Morphological and genomic responses of *Strongylocentrotus purpuratus* larval populations to experimental acidification

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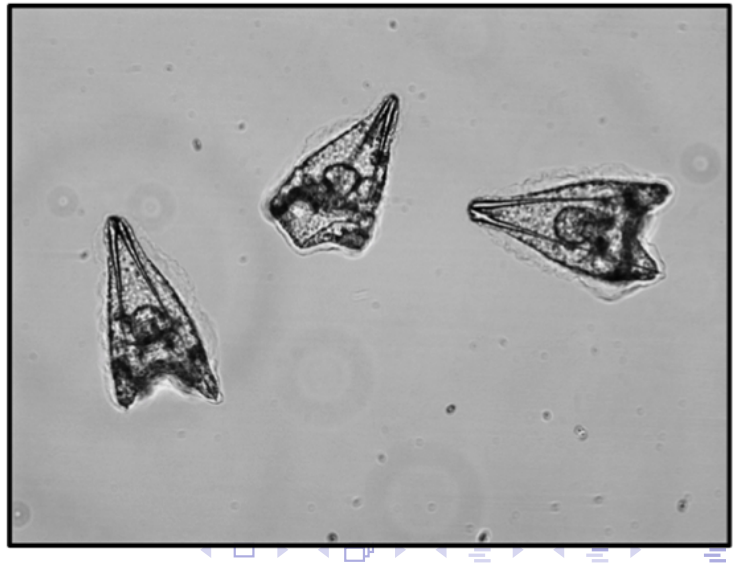
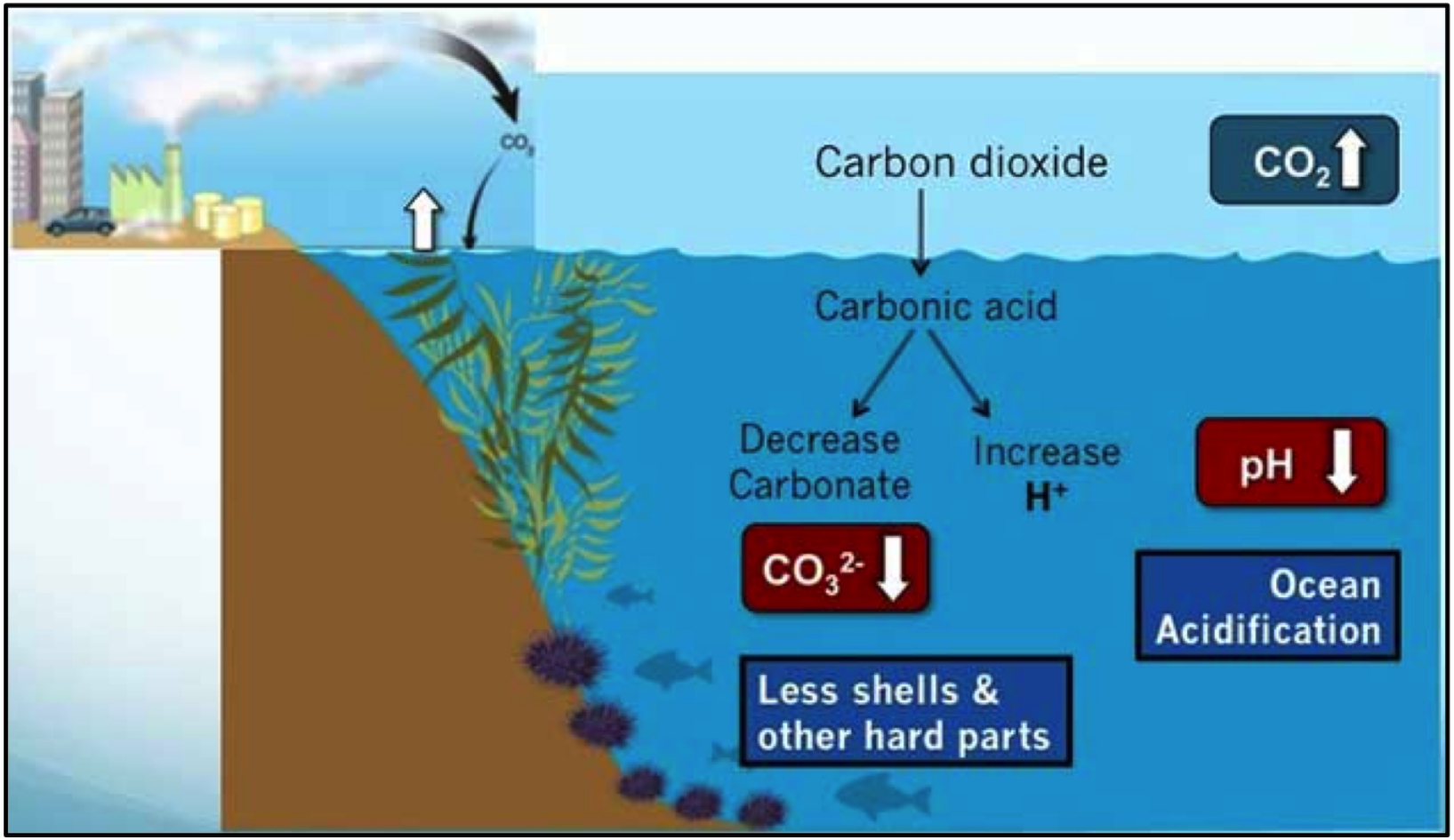
Computational Biology Research Presentation

May 3rd, 2017



Ocean Acidification:"The Other CO2 Problem"



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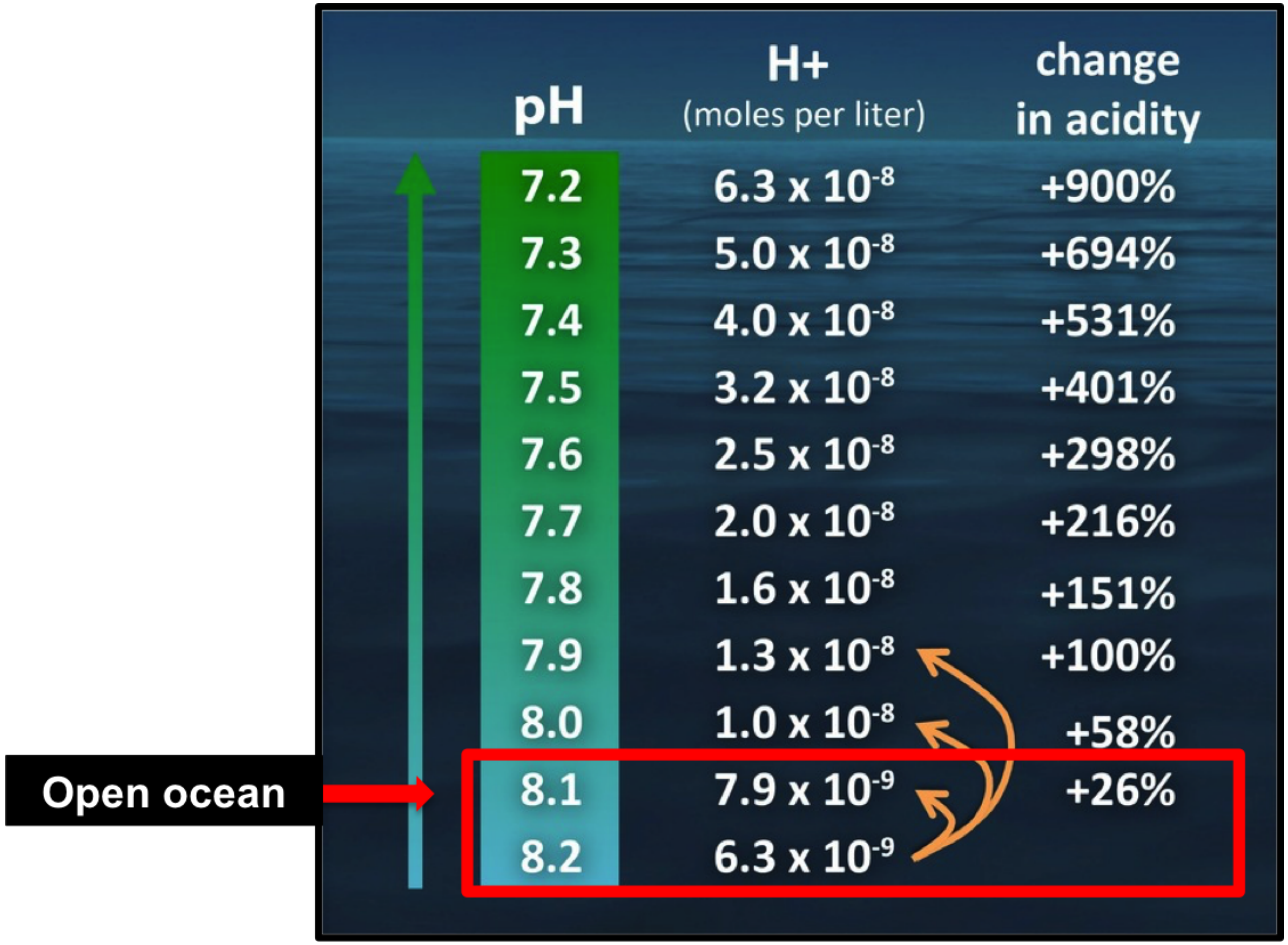

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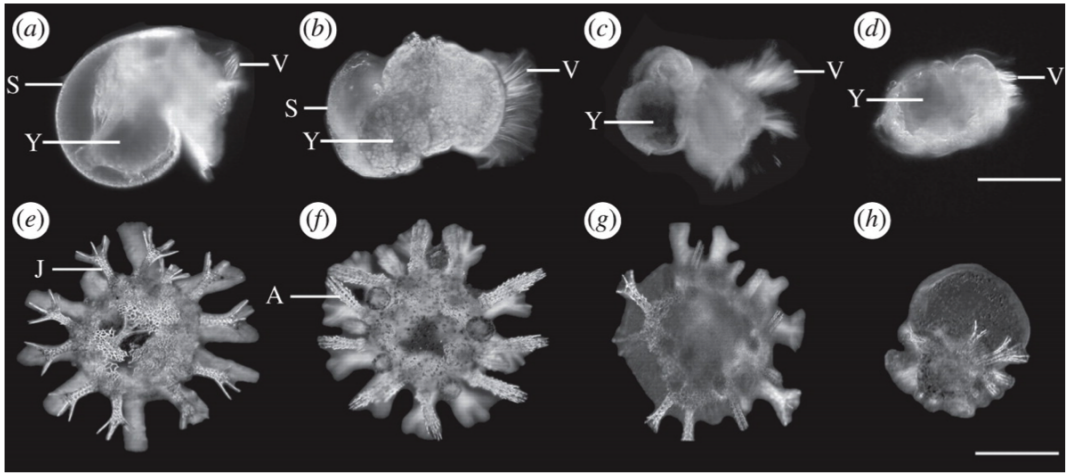

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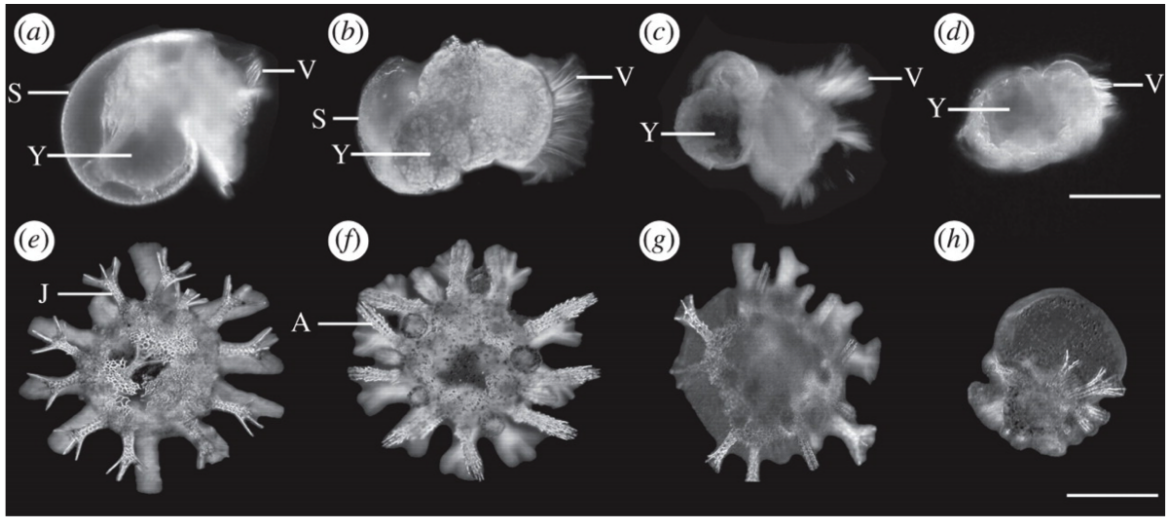
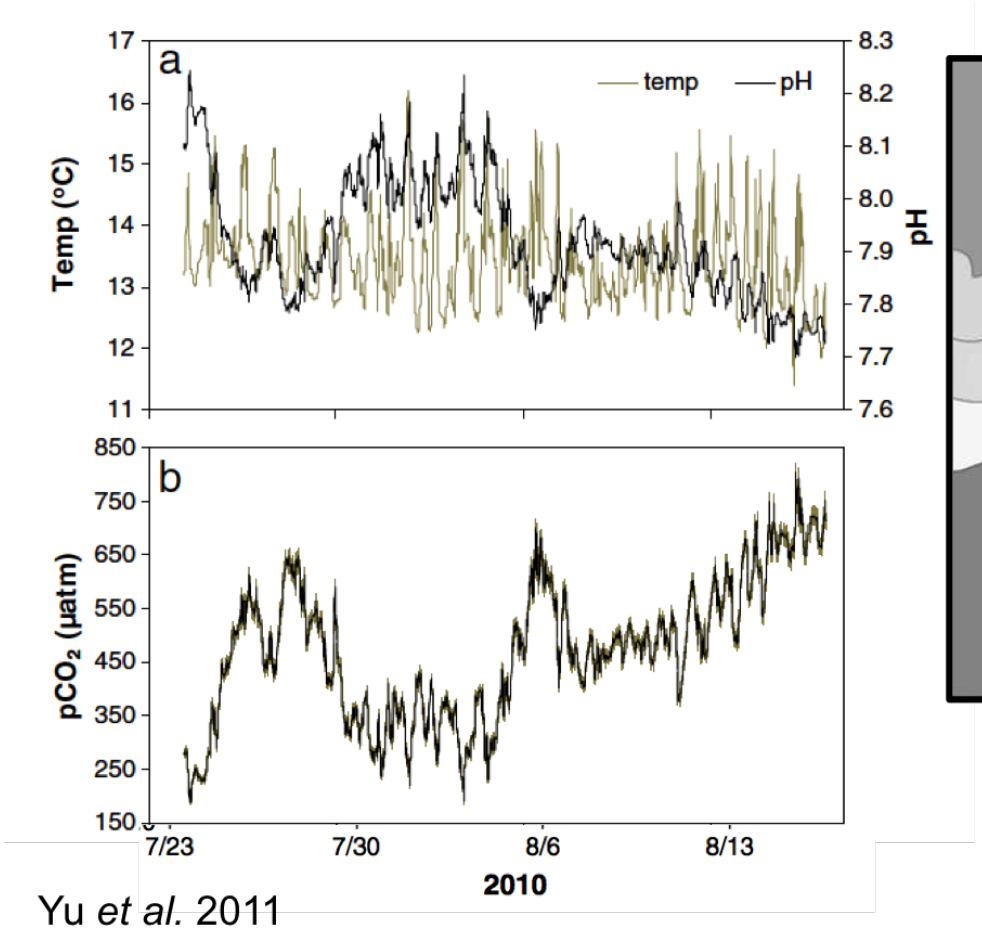
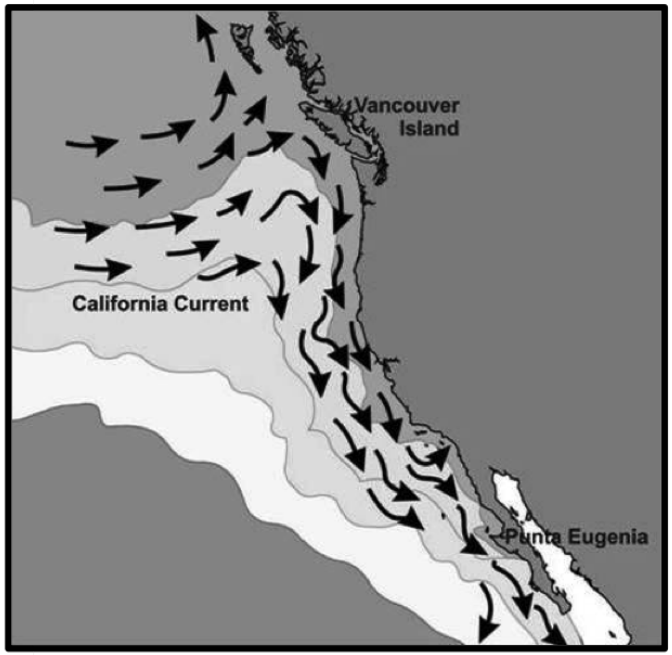


$\uparrow pCO_2 = \downarrow pH = \downarrow CO_3^-$
organismal survival?
population persistence?

CA Current System: extreme pH & variability





Yu *et al.* 2011

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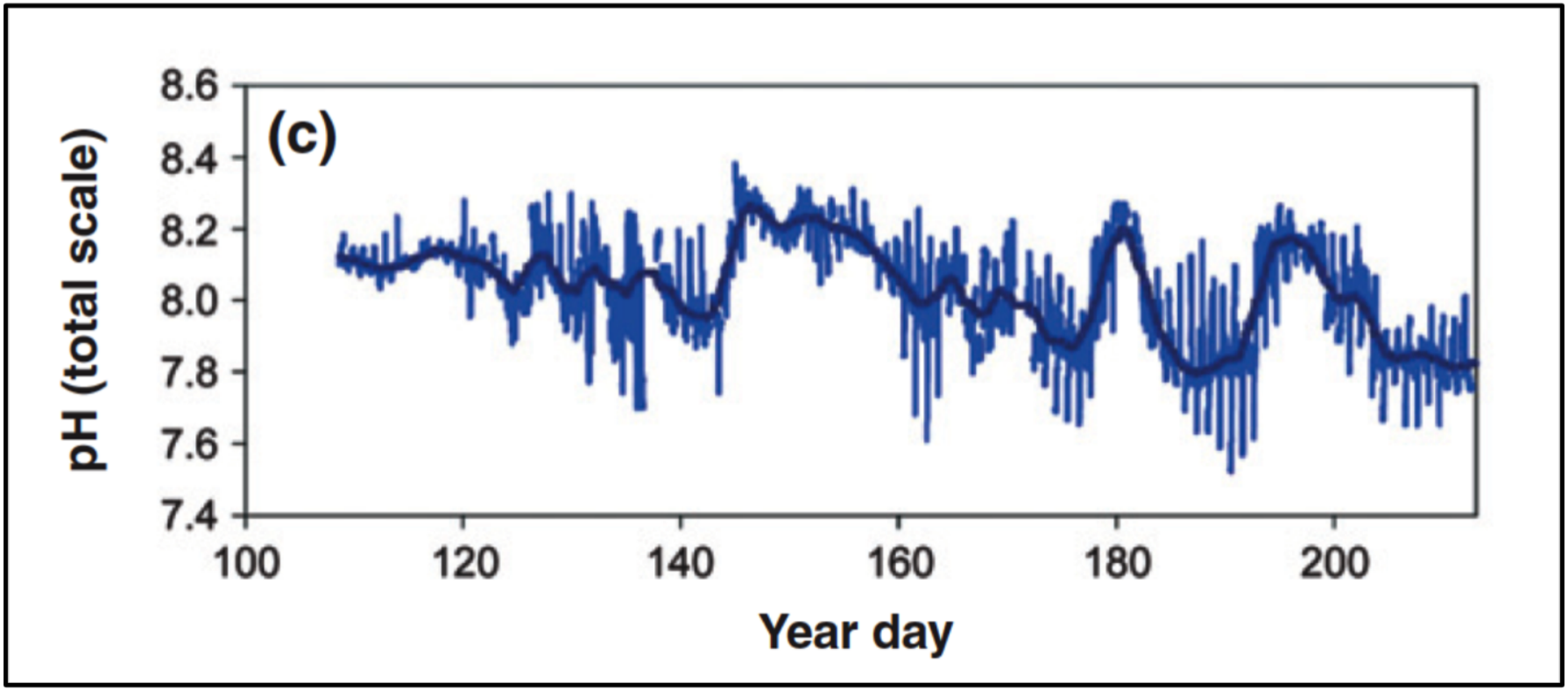

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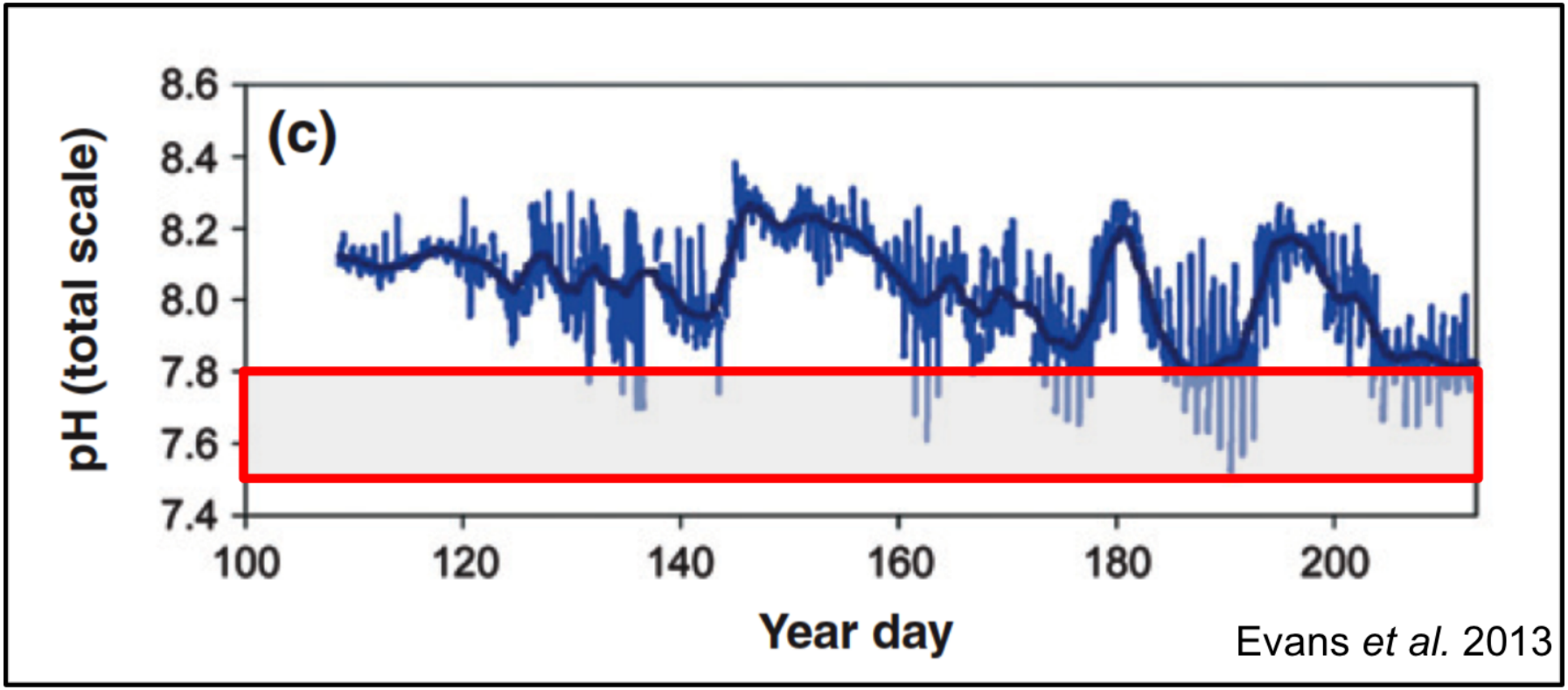

Pilot experiment: Questions & Hypotheses

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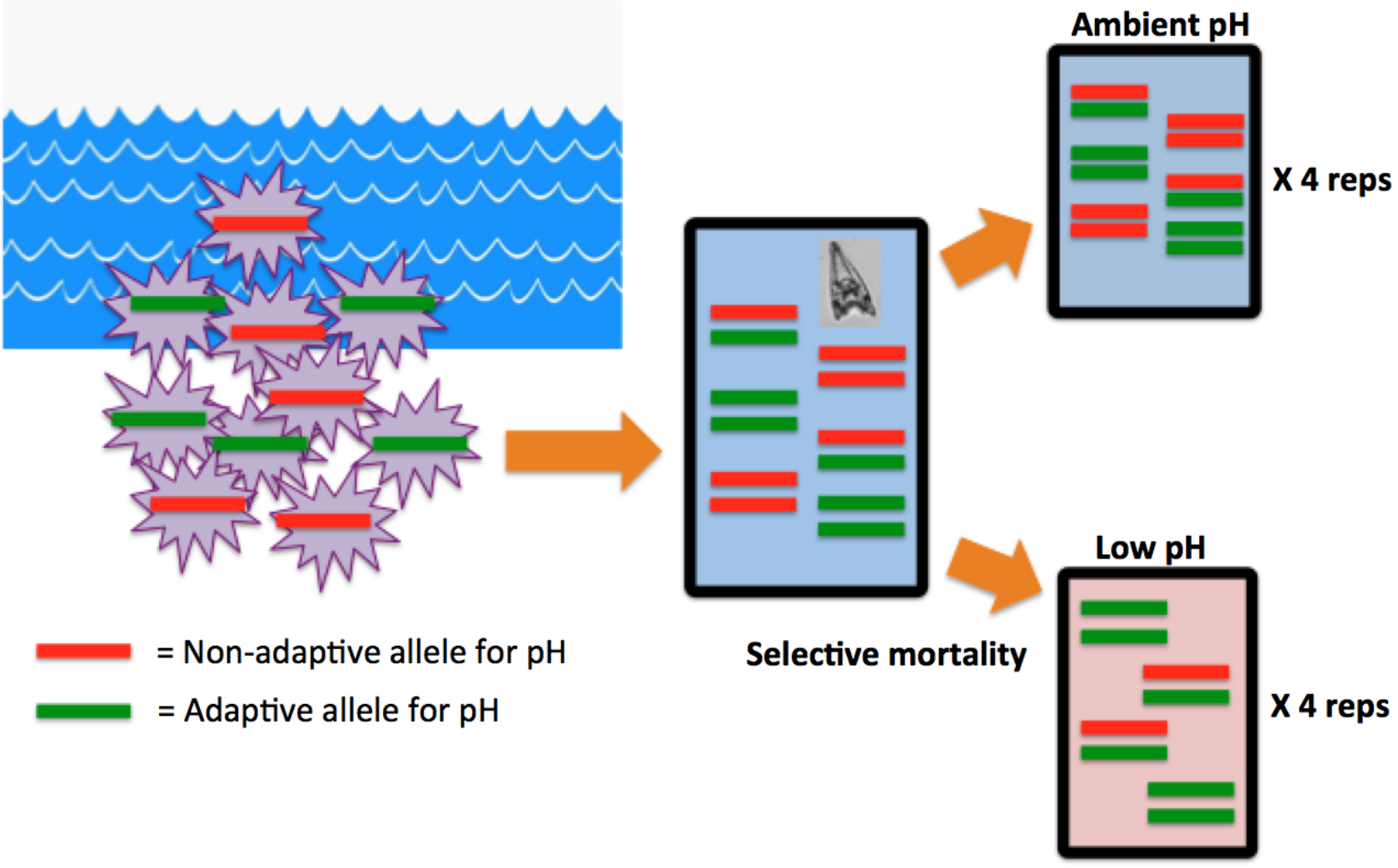
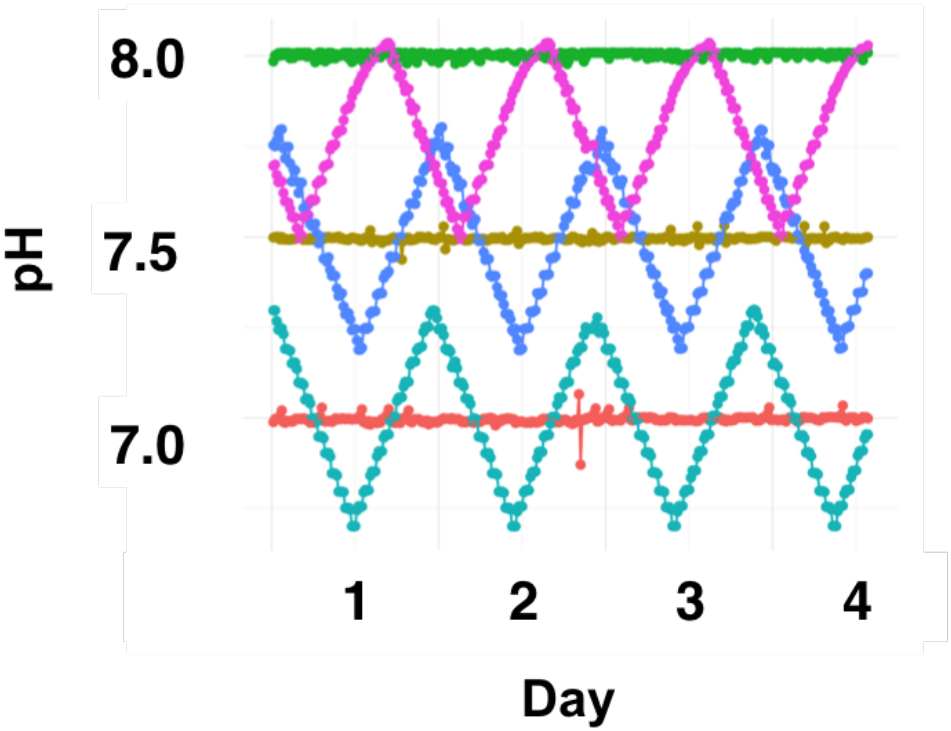
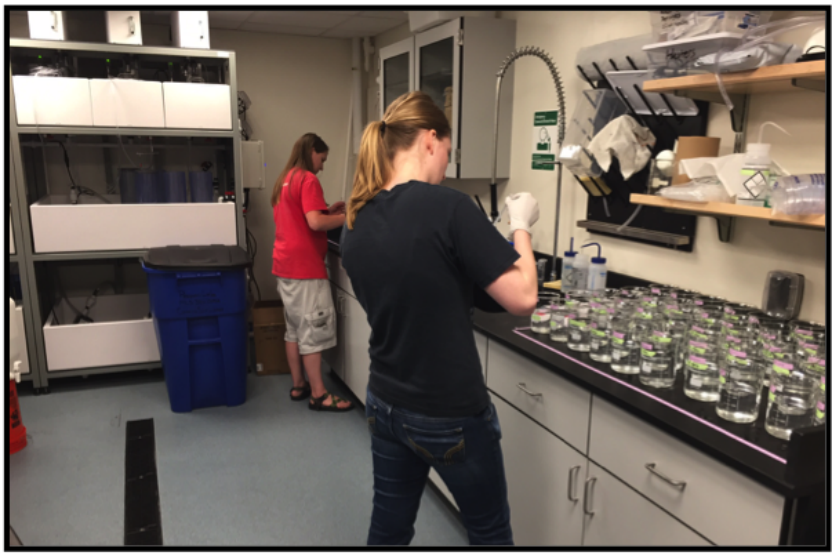
2) Does capture-sequencing pick up anticipated shifts in genomic diversity?

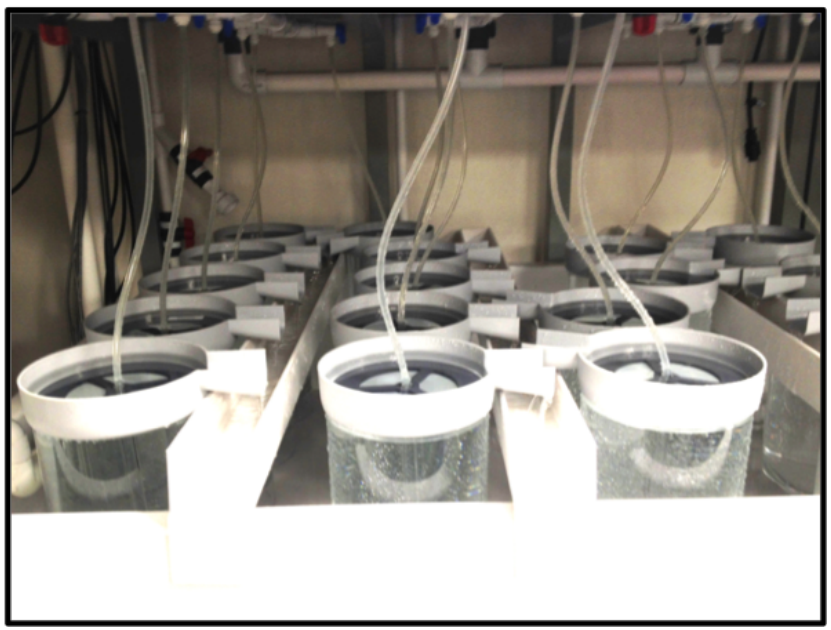
Power of larval selection experiments



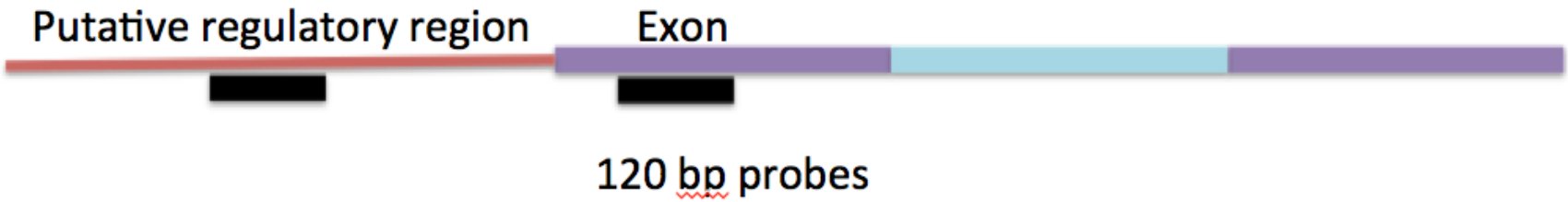
Methods: pH treatments & larval system







Methods: capture-sequencing

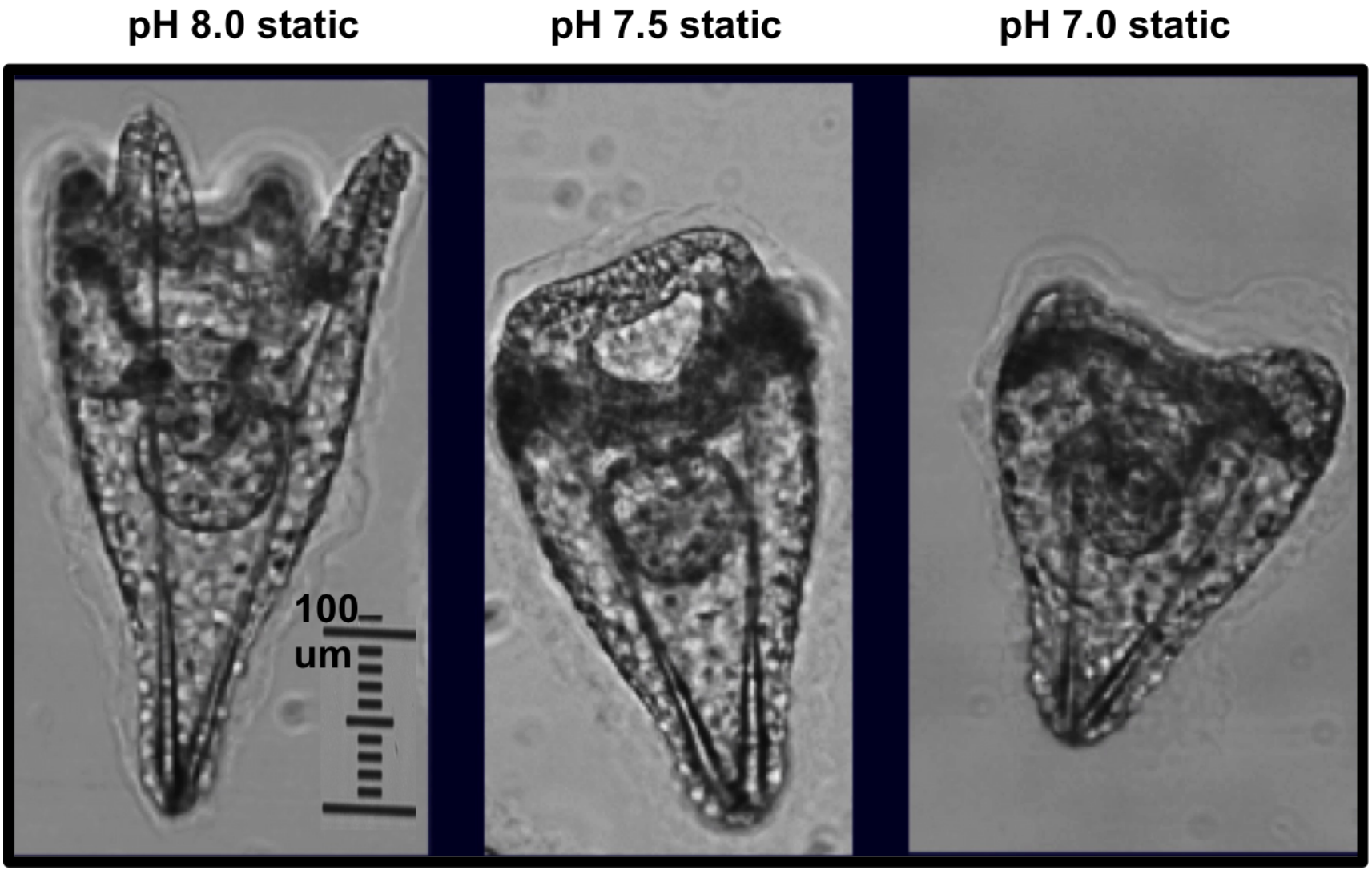


X 23,500 genes = 5.64Mbp sequenced to 50x coverage

- Cleaned reads from capture-seq
- Mapped to genome
- Created VCF file for Single Nucleotide Polymorphisms (SNPs)

289,431 high-quality SNPs

Results: Morphometrics



Morphometric data file

	A	B	C	D
1	Larval_ID	Vessel_ID	Treatment	Size
2	1	V15	8_0_S	257.035
3	2	V15	8_0_S	298.416
4	3	V15	8_0_S	256.064
5	4	V15	8_0_S	314.013
6	5	V15	8_0_S	322.715
7	6	V15	8_0_S	296.175
8	7	V15	8_0_S	342.825
9	8	V15	8_0_S	307.53
10	9	V15	8_0_S	278.099
11	10	V15	8_0_S	235.139
12	11	V15	8_0_S	341.037
13	12	V15	8_0_S	324.328
14	13	V15	8_0_S	317.779
15	14	V15	8_0_S	318.919
16	15	V15	8_0_S	250.125
17	16	V15	8_0_S	323.023
18	17	V15	8_0_S	290.918
19	18	V15	8_0_S	287.71
20	19	V15	8_0_S	333.9
21	20	V15	8_0_S	235.94
22	21	V15	8_0_S	254.61
23	22	V16	8_0_S	309.581
24	23	V16	8_0_S	335.052
25	24	V16	8_0_S	313.568
26	25	V16	8_0_S	346.353
27	26	V16	8_0_S	359.522

ANOVA code

```
# ANOVA For Morphometric Data

# read in data file
size<-read.csv("Spurp_OASV2_LarvalLengths.csv",header = TRUE)
head(size)

# run ANOVA
urchAnova<-aov(Size~Treatment,data = size)
summary(urchAnova)

# boxplot
boxplot(Size~Treatment,data=size,col=c("red","pink","green","lightgreen","blue"
,"lightblue"), main="Larval length decreases with decreasing pH, \n partial rescue
from variability", xlab = "pH Treatment", ylab = expression(paste("Larval length: ",
mu, "m")))

thsd<-TukeyHSD(urchAnova, conf.level = 0.95)
options(digits = 20)
print(thsd)
```

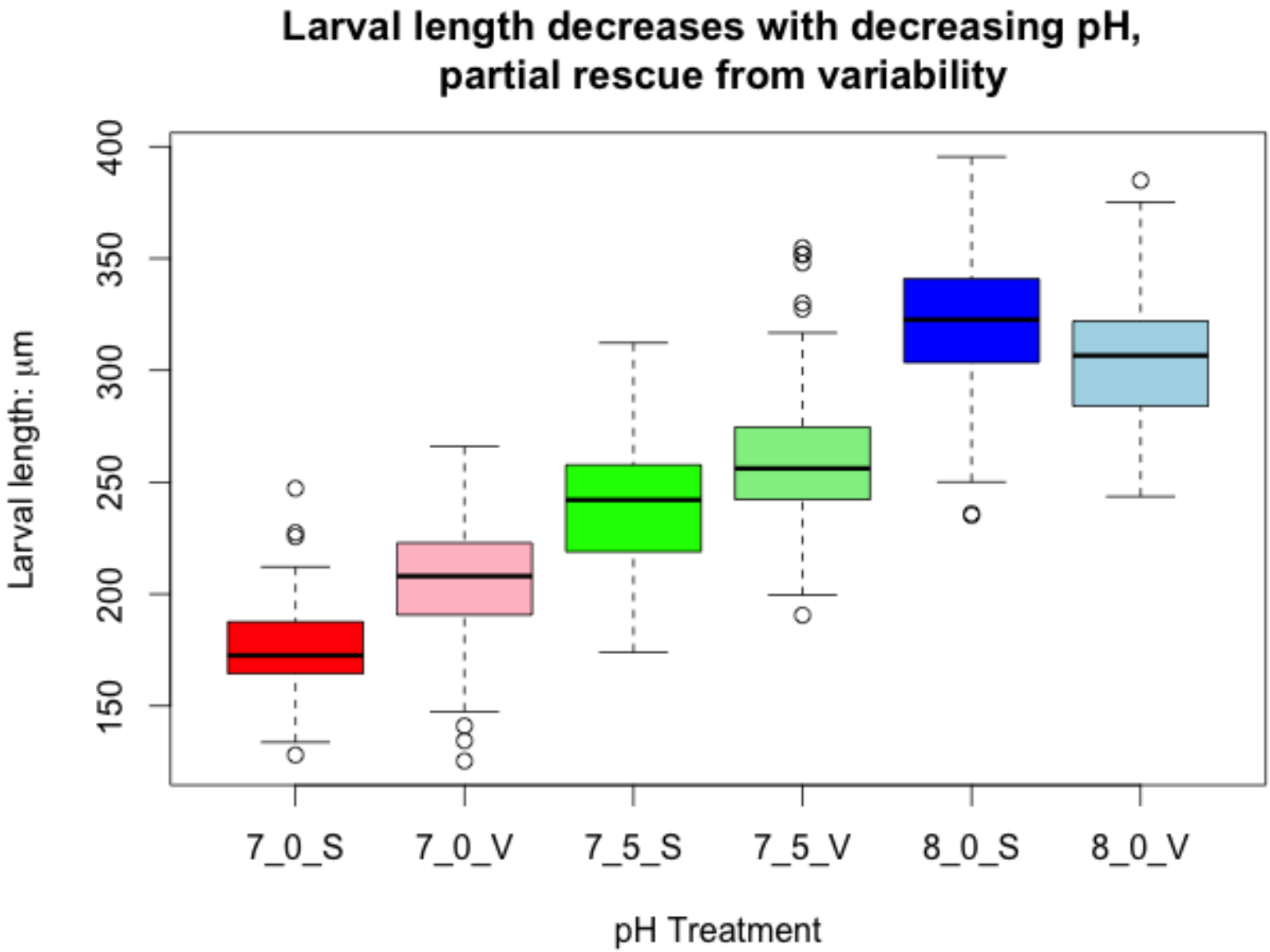
```
# 2-way ANOVA For Morphometric Data

# read in data file
size2<-read.csv("morphometrics_OASV2_separatedTreatments.csv",header =
TRUE, sep = ",")

# run 2-way ANOVA
urchAnova2<-aov(Size ~ pH*Condition, data = size2)
summary(urchAnova2)
```

ANOVA Results

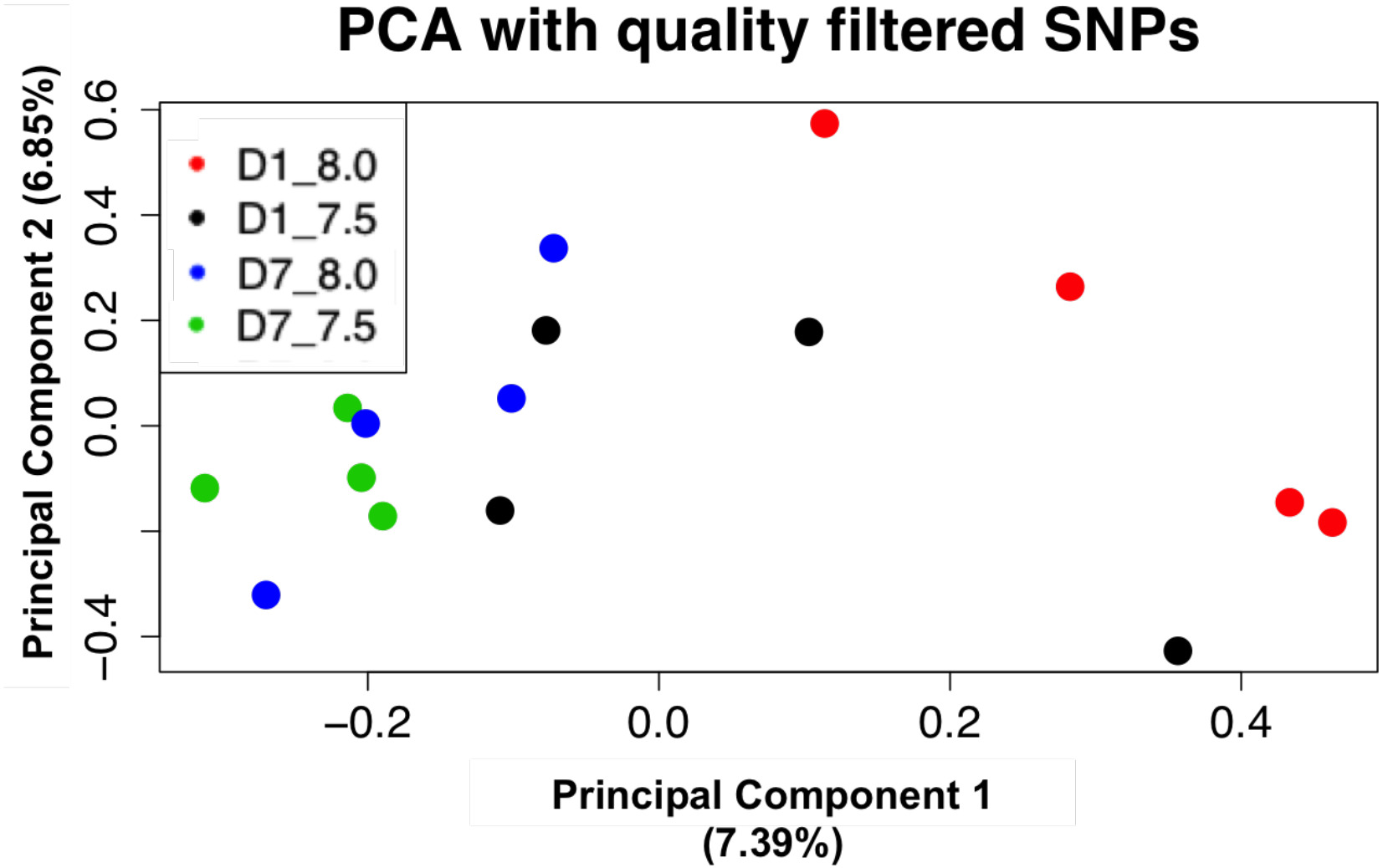
```
> summary(urchAnova)
             Df  Sum Sq Mean Sq F value Pr(>F)
Treatment     5 1421469  284294   355.1 <2e-16 ***
Residuals   582  465916     801
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> summary(urchAnova2)
               Df  Sum Sq Mean Sq F value   Pr(>F)
pH              1 1353954 1353954 1668.62  < 2e-16 ***
Condition       1   12468   12468   15.37 9.91e-05 ***
pH:Condition    1   47093   47093   58.04 1.04e-13 ***
Residuals     584  473870     811
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

ANOVA Boxplot



Capture-Seq Preliminary Results



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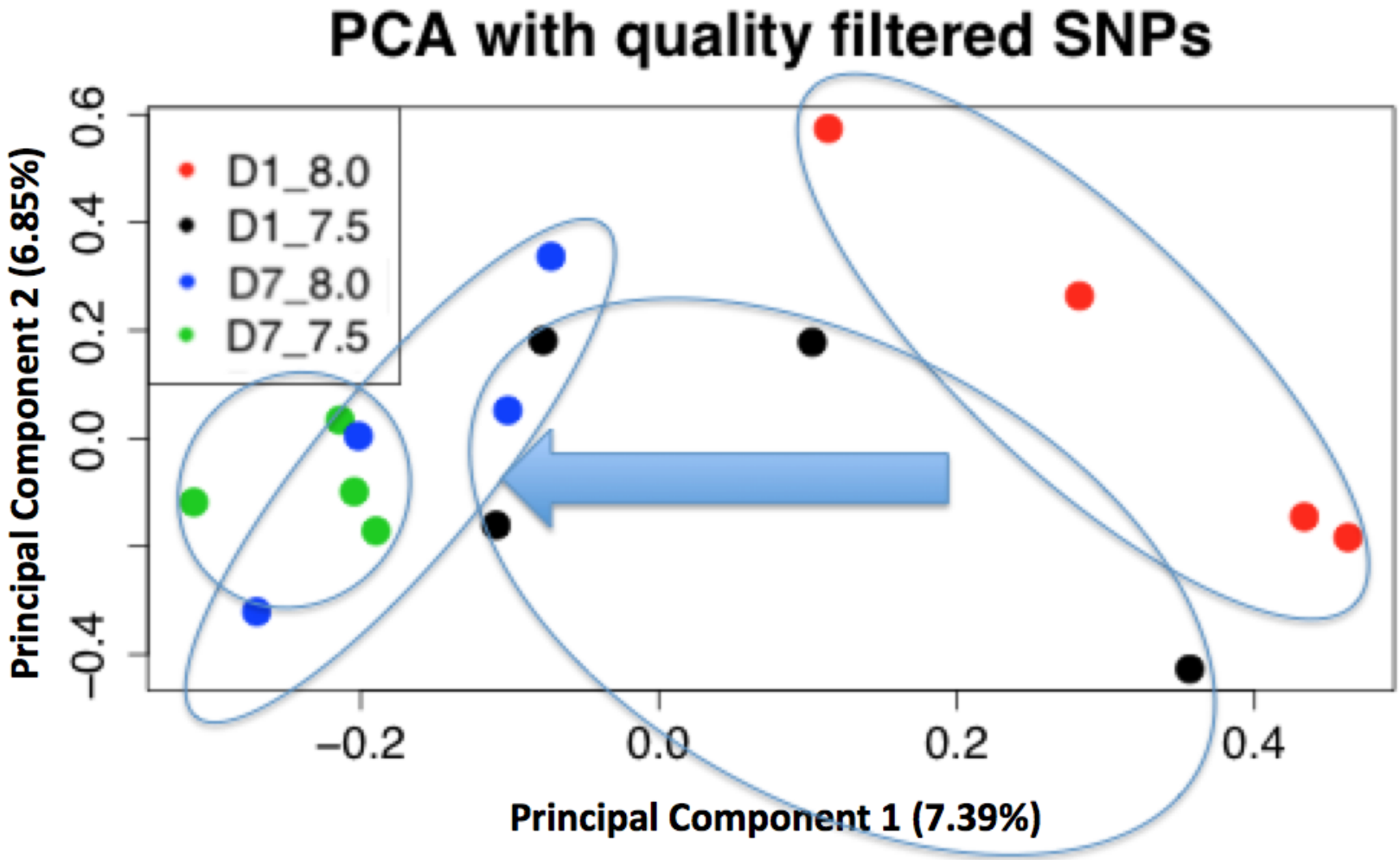

Conclusion

* Decrease in larval body length under extreme acidfication conditions - will they be able to further develop and metamorphose?

* Rescue effect of pH variability

* Loss of genetic diversity as consequence of selection in response to extreme acidification - capture-seq method appears promising

Acknowledgements

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Pete & Pat (San Diego)

Rapid Genomics

The UNIVERSITY of VERMONT