



Adaptation as a Response to Ocean Acidification – Is it Possible and How do We Look for it?

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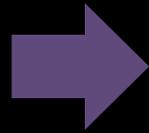
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*The National Adaptation Forum
2-4 April 2013, Denver, Colorado*

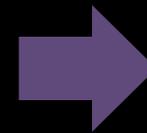
Hofmann Lab: Our Research

Global Change Biology in Marine Ecosystems

What are current ocean conditions?



How are species currently adapted to this environment?



How might species respond to future changes?



Collaborations:



Adaptation (the DNA kind) as a response to ocean acidification

- Is it possible?
- How do we look for it?
- What's the problem?



Ecosystem



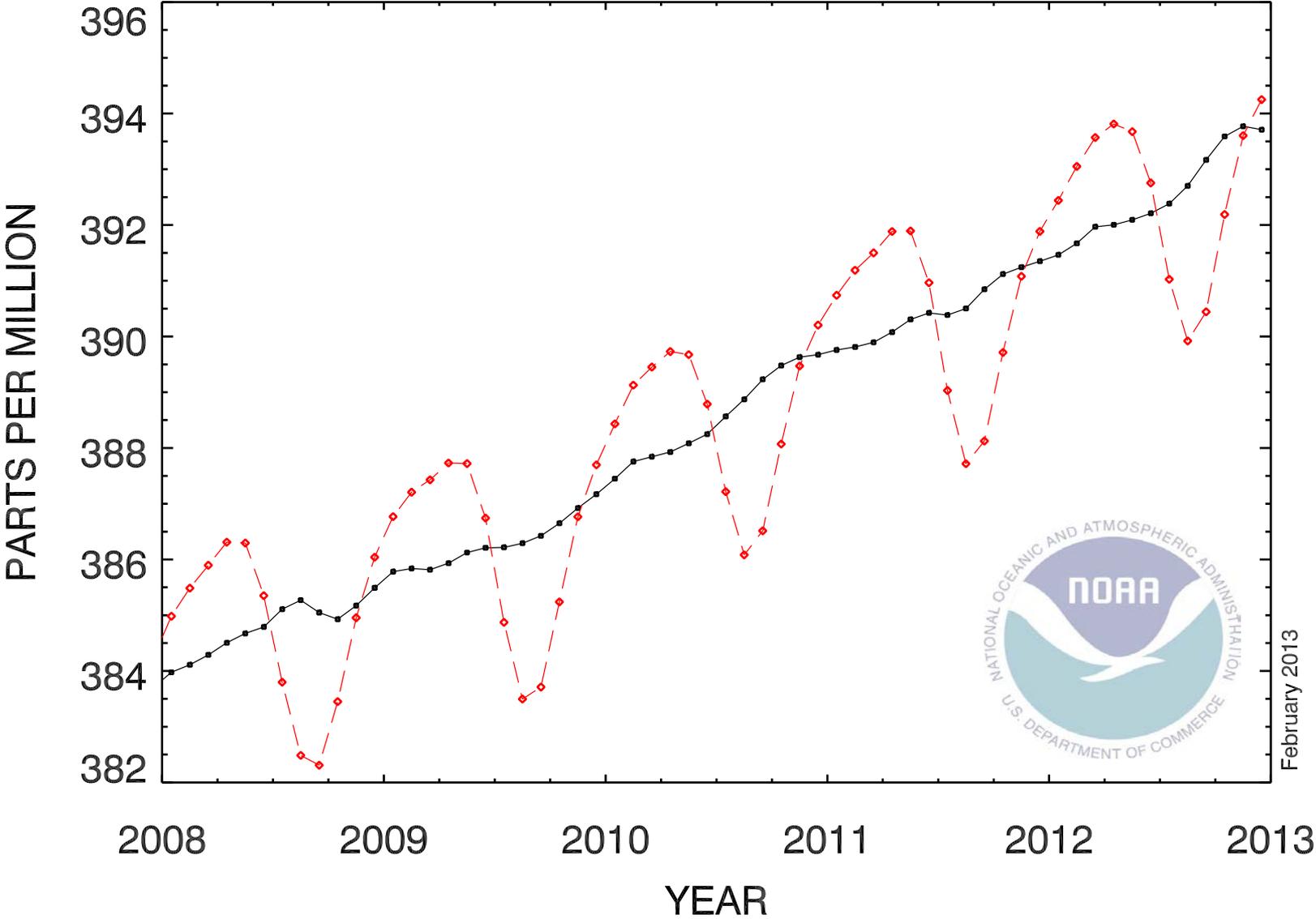
Organism



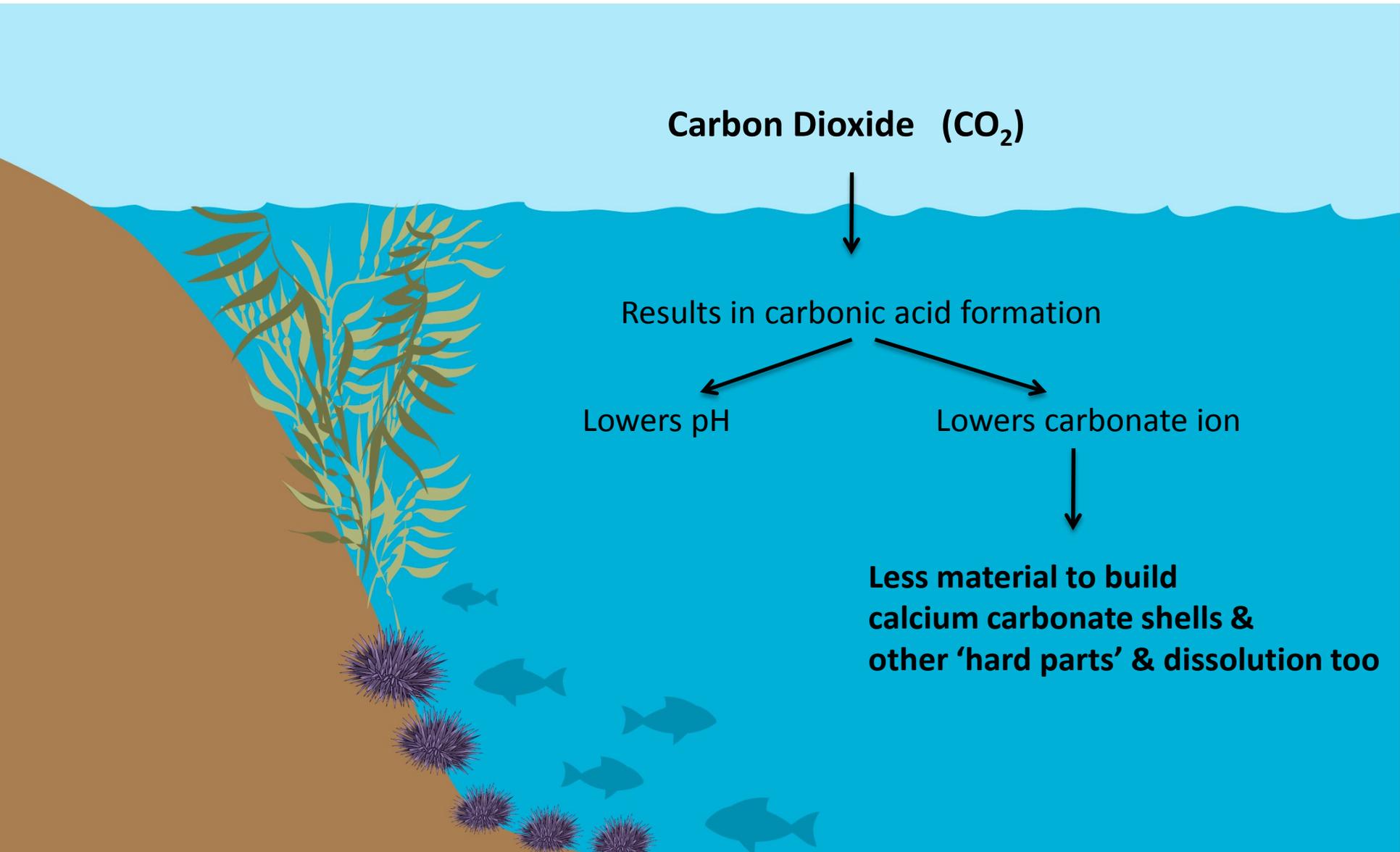
Food

Recent Global CO₂, December 2012: 394.25 ppm

RECENT GLOBAL MONTHLY MEAN CO₂

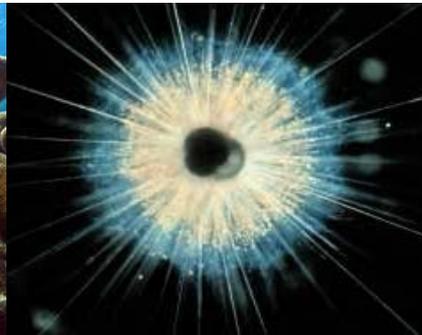


The Biological Consequences of Ocean Acidification



Huge challenge to calcifying organisms

- Reduced capacity to perform calcification
 - Effects on growth and development





How do we learn if key seafood species will adapt to future OA?

Is it possible?

How do we look for it?

Thinking about OA & Evolution: what do we know?

- First, evolution can occur on relatively short ecological times scales (rapid)

That is, evolutionary and ecological time scales are not always completely different

Carroll et al. (2007) Functional Ecology 21: 387-393



Trinidadian guppy (*Poecilia reticulata*)



Thinking about OA & Evolution: what do we know?

- Second, evolutionary rescue can occur

Bell and Gonzalez (2009) Ecology Letters 12: 942-948

Evolutionary rescue (ER) of yeast in an experimental evolution selection experiment – using high saline conditions

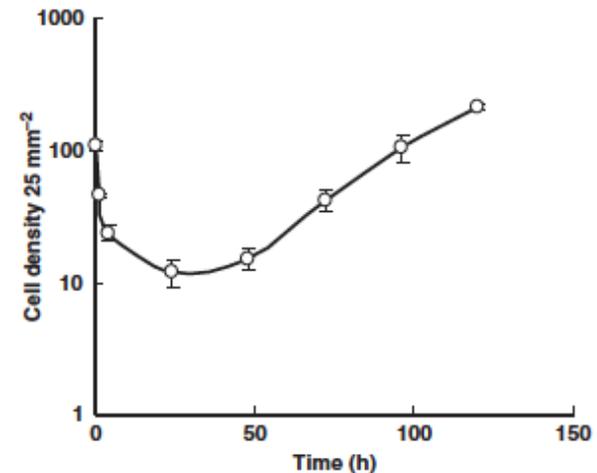


Figure 1 Collapse and recovery of yeast populations (mean \pm 1 SE) exposed to high-salt concentration. The concentration used was 125 g L⁻¹ of NaCl in yeast-peptone-dextrose medium. The initial inoculum was 10 μ L of a 24-hour YPD culture into 140 μ L medium, comprising $\sim 5 \times 10^5$ cells, with 4 replicate populations sampled on each occasion. Cell counts made on a 5 \times 5 mm² randomly selected on the surface of the YPD plate.



Adaptation and seafood: what do we need to know?

- **Rapid evolution can occur from two sources:**
 - ① Standing genetic variation
 - ② New mutations
- ***For OA studies, standing variation for pH tolerance in populations will determine the capacity for adaptation to OA in the future***
- **How to look for standing variation in populations?**



Three strategies in the search:

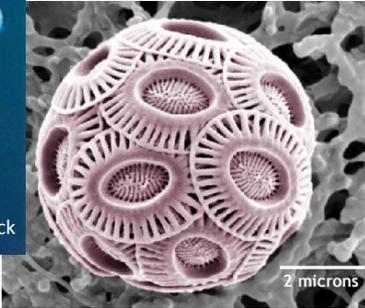
- 1. Genetic differences**
- 2. Local adaptation = “hot spots” for adaptation**
- 3. Breeding experiments**

We are learning about variation between genotypes, stocks & strains

1. Langer et al. (2009) *Biogeosciences*
Differences in response variables for 4 strains of coccolithophore *E. huxleyi*



© Jess Gorick



2 microns



© James Watanabe



2. Parker et al. (2011) *Marine Biology*
Sydney rock oyster *Saccostrea glomerata*
Differences between wild populations & wild oysters

3. Pistevos et al. (2011) *Oikos*
Clonal differences in *Celleporella hyalina*,
an encrusting bryozoan



Second Option

**Local adaptation –
Let Mother Nature help you....**



Local Adaptation & OA

the fine-tuning of populations to their local environment via natural selection

- Existing (and persistent) variation in environmental conditions may select for populations that evolve different performances, or phenotypes, and these have a fitness advantage

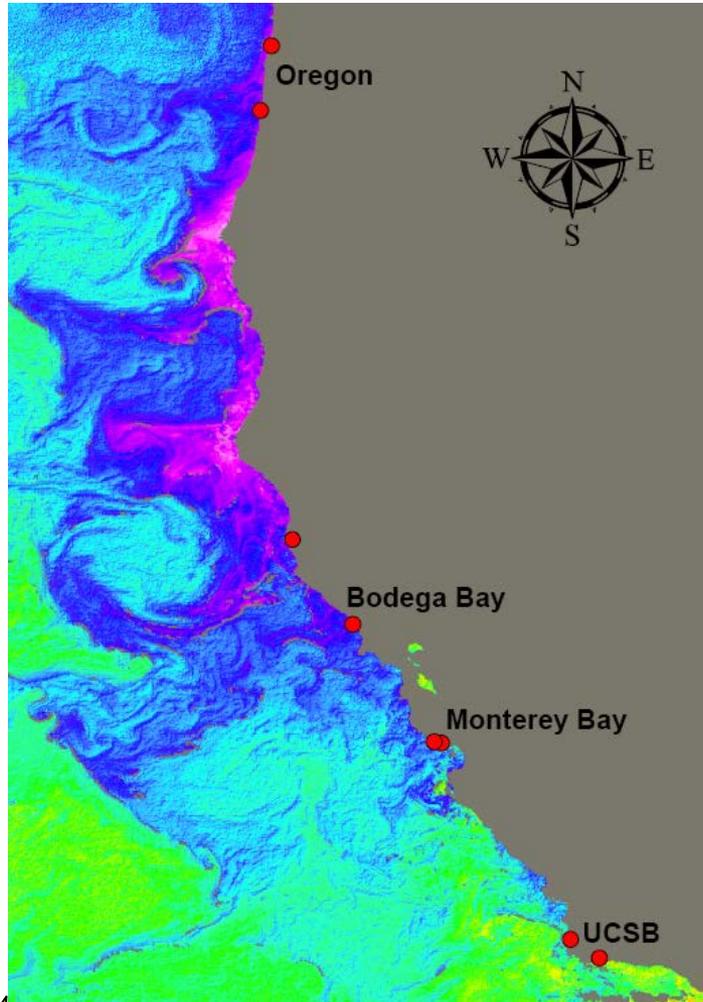


Local Adaptation & OA

Is there local adaptation to gradients in the “OA seascape” as we know it today?

Hot spots for adaptation?

OMEGAS: OA and local adaptation in the California Large Marine Ecosystem (CCLME)



- Co-locate sensors with biology**
- Capture the OA mosaic along the CCLME
 - Measure variability of populations in OA tolerance

Design: Pairs of sites in contrasting oceanographic settings, in four regions of the CCLME from Oregon to southern California



<http://hofmannlab.msi.ucsb.edu/omegas>

Local adaptation in wild invertebrates of the CCLME

1. Mosaic of pH on the coast



2. There are major differences in performance of calcifying organisms



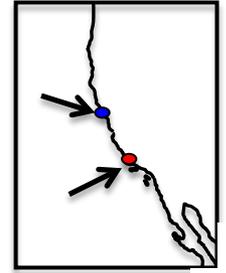


Third Option

**Breeding experiments –
Is that tolerance heritable?**

CRITICAL ISSUE

Breeding experiment: Cross Design



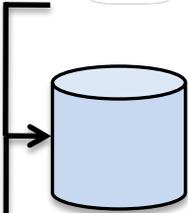
N=8 males/site



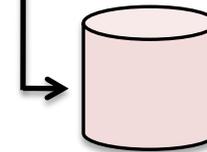
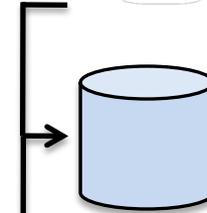
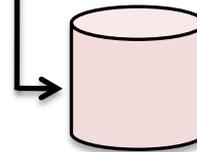
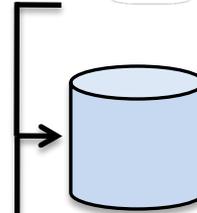
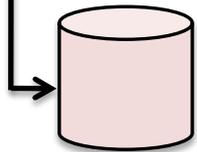
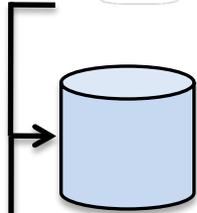
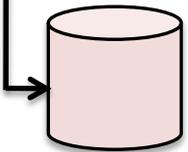
N=15 females
/site



Low pCO₂
424 μatm
(±4ppm, SE)

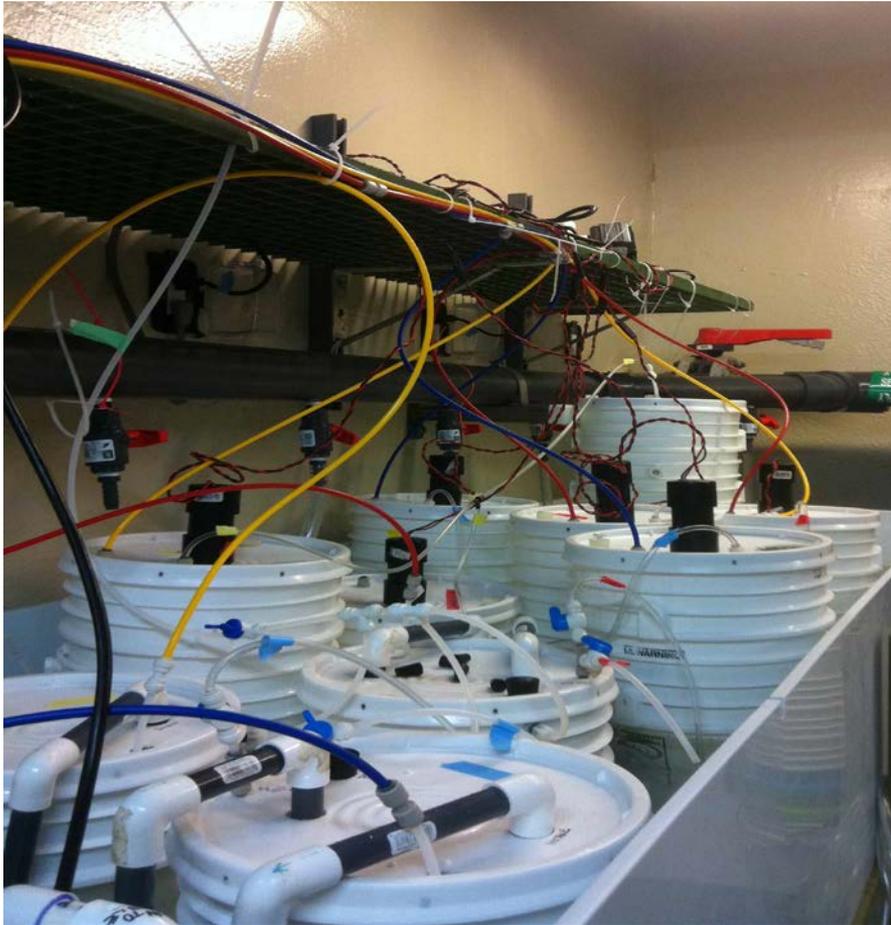


High pCO₂
1210 μatm
(±9ppm, SE)

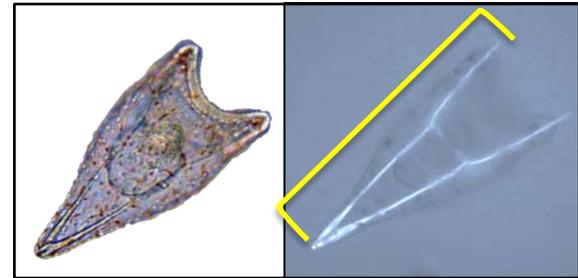


Total:
64 crosses/
treatment

Larval culture

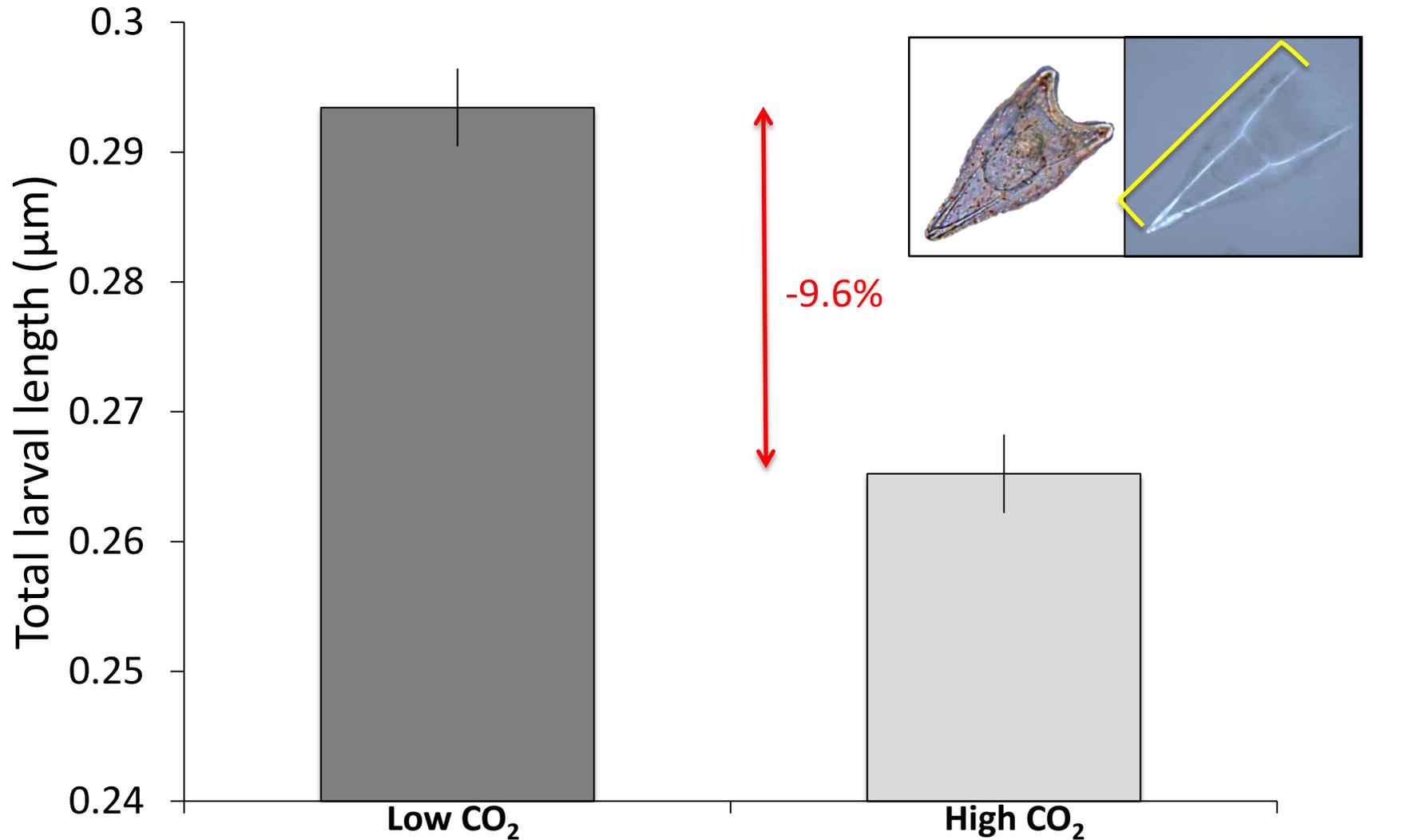


- Larvae reared for 5 days @ 13°C
- Response variable= total larval length



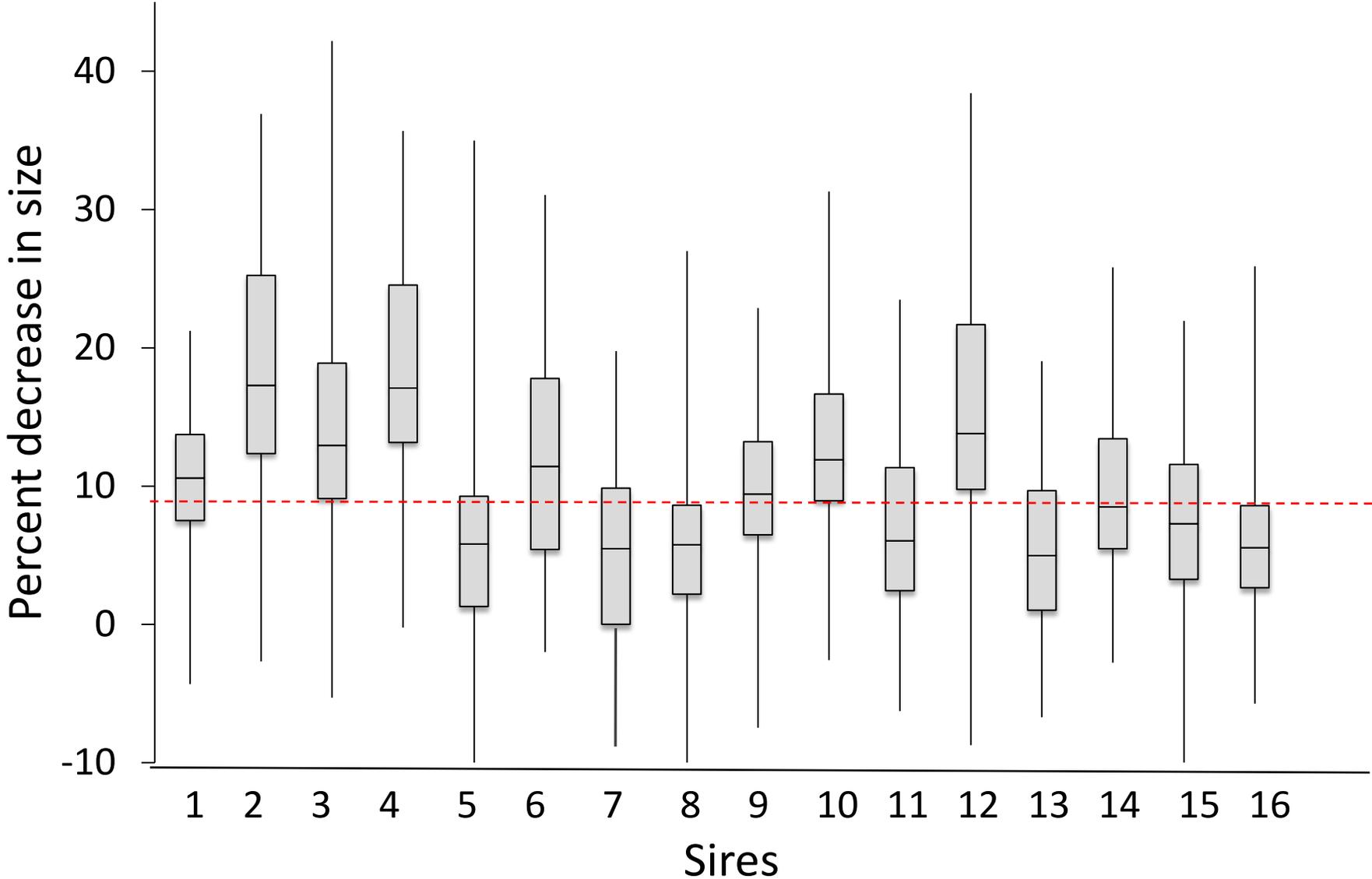
N=25 larvae/cross x pCO₂ treatment. (Total of 3,200 larvae)

Larvae raised under elevated CO₂ are smaller

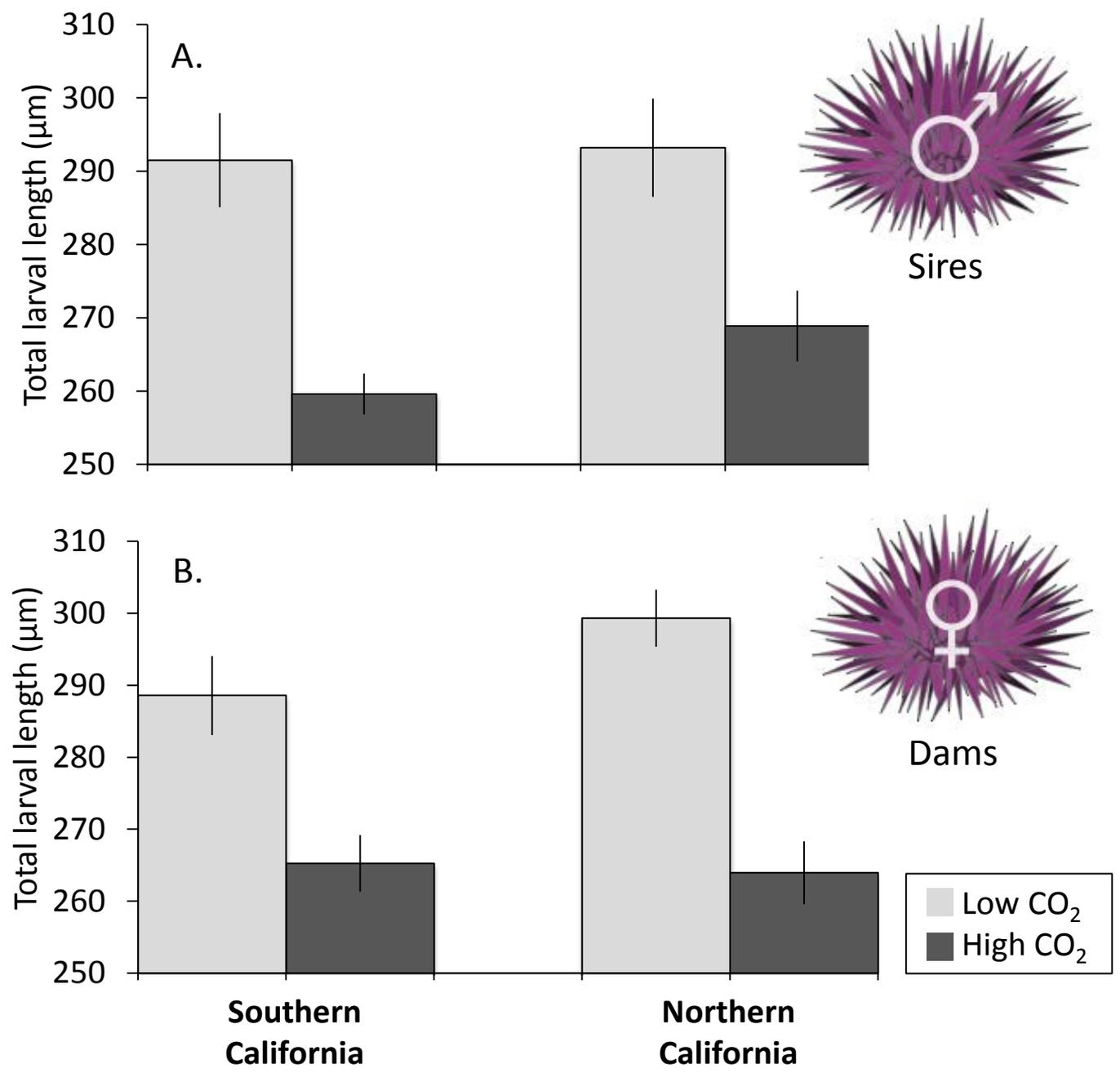


$F_{1,3180}=1088$ $p<0.0001$

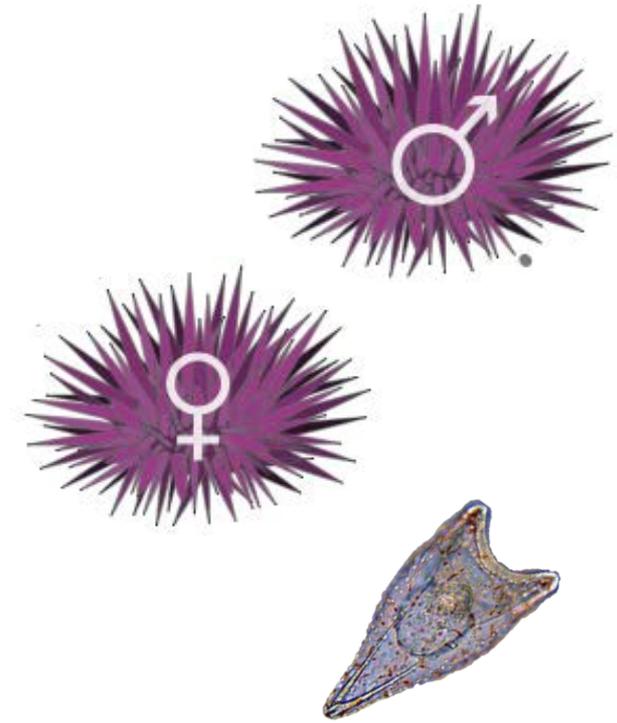
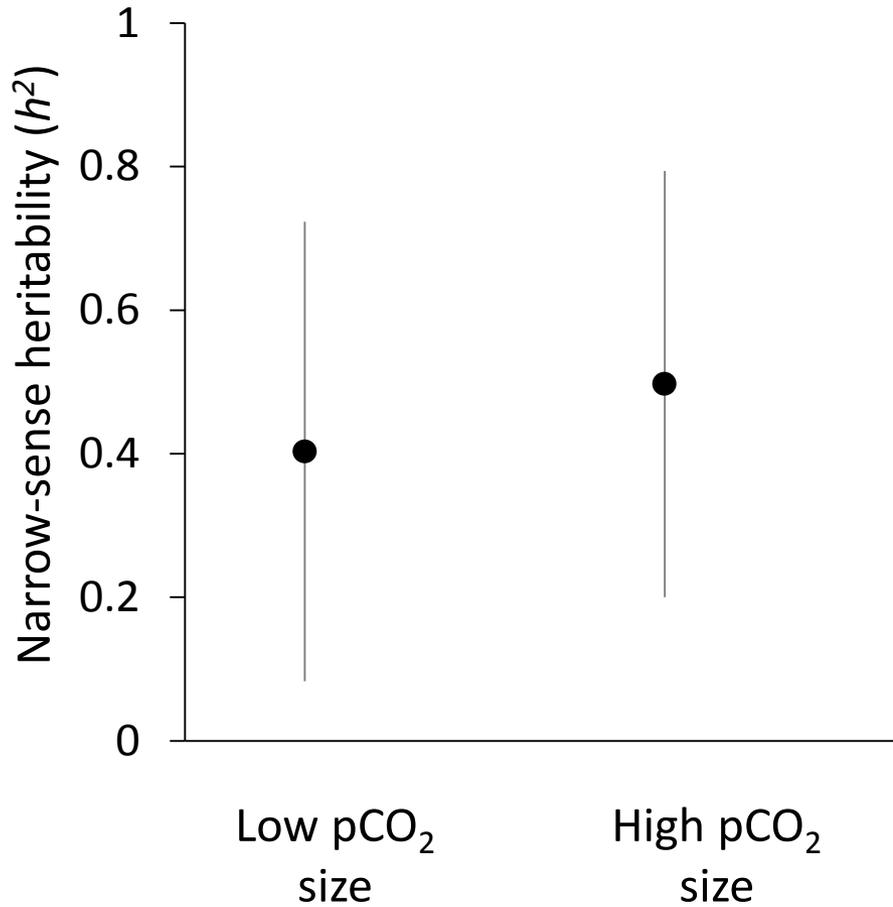
Sensitivity to elevated pCO₂ varies among and within families



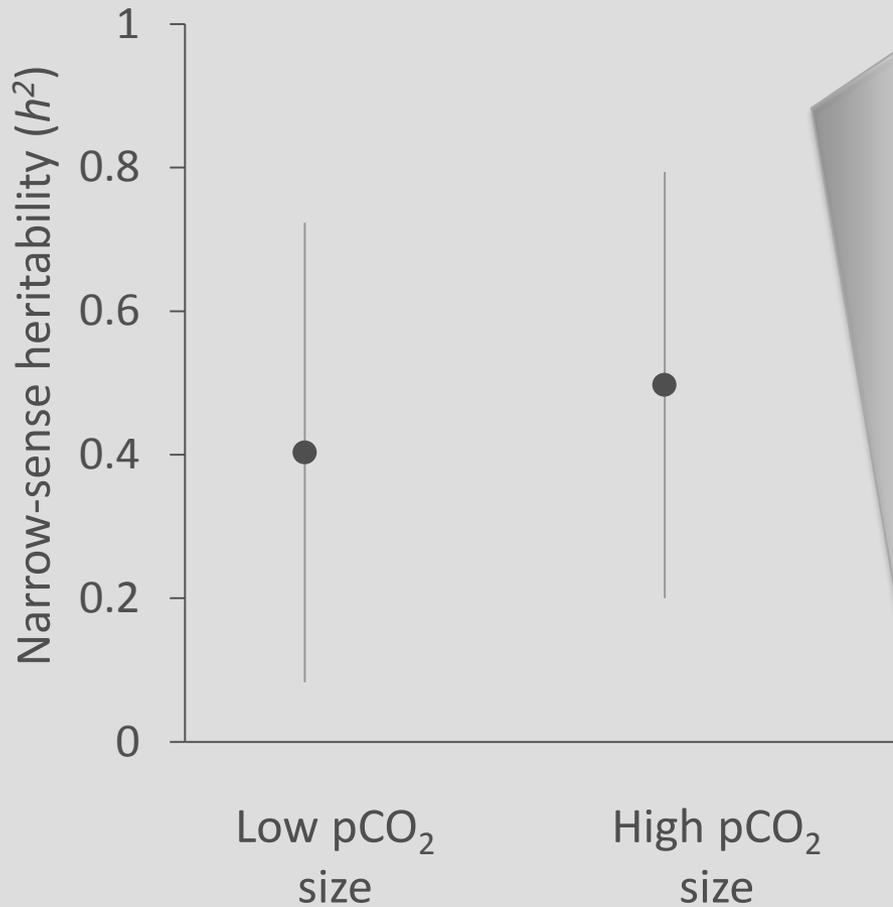
Preliminary analysis:
Offspring of northern CA sires are **larger** than the offspring of southern CA sires under high pCO₂



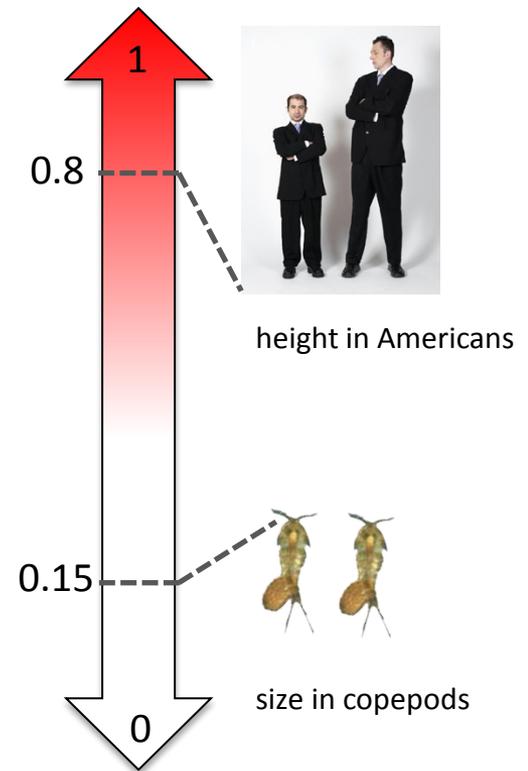
Significant genetic variation for size under high pCO₂



Significant genetic variation for size under high pCO₂



heritability: proportion of variation controlled by additive genetic effects



Will there be sushi?

Approaches that can look for genetic variation, resilience and tolerance in key food species.



Red sea urchin - uni



Mussel seed