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

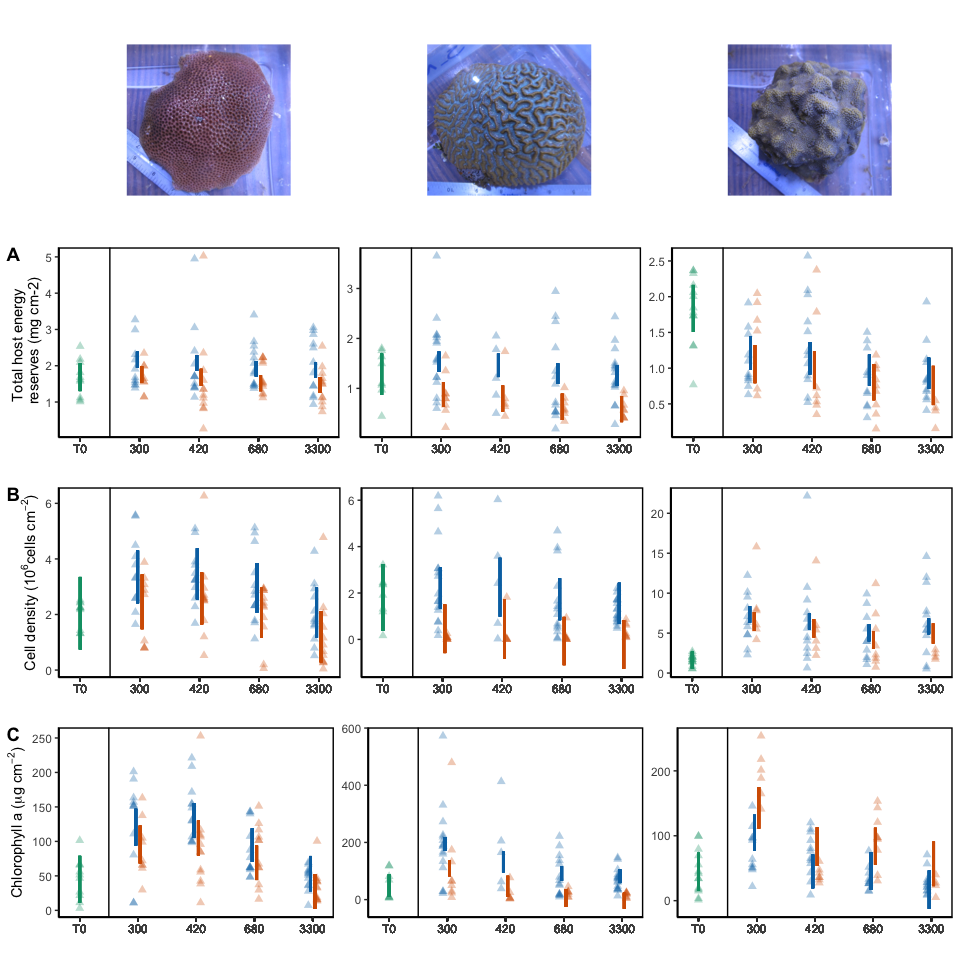
I will talk about HOST trends/findings about gene expression here.

#### (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.

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] stats graphics grDevices utils datasets methods 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 plyr\_1.8.4   
## [9] lattice\_0.20-38 shiny\_1.4.0 forcats\_0.4.0 stringr\_1.4.0   
## [13] purrr\_0.3.3 tibble\_2.1.3 tidyverse\_1.2.1 plotly\_4.9.0   
## [17] openxlsx\_4.1.0.1 tidyr\_1.0.0 dplyr\_0.8.3 ggplot2\_3.2.1   
## [21] readr\_1.3.1 knitr\_1.25   
##   
## loaded via a namespace (and not attached):  
## [1] httr\_1.4.1 jsonlite\_1.6 viridisLite\_0.3.0  
## [4] splines\_3.5.2 modelr\_0.1.5 assertthat\_0.2.1   
## [7] highr\_0.8 cellranger\_1.1.0 yaml\_2.2.0   
## [10] pillar\_1.4.2 backports\_1.1.5 glue\_1.3.1   
## [13] digest\_0.6.22 promises\_1.1.0 rvest\_0.3.4   
## [16] minqa\_1.2.4 colorspace\_1.4-1 htmltools\_0.4.0   
## [19] httpuv\_1.5.2 pkgconfig\_2.0.3 broom\_0.5.2   
## [22] haven\_2.1.1 xtable\_1.8-4 scales\_1.0.0   
## [25] webshot\_0.5.1 later\_1.0.0 generics\_0.0.2   
## [28] ellipsis\_0.3.0 withr\_2.1.2 lazyeval\_0.2.2   
## [31] cli\_1.1.0 magrittr\_1.5 crayon\_1.3.4   
## [34] readxl\_1.3.1 mime\_0.7 evaluate\_0.14   
## [37] nlme\_3.1-141 MASS\_7.3-51.4 xml2\_1.2.2   
## [40] tools\_3.5.2 data.table\_1.12.6 hms\_0.5.1   
## [43] lifecycle\_0.1.0 munsell\_0.5.0 zip\_2.0.4   
## [46] compiler\_3.5.2 rlang\_0.4.1 grid\_3.5.2   
## [49] nloptr\_1.2.1 rstudioapi\_0.10 htmlwidgets\_1.5.1  
## [52] labeling\_0.3 rmarkdown\_1.16 boot\_1.3-23   
## [55] gtable\_0.3.0 R6\_2.4.0 gridExtra\_2.3   
## [58] lubridate\_1.7.4 fastmap\_1.0.1 zeallot\_0.1.0   
## [61] stringi\_1.4.3 Rcpp\_1.0.2 vctrs\_0.2.0   
## [64] tidyselect\_0.2.5 xfun\_0.10