Chapter 3: Physiology

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# 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 pCO2 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**).

#### (B) Host transcriptomic responses

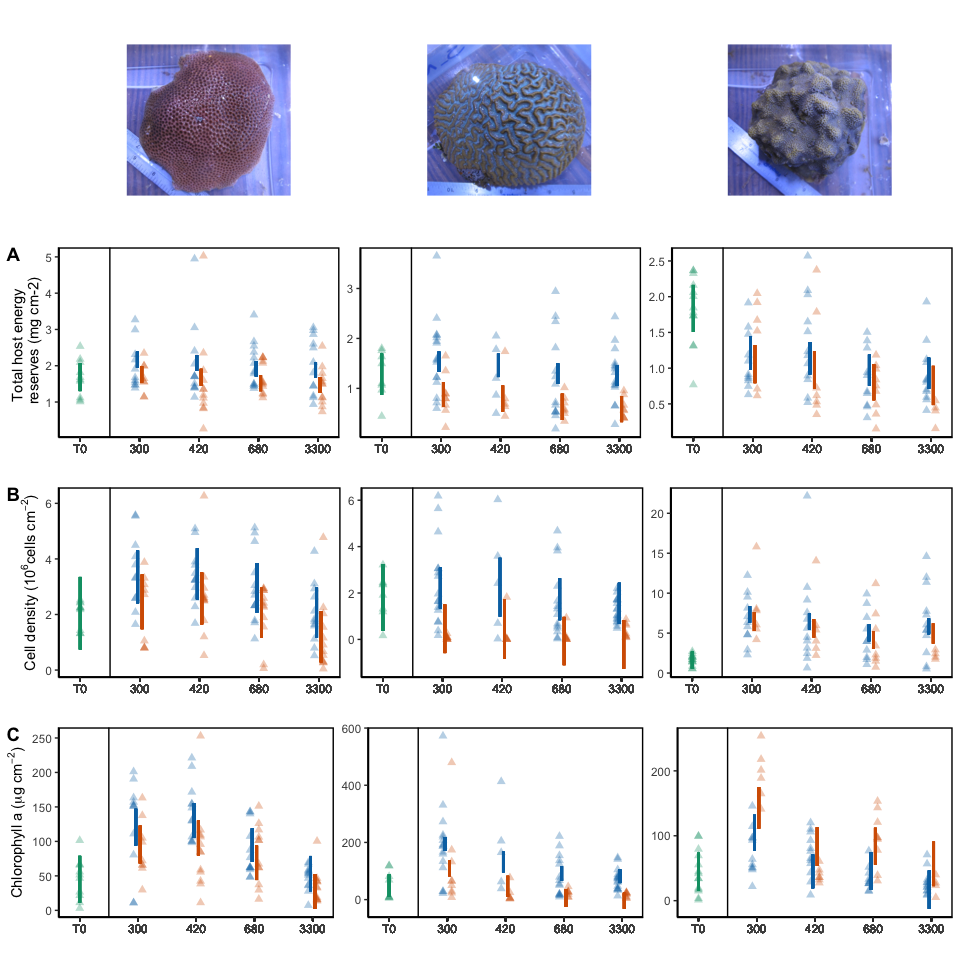
I will talk about HOST trends/findings about gene expression here.

#### (C) Algal endosymbiont transcriptomic responses

I will talk about symbiont trends/findings about gene expression here.

#### (D) Overall physiological response

This will discuss overall responses and the WGCNA here.

 **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.

### PCAs

## Loading required package: scales

##   
## Attaching package: 'scales'

## The following object is masked from 'package:purrr':  
##   
## discard

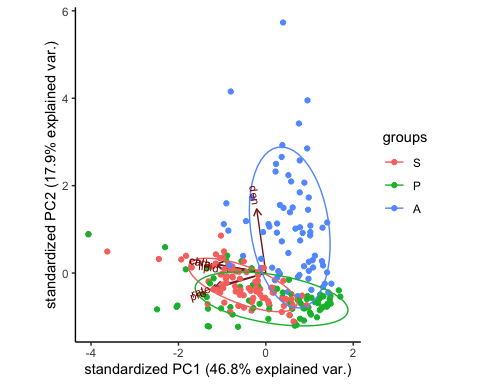
## The following object is masked from 'package:readr':  
##   
## col\_factor

## Loading required package: grid

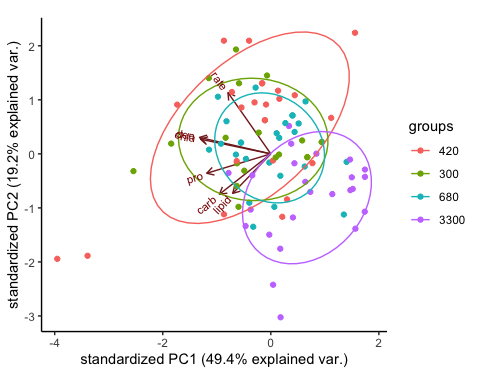
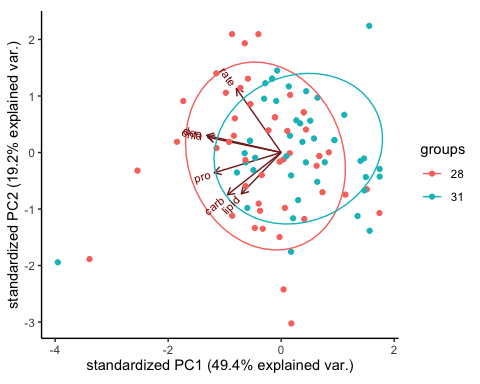
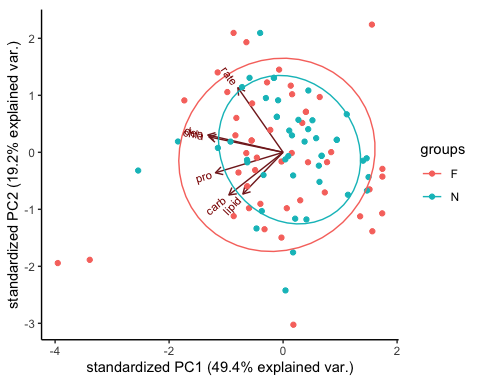
##   
## Attaching package: 'ggbiplot'

## The following object is masked from 'package:ggfortify':  
##   
## ggbiplot

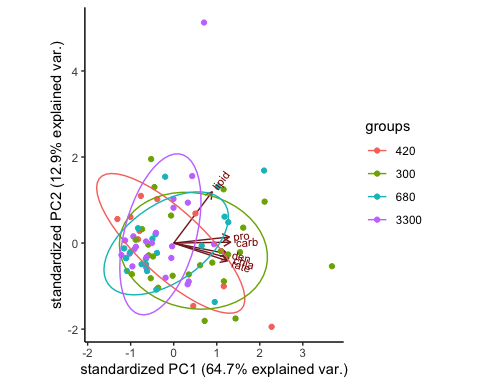
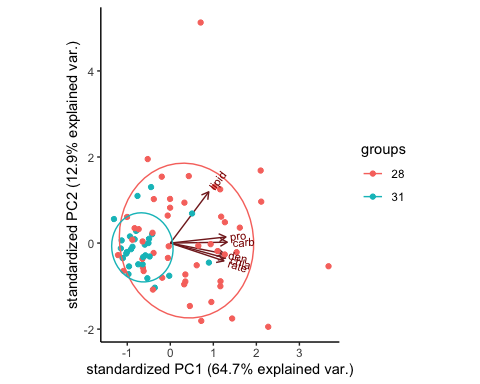
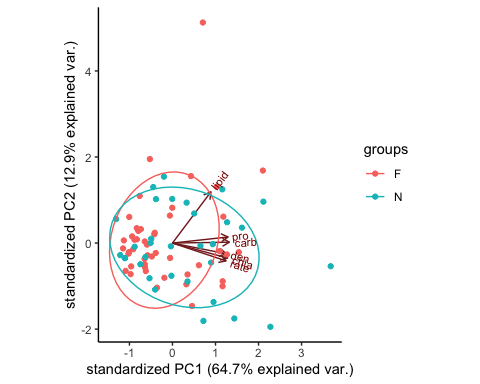
## Importance of components:  
## PC1 PC2 PC3 PC4 PC5 PC6  
## Standard deviation 1.6754 1.0352 0.8997 0.75012 0.64963 0.57192  
## Proportion of Variance 0.4678 0.1786 0.1349 0.09378 0.07034 0.05452  
## Cumulative Proportion 0.4678 0.6465 0.7814 0.87515 0.94548 1.00000



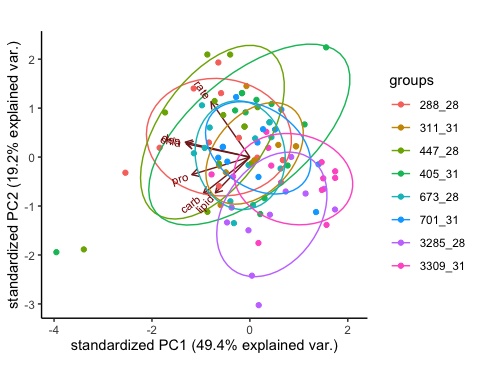
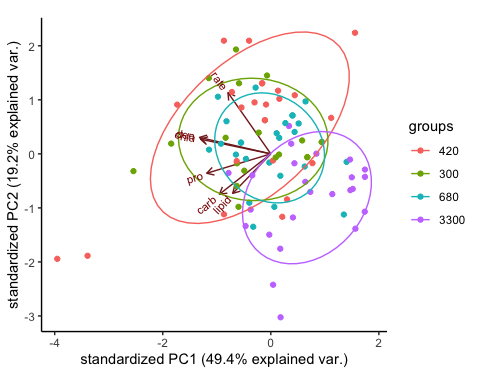
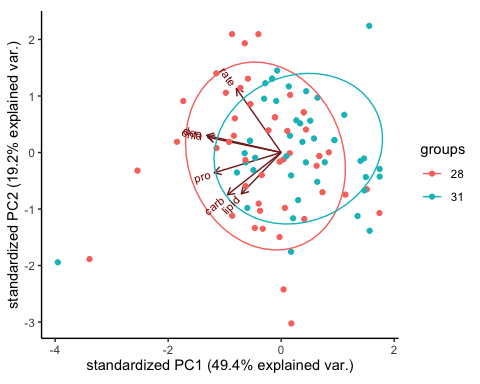
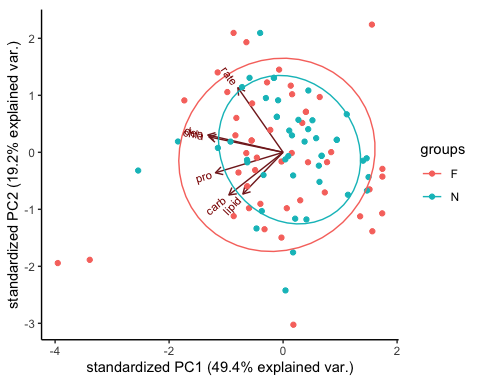
##   
## Call:  
## adonis(formula = value ~ ftemp + fpco2 + param + ftemp:fpco2 + ftemp:param + fpco2:param, data = s.df.l, method = "eu")   
##   
## Permutation: free  
## Number of permutations: 999  
##   
## Terms added sequentially (first to last)  
##   
## Df SumsOfSqs MeanSqs F.Model R2 Pr(>F)   
## ftemp 1 3111 3111 9.50 0.00376 0.004 \*\*   
## fpco2 3 14260 4753 14.51 0.01722 0.001 \*\*\*  
## param 5 559386 111877 341.49 0.67541 0.001 \*\*\*  
## ftemp:fpco2 3 1691 564 1.72 0.00204 0.156   
## ftemp:param 5 13795 2759 8.42 0.01666 0.001 \*\*\*  
## fpco2:param 15 65936 4396 13.42 0.07961 0.001 \*\*\*  
## Residuals 519 170031 328 0.20530   
## Total 551 828211 1.00000   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1



##   
## Call:  
## adonis(formula = value ~ reef + ftemp + fpco2 + param + reef:param + ftemp:param + fpco2:param, 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 8.252 0.00709 0.007 \*\*   
## ftemp 1 18776 18776 14.333 0.01231 0.001 \*\*\*  
## fpco2 3 31998 10666 8.142 0.02098 0.001 \*\*\*  
## param 5 600292 120058 91.650 0.39353 0.001 \*\*\*  
## reef:param 5 50718 10144 7.743 0.03325 0.001 \*\*\*  
## ftemp:param 5 85223 17045 13.011 0.05587 0.001 \*\*\*  
## fpco2:param 15 153837 10256 7.829 0.10085 0.001 \*\*\*  
## Residuals 438 573767 1310 0.37614   
## Total 473 1525422 1.00000   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1



##   
## Call:  
## adonis(formula = value ~ ftemp + fpco2 + param + ftemp:param + fpco2:param, 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 3111 3111 9.46 0.00376 0.002 \*\*   
## fpco2 3 14260 4753 14.45 0.01722 0.001 \*\*\*  
## param 5 559386 111877 340.08 0.67541 0.001 \*\*\*  
## ftemp:param 5 13795 2759 8.39 0.01666 0.001 \*\*\*  
## fpco2:param 15 65936 4396 13.36 0.07961 0.001 \*\*\*  
## Residuals 522 171723 329 0.20734   
## Total 551 828211 1.00000   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1



sessionInfo()

## R version 3.5.2 (2018-12-20)  
## Platform: x86\_64-apple-darwin15.6.0 (64-bit)  
## Running under: macOS Mojave 10.14.6  
##   
## 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] ggbiplot\_0.55 scales\_1.0.0 magick\_2.2 lme4\_1.1-21   
## [5] Matrix\_1.2-17 kableExtra\_1.1.0 ggfortify\_0.4.7 cowplot\_1.0.0   
## [9] Rmisc\_1.5 plyr\_1.8.4 shiny\_1.4.0 vegan\_2.5-6   
## [13] lattice\_0.20-38 permute\_0.9-5 forcats\_0.4.0 stringr\_1.4.0   
## [17] purrr\_0.3.3 tibble\_2.1.3 tidyverse\_1.2.1 plotly\_4.9.0   
## [21] openxlsx\_4.1.0.1 tidyr\_1.0.0 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\_3.1-141 lubridate\_1.7.4 webshot\_0.5.1   
## [4] httr\_1.4.1 tools\_3.5.2 backports\_1.1.5   
## [7] R6\_2.4.0 lazyeval\_0.2.2 mgcv\_1.8-28   
## [10] colorspace\_1.4-1 withr\_2.1.2 tidyselect\_0.2.5   
## [13] gridExtra\_2.3 compiler\_3.5.2 cli\_1.1.0   
## [16] rvest\_0.3.4 xml2\_1.2.2 labeling\_0.3   
## [19] digest\_0.6.22 minqa\_1.2.4 rmarkdown\_1.16   
## [22] pkgconfig\_2.0.3 htmltools\_0.4.0 highr\_0.8   
## [25] fastmap\_1.0.1 htmlwidgets\_1.5.1 rlang\_0.4.1   
## [28] readxl\_1.3.1 rstudioapi\_0.10 generics\_0.0.2   
## [31] jsonlite\_1.6 zip\_2.0.4 magrittr\_1.5   
## [34] Rcpp\_1.0.2 munsell\_0.5.0 lifecycle\_0.1.0   
## [37] stringi\_1.4.3 yaml\_2.2.0 MASS\_7.3-51.4   
## [40] parallel\_3.5.2 promises\_1.1.0 crayon\_1.3.4   
## [43] haven\_2.1.1 splines\_3.5.2 hms\_0.5.1   
## [46] zeallot\_0.1.0 pillar\_1.4.2 boot\_1.3-23   
## [49] glue\_1.3.1 evaluate\_0.14 data.table\_1.12.6  
## [52] modelr\_0.1.5 vctrs\_0.2.0 nloptr\_1.2.1   
## [55] httpuv\_1.5.2 cellranger\_1.1.0 gtable\_0.3.0   
## [58] assertthat\_0.2.1 xfun\_0.10 mime\_0.7   
## [61] xtable\_1.8-4 broom\_0.5.2 later\_1.0.0   
## [64] viridisLite\_0.3.0 cluster\_2.1.0 ellipsis\_0.3.0