

# Opening Thought Question – 4/27

Last lecture, we learned that whales have incredibly low cancer rates despite being large and having many cells in their bodies.

How do they manage this?

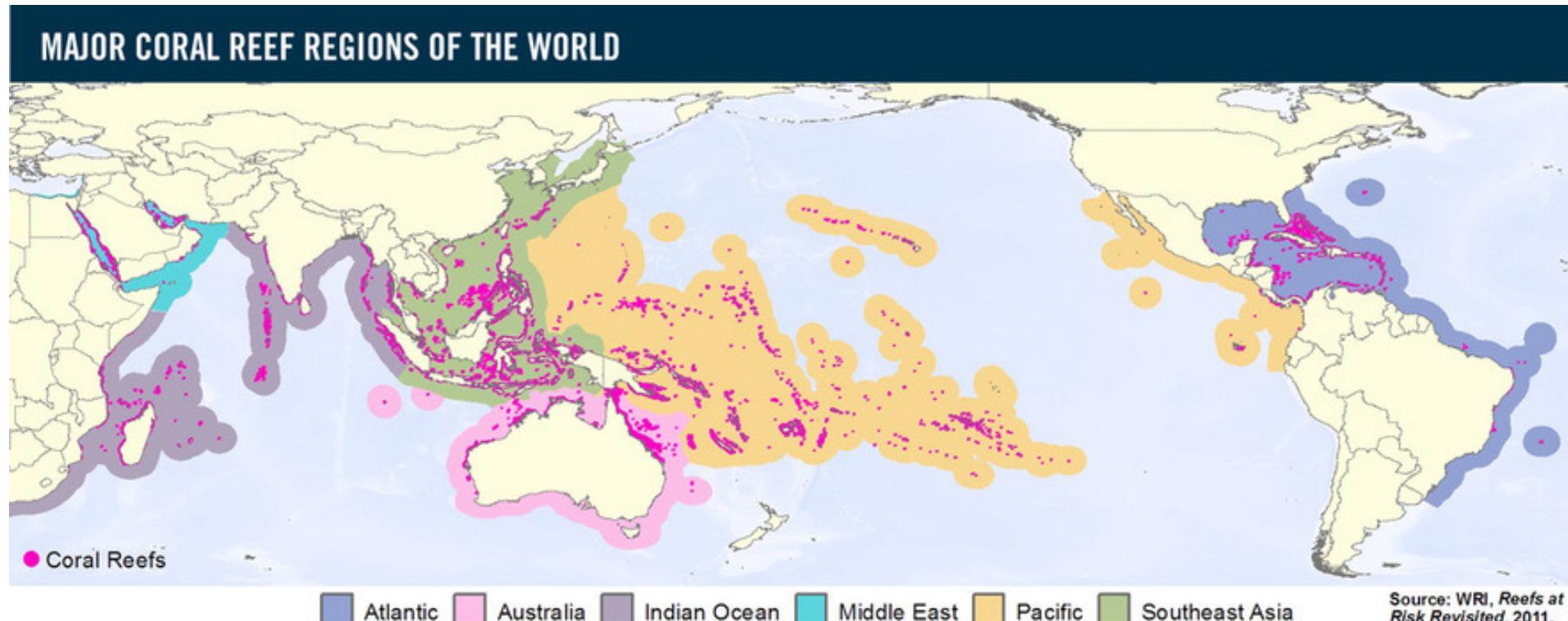
How have bioinformaticians figured this out?

# Coral reefs: oceanographic influences and mutualisms transform communities

1. Coral reefs are incredibly biodiverse
2. How do corals survive and form reefs?
3. How do corals thrive in warm, shallow, clear water that is nutrient poor (i.e., oligotrophic)?
4. How resilient are coral reefs to stress?

# Coral Paradox (“Darwin’s Paradox”)

Corals thrive in warm, shallow, clear water that is nutrient poor. How?



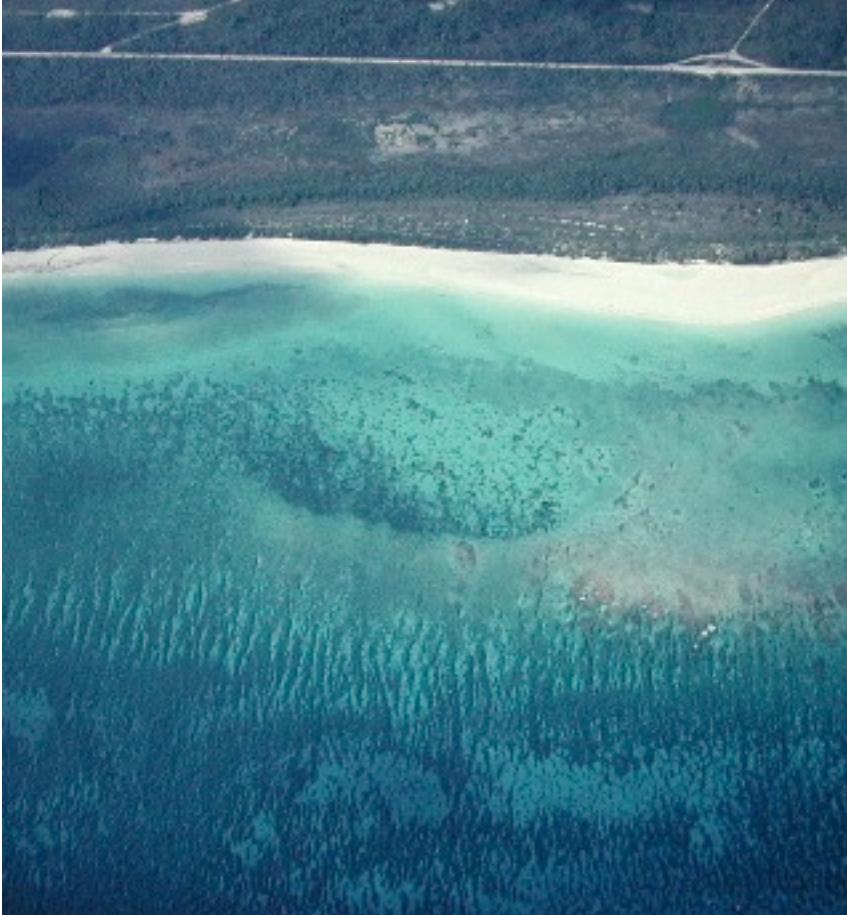
Possible because of:

- symbionts
- key herbivores that reduce algal biomass
- positive feedback loop from reef building corals keeps phytoplankton and nutrients within system

## What is a coral reef? How is it made?

A coral reef is a biogenic structure built over 1000's of years by tiny coral polyps that make up coral colonies.

Scleractinian (reef-building) corals secrete  $\text{CaCO}_3$  to build an external skeleton.



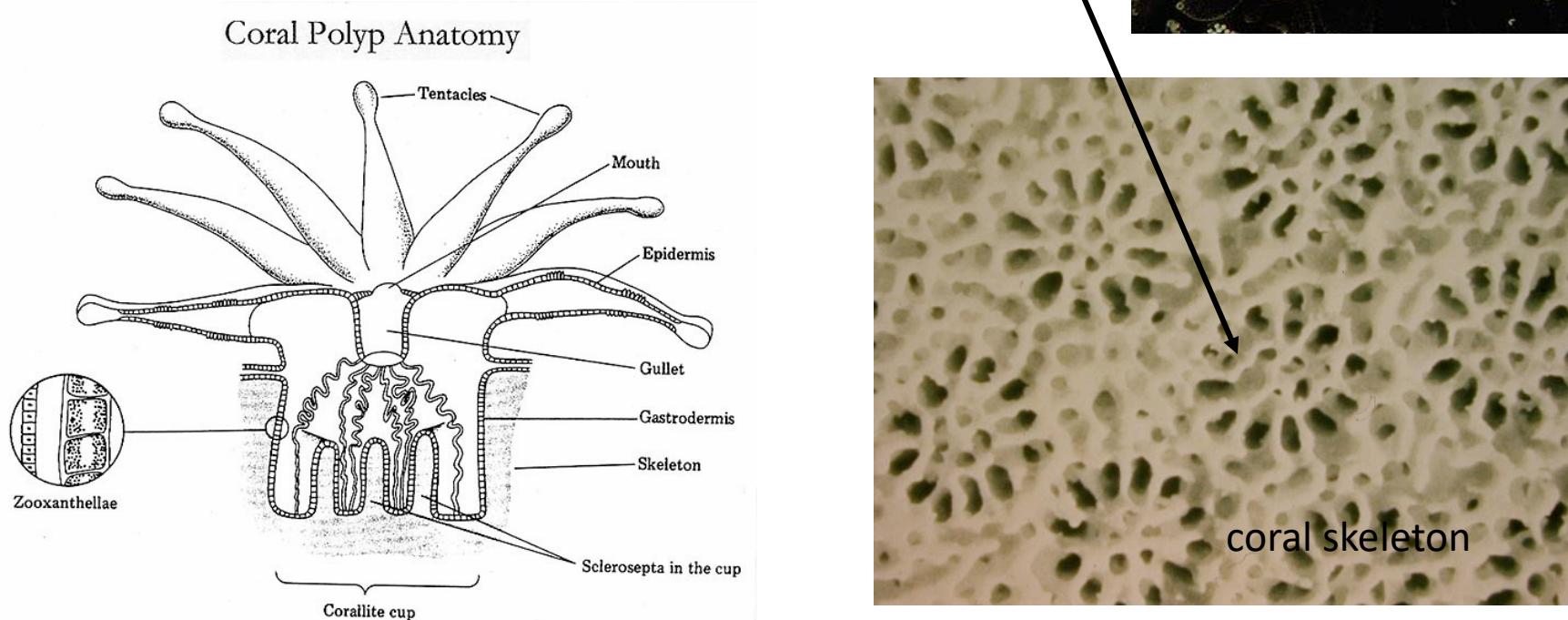
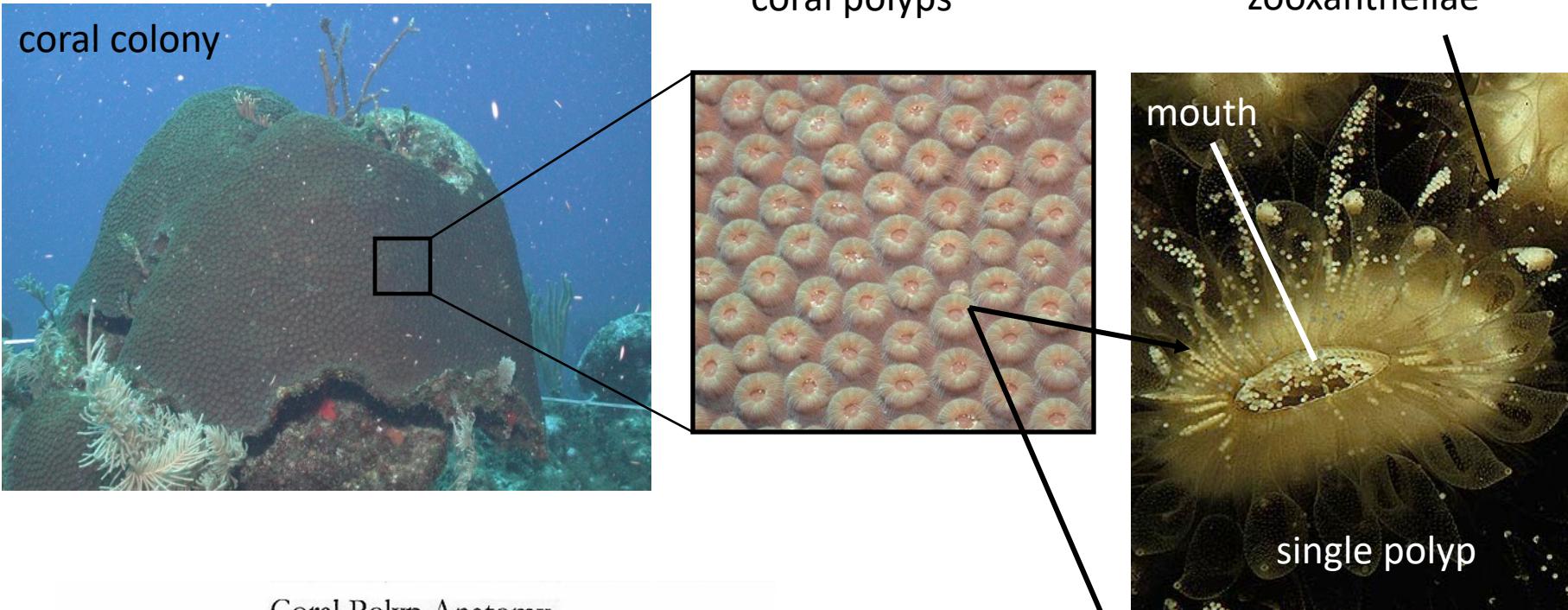


Figure 9.3 Anatomy of a coral polyp.

Corals are both autotrophs and heterotrophs: a symbiosis

**Benefits to coral:**

- 1) food
- 2) calcification
- 3) nutrient recycling
- 4) provision of O<sub>2</sub>

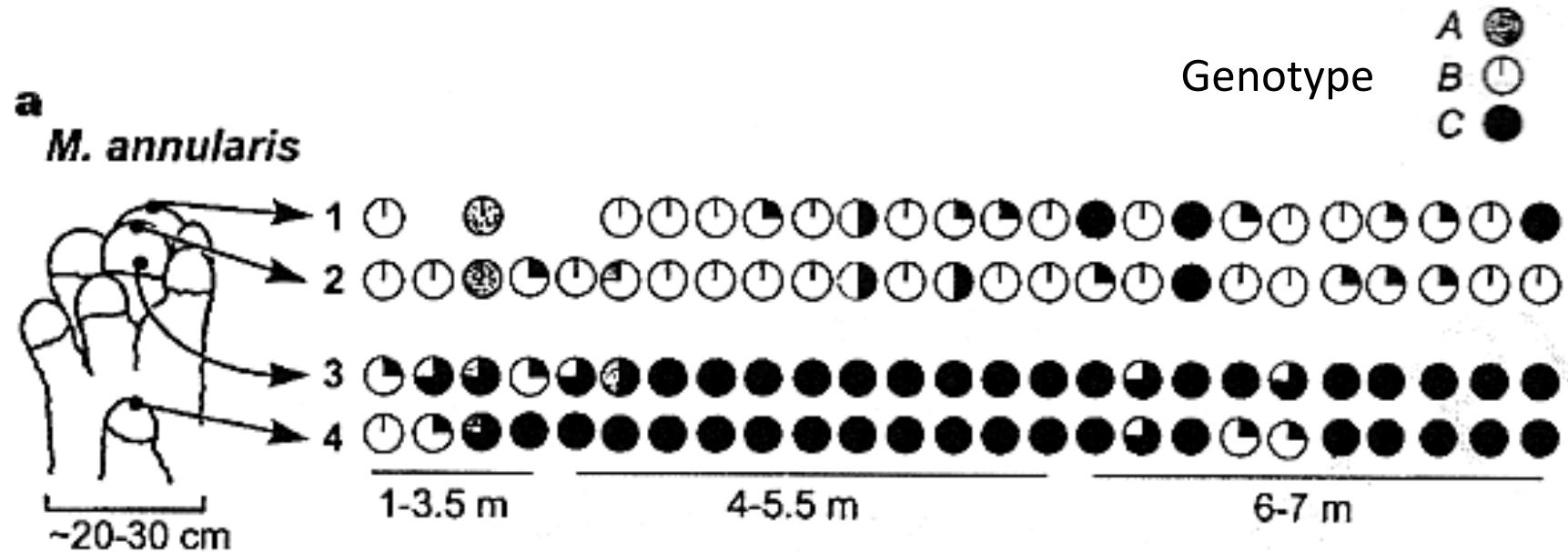
**Benefits to zooxanthellae:**

- 1) protection from predators
- 2) regulation of environment
- 3) nutrient recycling
- 4) provision of CO<sub>2</sub>

Zooxanthellae  
(dinoflagellates)

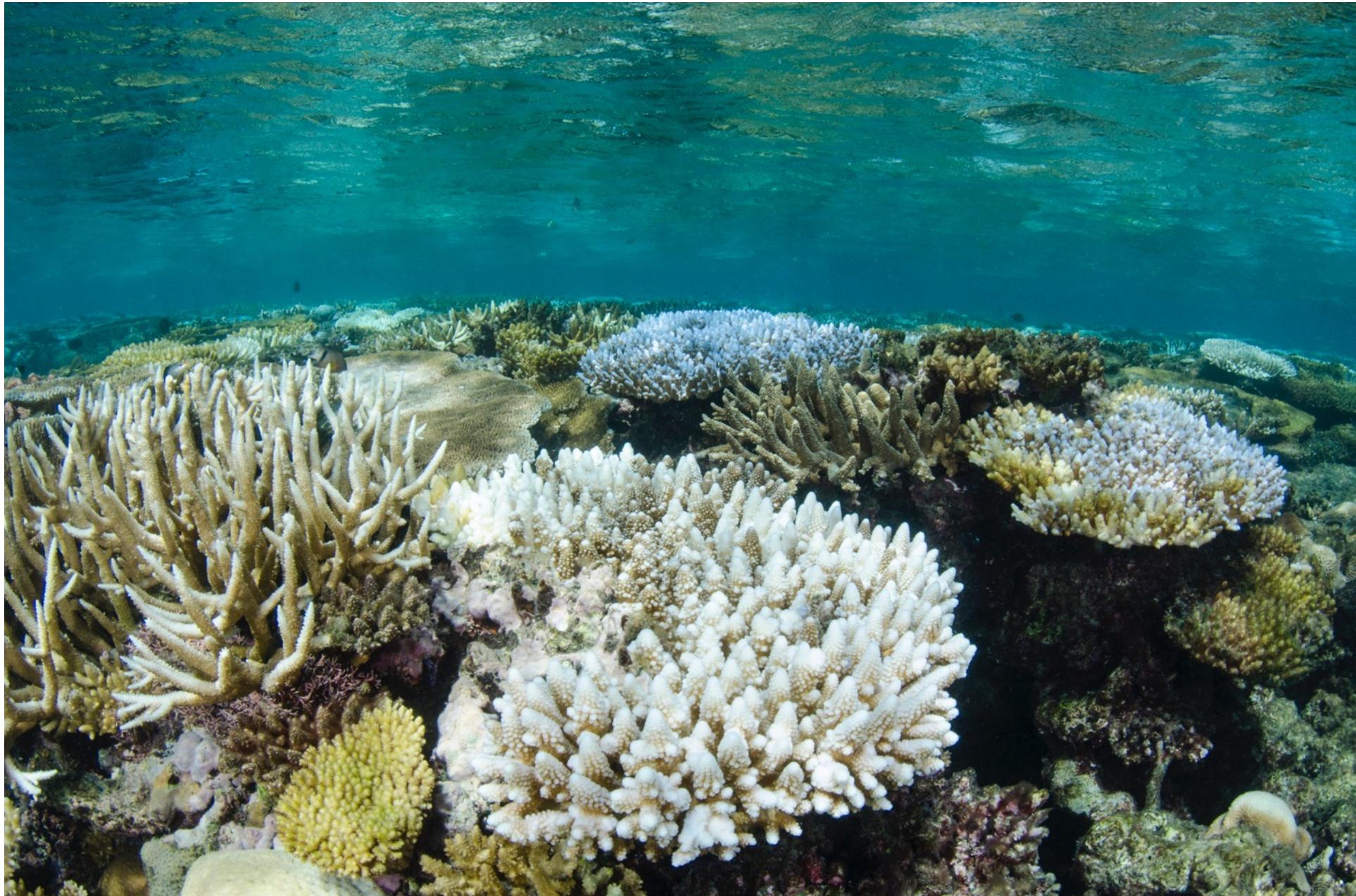


Many corals have multiple ‘species’ of zooxanthellae

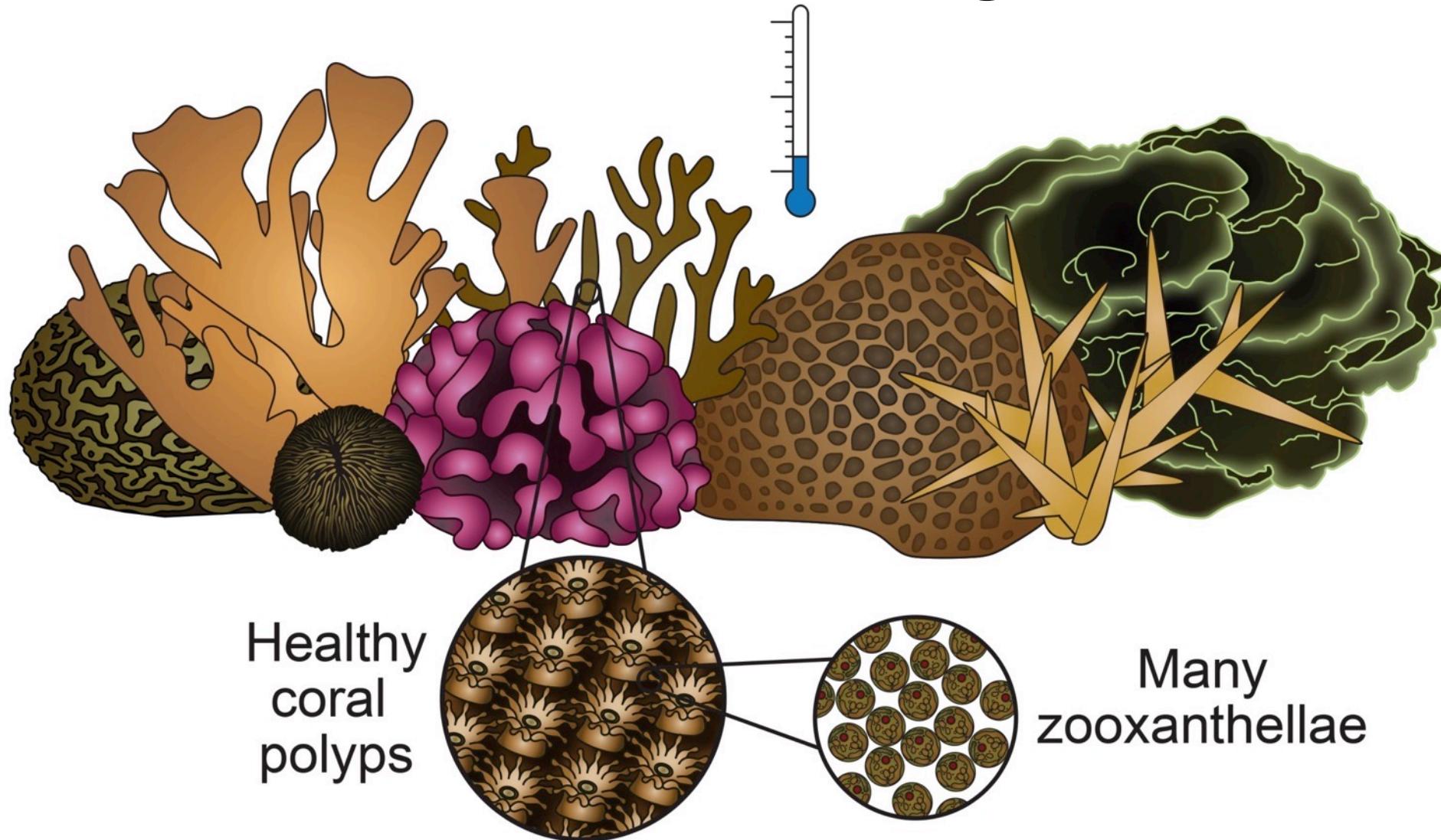


Different zooxanthellae found in different zones of the coral:  
Genotype B dominant in high light areas, C in shaded areas.

Coral bleaching: expulsion of zooxanthellae  
due to high temperature or light

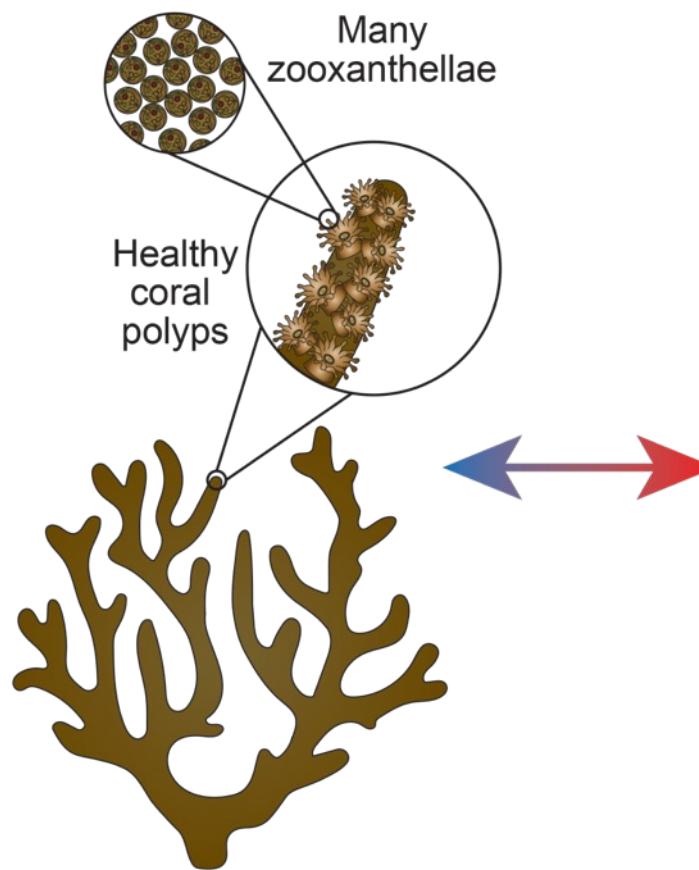


# Coral bleaching

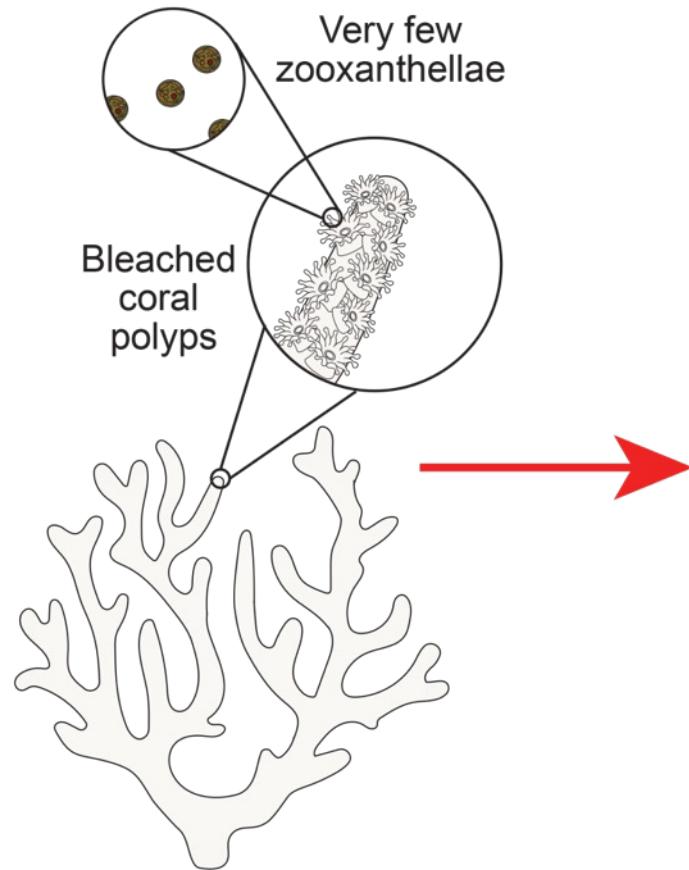


Corals can expel their zooxanthellae during bleaching, which can occur when corals are exposed to higher than average water temperatures and/or light.

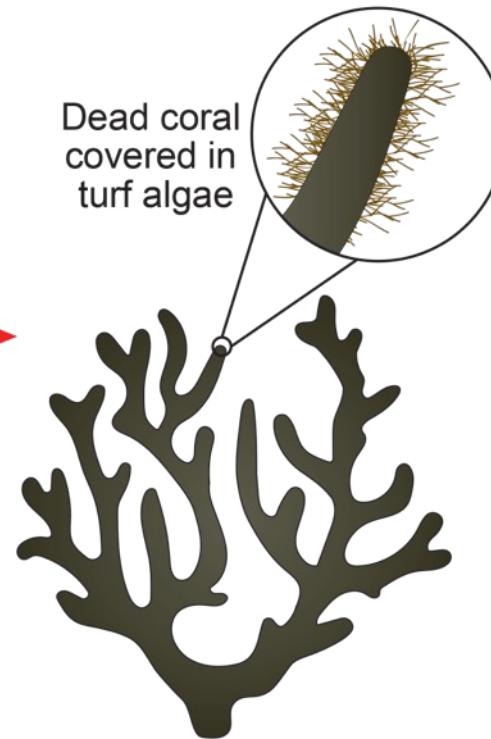
## Survival



## Bleaching



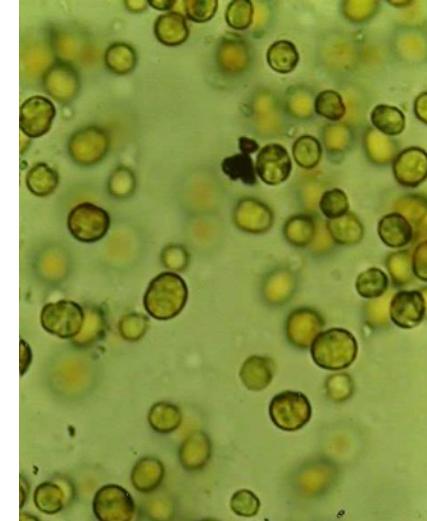
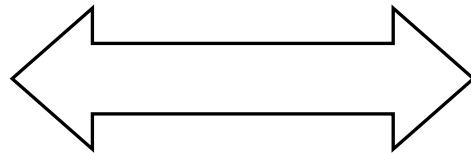
## Mortality



If water temperatures return to normal, the corals can regain their zooxanthellae and recover. If water temperatures remain warm, however, corals can die.



## Coral Bleaching



- what is it? a stress response to unfavorable environmental conditions that disrupts the symbiosis  
loss of algal pigments or zooxanthellae expulsion or both
- causes: -change in seawater temperature outside of normal range  
-increase in visible or UV light  
-decreased salinity  
-synergism of many stressors
- mechanism: -possibly production of toxic compounds such as reactive oxygen species (but cellular mechanism is still unknown!)
- effects: variable - recovery from short term bleaching possible;  
longer-term bleaching can be fatal.

## Corals can and often do recover from bleaching

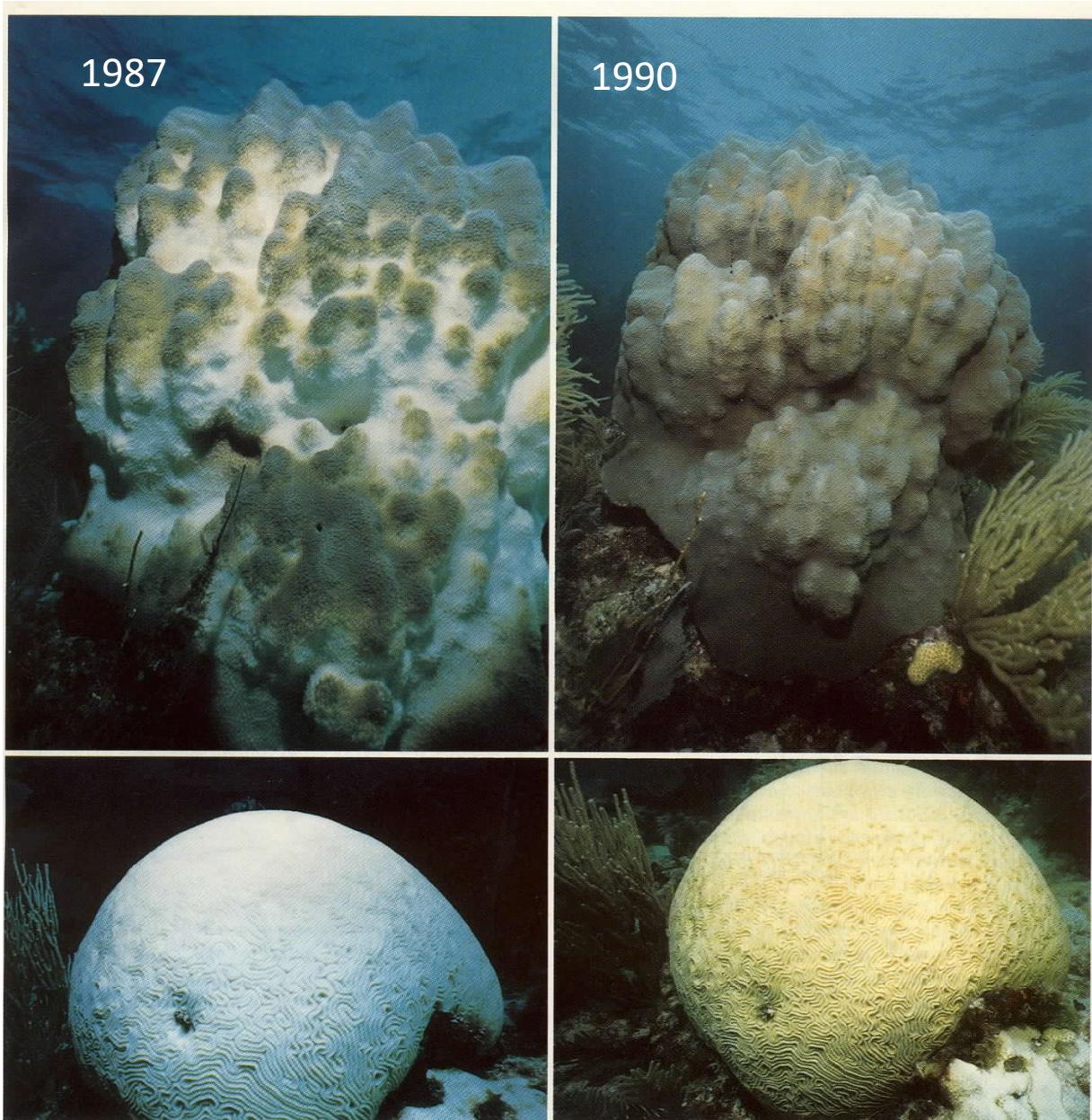
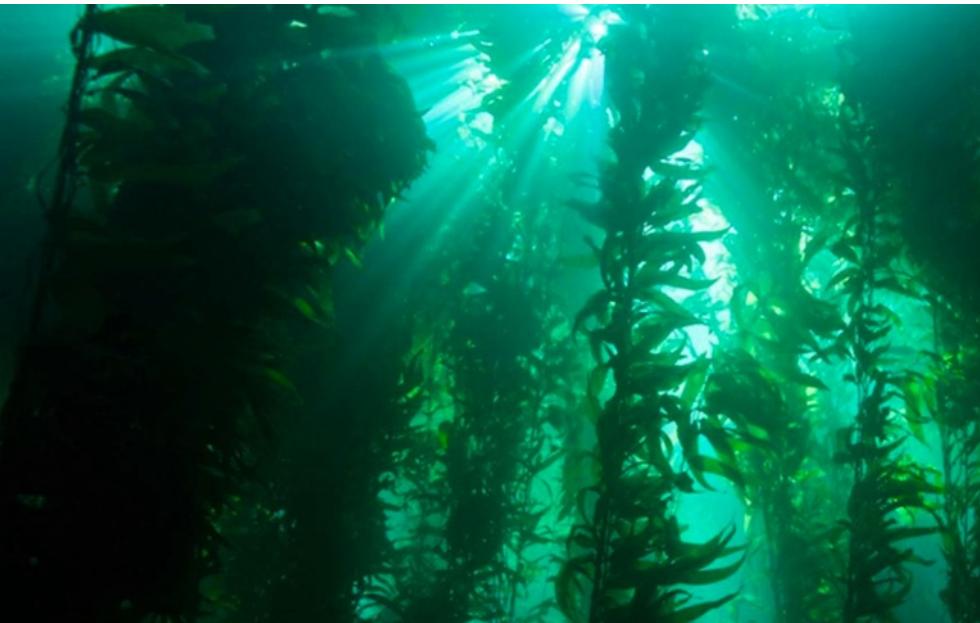


Fig. 1. *Montastrea annularis* (above) and *Diploria labyrinthiformis* (below) on Grecian Rocks Reef in the Key Largo National Marine Sanctuary during the “bleaching event”, October of 1987 (left), and after recovery of normal coloration in August of 1990 (right)



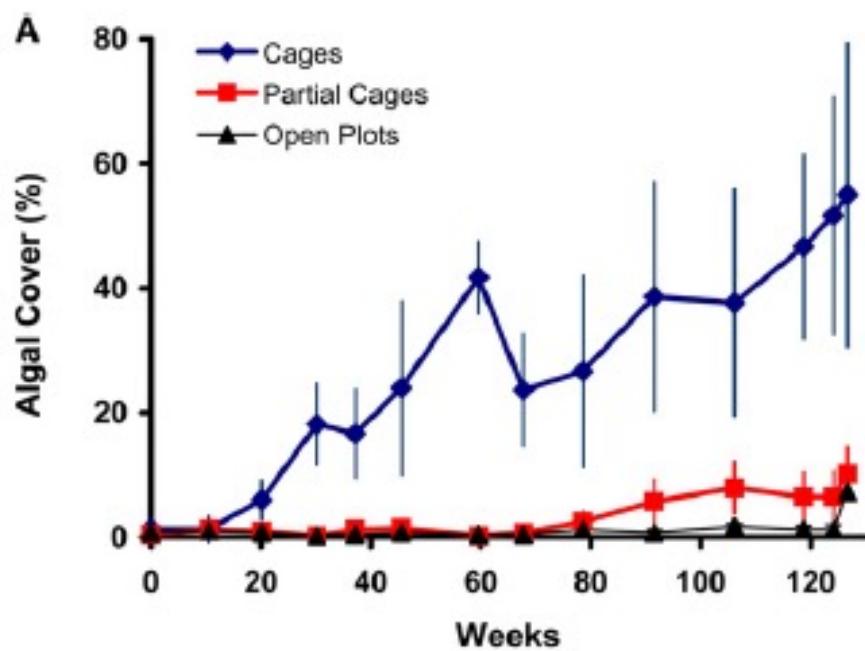
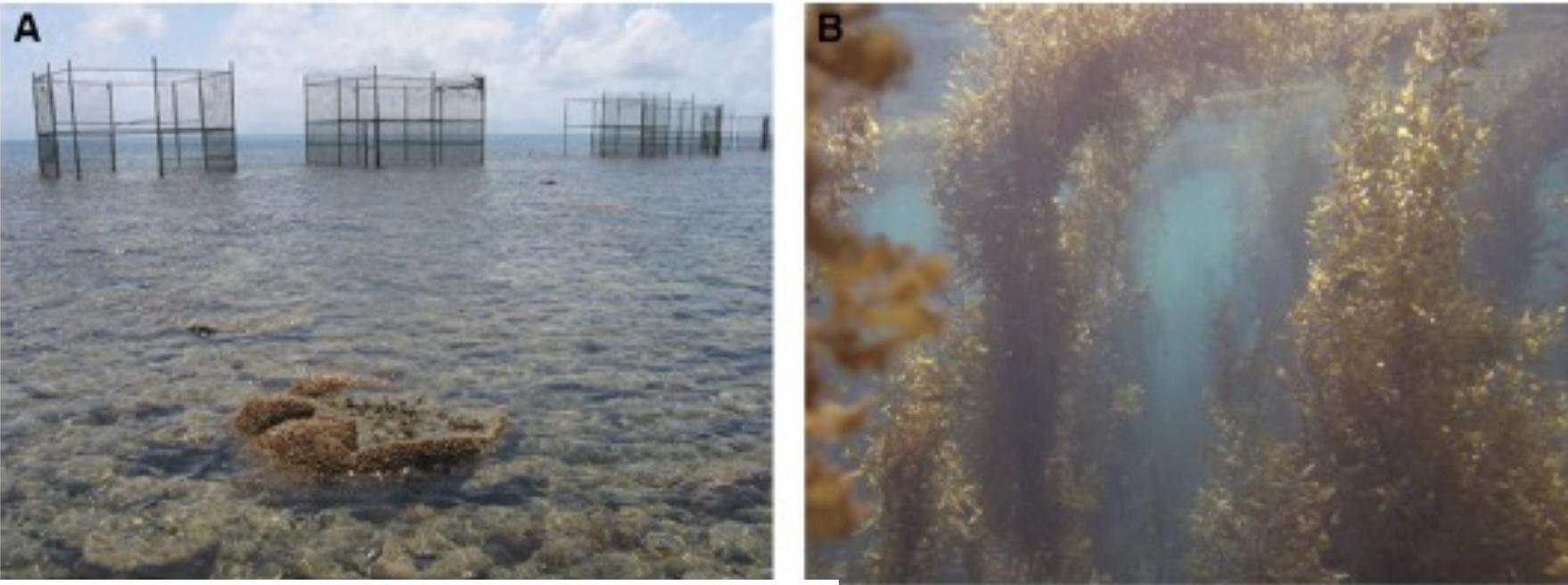
Tropical reefs:

- low nutrients
- lots of herbivorous fishes and invertebrates ( $\sim 156,000$  fish bites  $m^{-2} day^{-1}$ )
- High coral cover, low algal cover

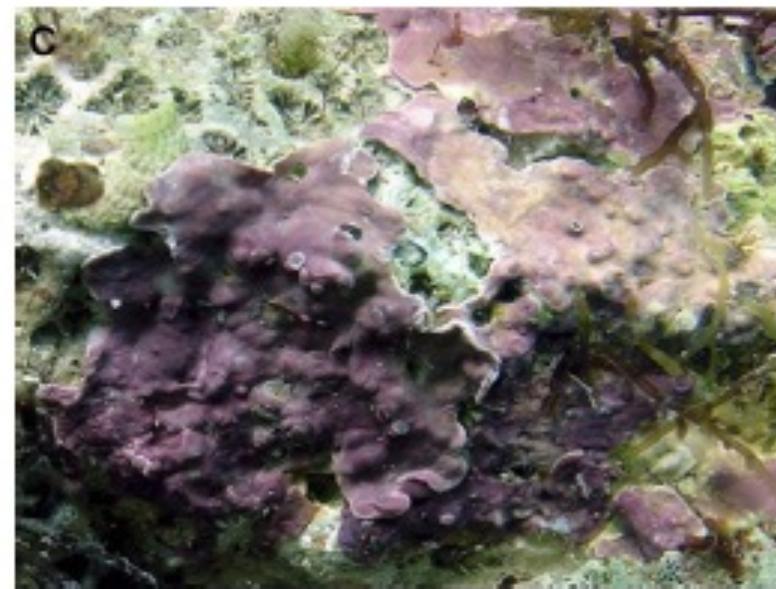
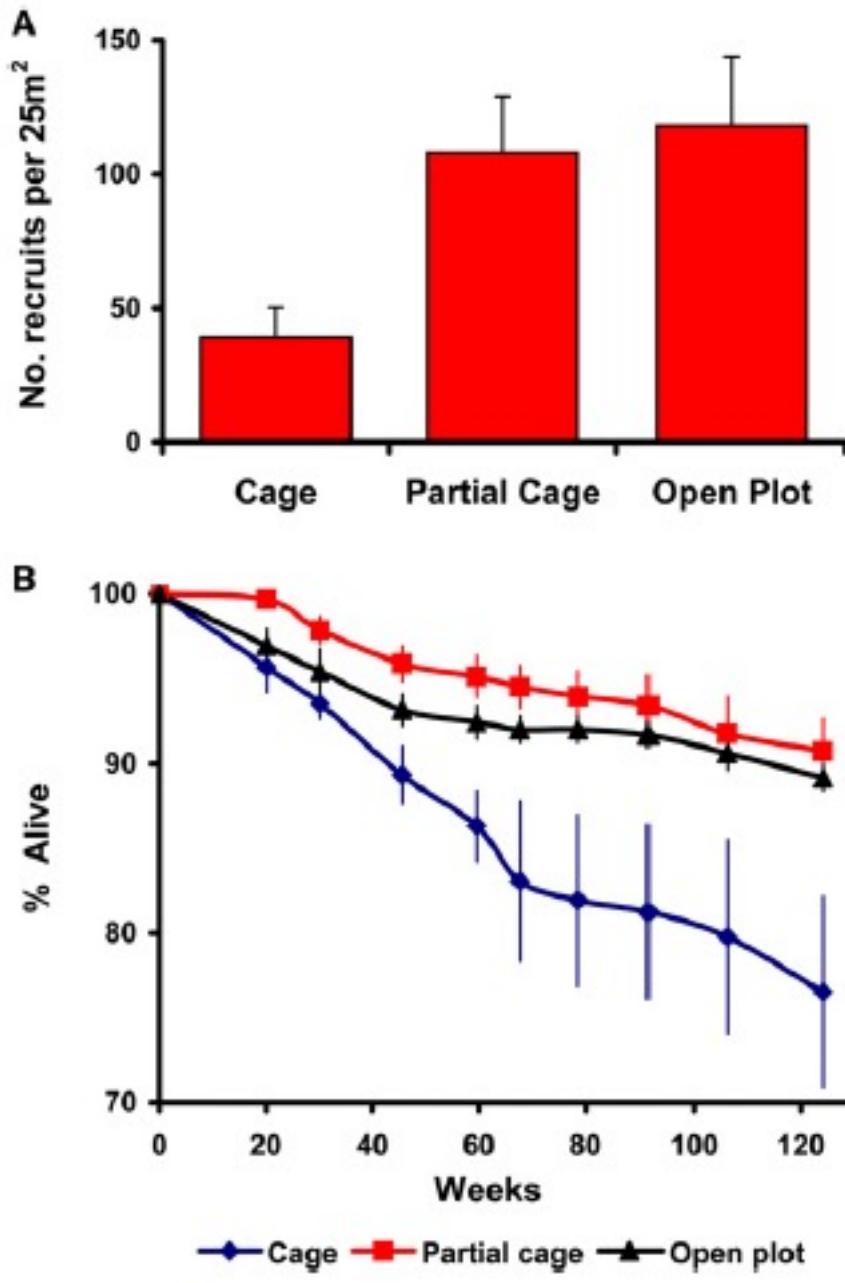


Temperate habitats (e.g., kelp forests):

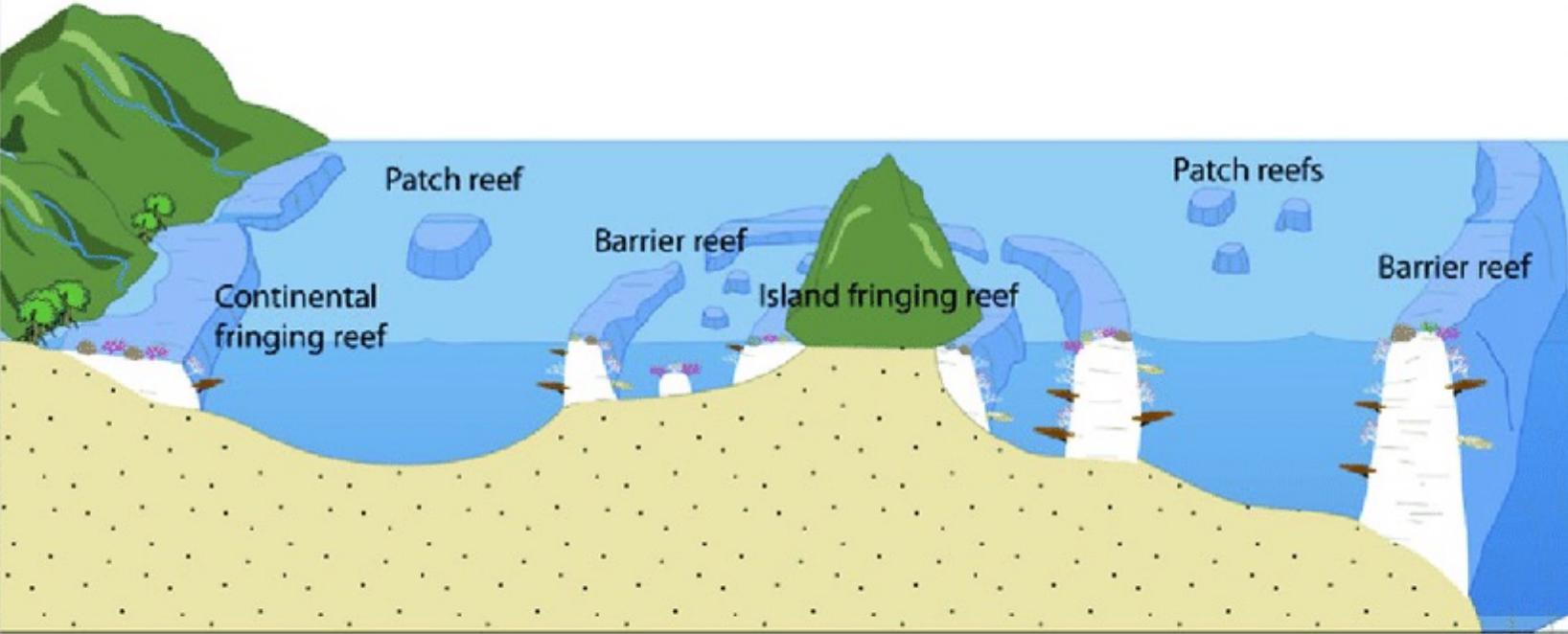
- high nutrients, few herbivorous fishes
- High algal cover, low coral cover



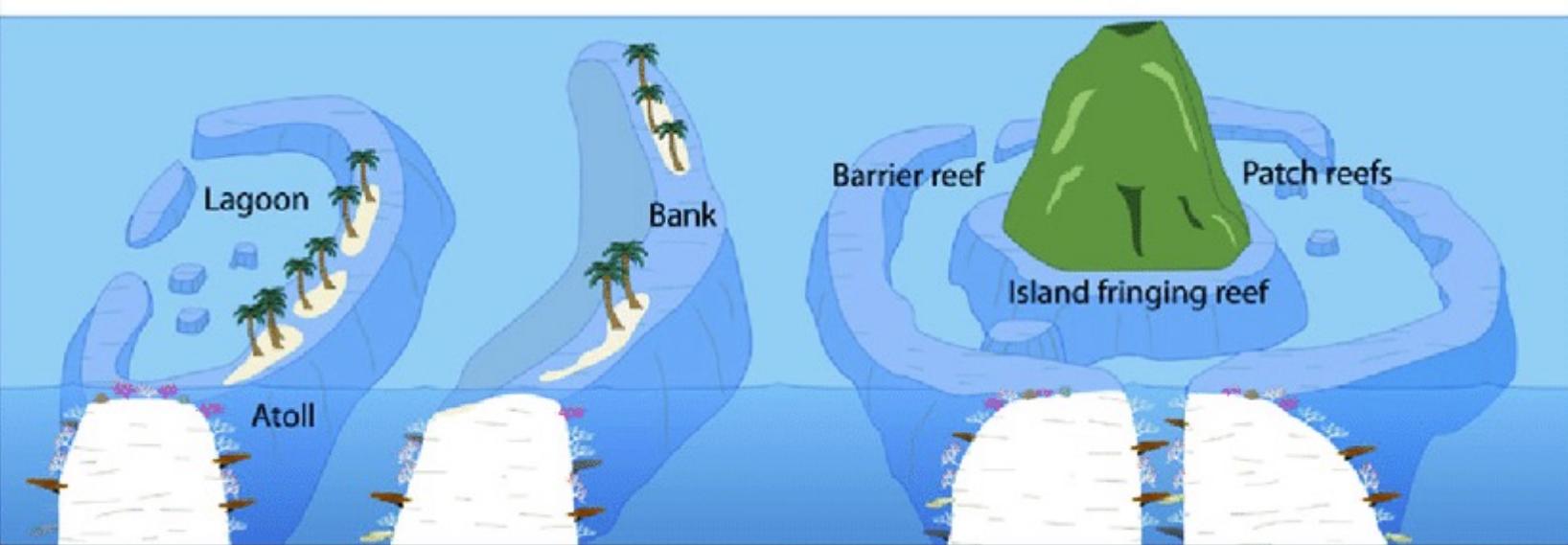
Hughes et al. 2007  
Current Biology



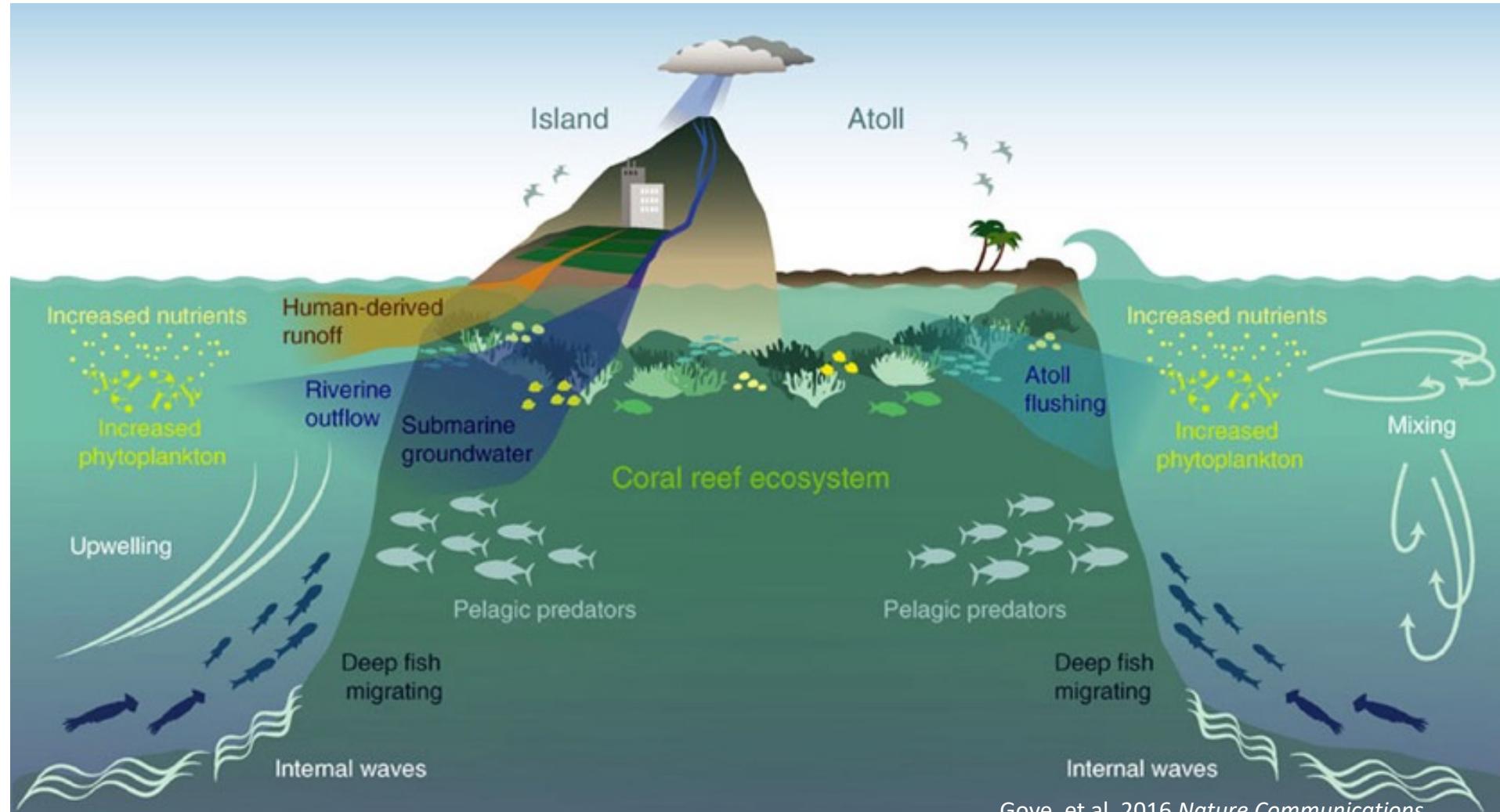
### Continental reefs



### Oceanic reefs

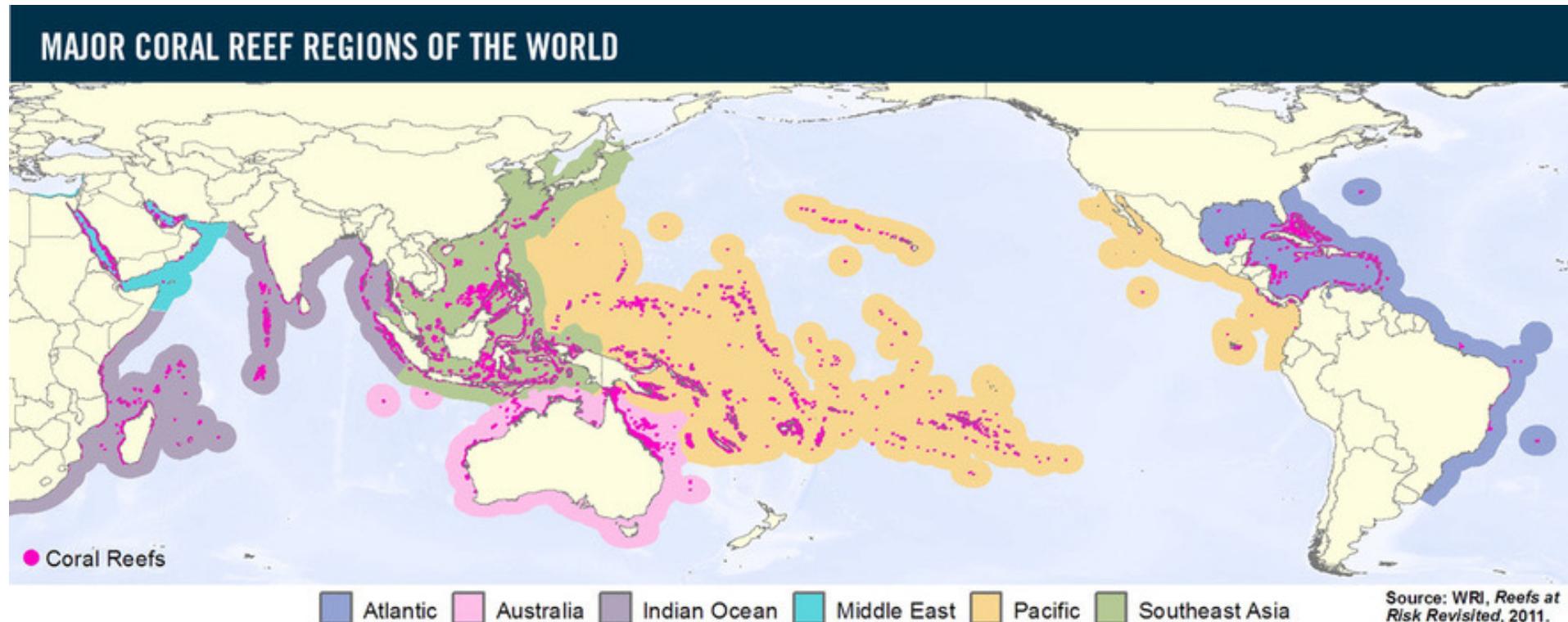


- Land masses promote mixing and upwelling, which promotes phytoplankton growth
- Supply coral growth and reef development. Coral reefs, especially atolls and large barrier reefs, further increase "Island Mass Effect"
- Positive feedback: the larger the reef, the more phytoplankton retained



# Coral Paradox (“Darwin’s Paradox”)

Corals thrive in warm, shallow, clear water that is nutrient poor. How?



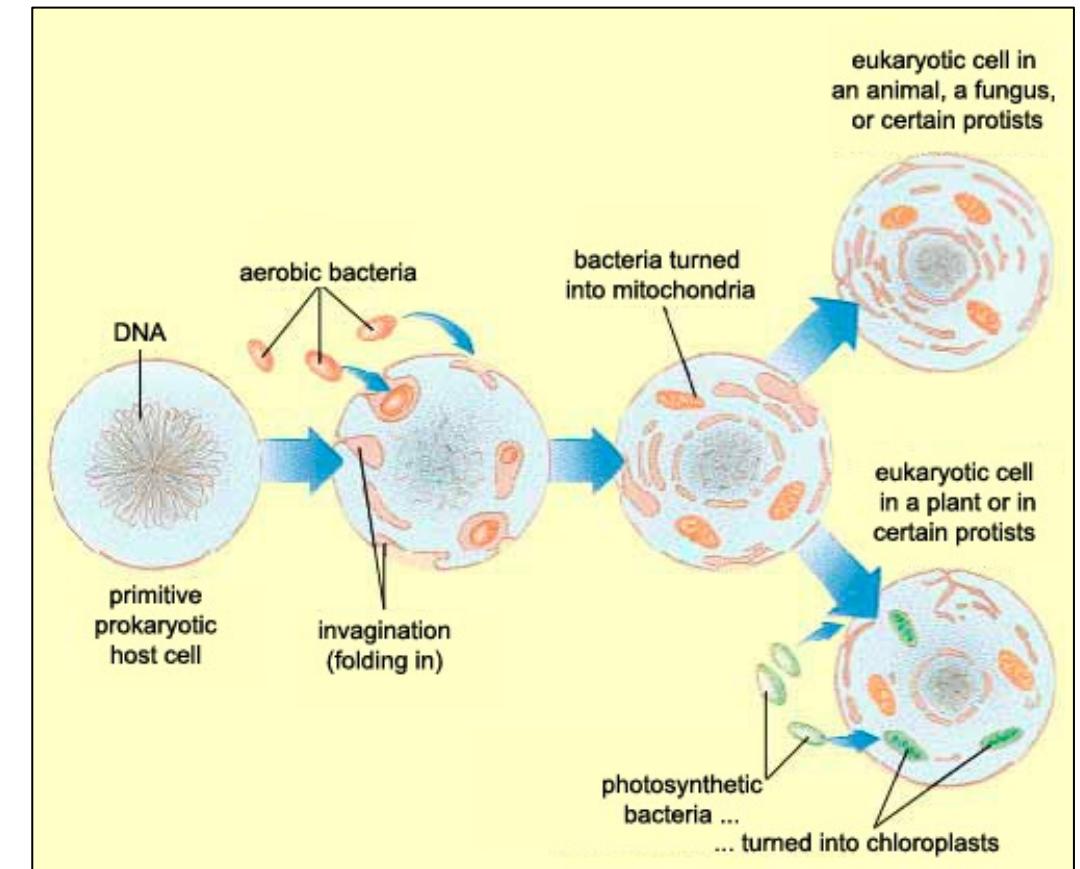
Possible because of:

- symbionts
- key herbivores that reduce algal biomass
- positive feedback loop from reef building corals keeps phytoplankton and nutrients within system

# Barcode



Crédit photo : Grégoire Le Bacon/TNH



# DNA Barcoding

- Analogy to product barcodes
- Scanning a barcode sticker is easier than scanning an apple
- A database of barcodes provides lookup table for easy identification
- 2 de-facto standard genes: 16S/18S rRNA and COI



# Requirements for a barcode gene

1. Universal
2. Easy to extract and sequence
3. Unique in each species
4. Bonus points: a *barcode gap*

## The 2 most common barcode genes

- 16S / 18S ribosomal RNA
  - Better for single-cell and very small protist metagenomics
- COI (“See-Oh-Won”)

# Advantages of COI over rRNA (other than in metagenomic studies)

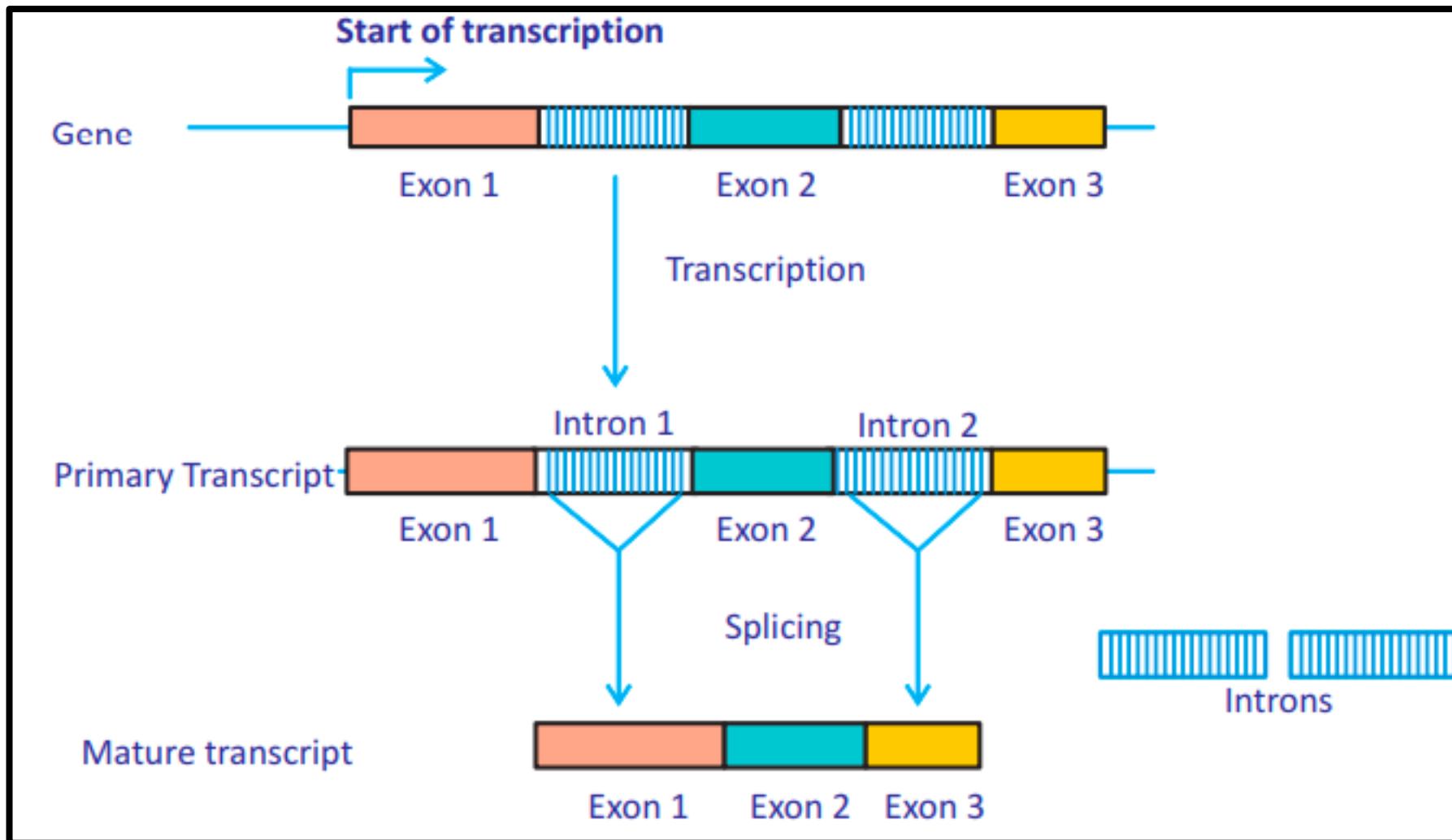
- Shorter than rRNA
  - Fewer chances for sequencing errors, easier bioinformatic analysis
- More reliable amplification than rRNA
  - Especially of degraded samples, e.g. museum specimens
- More variable than rRNA
  - Less possibility of 2 species with same barcode

# COI: The de-facto standard barcoding gene for animal life



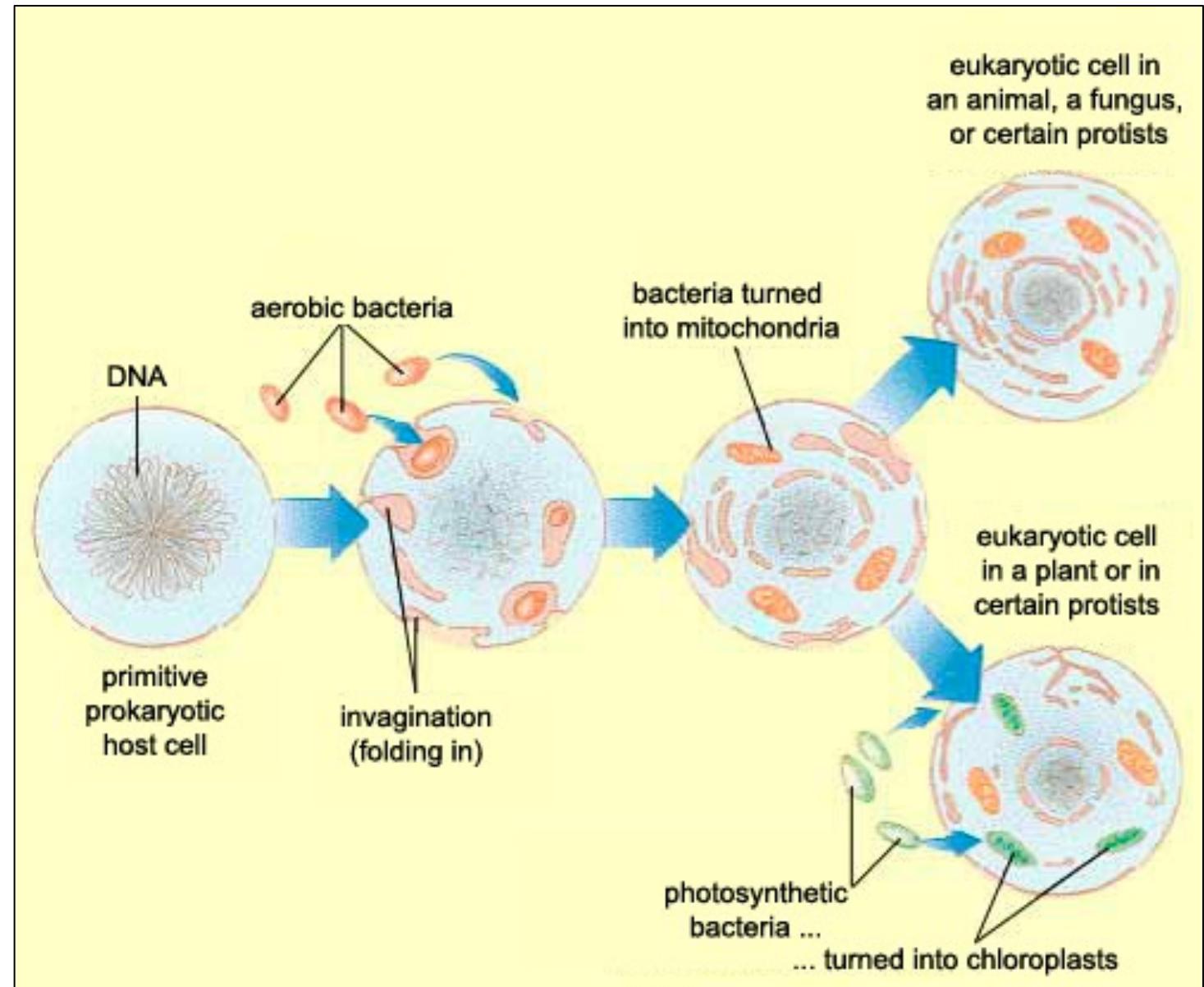
- 2002: Hebert & al propose COI as barcoding standard
  - All animals have it
  - Good primers
  - Mitochondrial → no introns → easy to align
  - Indel mutations are rare → easy to align
  - High substitution rate in 3<sup>rd</sup> codon position → lots of diversity
- BOLD database
  - “Barcode Of Life Database”
  - Vouchered, expensive, highly COI-specific
- CO-ARBitrator algorithm & database: software curated from GenBank, equally specific, more sensitive

Eukaryote DNA has introns and exons. These are spliced out of the mRNA transcript before translation to protein



# COI is mitochondrial

We got it through  
endosymbiosis



# So we animals really have 2 genomes

## The *nuclear* genome

- In the cell nucleus
- Half from each parent
- Introns, exons

## The *mitochondrial* genome

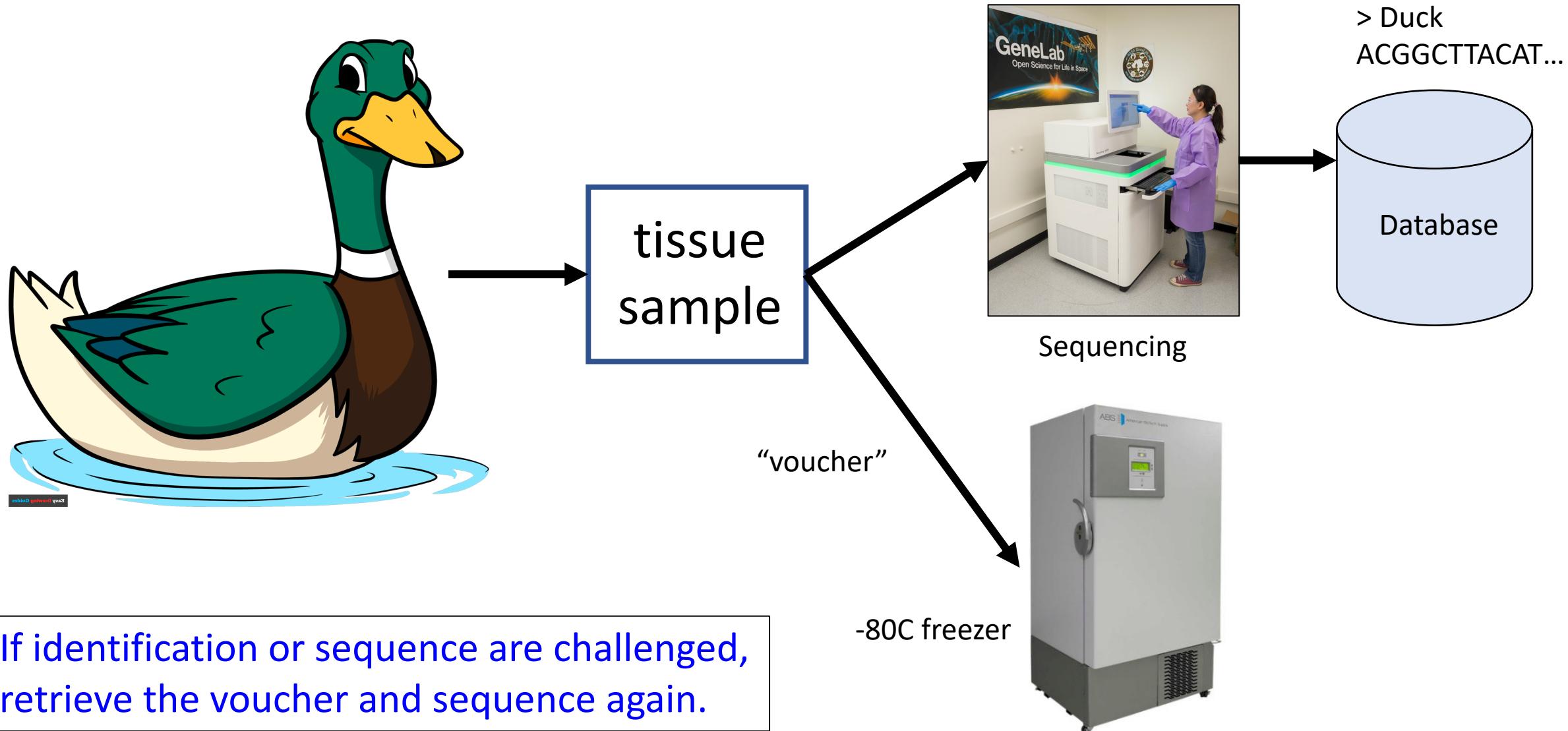
- In each mitochondrion
- All from mother, none from father
- No introns/exons

Introns are long, highly variable regions that mess with alignment algorithms.

➔ A barcode gene without introns is an advantage.

COI gene is mitochondrial.

# Vouchered sequence databases

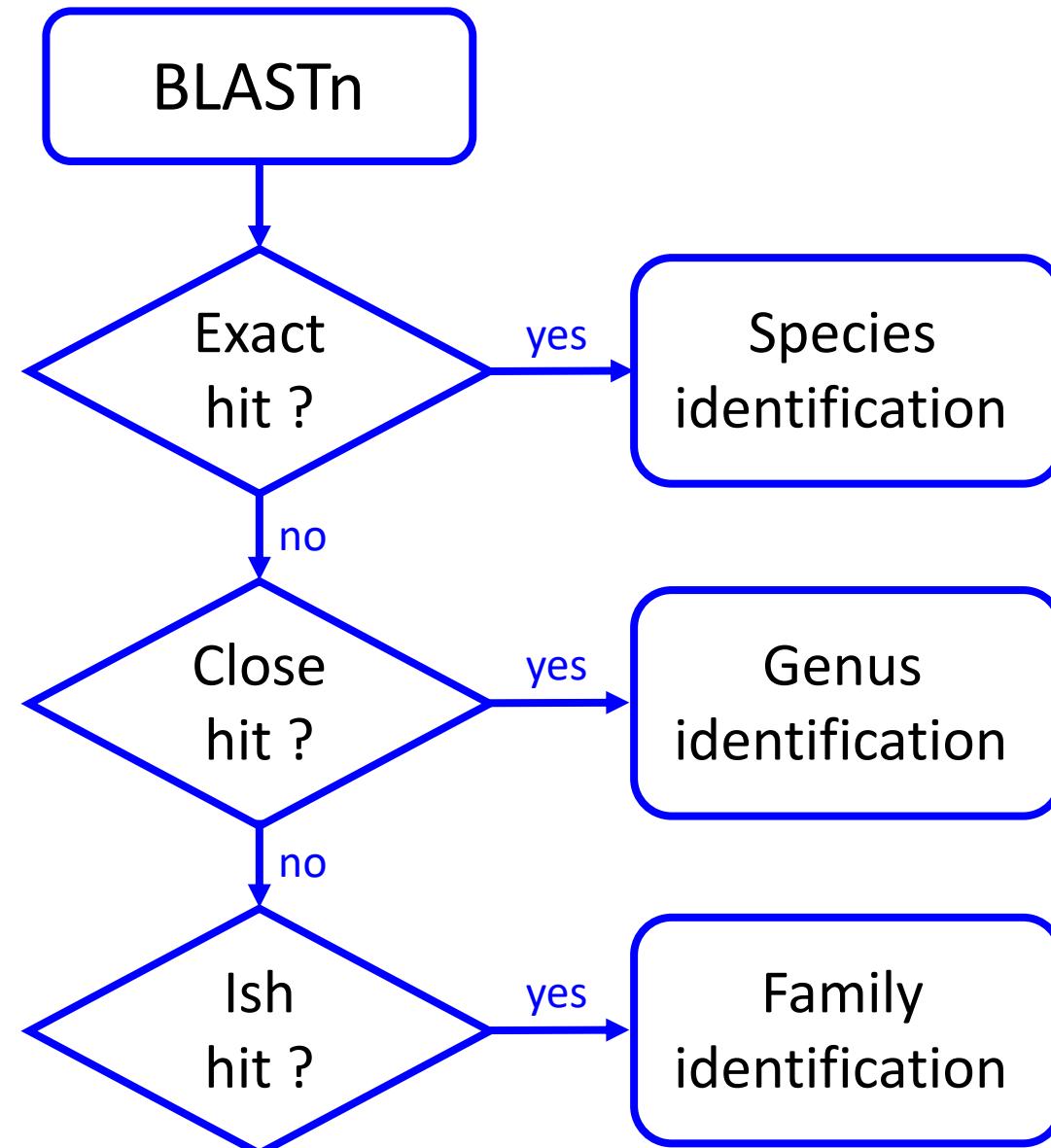


# The BOLD database is highly COI specific

- Specific: (nearly) everything in the database really is COI.
- Not very sensitive: there are lots of COI sequences in the world that aren't in BOLD.
- This isn't surprising, and isn't a problem.
- BOLD's stringent submission requirements, including voucher requirement, make submission slow and expensive.

# The trouble with COI: the “barcode gap”

- A reasonable expectation: given any 2 samples, COI nucleotide sequence similarity reflects species similarity
- Therefore if you find a novel species, blasting its COI against BOLD should tell you the right genus
- Et cetera



# The reasonable expectation requires a “Barcode gap”

- Given any clade, every member should be more similar to every other member, than it is to every non-member
- $d(x, y)$  means evolutionary “distance” between x and y, e.g. # of mutations



Genus *Ursus*

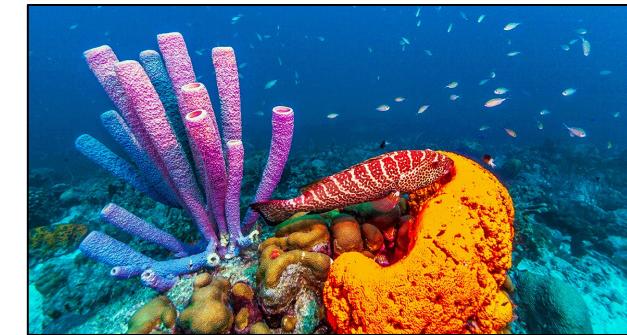
$d(\text{Panther, Panda})$   
should be >  
 $d(\text{Panther, Lion})$



Genus *Pantera*

# But the barcode gap is not universal

- Sep 30, 2022: downloaded all BOLD metazoan COI sequences.
- Converted to blastable.
- BLASTed every sequence against this database, ignoring hits to species of query.
- Simulates considering each species as novel, therefore not yet in BOLD.
- Best hit not always to different species in correct genus.
- Within phylum *Porifera*, 38% of species identified with wrong genus.
- Within phylum *Nematoda*, 39% of species identified with wrong genus.



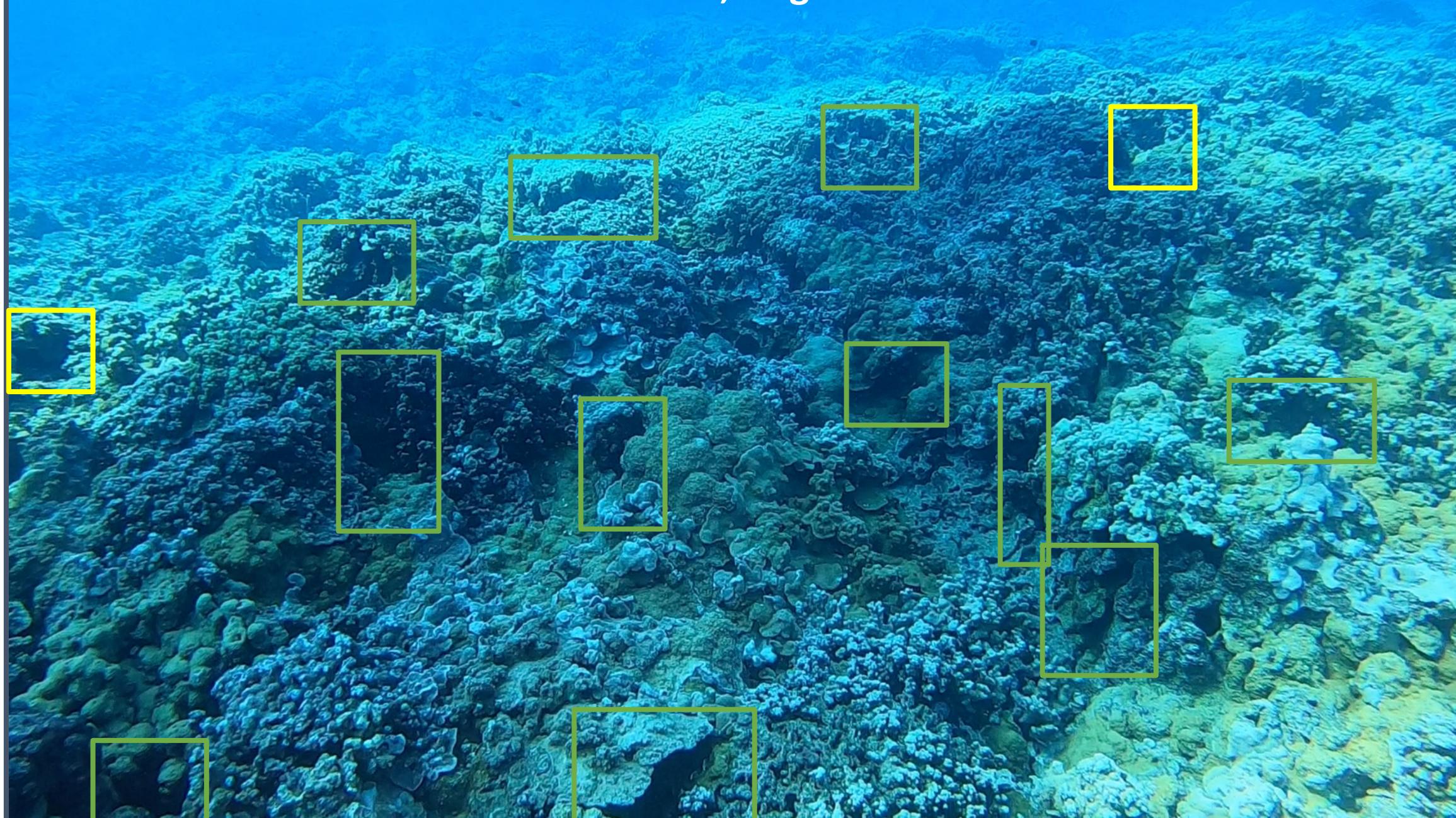
# Dos and Don'ts of identifying a mystery sequence using COI barcoding

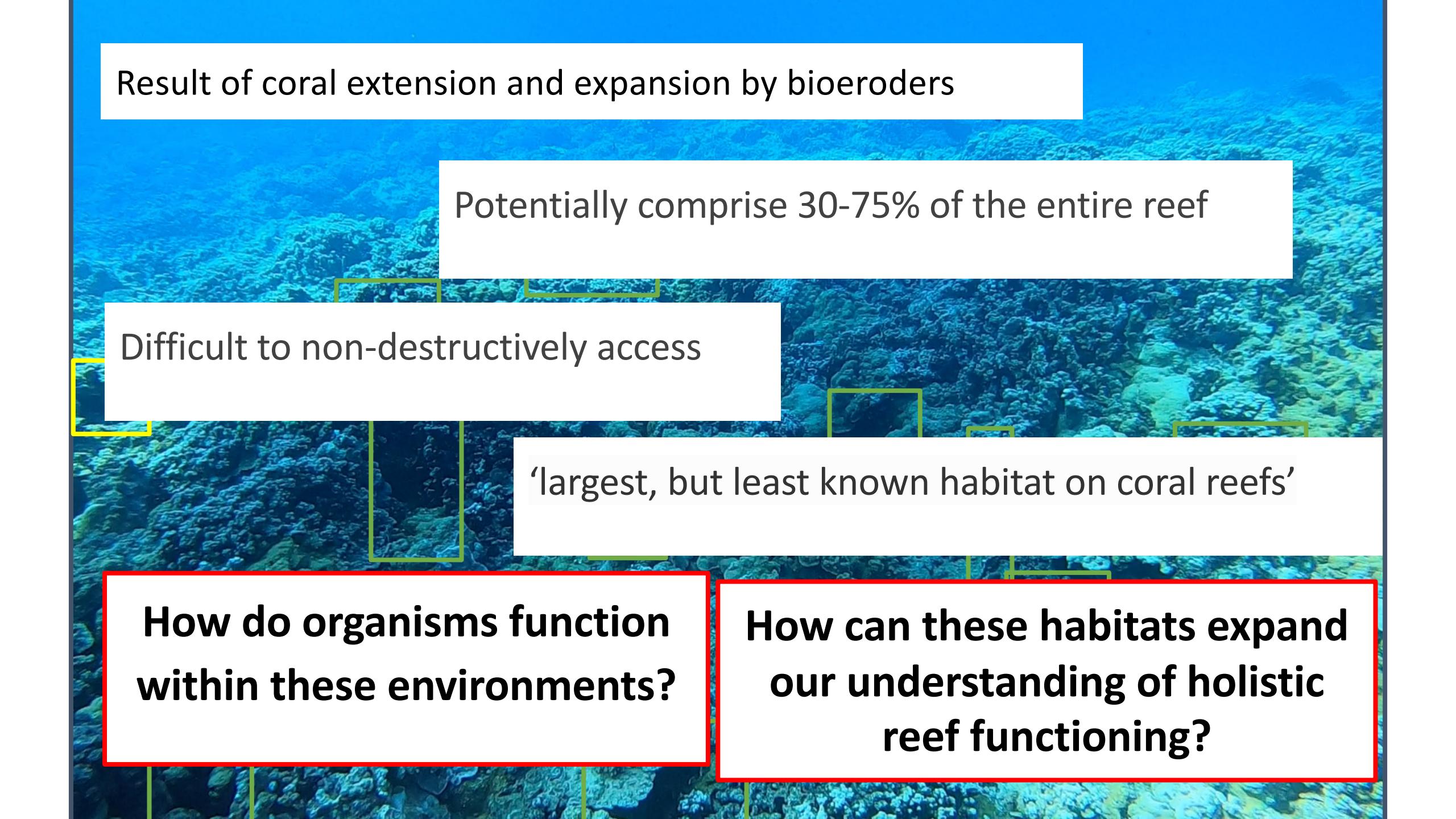
- BLAST the mystery against a COI database
- Do trust any exact hit
- Don't use a close but inexact hit to infer genus

## Opening Thought Question – 3/15

List some of the stressors that can lead to coral bleaching

# Molokini Crater, August 2022





Result of coral extension and expansion by bioeroders

Potentially comprise 30-75% of the entire reef

Difficult to non-destructively access

'largest, but least known habitat on coral reefs'

**How do organisms function  
within these environments?**

**How can these habitats expand  
our understanding of holistic  
reef functioning?**

# Crustose Coralline Algae (CCA)

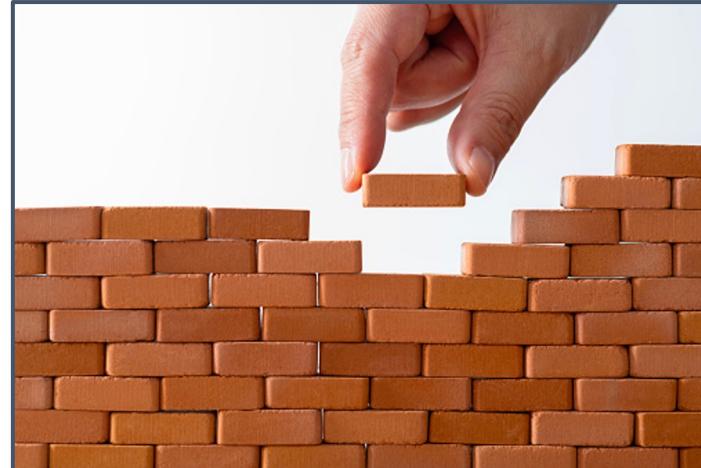
Coral Recruitment Habitat



Low light, no problem!



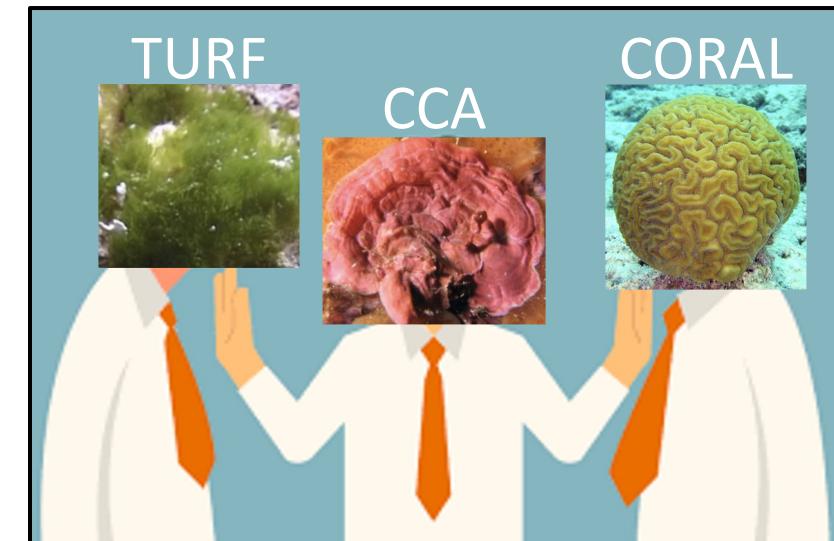
Accretion



Stabilizes Sediments

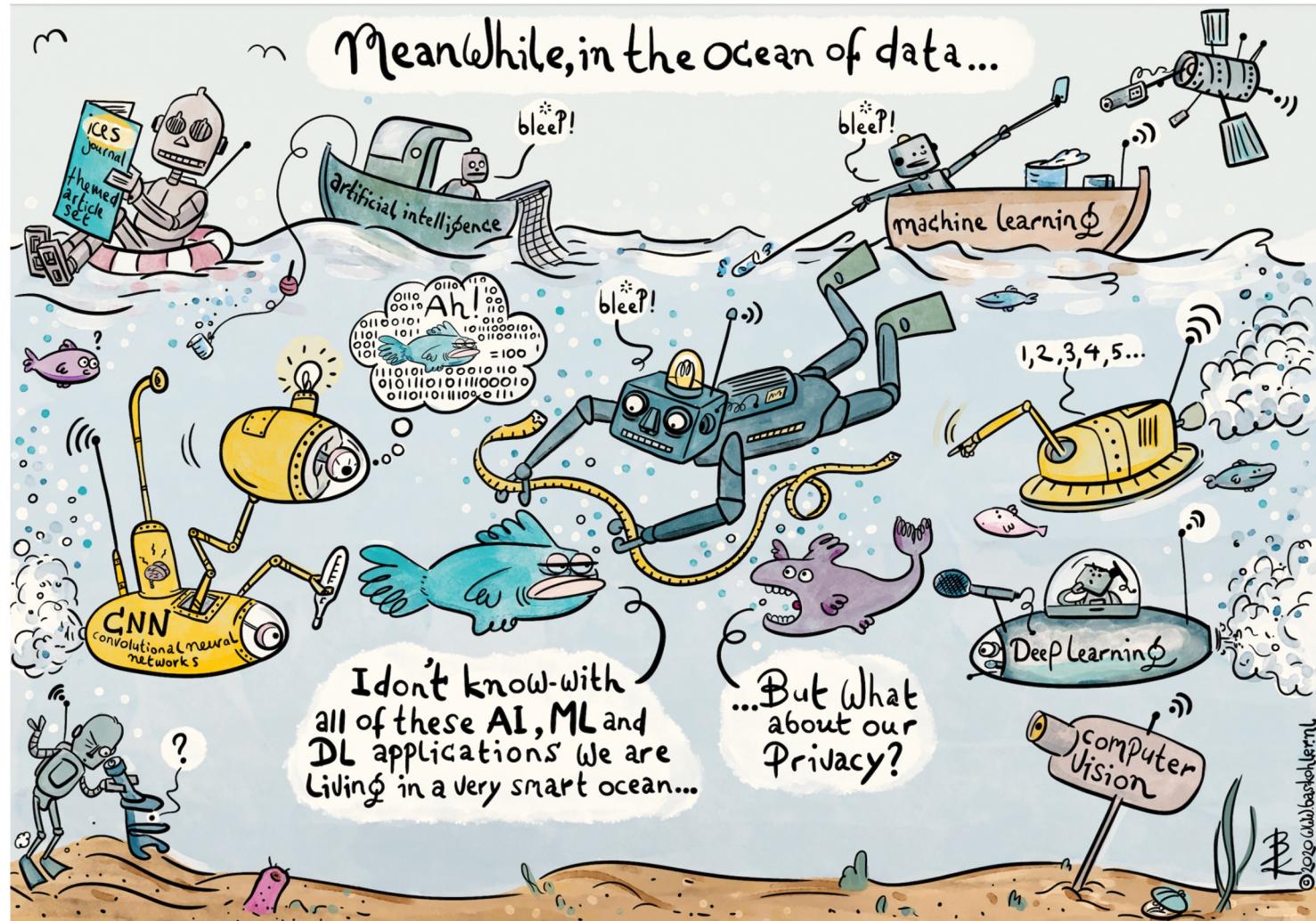


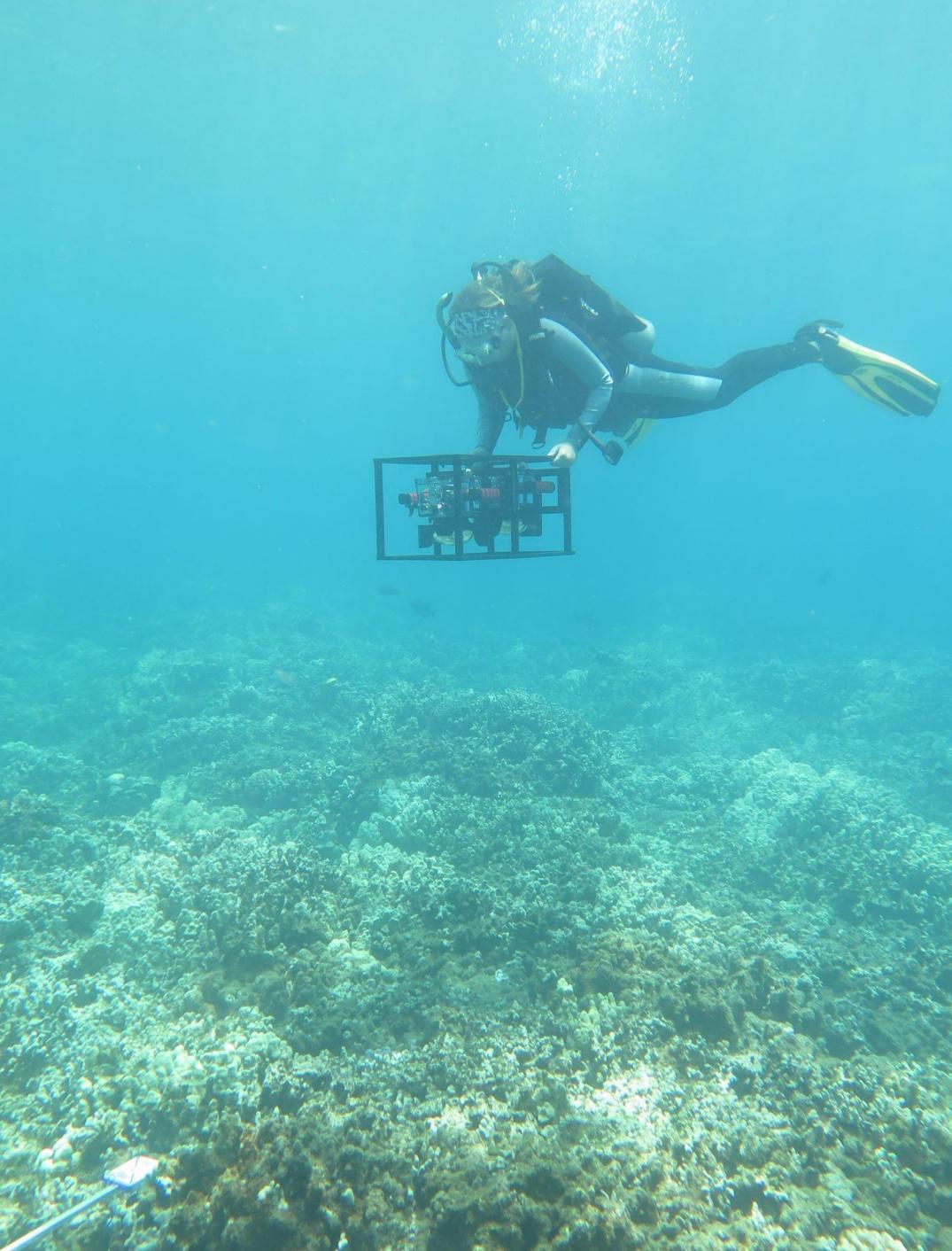
Ecological Mediators



# Artificial Intelligence and the Ocean

- Can deep machine learning models analyze percent cover of benthic organisms autonomously?

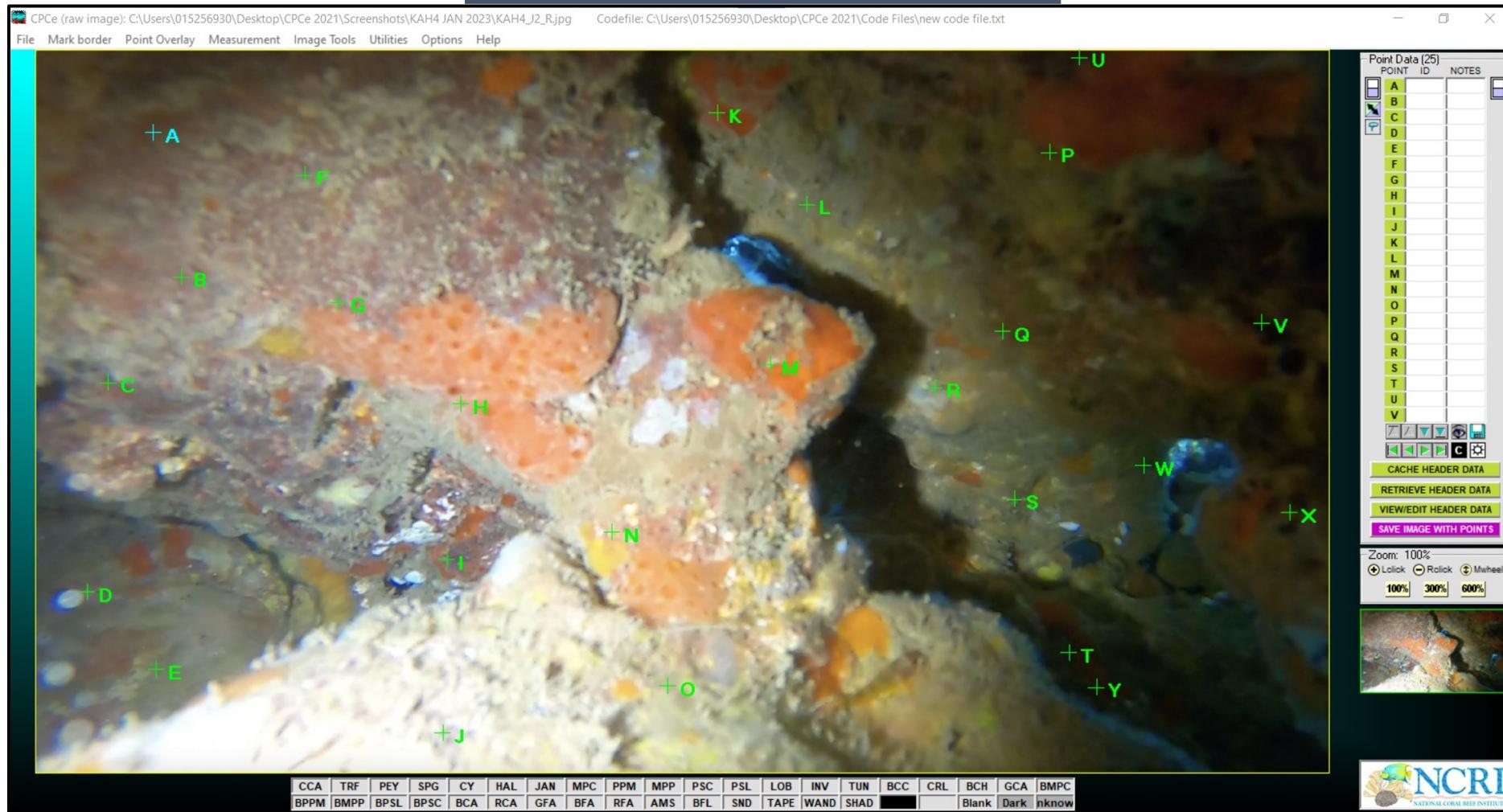




# Quantifying CCA % Cover

- Calculated percent cover of benthic species

## Coral Point Count (CPCe)





# Quantifying benthic cover: CPCe vs. AI

- **Deep Machine Learning Technique**
  - Fully automated- improves accuracy and removes human user.
  - Trained to trace CCA “patches”
    - calculates percent cover by comparing # of pixels traced (pink) to total # of pixels of image.

To Review:

### **Question 1: Where is CCA found in crevices?**

- Most CCA found on the ceiling at crevice openings

### **Question 2: What abiotic factors may govern CCA distribution inside crevices?**

- More light = more CCA
- More sediment = less CCA

### **Question 3: How does internal CCA contribution compare to top-reef?**

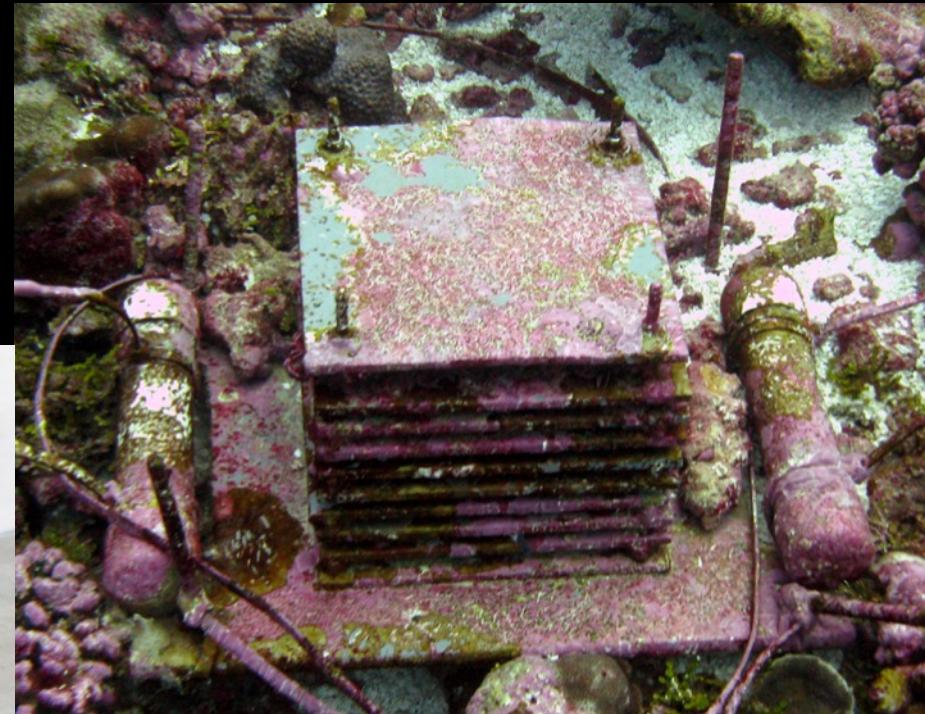
- More CCA inside the reef than outside (all sites but one)

# Opening Thought Question 3/20

1. What is CCA and how does it contribute to coral reef ecosystems?
2. Anna told us that the distribution of CCA changes with light and depth. What were the patterns that she described and how do these patterns relate to the broad ecological theory of zonation?
3. How can bioinformatics help Anna to analyze her data?

# ARMS

## Autonomous Reef Monitoring Structures



Images: [https://www.pifsc.noaa.gov/cred/survey\\_methods/arms/overview.php](https://www.pifsc.noaa.gov/cred/survey_methods/arms/overview.php)  
Leray and Knowlton. 2014. *PNAS*  
Pearman et al. 2016. *Mar Environ. Res.*

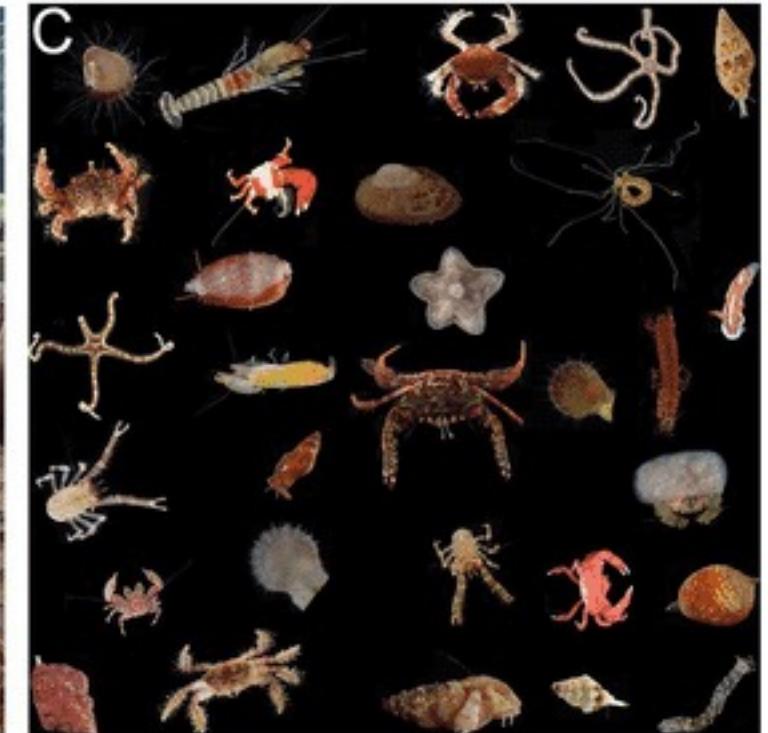
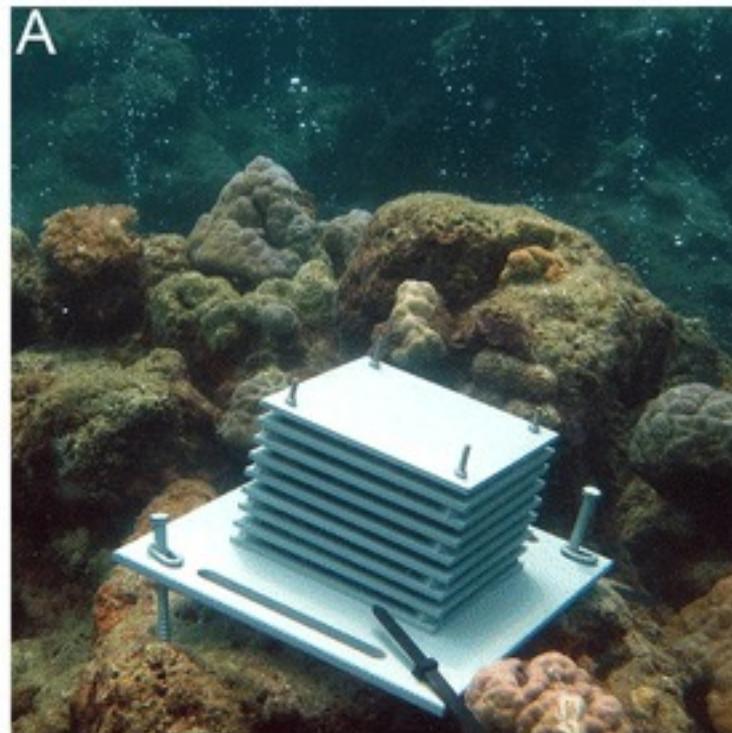
# ARMS Research



<https://naturalhistory.si.edu/research/global-arms-program>

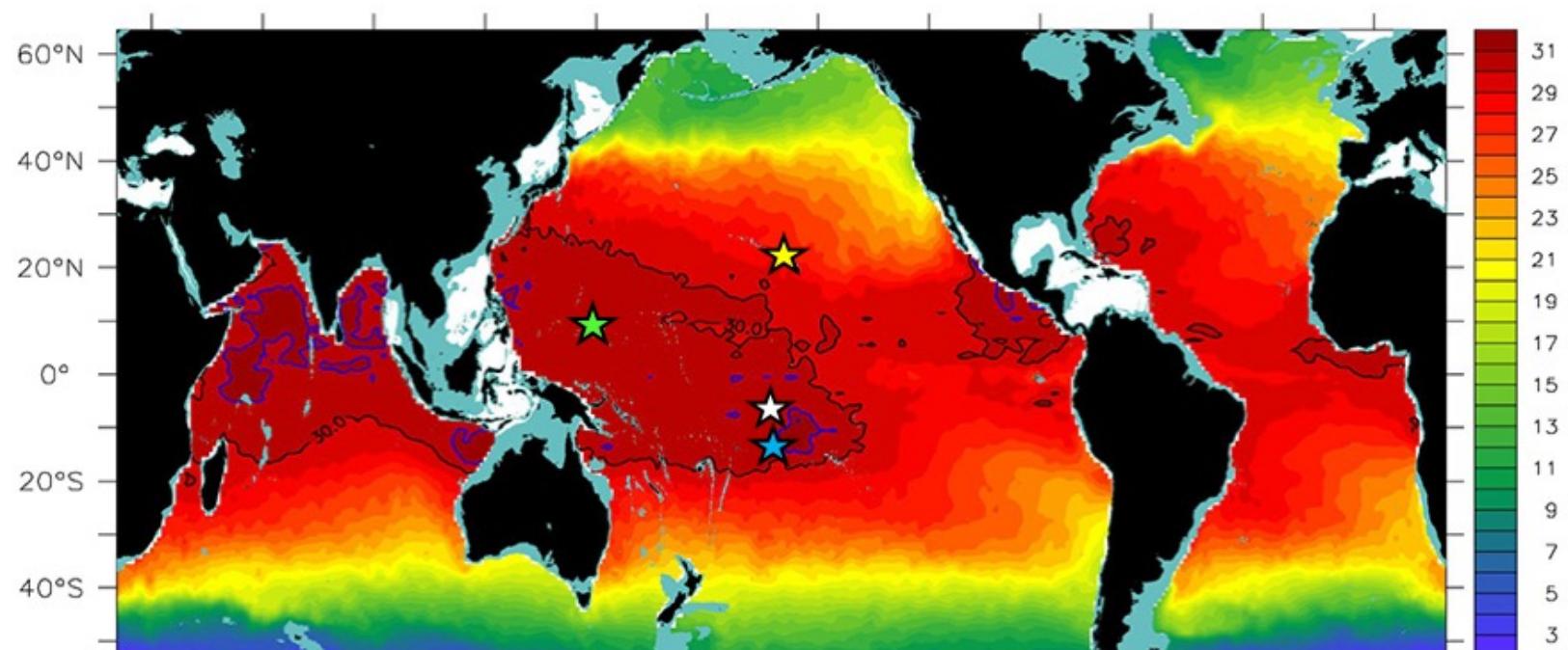
# What are the limitations of ARMS?

Difficult to learn about the ecology of cryptic coral habitats *in situ*  
(i.e. in the wild)



# The Biggest ARMS data set

- NOAA's Pacific Reef Assessment and Monitoring Program (Pacific RAMP), 2004-2017.
- Hundreds of multi-plate deployments at pristine coral reefs in the Pacific basin.
  - Marianas
  - Hawai'i
  - Line Islands
  - Samoa
- Thousands of plate photos.
- COI barcode sequences.



# ARMS Analysis Challenges

## DNA analysis

- Not quantitative
- Dependent on high-quality local databases of barcode gene

## Photo analysis

- Human → doesn't scale up
- Semi-automated → CPCe
- Fully automated → significant progress on the difficult first half

# Can ARMs photos be analyzed computationally?



Original jpeg



Segmented

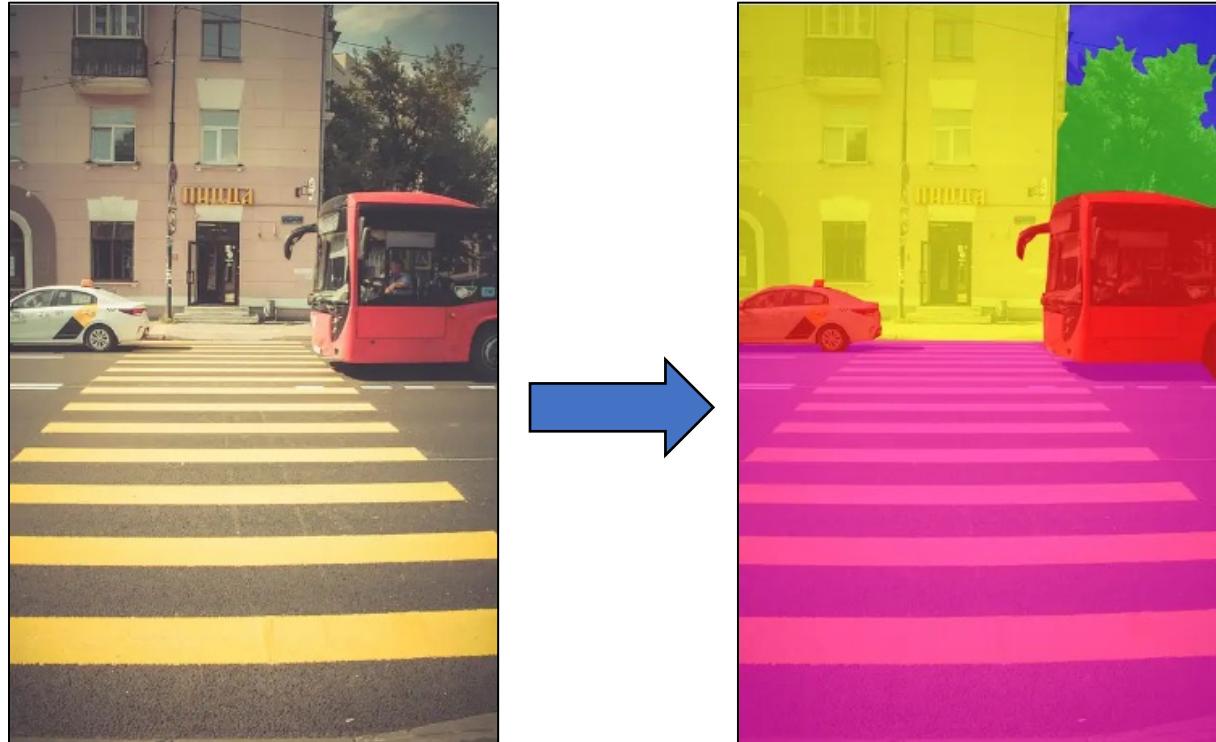
*Suberitidae*  
(just guessin')

Turf

CCA

Identified

# Segmentation: the hardest step (by a factor of a gazillion)



- Given a digitized photo, identify the pixels that belong to individual objects
- Classify the individuals in a later step
- Impossible in the general case without deep-learning neural networks

# Opening Thought Question – 4/3

How do coral reefs survive and grow in warm, oligotrophic (e.g., nutrient poor) waters?

- List the “support systems” that corals have that allows them to survive and grow.

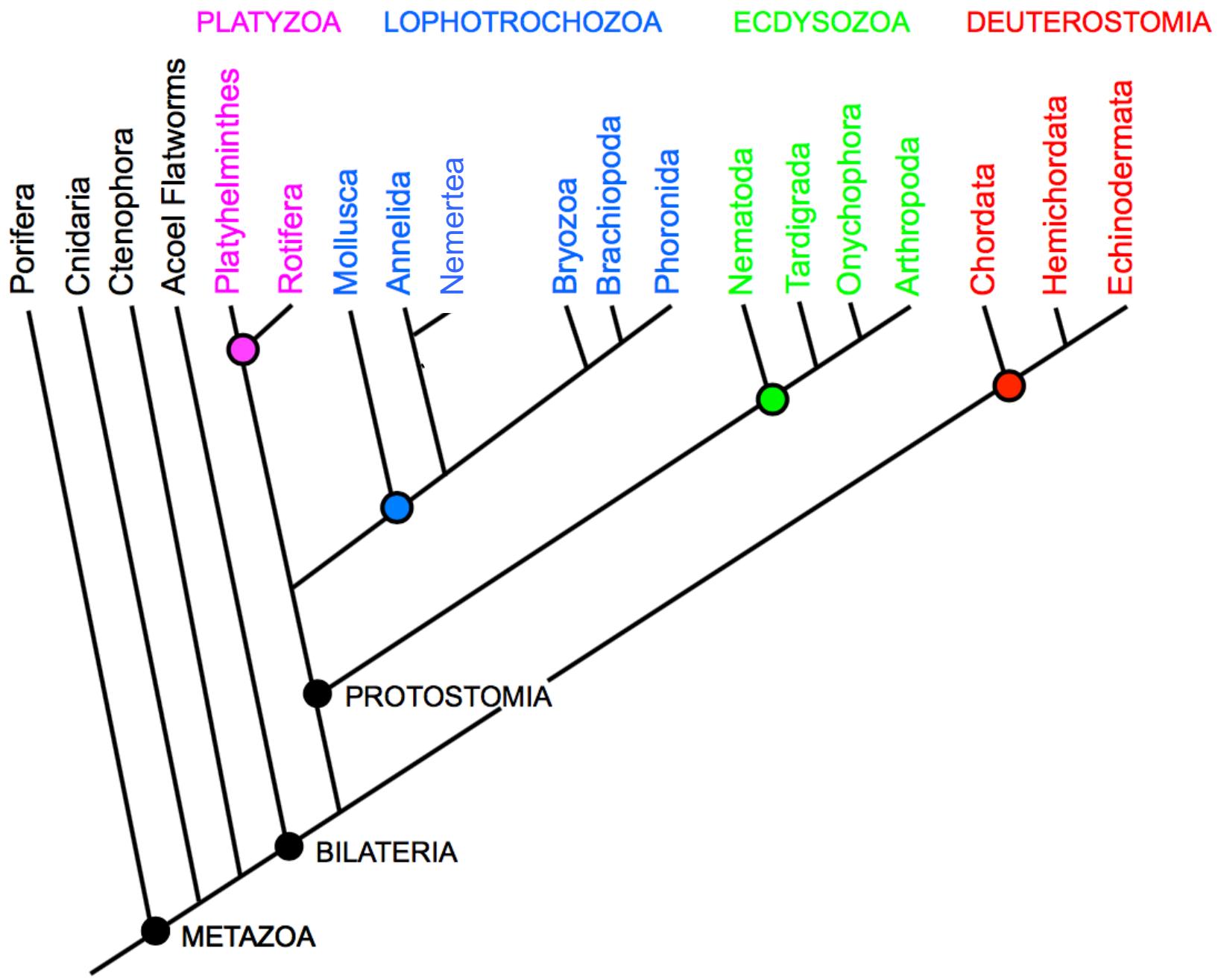
# Sponges: Phylum Porifera



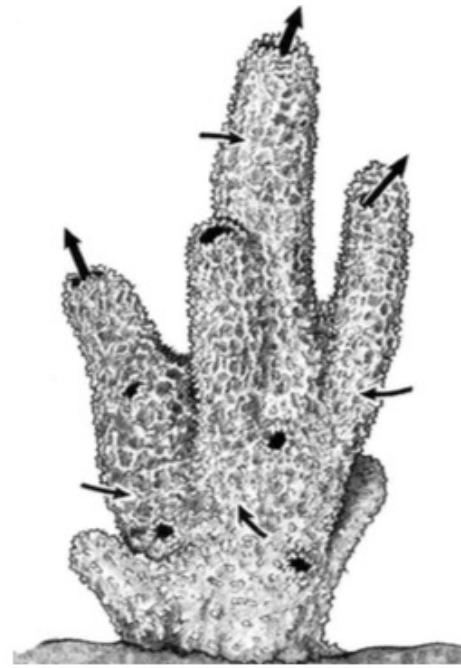
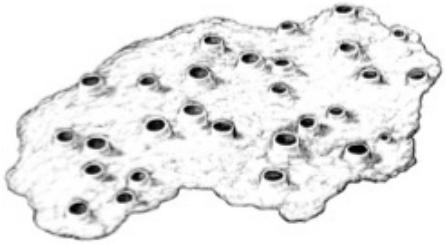
## PHYLUM PORIFERA: The Sponges

- (1) simplest body plan of any multicellular animal
- (2) cellular level of organization (no real tissues or organs)
- (3) cells exhibit high degree of plasticity (“totipotency”)
- (4) sessile filter feeders, with body constructed around system of water canals
- (5) asexual & sexual reproduction
- (6) ecologically very important

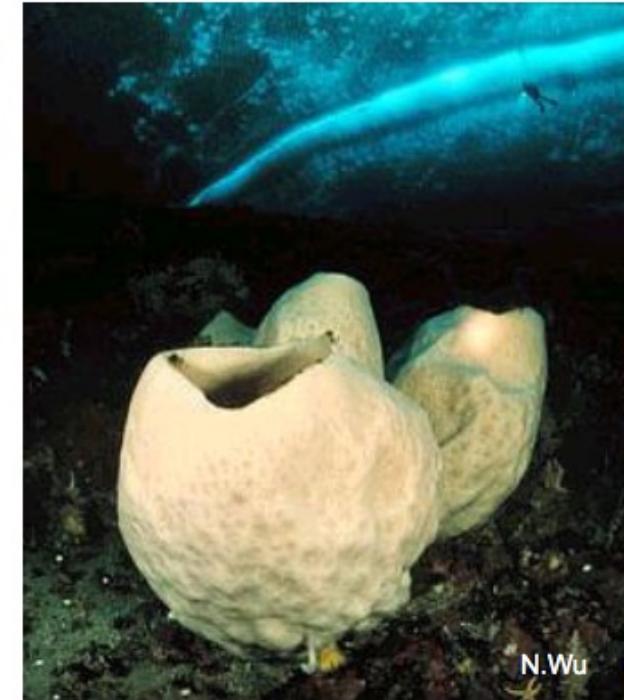




# Sponge Diversity

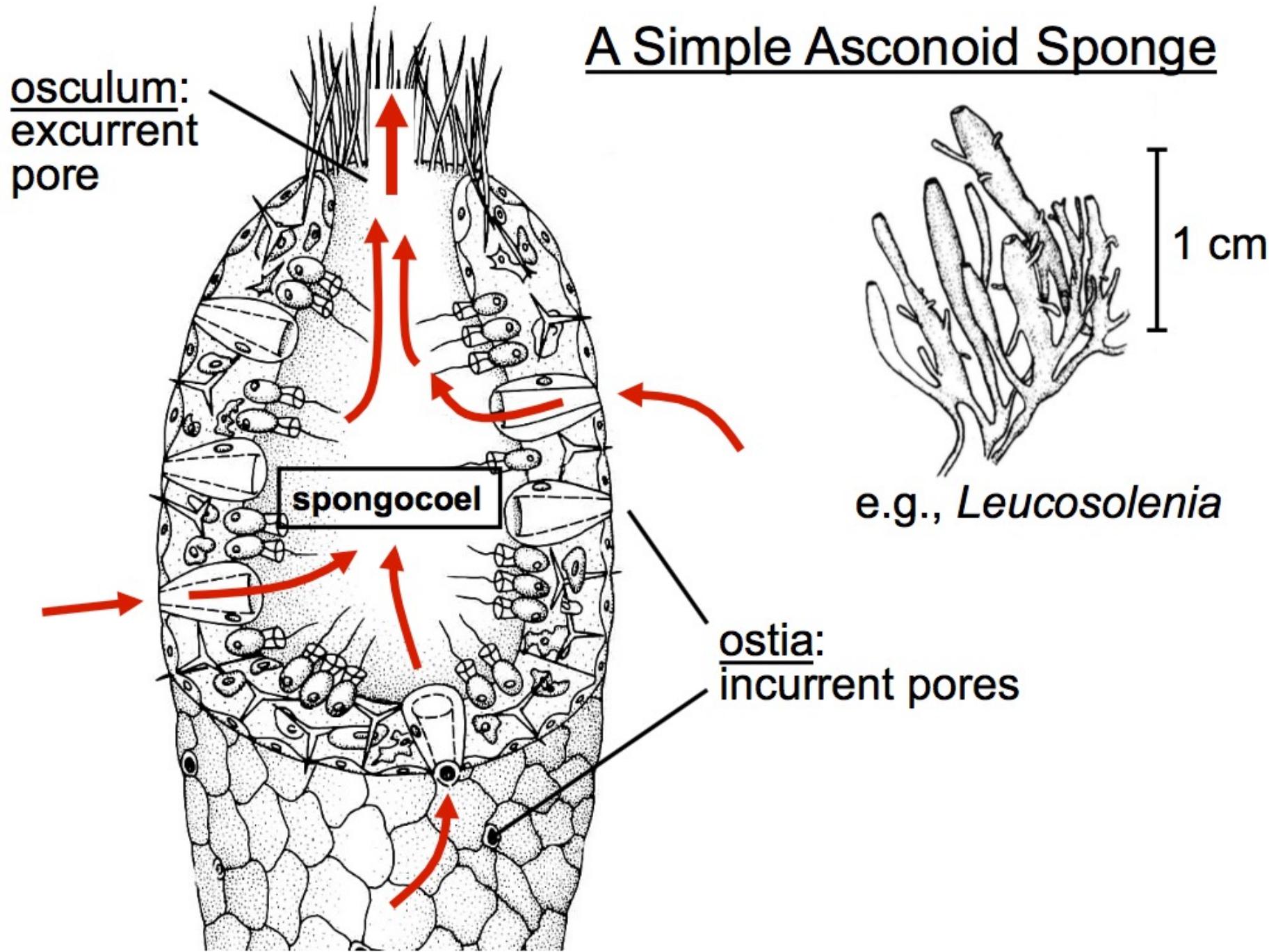


E.Sanford

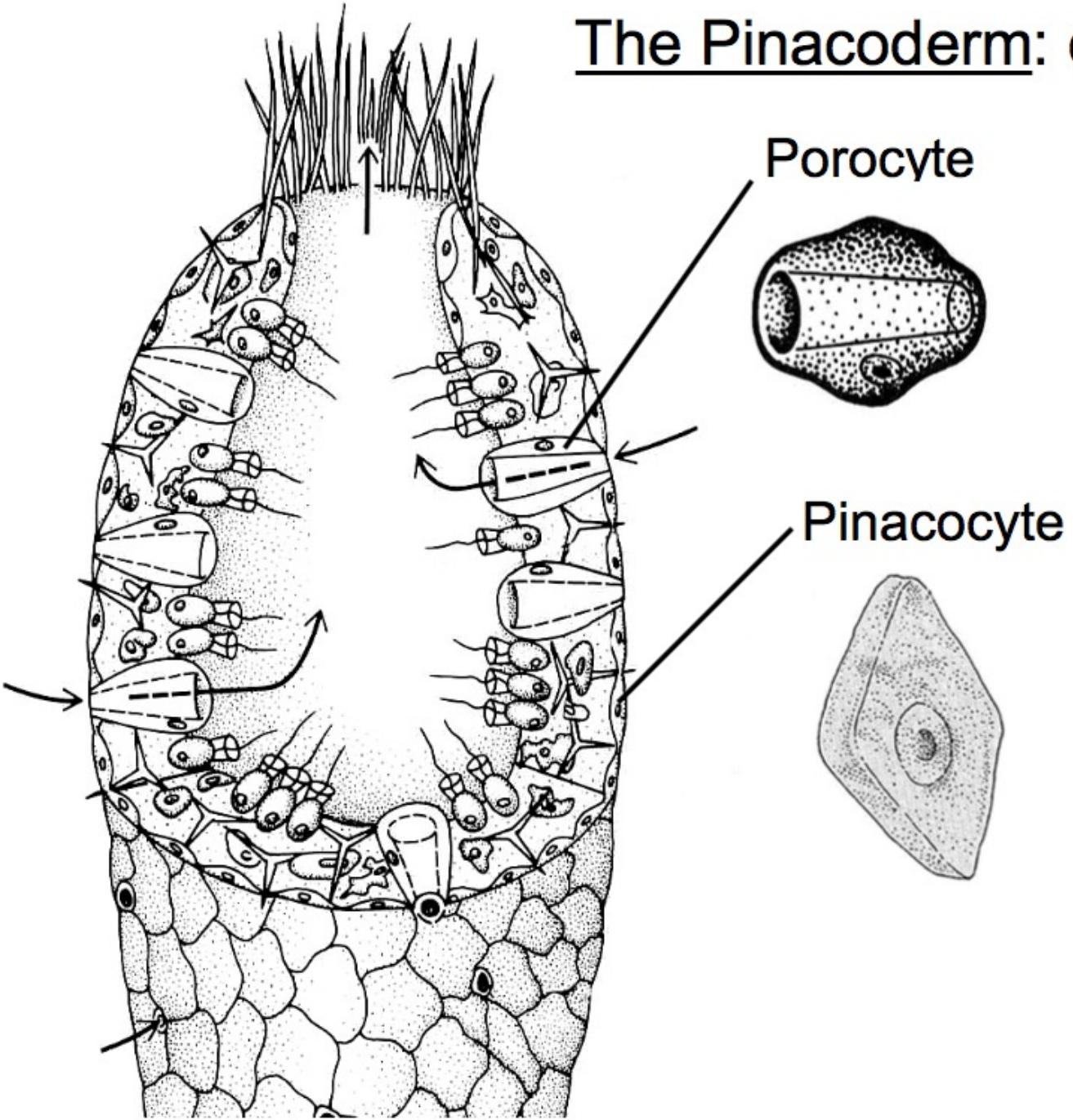


N.Wu

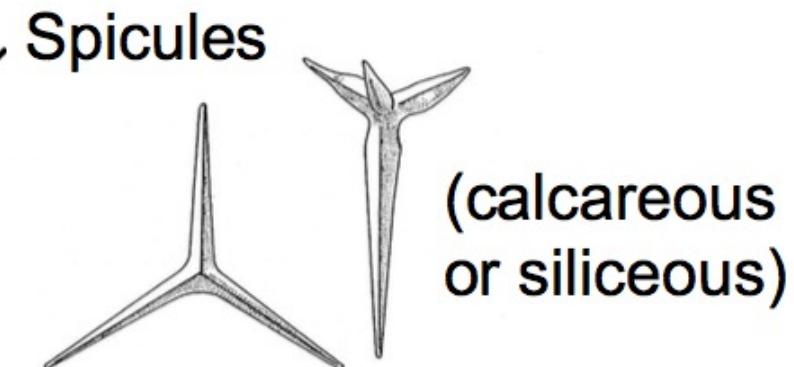
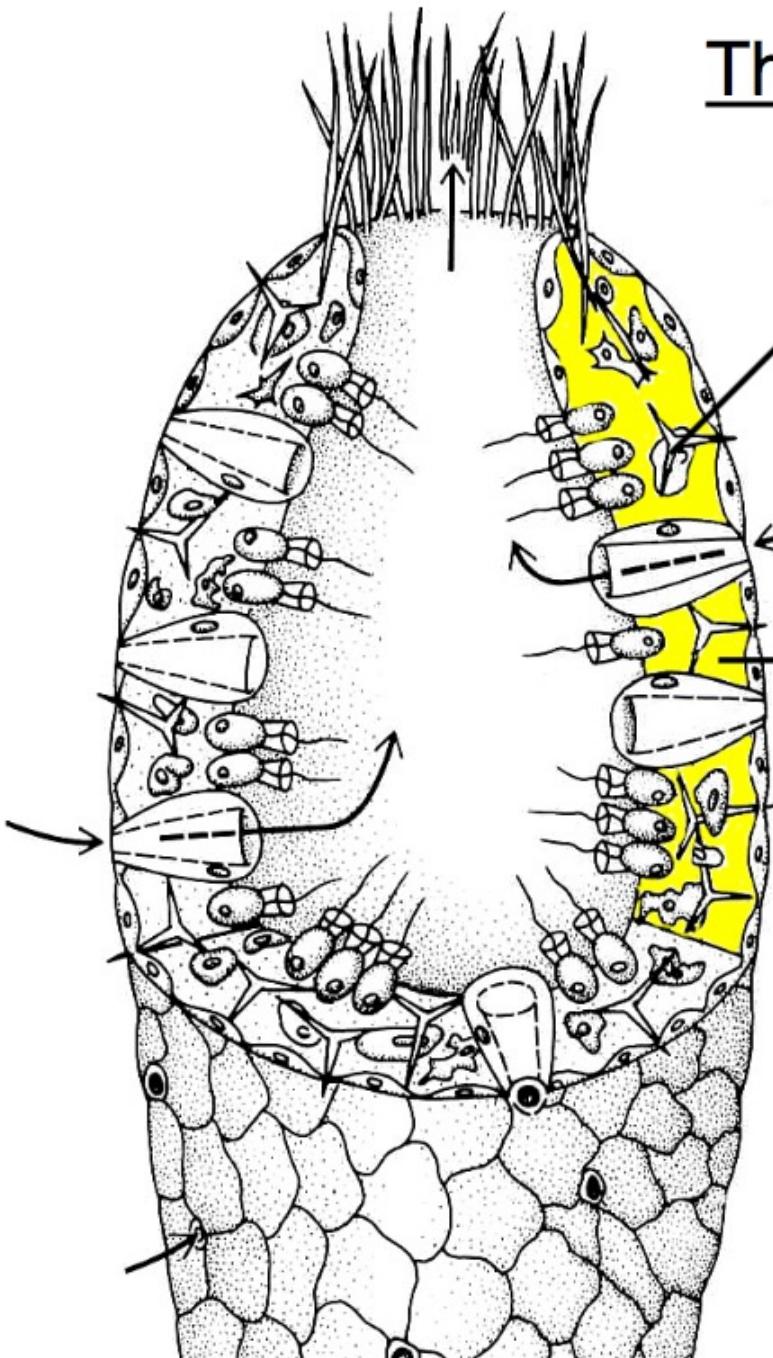
## A Simple Asconoid Sponge



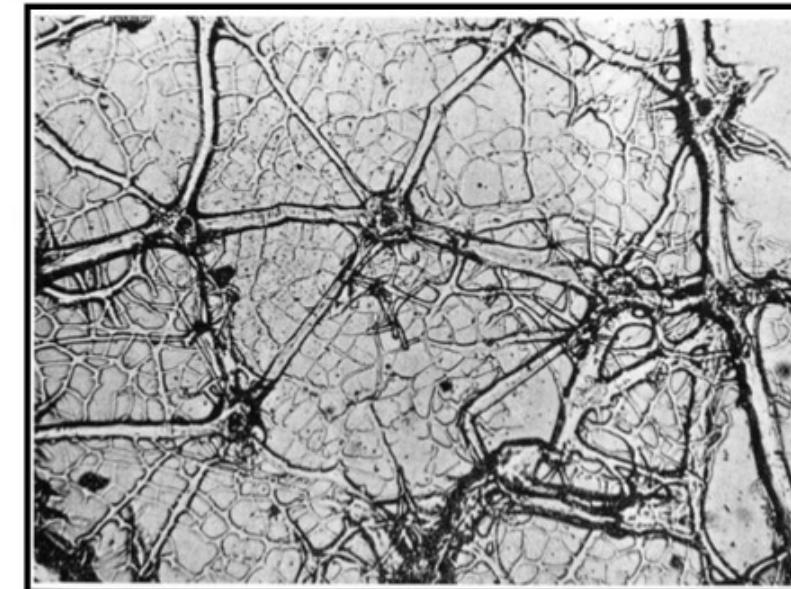
## The Pinacoderm: outer layer



## The Mesohyl: middle layer

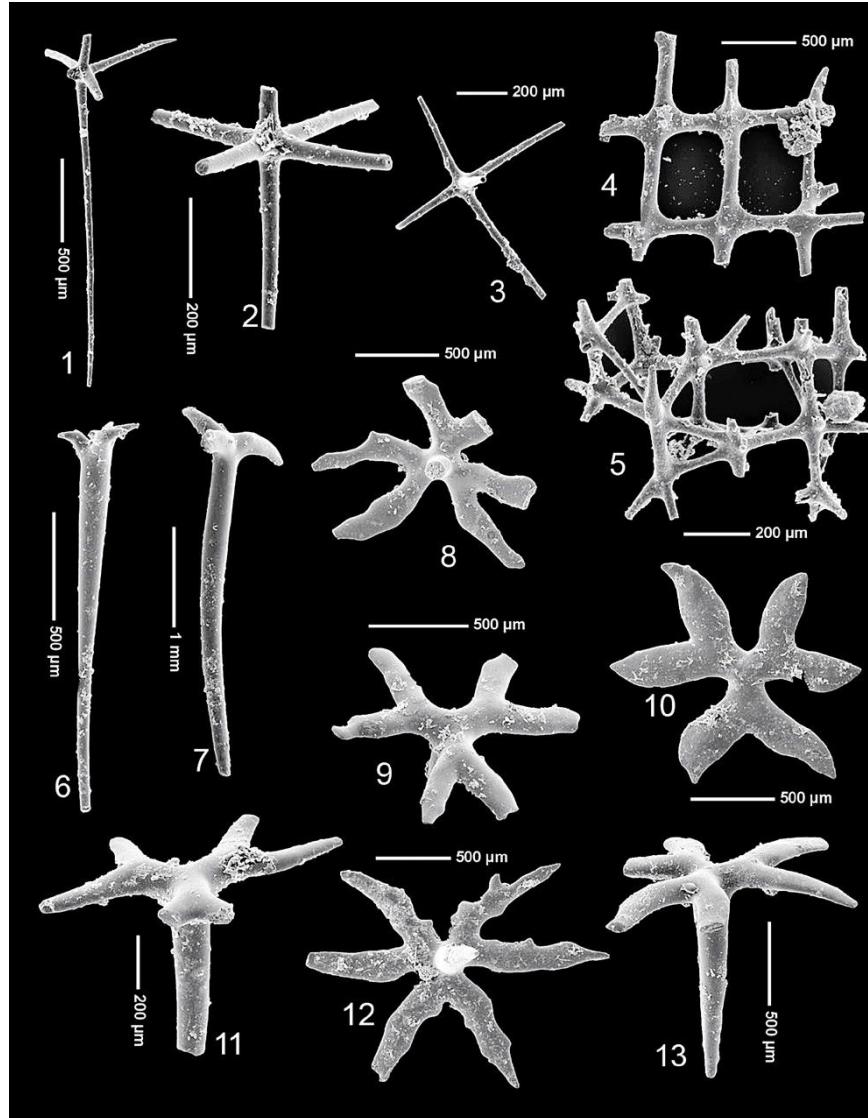


Spongin fibers

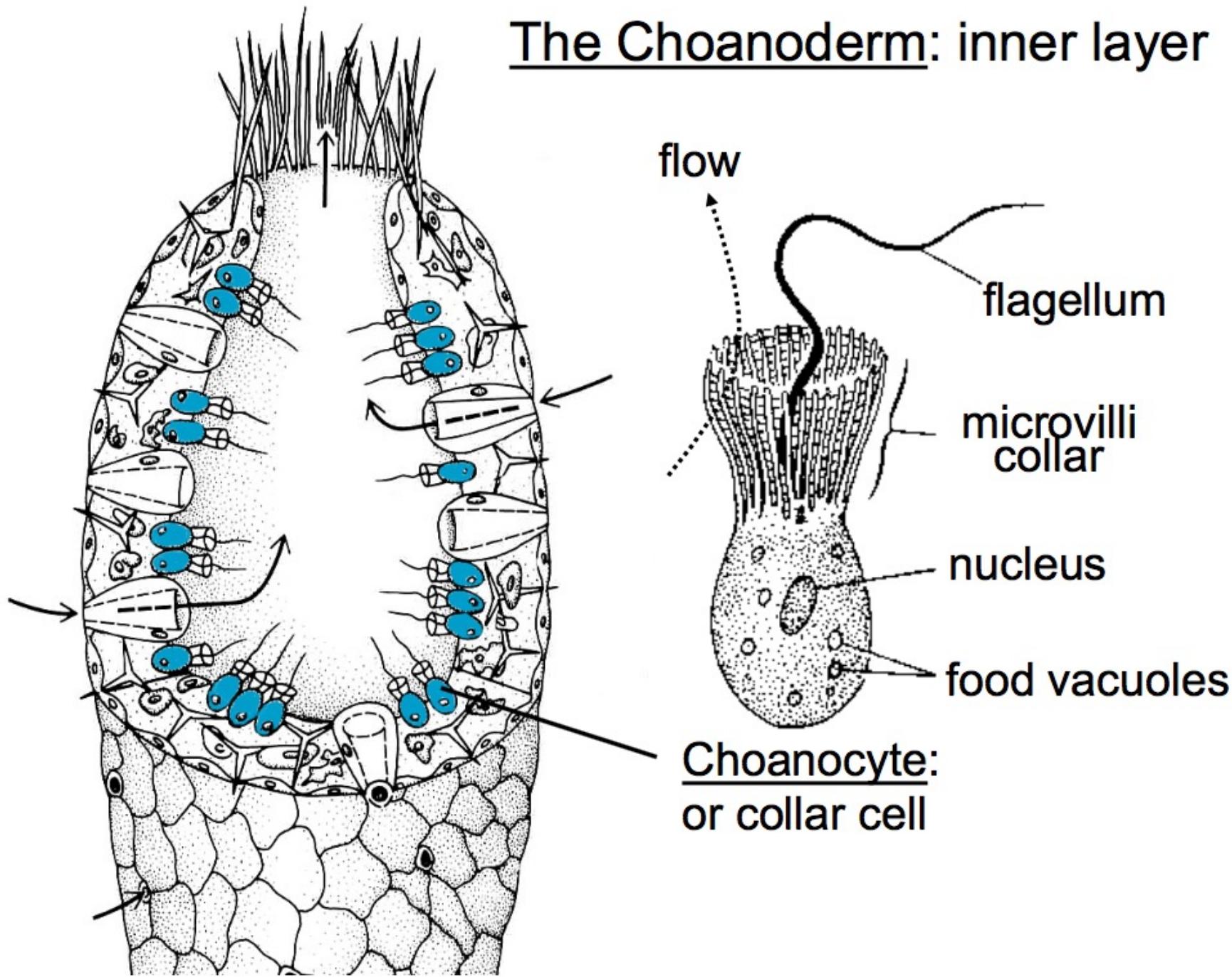


# Sponges and spicules

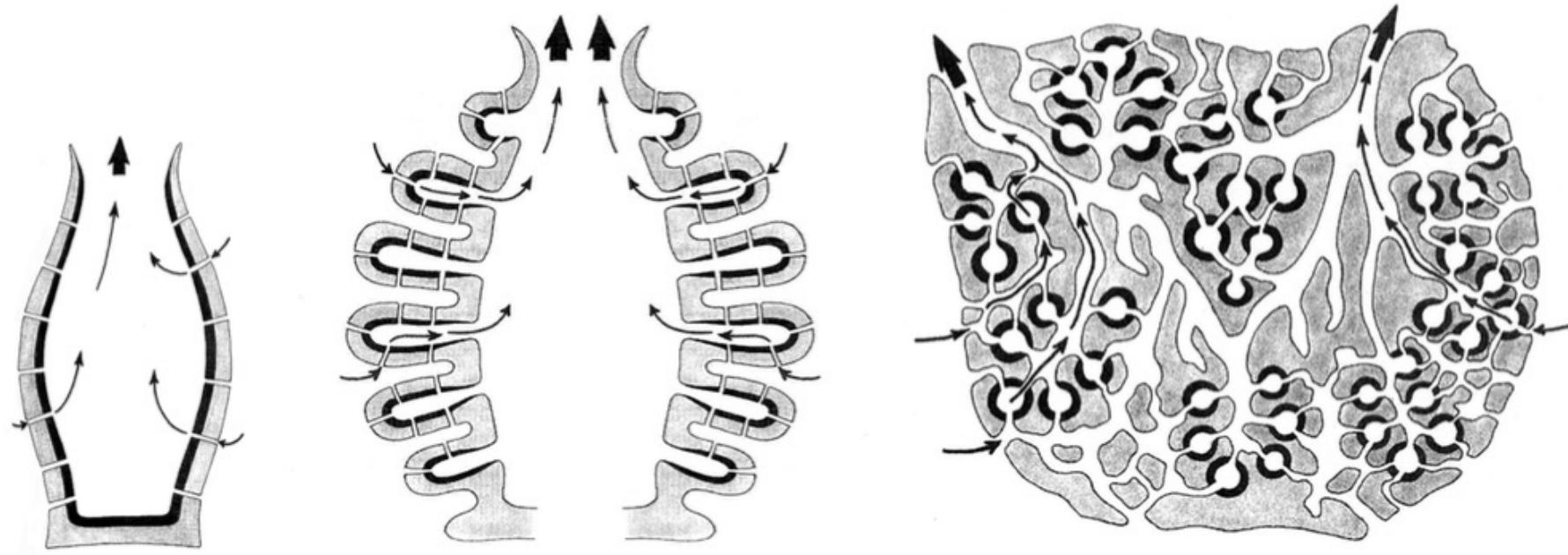
- Sponges filter dissolved inorganics from seawater
- Build spicules = structural elements of skeletons
- Some filter calcium, make calcium carbonate spicules



## The Choanoderm: inner layer



## Architectural Grades of Sponge Construction:



ASCONOID

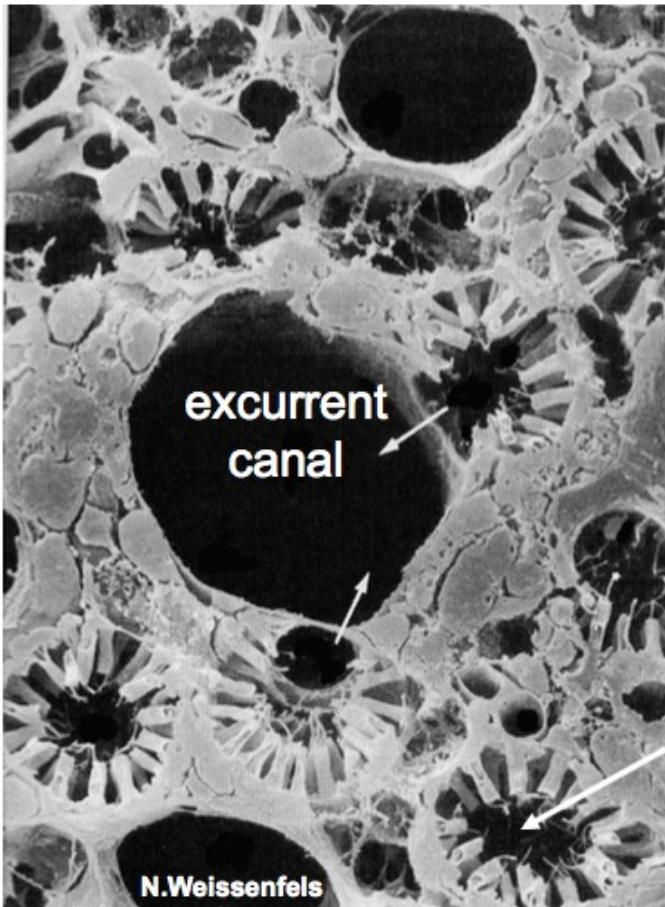
SYCONOID

LEUCONOID

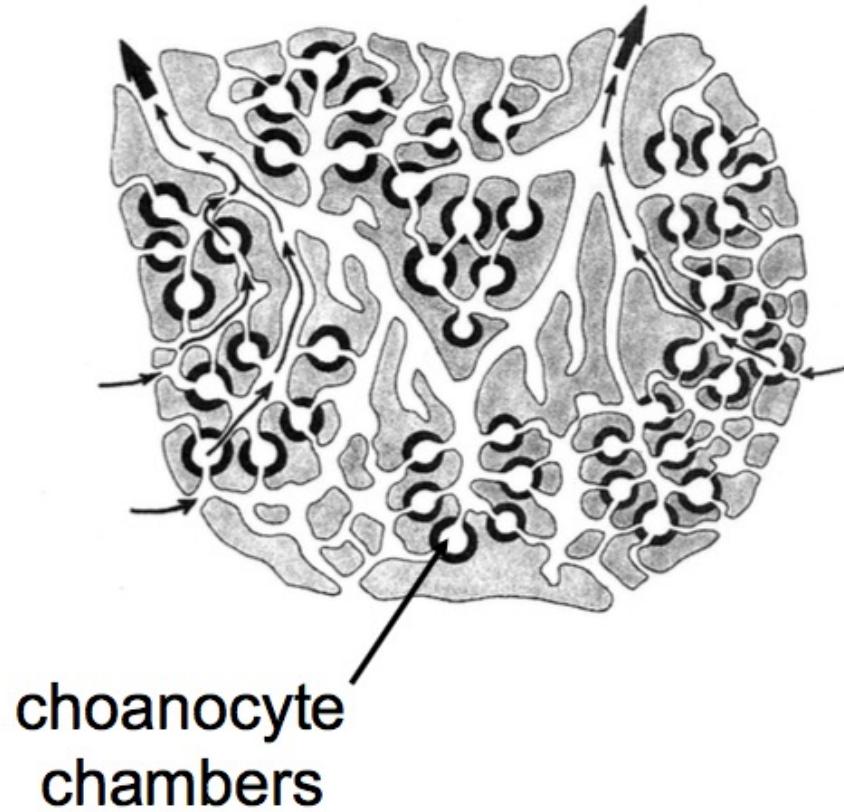
SPONGE HISTORY? →

- Evolutionary trend toward increased SA of choanocyte layer relative to water volume?
- Water currents = nutrition, excretion, gas exchange

## LEUCONOID



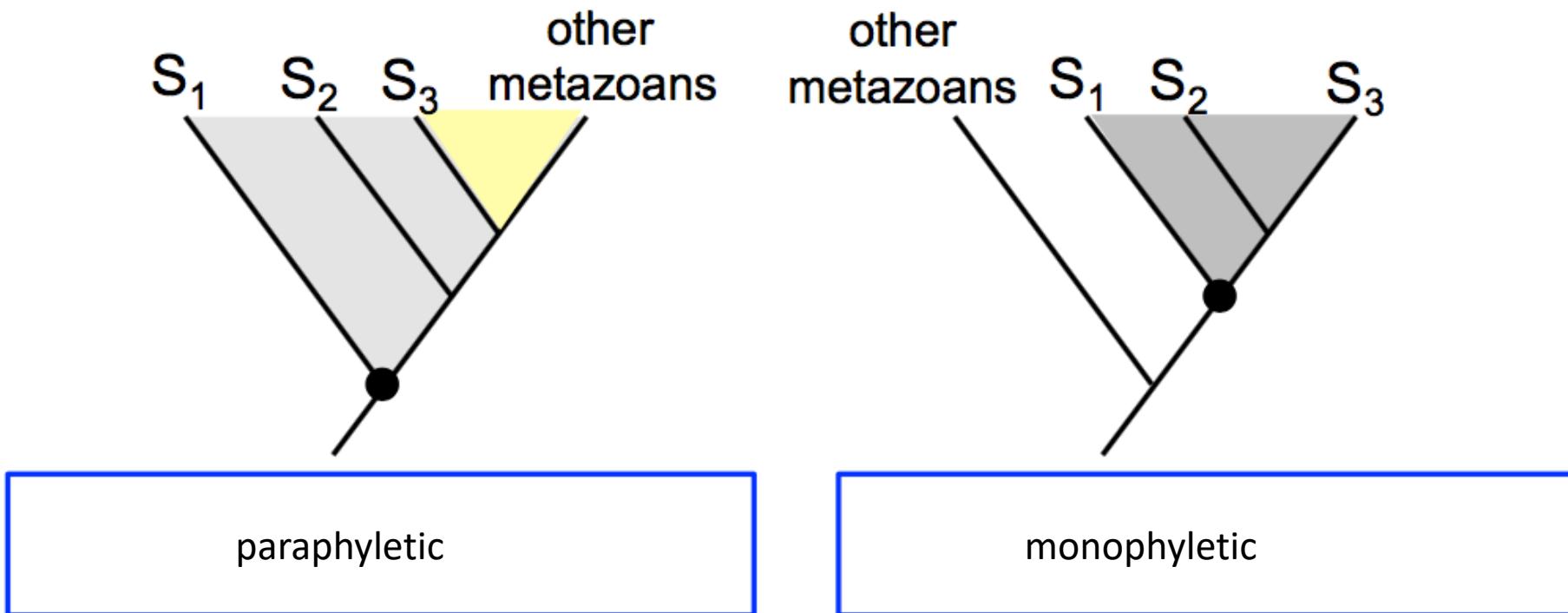
SEM



choanocyte  
chambers

10,000 chambers/ mm<sup>3</sup>  
~ 30 µm diameter

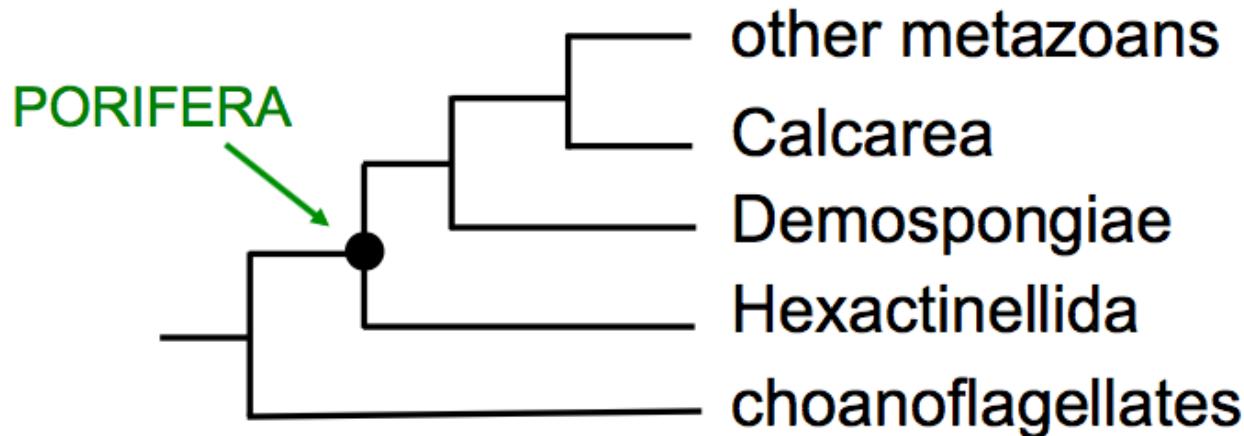
## Are sponges monophyletic or paraphyletic?



Monophyletic: A group that evolved from a single ancestor and includes all descendants of that most recent common ancestor

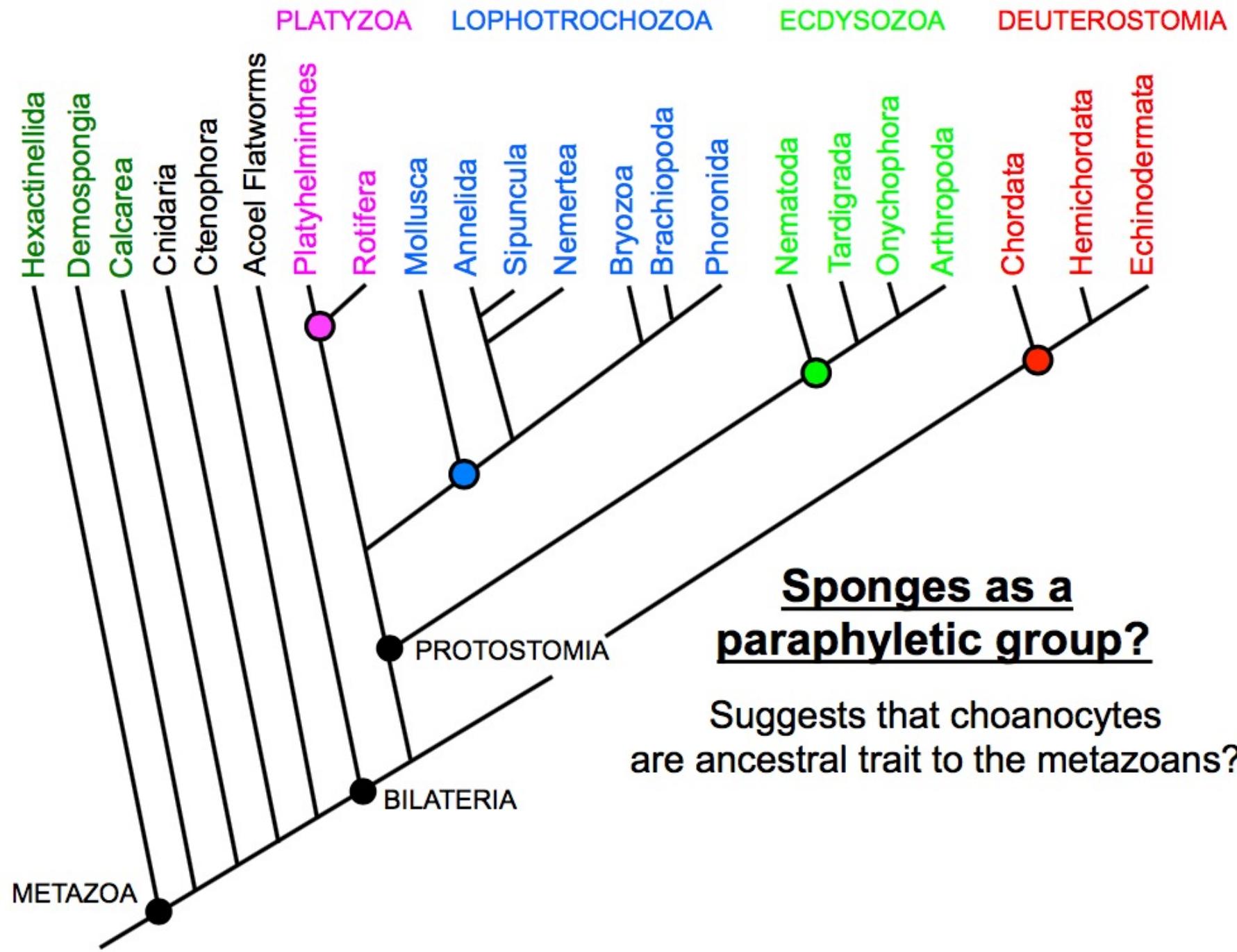
Paraphyletic: A group that does not include all descendants of an ancestor

Phylogeny based on seven nuclear housekeeping genes  
(Sperling et al. 2009. *Molecular Biology and Evolution*)



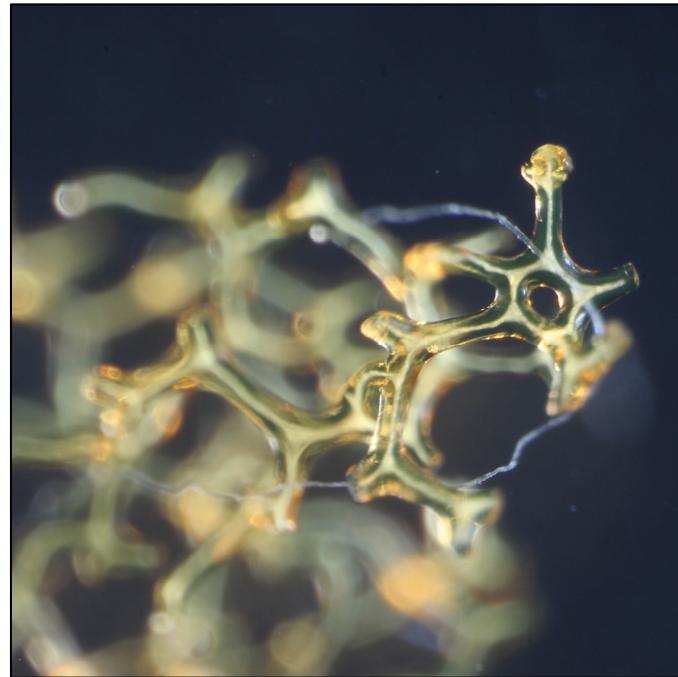
Suggests sponges might be a paraphyletic group  
(a monophyletic group must include all  
descendants of MRCA – i.e., all other metazoans)

But see also: Wörheide et al. 2012 *Adv Mar Biol*,  
Simion et al. 2017 *Current Biology*



# The glass sponges

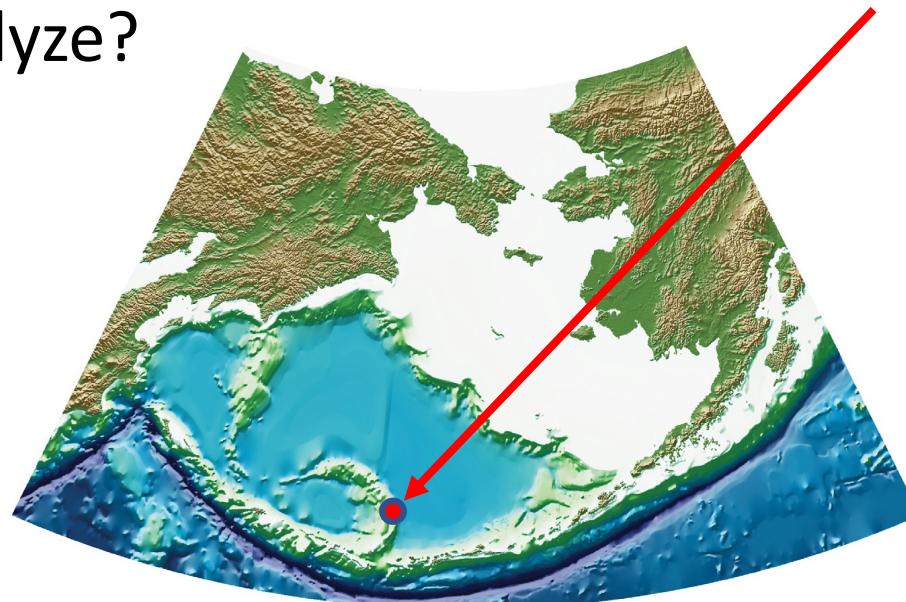
- Classes *Demospongia* and *Hexactinellidae*
- Filter silica
- Spicules are made of biosynthetic glass



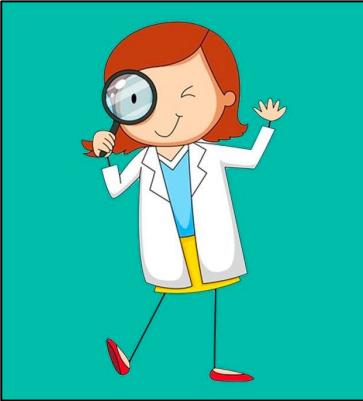
Vanderbilt news

# The Pliocene Warm Period

- ~3 Ma
- The last time the planet warmed like this
- High productivity in the Bering Sea
- Integrated Ocean Drilling Program Expedition 323
- Core samples of Site U130 (Bowers Ridge, depth 1295m)
- How to analyze?



# Glass spicules: a tool for quantifying/qualifying ancient sponge communities



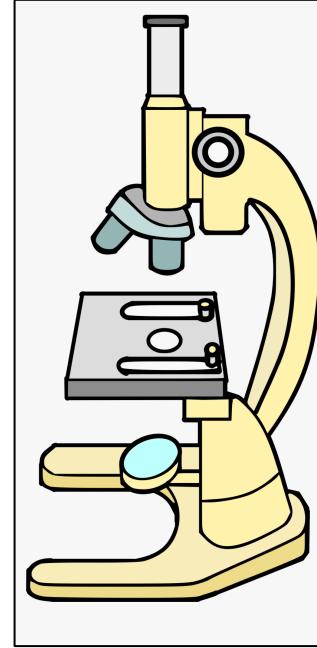
+



+



+

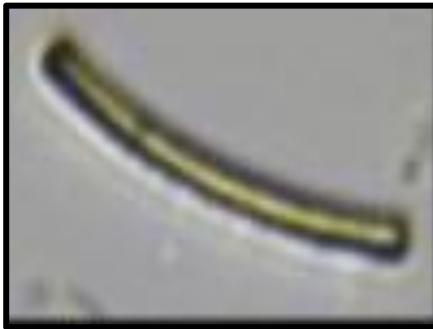


- Grad student inserts toothpick into core
- Collects a little material onto tip of toothpick
- Smears tip onto a slide
- Visual identification

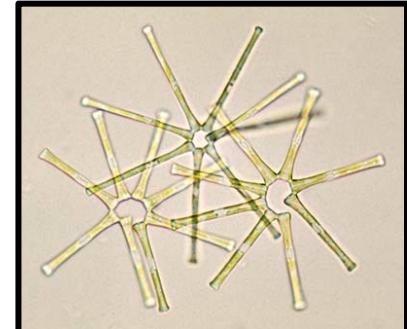
# Drawback #1: Sponges aren't the only ones with glass skeletons



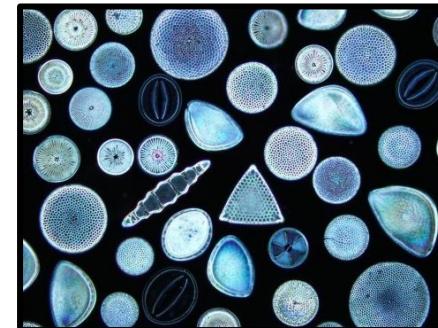
Sponge



Radiolarian

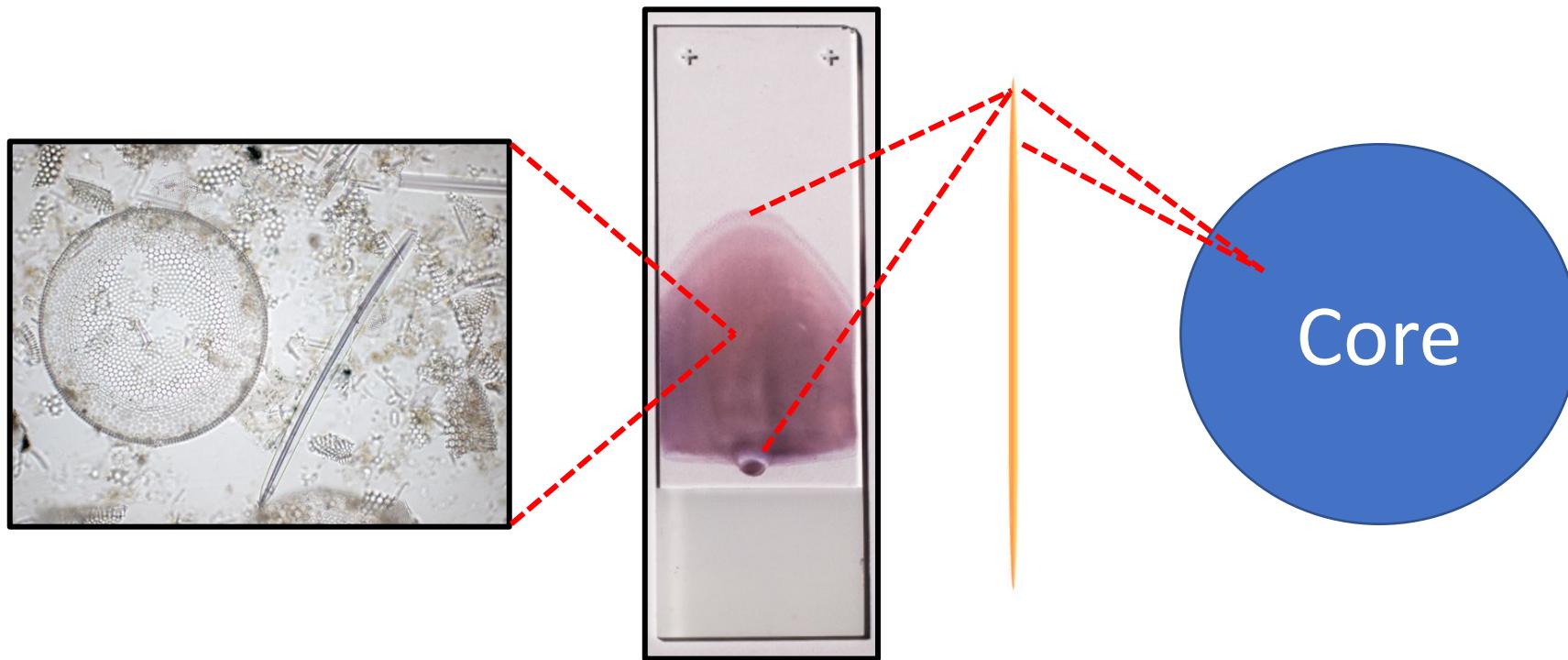


Diatom



## Drawback #2: Low statistical strength

- No mechanized steps → slow
- Microscope view is a sub-sub-subsample



## Drawback #3: Spicule shapes are not diagnostic

- Original shapes are shared across taxa
- Individual taxa can use diverse of shapes
- *Distribution* of shapes seems to be diagnostic
- Spicules can break at (1295m = ) 128 atm over 3m years

# Opening Thought Question – 4/11

1. Why are sponges challenging to classify, especially when they've been in the sediment for a long time?
2. How can deep machine learning techniques help meet these challenges?

# stomatopod crustaceans (mantis shrimp)

500+ extant species

First see in the fossil record 400 mya

tropical and subtropical

raptorial appendage moves extremely fast

incredible vision



Slide: M. Porter; Photos: R. Caldwell, M. Bok

# Smashers



# Speakers



Photos: R. L. Caldwell and S. N. Patek

This is where smashers live



# Smashing



Filmed at 30 fps



Filmed at 5000 fps, played at 15 fps

speed: 14-23 m/s

acceleration: 65,000-104,000 m/s<sup>2</sup>

This is where spearers live



# Spearing



Filmed at 30 fps

speed:  $2.3 \pm 0.9$  m/s

acceleration:  $0.4 \pm 0.3$  m/s<sup>2</sup>



Filmed at 3000 fps, played at 30 fps



speaker

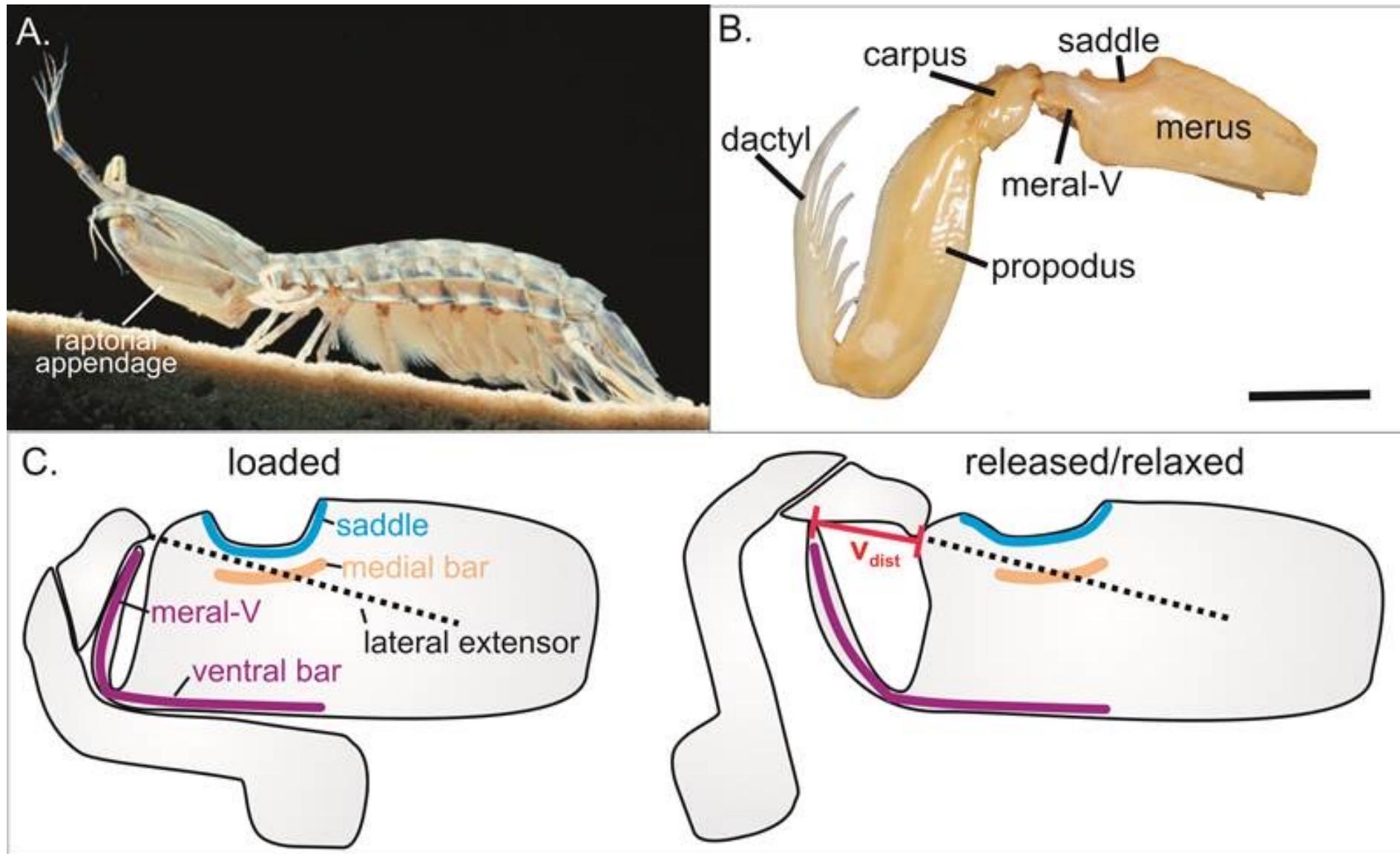


smasher

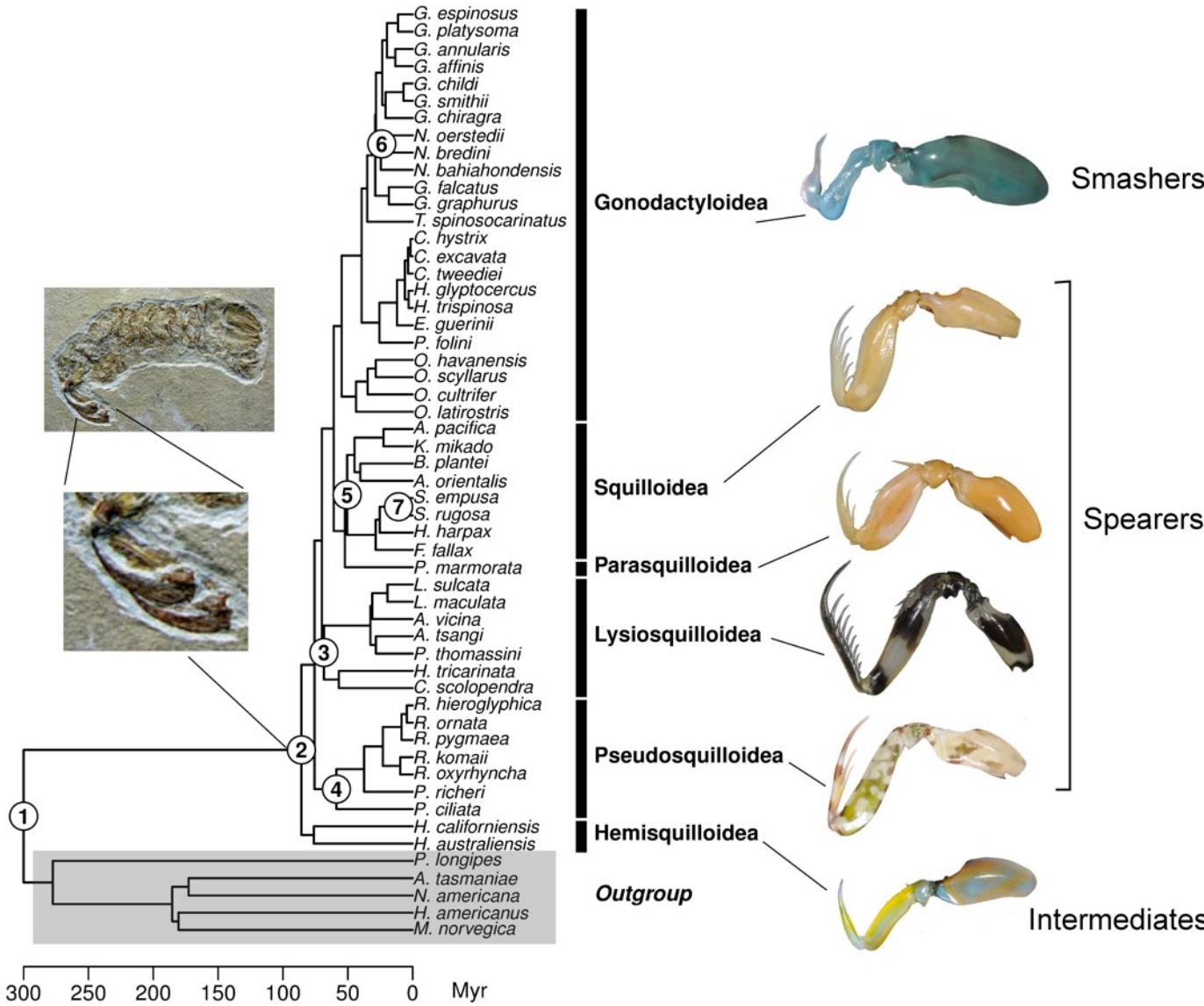
---

	speaker	smasher
Duration (ms)	25.0	3
Speed (m/s)	2.3	14-23
Acceleration (m/s <sup>2</sup> )	0.4	65,000-104,000

# Raptorial appendage functions as a spring



# Appendage morphology across mantis shrimp



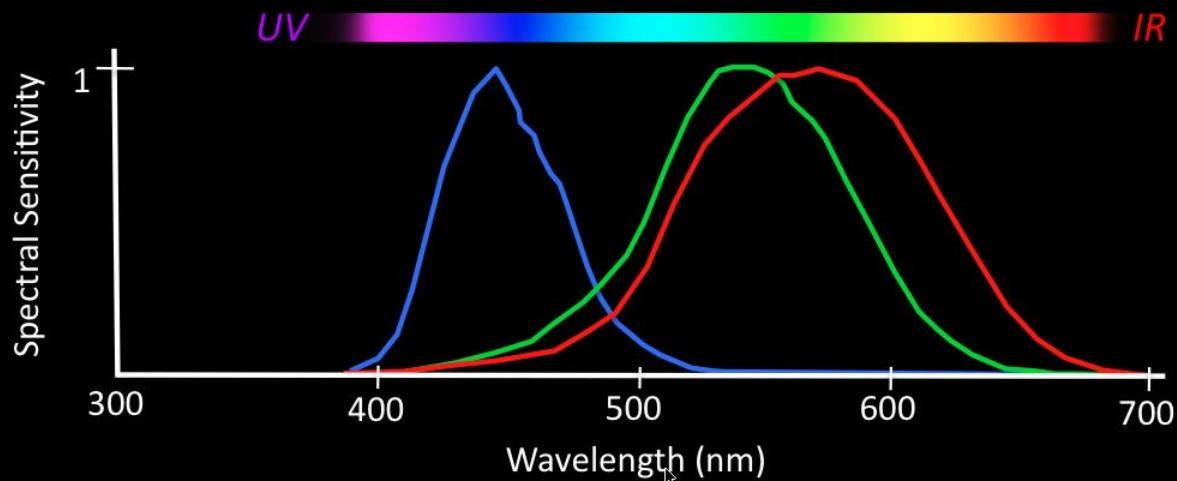
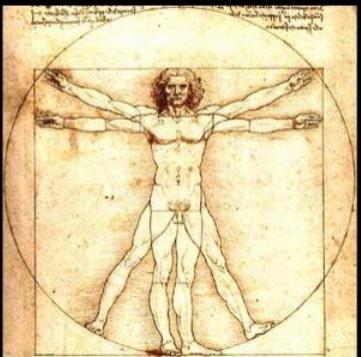
Phylogeny: Porter et al. (2010) *J. Exp. Biol.*; Figure: Claverie & Patek (2012) *Evolution*.

# Opening Thought Question – 4/13

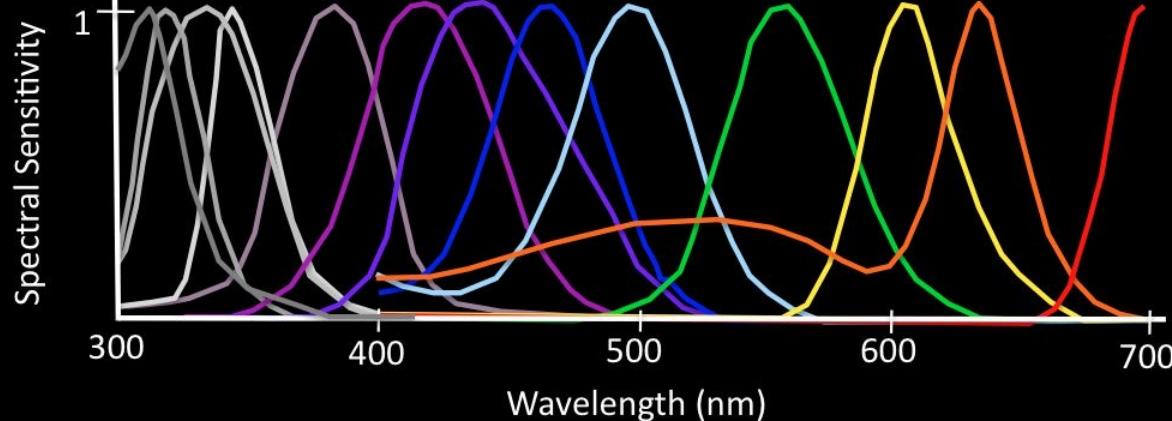
What are the tradeoffs associated with  
spearing vs smashing mantis shrimp strikes?

# Mantis Shrimp: Extraordinary Eyes

*Homo sapiens*

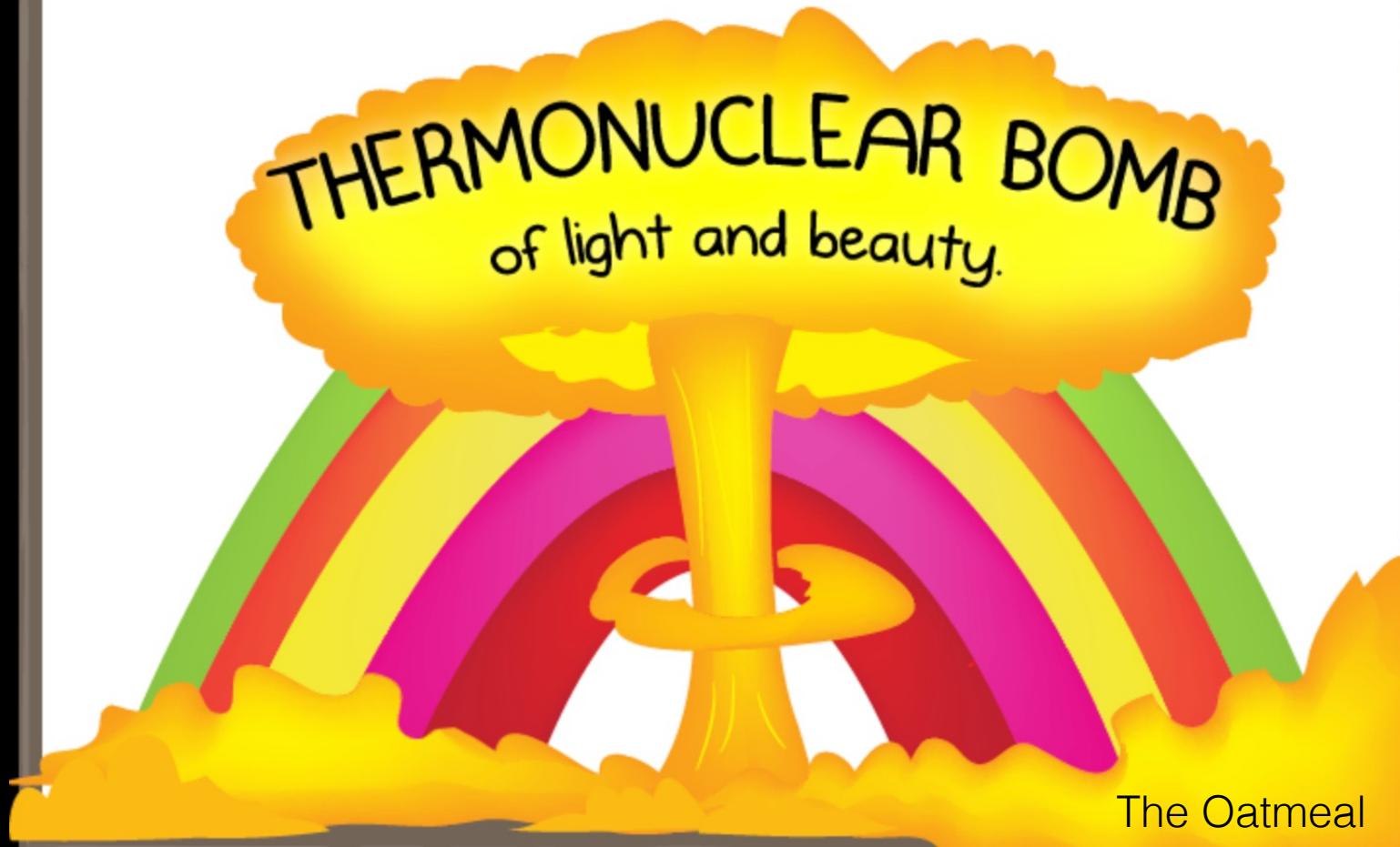


*Neogonodactylus oestedii*



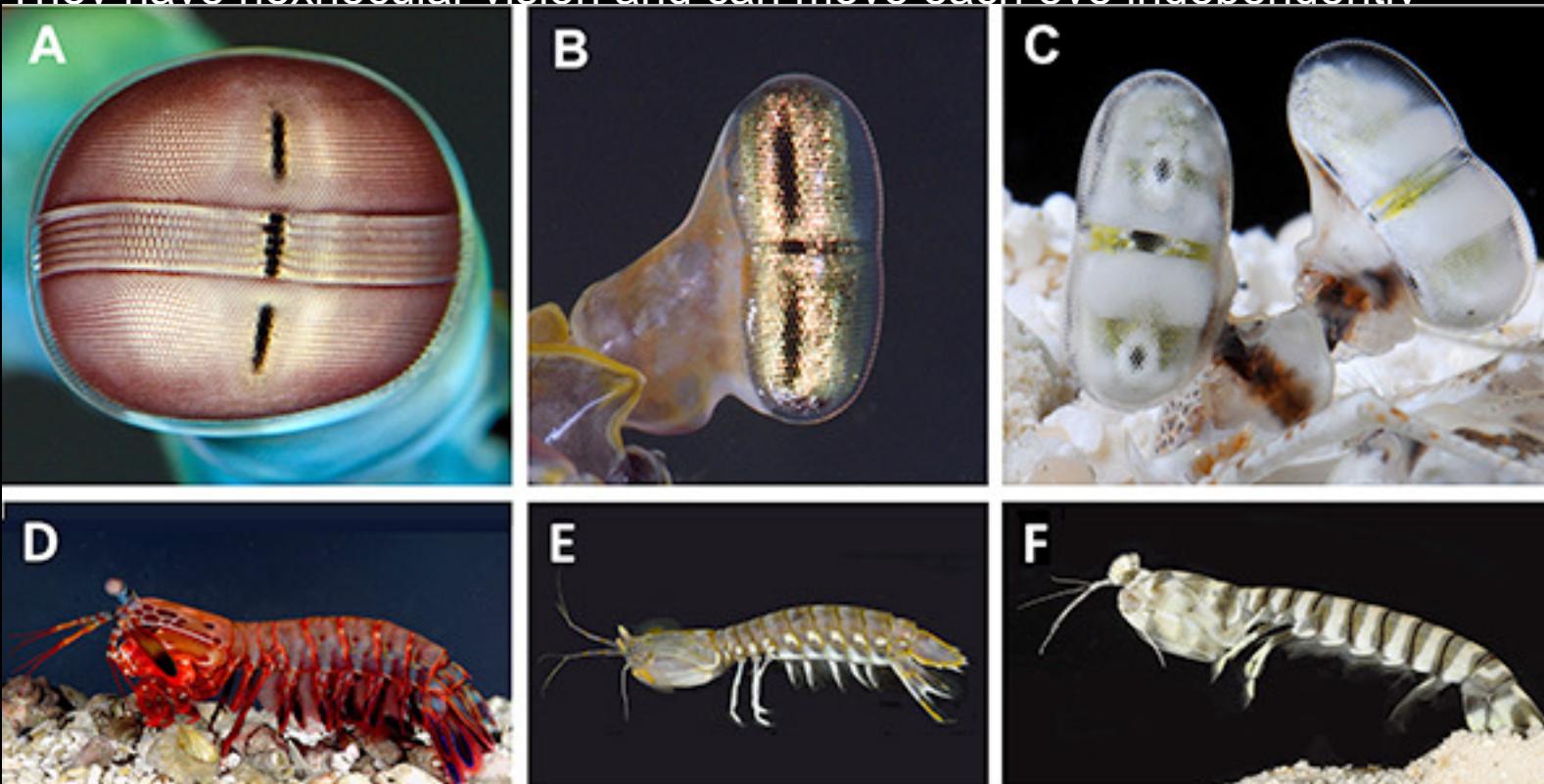
so try to imagine a mantis' rainbow  
created from SIXTEEN colors.

Where we see a rainbow,  
the mantis shrimp sees a



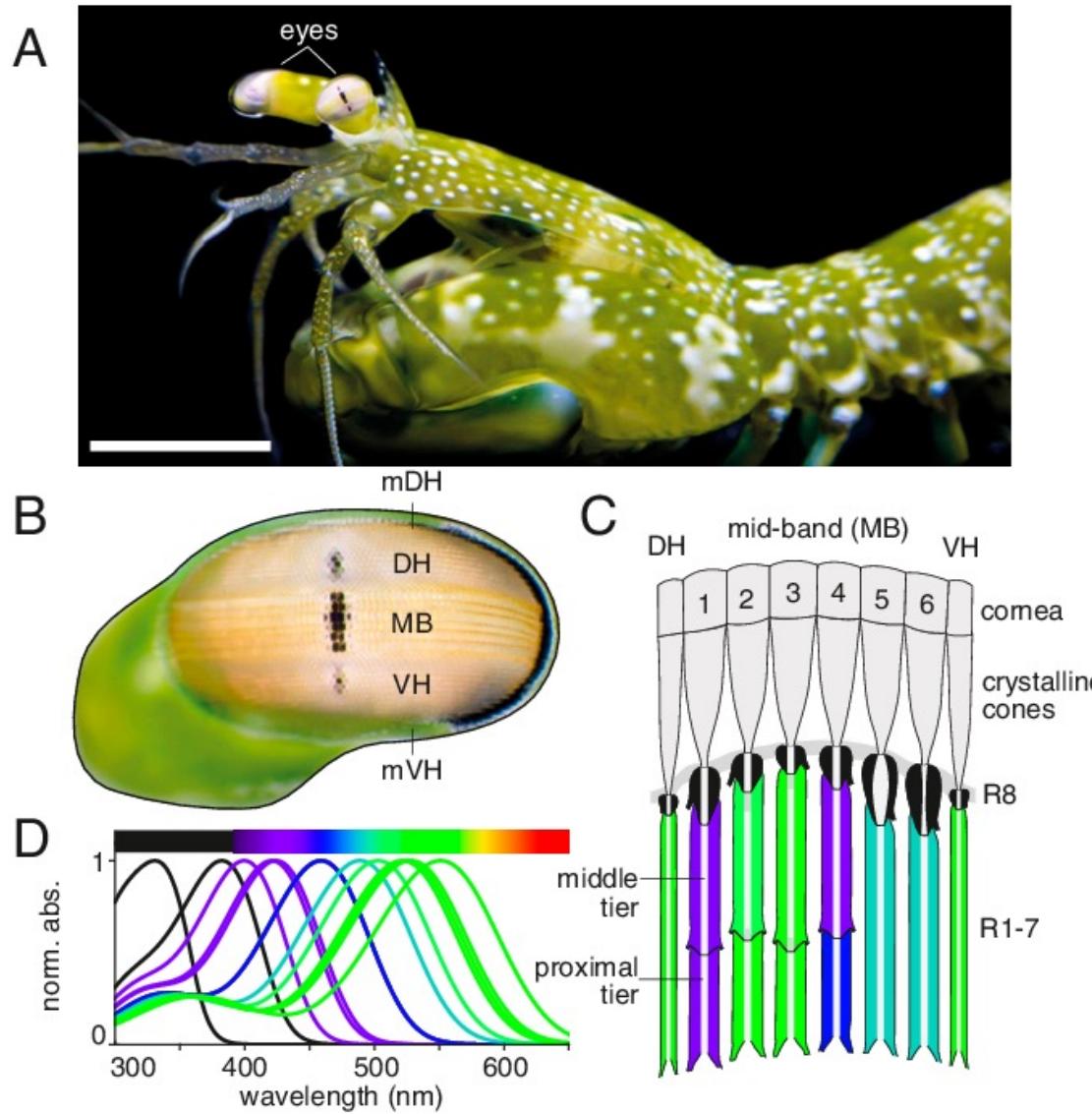
# How do mantis shrimp see so many colors?

- They have 16 color receptive cones! (We have 3)
- They can see visible and UV light, and even into the infrared spectrum
- They can see linearly and circularly polarized light
- They have hexnocular vision and can move each eye independently



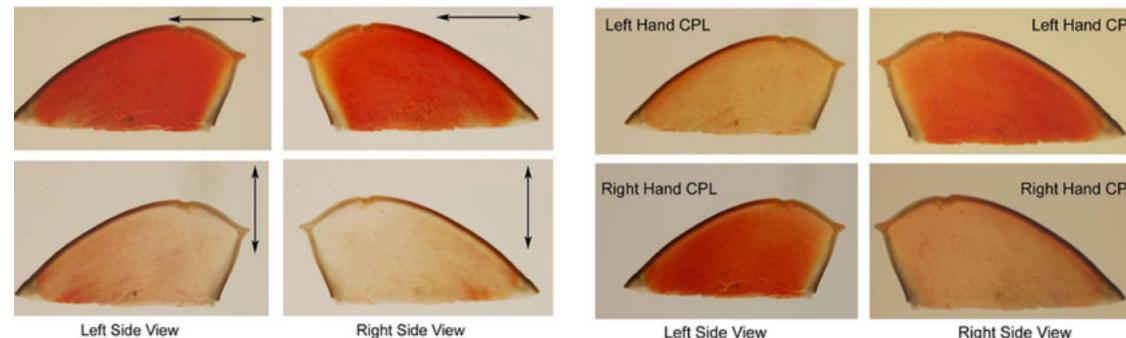
# Compound eyes in mantis shrimp

- All arthropods have eyes that are composed of separate light sensing organs called ommatidia
- The ommatidia have light sensing proteins in them called **opsins**
- Examining the genetic diversity of opsins in mantis shrimp has revealed that they have a wide diversity of transcripts that code for opsin proteins.
- The organization of the eye with the central “midband” is also important. This midband has 6 organized rows of specialized ommatidia for UV and polarized light

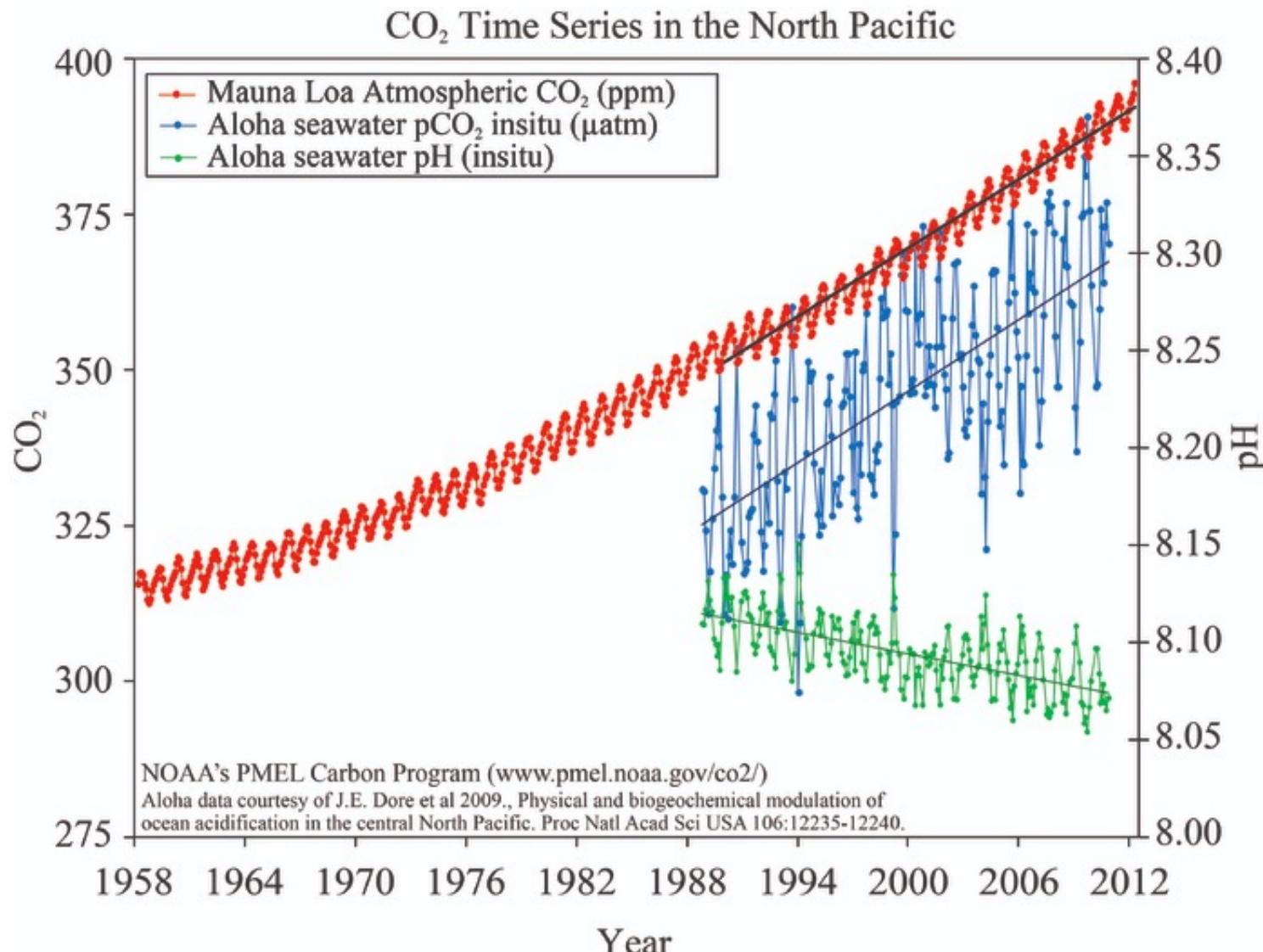


# What do mantis shrimp actually see?

- They do not see shades of color in the same way that we do.
- Colors turn neurons on and off, which signals a mantis shrimp to do something.
- So they have 16 "channels" in which to fewer colors than we can see overall.
- Behaviorally, they use these amazing colors to signal to each other to attract mates and ward off competitors.

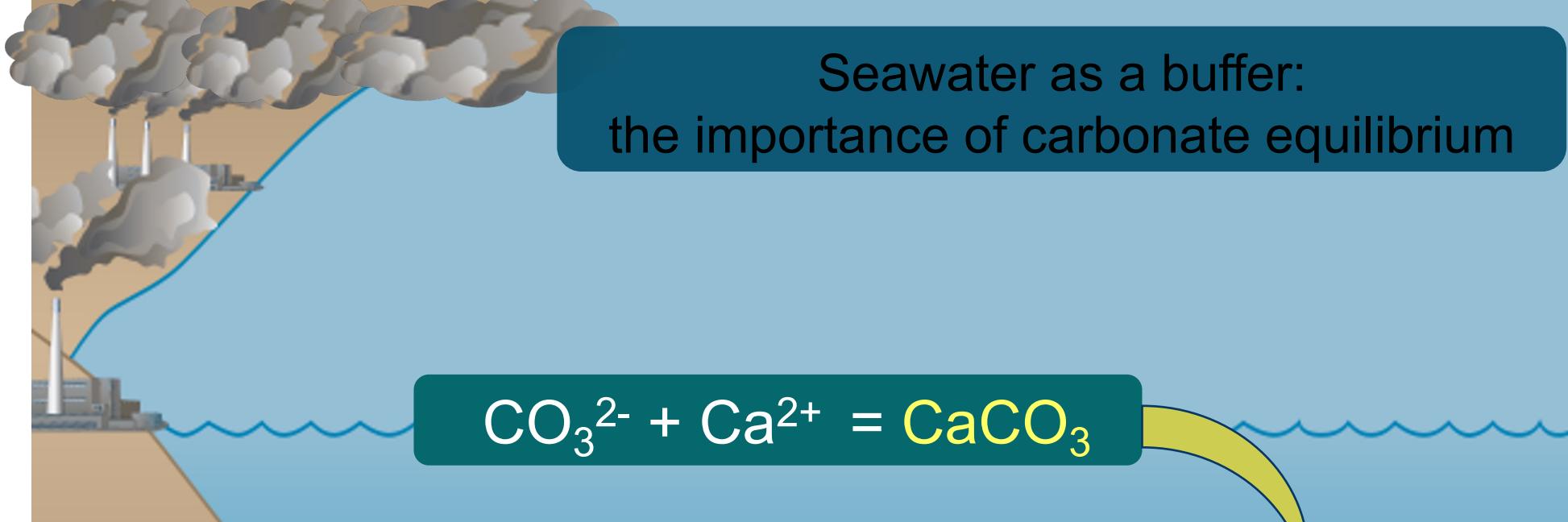


# Decrease in pH with increase CO<sub>2</sub> in atmosphere and seawater



<https://scripps.ucsd.edu/programs/keelingcurve/2019/06/04/animation-of-keeling-curve-history-updated-to-include-2019-milestone/>

~30% increase in [H<sup>+</sup>] over pre-industrial time



## Seawater as a buffer: the importance of carbonate equilibrium



carbonic acid

bicarbonate

carbonate

Carbonic acid breaks down to form bicarbonate and carbonate with H<sup>+</sup> and 2H<sup>+</sup>

# Ocean acidification affects calcified structures



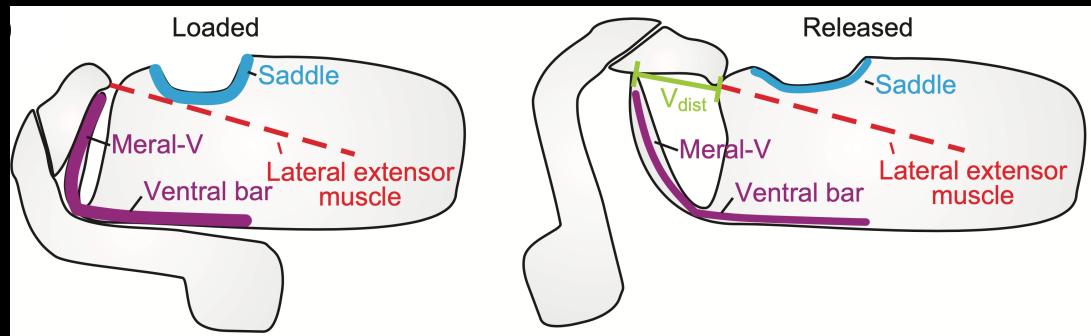
How does feeding morphology change in response to  $\downarrow$  pH and  $\uparrow$  temperature?

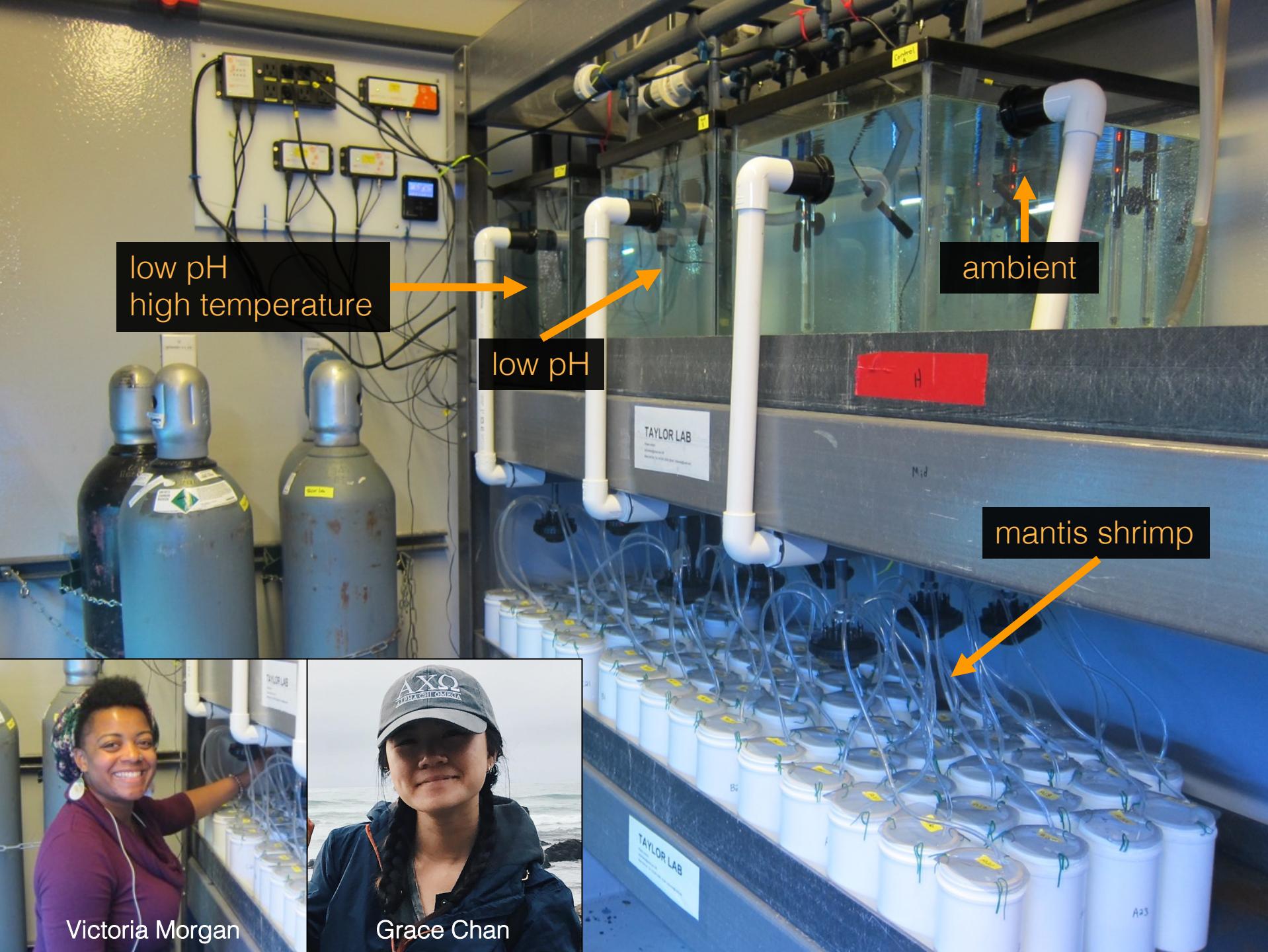


Photo: R. L. Caldwell

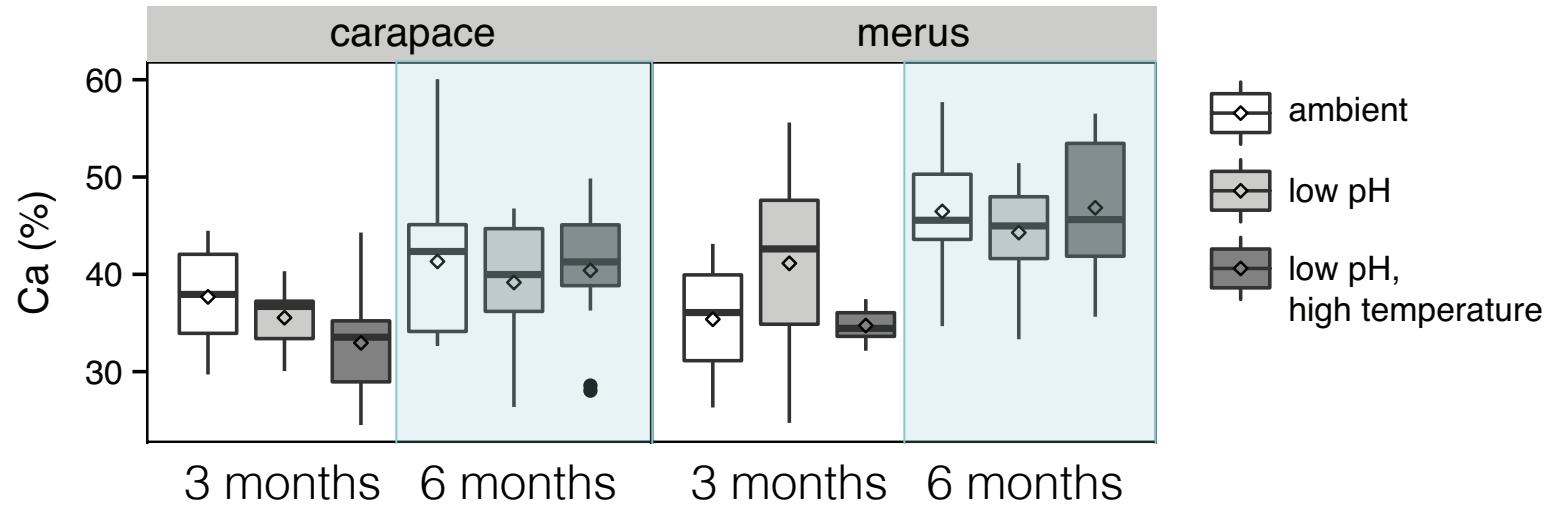
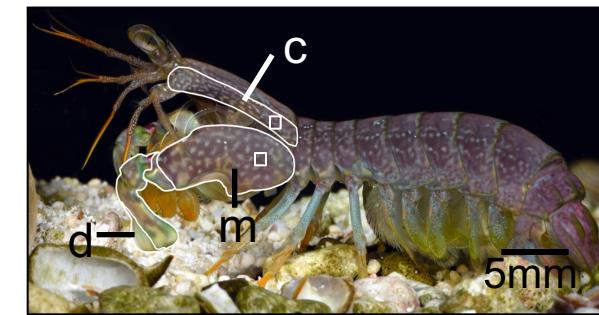
*Neogonodactylus bredini*

Exoskeleton behaves  
like a spring



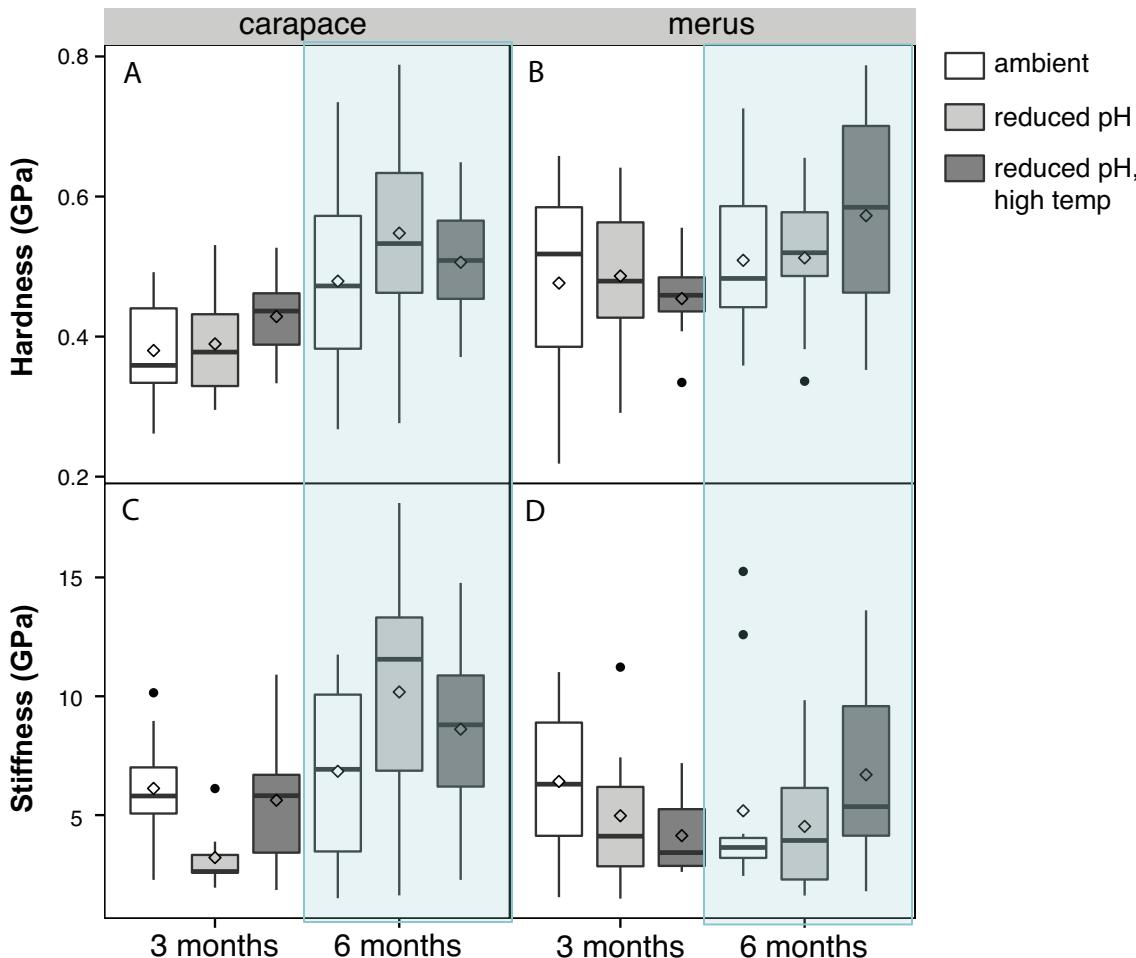
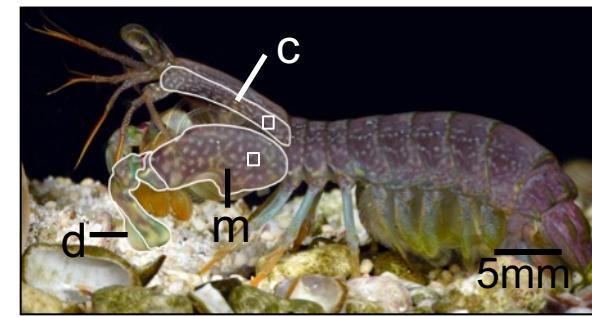


# Mineral composition



- Ca %: no significant differences between treatments.
- Mg %: no significant differences between treatments.

# Material properties



- No changes in material properties between treatments.



Tessa Pierce-Ward

Differential  
expression of genes  
under OA conditions

*N. bredini* may be able to exploit less tolerant, hard-shelled prey that are predicted to break more easily in future ocean conditions.

Affected prey



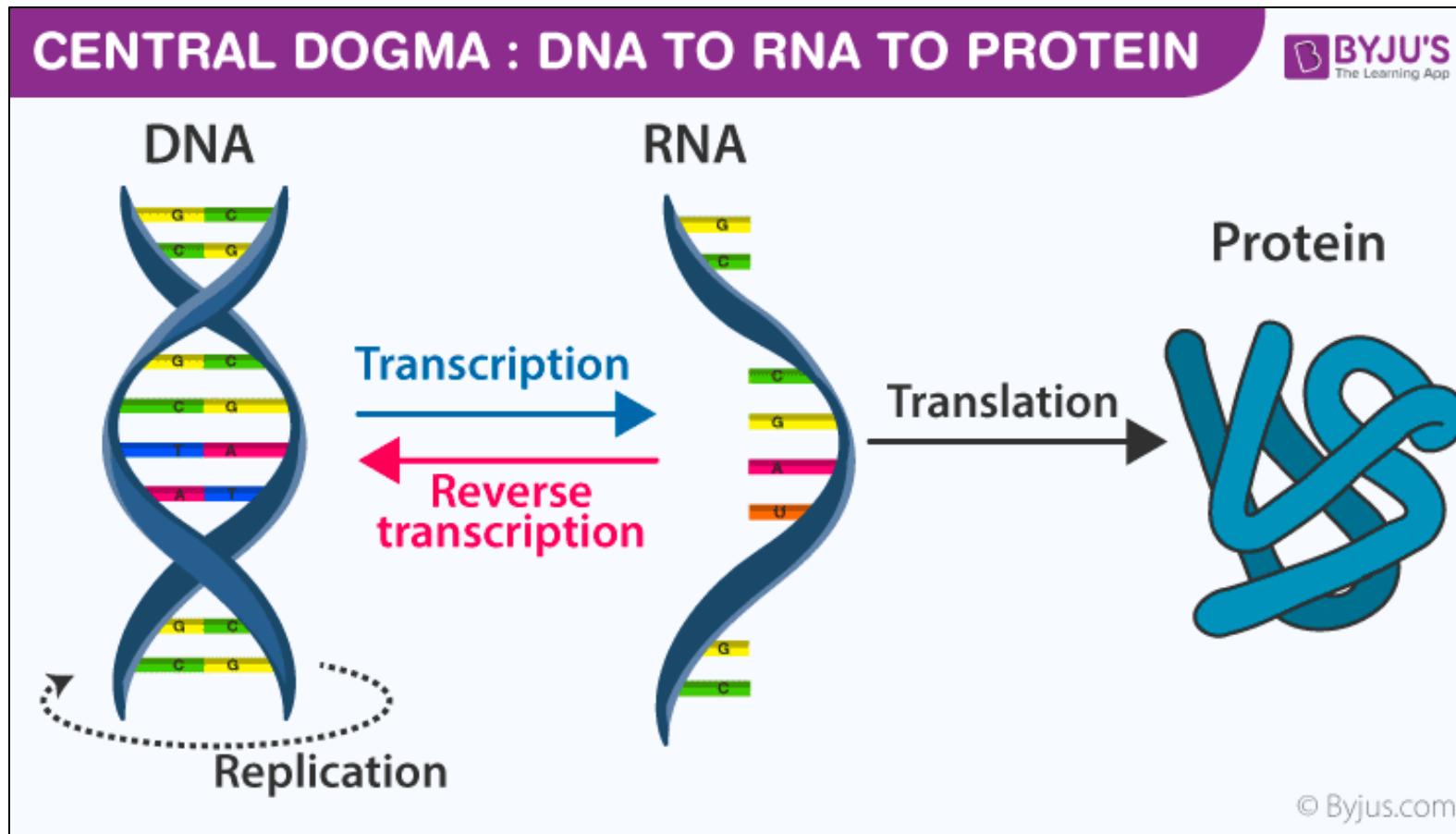
Unaffected prey



# Mantis Shrimp Transcriptomics



Transcriptomics: Study the transcriptome rather than the genome.



Genomics  
Genetic potential

Transcriptomics  
What proteins are getting made

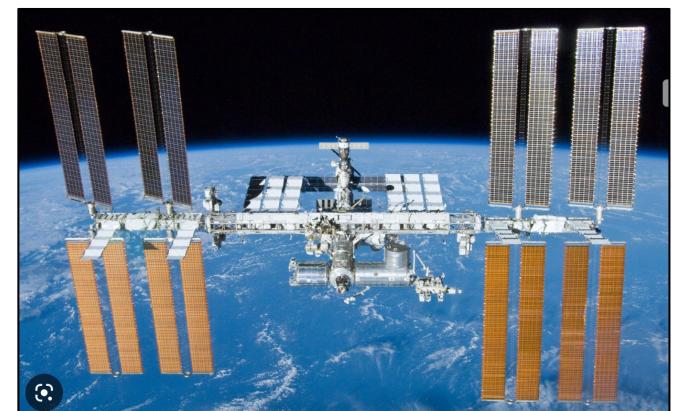
Proteomics

# What genomics can't tell you

- Is a gene of interest ever transcribed?
- How frequently is it transcribed?
- Under what circumstances is it transcribed (or not)?
- What other genes are transcribed (or not) at the same time?

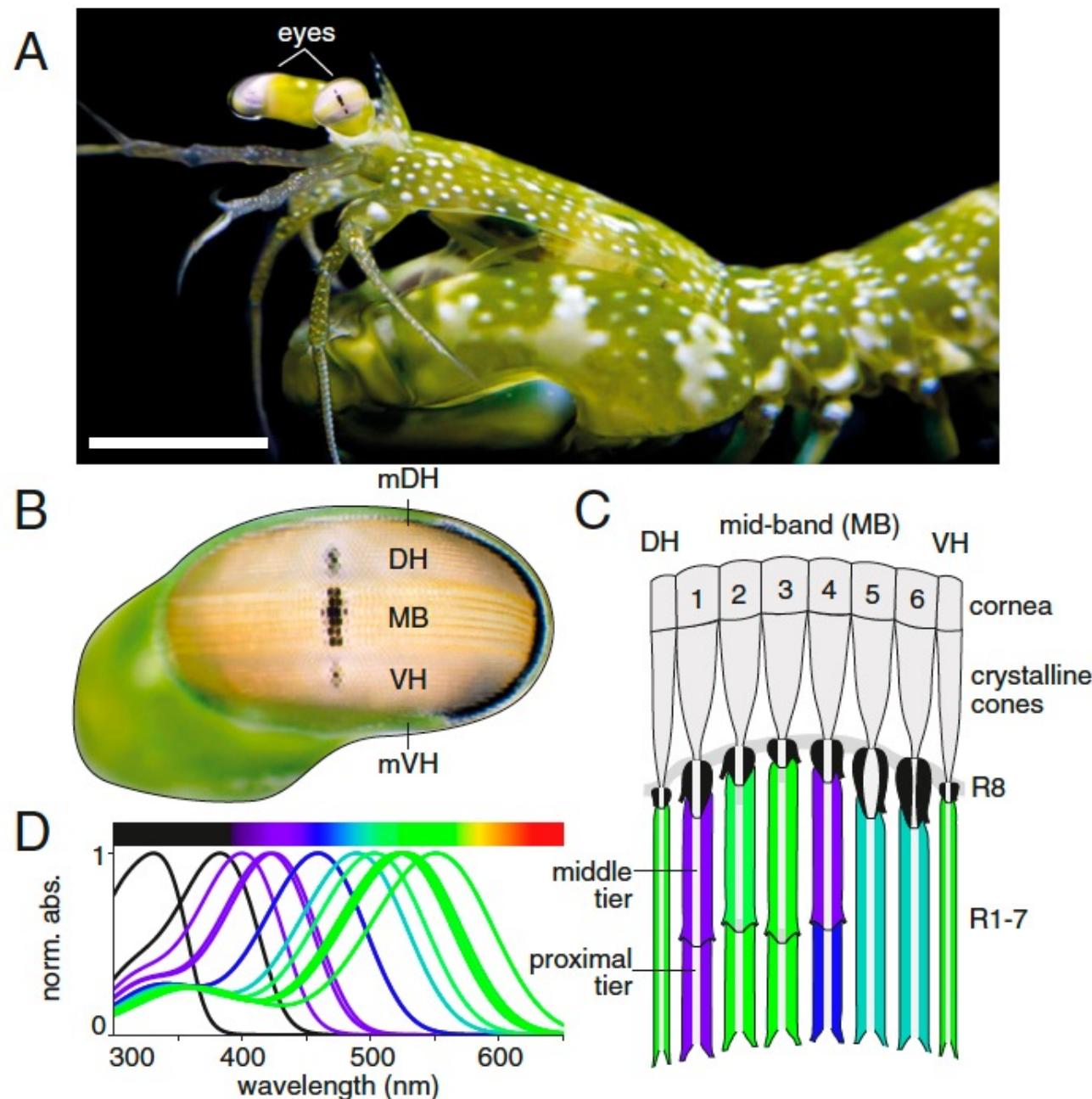
# Differential Gene (DGE) Expression in LEO

- How is gene expression different between a control group and an experimental group?
- Control = ground
- Experimental = LEO (low-Earth orbit)
  - Space shuttles
  - International Space Station
- Capture and sequence mRNA from each group
- Identify genes with significant differential expression
- → Insight into astronaut health issues



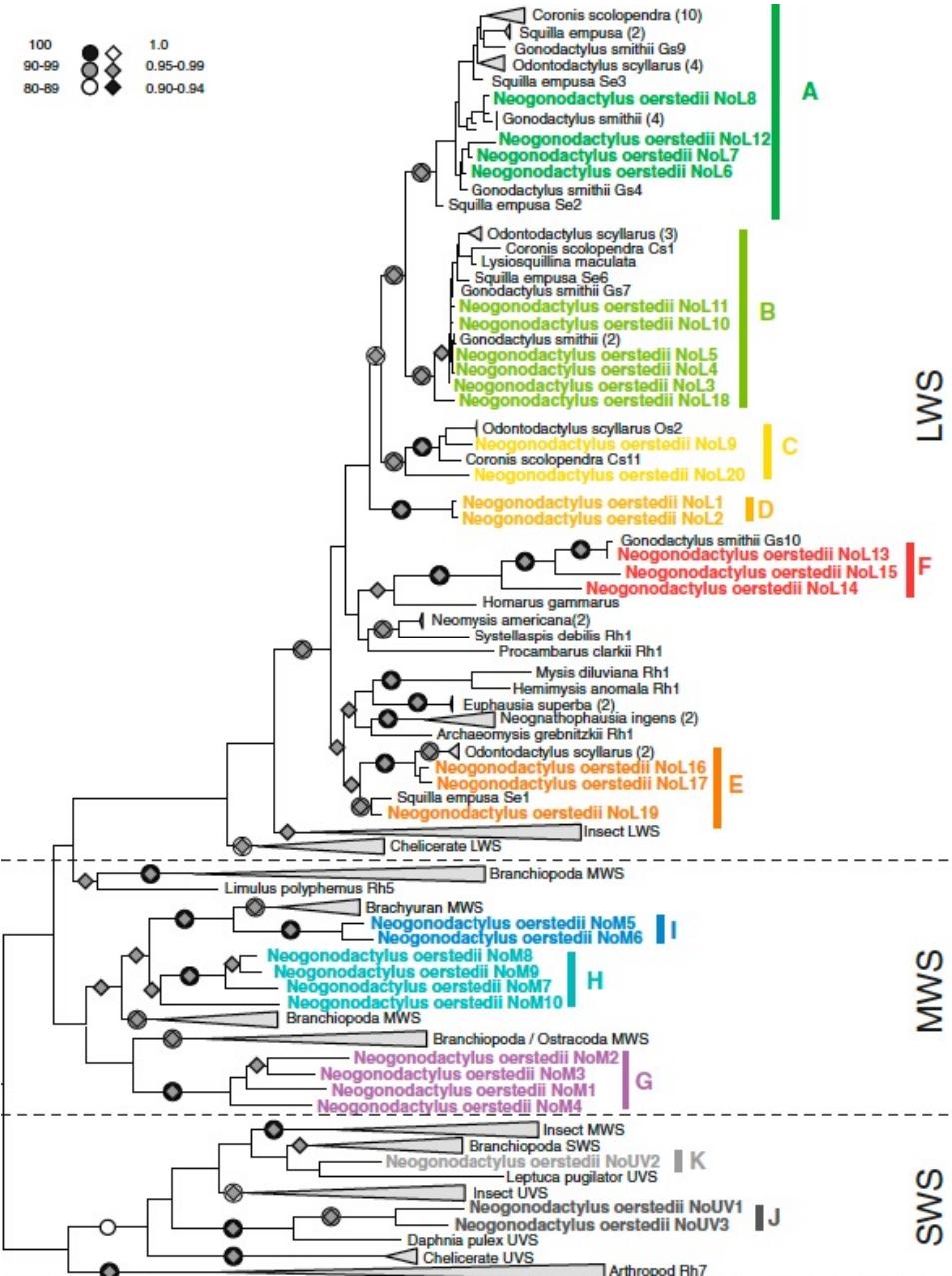
# Mantis shrimp eye

- From Porter et al., PNAS 2020.
- *Neogonodactylus oerstedii*: The most sophisticated eye on the planet.
- Scale bar in A is 5 mm.
- Many kinds of receptor pigment (33 versus 3 in humans), sensitive to different ranges of light color: ultraviolet through red.
- Study by measuring expression of different opsin genes in different parts of eye.



# Why transcriptomics?

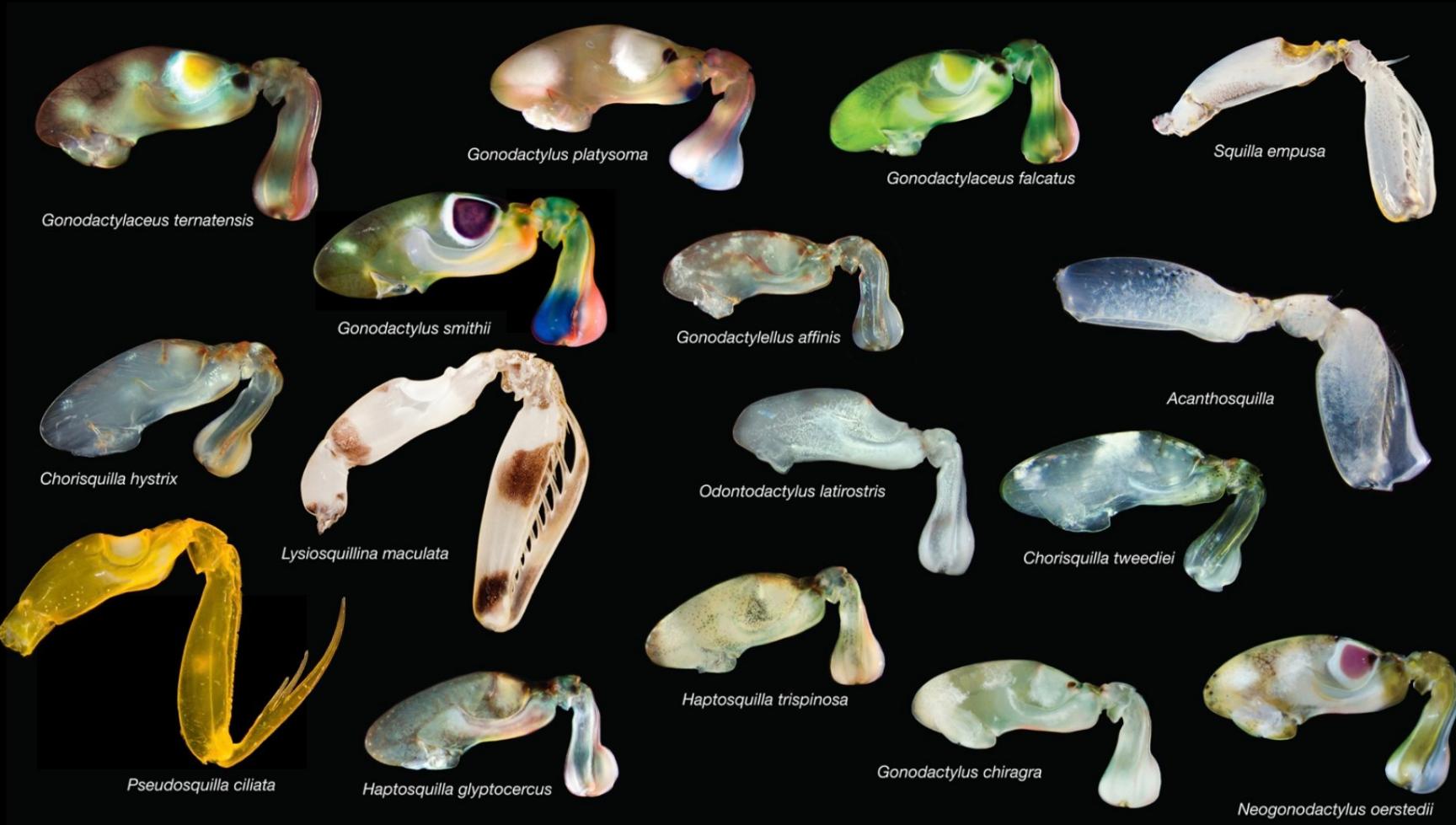
- Genomics would be so much easier!
  - Genome is the same in all cells, so don't have to sequence 33 cell types.
  - Sequencing genes is easier than sequencing mRNA.
- With transcriptomics, you learn what opsins are being expressed in each cell type.
- Genomics only tells you what genes are present, not what genes are expressed.
- Genomics won't explain differences among cell types.



# Results

- LWS = long wavelength sensitive
  - Red, orange ... green
- MWS = middle wavelength sensitive
  - Cyan, blue, purple
- SWS = short wavelength sensitive
  - Ultraviolet
- Identified 15 new opsin proteins
- Sequences cluster by group and color

Those club arms must be really tough ... how are they made?



# Amini & al., 2019 PNAS: “A diecast mineralization process forms the tough mantis shrimp dactyl club”

Diecast: made by injecting material into a mold



Dactyl: from the Greek for finger



Polydactyl  
(many fingers)



Pterodactyl  
(wing finger)

# What is the molecular process of club formation?

- “Having established that proteins within the flexible membrane could regulate apatite nucleation and growth, we sought to identify and sequence these putative mineralization proteins...”
- Extracted mRNA from flexible membranes immediately after shedding.
- “We identified five proteins containing chitin-binding domains in the club transcriptome one of which (*had*) no homology to any known protein, which we termed Club Mineralization Protein 1 (CMP-1).”

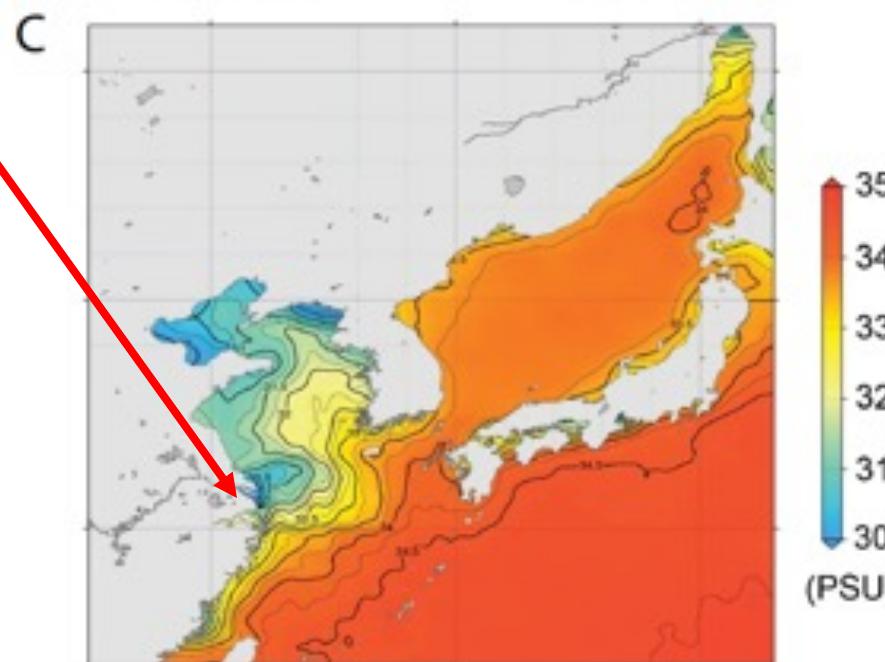
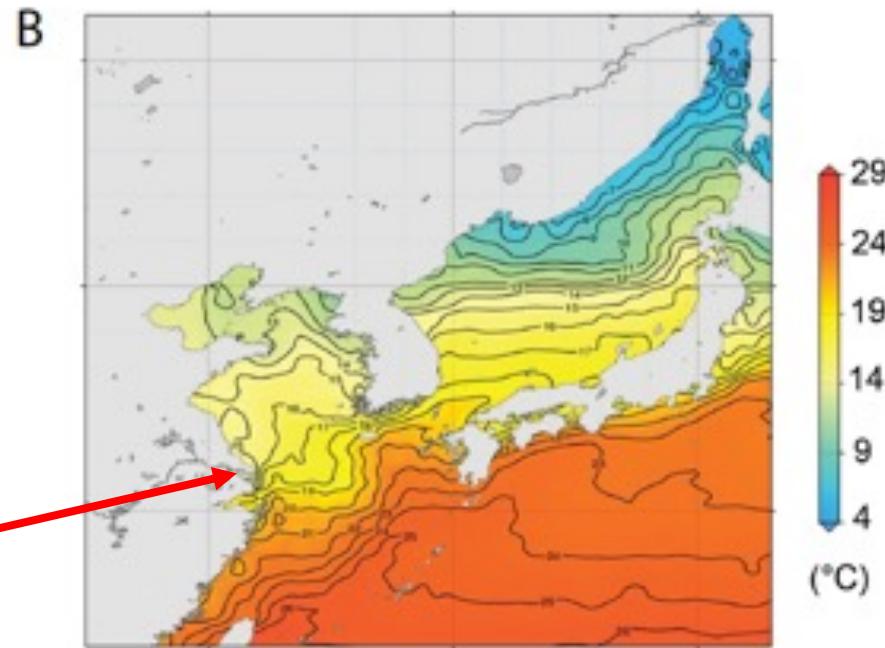
# Insights into adaptive divergence of Japanese mantis shrimp *Oratosquilla oratoria* inferred from comparative analysis of full-length transcriptomes

Jiao Cheng<sup>1,2,3</sup>, Liwen Zhang<sup>4</sup>, Min Hui<sup>1,2,3</sup>, Yuan Li<sup>5</sup>  
and Zhongli Sha<sup>1,2,3,4\*</sup>

Frontiers in Marine Science  
Aug 2022

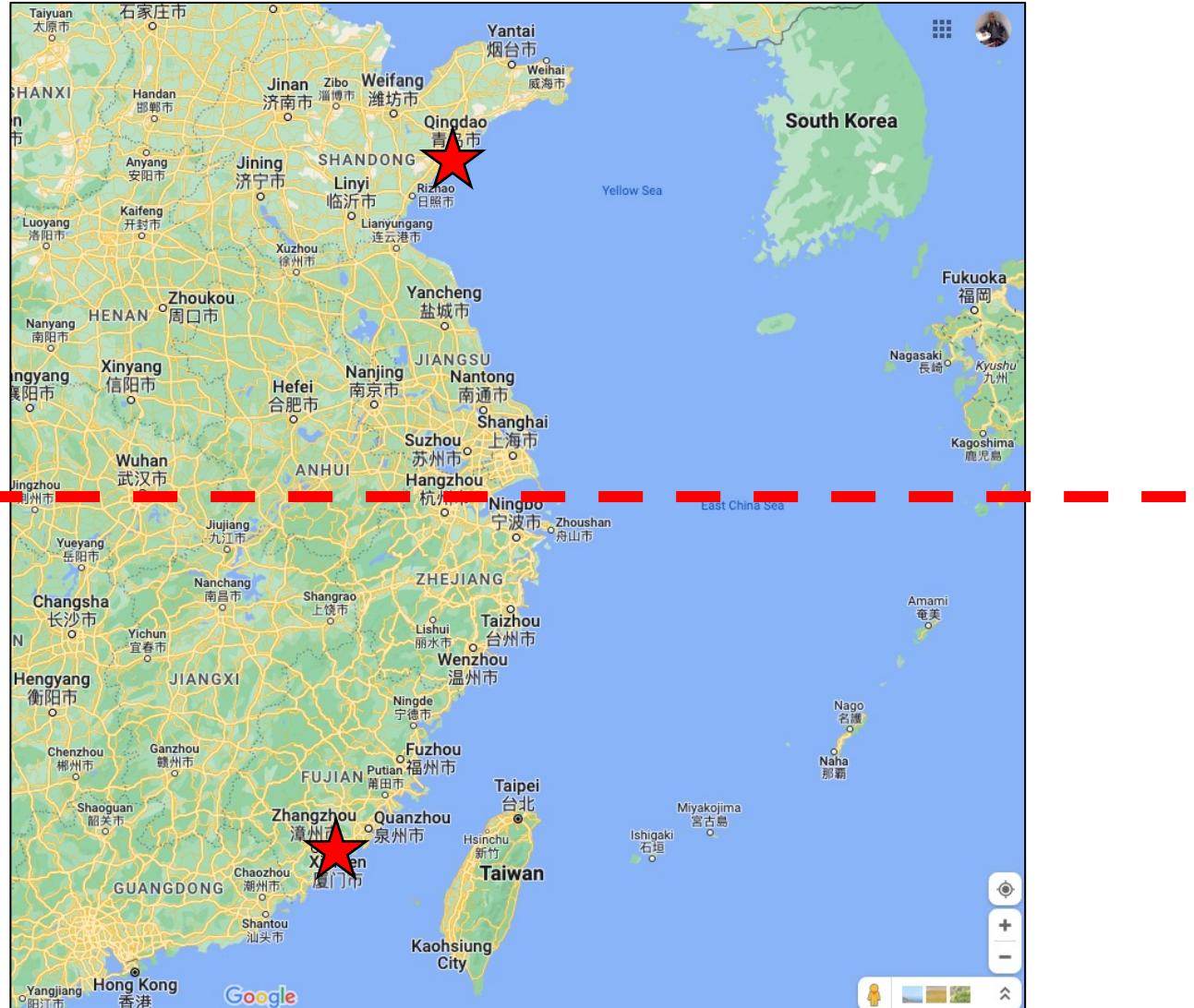


Horizontal  
thermocline/halocline  
north and south of the  
Yangtze River estuary



# Methods

- Collect individuals at Qingdao and Xiamen.
- All same species → expect (nearly) identical genomes, so sequencing DNA won't be informative.
- Sequence mRNA, determine differentially expressed genes.



# Results

- Identified different genes between north & south groups that appear to be undergoing positive or purifying selection
  - Positive selection: an advantageous trait spreads through a population
  - Purifying selection: a disadvantageous trait is removed from a population
- Identified genes are involved in stress response, immunity, cytoskeletal organization
- Water temperature difference is a more important factor than salinity

# Opening Thought Question – 4/20

Transcriptomics has helped to reveal several mantis shrimp mysteries.

What is one of the mysteries that we discussed in class, and how has transcriptomics helped to unravel this mystery?

We usually think of a kelp forest as looking like this...



But sometimes it looks more like this... WHY?

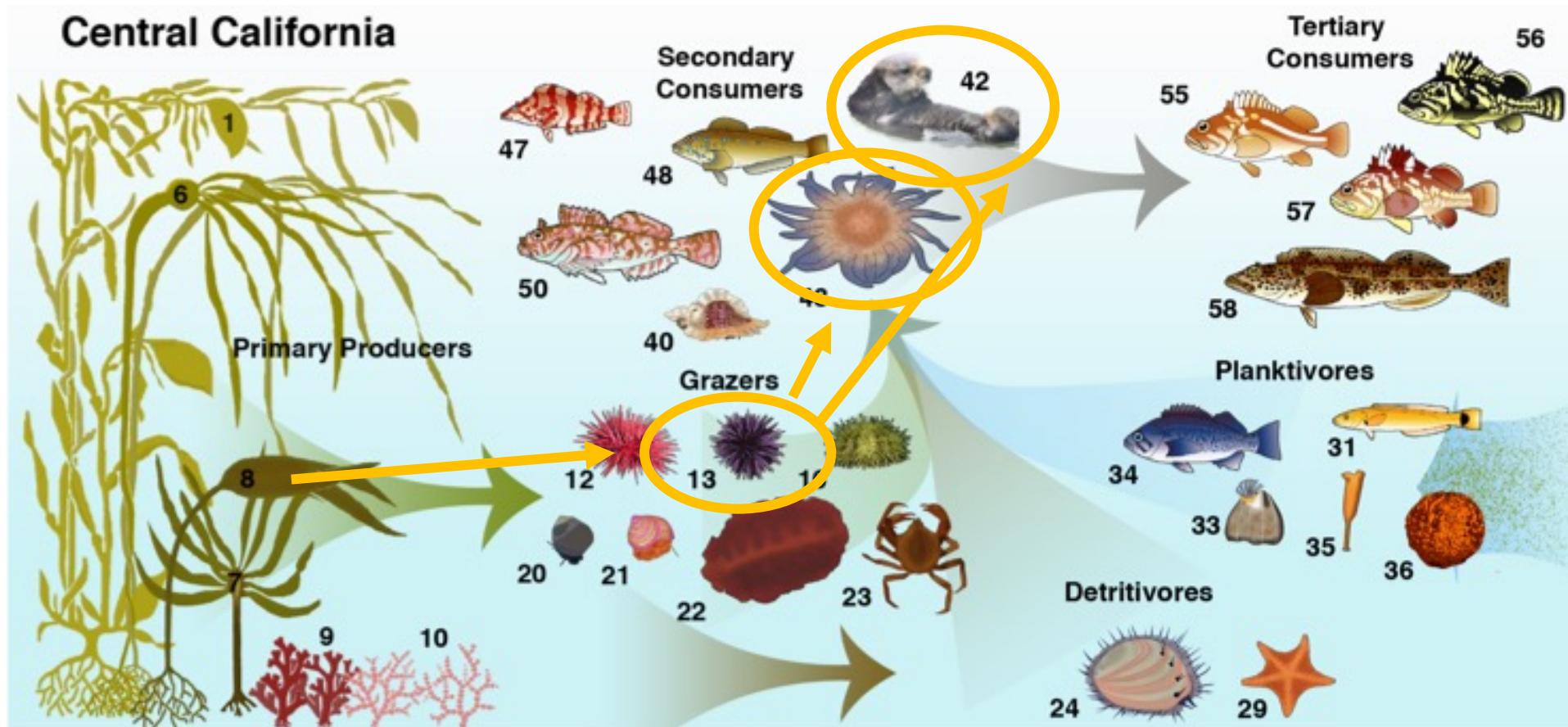


# Kelp forests, sea otters, and trophic cascades

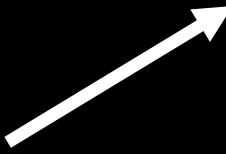
1. What is a trophic cascade?
2. What is a keystone species?
3. What is a genetic bottleneck and how does bioinformatics help to reveal these bottlenecks?

# The main players in kelp forests

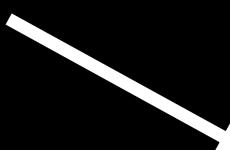
Who helps keep urchin populations from getting too large?



Otters  
present



Otters  
absent



# Sea otter historical range (pre-1940) and current range

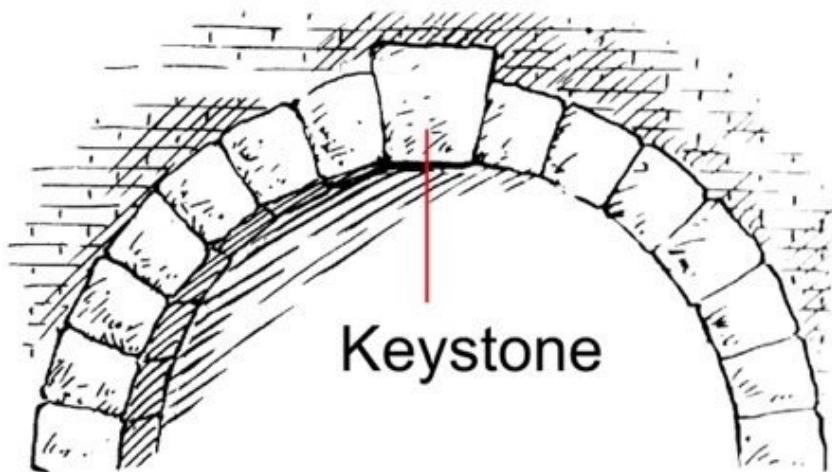


Sea otters have a huge effect on community composition



**Keystone species:** have an effect on community composition that is disproportionately large, given their abundance

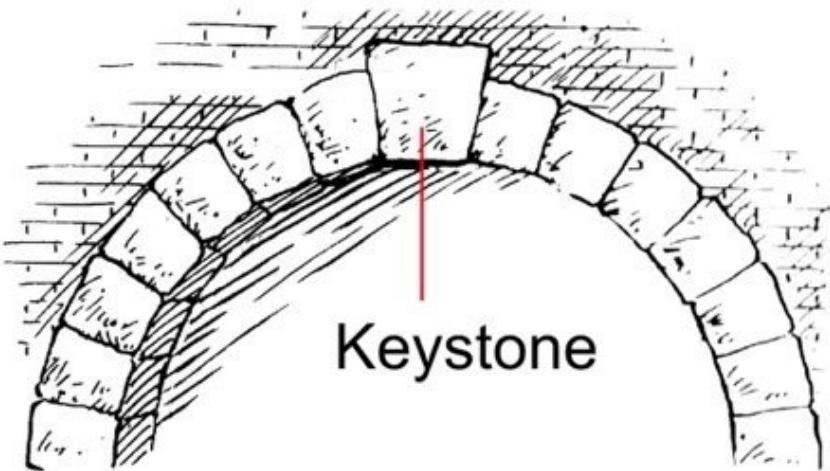
Keystone species: have a big effect despite low abundance



other examples of keystones in nature



Keystone species: have a big effect despite low abundance



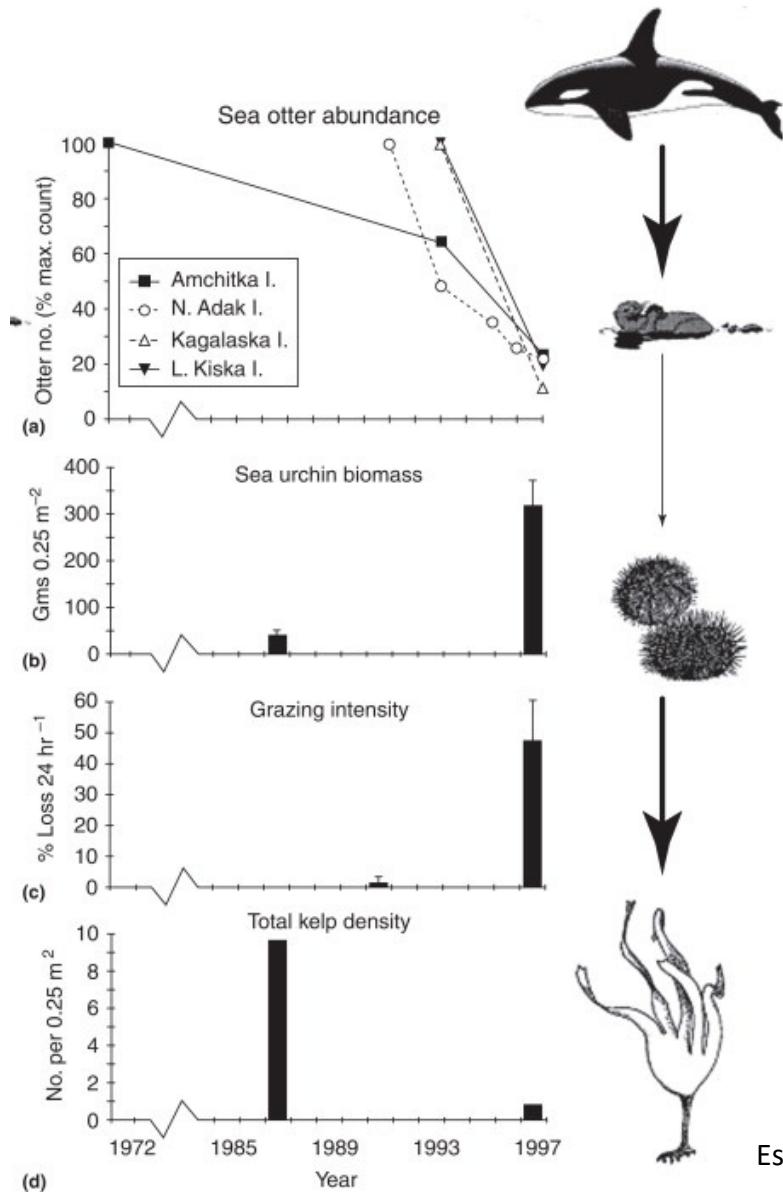
in contrast

Foundation species: have a big effect because of their abundance/size



Trophic Cascade: indirect control of basal species biomass (e.g., primary producers) by high order consumers (e.g., carnivores)

- effects propagate over two or more trophic levels



Adding a new trophic level  
reverses the switch, back  
to barrens

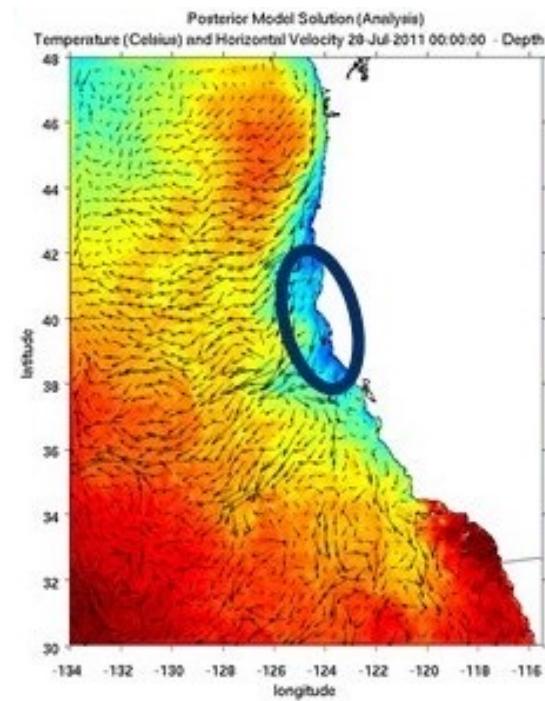
But you can get kelp  
forests even in the  
absence of otters... what  
else controls urchin  
grazing?

# What has been happening on along the coast of California in recent years?

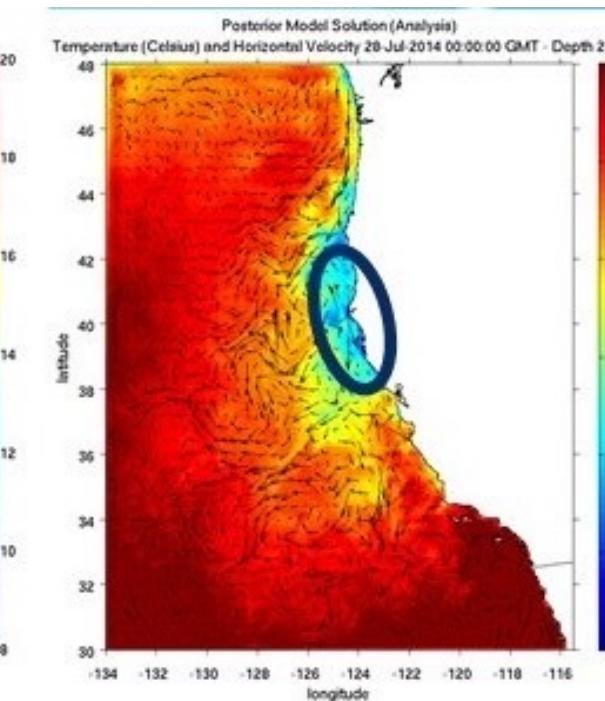
Observations:

1. Few otters in Northern California and currently few kelp forests
2. No otters in Southern California and currently recovering help forests

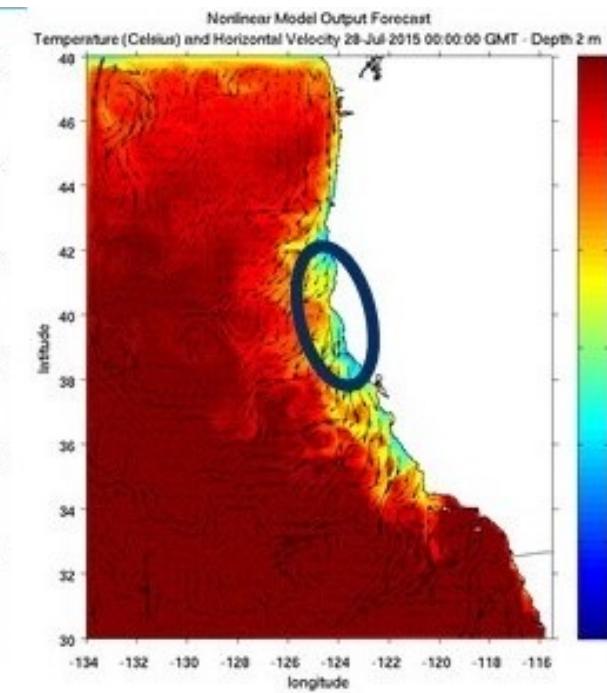
# Decline of kelp forests due to high temperatures across California



**July 28, 2011**  
**Normal Conditions**

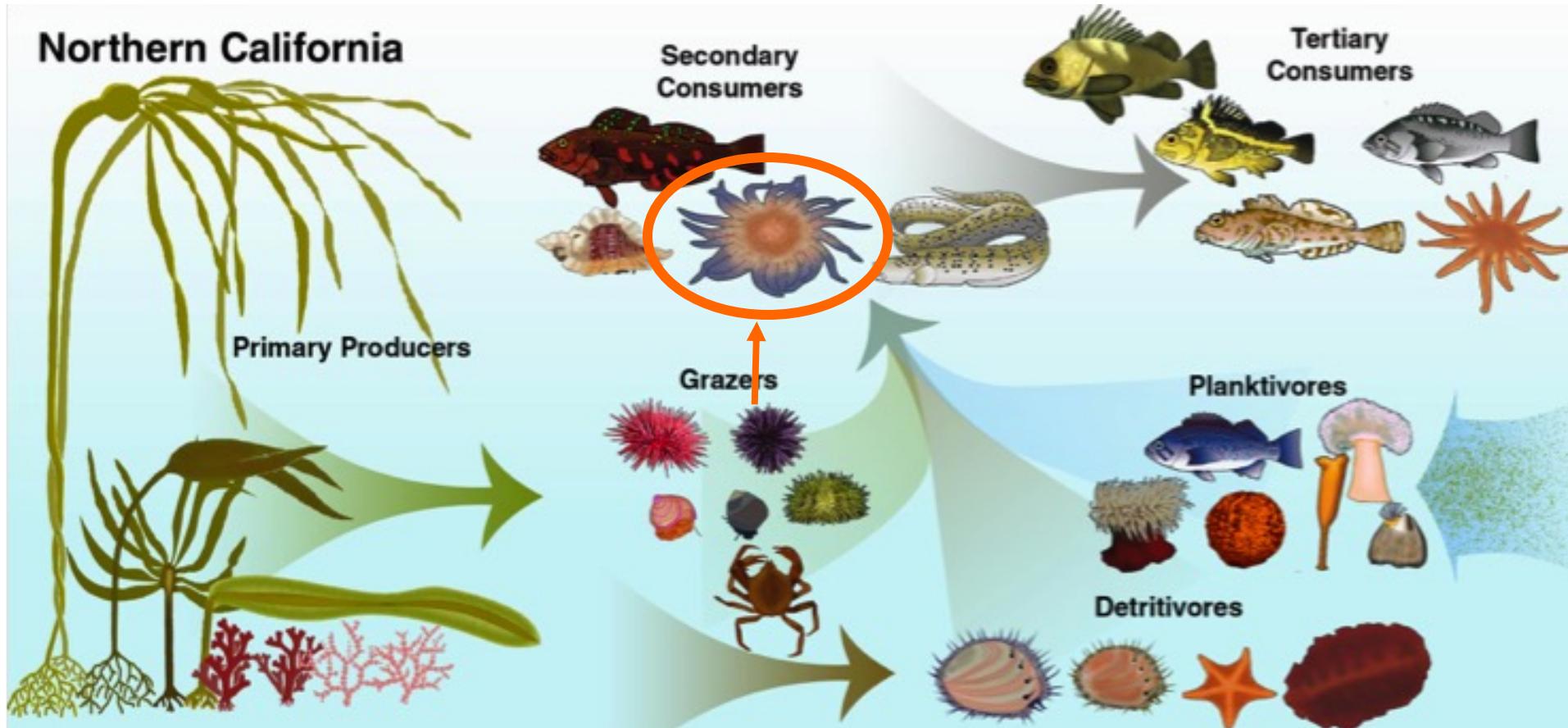


**July 28, 2014**  
**“Warm Blob”**



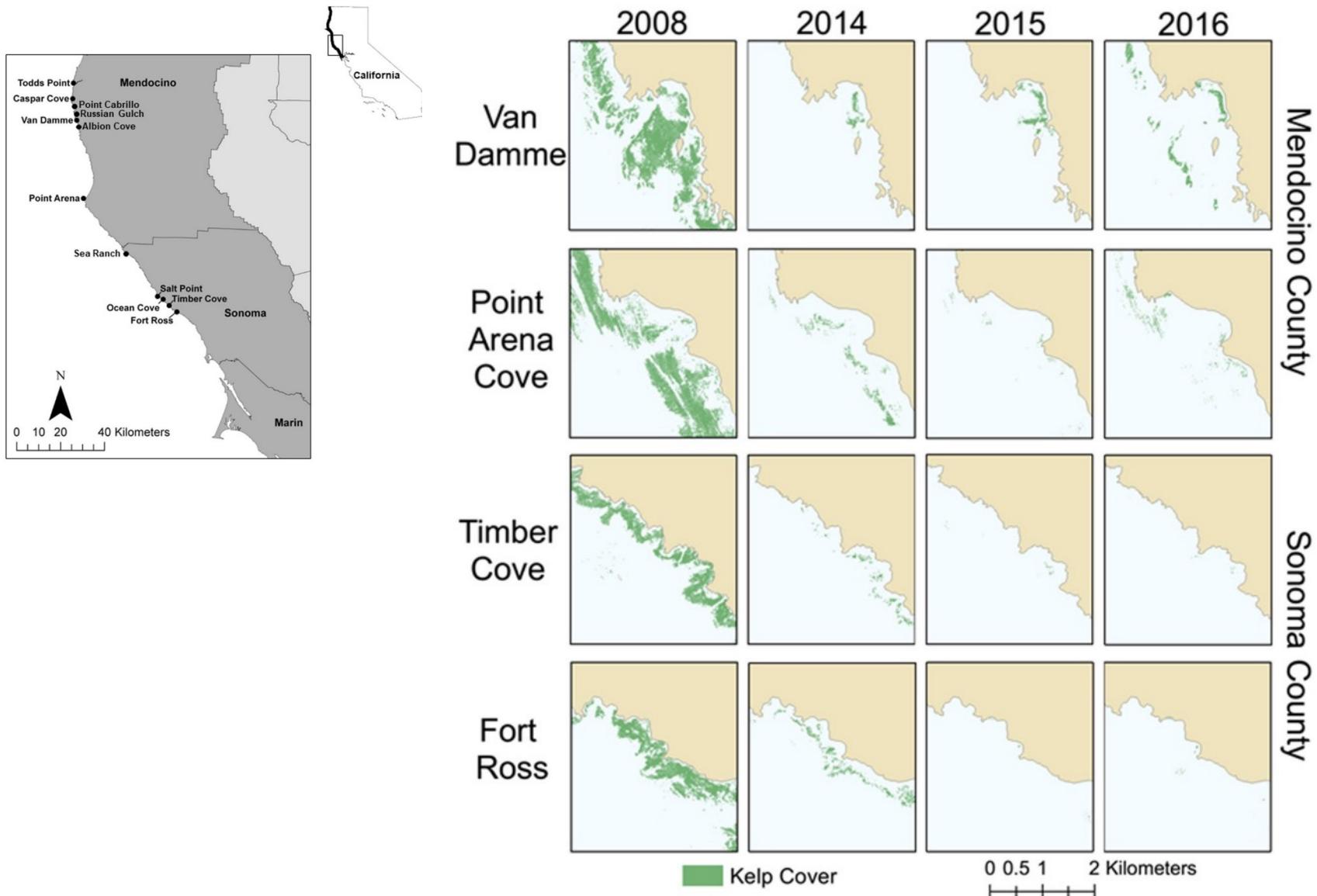
**July 28, 2015**  
**“Warm Blob” + Strong El Niño**

# Typical Northern California food web with bull kelp

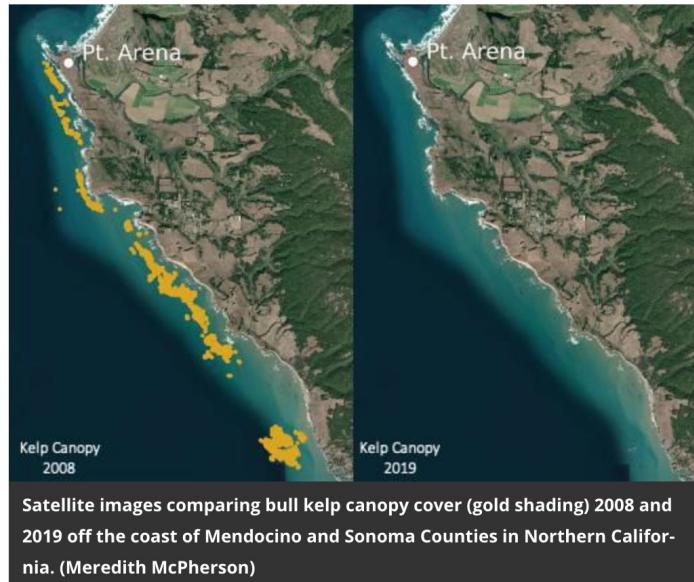
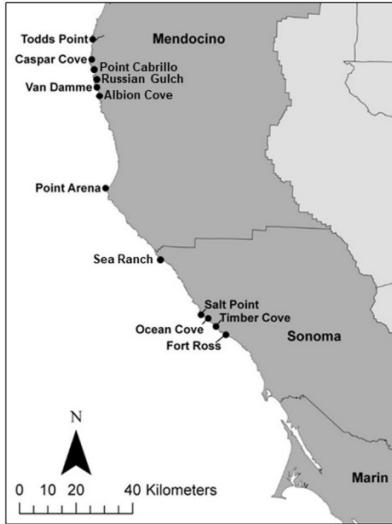


Few otters present, but also have *Pycnopodia* (sunflower star) as main urchin predator

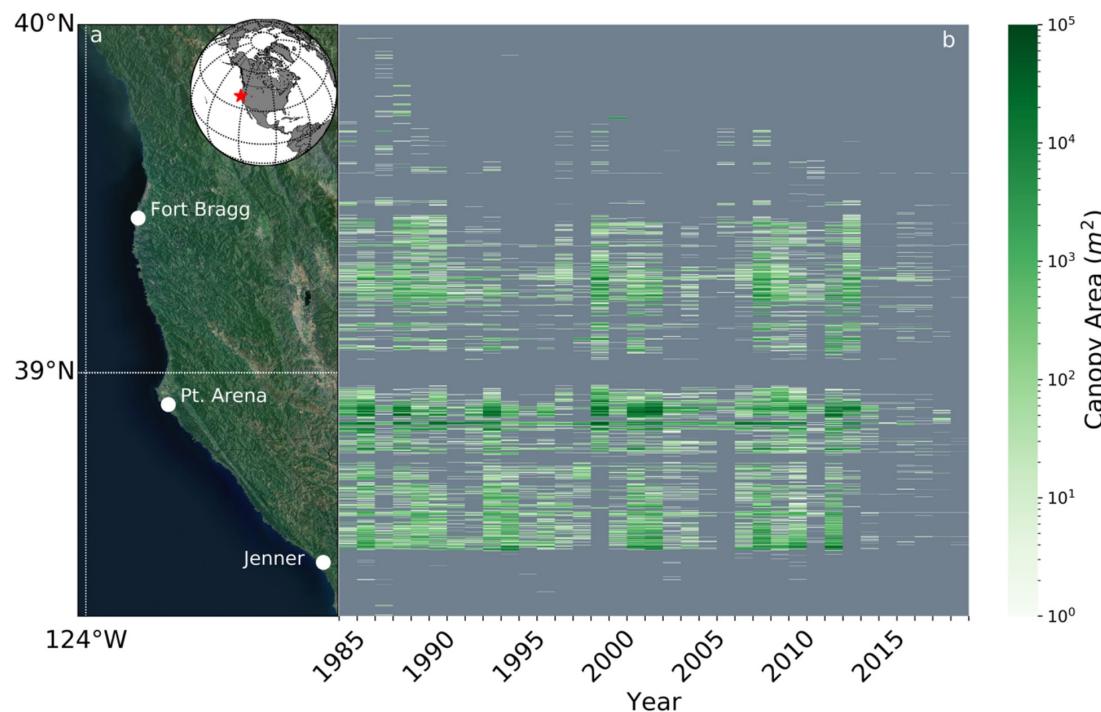
# Kelp forest decline in Northern California

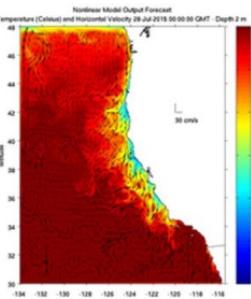
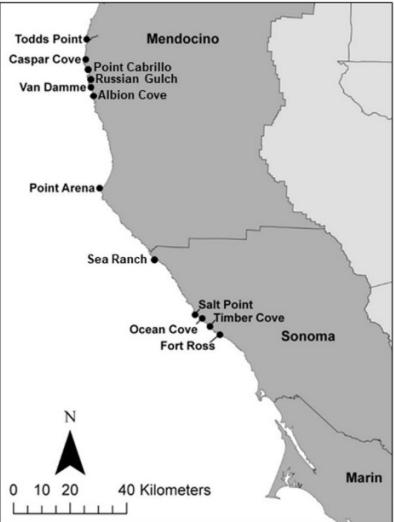


# Kelp forest decline in Northern California

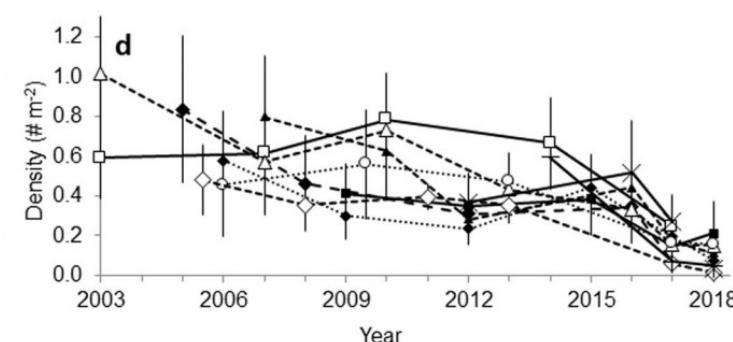
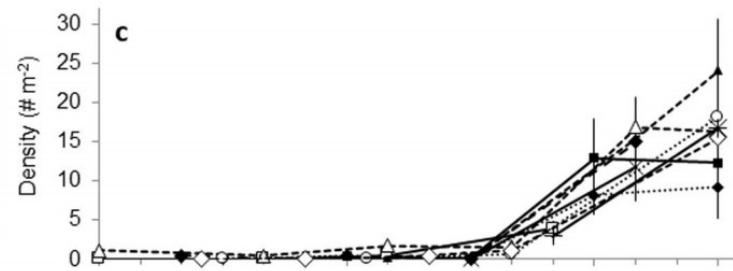
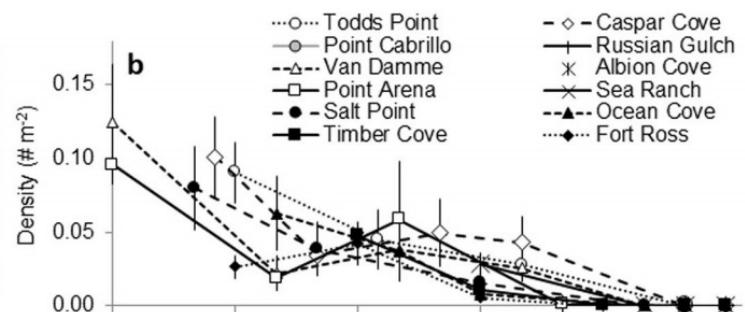
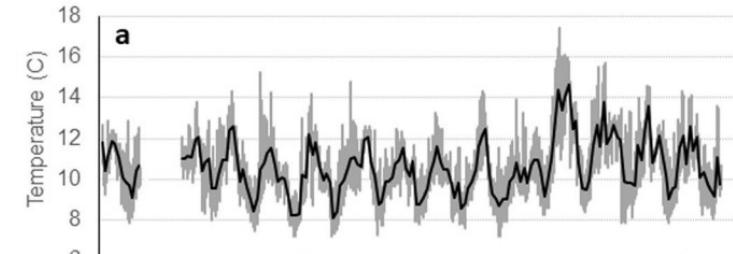


Satellite images comparing bull kelp canopy cover (gold shading) 2008 and 2019 off the coast of Mendocino and Sonoma Counties in Northern California. (Meredith McPherson)

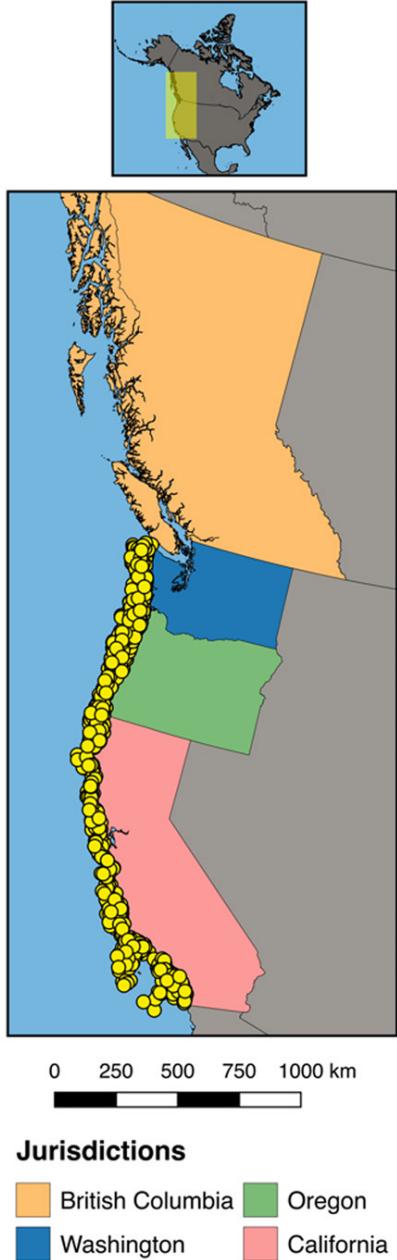
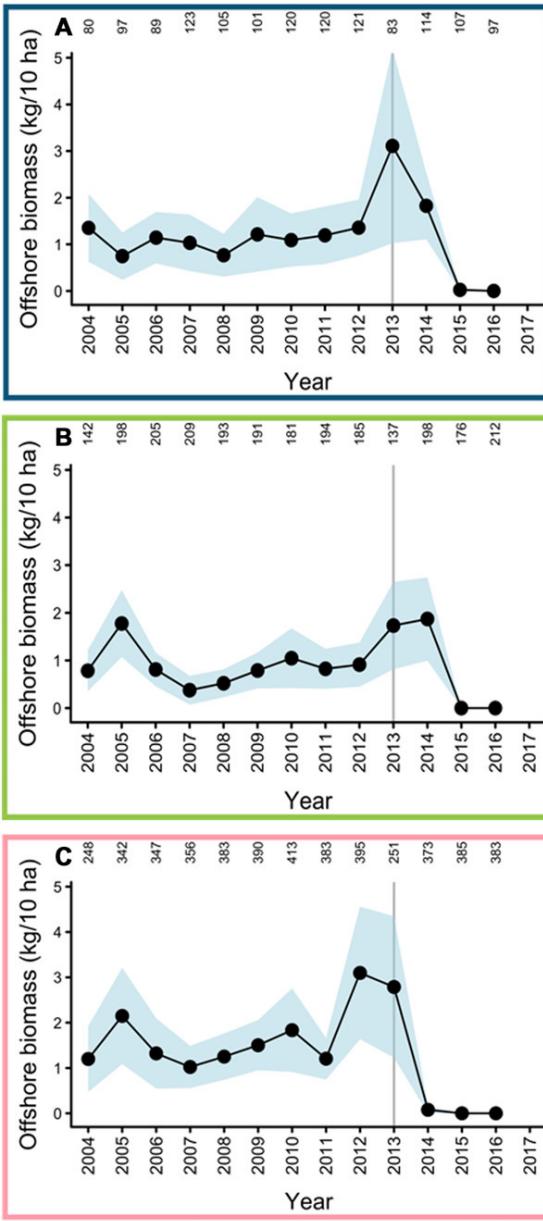




Warm waters coincided with decrease in sunflower star and abalone densities and increase in urchin densities



## sunflower star biomass

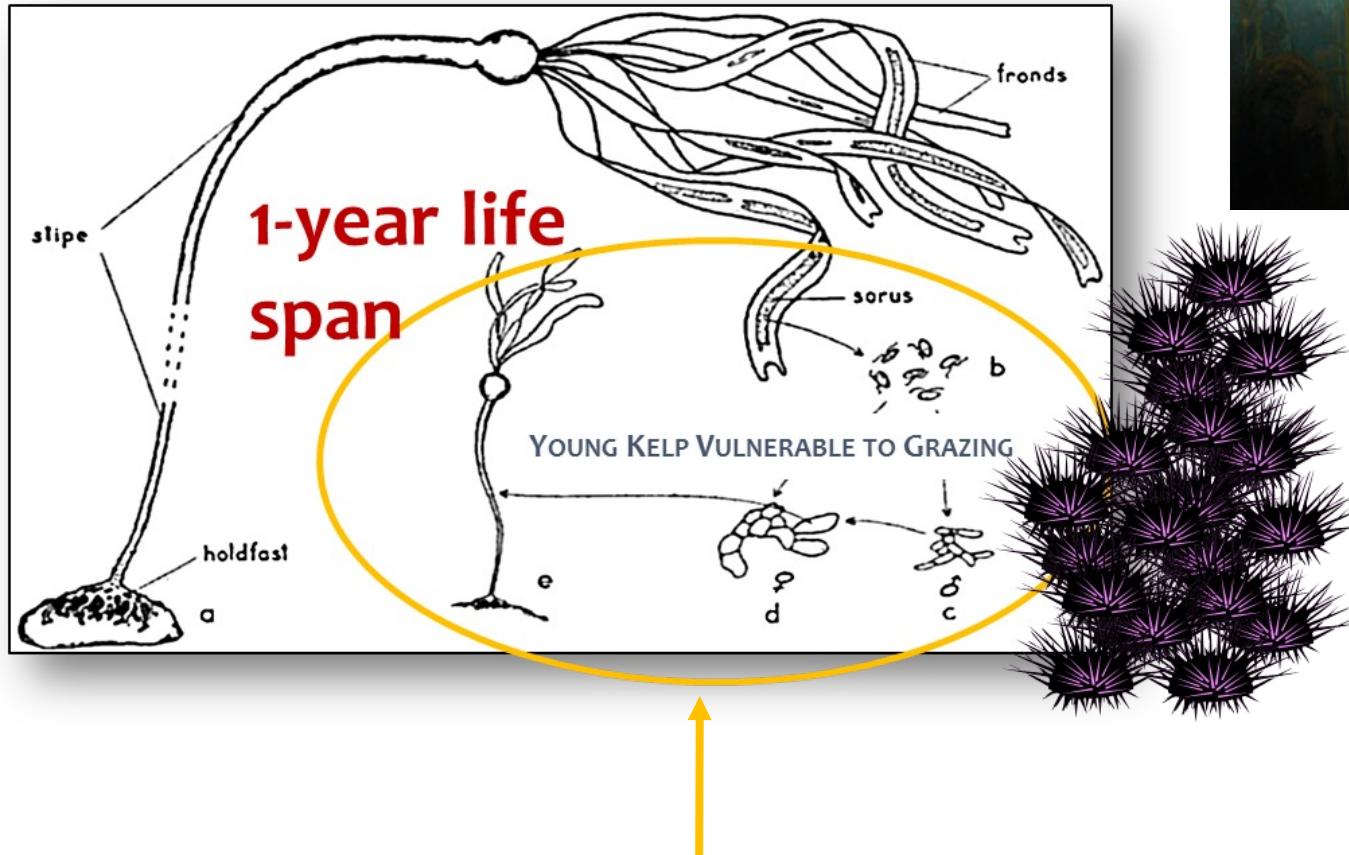


*Pycnopodia* sunflower star

Bull kelp recruits and urchin predators have been wiped out

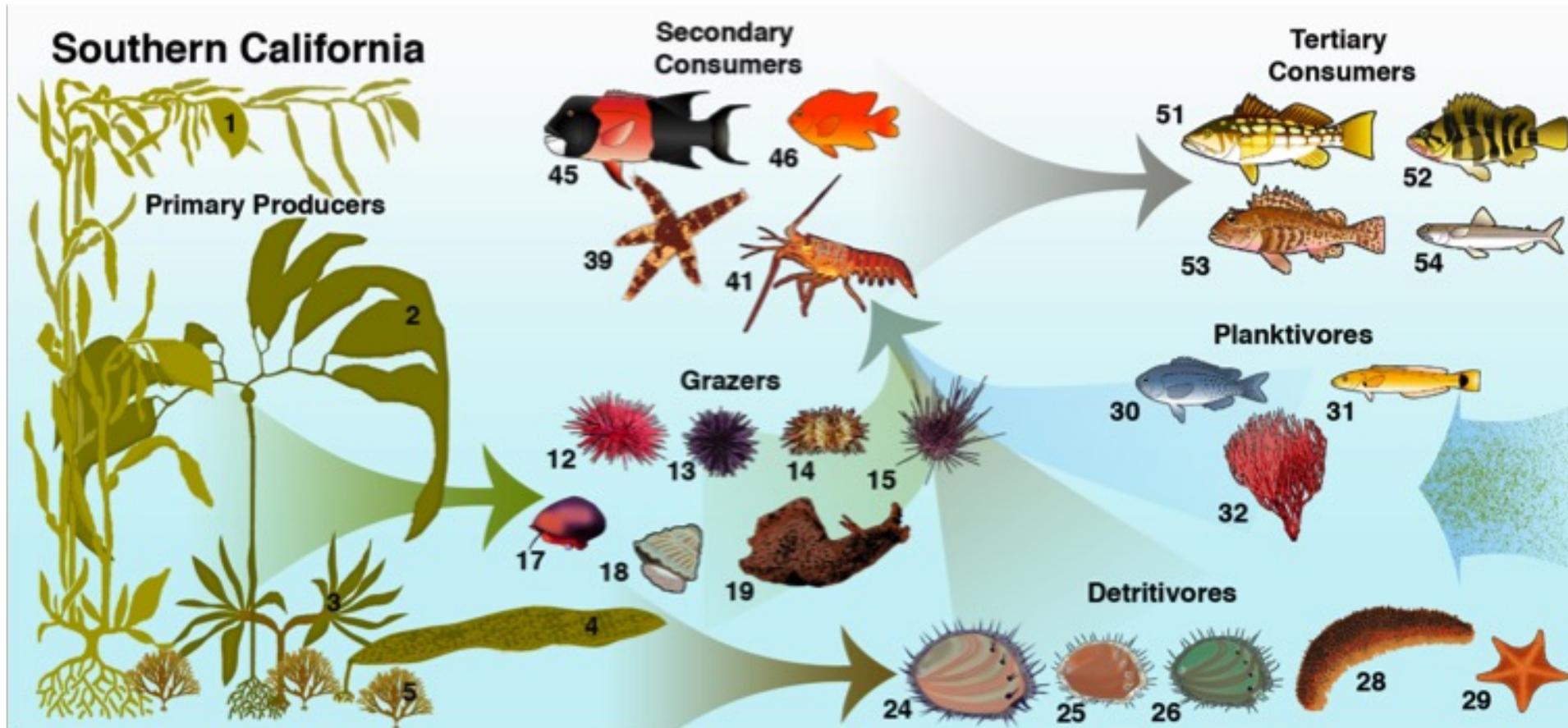
Harvell et al. 2019

Bull kelp is an annual species meaning that it must settle and re-establish every year



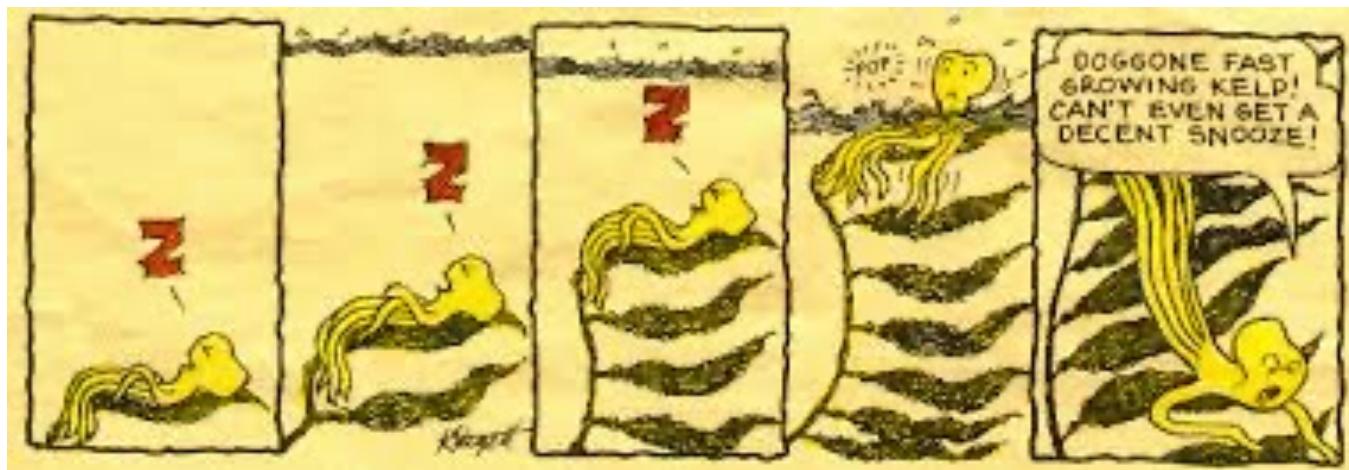
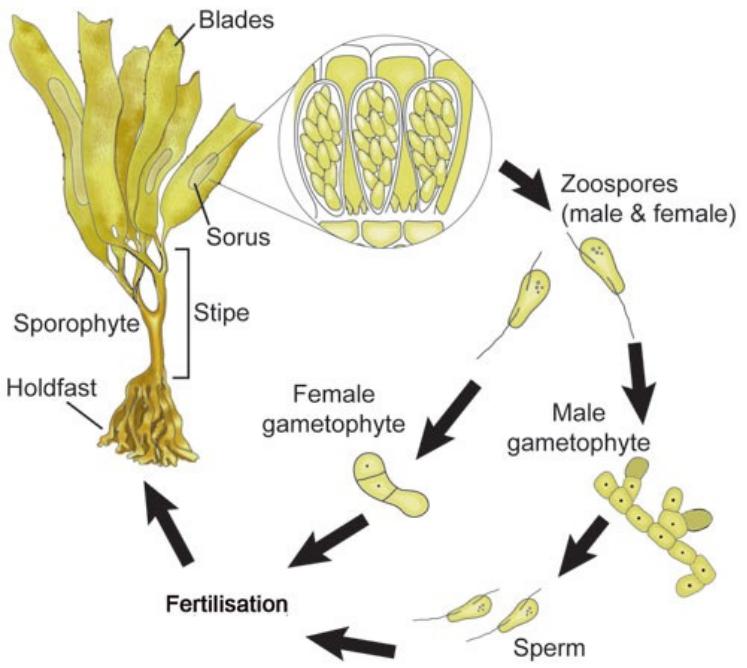
Young kelp are vulnerable to urchin grazing

# Typical Southern California food web with giant kelp

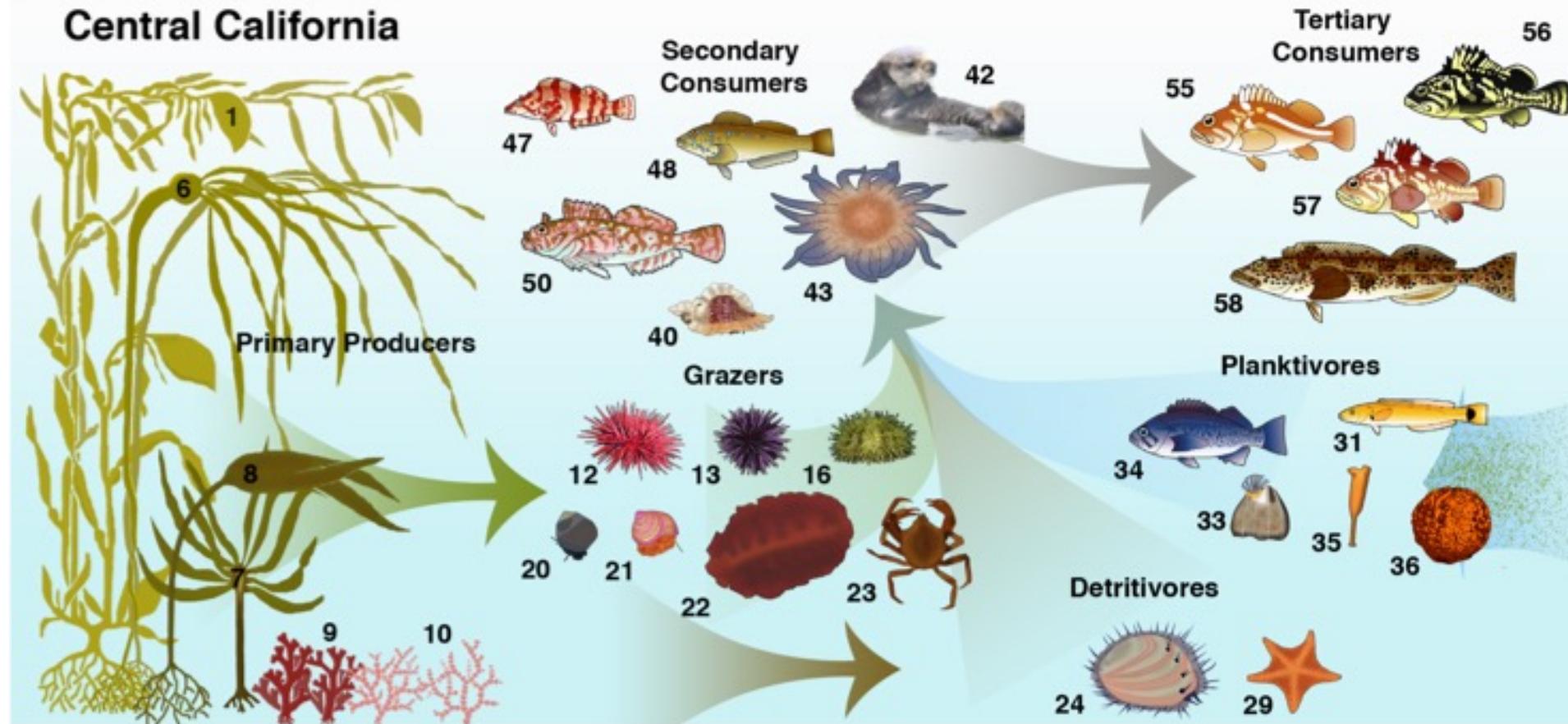


No otters present, *but* have lobsters, sheepshead wrasse, sunflower seastars and as main urchin predators

Giant kelp is a perennial species meaning that once it settles, it will usually become established and keep growing for a number of years



# Typical Central California food web with both giant and bull kelp

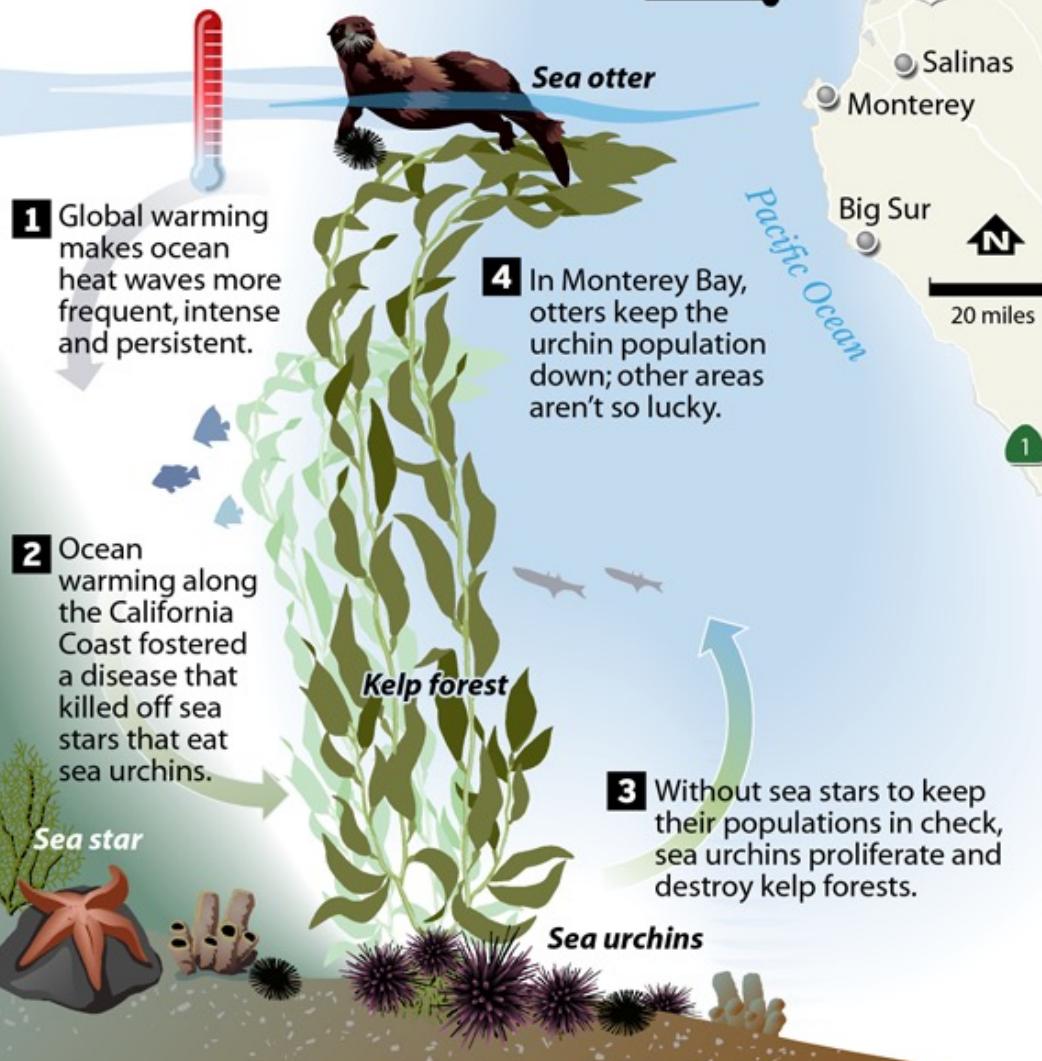


Otters are present as main urchin predators, sunflower sea star populations still recovering

# Vicious Cycle

Oceans have absorbed about 93 percent of the heat trapped by Industrial Age greenhouse gas pollution, with devastating consequences for marine life.

## CYCLE OF EVENTS



# The Sea Otter Bottleneck



Siberian Husky: 4,000 hairs per square inch



Norwegian Forest Cat: 9,000 hairs per square inch



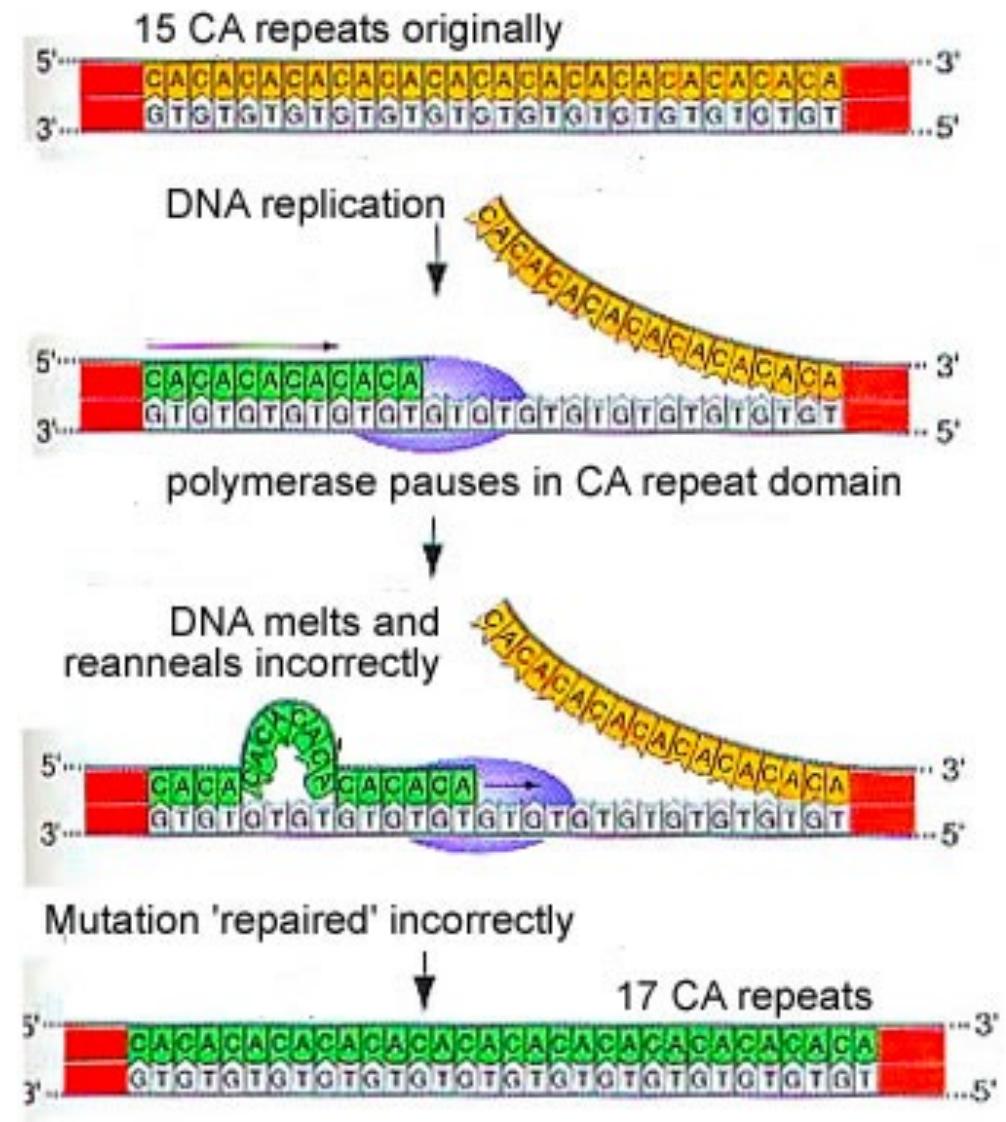
Mink: 45,000 hairs per square inch



Sea otter: 1,000,000 hairs per square inch

# Microsatellites: a tool for reconstructing population bottlenecks

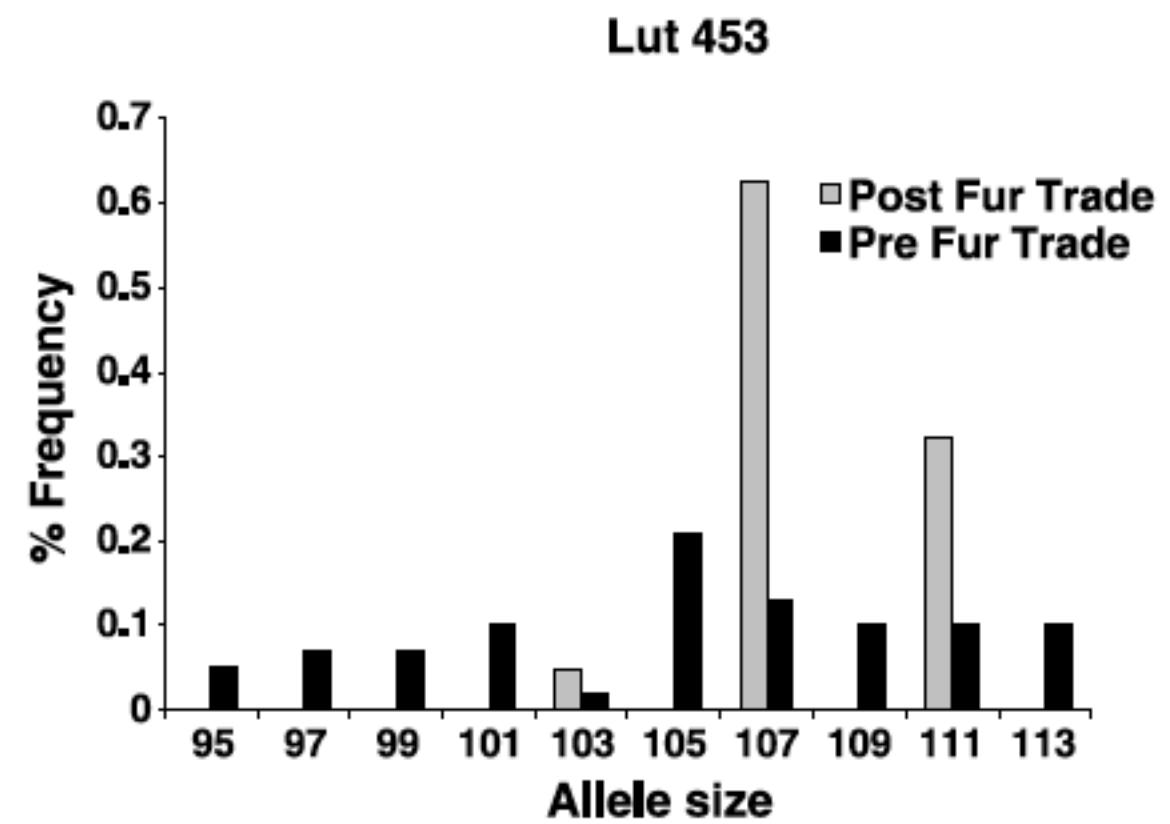
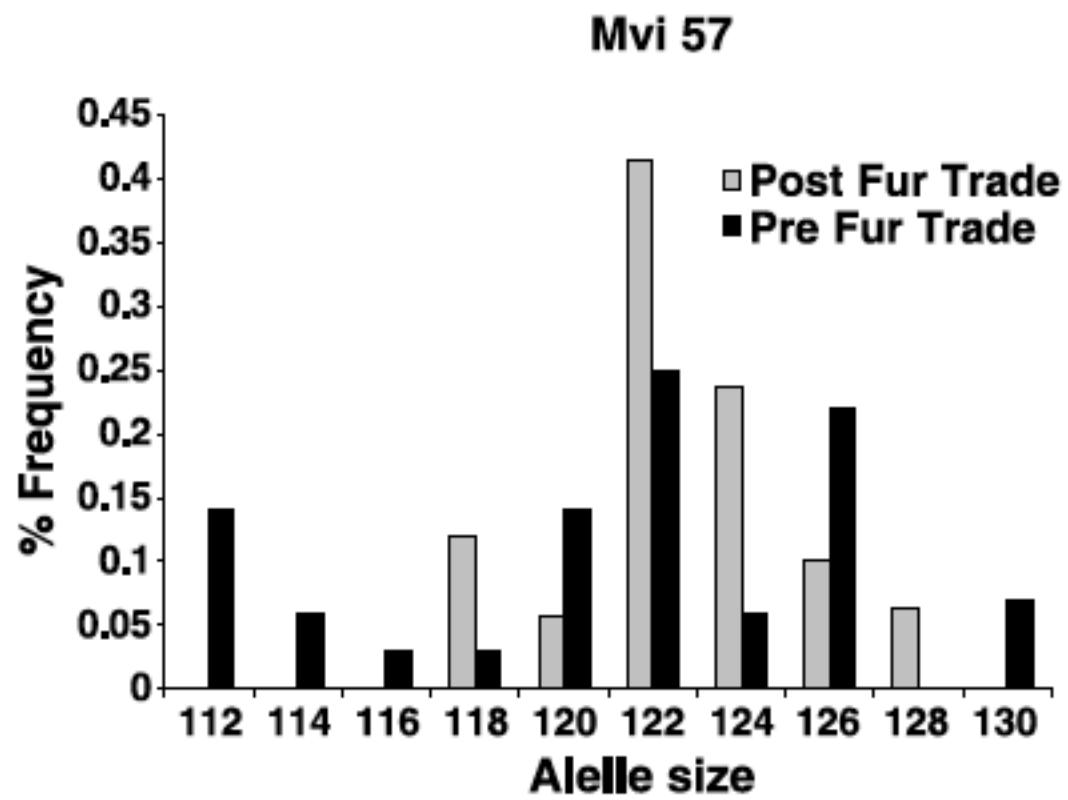
- Short Tandem Repeats (STRs)
  - Microsatellite: repeating pattern of 1-6 nucleotides
  - Minisatellite: repeating pattern of 10-100 nucleotides
  - Macrosatellite: repeating pattern of 100-1000 nucleotides
- Caused by polymerase slippage
- Higher than average rate of mutations that gain or lose a repeat
- Mutation rate is a good match for evolutionary history after recent events



# The experiment

- Control: DNA from remains of 34 individuals from before the fur trade.
- Experiment: 5 current sea otter populations.
- Sequence 4 microsatellites.
- Hypothesis: sea otters from before the fur trade will show more genetic variation than those from current populations.

# Results (2 of the 4 microsatellites)



# Conclusions

- Sea otter population is recovering to low end of estimated pre-hunting counts.
- Genetic diversity is significantly lower than pre-hunting, which can lead to...
  - Inbreeding depression (offspring inherit 2 copies of harmful genes, zero copies of healthy allele).
  - Increased probability of extinction (local population or species) due to random events.
- “We recommend continued monitoring of wild sea otter populations...”

# Opening Thought Question – 4/25

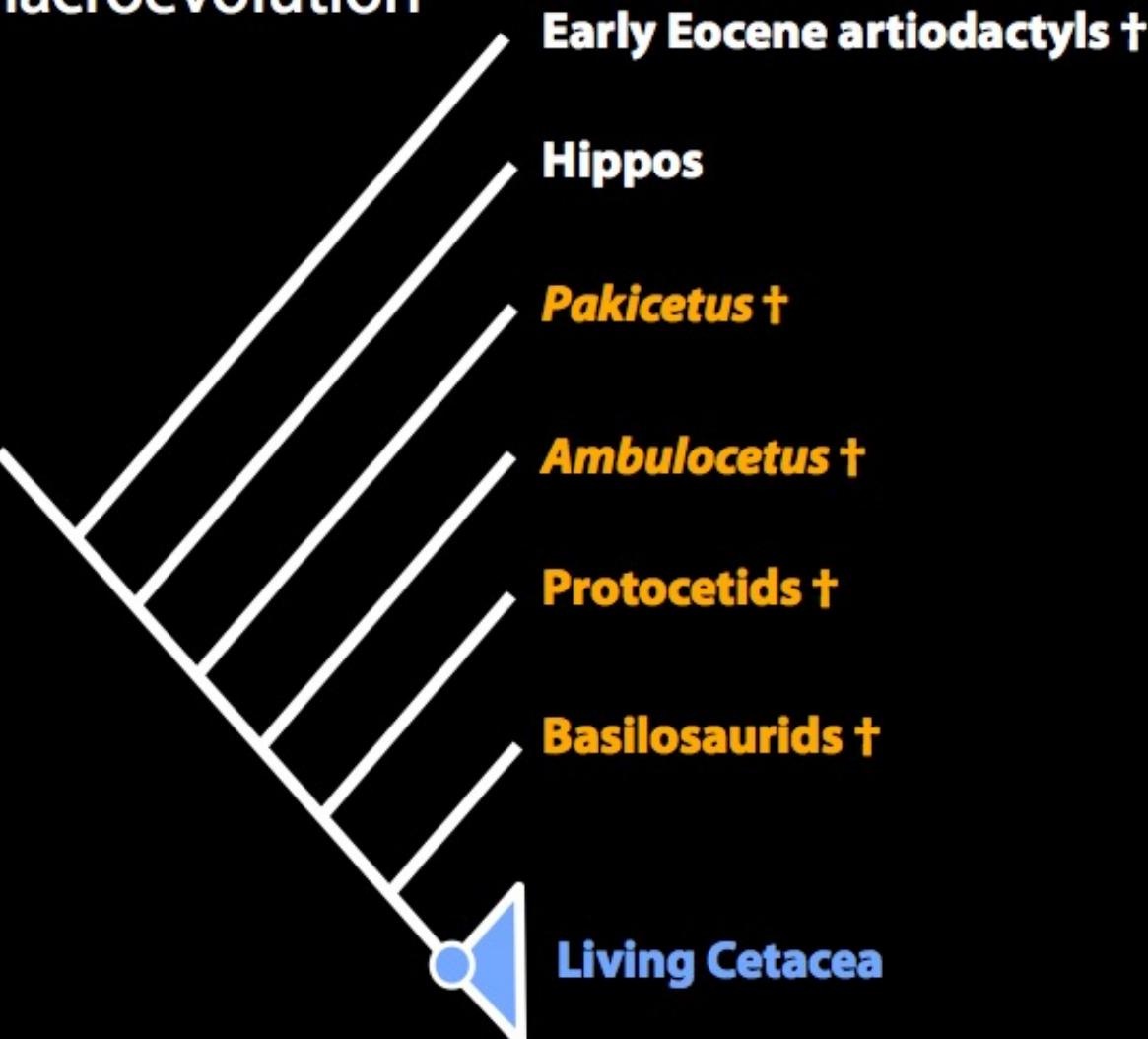
Last week we learned that sea otters underwent a genetic bottleneck.

1. What is a bottleneck? (Define bottleneck)
2. Predict whether sunflower sea stars have experienced a bottleneck due to sea star wasting disease.
3. How would you test your prediction?

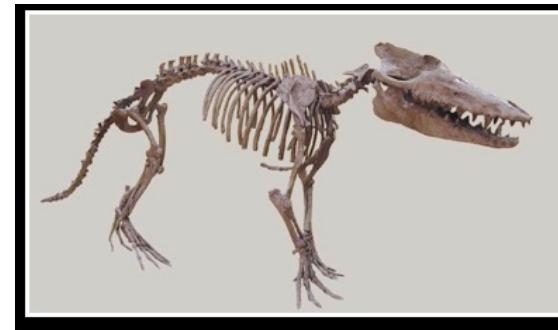
# What are Marine Tetrapods?

- “Four-footed”
  - Evolved from ancestors with 2 sets of limbs
- Terrestrial ancestry
- Obtain food from the sea
- Seabirds, Marine Reptiles, Marine Mammals

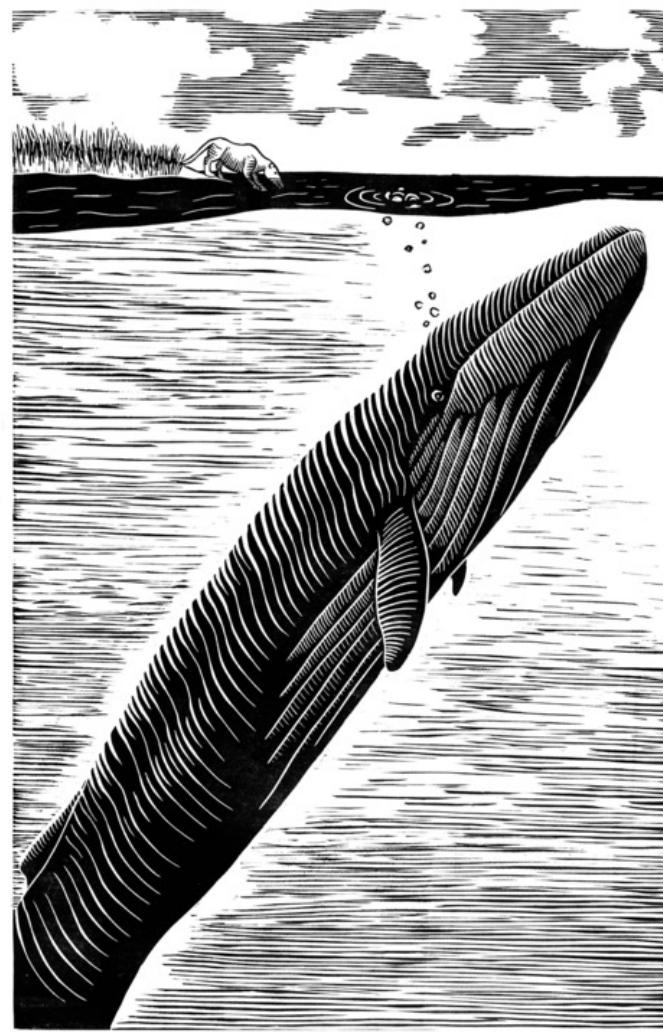
# macroevolution



Slide for Kitzmiller v. Dover, 2005; available online at NCSE

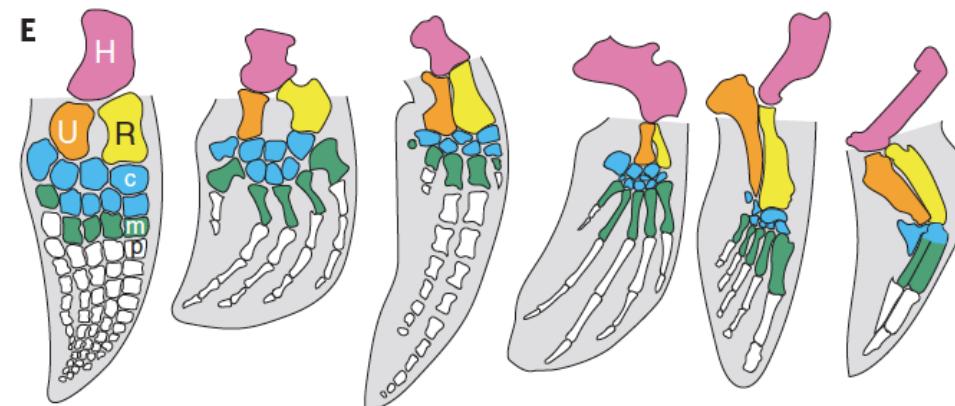


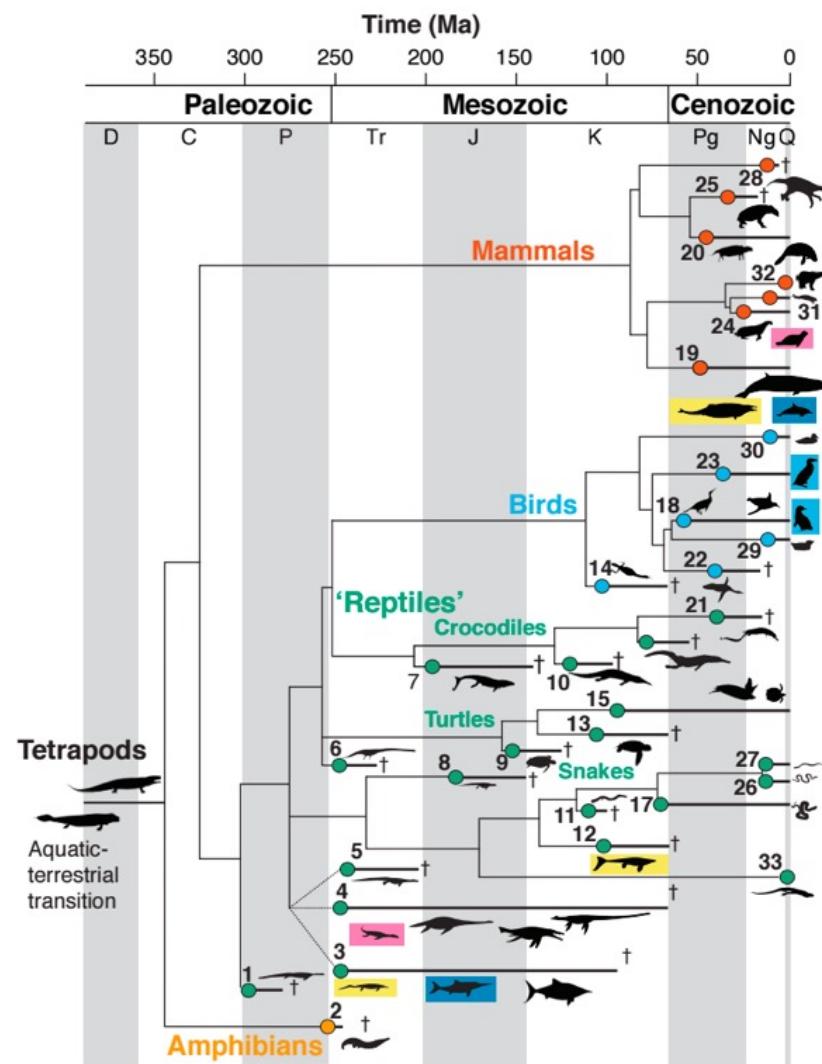
Art by Carl Buell & Alex Boersma



# Adaptations to Oceanic Life

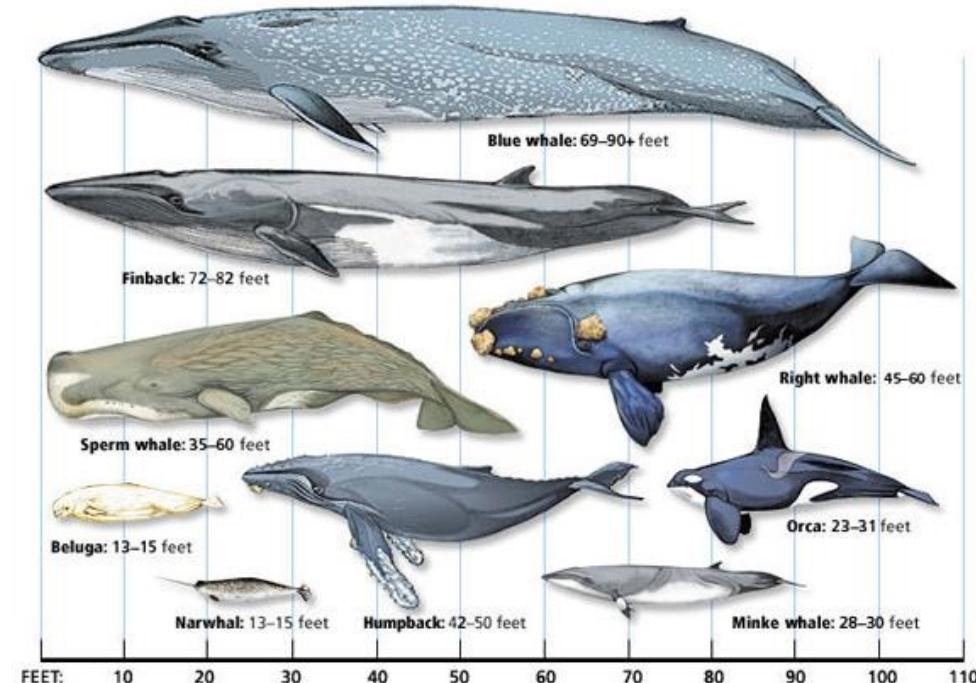
- Locomotion





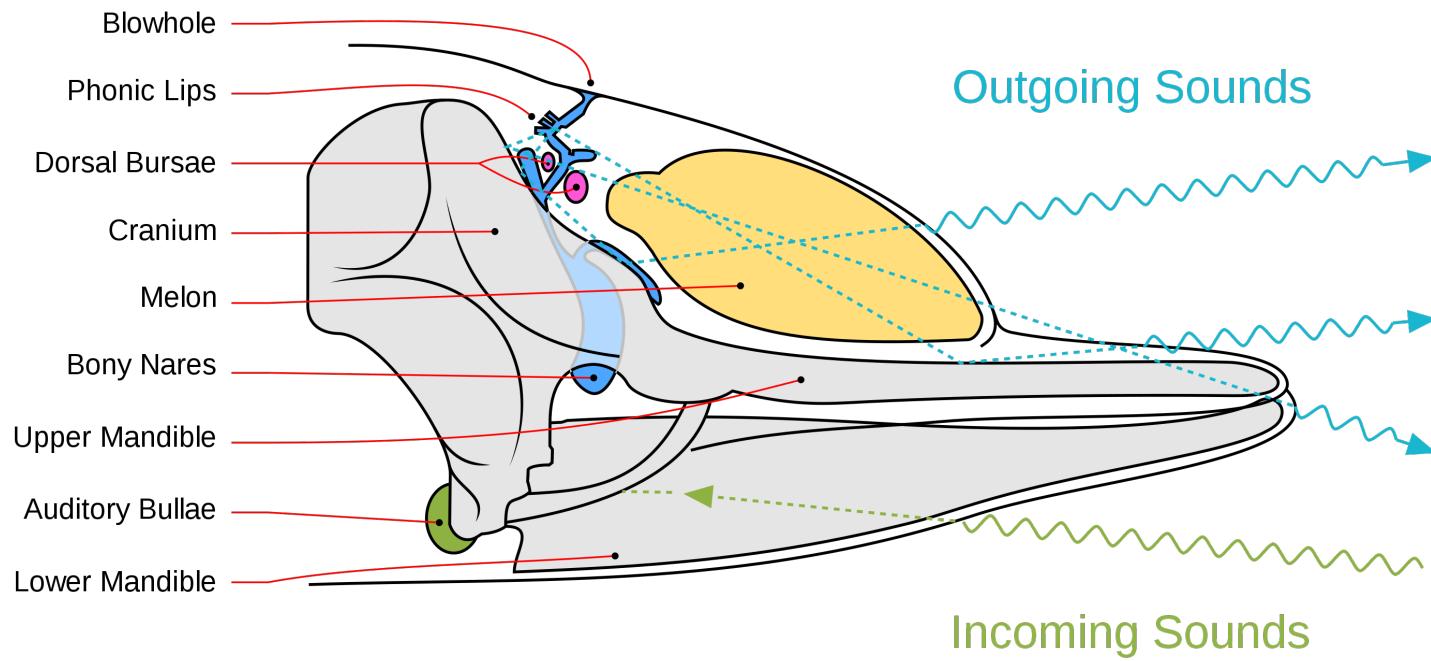
# Adaptations to Oceanic Life

- Locomotion
- Gravity effects

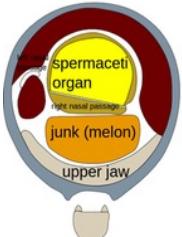


# Adaptations to Oceanic Life

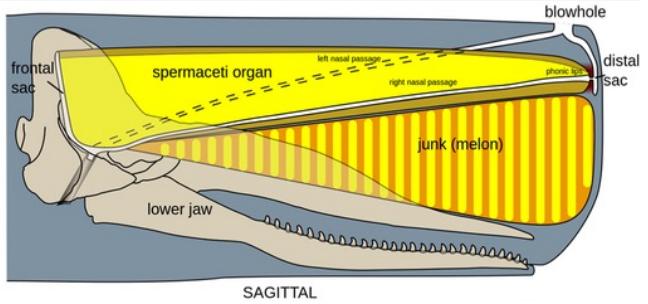
- Locomotion
- Gravity effects
- Alternative sensory systems



# Echolocation in sperm whales



TRANSVERSE



SAGITTAL



# Adaptations to Oceanic Life

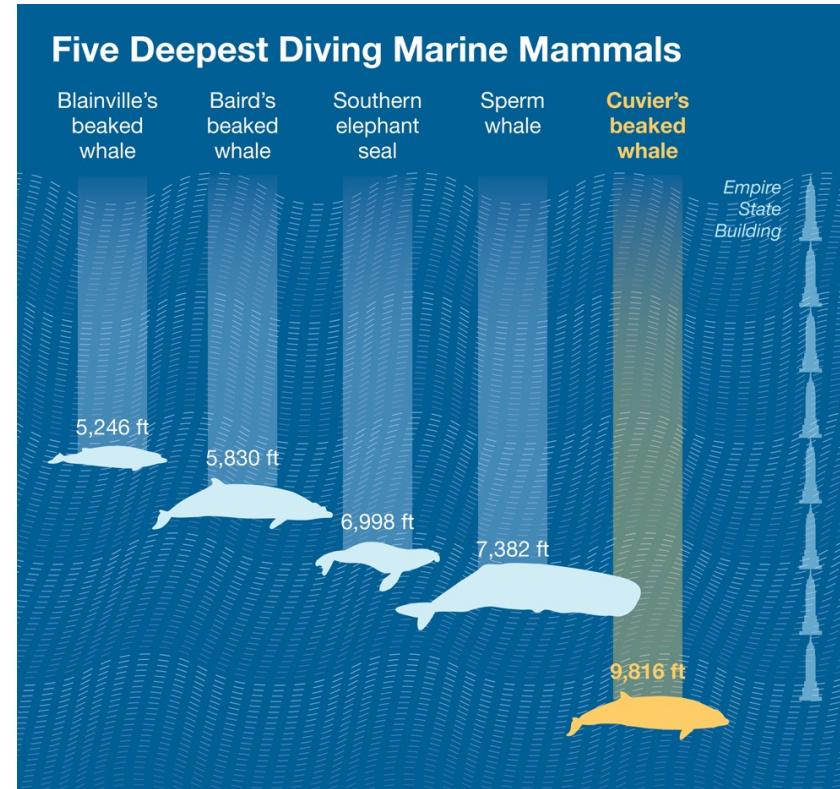
- Locomotion
- Gravity effects
- Alternative sensory systems
- O<sub>2</sub> capture



Photo copyright of Hadoram Shirihai

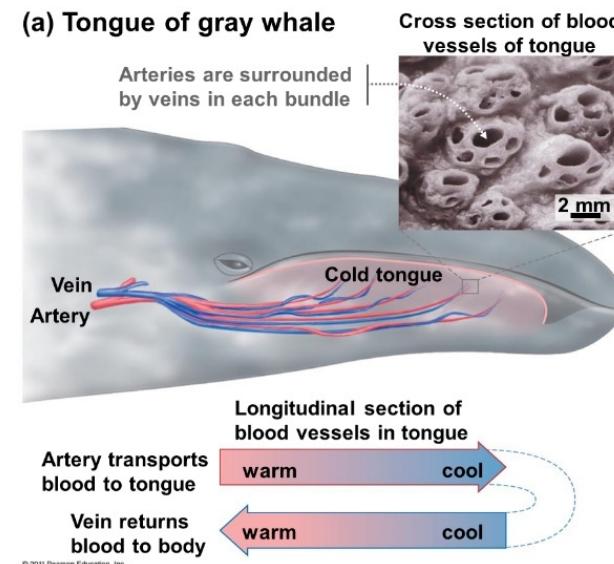
# Adaptations to Oceanic Life

- Locomotion
- Gravity effects
- Alternative sensory systems
- O<sub>2</sub> capture
- Diving physiology



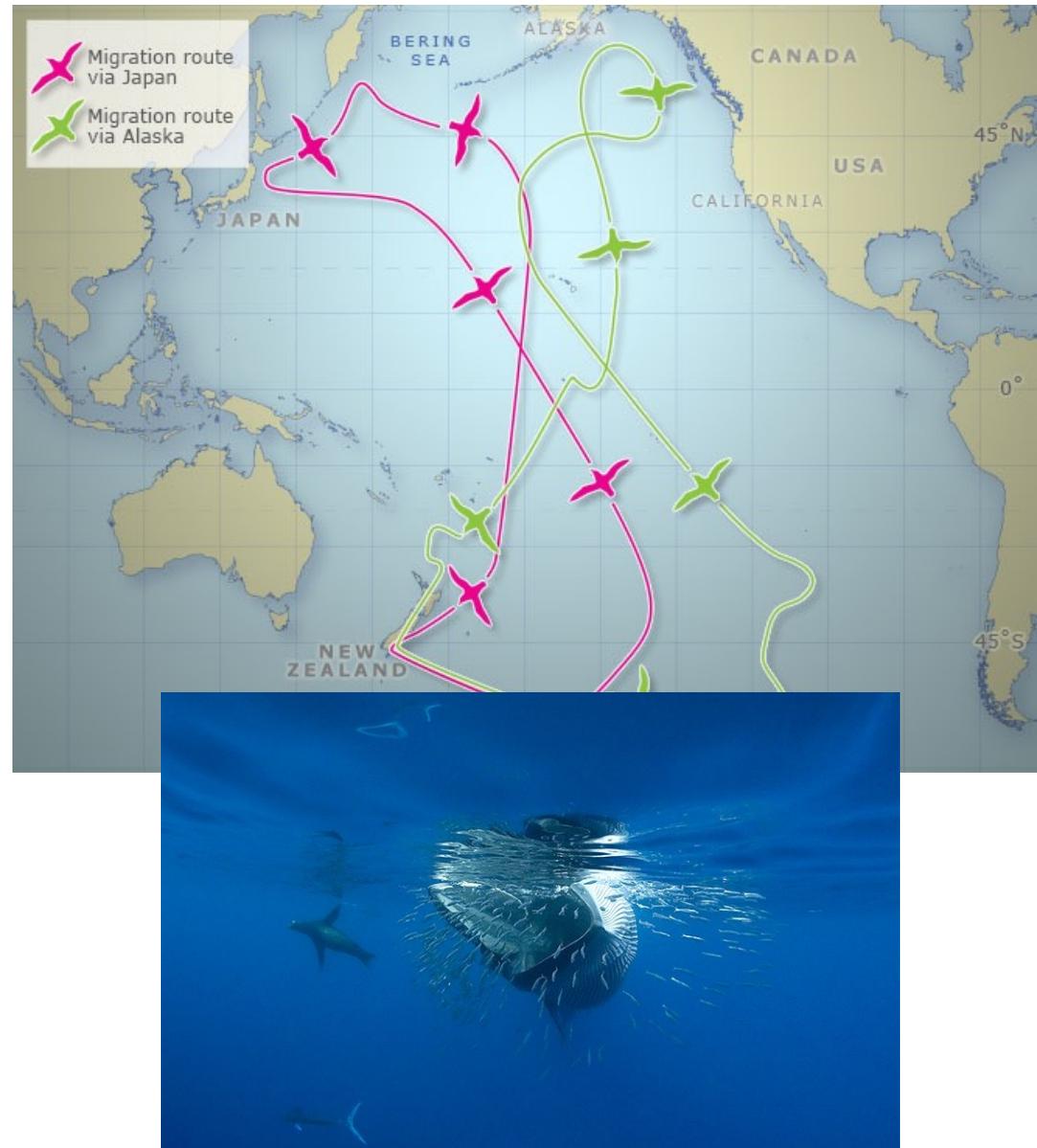
# Adaptations to Oceanic Life

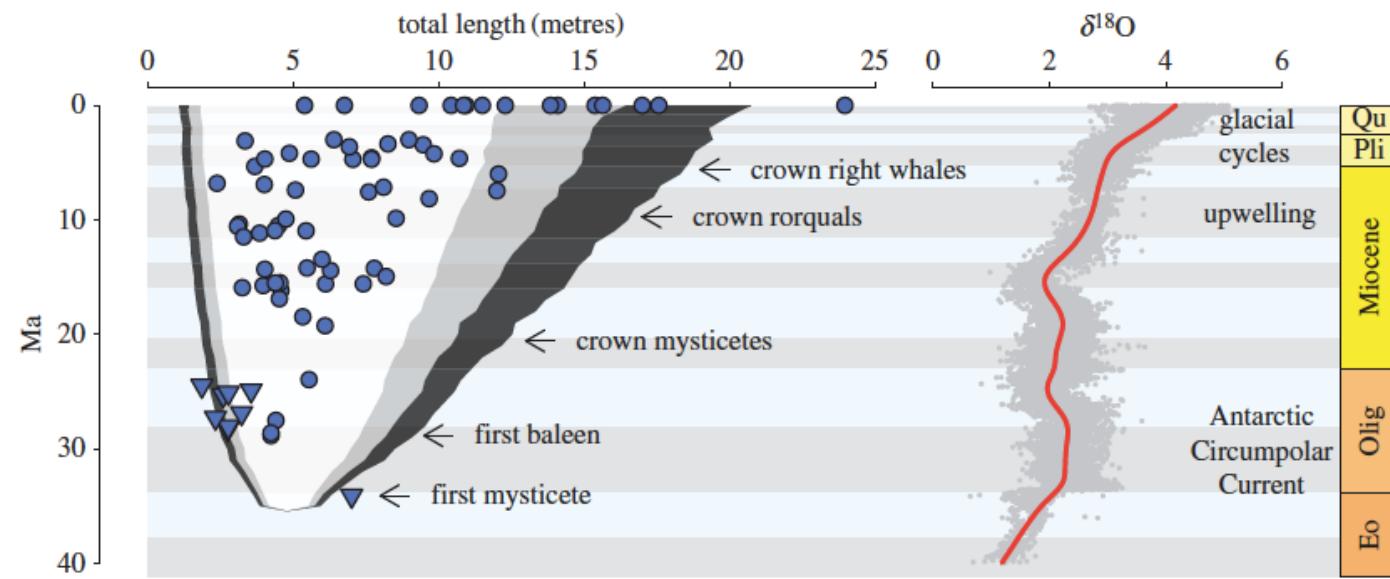
- Locomotion
- Gravity effects
- Alternative sensory systems
- O<sub>2</sub> capture
- Diving physiology
- Heat conservation



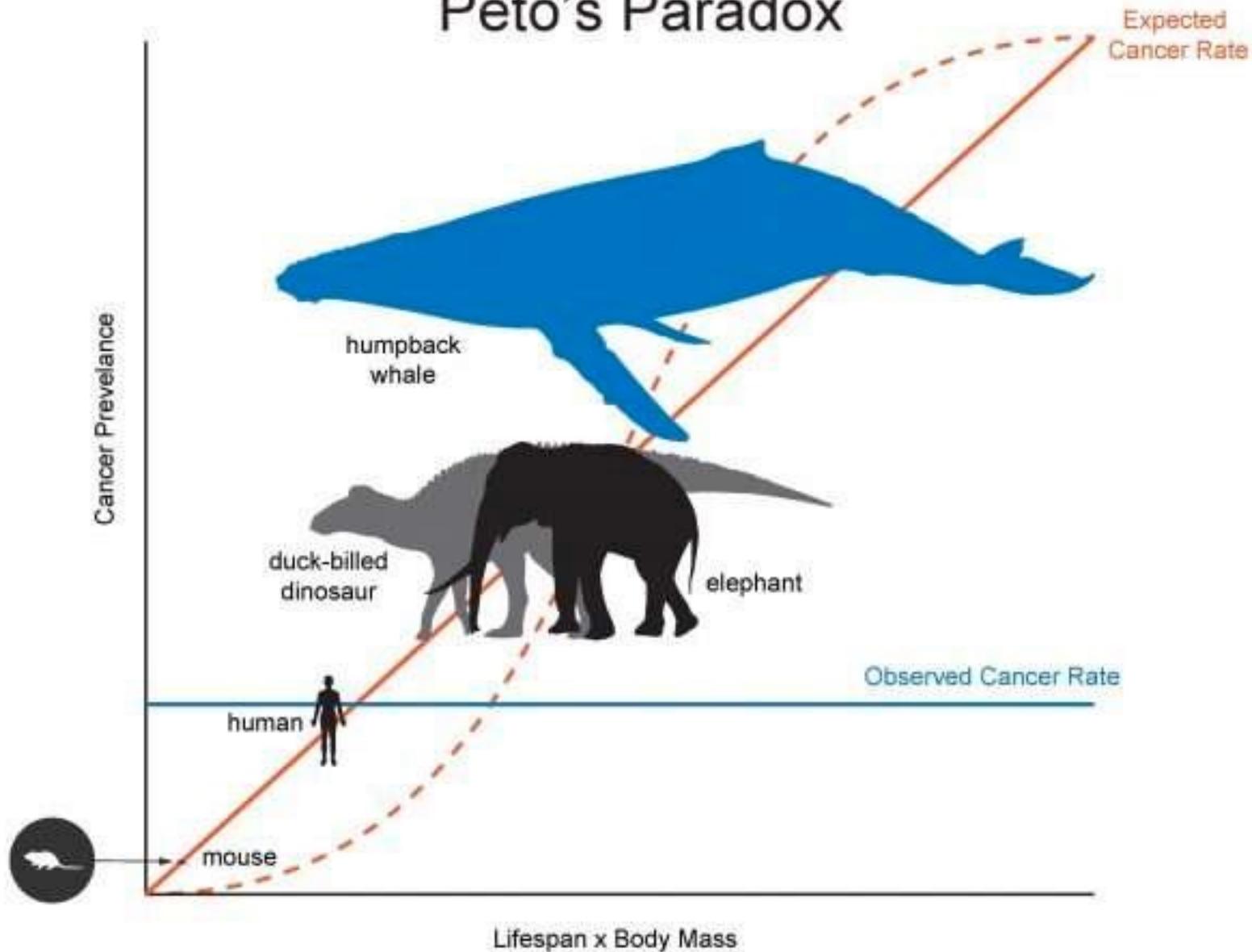
# Adaptations to Oceanic Life

- Locomotion
- Gravity effects
- Alternative sensory systems
- O<sub>2</sub> capture
- Diving physiology
- Heat conservation
- Migrations & Ecology





# Peto's Paradox



# TP53

- Tumor suppressor
- Mutations found in up to half of human cancers
- Cell cycle arrest, DNA repair, apoptosis
- Washing machine analogy:
  - Start the machine, notice water leaking out
  - Stop the cycle!
  - Call the repair agent
  - If necessary, throw away the washer

# Depth analysis

- When you sequence a genome, you:
  - Amplify all the DNA.
  - Fragment amplified DNA at random places → reads.
  - Determine sequence of each reads.
  - Hire a bioinformatician.
- Sequencing depth = average number of times a nucleotide in the genome is represented in a read
- There's always fluctuation, but depth anywhere is roughly within 20% of the average.

# Reference genome: fictitious example

- The Green Martian genome has been fully sequenced and annotated.



- The Blue Martian Genome Project has a partial assembly. Before they annotate (find and determine function of each gene), they hire you to analyze their reads.



- You decide that Green Martian is a close enough relative to use as a reference genome. You blast all your reads against the Green Martian genome

# Reference genome: fictitious example

- Average read depth over the entire reference genome is 50.
- For the references genome's COI sequence, average read depth is 48.
  - Yes, Martians have COI.
  - 48 is within 4% of the overall average → nothing unusual here.
- For the references genome's Photosystem II sequences, average read depth is .05.
  - Yes, Green Martians photosynthesize. That's why they're green.
  - Conclude that Blue Martians don't have Photosystem II. Maybe they are related to UCYN-A?
- For the references genome's TP53 sequences, average read depth is 96.
  - Nearly 2x average depth.
  - Hard to explain if Blue Martians only have 1 TP53 gene.
  - Expected depth if Blue Martians have 2 TP53 genes.

# What we've seen

- Salt was the first Humpback Whale to be sequenced.
- Depth analysis, using Blue Whale genome as a reference, suggested that the Humpback has (at least) 2 copies of TP53.
- Thank you, Salt.

