Chapter 3: Physiology

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14 January 2020

# Results

### (A) Coral host and algal endosymbiont physiology

Coral host total tissue energy reserves (mg cm-2) was calculated as the sum of each protein, lipid, and carbohydrate value per coral host. Total host energy reserves of *P. astreoides* at T0 were clearly greater than the total energy reserves quantified in coral hosts maintained under at control treatment at T90 (**Figure 1A**). There was no difference in total energy reserves between T0 and T90 control coral hosts in either *S. siderea* or *P. strigosa*. Elevated temperature (31°C) resulted in a clear reduction in total coral host energy reserves in only *P. strigosa* across all *p*CO2 treatments (**Figure 1A**). No overall effect of *p*CO2 was quantified in any of the four species examined.

Algal endosymbiont cell density (106 cells cm-2) in *P. astreoides* T0 densities were clearly lower than those measured under all treatments at T90 (**Figure 1B**). Algal endosymbiont cell densities did not exhibit a statistically clear difference between T0 fragments and T90 fragments maintained at the control treatment in *S. siderea* or *P. strigosa*. Neither *p*CO2 nor temperature exhibited a statistically clear overall effect on algal endosymbiont cell densities quantified at T90 in any of the three coral species (**Figure 1B**). Algal endosymbiont chlorophyll a content (ug cm-2) of *S. siderea* and *P. strigosa* at T0 was lower than the measured chlorophyll a in fragments maintained in the control treatment at T90 (**Figure 1C**). Conversely, chlorophyll a measured at T0 was not clearly different than in fragments reared in the control treatment at T90 for *P. astreoides*. All species exhibited reduced algal endosymbiont chlorophyll a in the highest *p*CO2 treatment, while elevated temperature (31°C) only clearly reduces chlorophyll a in the algal endosymbionts associated with *P. strigosa* (**Figure 1C**).

*Need a statement about PCAs* (**Figure 2**)

### (B) Host transcriptomic responses

I will talk about HOST trends/findings about gene expression here. (**Figure 3**)

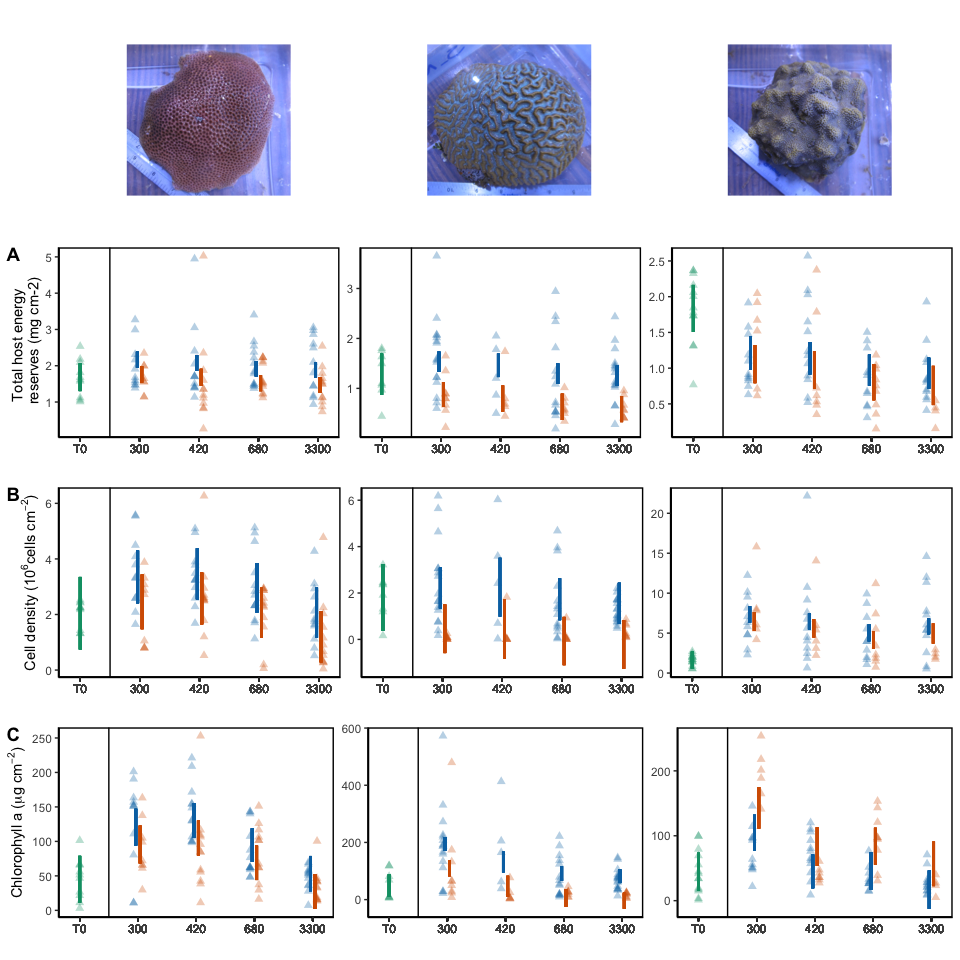
### (C) Algal endosymbiont transcriptomic responses

I will talk about symbiont trends/findings about gene expression here. (**Figure 4**)

### (D) Overall physiological response

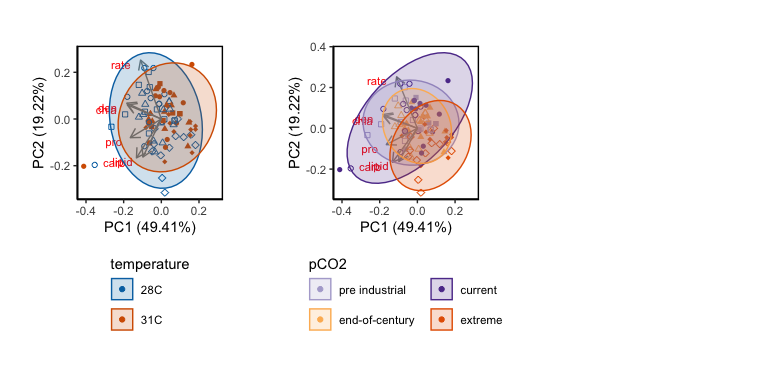
This will discuss overall responses and the WGCNA here. *– This will be excluded from my dissertation, but included in the manuscript*

# Figure 1: Holobiont physiology

 **Figure 1.** Modeled 95% confidence interval of (**A**) total host energy reserves (mg cm-2), (**B**) cell density (106 cells cm-2), and (**C**) Chlorophyll a (ug cm-2) for *S. siderea*, *P. strigosa*, and *P. astreoides* at T0 (green) or T90 (red/blue), with individual coral fragment physiology denoted by points. Blue denotes 28°C and red denotes 31°C, with *p*CO2 treatment along the x axis.

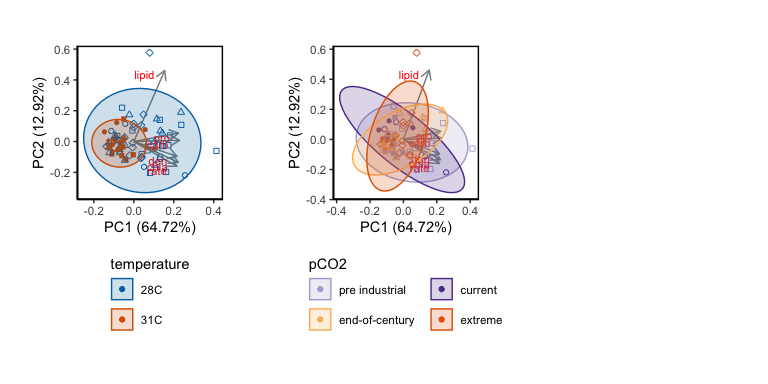
# Figure 2: Holobiont PCAs

#### **A |** *Siderastrea siderea*



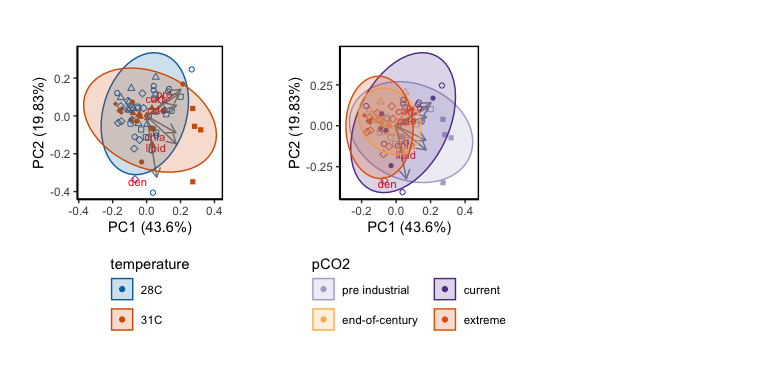
##   
## Call:  
## adonis(formula = value ~ ftemp + fpco2 + reef, data = s.df.l, method = "eu")   
##   
## Permutation: free  
## Number of permutations: 999  
##   
## Terms added sequentially (first to last)  
##   
## Df SumsOfSqs MeanSqs F.Model R2 Pr(>F)   
## ftemp 1 3111 3111.1 2.0968 0.00376 0.145   
## fpco2 3 14260 4753.4 3.2037 0.01722 0.024 \*  
## reef 1 736 736.2 0.4962 0.00089 0.485   
## Residuals 546 810104 1483.7 0.97814   
## Total 551 828211 1.00000   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### **B |** *Pseudodiploria strigosa*



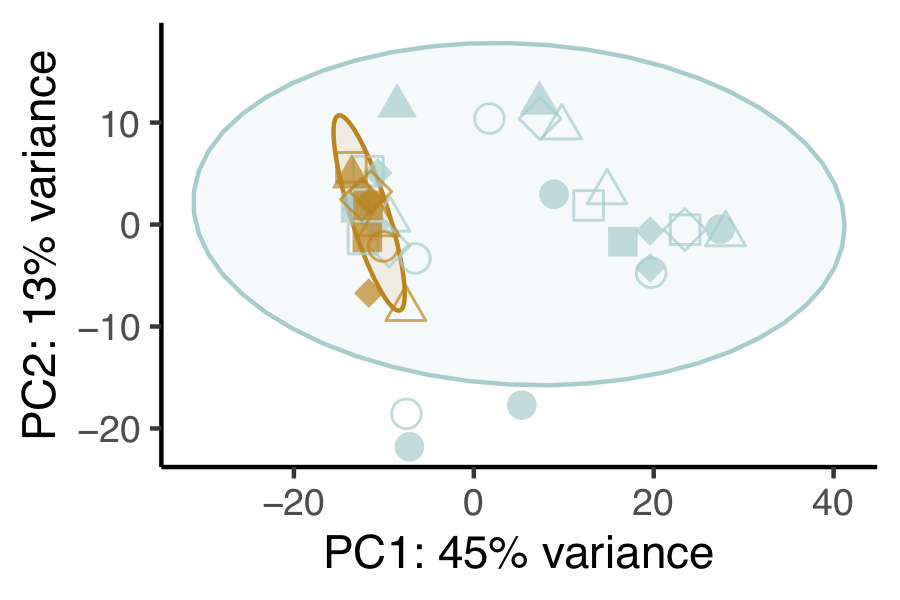
##   
## Call:  
## adonis(formula = value ~ reef + ftemp + fpco2, data = p.df.l, method = "eu")   
##   
## Permutation: free  
## Number of permutations: 999  
##   
## Terms added sequentially (first to last)  
##   
## Df SumsOfSqs MeanSqs F.Model R2 Pr(>F)   
## reef 1 10809 10809.2 3.4558 0.00709 0.071 .  
## ftemp 1 18776 18775.5 6.0027 0.01231 0.013 \*  
## fpco2 3 31998 10666.2 3.4100 0.02098 0.019 \*  
## Residuals 468 1463839 3127.9 0.95963   
## Total 473 1525422 1.00000   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#### **C |** *Porites astreoides*

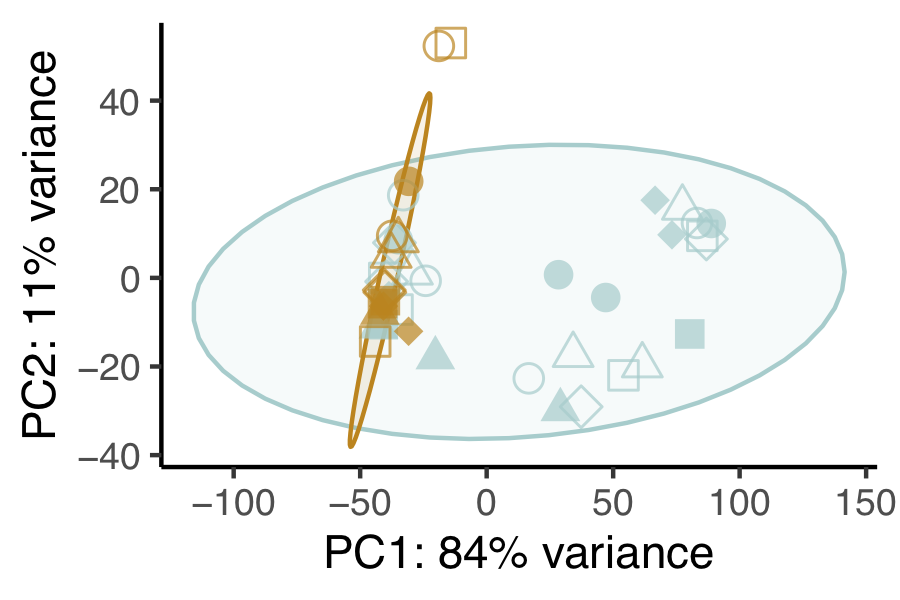


##   
## Call:  
## adonis(formula = value ~ ftemp + fpco2 + reef + ftemp:fpco2, data = a.df.l, method = "eu")   
##   
## Permutation: free  
## Number of permutations: 999  
##   
## Terms added sequentially (first to last)  
##   
## Df SumsOfSqs MeanSqs F.Model R2 Pr(>F)   
## ftemp 1 4401 4401.1 4.1700 0.00972 0.056 .   
## fpco2 3 12017 4005.7 3.7953 0.02654 0.005 \*\*  
## reef 1 116 116.4 0.1103 0.00026 0.737   
## ftemp:fpco2 3 8889 2963.0 2.8074 0.01963 0.049 \*   
## Residuals 405 427447 1055.4 0.94386   
## Total 413 452871 1.00000   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# Figure 3: Gene expression by reef environment

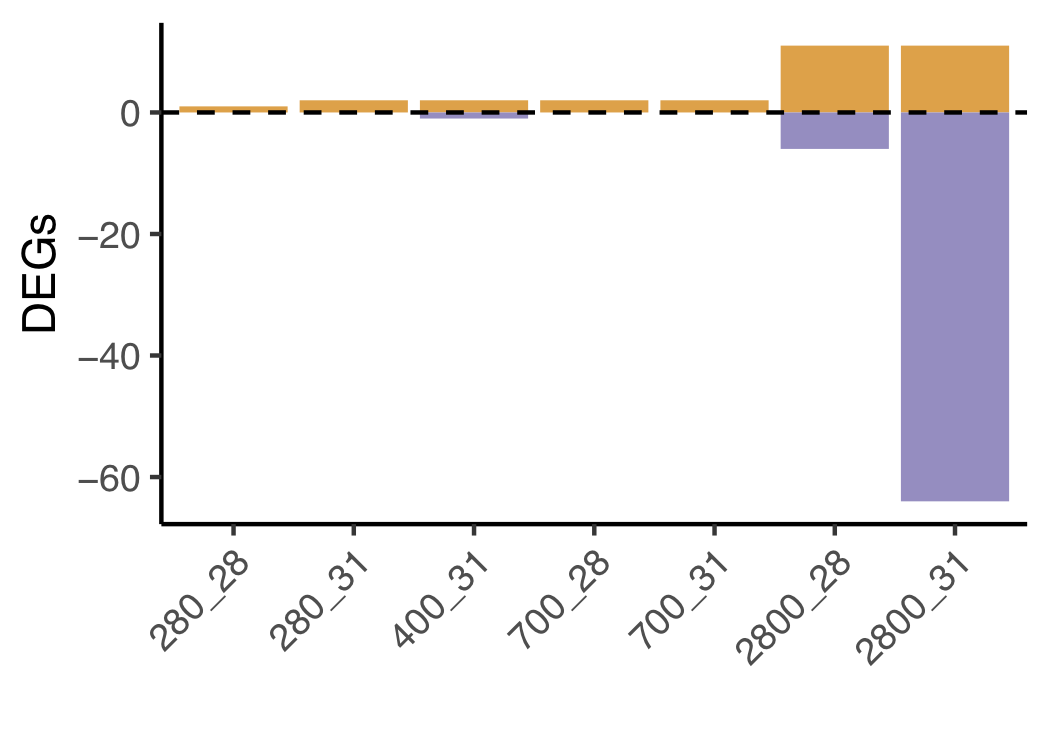


**A |**  Host gene expression by treatment

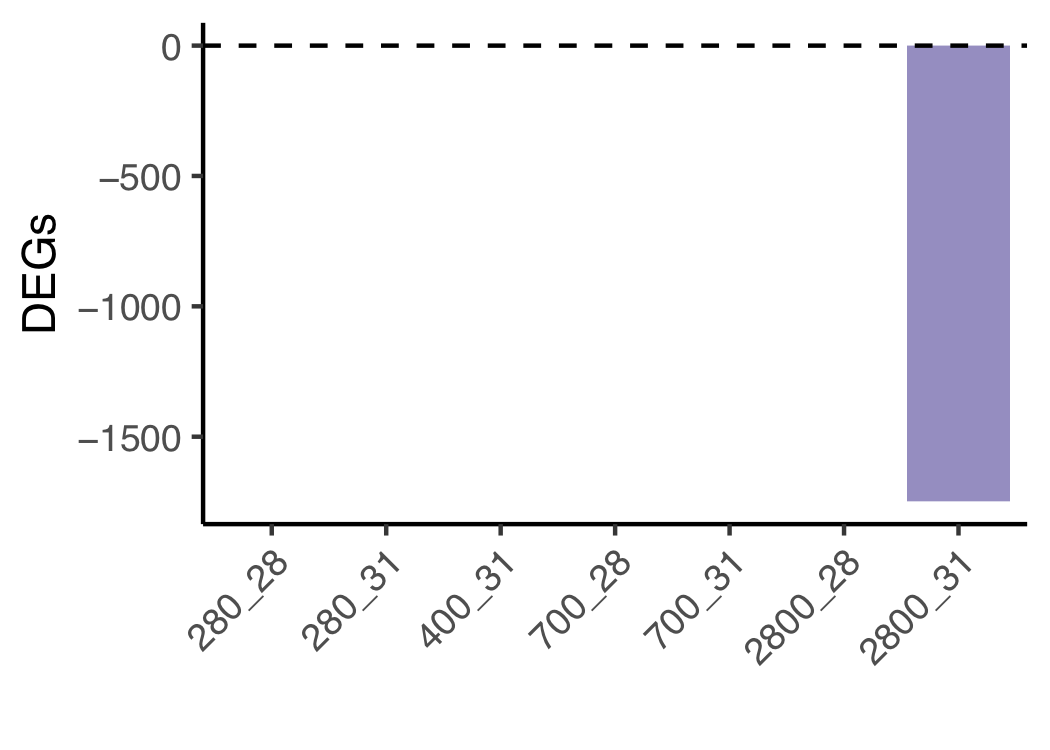


**B |**  Endosymbiont gene expression by treatment

# Figure 4: Differentially expressed genes by treatment



**A |**  Host significantly differentially expressed genes



**B |**  Endosymbiont significantly differentially expressed genes

sessionInfo()

## R version 3.5.1 (2018-07-02)  
## Platform: x86\_64-apple-darwin15.6.0 (64-bit)  
## Running under: macOS High Sierra 10.13.6  
##   
## Matrix products: default  
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib  
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib  
##   
## locale:  
## [1] en\_US.UTF-8/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8  
##   
## attached base packages:  
## [1] grid stats graphics grDevices utils datasets methods   
## [8] base   
##   
## other attached packages:  
## [1] magick\_2.2 lme4\_1.1-21 Matrix\_1.2-17 kableExtra\_1.1.0  
## [5] ggfortify\_0.4.7 cowplot\_1.0.0 Rmisc\_1.5 shiny\_1.4.0   
## [9] vegan\_2.5-5 lattice\_0.20-38 permute\_0.9-5 forcats\_0.4.0   
## [13] stringr\_1.4.0 purrr\_0.3.3 tibble\_2.1.3 tidyverse\_1.3.0   
## [17] plotly\_4.9.0 openxlsx\_4.1.2 tidyr\_1.0.0 ggbiplot\_0.55   
## [21] scales\_1.1.0 plyr\_1.8.5 dplyr\_0.8.3 ggplot2\_3.2.1   
## [25] readr\_1.3.1 knitr\_1.25   
##   
## loaded via a namespace (and not attached):  
## [1] nlme\_3.1-140 fs\_1.3.1 lubridate\_1.7.4   
## [4] webshot\_0.5.1 httr\_1.4.1 tools\_3.5.1   
## [7] backports\_1.1.5 R6\_2.4.1 DBI\_1.0.0   
## [10] lazyeval\_0.2.2 mgcv\_1.8-28 colorspace\_1.4-1   
## [13] withr\_2.1.2 tidyselect\_0.2.5 gridExtra\_2.3   
## [16] compiler\_3.5.1 cli\_2.0.1 rvest\_0.3.5   
## [19] xml2\_1.2.2 labeling\_0.3 digest\_0.6.23   
## [22] minqa\_1.2.4 rmarkdown\_1.16 pkgconfig\_2.0.3   
## [25] htmltools\_0.4.0 highr\_0.8 dbplyr\_1.4.2   
## [28] fastmap\_1.0.1 htmlwidgets\_1.3 rlang\_0.4.2   
## [31] readxl\_1.3.1 rstudioapi\_0.10 farver\_2.0.1   
## [34] generics\_0.0.2 jsonlite\_1.6 zip\_2.0.3   
## [37] magrittr\_1.5 Rcpp\_1.0.3 munsell\_0.5.0   
## [40] fansi\_0.4.1 lifecycle\_0.1.0 stringi\_1.4.5   
## [43] yaml\_2.2.0 MASS\_7.3-51.4 parallel\_3.5.1   
## [46] promises\_1.1.0 crayon\_1.3.4 haven\_2.2.0   
## [49] splines\_3.5.1 hms\_0.5.3 zeallot\_0.1.0   
## [52] pillar\_1.4.3 boot\_1.3-23 reprex\_0.3.0   
## [55] glue\_1.3.1 evaluate\_0.14 data.table\_1.12.2  
## [58] modelr\_0.1.5 nloptr\_1.2.1 vctrs\_0.2.1   
## [61] httpuv\_1.5.2 cellranger\_1.1.0 gtable\_0.3.0   
## [64] assertthat\_0.2.1 xfun\_0.8 mime\_0.7   
## [67] xtable\_1.8-4 broom\_0.5.2 later\_1.0.0   
## [70] viridisLite\_0.3.0 cluster\_2.1.0 ellipsis\_0.3.0