



# The Combined Effects of Temperature and Ocean Acidification on the Resident Microbial Communities of South Florida Reef Corals

Emma Weber<sup>1</sup>, James Klaus<sup>1</sup>

<sup>1</sup>Rosenstiel School of Marine and Atmospheric Science, University of Miami, FL

## Introduction

Coral species face threats due to climate change in the form of many factors including increasing sea surface temperatures and ocean acidification.

Microbial communities are an important but understudied component of coral health<sup>1</sup> that assist in functions such as nutrient cycling, larval recruitment and settlement, and protection from pathogens<sup>2</sup>.

Few studies have observed the combined effects of rising temperature and ocean acidification on coral microbial communities. The stability of coral microbiomes under these stressful conditions may serve as an indicator of their resilience or sensitivity to future climate change conditions.

## Methods

Samples from five South Florida coral species were collected, fragmented, and allowed to recover for one month before being exposed to treatments of varying temperatures and pCO<sub>2</sub> levels for 8 weeks.<sup>3</sup>

RSMAS Climate Change Facility



Six treatments were created in 12 tanks, composed of two temperatures crossed with three pCO<sub>2</sub> levels.

Temperature (°C)	pCO <sub>2</sub> (µatm)
27 (control)	390 (control)
30.3	900
	1400

*Agaricites agaricia*  
Lettuce Coral



*Solenastrea hyades*  
Knobby Star Coral



Tissue scrapings were taken from the surfaces of the 86 coral samples. Microbes were characterized using 454 Pyrosequencing of 16s rRNA.<sup>3</sup>

Data was then analyzed at two microbial taxonomic levels with the goal of observing changes in microbial community composition within and between coral species and experimental treatments. Analysis was performed using PAST and Microsoft Excel.

## Results

The total number of microbial sequences across all coral samples was 620,844 and the average number of sequences per sample was 5,640. Microbes represented 55 phyla and 927 taxonomic groups at the genus level.

DCA for all Coral Samples

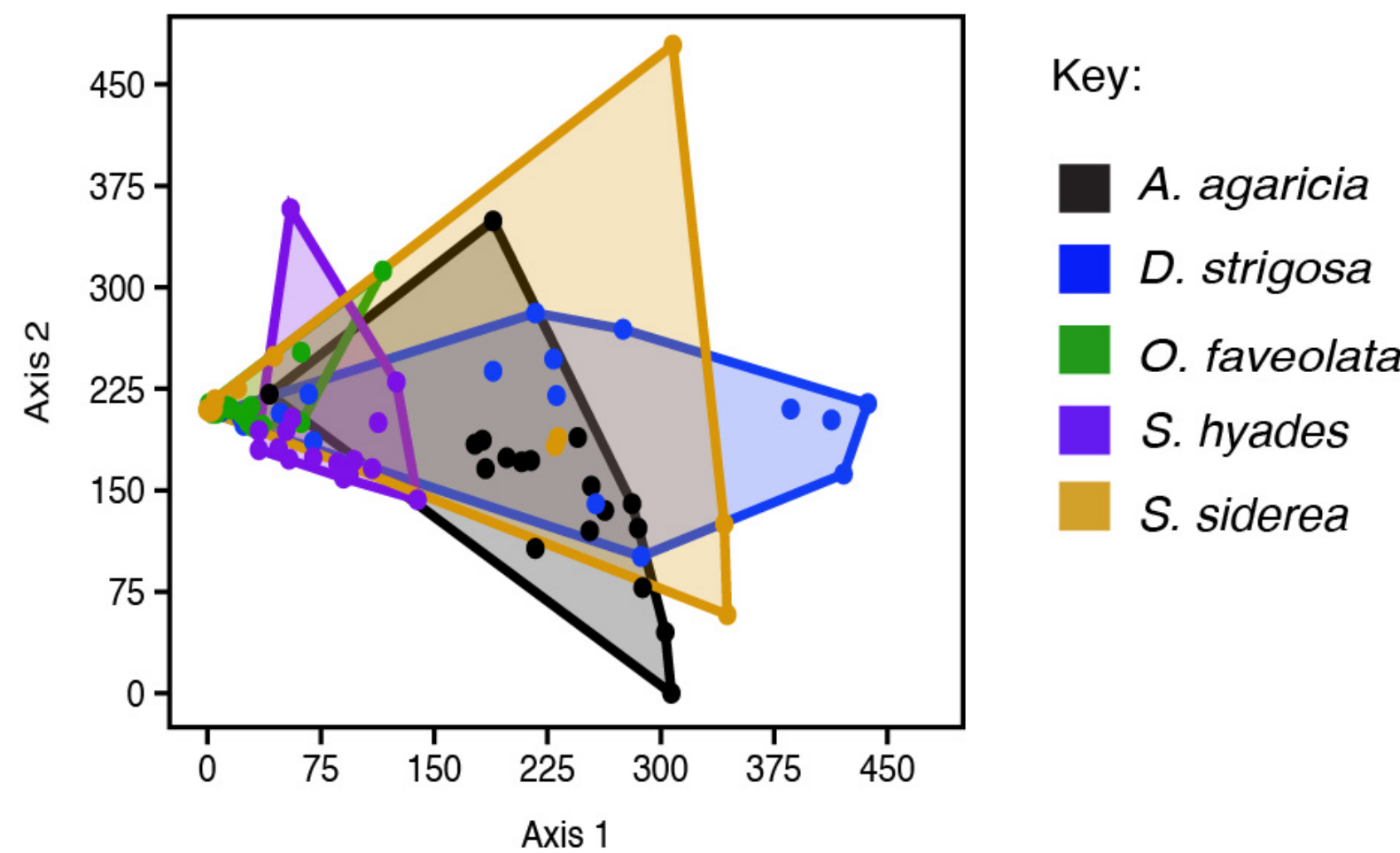


Figure 1. DCA plot compares microbial communities of all coral samples using microbial data at the genus level. Colored hulls each represent a coral species, and each dot represents a sample. Axis 1 accounts for 36.8% of total variance, and Axis 2 for 27.9% of variance. *Orbicella faveolata* and *S. hyades* form tight clusters at the lower end of Axis 1, while *A. agaricia*, *D. strigosa*, and *S. siderea* are more widely spread along both axes and broadly overlap with each other.

Microbial Percentages at Phylum Level for all Coral Samples

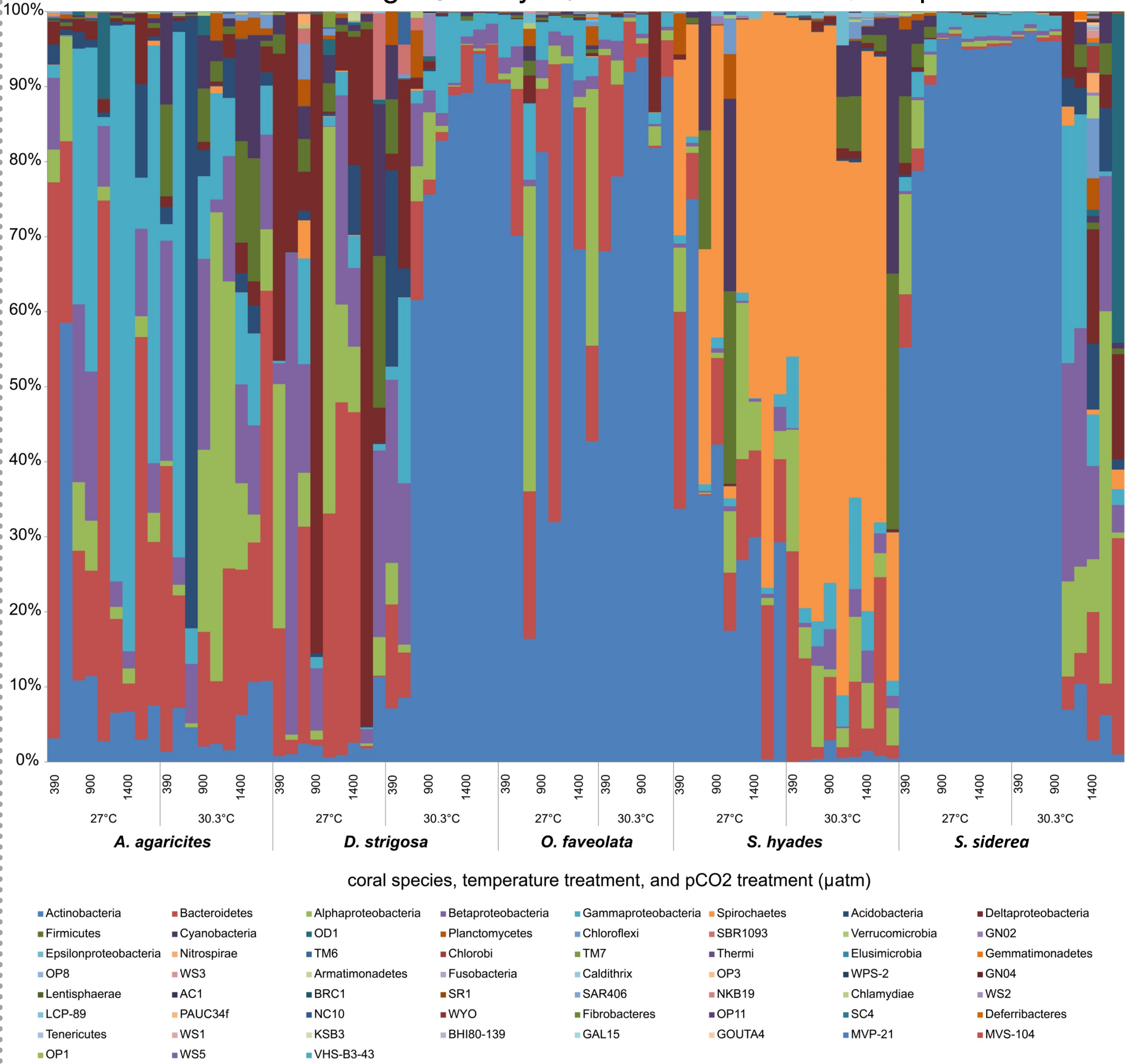
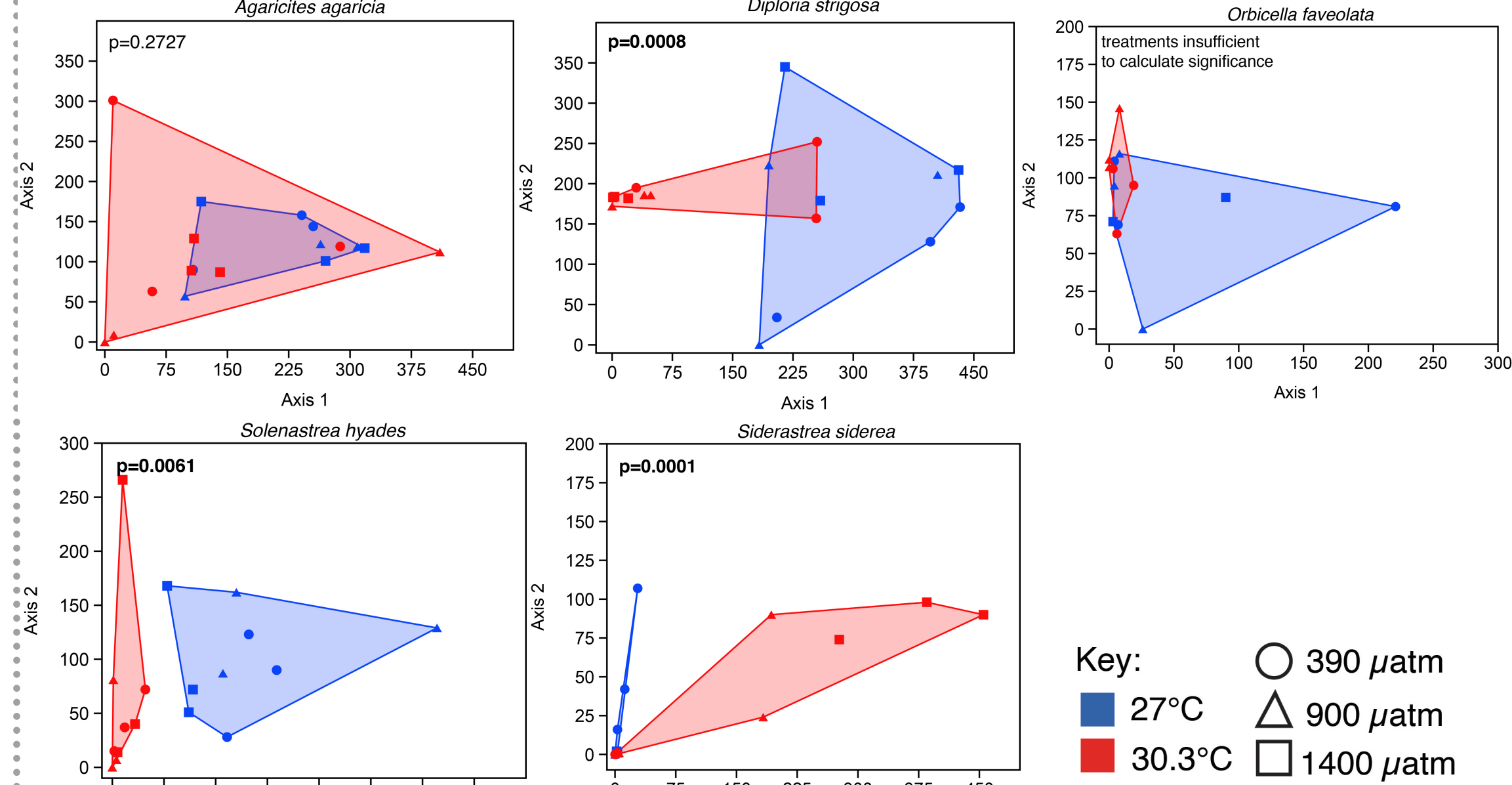


Figure 2. Column chart showing microbial phylum percentage compositions for all coral samples, subdivided by coral species, temperature treatment, and pCO<sub>2</sub> treatment.

The column chart displays differences in microbial community composition between and within coral species. Microbial community diversity was significantly lower with increasing pCO<sub>2</sub> level in *D. strigosa* (p=0.0077), and higher with increasing pCO<sub>2</sub> level and temperature in *S. siderea* (p=0.0007, p=0.0019). Diversity in microbial communities of *O. faveolata* was not tested for significance because insufficient treatments were sampled; no significance was found for the other two coral species.

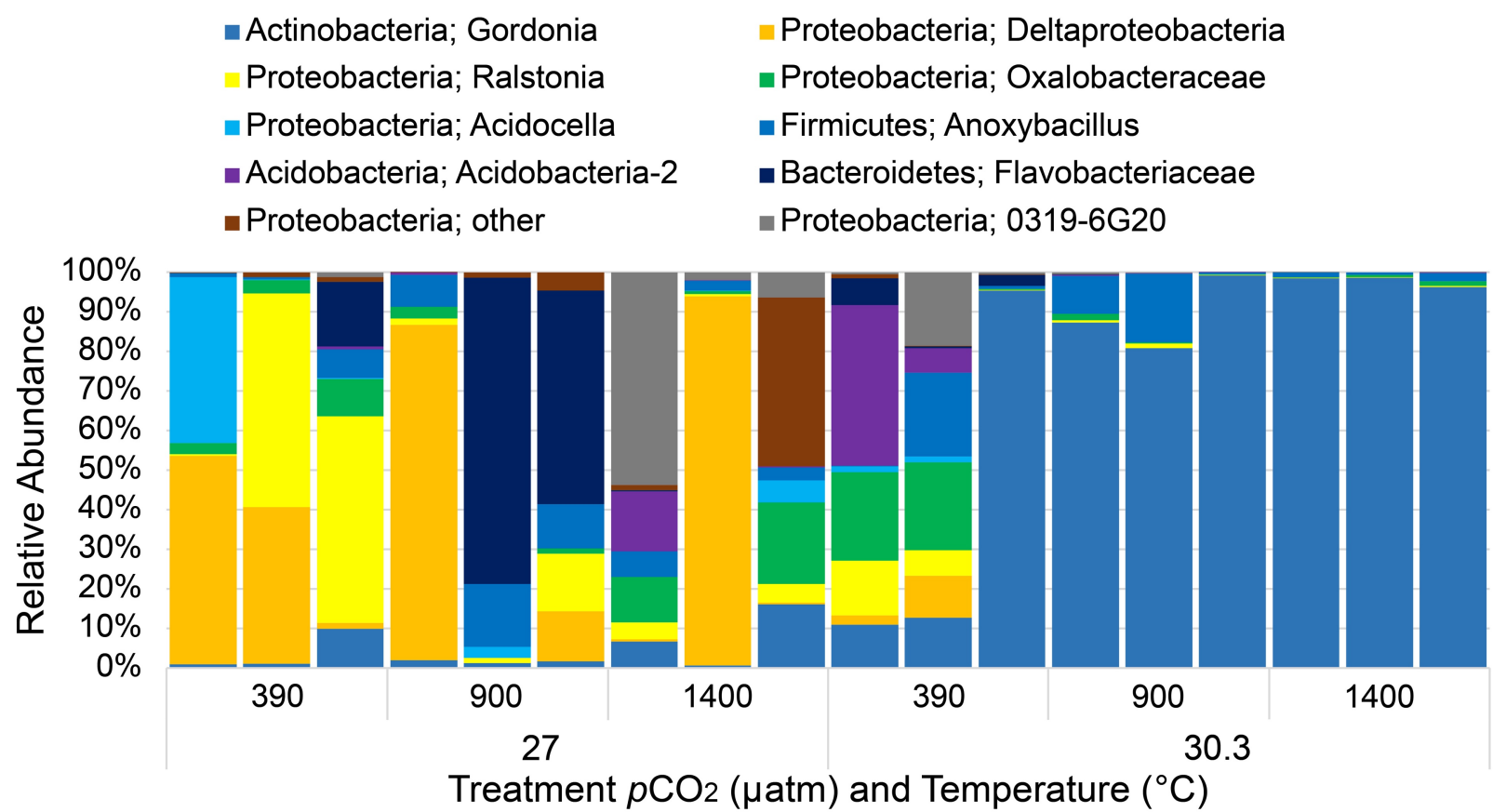
Figure 3. DCA plots for each coral species, showing differences in temperature treatments using colored hulls and pCO<sub>2</sub> treatments using symbol shapes. Significance between temperatures was tested for using two-way ANOSIM, shown with bolded p-values if significant.



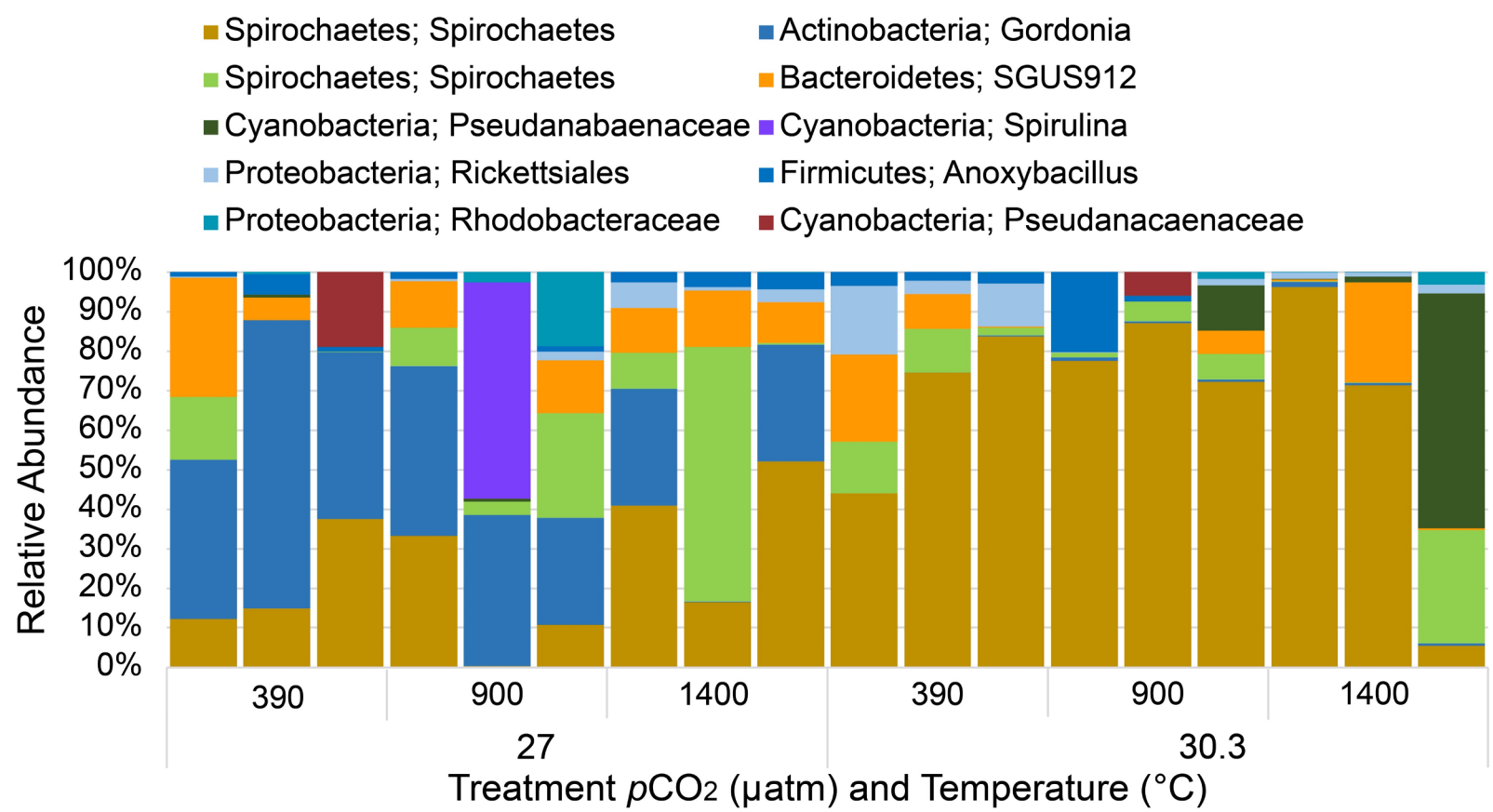
*Diploria strigosa*, *S. hyades*, and *S. siderastrea* showed significant differences in microbial community composition between temperature treatments. SIMPER analyses were performed for these species to find the top microbial taxa contributing to dissimilarity between temperature treatments, which are shown below in column charts.

Figures 4, 5, 6. Column charts show relative abundances of microbial genera contributing to dissimilarity between communities at different temperature treatments. Microbial taxa are labeled by phylum and the lowest taxonomic identification available for each group.

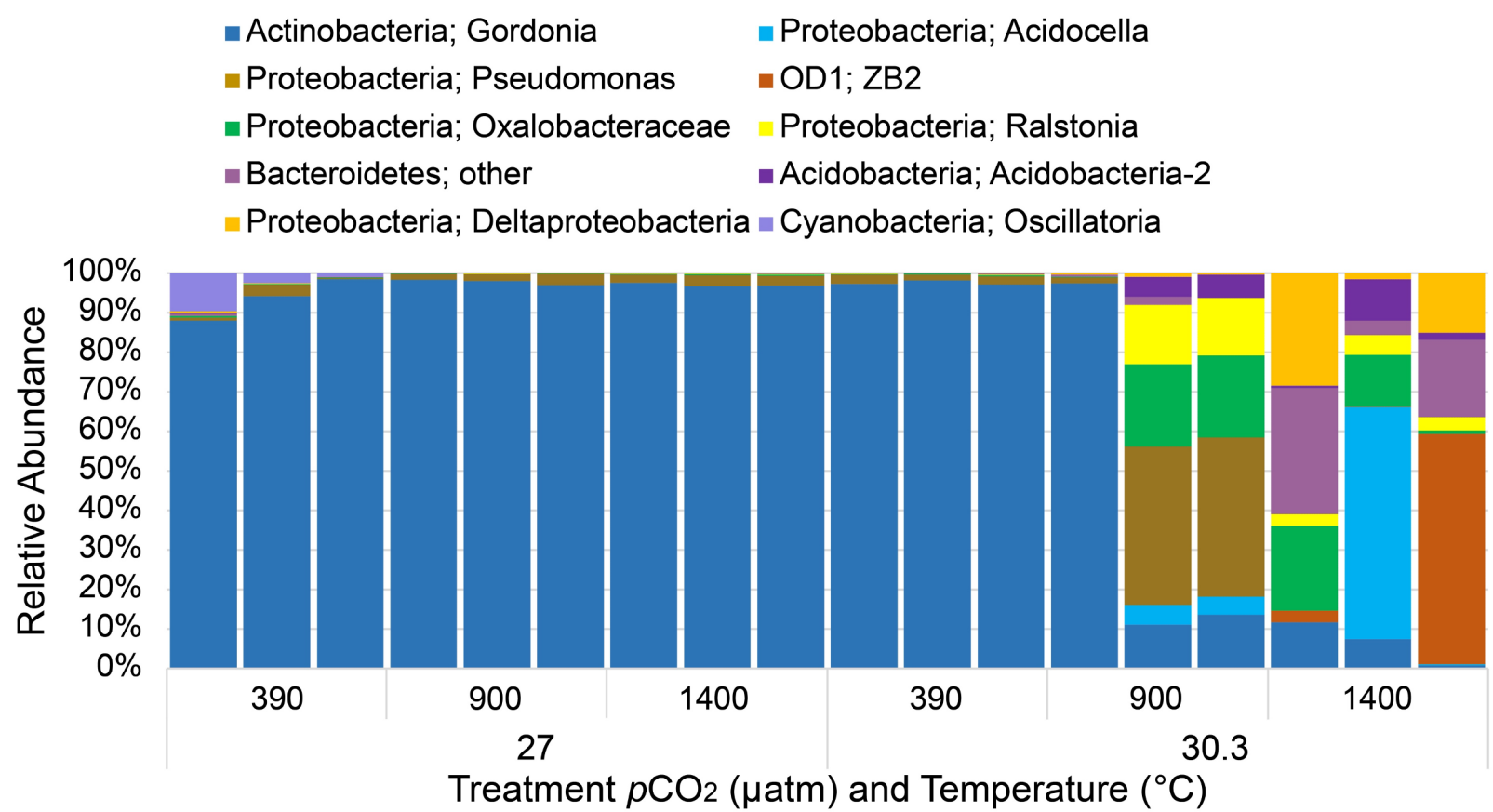
*D. strigosa* Top 10 Microbial Genera Based on SIMPER between Temperature Treatments



*S. hyades* Top 10 Microbial Genera Based on SIMPER between Temperature Treatments

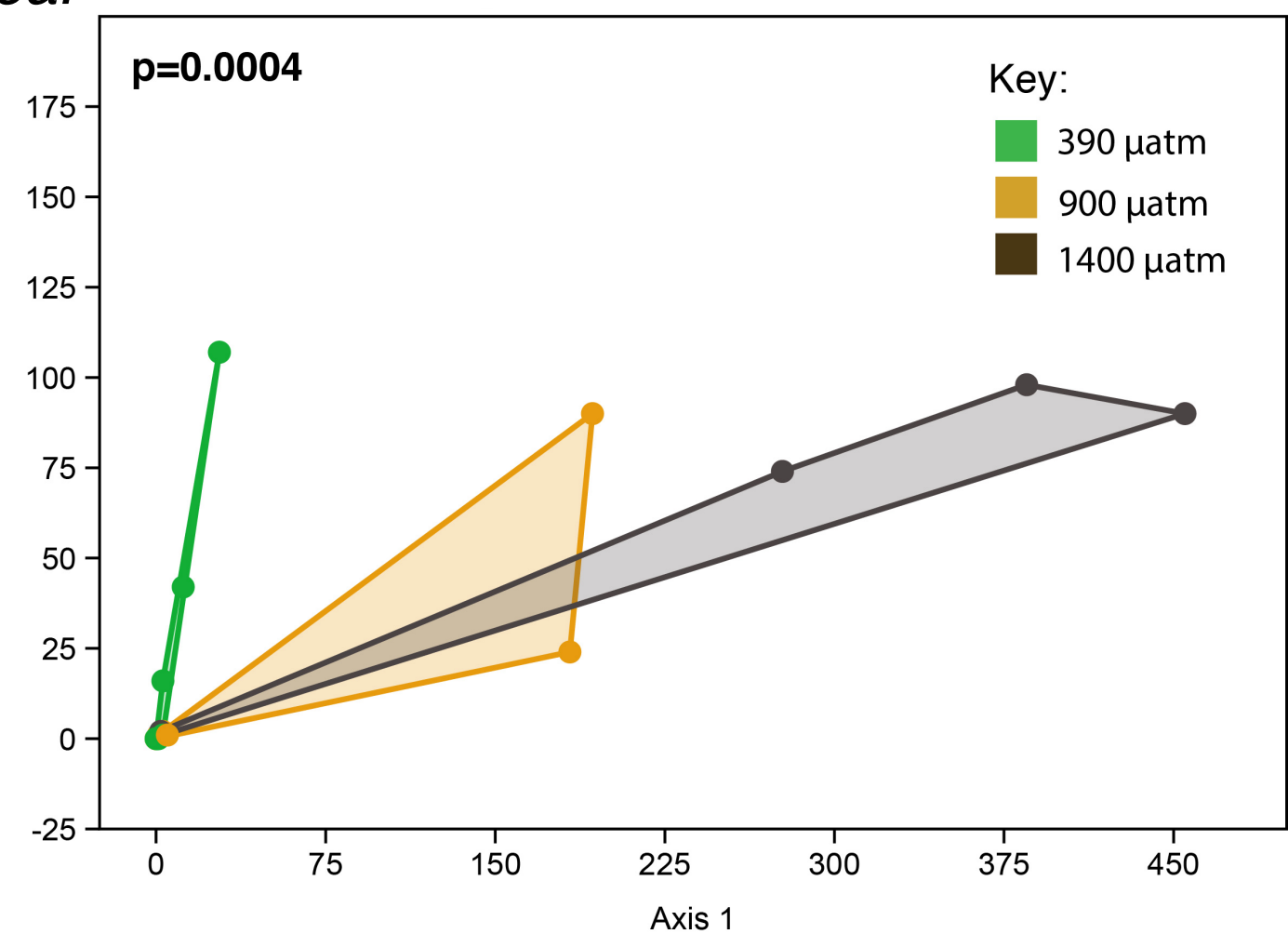


*S. siderea* Top 10 Microbial Genera Based on SIMPER between Temperature Treatments



Microbial communities of *S. siderea* showed significant differences in composition between different pCO<sub>2</sub> treatments.

Figure 7, 8. DCA Plot shows different pCO<sub>2</sub> treatments within *S. siderea*.



## Conclusions

Increasing temperature significantly changed microbial community composition in three of the five coral species: *D. strigosa*, *S. hyades*, and *S. siderea*; two of these species additionally showed a significant change in microbial community diversity between temperature and/or pCO<sub>2</sub> treatments. No significant differences were observed between controls and experimental treatments in *A. agaricia*. *Orbicella faveolata*, though lacking full data needed to test significance, appeared to show some differences in temperature treatments (Figures 1, 3).

Stability in microbial community composition and diversity during exposure to increased temperature and atmospheric carbon dioxide concentrations could be an indicator of resilience for a coral species during future climate change; disruptions in microbial communities may indicate sensitivity.

Based on this, *D. strigosa*, *S. hyades*, and *S. siderea* are predicted to be sensitive to future environmental changes, while *A. agaricia* may be more resilient.

It is also possible that coral species that can tolerate shifts in their microbiome may be less susceptible to environmental changes. Coral species show unique responses to stressors, and future research and conservation efforts may require species-specific strategies.

## References

- Hernandez-Agreda, Alejandra, Ruth D. Gates, and Tracy D. Ainsworth. "Defining the core microbiome in corals' microbial soup." *Trends in Microbiology* 25.2 (2017): 125-140.
- Okazaki, Remy R., et al. "Species-specific responses to climate change and community composition determine future calcification rates of Florida Keys reefs." *Global change biology* 23.3 (2017): 1023-1035.
- Van Oppen, Madeleine JH, and Linda L. Blackall. "Coral microbiome dynamics, functions and design in a changing world." *Nature Reviews Microbiology* 17.9 (2019): 557-567.

## Acknowledgements

Thanks to James Klaus, Al Piggot, Peter Swart, Chris Langdon, and Remi Okazaki, whose research started this project.