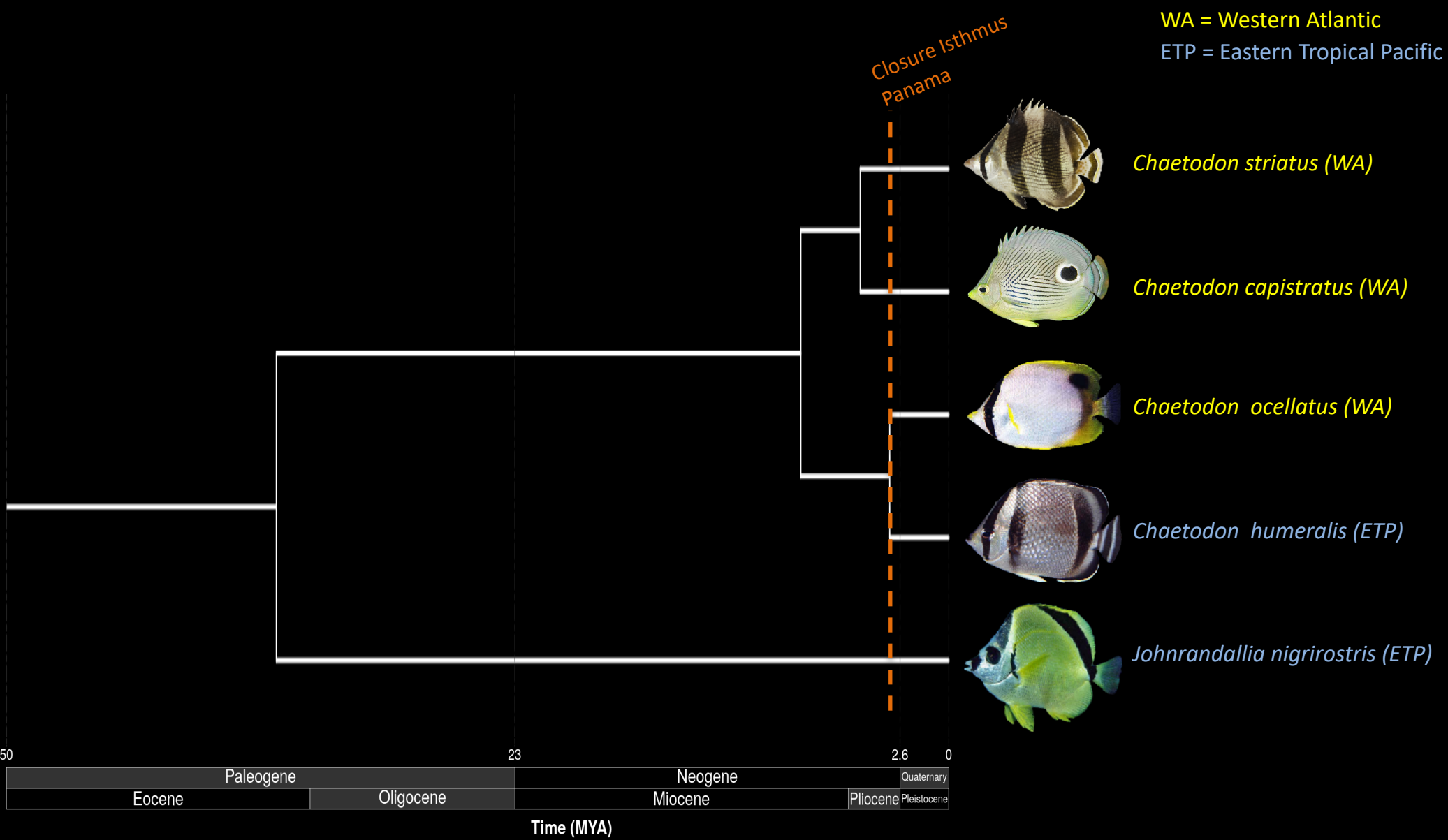
Sampling locations



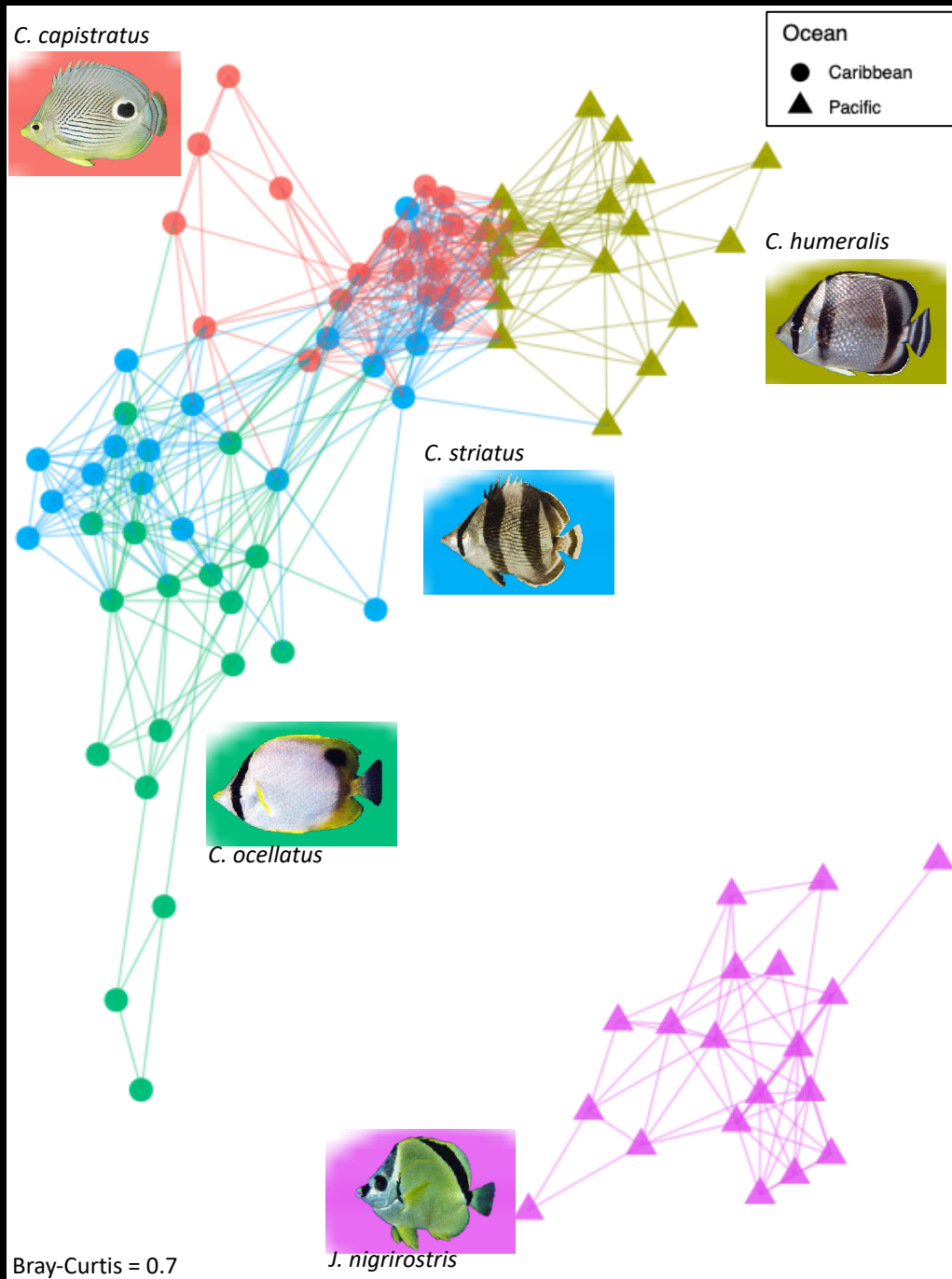
Sample types



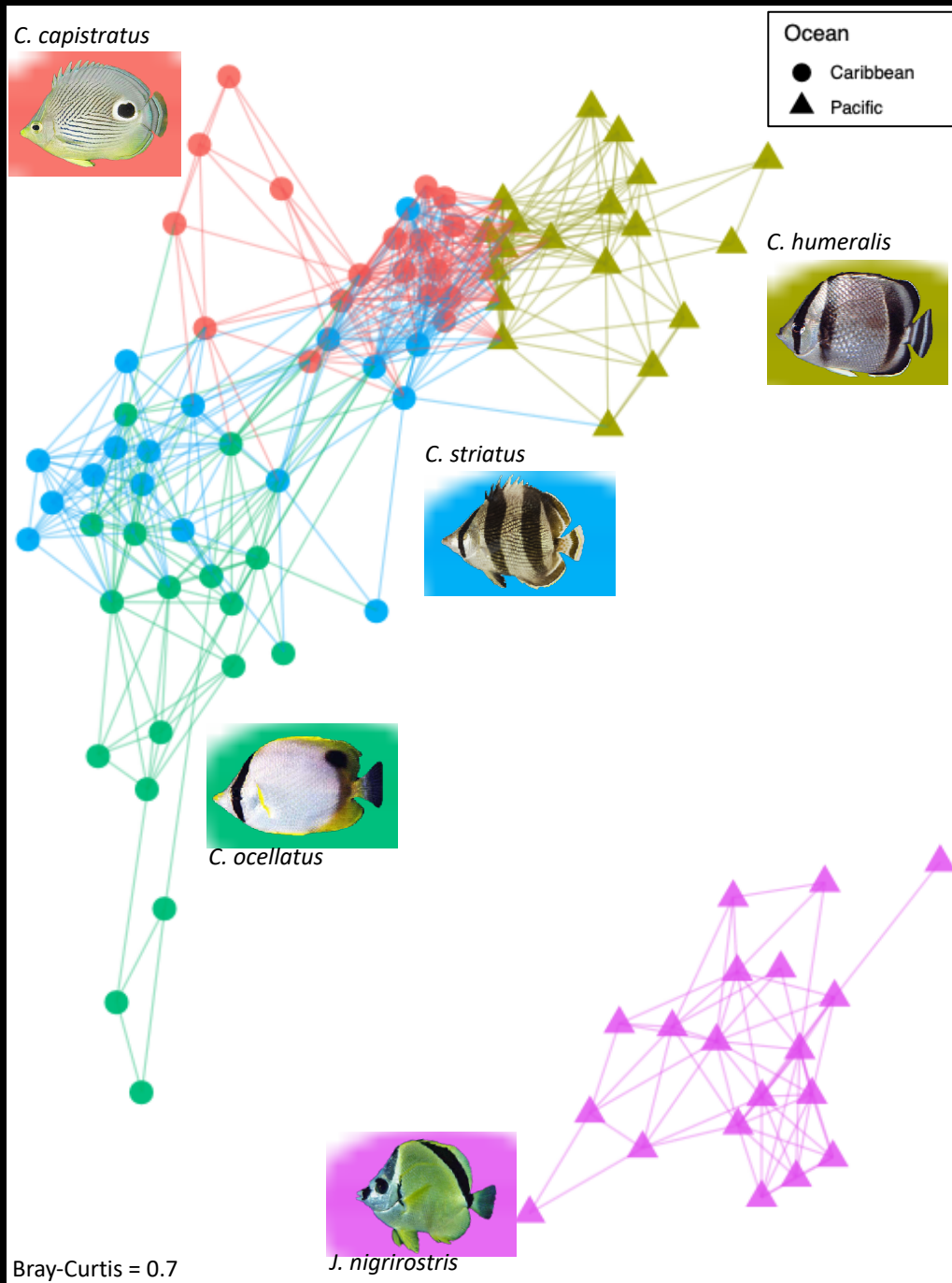
16S rRNA
Earth Microbiome Project
protocols



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

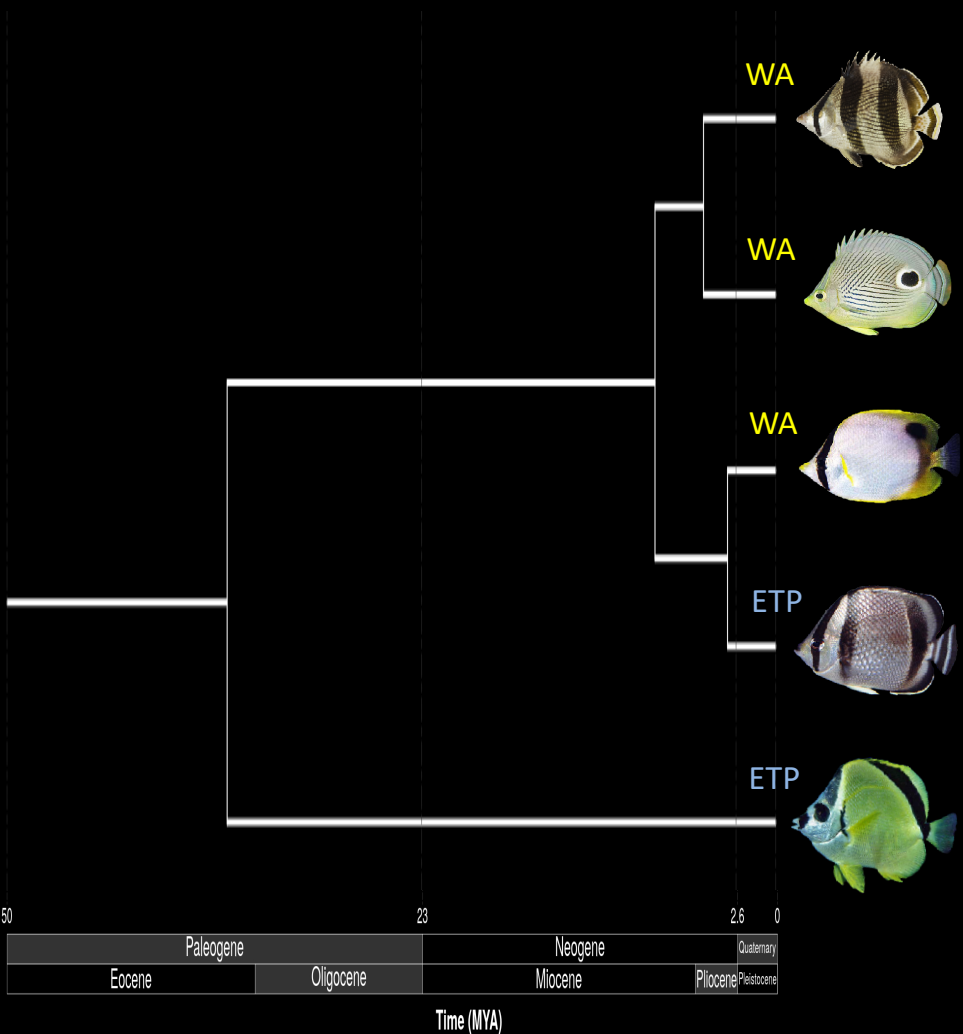
(UPGMA tree based on Bray Curtis distances of 16S rRNA ASVs)

Phyllosymbiosis?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

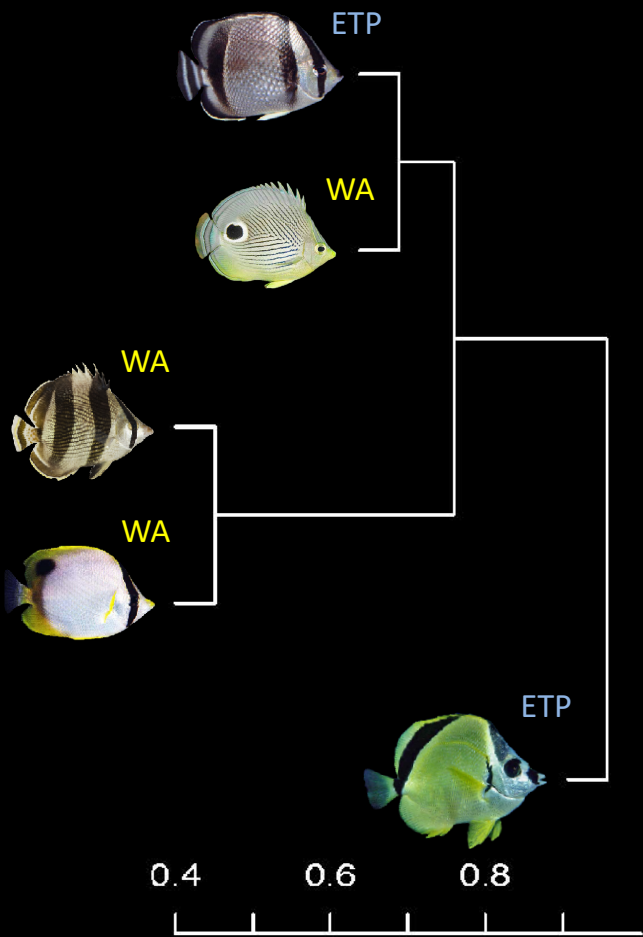
Host tree

(based on molecular markers)



Gut microbiome

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

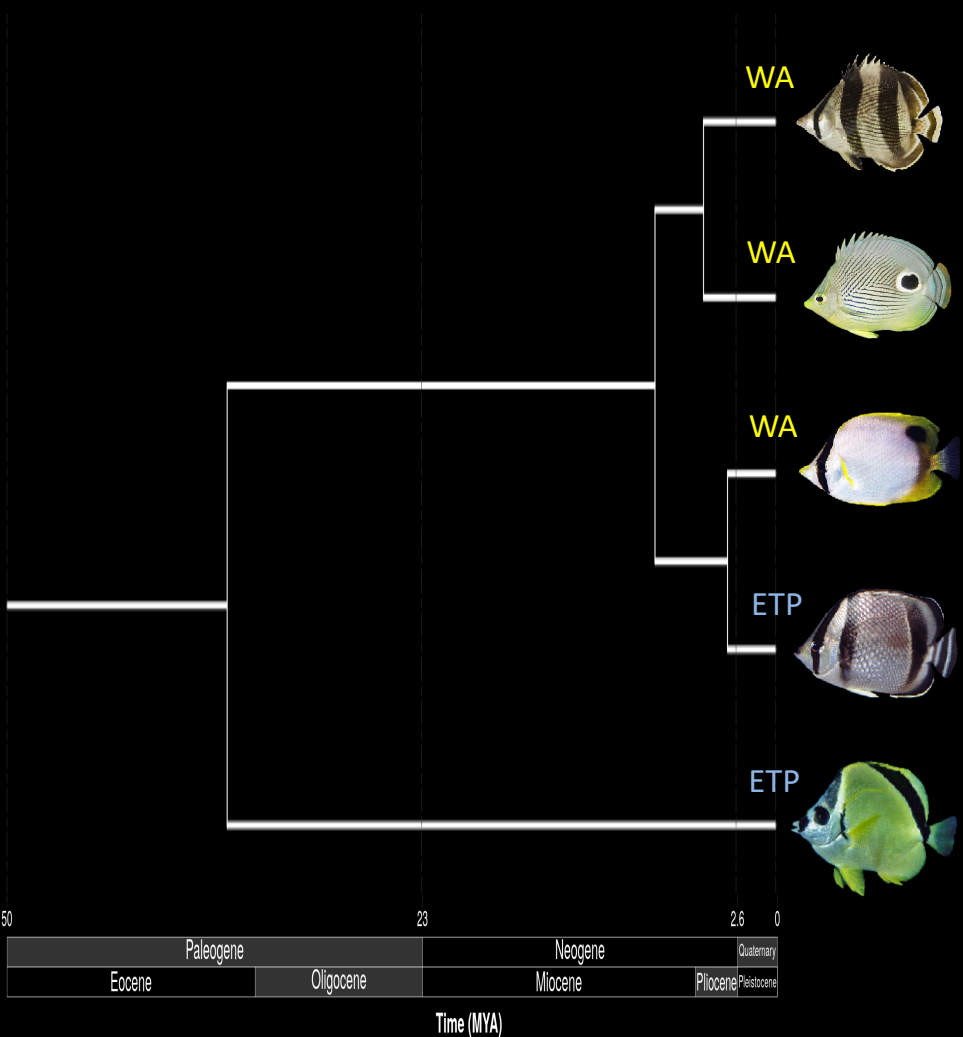


Phyllosymbiosis?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

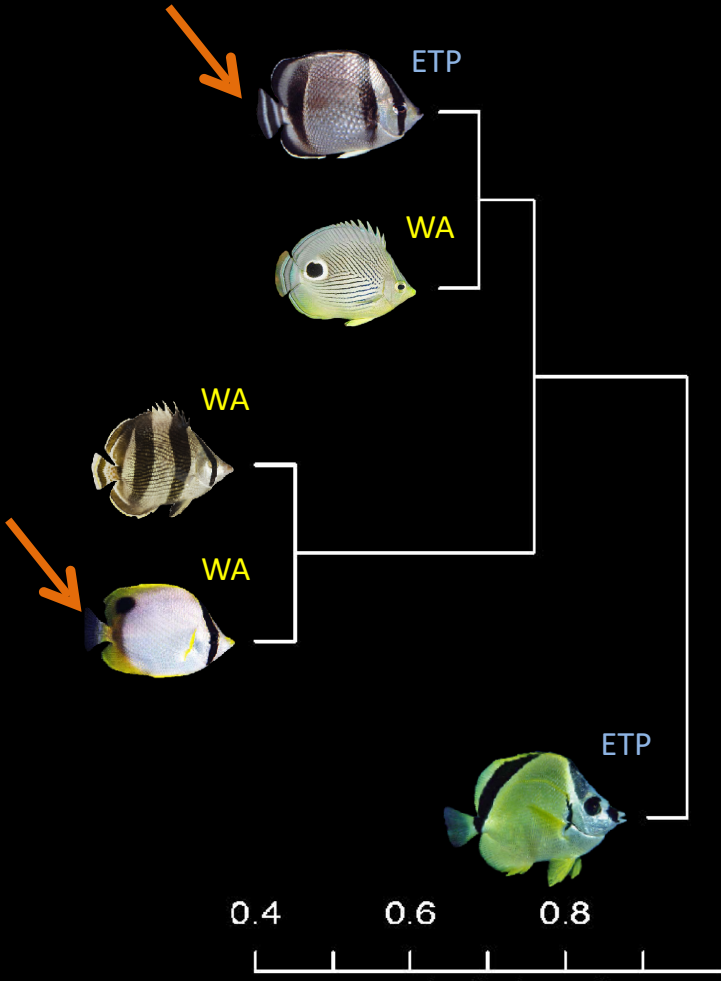
Host tree

(based on molecular markers)



Gut microbiome

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



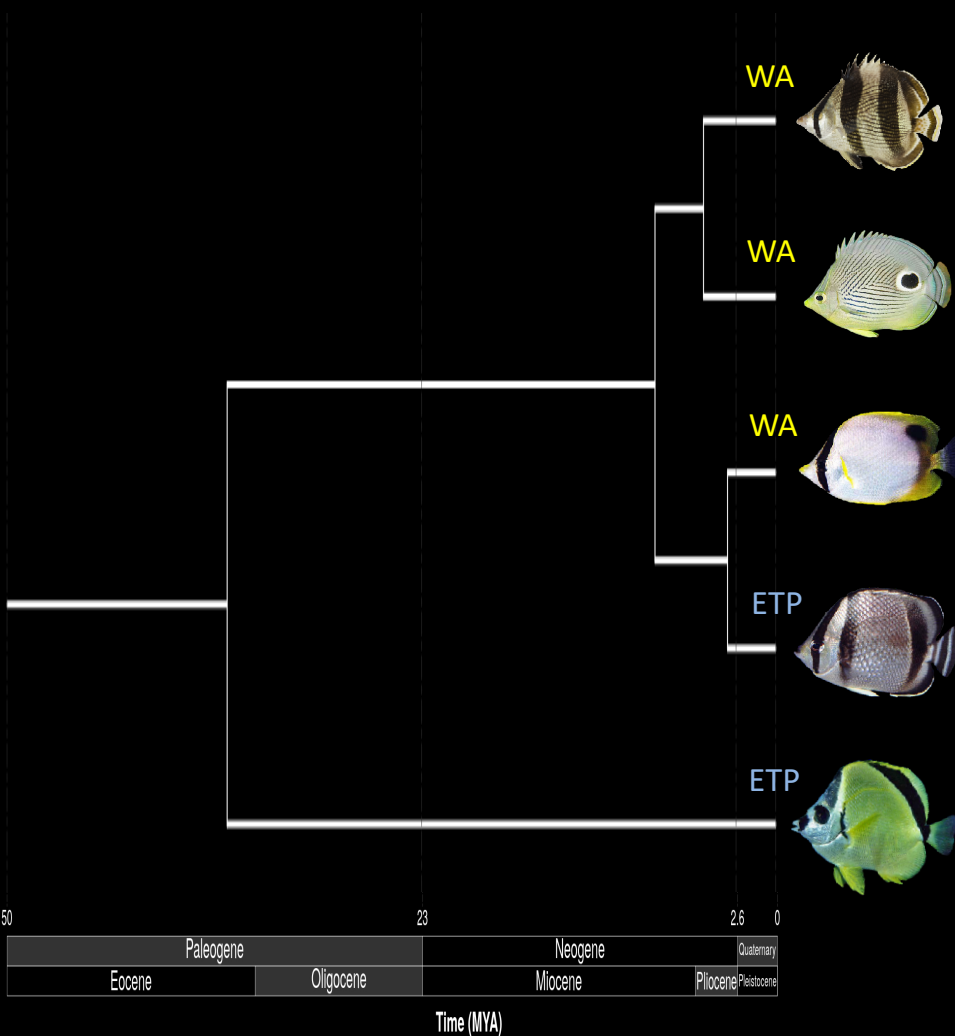
Phylosymbiosis?

WA = Western Atlantic

ETP = Eastern Tropical Pacific

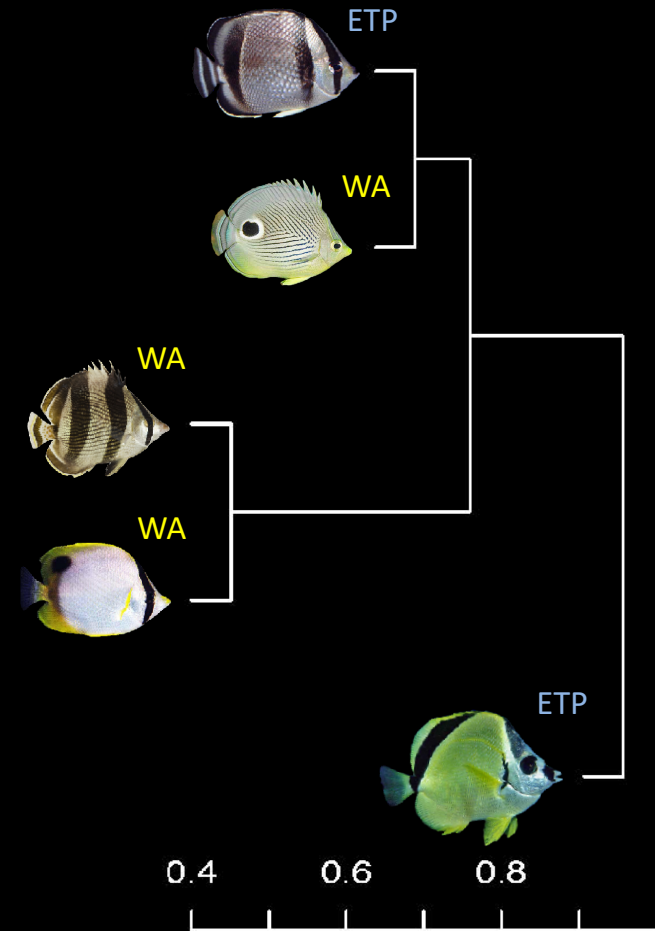
Host tree

(based on molecular markers)



Gut microbiome

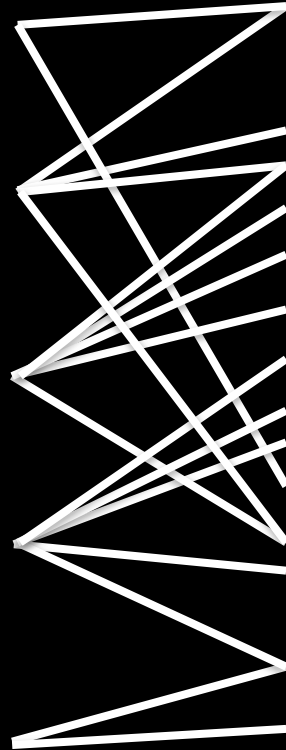
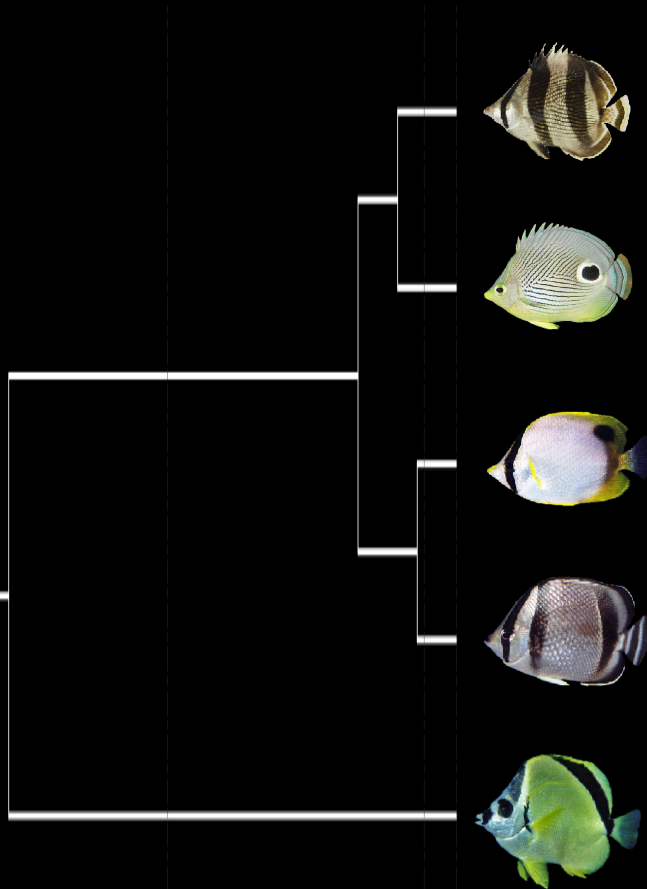
(UPGMA tree based on Bray Curtis distances of 16S rRNA ASVs)



➔ Community similarity of gut microbiome does not mirror host phylogeny

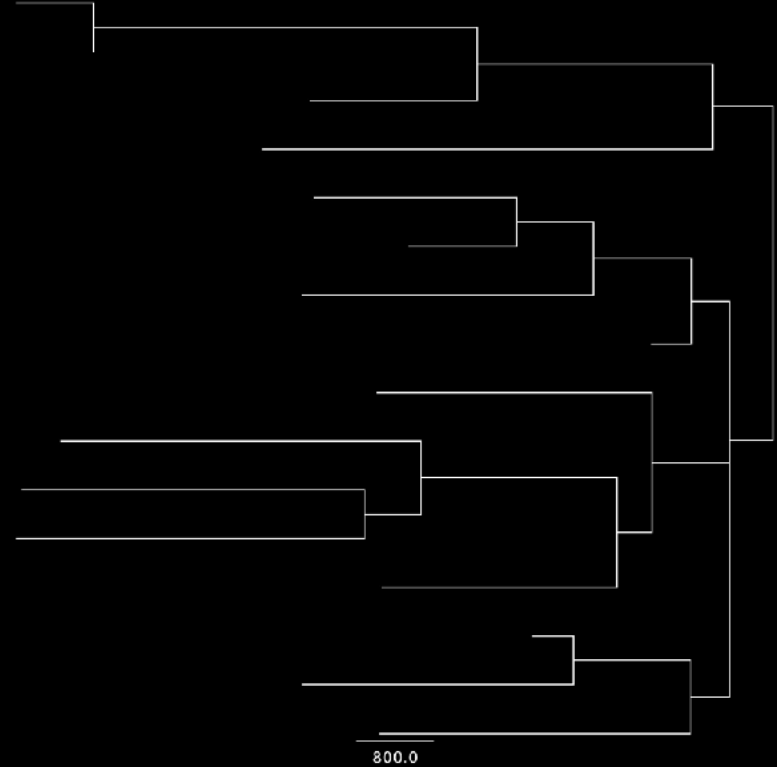
Cophylogeny?

Host tree



Bacterial trees

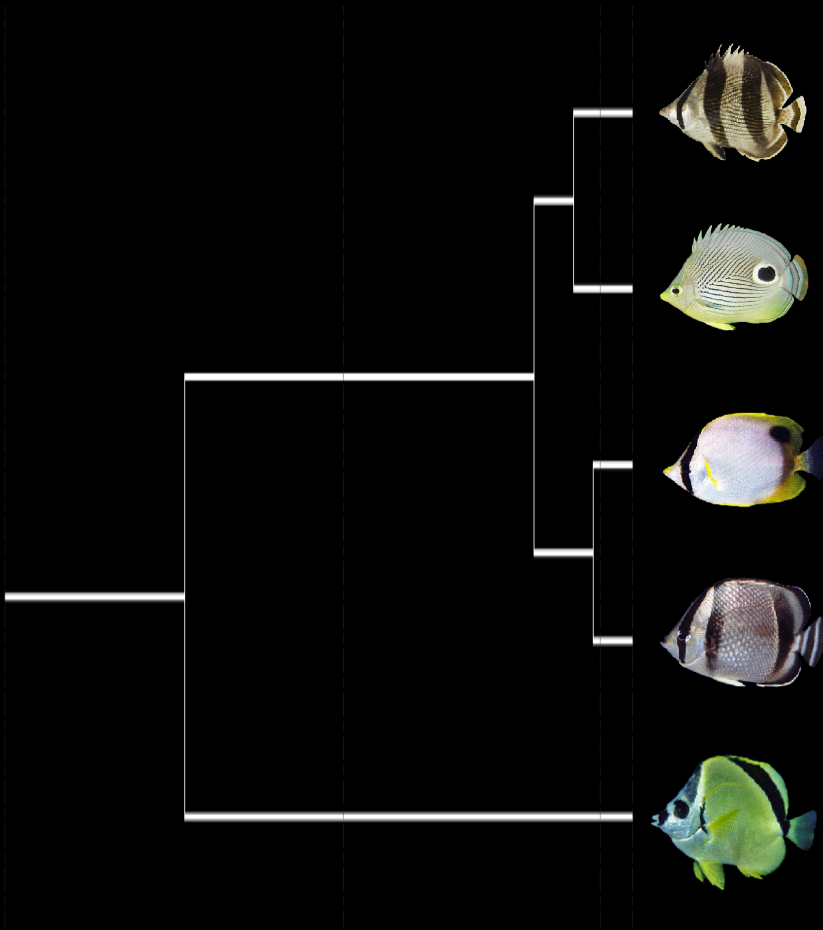
e.g., genus *Coxiella*



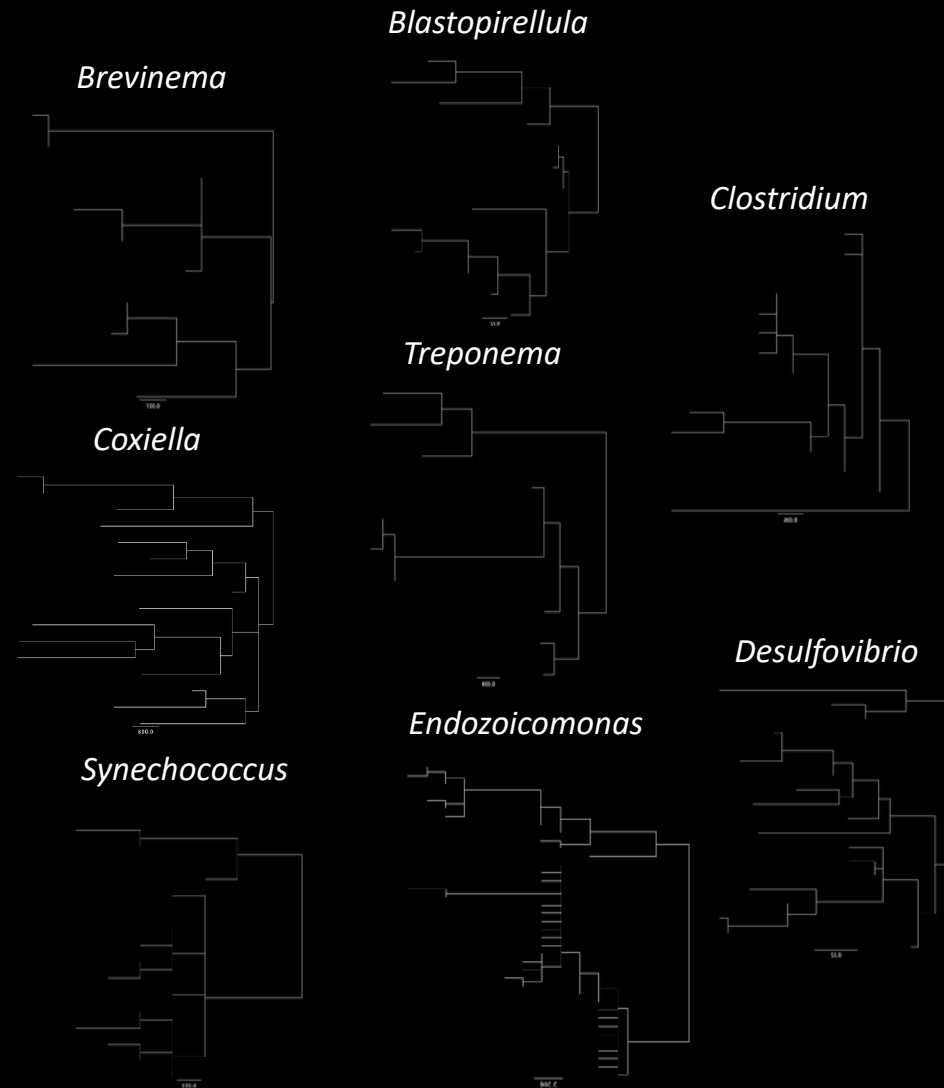
Is at least some part of the bacteria phylogeny
constrained by the one of the host?

Cophylogeny?

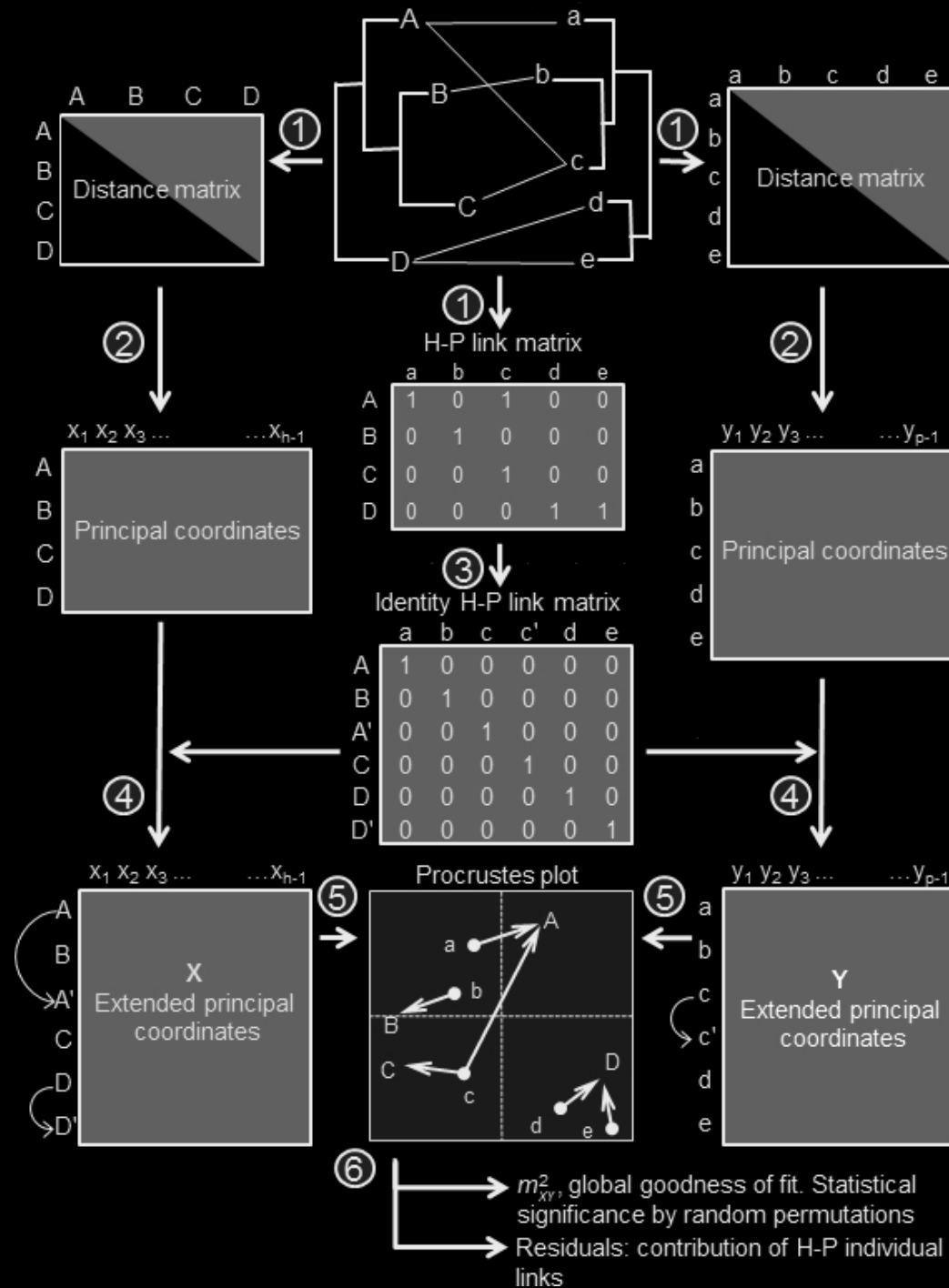
Host tree



Bacterial trees



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

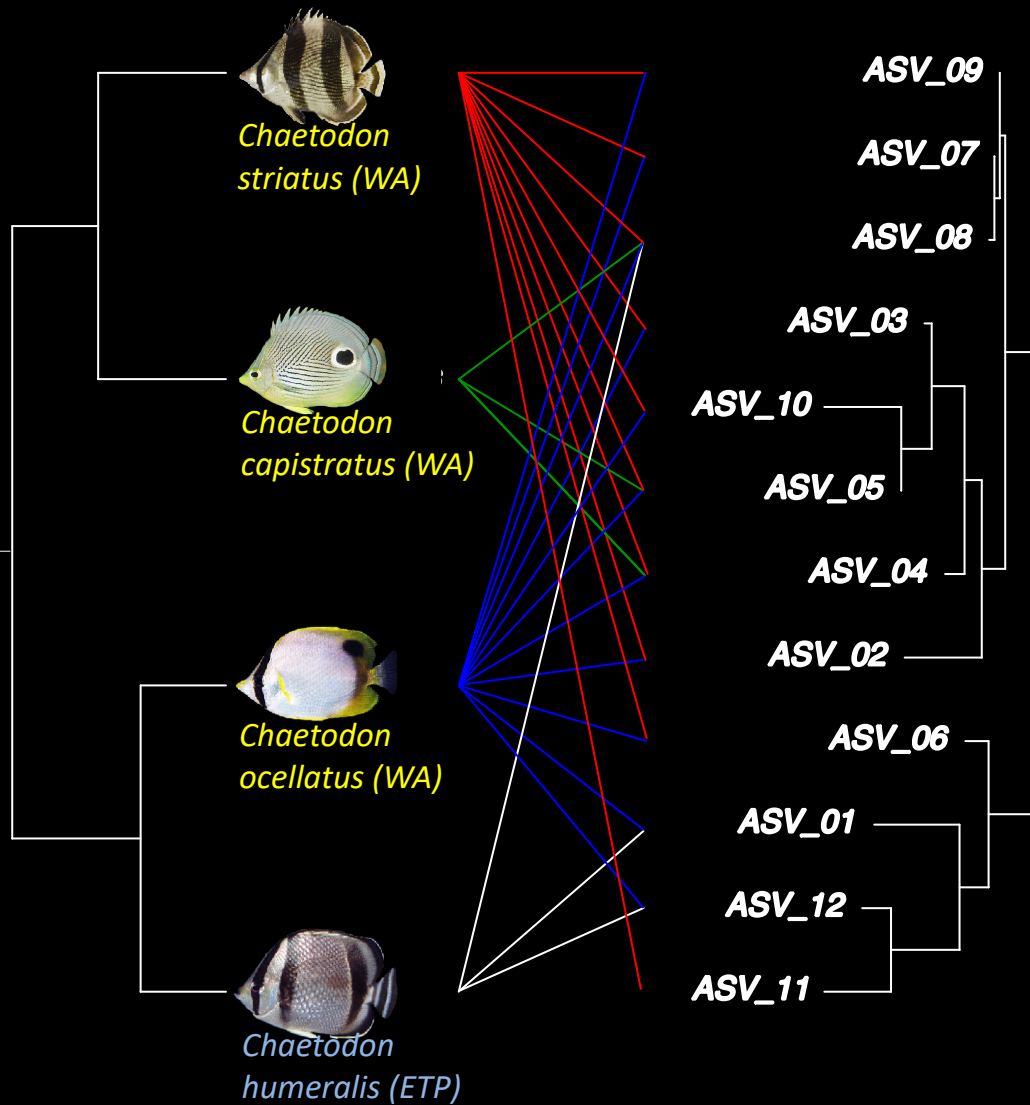


Cophylogeny?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Host tree

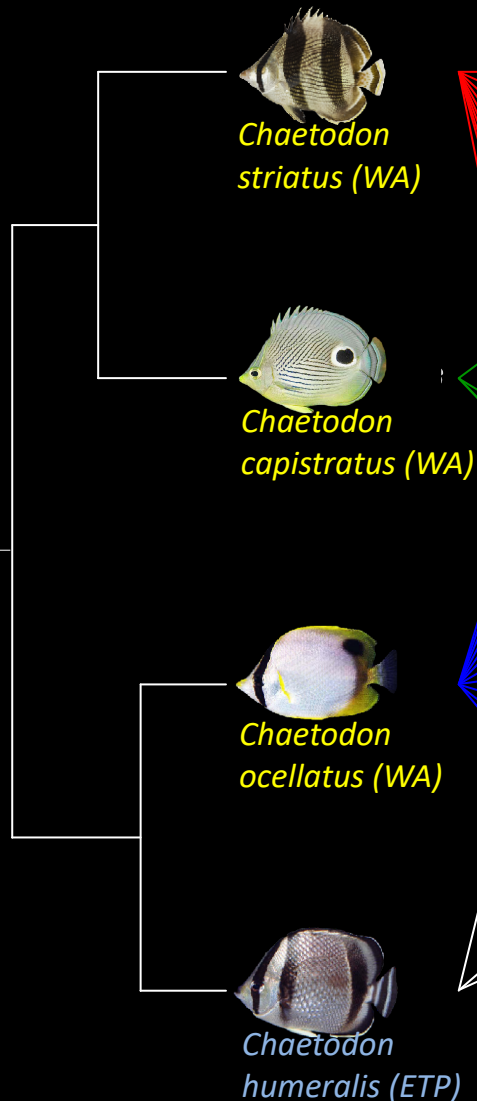
Blastopirellula 16S tree



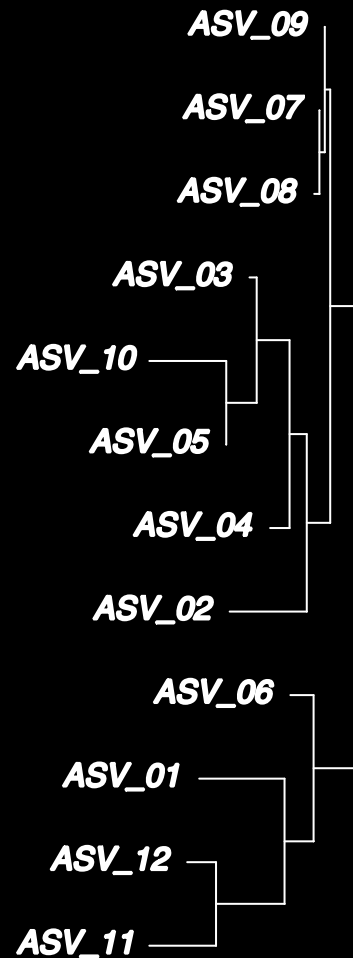
Cophylogeny?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Host tree



Blastopirellula 16S tree



Procrustes analysis

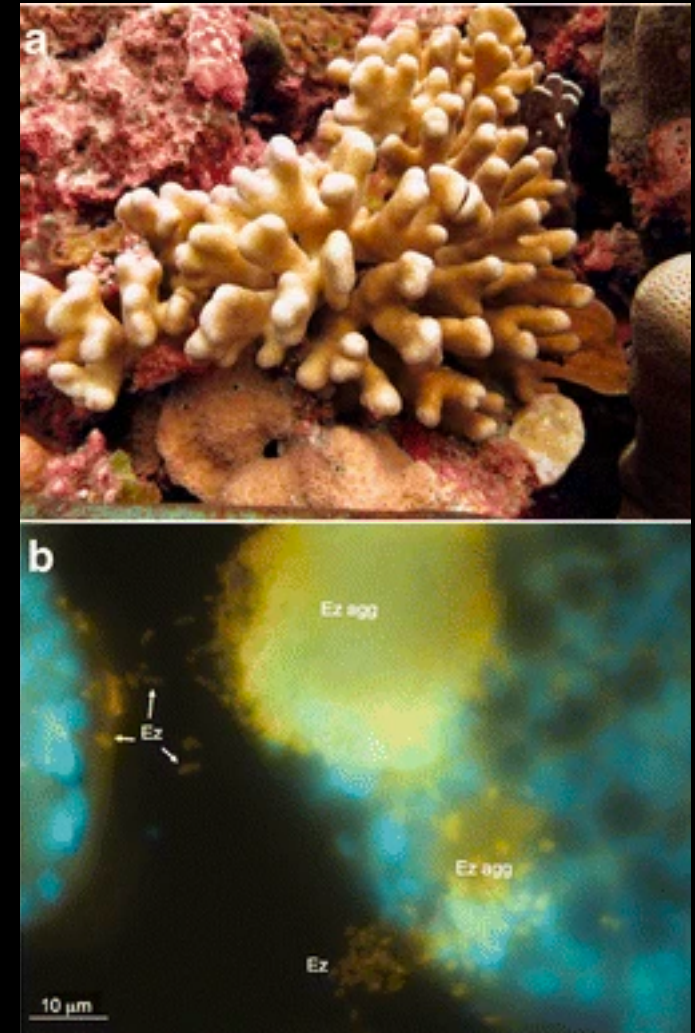
Param	<i>Endozoicomonas</i>
\$p	0.027*
\$ss	5765.733
\$n	1000

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

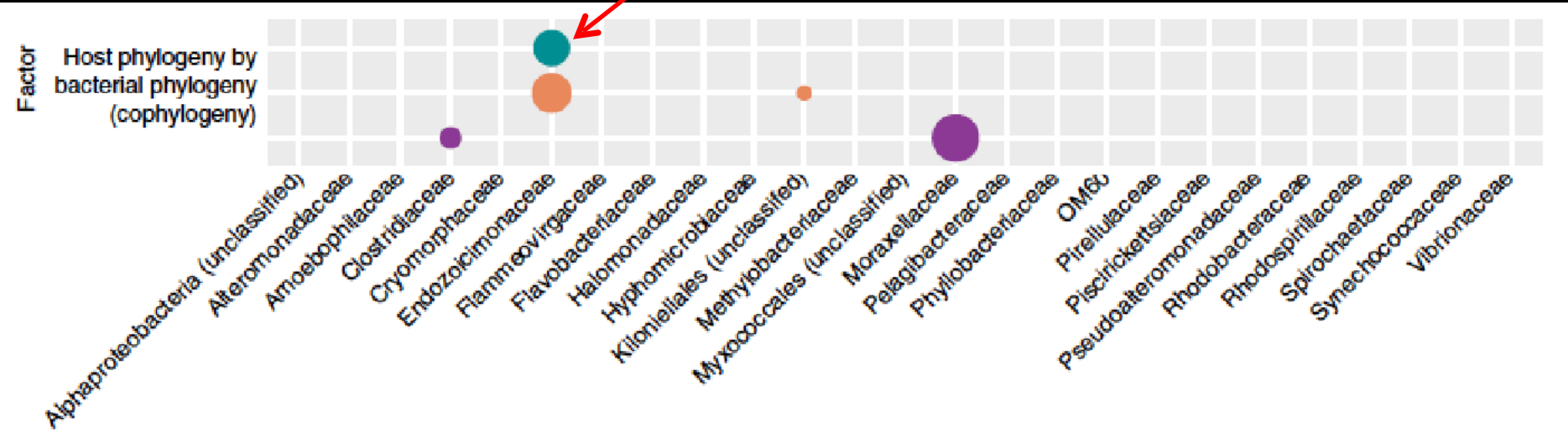
DOI: 10.1038/s41467-018-07275-x

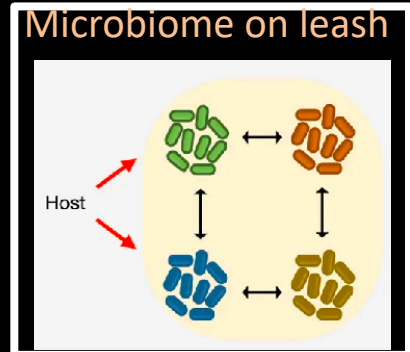
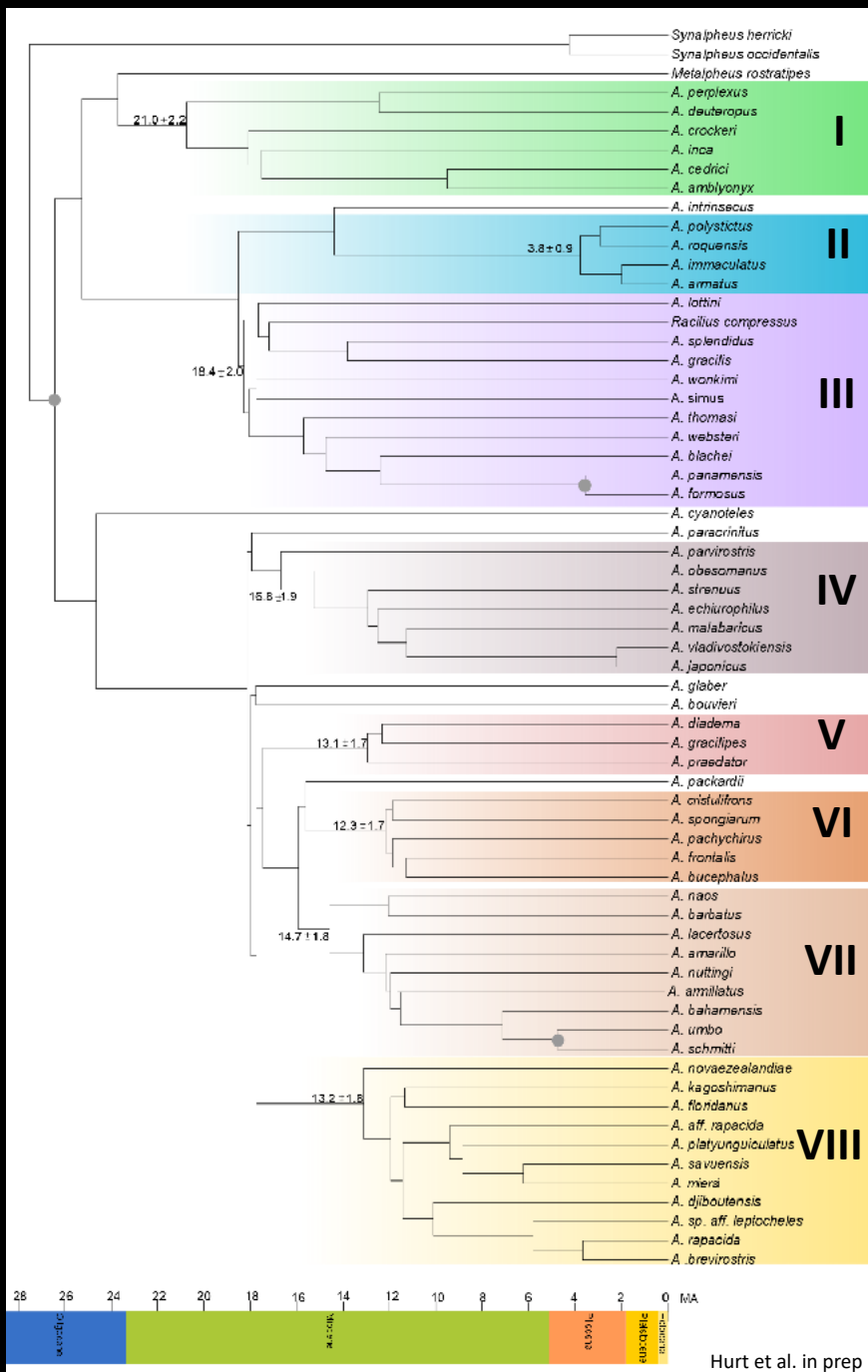
OPEN

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 host tree

>500 Loci
using Anchored Hybrid Enrichment

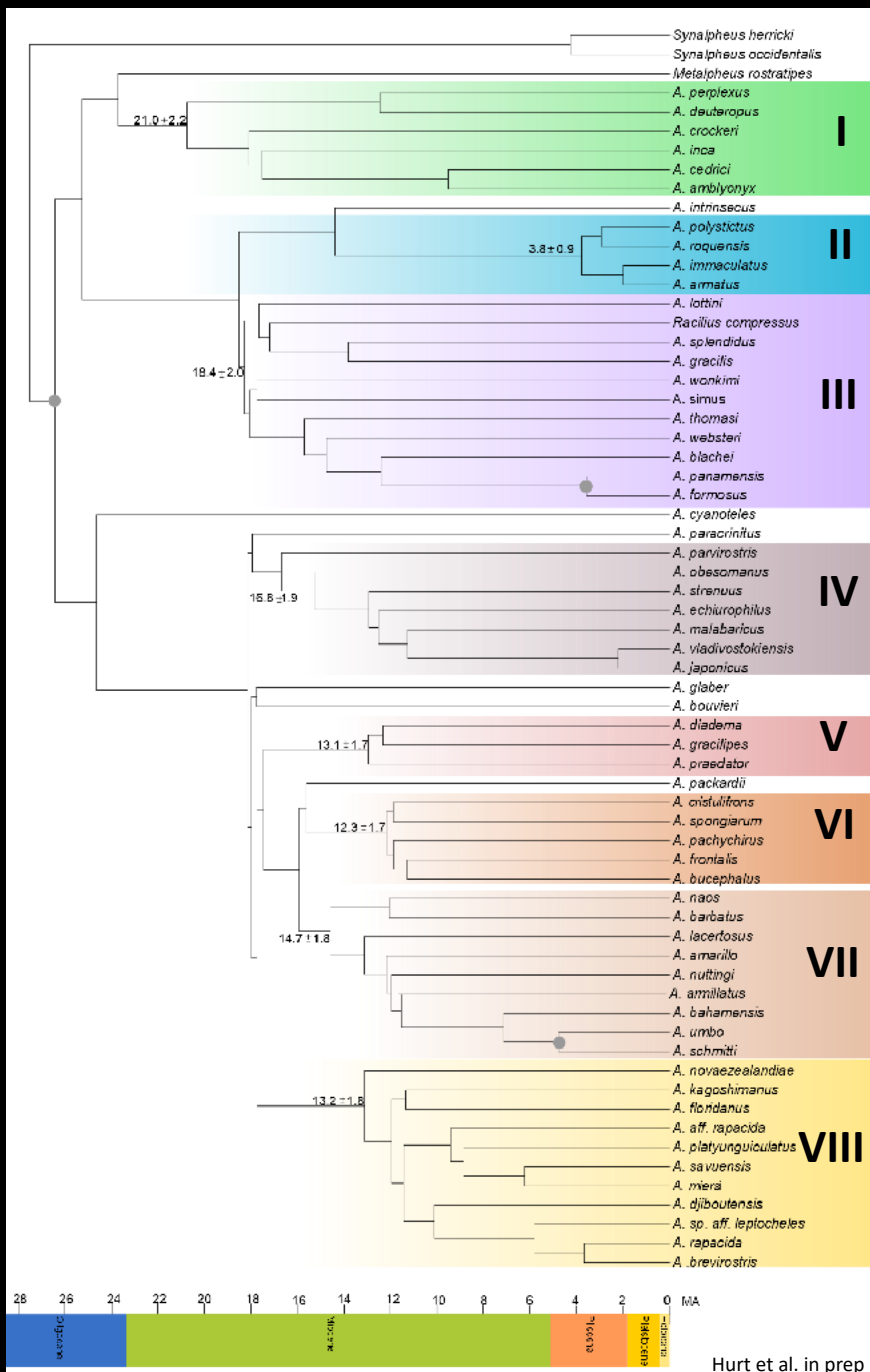


Carla Hurt



Kristin Hultgren

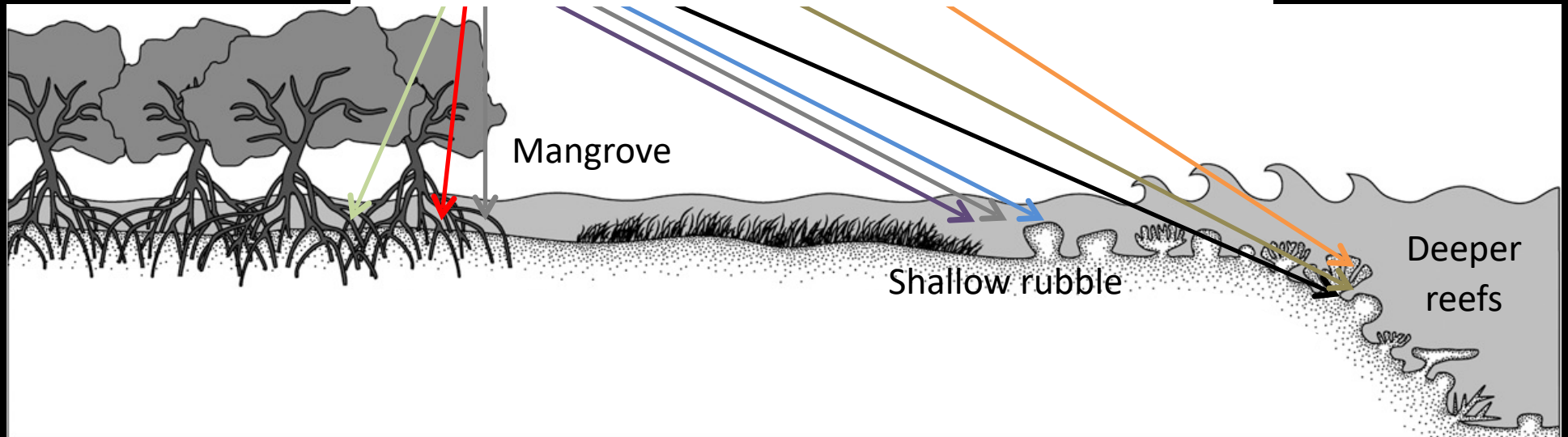
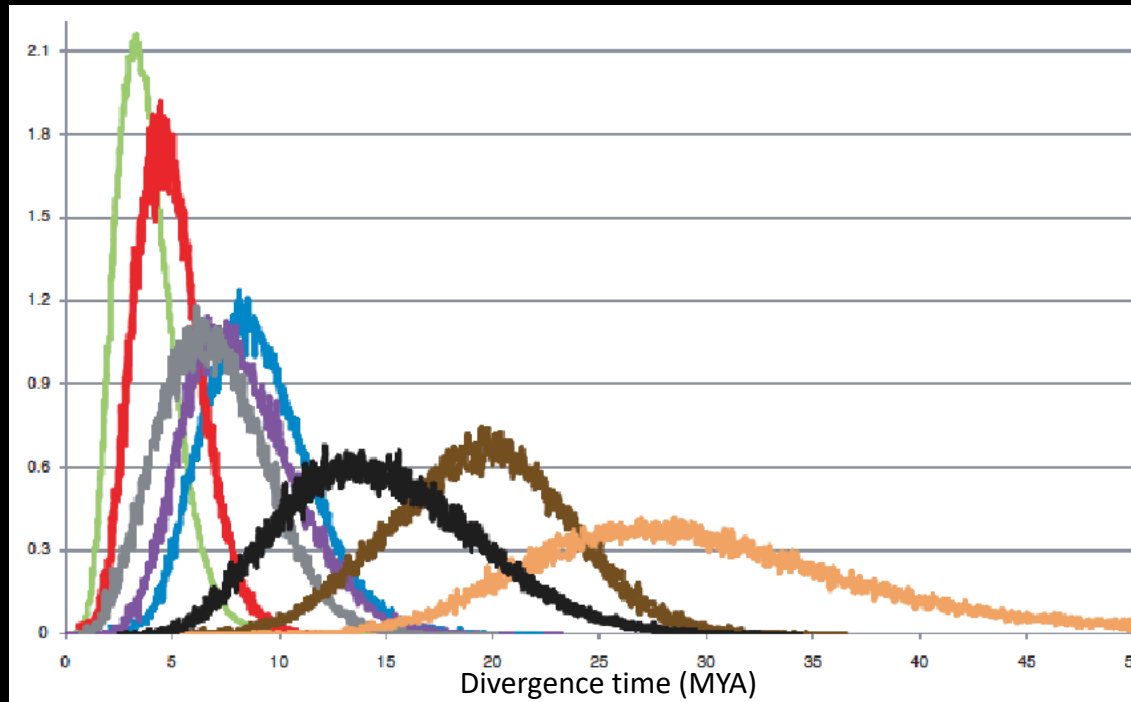
Backbone phylogenomic tree



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

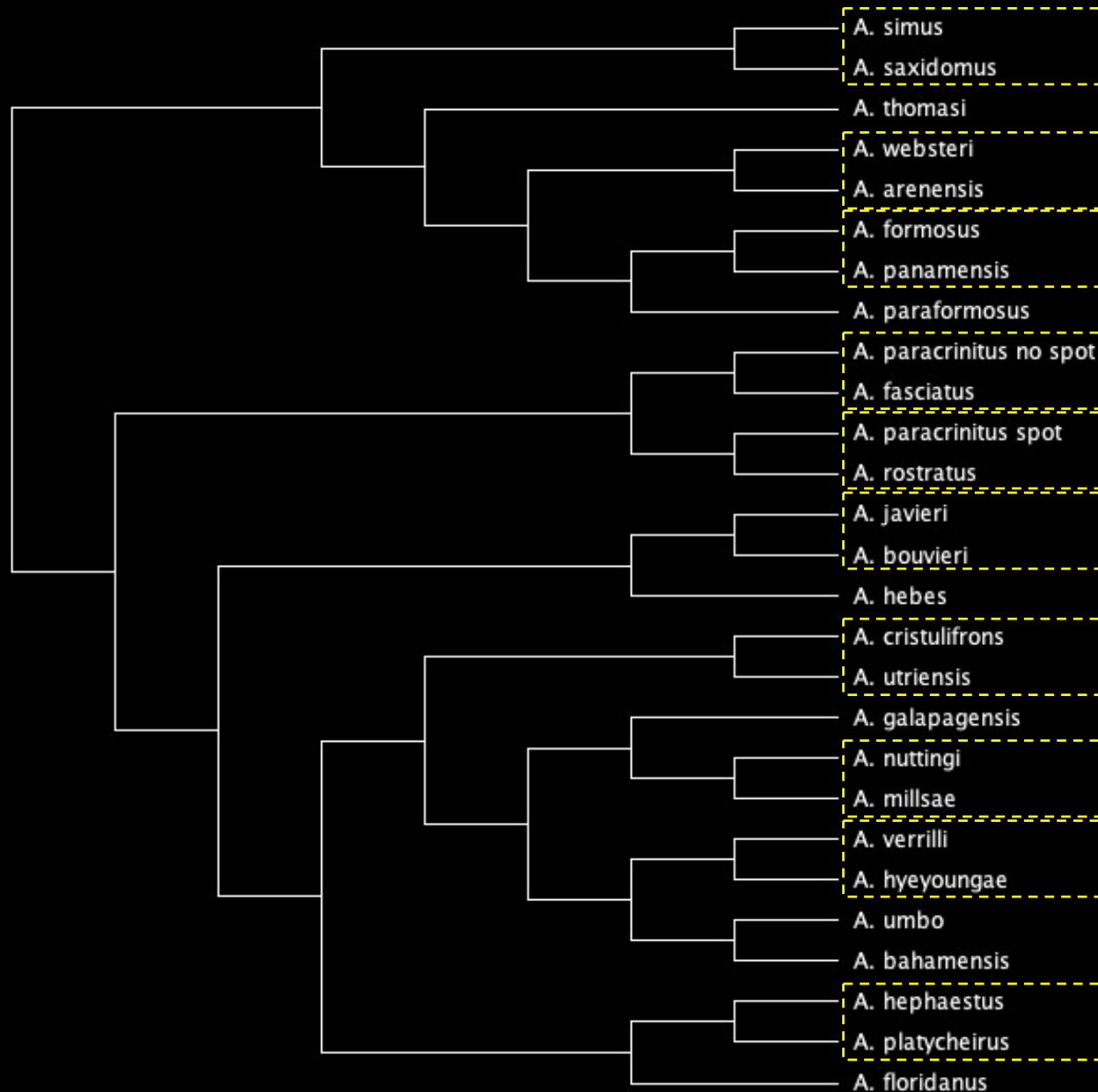
Azevedo Ferreira et al. 2020 Zootaxa



Unesconia coibensis

Anker 2020 Zootaxa

27 species across 6 major clades



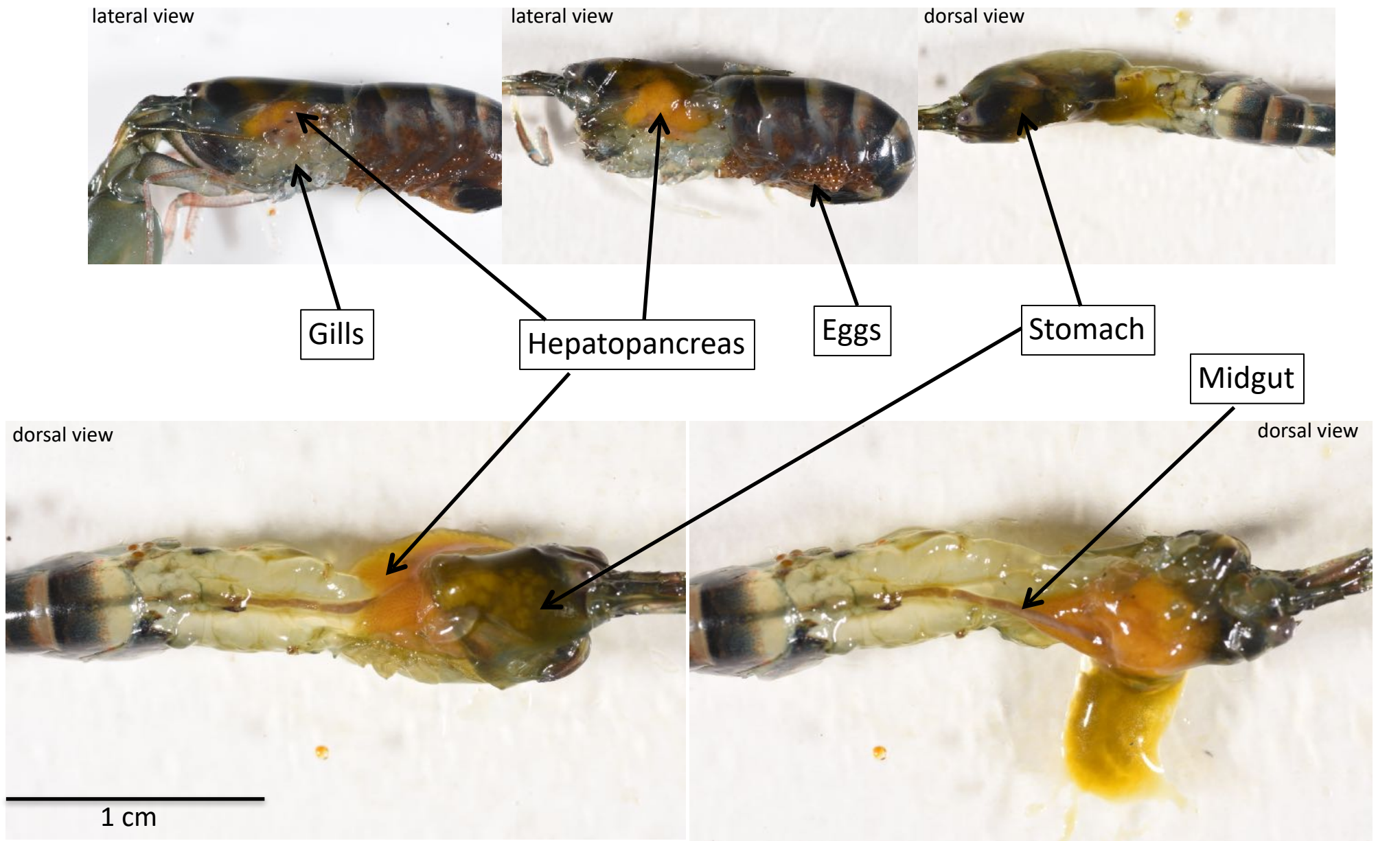
Eastern Pacific

Caribbean



10 transisthmian pairs

Internal anatomy of *Alpheus javieri*





Catalina
Rodriguez

Helio
Quintero



dorsal view

426 specimens
1799 tissues



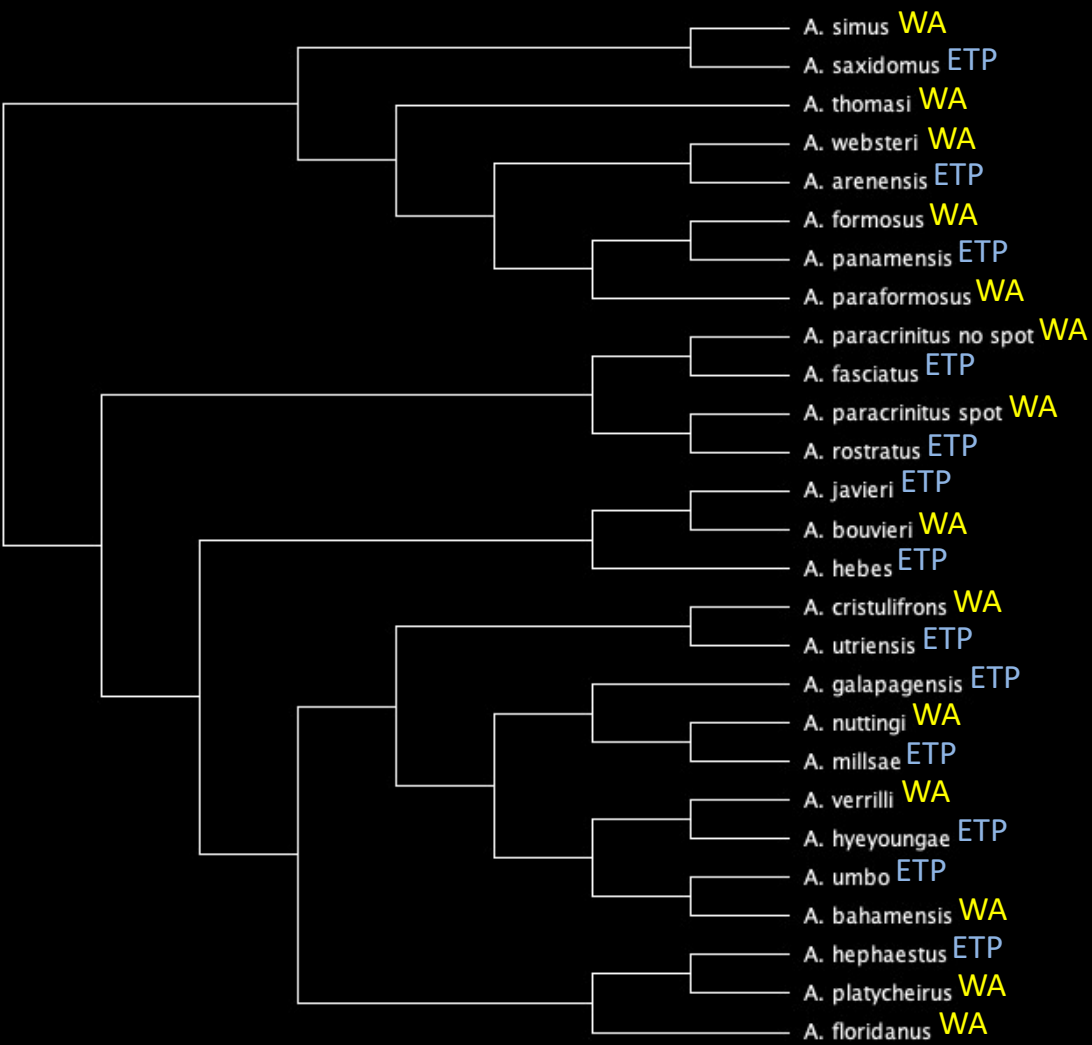
dorsal view

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)



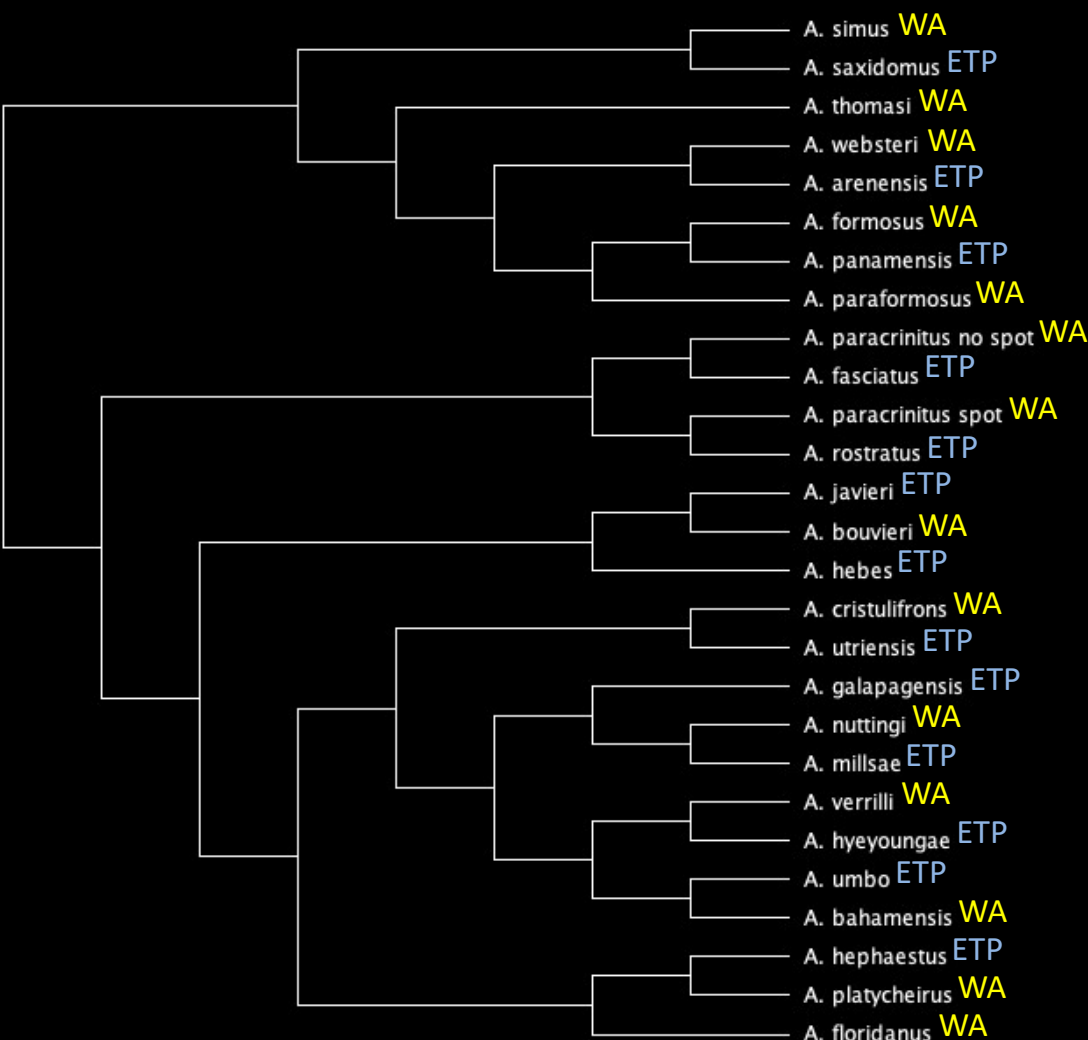
Phylosymbiosis?

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Host tree

(based on molecular markers)



Midgut microbiome

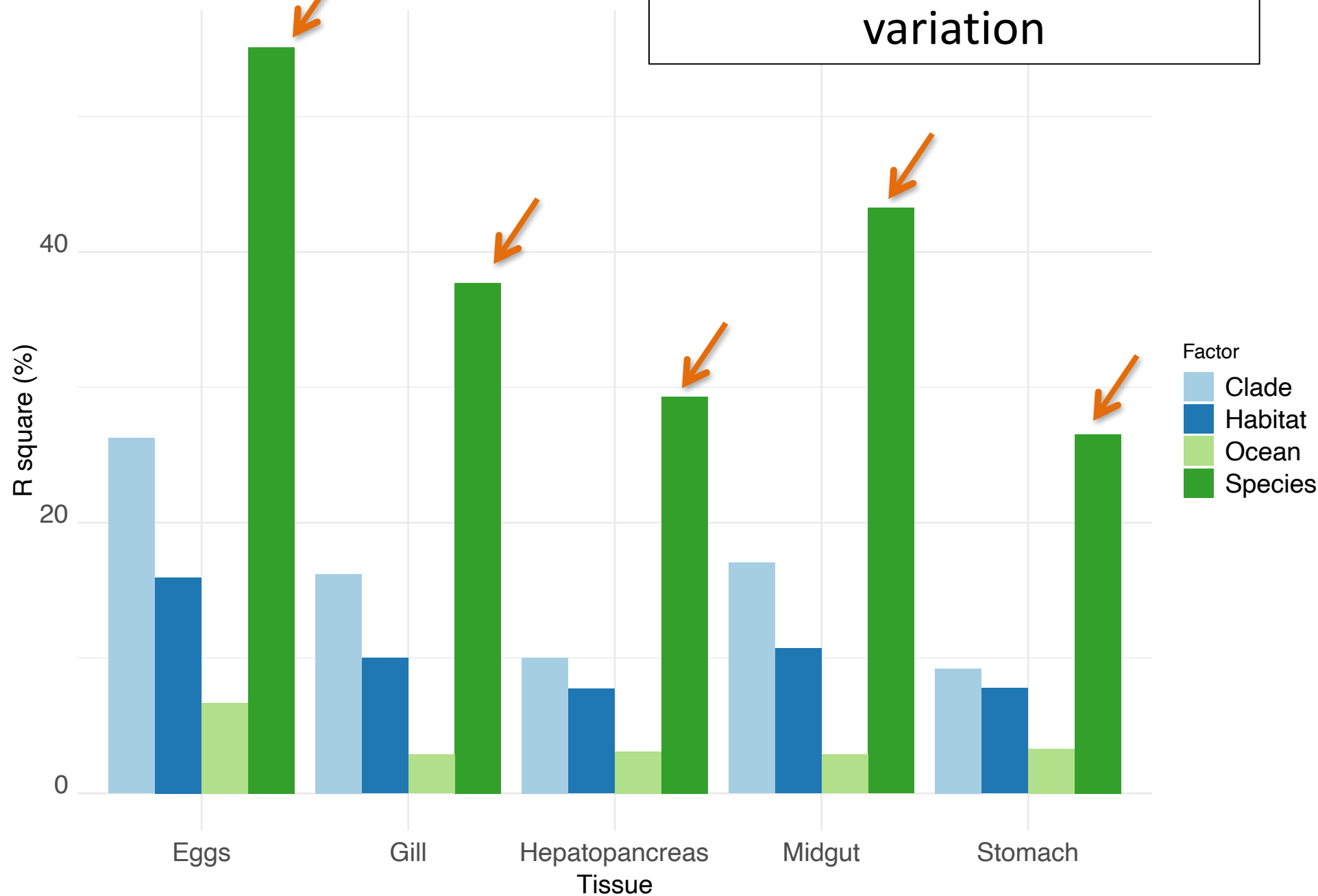
(UPGMA tree based on Bray Curtis distances of 16S rRNA ASVs)



Variance explained

PERMANOVA

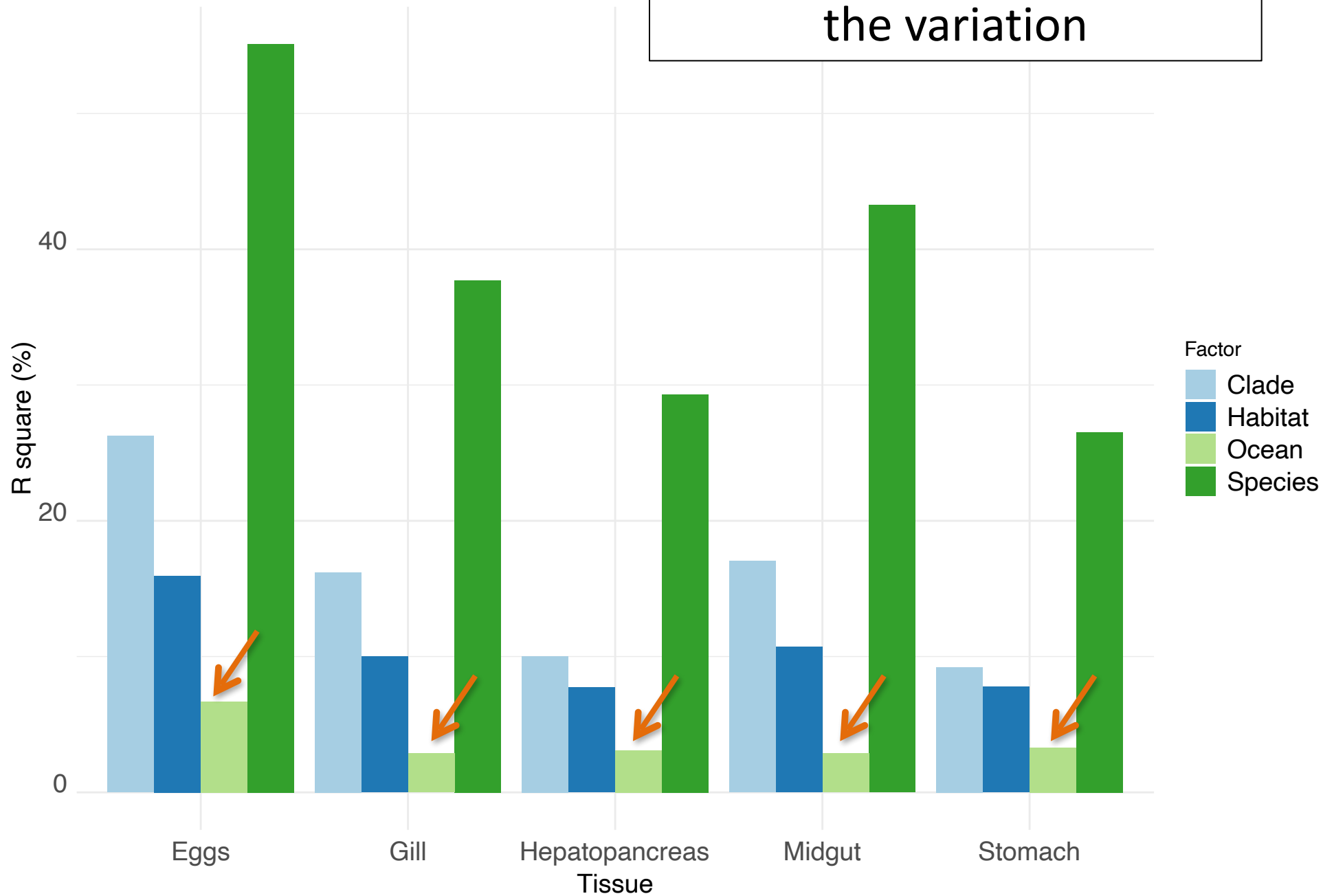
Species explains most of the variation



Variance explained

PERMANOVA

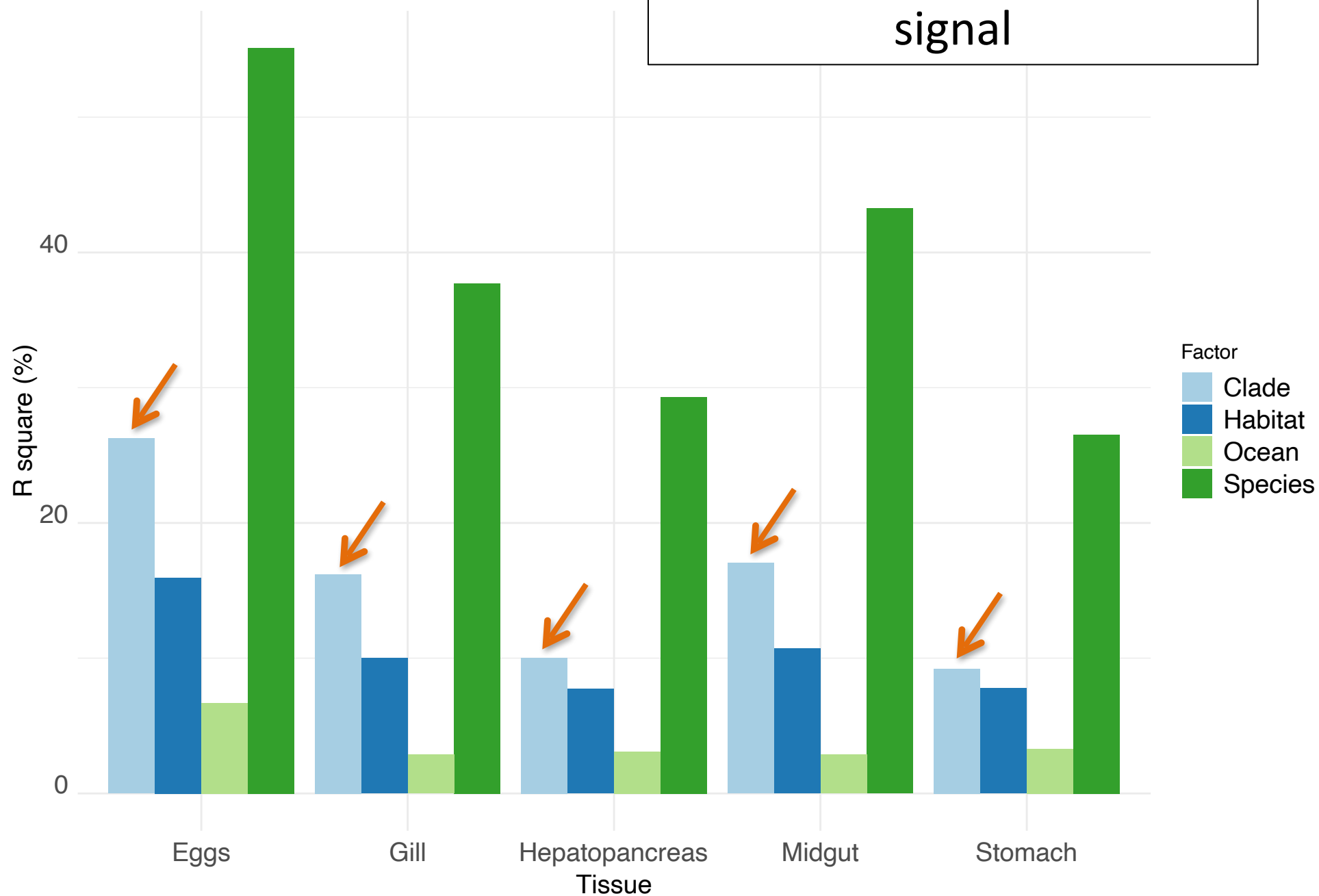
Ocean explains very little of the variation



Variance explained

PERMANOVA

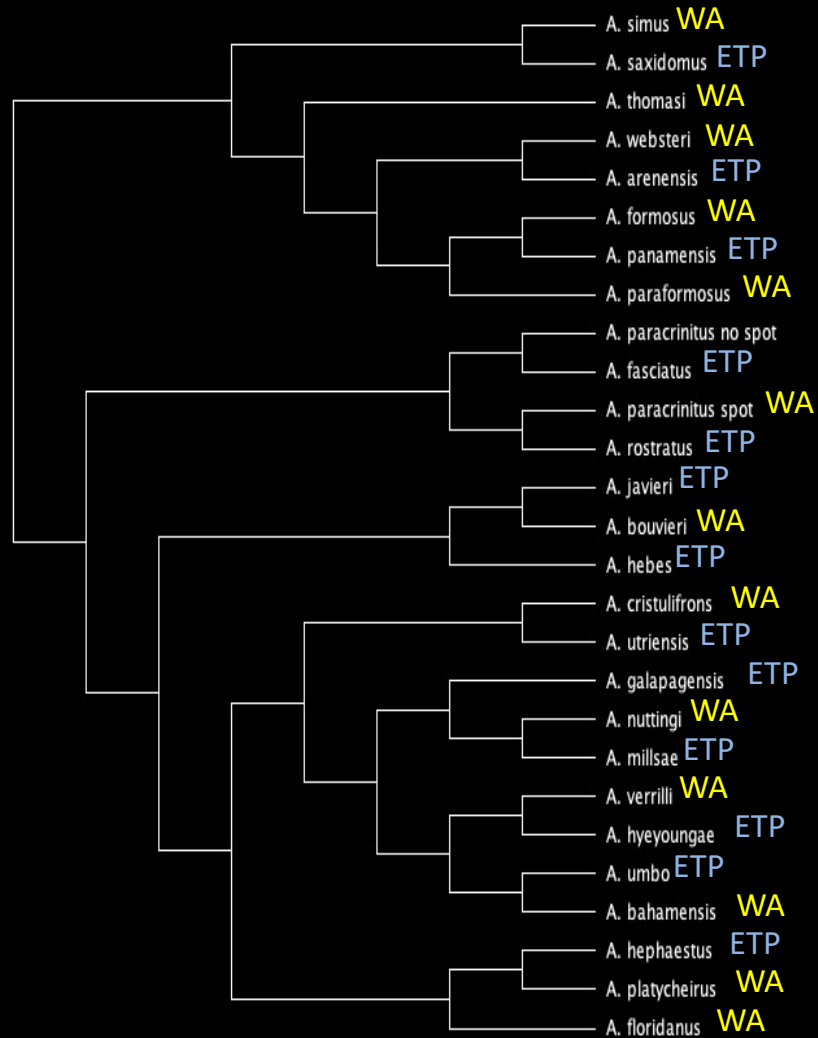
Significant phylogenetic
signal



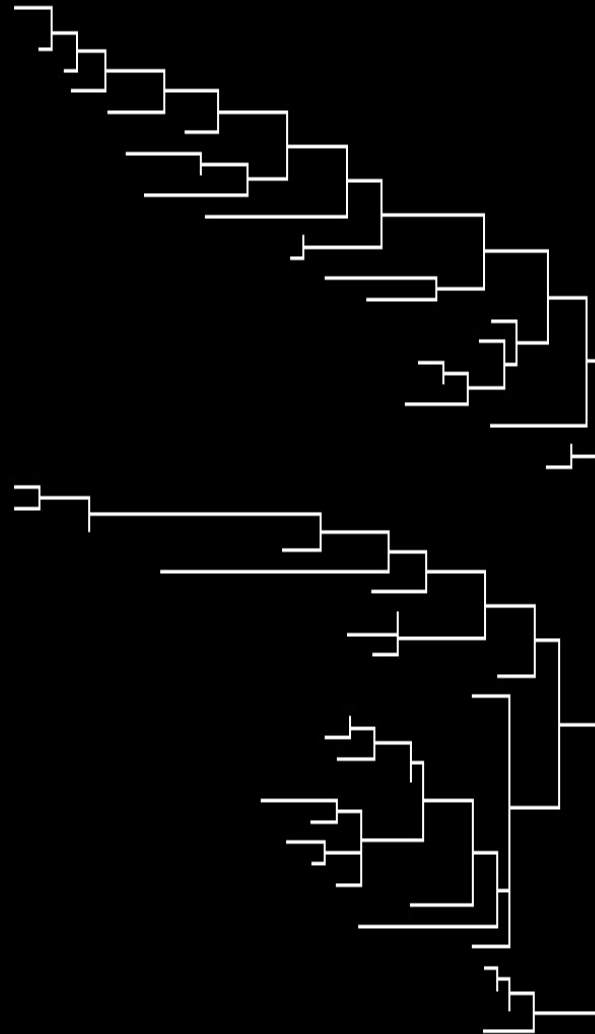
Cophylogeny?

WA = Western Atlantic
ETP = Eastern Tropical Pacific

Host tree



e.g., *Blastopirellula* 16S tree

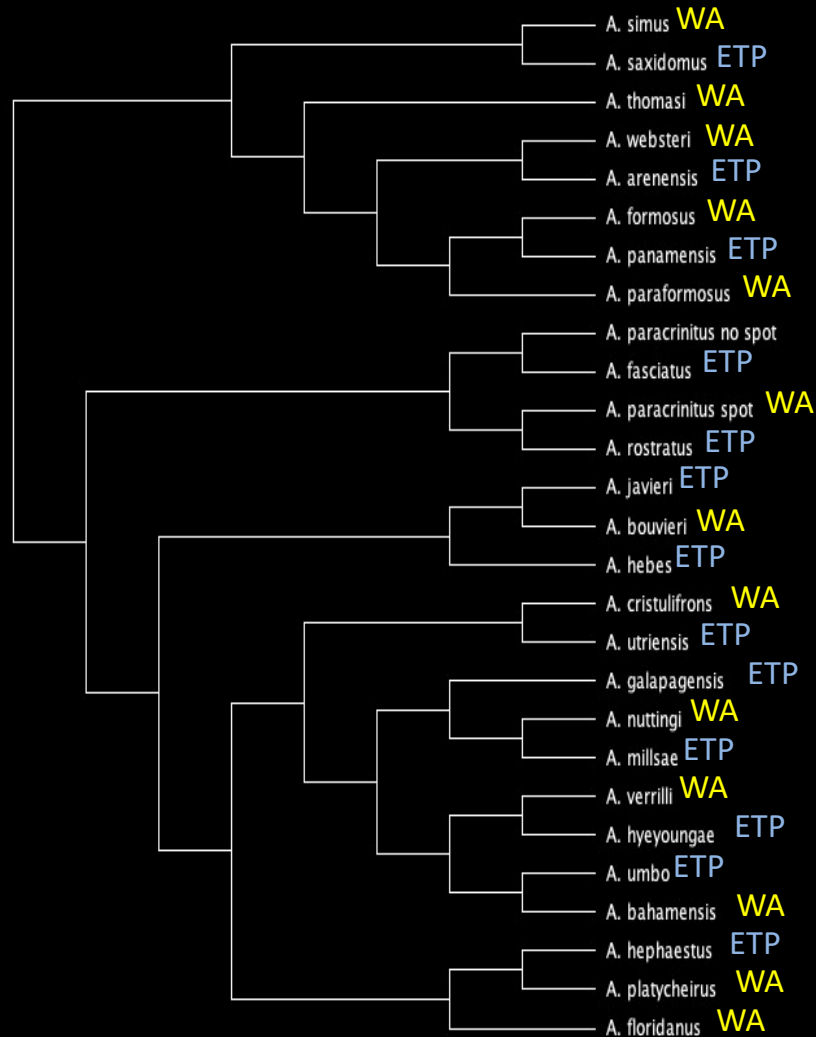


Cophylogeny?

WA = Western Atlantic

ETP = Eastern Tropical Pacific

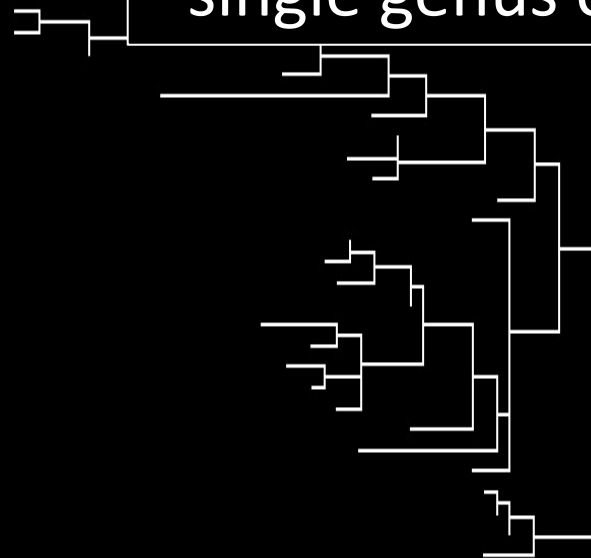
Host tree



Midgut microbiome

	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

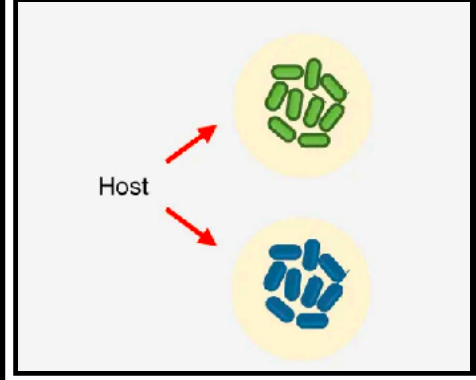
Significant co-divergence
between hosts and a
single genus of bacteria



Lucinid clams



Host control

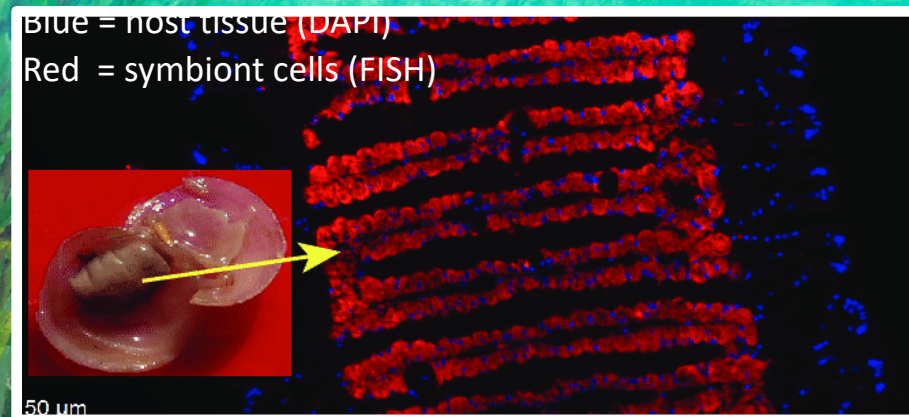


Laetitia Wilkins,
UC Davis

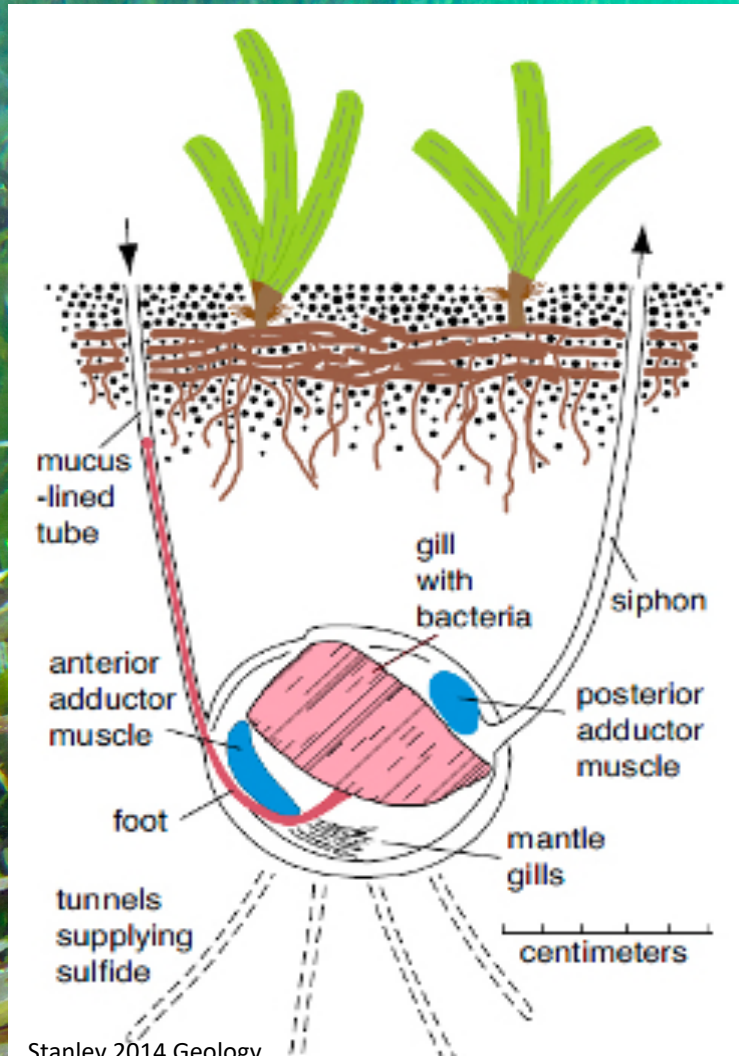
Jillian Petersen,
DOME Uni Vienna

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?

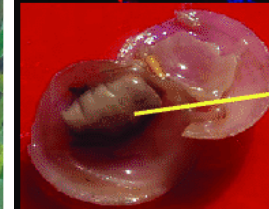


A nutritional symbiosis that is believed to be the foundation of seagrass ecosystems

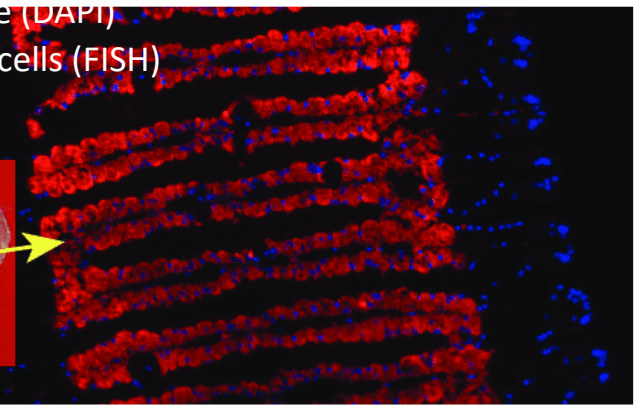


Lucinid clams and their gill sulfur oxidizing symbionts remove toxic sulfide from the sediment

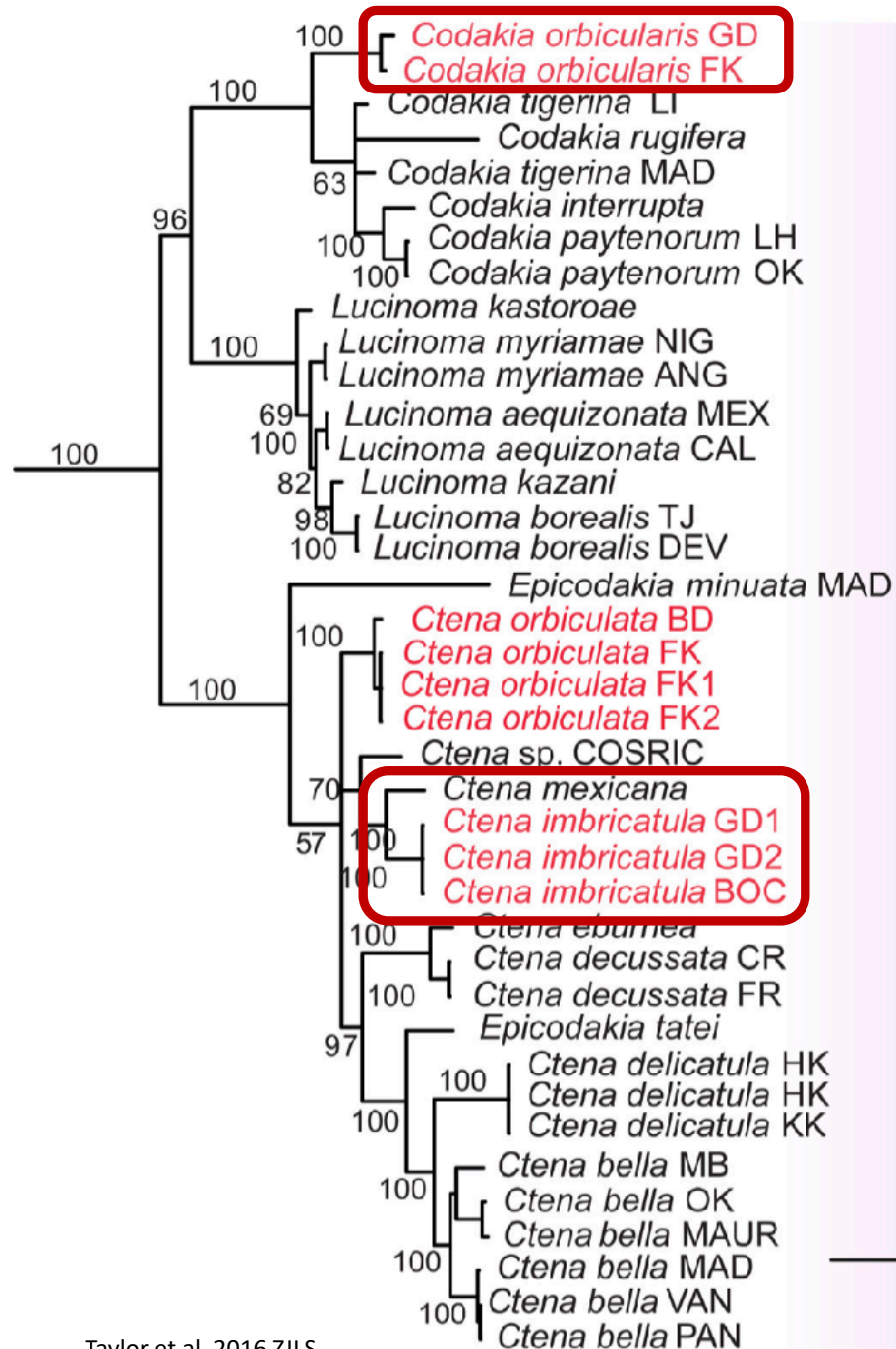
Blue = host tissue (DAPI)
Red = symbiont cells (FISH)



50 μ m

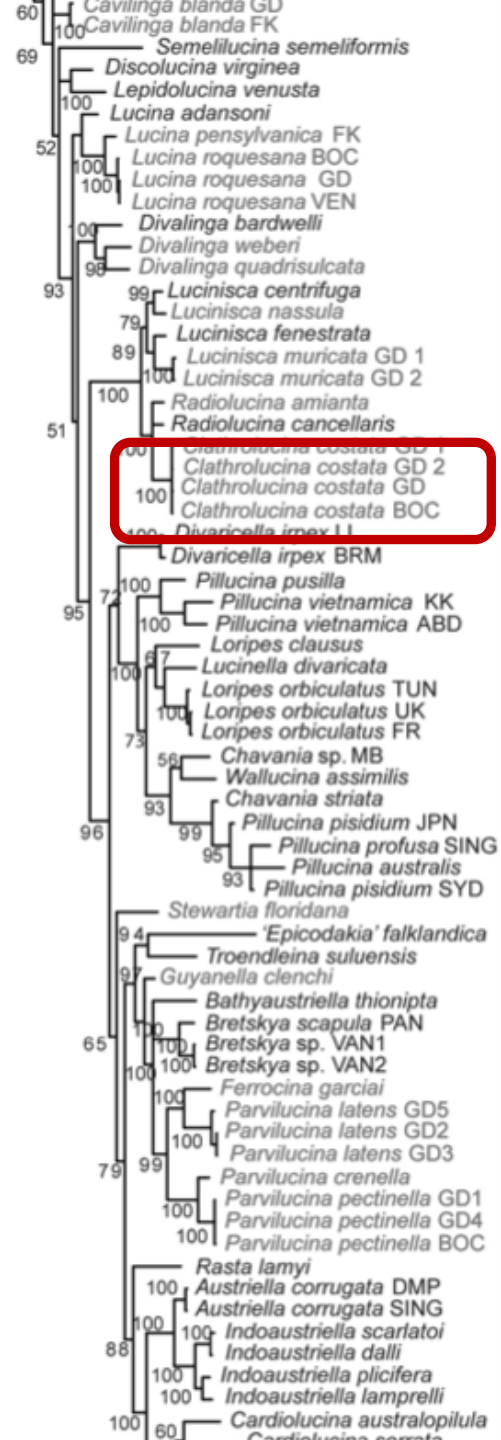


Making suitable conditions for seagrass plants to thrive



CODAKIINAE

0.3



LUCININAE

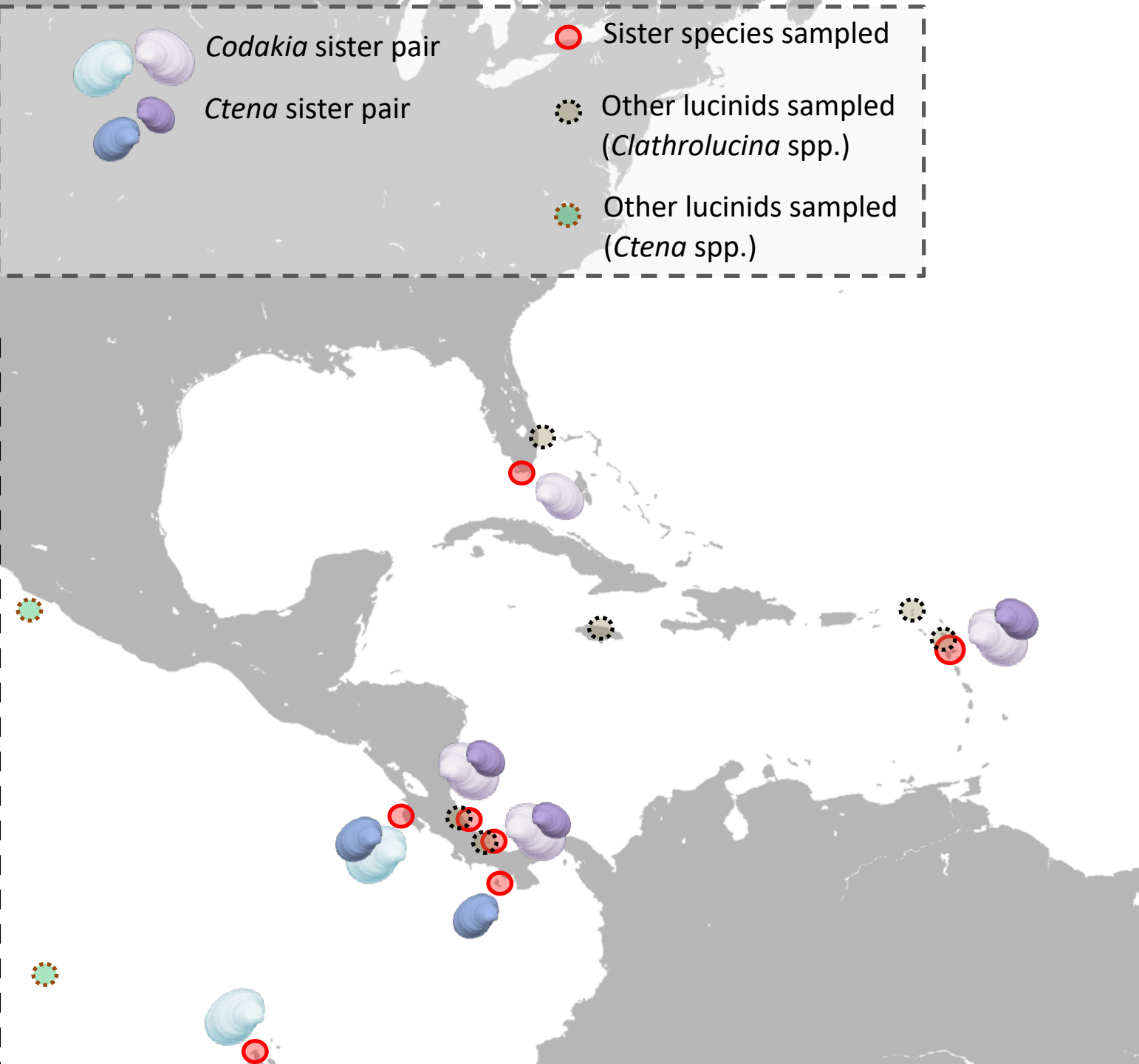
We also included
Clathrolucina costata as an
outgroup

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

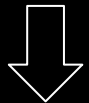
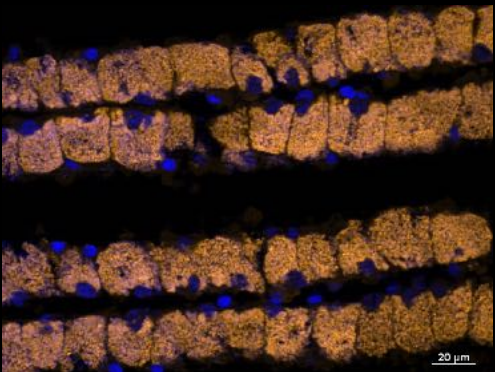
Sampling



Gustav Paulay,
Florida Museum of Natural History

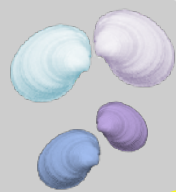


Symbiont Genome Sequencing

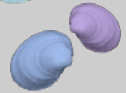


Shotgun metagenomics

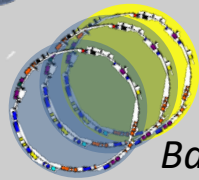
B



Codakia sister pair



Ctena sister pair



Yellow: Caribbean

Blue: Pacific

Bacterial symbiont genomes



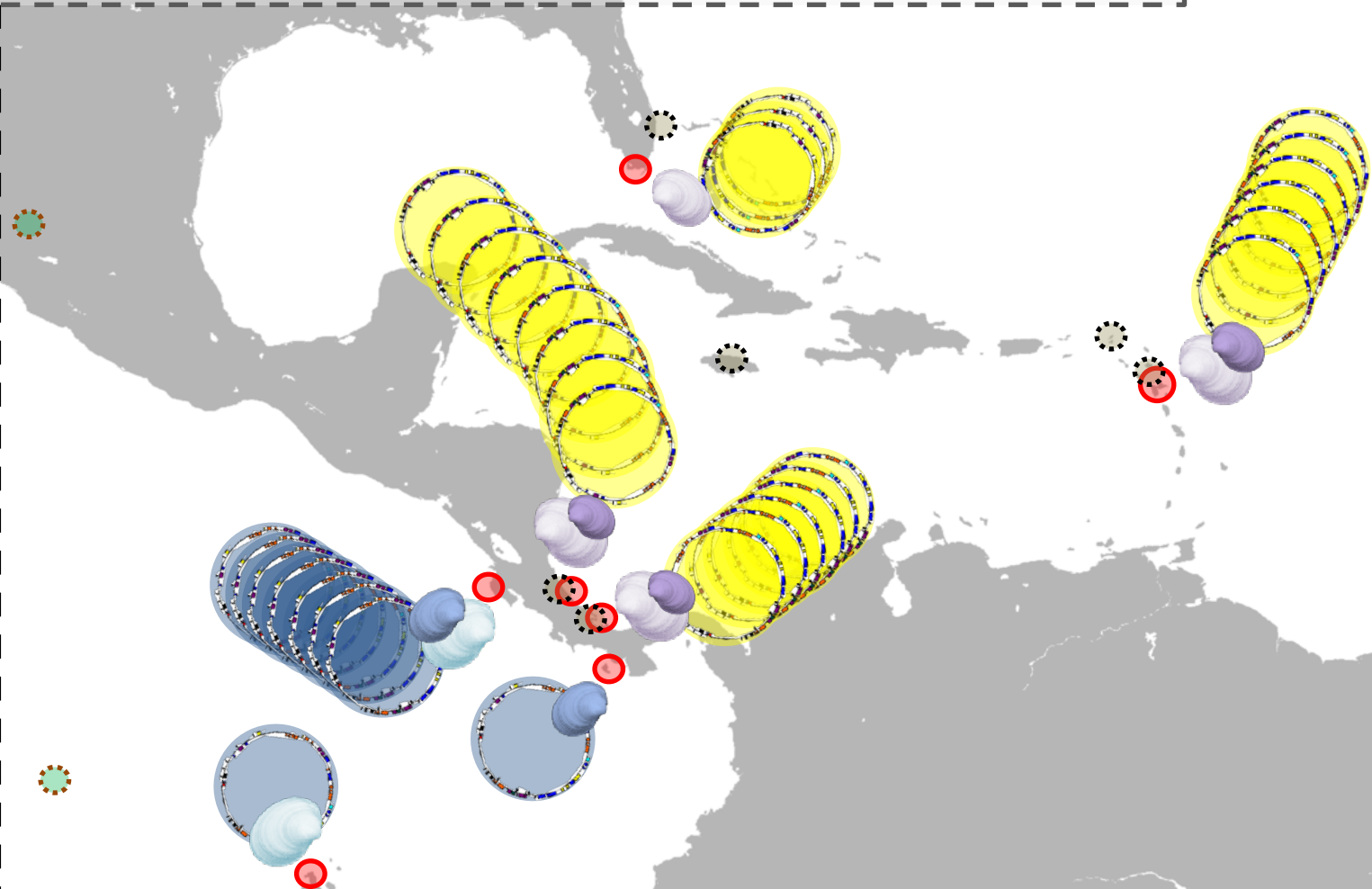
Sister species locations



Other lucinids sampled
(*Clathrolucina* spp.)



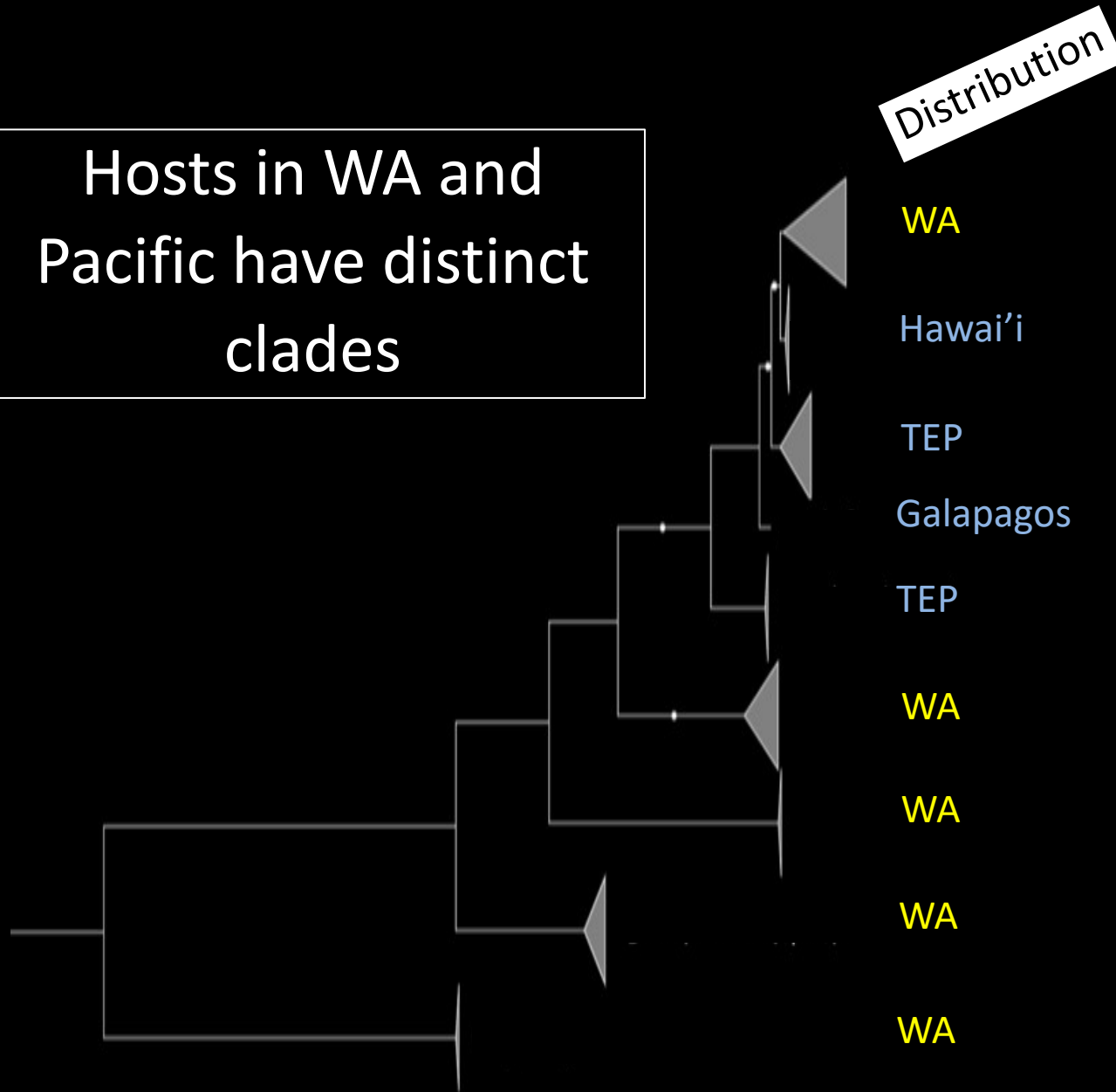
Other lucinids sampled
(*Ctena* spp.)



233 high quality genomes clustered into 8 clades

WA = Western Atlantic
ETP = Eastern Tropical Pacific

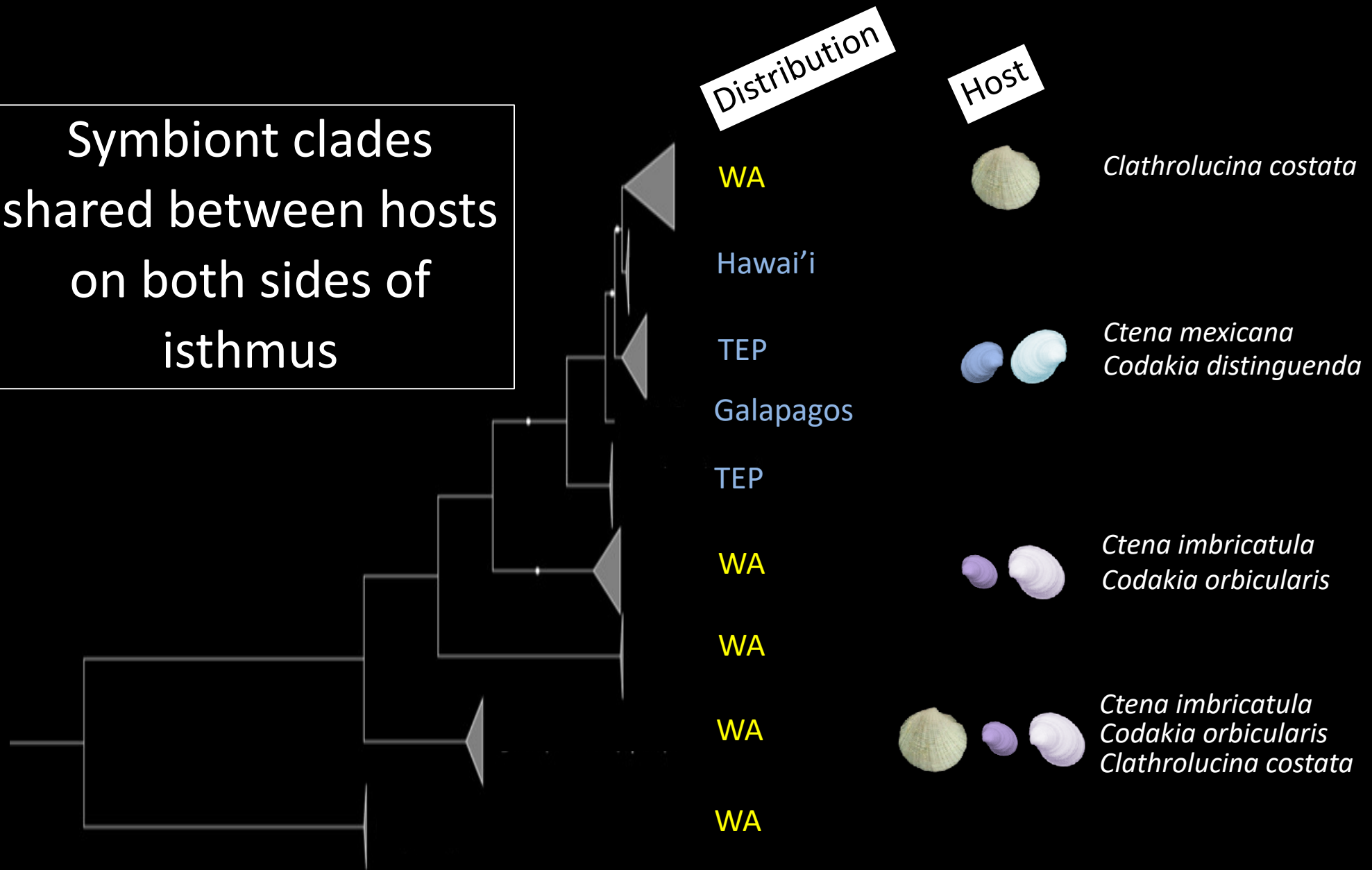
Hosts in WA and Pacific have distinct clades



233 high quality genomes clustered into 8 clades

WA = Western Atlantic
ETP = Eastern Tropical Pacific

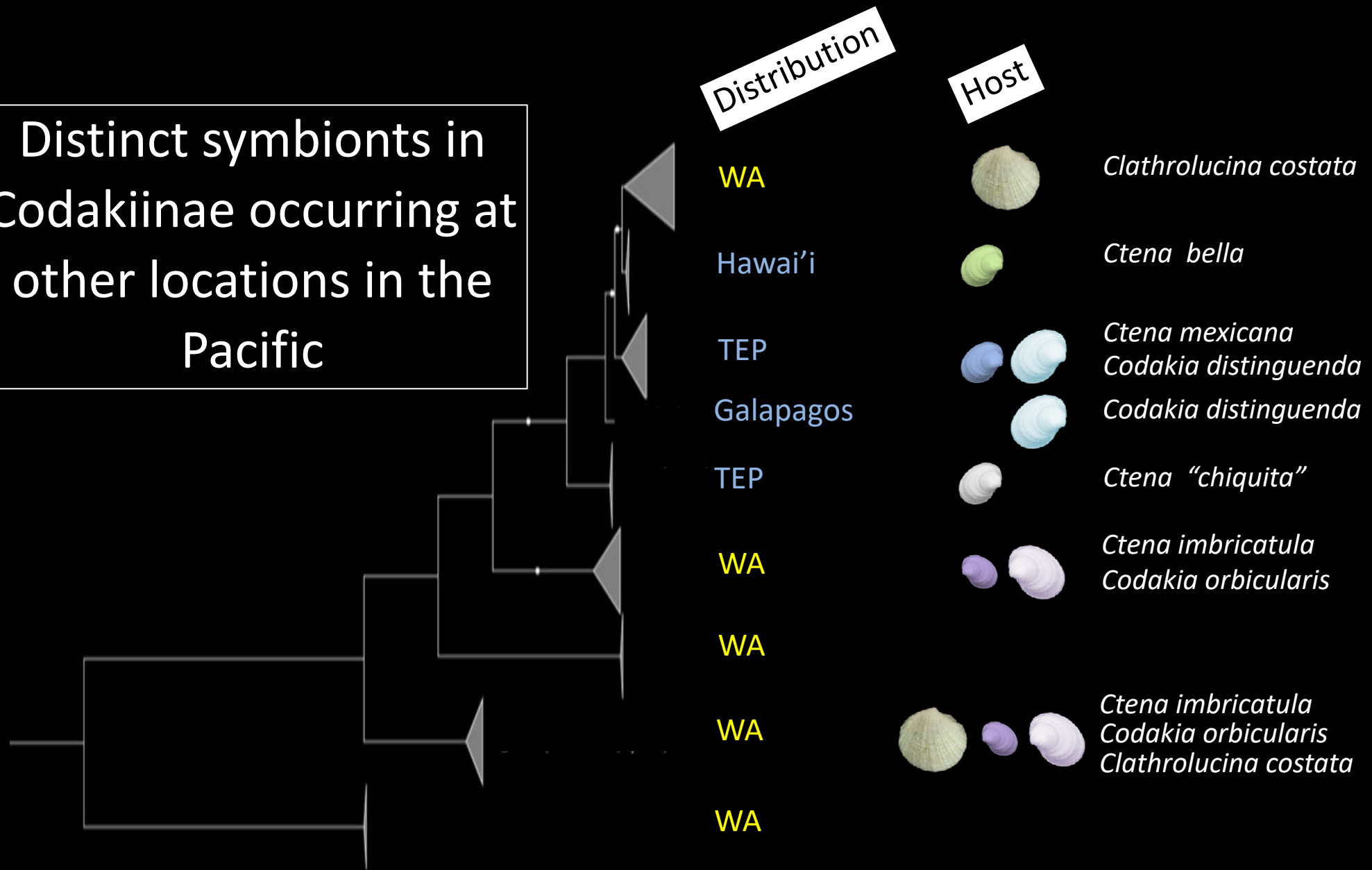
Symbiont clades shared between hosts on both sides of isthmus



233 high quality genomes clustered into 8 clades

WA = Western Atlantic
ETP = Eastern Tropical Pacific

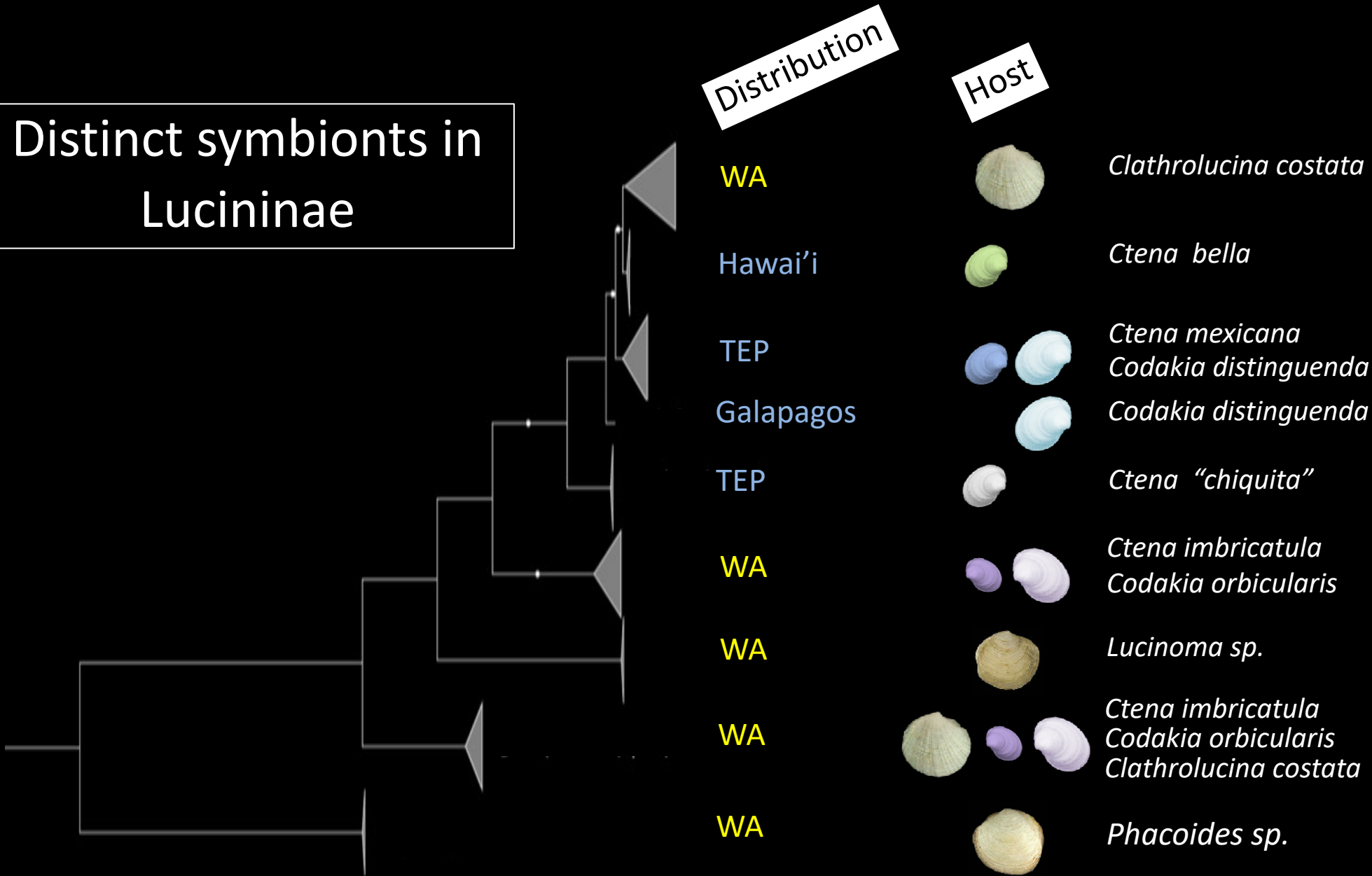
Distinct symbionts in
Codakiinae occurring at
other locations in the
Pacific



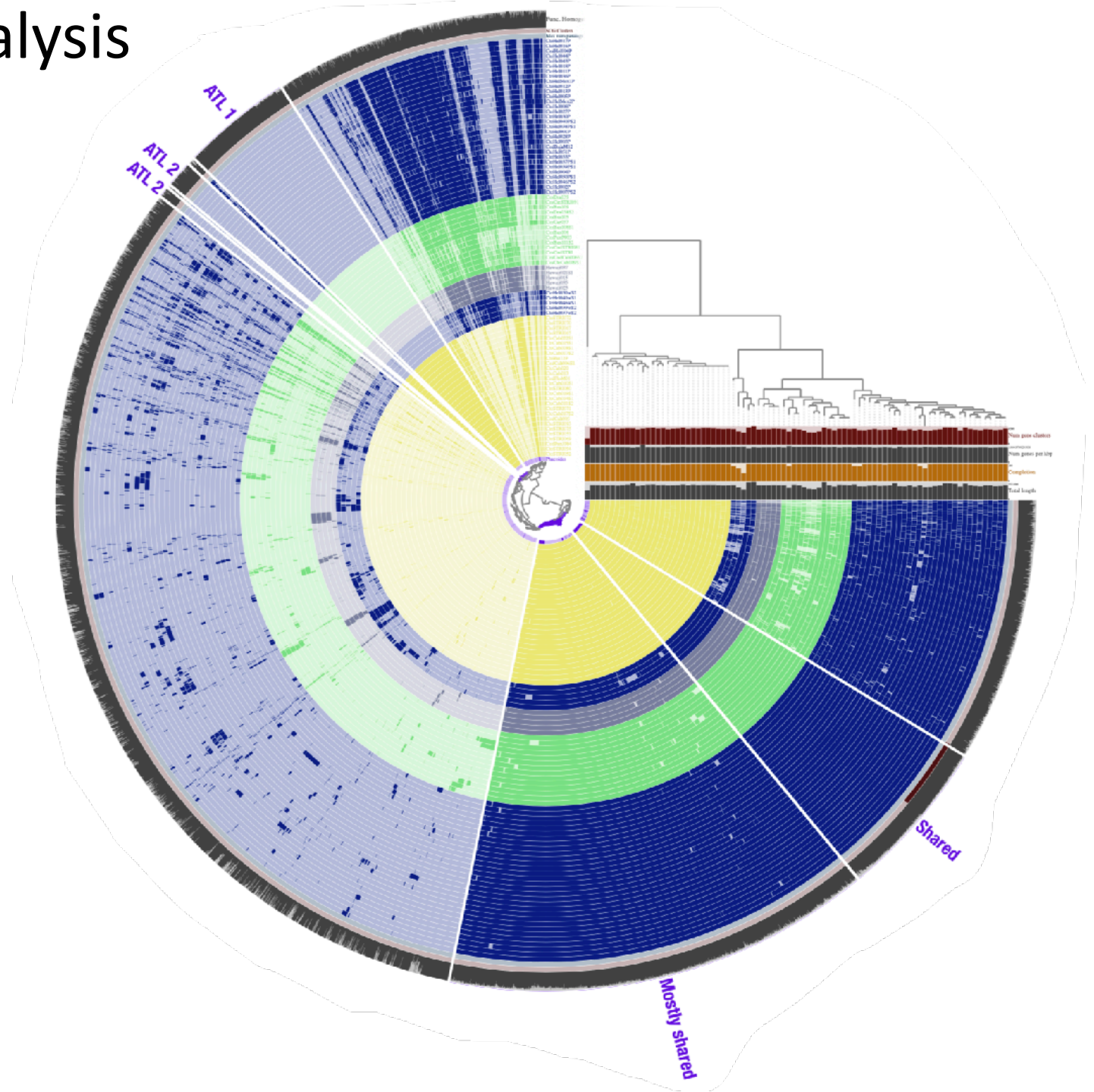
233 high quality genomes clustered into 8 clades

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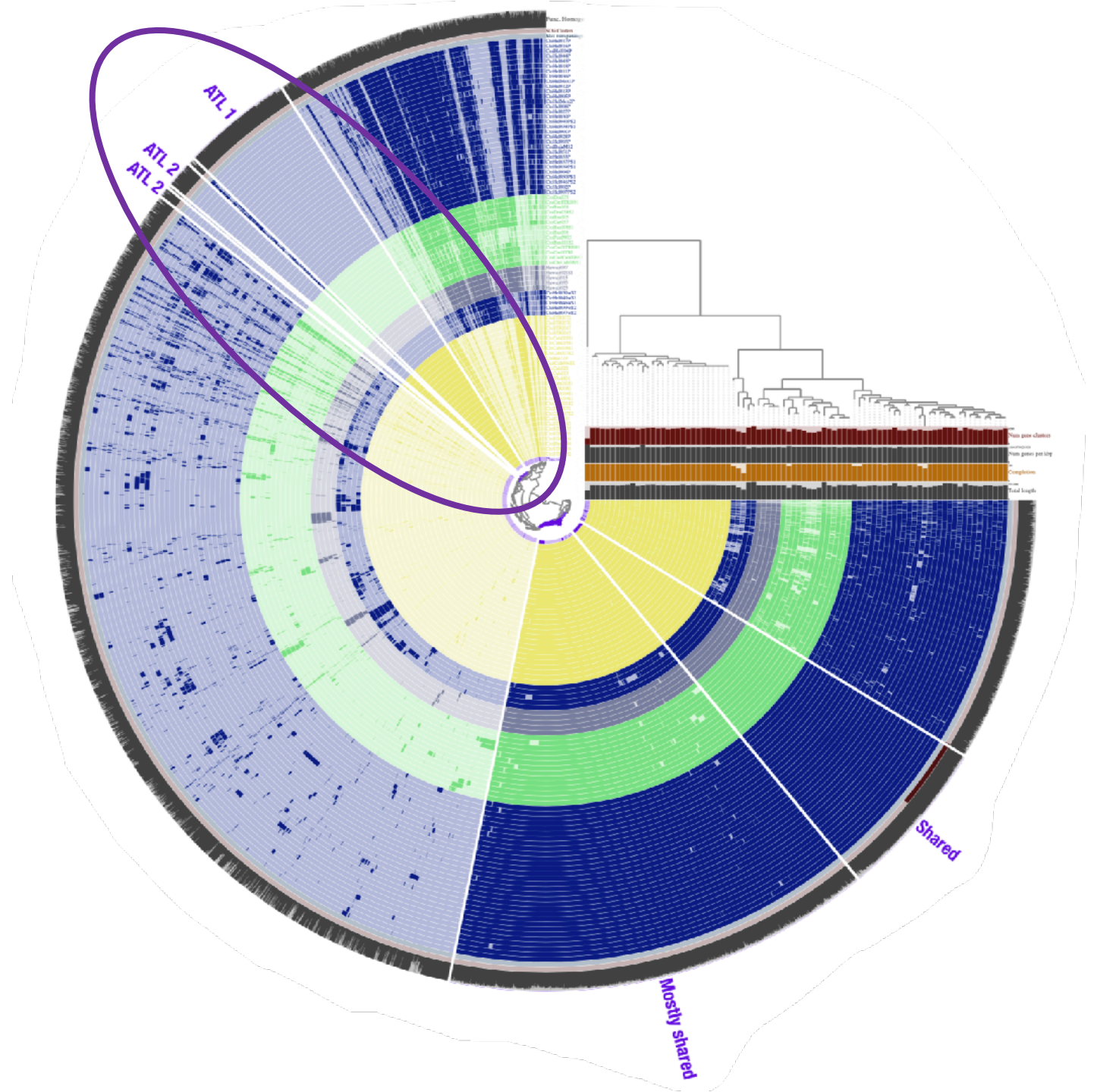
Distinct symbionts in
Lucininae



Pangenome analysis

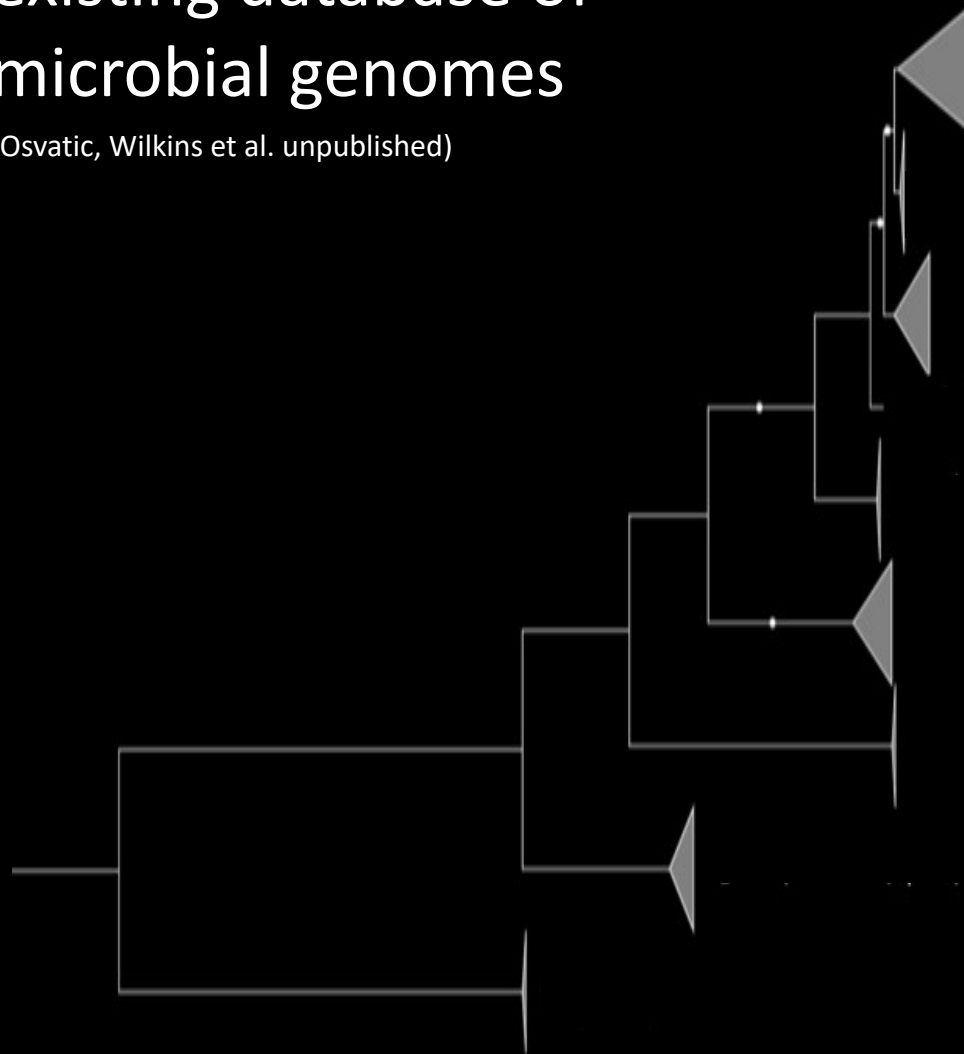


Gene families only found in the Caribbean (Atlantic)



Comparison with existing database of microbial genomes

(Osvatic, Wilkins et al. unpublished)



WA = Western Atlantic

ETP = Eastern Tropical Pacific

Distribution

Host

WA



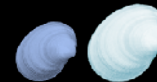
Clathrolucina costata

Hawai'i



Ctena bella

TEP



Ctena mexicana
Codakia distinguenda

Galapagos



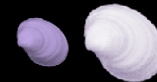
Codakia distinguenda

TEP



Ctena "chiquita"

WA



Ctena imbricatula
Codakia orbicularis

WA



Lucinoma sp.

WA



Ctena imbricatula
Codakia orbicularis
Clathrolucina costata

WA

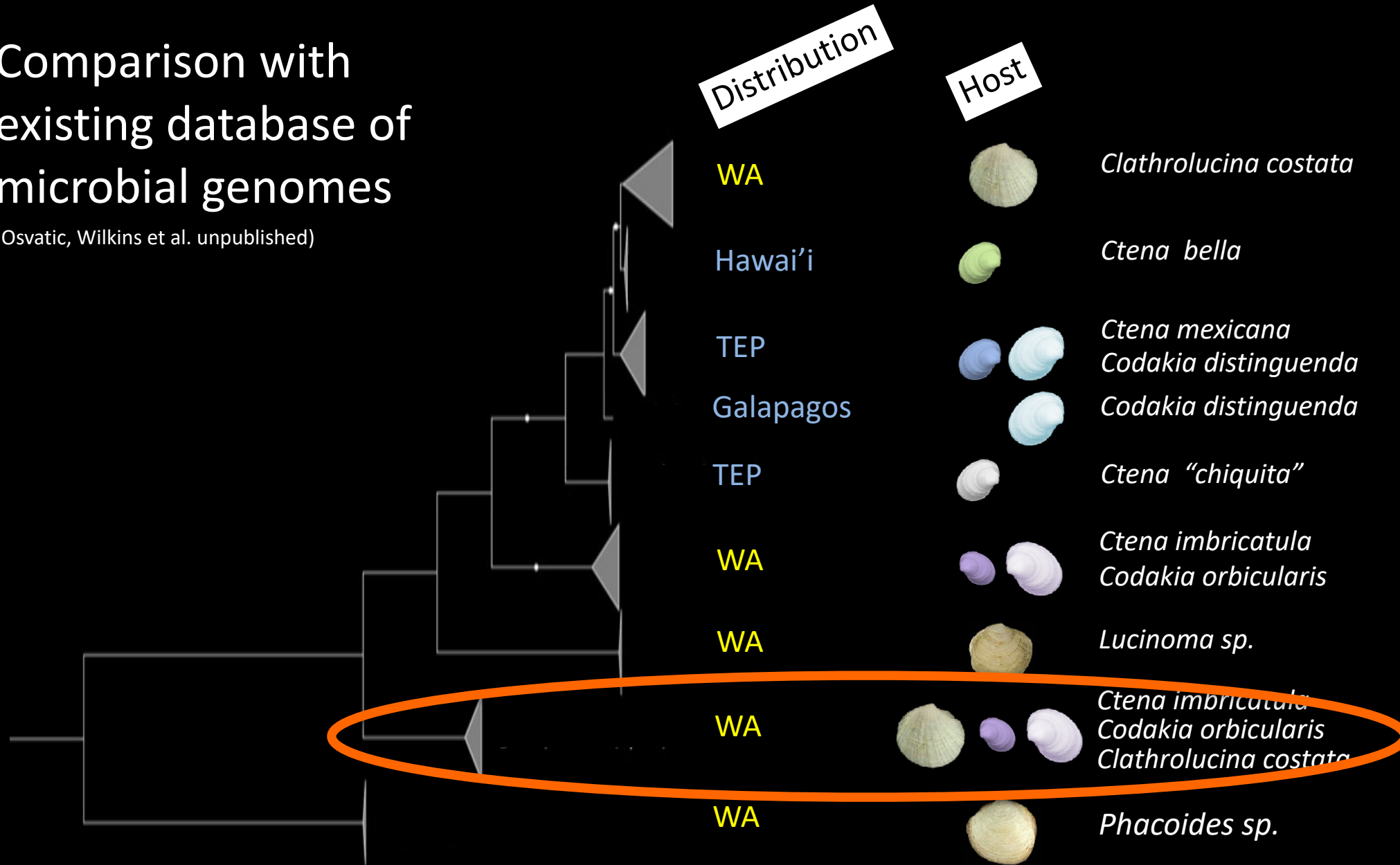


Phacoides sp.

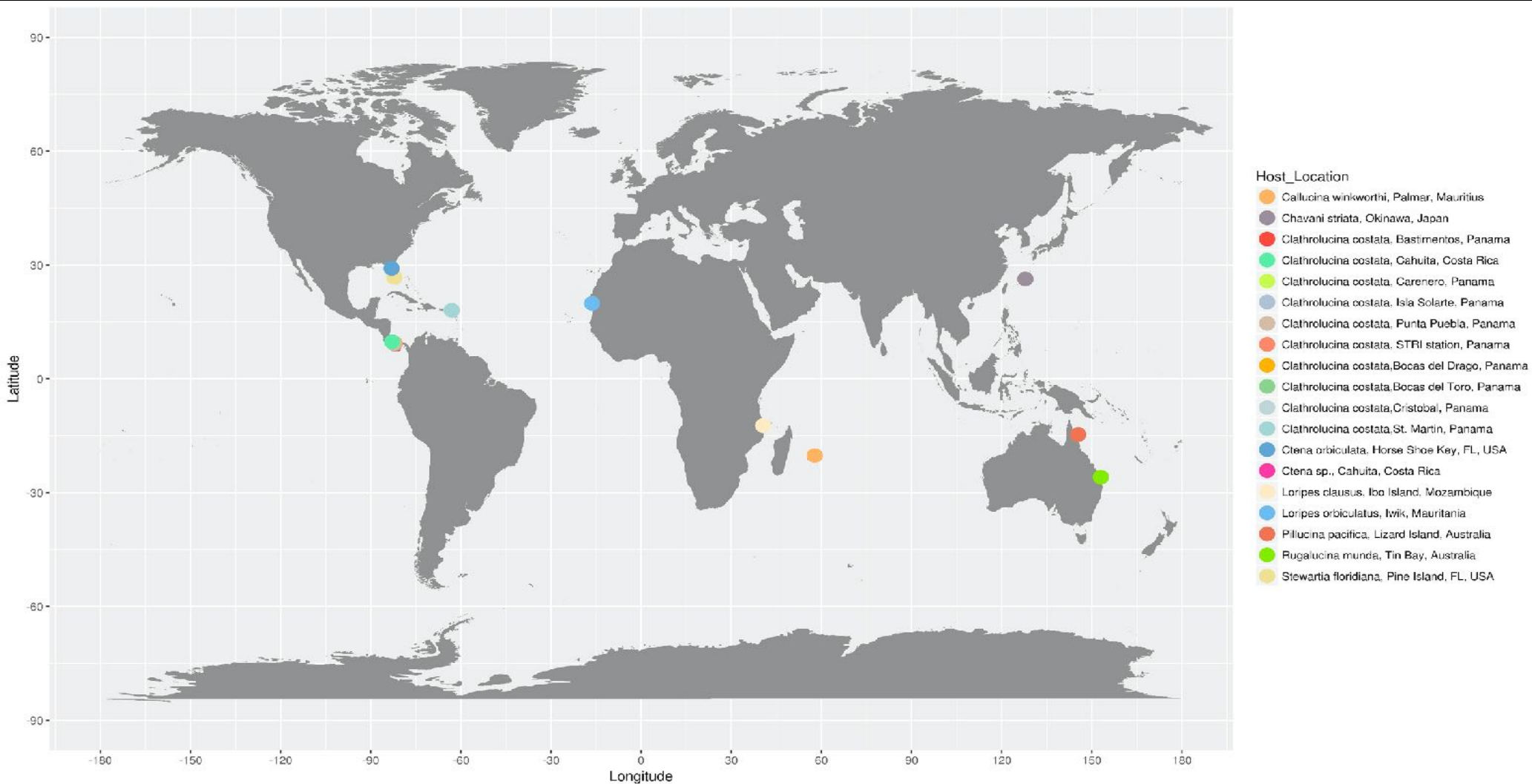
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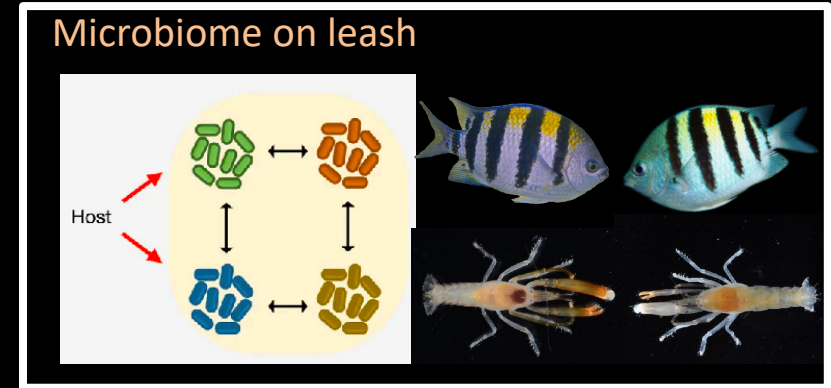
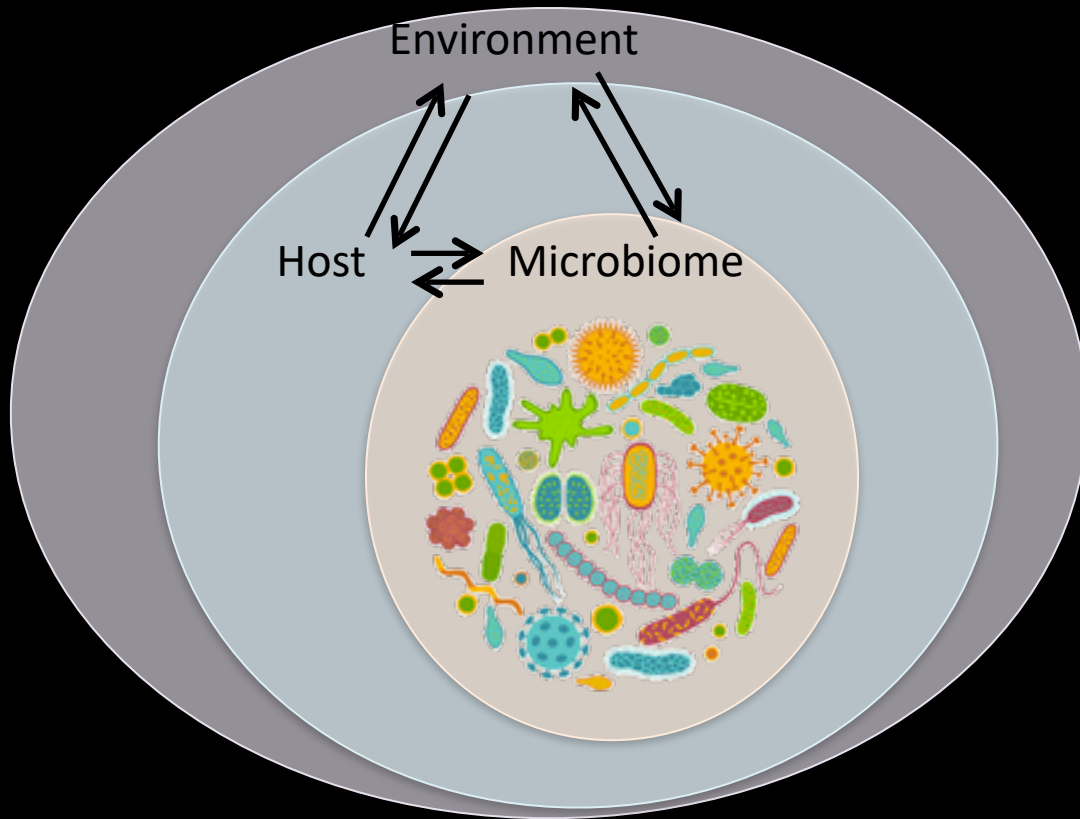


One clade of symbiont is widespread (but absent in TEP)



What have we learned so far?

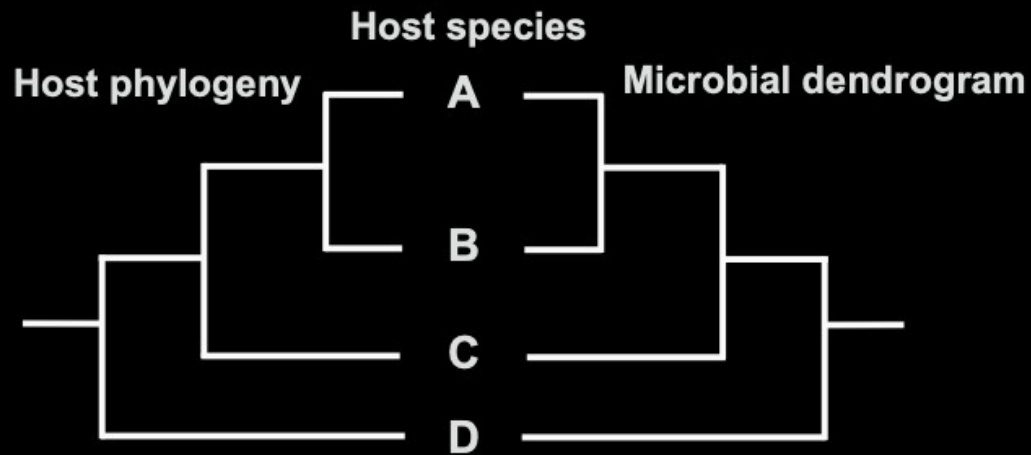
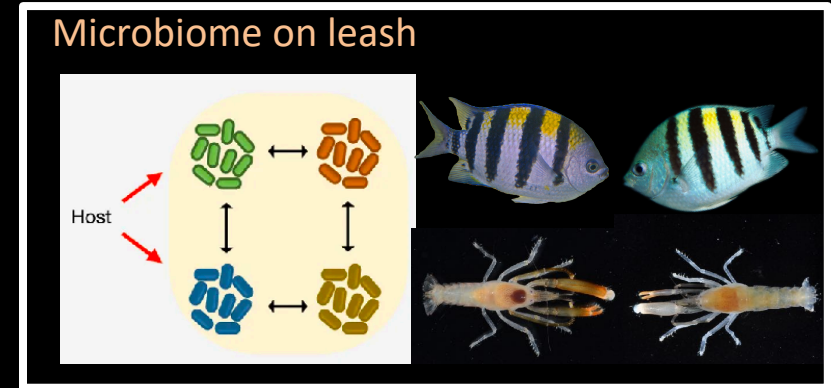
1) Identifying ecological and evolutionary drivers of the microbiome



- 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

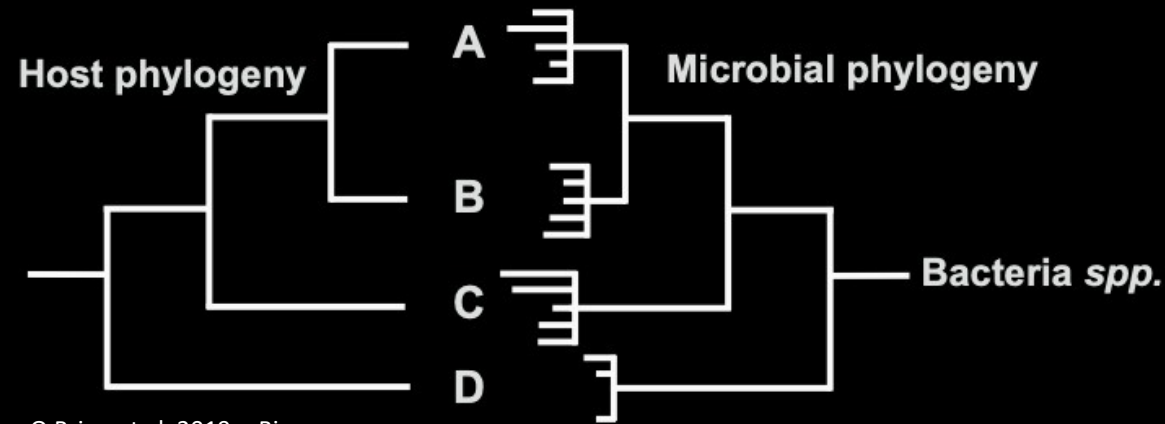


O.Brien et al. 2019 mBio

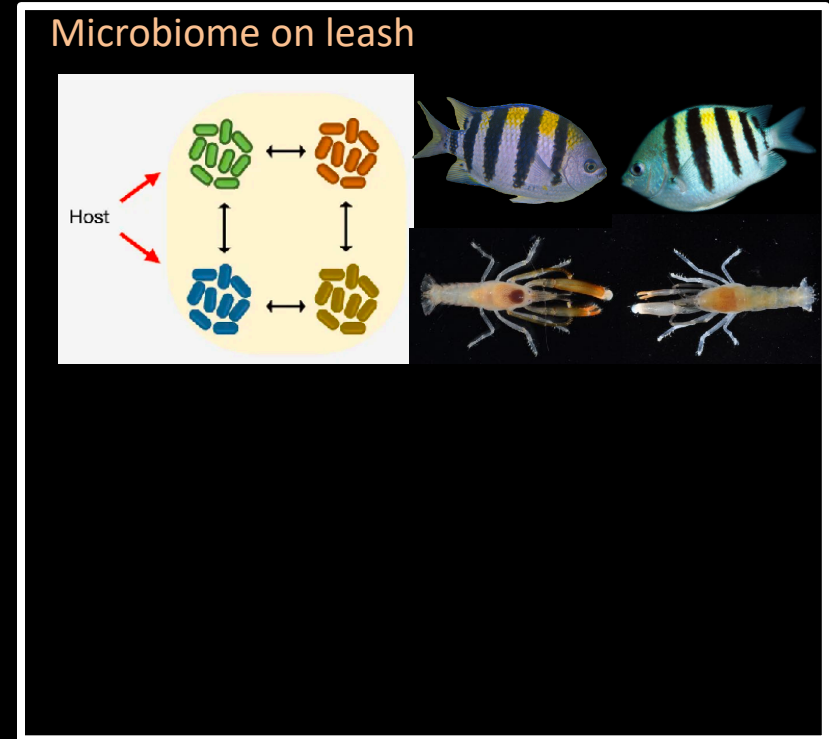
- Species and tissue specific microbiomes
= microbiome on leash
- Limited effect of the “Ocean” on community structure
- Phylogenetic signal

What have we learned so far?

2) Co-divergence between hosts and microbes



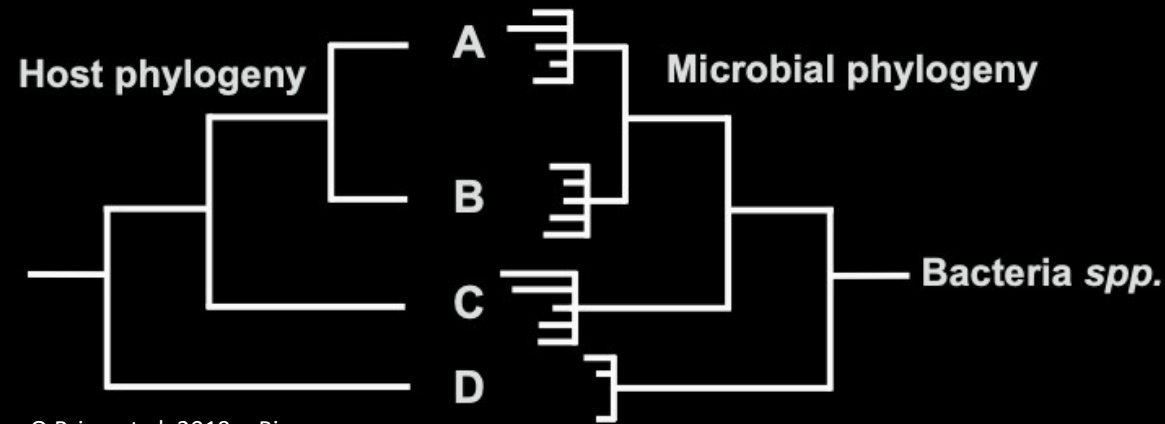
O'Brien et al. 2019 mBio



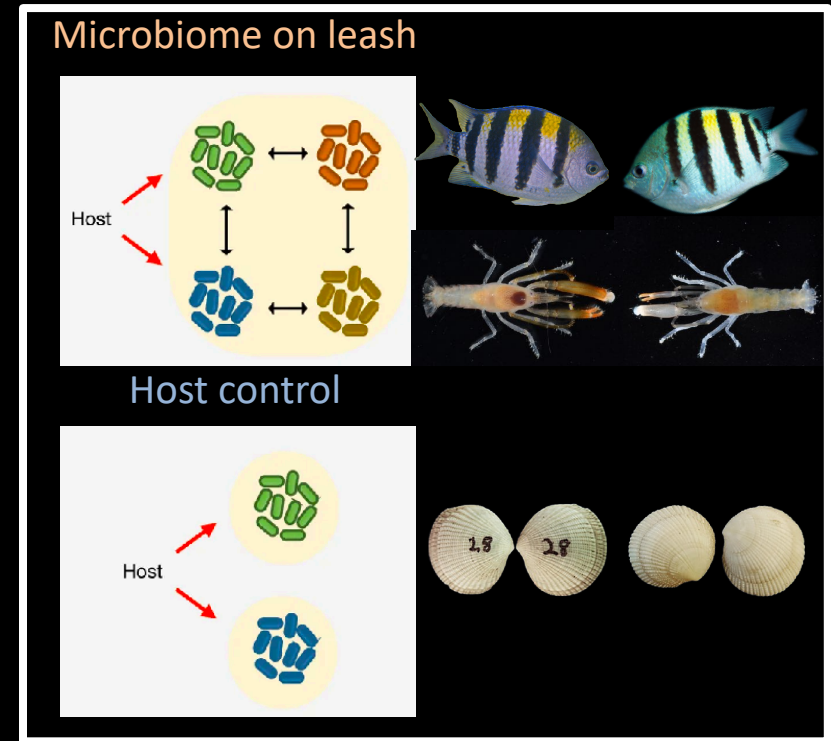
- Evidence of co-divergence between hosts and very few microbes

What have we learned so far?

2) Co-divergence between hosts and microbes



O'Brien et al. 2019 mBio

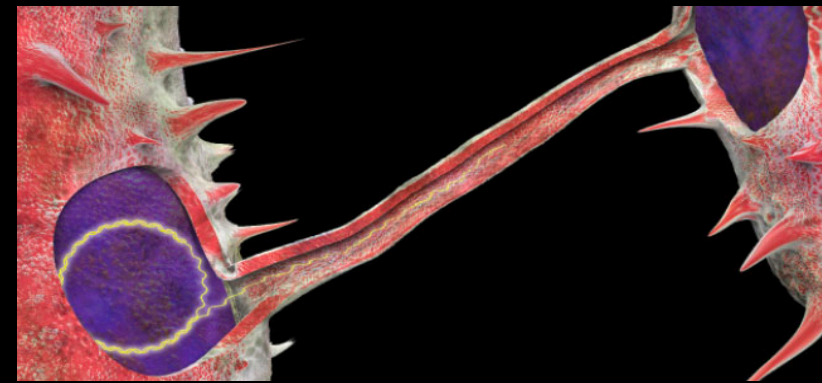
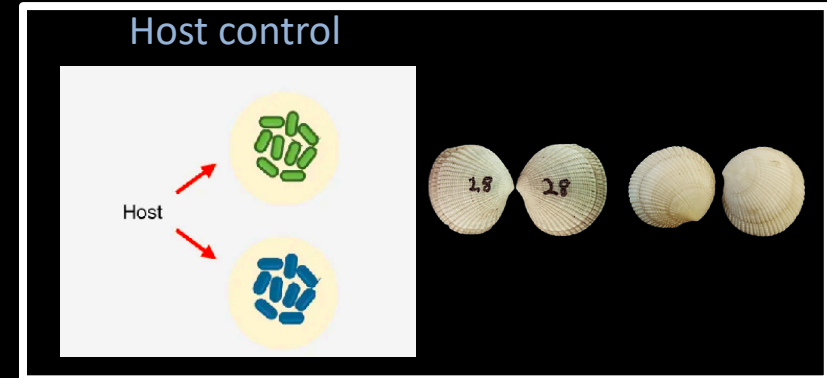
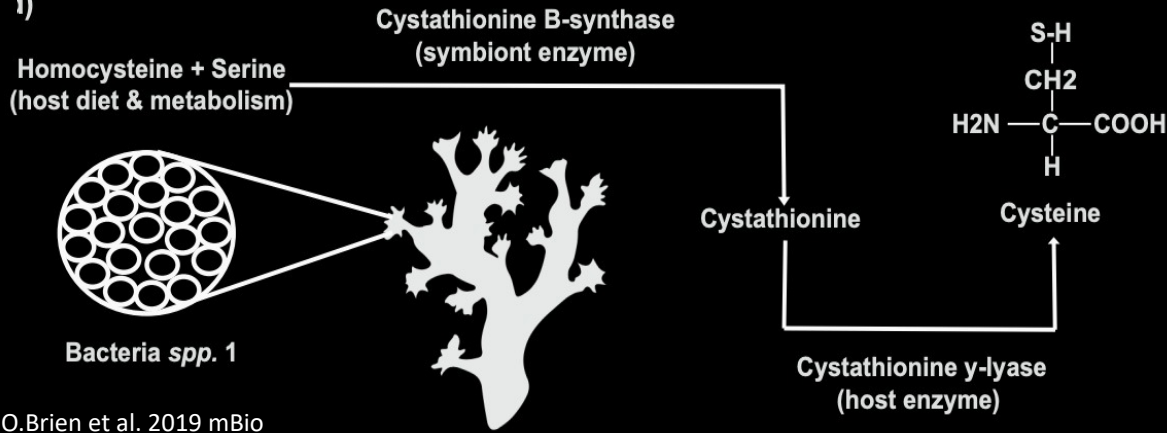


- Evidence of co-divergence between hosts and very few microbes
- Beneficial microbes are promiscuous (not host specific)
- Beneficial microbe with wide geographical distribution

What have we learned so far?

3) Adaptation and metabolic cooperation

1)



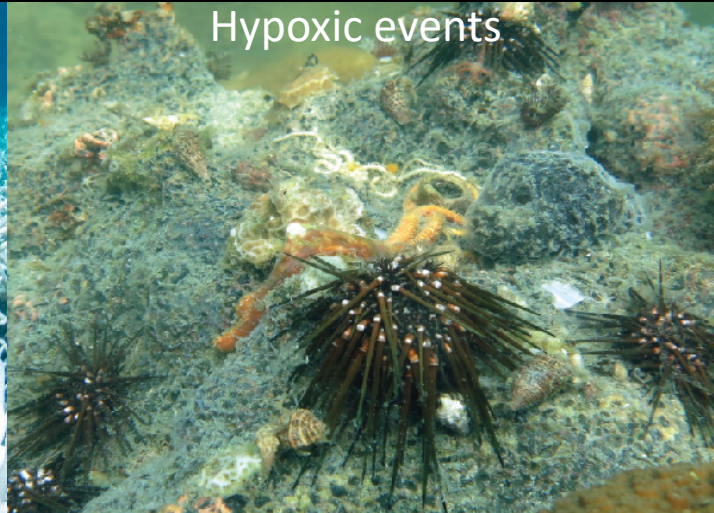
- Set of genes present only in genome of the Caribbean symbionts

Breakdown of interactions between hosts and microbes/microbiomes

Coral bleaching



Hypoxic events



Disease



EVERY YEAR WE LOSE



2-8%
mangroves

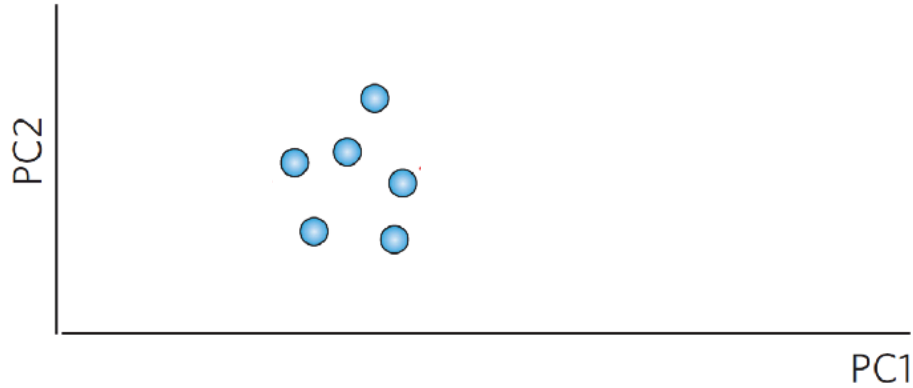


5%
seagrass meadows

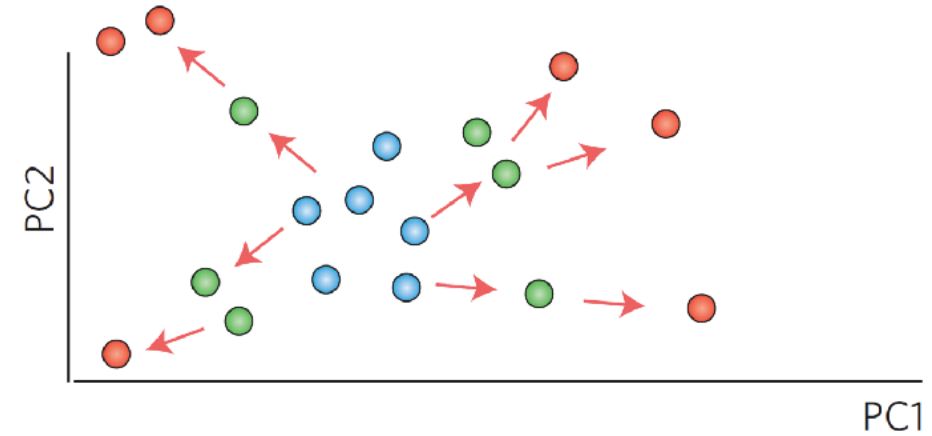


5%
coral reefs

Healthy microbiome

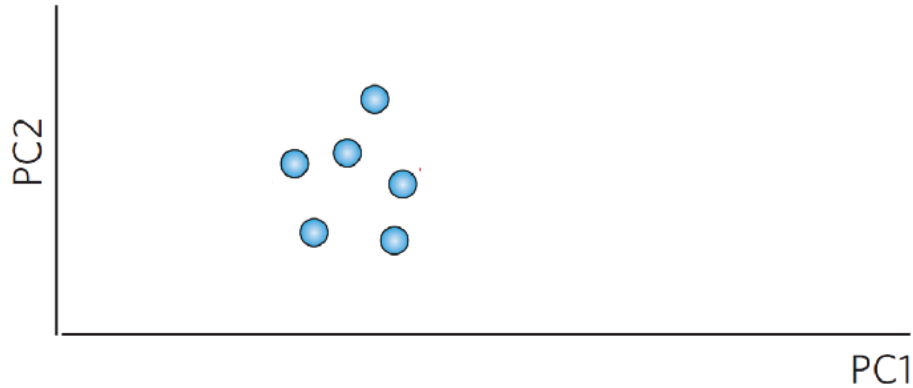


Dysbiotic microbiome

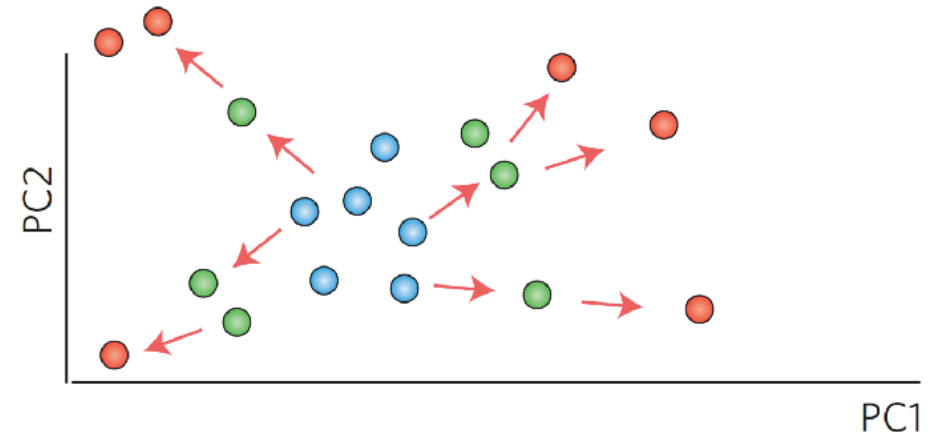


Zaneveld et al. 2017 Nature Microb.

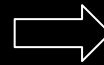
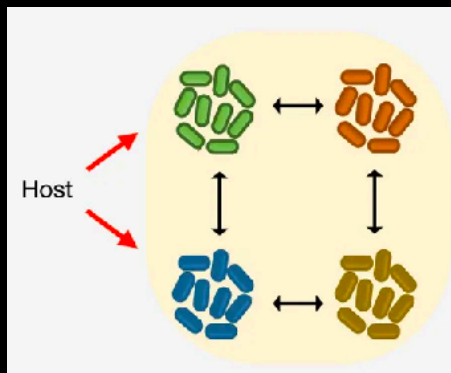
Healthy microbiome



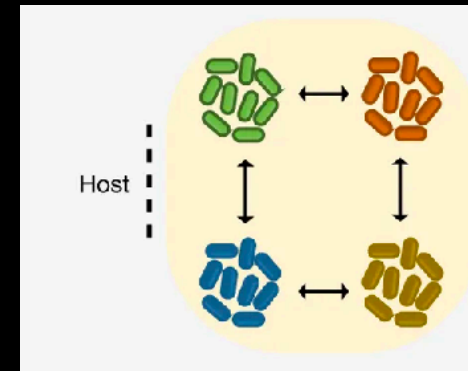
Dysbiotic microbiome



Microbiome on leash

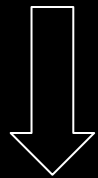


Open ecosystem

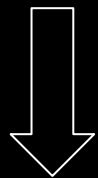


The host can no longer keep its microbiome on a leash

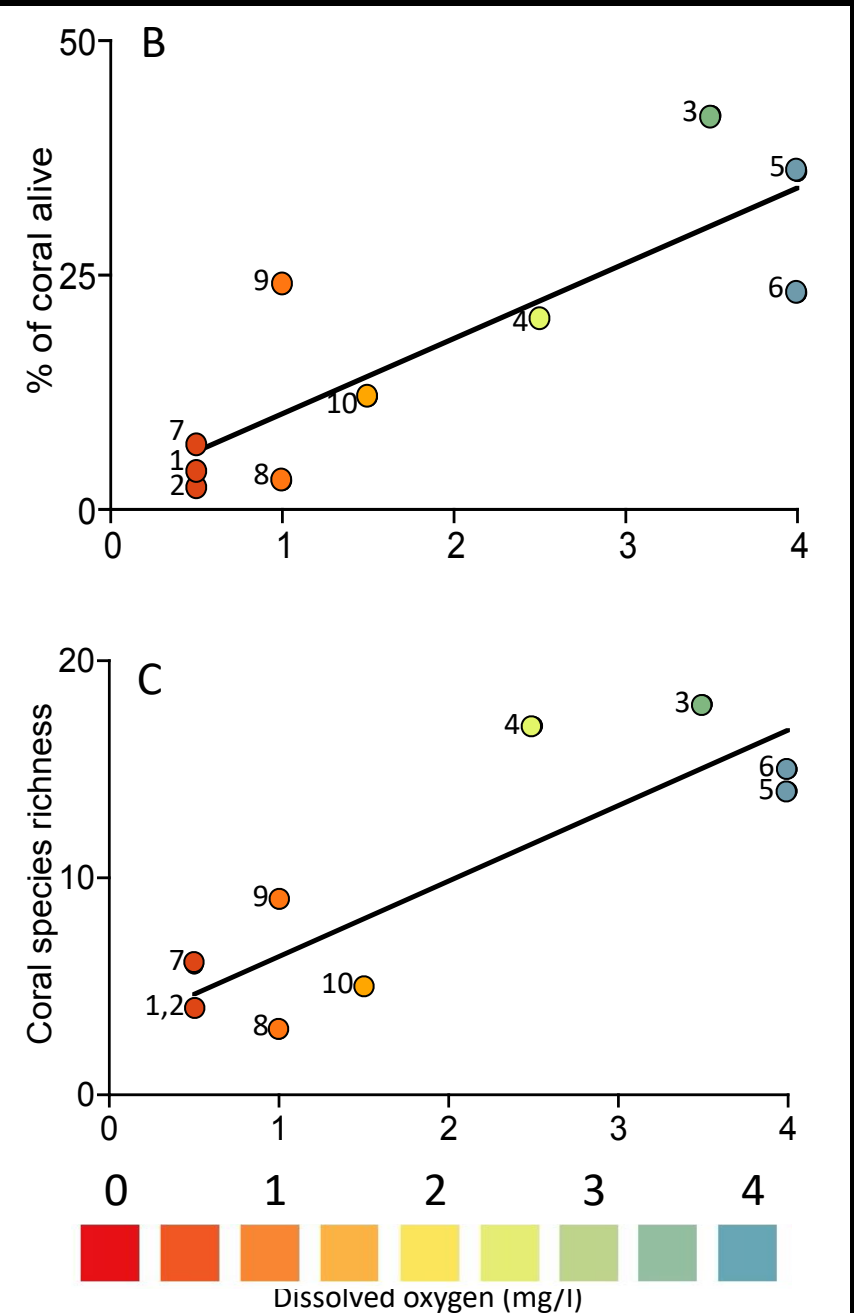
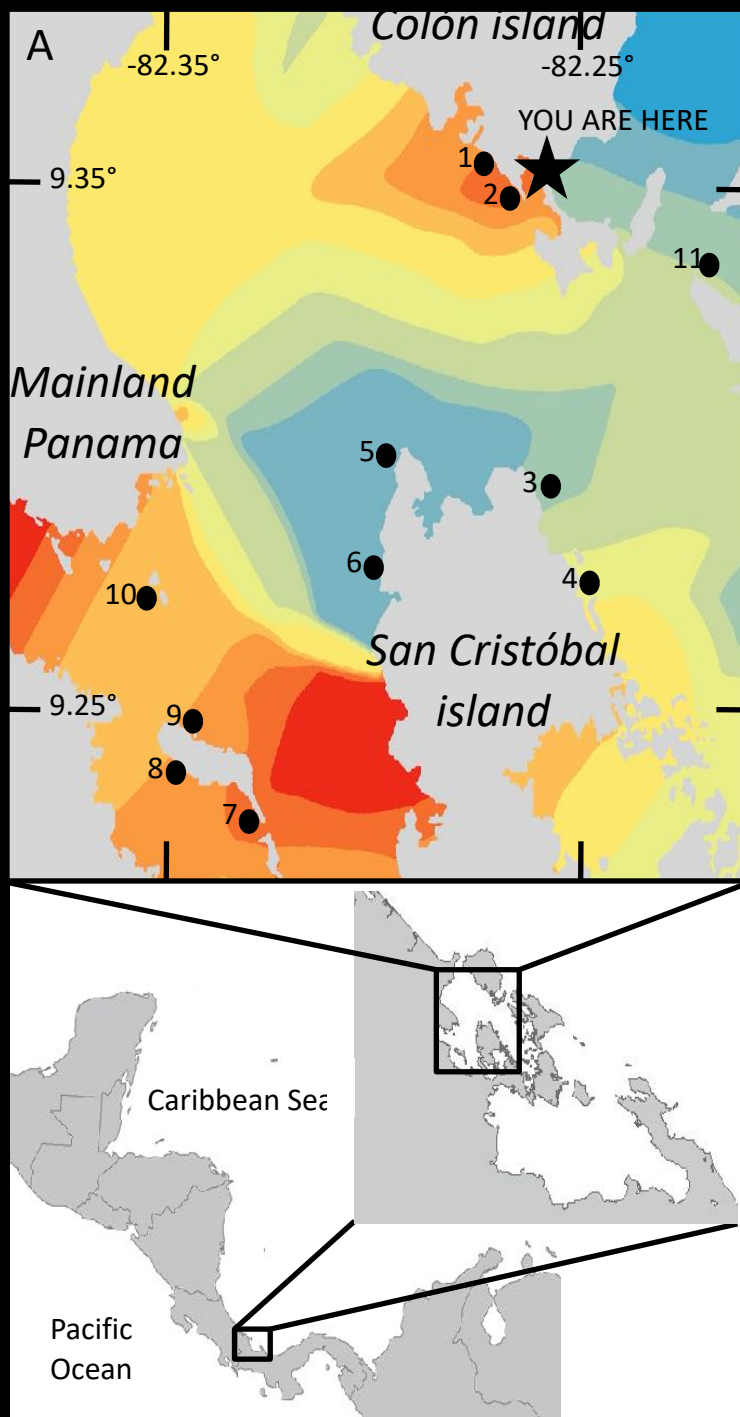
Hypoxia
in 2010



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?

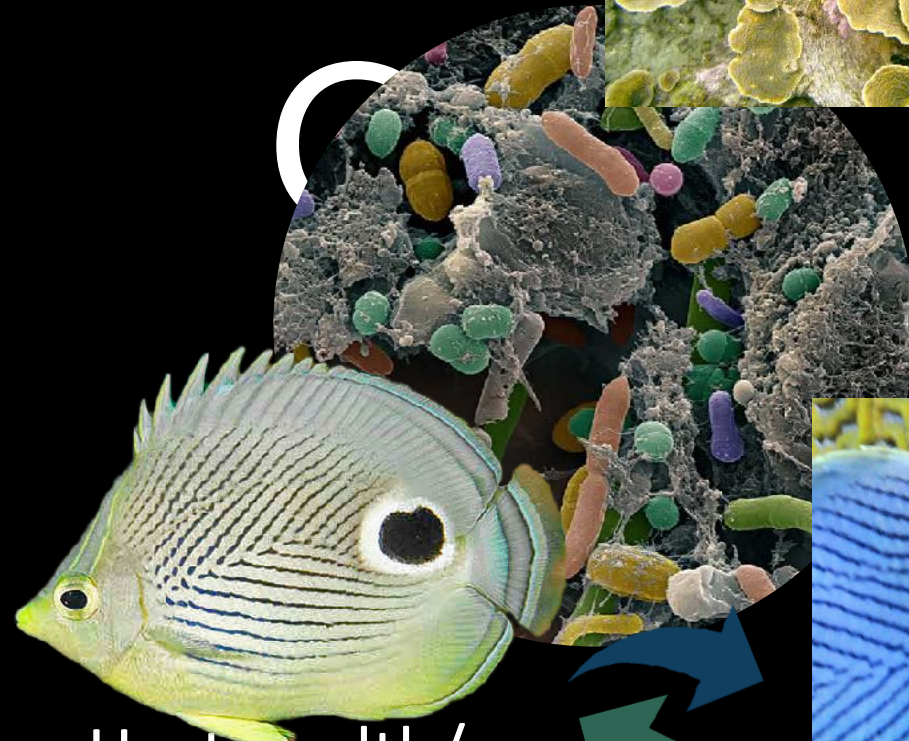
HOST:

Foureye butterflyfish
Preferentially feeds on corals

MICROBIOME:

Gut microbiome
linked to host health, diet &
habitat

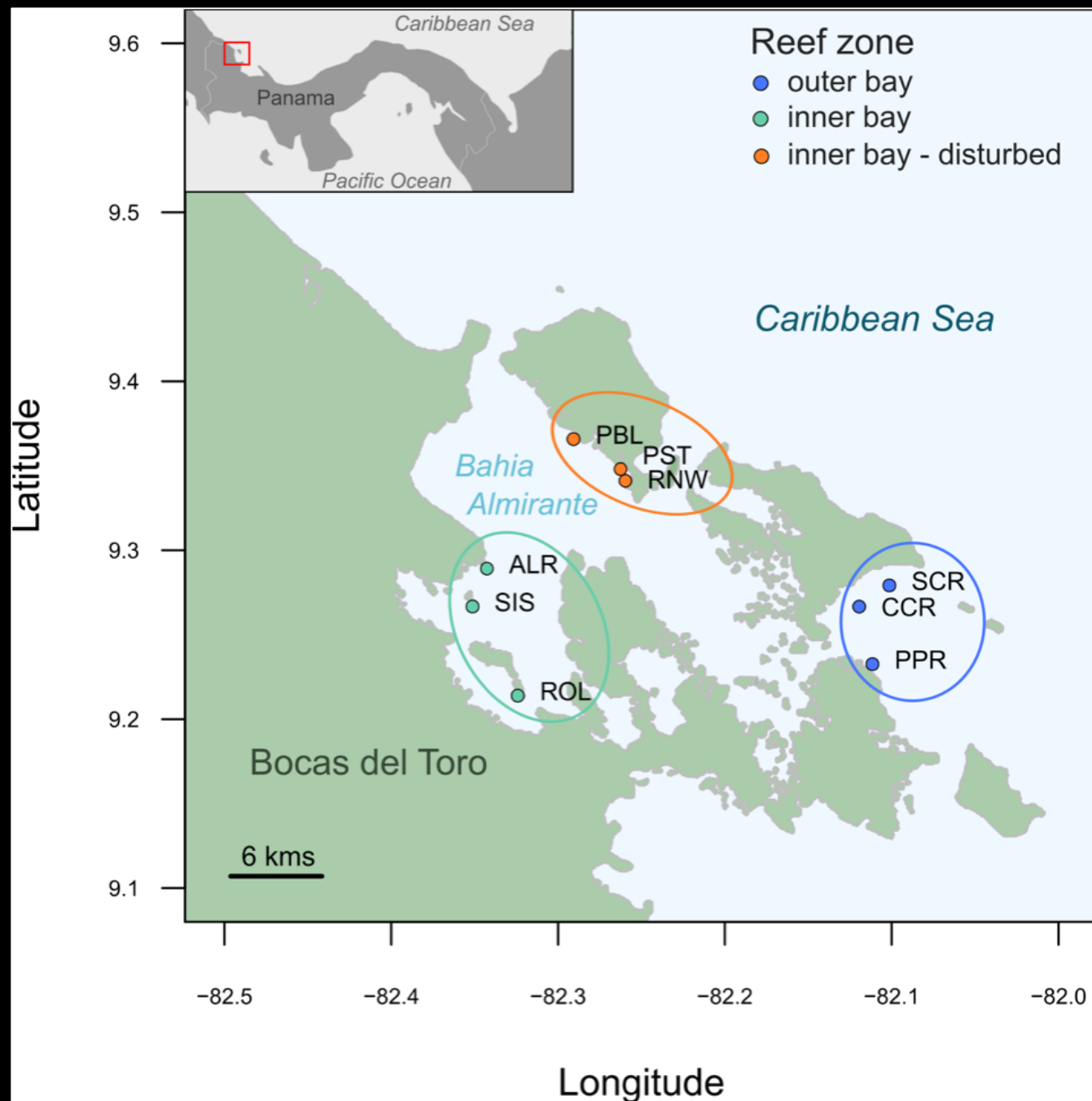
Habitat



Host health/
genetics

Diet





COLLECTION OF FISH



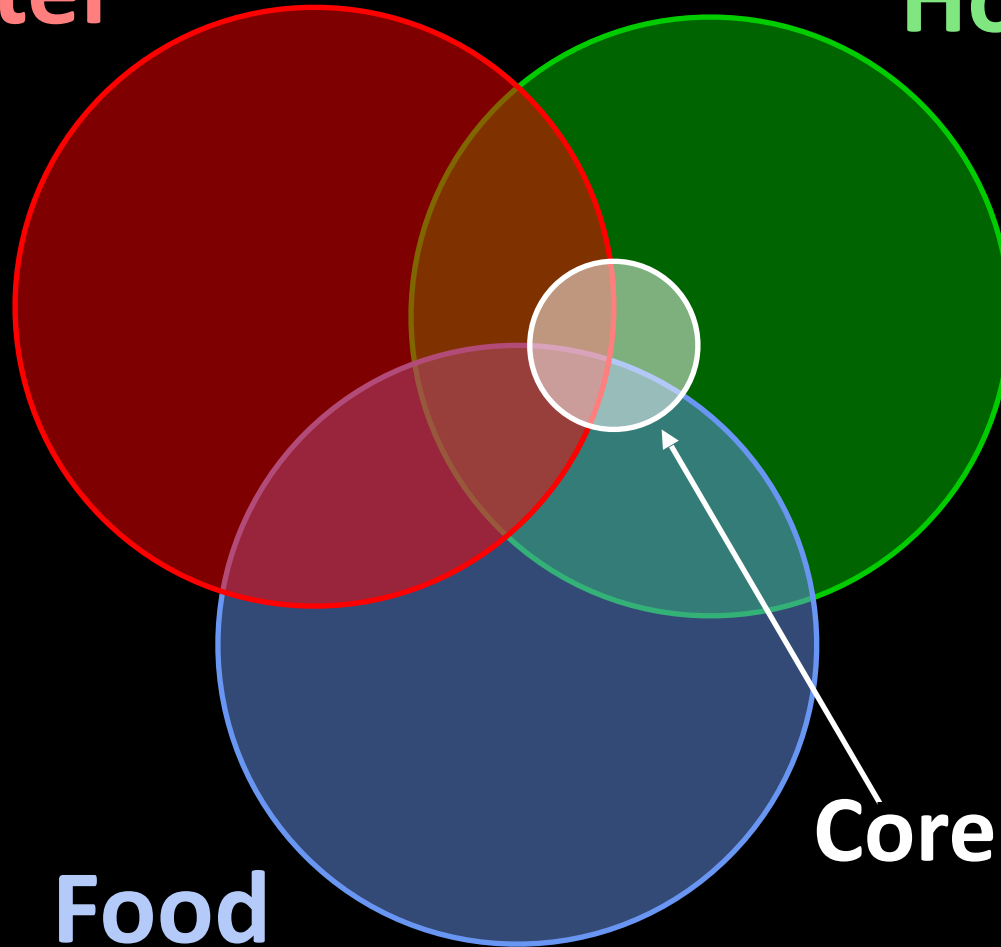
20 specimens per reef
Four-eye butterflyfish

COLLECTION IN THE SURROUNDING ENVIR.

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

Seawater

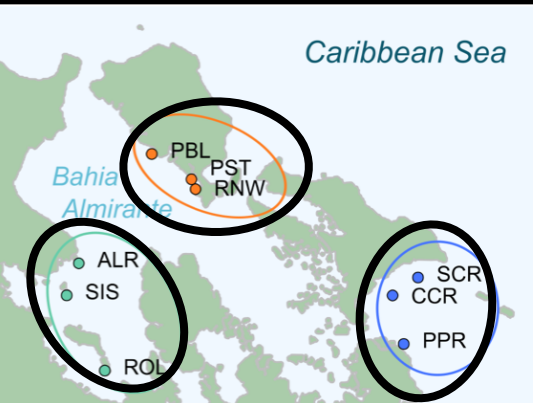
Host



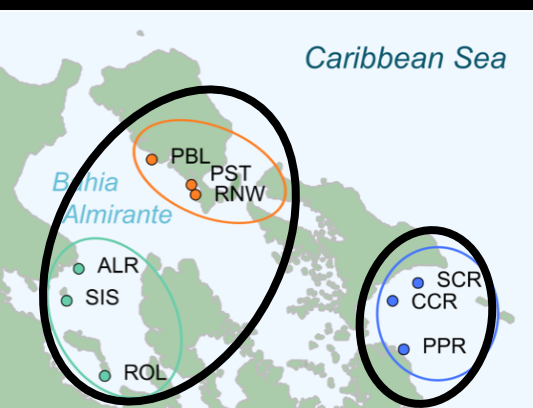
Food

Core microbiome

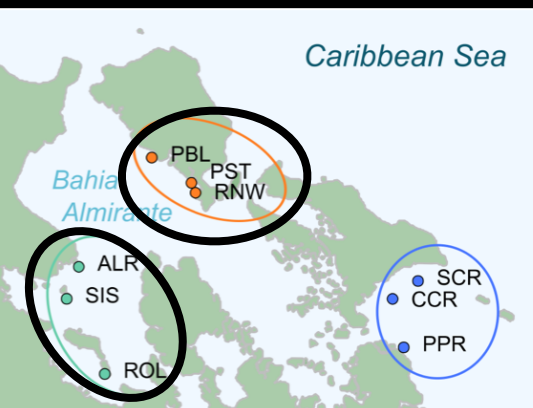
Zone



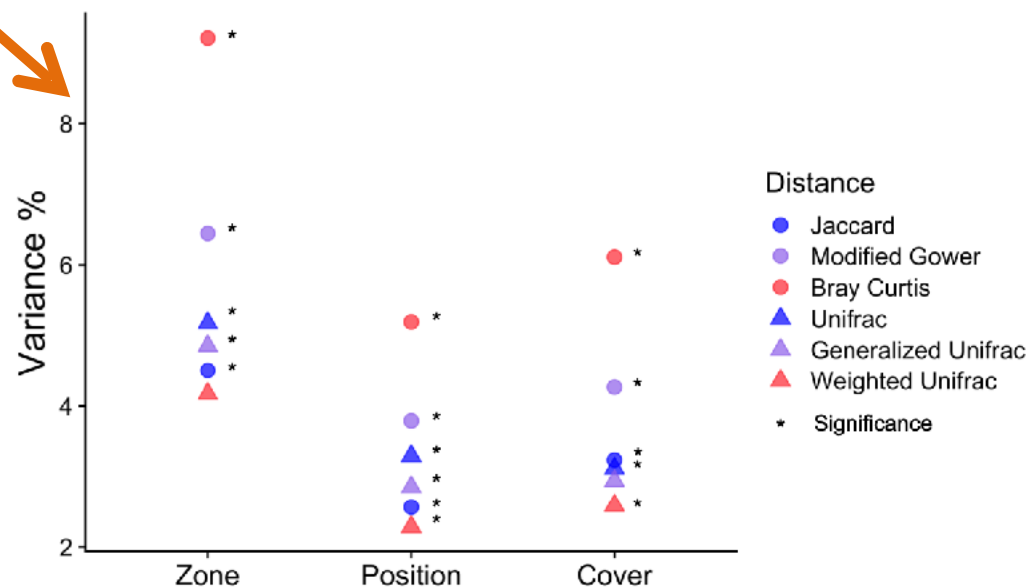
Position



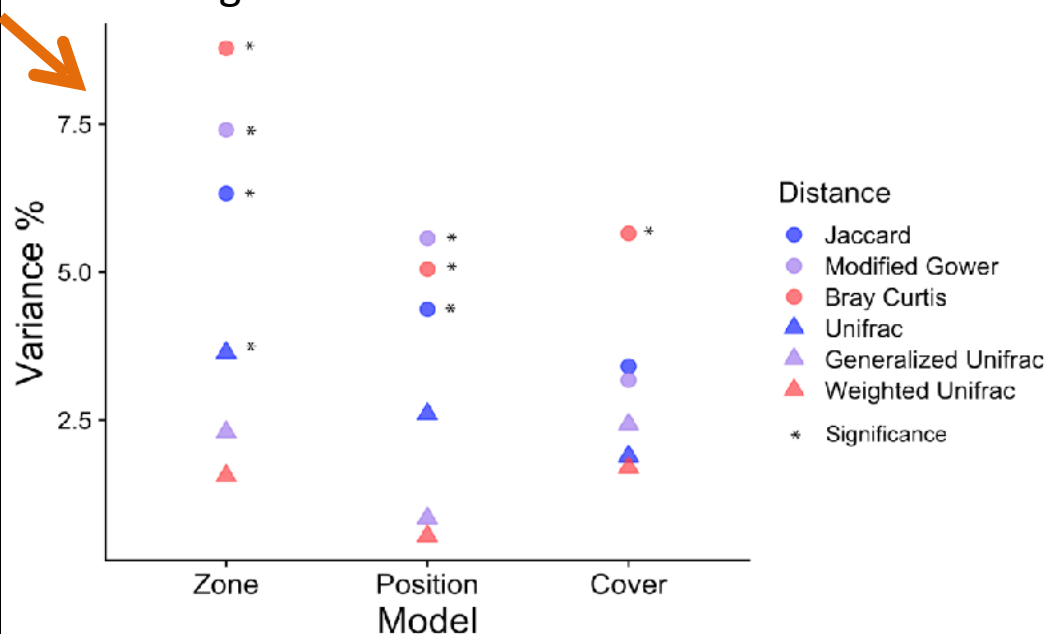
Cover



Whole gut microbiome



Core gut microbiome

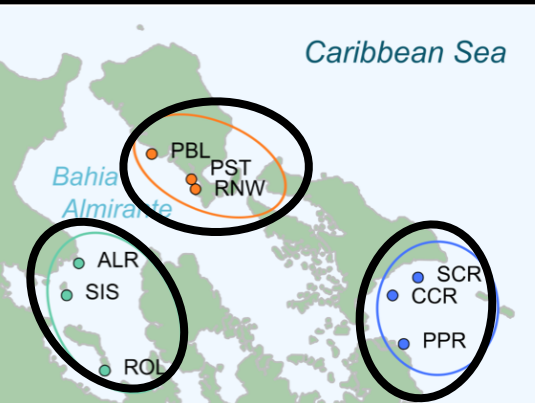


Significant differences in the composition of gut microbiomes across space

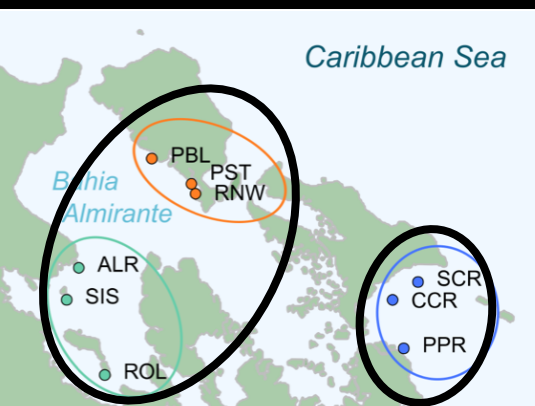
BUT

A very small proportion of the variance is explained

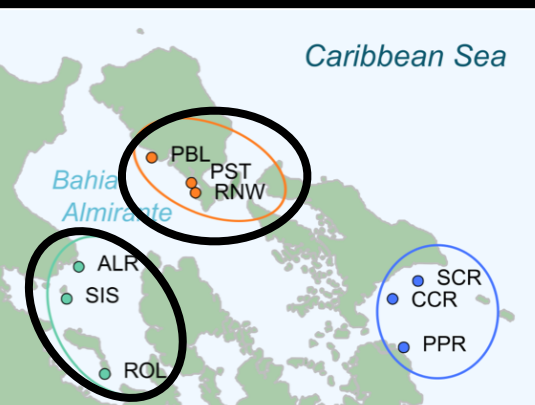
Zone



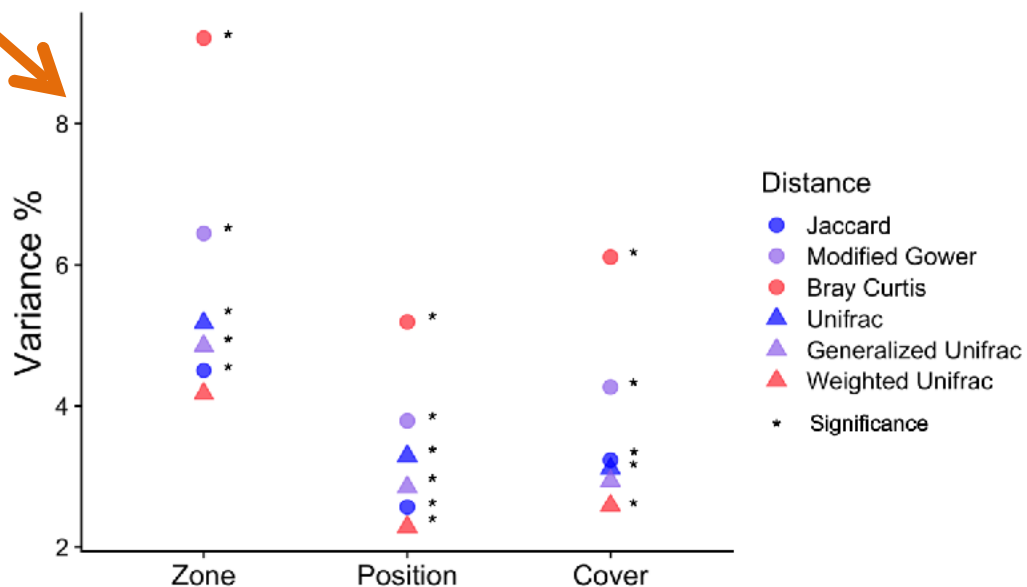
Position



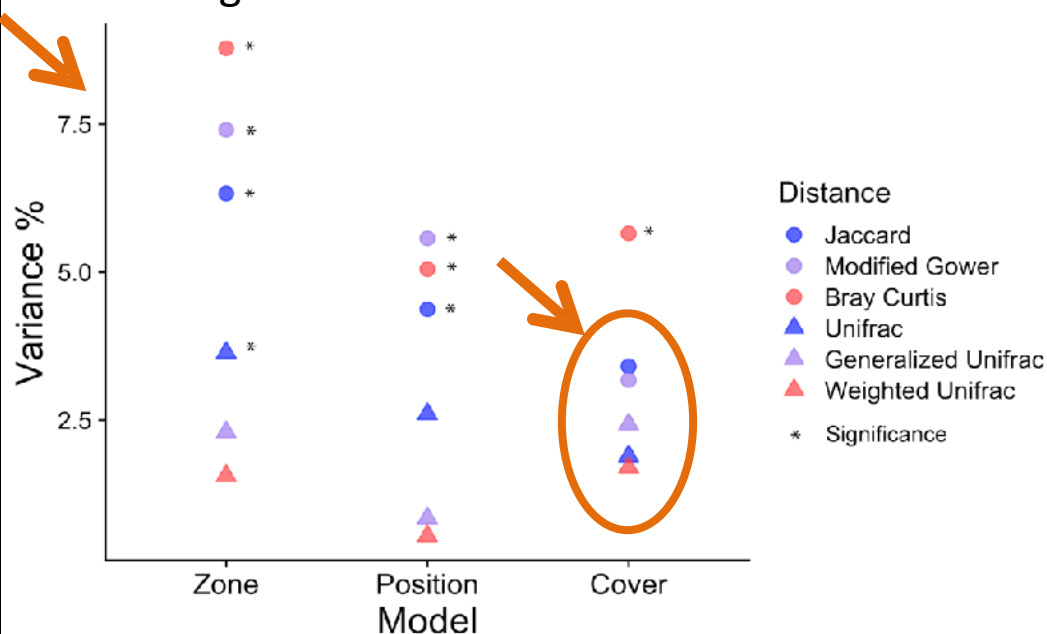
Cover



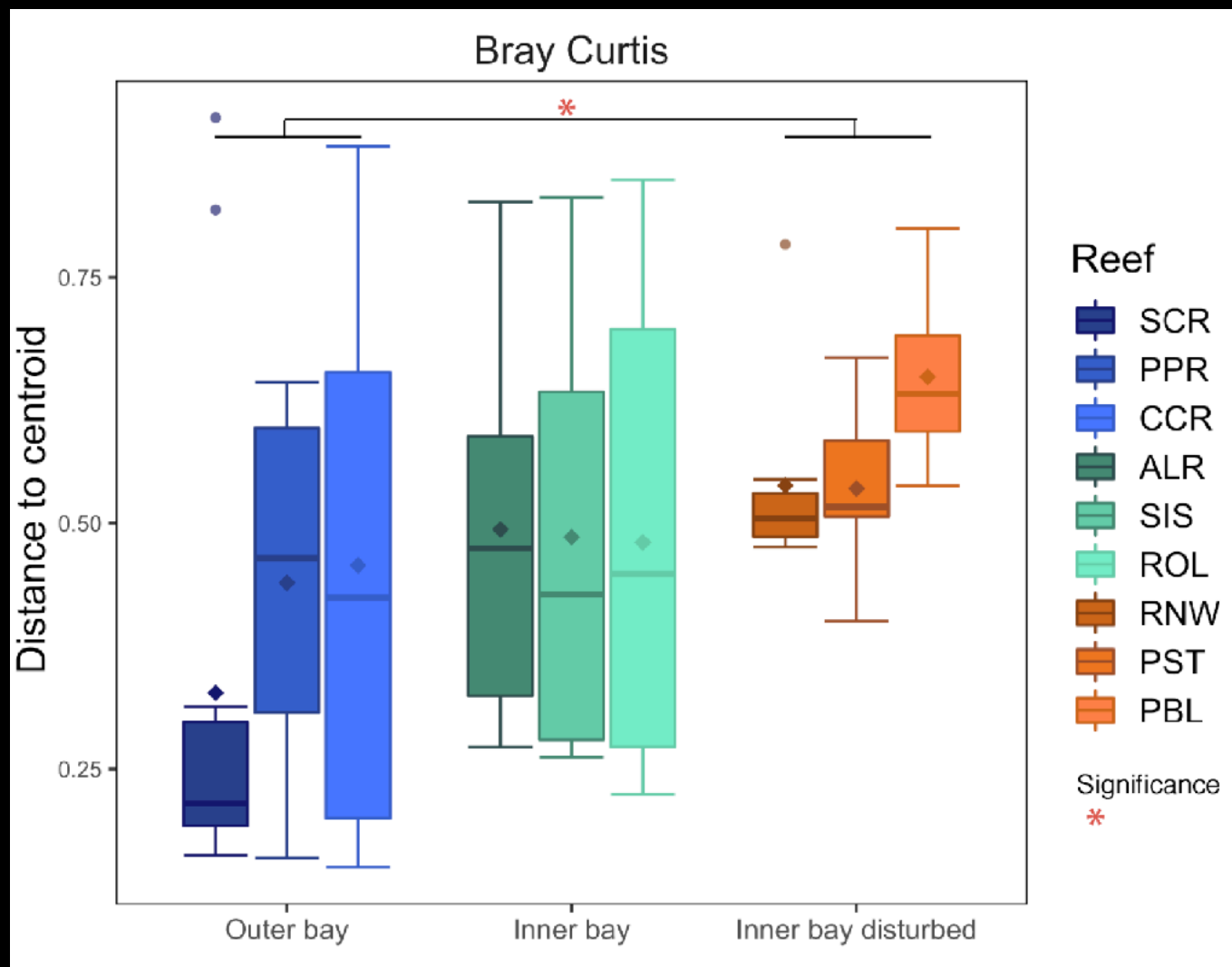
Whole gut microbiome

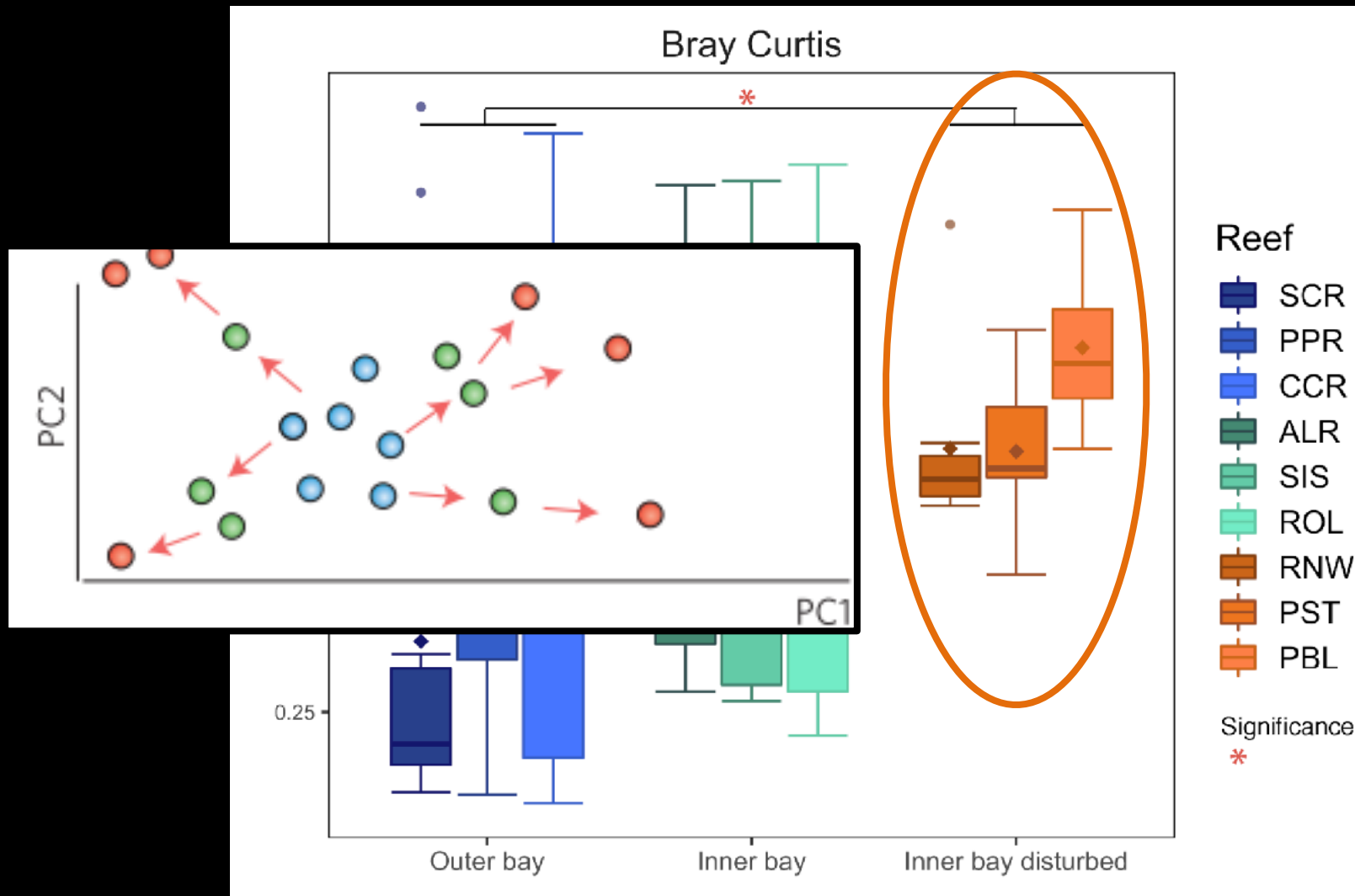


Core gut microbiome



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

UC DAVIS

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
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Diana	Chin	Stony Brook University	Gustav	Paulay	University of Florida
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			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



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THANK YOU!

