

Introduction

Corals have a symbiotic relationship with dinoflagellate algae within their cells.

Corals and their symbiont can be dispersed over great distances, but organisms that live at different depths experience different conditions.

We used extensive genomic tools to understand the major physiological differences between two symbiont species that are specialized to live in different habitats that are as close as 200 meters.

Methods

- Transcriptome Data was taken from symbionts of Caribbean octocorals at two depth ranges.
- SNP data was used to run PCAs and Admixture.
- Phylogenetic tree made using 28S genetic marker for each *Symbiodiniaceae* genus.
- Go enrichment analysis of genes associated with Biological processes between the two populations.

Discussion

- As seen in the PCA graphs there is a very clear genetic difference between the two symbiont populations. Enough difference to classify the populations as different species (30%), could even be enough to consider them indifferent genera.
- Transcriptome data was unused prior – allows for more accurate identification as well as identification of the genes under selection.
- Becoming more common in identification studies in other animals.
- Genes that encode for metabolism and photosynthesis were found to be under selection.
- Identifying and understanding the differences in symbionts can help better inform conservation efforts.

Future work: taxonomically identify the shallow species seen in this research, and use transcriptome data to identify more symbiont species, and use it to identify how they differ in mechanisms related to photosynthesis

RNA-seq data uncovers cryptic species of coral symbionts and determines genes under selection.



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Results

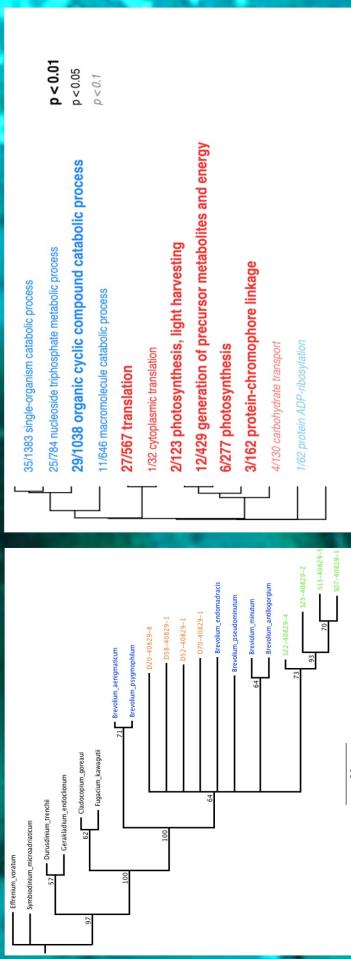


Figure 1. This is a 1000 bootstrap RAxML phylogenetic tree built using Geneious using the 28S molecular marker. Four samples from the deep population (orange) and Four from the Shallow species (green) were compared to each type species of the seven described *Symbiodiniaceae* genera, as well as each described *Breviolum* species (blue).



Figure 2. Gene Ontology enrichment analysis of the genes controlling biological processes that are under selection for the deep species after being transplanted to shallower depths. The font indicates the level of significance. Blue indicates up regulated genes.

Extra tables and graphs

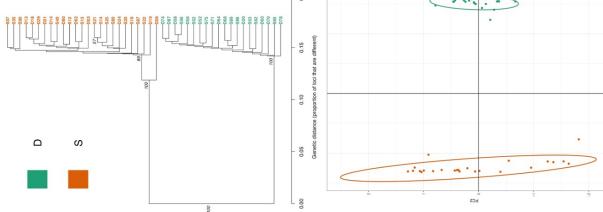


Figure 3: Distance Tree
Orange is the shallower group and Green is the deeper group

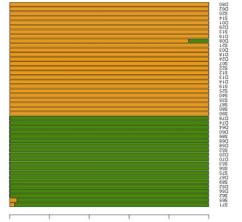


Figure 4: PCA graph
Principle component analysis of PCR1 vs PCR2



Figure 5: Admixture plot
Using K=2 as the assumption of # of populations

Larger versions with full figure descriptions found on website (Scan QR code)



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