EFFECTS OF AGE AND CLIMATE ON THE MICROBIOME OF TROPICAL URCHINS ACROSS GENERATIONS

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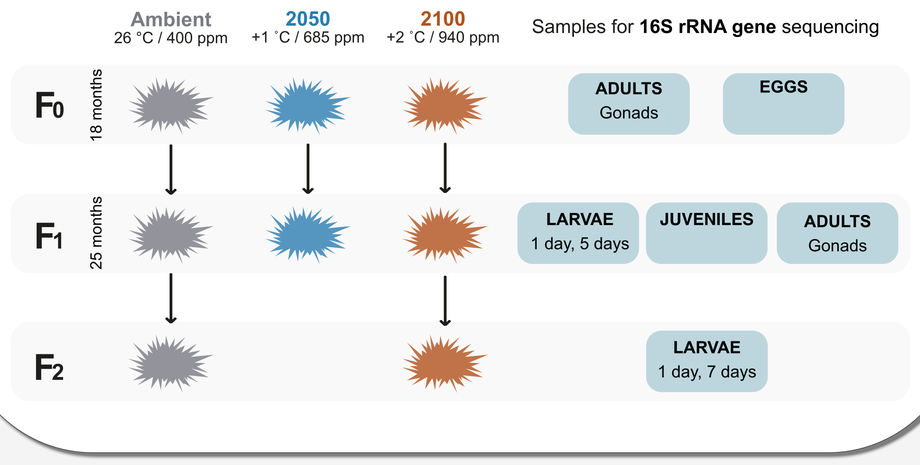
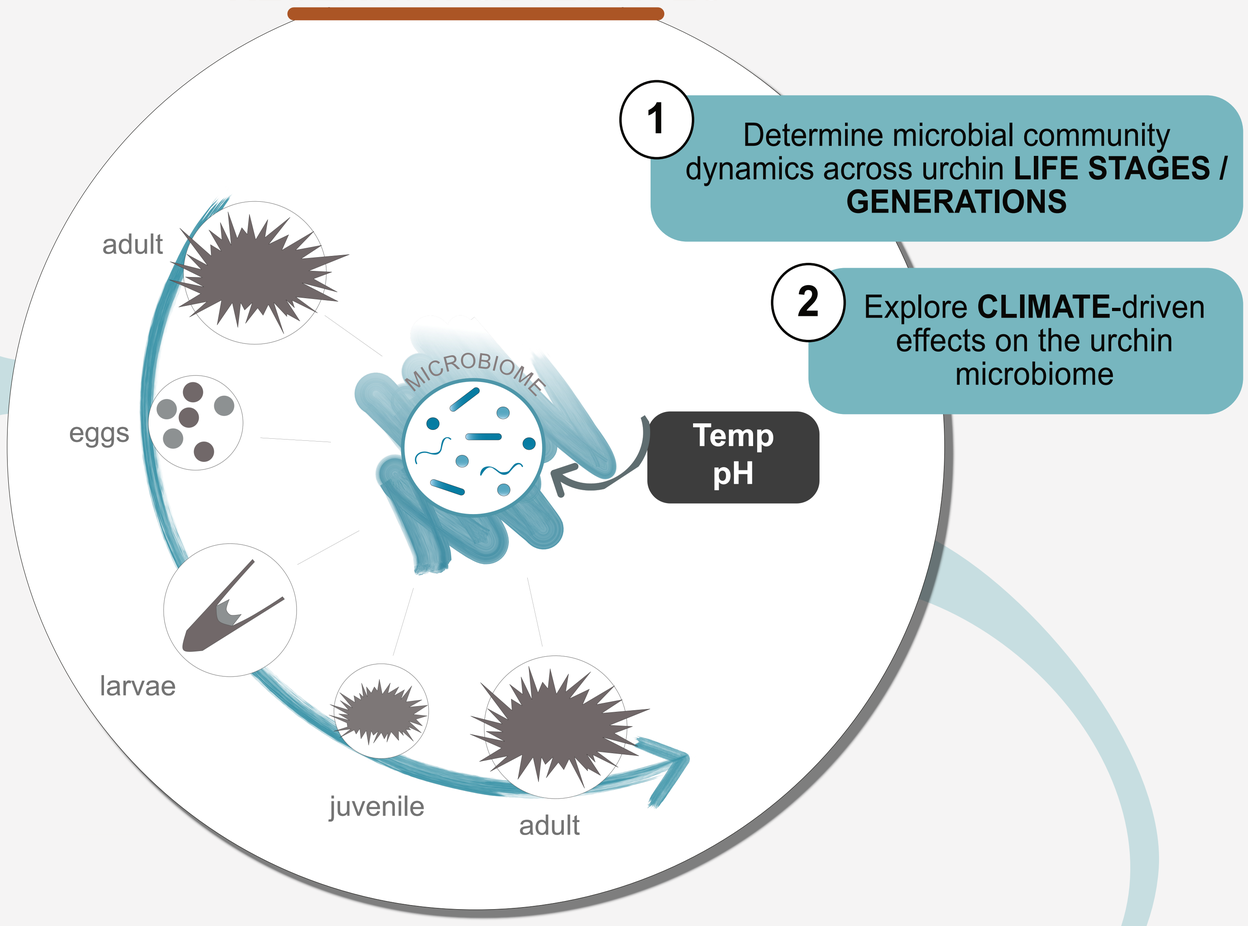
INTRODUCTION

Climate change is a major threat to reef species[1,2]. Despite the fundamental contribution of **microbes** to host health[3,4,5], microbiome dynamics across host generations remain poorly understood in most reef species, especially in the context of climate change. Here, we explore microbial changes across life stages in the **tropical sea urchin** Echinometra sp. A exposed to ocean warming (OW) and acidification (OA) over a 4-year multigenerational experiment.

METHODS



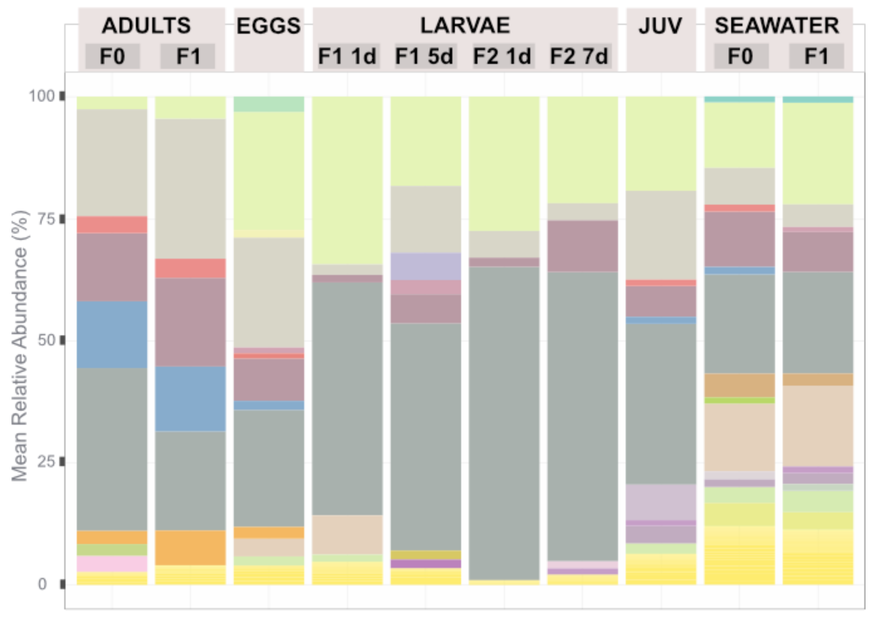
RESEARCH OBJECTIVES



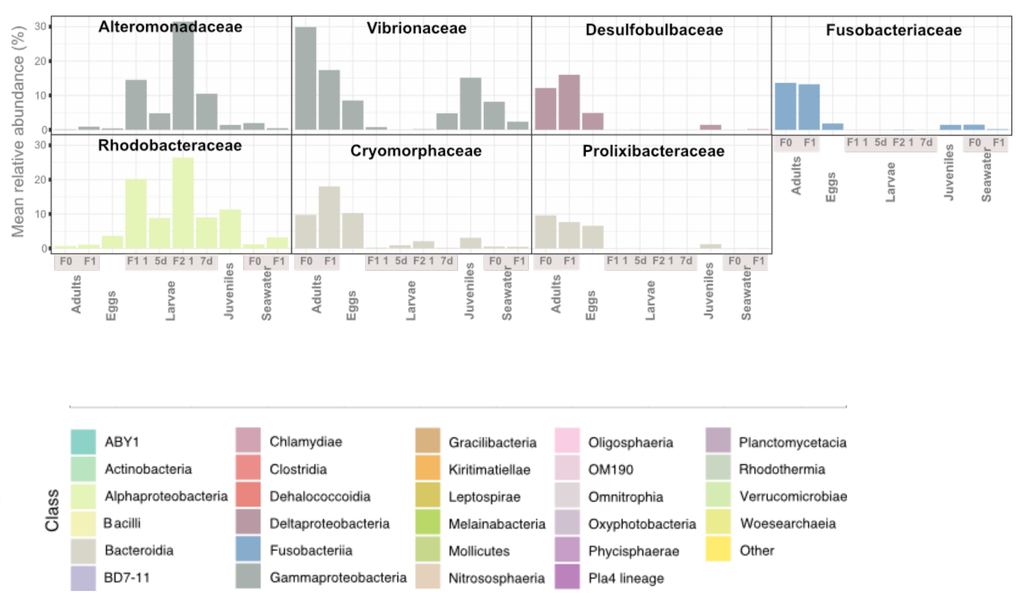
RESULTS

1

Microbial communities shift during major urchin life stages and generations under AMBIENT conditions

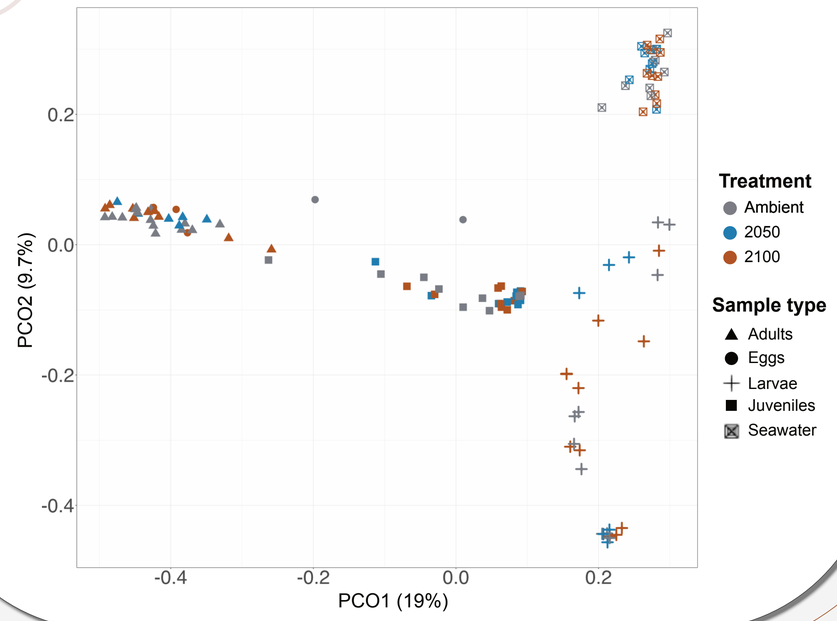


Relative abundances of prevalent microbial families differ across major urchin life stages under AMBIENT conditions



2

Temperature and pCO_2 levels are not the main drivers of microbial shifts in the urchin microbiome



CONCLUSIONS

1. Our multigenerational study reveals that **microbial communities are distinct across major urchin life stages**. The high relative abundance of Alteromonadaceae and Rhodobacteraceae in larvae suggests that these taxa may play an important role during early developmental stages. Following larval metamorphosis, a shift from Alteromonadaceae to Vibrionaceae is observed, with Vibrionaceae representing the most abundant family in juveniles.
2. Our results show that **OW/OA do not drive major changes in the urchin microbiome**

This multigenerational study provides new insights into the ontogeny of a reef species from a microbial perspective, and explores for the first time the effects of OW/OA on the urchin microbiome across life stages.

References

1. Hughes et al. 2018 Nature.
2. Doney et al. 2009 Mol Ecol.
3. McFall-Ngai et al. 2013 PNAS
4. Carrier et al. 2021 PNAS.
5. Schuh 2020 Front Microbiol.

AUTHOR INFORMATION

Emma Marangon is an AIMS@JCU PhD candidate investigating the effects of climate change on reef species (urchins, corals, sponges) from a microbial perspective, using 16S rRNA gene analyses, metagenomics and transcriptomics.

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