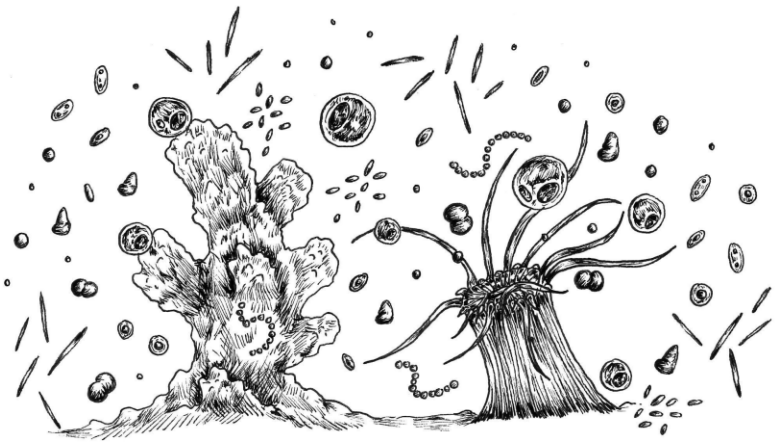
Host-microbiome dynamics impact the thermotolerance of cnidarian holobionts



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A mi madre, padre y hermano: por alentarme en los momentos en los que más me sentía sola y por ser la motivación de todo lo que hago.

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Abstract

Understanding the mechanisms underlying organismal responses to environmental stress has been a long-standing pursuit in evolutionary biology, but anthropogenic climate change has turned this interest into an imperative. There is growing appreciation for the importance of interactions between a host and its microorganisms ("microbiome") for species resilience to environmental change. The holobiont theory emerged in response to this rapidly evolving field, arguing that a host and its microbiome are a single unit under selection, reciprocally impacting each other's development, fitness, and evolution. In this dissertation, I explore these interactions through a holobiont lens using the reef-building *Pocillopora* coral and the sea anemone *Aiptasia* as model organisms.

In Chapter 1, I explore how environmental and geographic factors are structuring *Pocillopora* corals' Symbiodiniaceae algal symbioses across the Indo-Pacific. In analyzing publicly available data for these symbioses, sea surface temperature emerged as the primary driver of algal community differences, with geographical isolation explaining these patterns to a lesser extent. My meta-analysis is one of the few studies to explicitly explore coral holobionts from a biogeographical perspective, further supporting the hypothesis that algal symbionts may be implicated in coral host thermotolerance.

In Chapter 2, I focus on *Pocillopora* coral reefs in Panama's Tropical Eastern Pacific (TEP) to assess how seasonal upwelling influences host-microbiome configurations and holobionts' resistance to increasing water temperatures. To do so, I studied colonies in-situ and subjected them to a thermal assay known as the Coral Bleaching Automated Stress System (CBASS).

Contrary to expectations, I found little host genetic differentiation across upwelling regimes, yet there were signatures of divergent selection on genes with functions previously implicated in bleaching. During the CBASS, genetic lineage, region, and temperature collectively mediated algal symbiont shifts in response to thermal stress. This pattern with algal symbionts strongly contrasted with temperature-driven dysbiosis for the prokaryotic community. Additionally, corals under seasonal upwelling experienced more stressful baseline conditions, which may contribute to their higher predicted thermal thresholds. My holobiont approach reveals how corals' adaptation and acclimation mechanisms are potentially impacted by upwelling, providing new insights into how host and microbiome responses synergistically impact resilience to climate change.

In Chapter 3, I build upon my findings in Chapter 2 using the sea anemone *Aiptasia* as a model for corals. I investigated how algal symbiont's thermal sensitivity impacted prokaryotic dynamics by subjecting clonal *Aiptasia* lines hosting either a thermotolerant or thermally sensitive algae to a heat stress assay that triggers bleaching. I found that algal strain was the strongest driver of the *Aiptasia* prokaryotic microbiome, presenting prokaryotic taxa that may be potential indicators of both improved and reduced bleaching resilience. Additionally, I propose that sustained community variance, as opposed to increased variance as a function of temperature, may be characteristic of more thermally sensitive cnidarian holobionts. My work is the first to explicitly control for *Aiptasia* host genetic lineage in characterizing prokaryotic community dynamics under heat stress, underscoring how algal and prokaryotic dynamics together may result in different bleaching trajectories.

Collectively, my thesis presents that the host and its microbiome are not only a single unit under selection, but also one collectively responding to climate change. In studying corals and sea anemones, my work's holobiont approach emphasizes that considering how microorganisms influence the ecology and evolution of organisms can reveal novel perspectives into the factors that contribute to climate resilience.

Résumé

Comprendre les mécanismes qui sous-tendent les réponses des organismes au stress environnemental est une quête de longue date en biologie évolutive, mais le changement climatique anthropogénique a changé cet intérêt à un impératif. De plus en plus, l'importance des interactions entre un hôte et ses micro-organismes ("microbiome") est reconnue pour aider la résilience des espèces aux changements environnementaux. La théorie de l'holobionte est apparue en réponse à ce domaine en pleine évolution, soutenant qu'un hôte et son microbiome constituent une unité soumise à la sélection, ayant un impact réciproque sur le développement, la condition physique et l'évolution de chacun. Dans cette thèse, j'explore ces interactions sous l'angle de l'holobionte en utilisant le corail *Pocillopora* qui construit les récifs et l'anémone de mer *Aiptasia* comme organismes modèles.

Dans le Chapitre 1, j'étudie comment les facteurs environnementaux et géographiques structurent les symbioses algales Symbiodiniaceae des coraux *Pocillopora* dans l'Indo-Pacifique. En analysant les données publiques disponibles pour ces symbioses, la température de surface de la mer est apparue comme le principal moteur des différences entre les communautés d'algues, avec un effet secondaire de l'isolement géographique. Ma méta-analyse est l'une des rares études à explorer explicitement les holobiontes coralliens d'un point de vue biogéographique, ce qui renforce l'hypothèse que les symbiotes algaux peuvent être impliqués dans la tolérance thermale de l'hôte corallien.

Dans le Chapitre 2, je me concentre sur les récifs coralliens de *Pocillopora* dans le Pacifique tropical oriental (PTO) du Panama afin d'évaluer comment la remontée saisonnière des eaux

influence les configurations hôte-microbiome et la résistance des holobiontes à l'augmentation des températures de l'eau. Pour ce faire, j'ai étudié les colonies in situ et les ai soumises à un test thermique nommé Coral Bleaching Automated Stress System (CBASS). Contrairement aux attentes, j'ai observé peu de différenciation génétique des hôtes entre les régimes de remontée d'eau, mais il y avait des signatures de sélection divergente sur des gènes dont les fonctions avaient déjà été impliquées dans le blanchiment. Au cours de la CBASS, la lignée génétique, la région et la température ont collectivement contribué aux ajustements de symbiotes d'algues en réponse au stress thermique. Ce modèle de symbiotes algaux contraste fortement avec la dysbiose induite par la température pour la communauté procaryote. En outre, les coraux soumis à une remontée d'eau saisonnière ont connu des conditions de base plus stressantes, ce qui peut contribuer à leurs seuils thermiques prédits plus élevés. Mon approche holobionte révèle comment les mécanismes d'adaptation et d'acclimatation des coraux sont potentiellement affectés par la remontée d'eau, fournissant de nouvelles informations sur comment les réponses de l'hôte et du microbiome ont un impact synergique sur la résilience au changement climatique.

Dans le Chapitre 3, je m'appuie sur les résultats du Chapitre 2 en utilisant l'anémone de mer *Aiptasia* comme modèle pour les coraux. J'ai étudié l'impact de la sensibilité thermique du symbiote algal sur la dynamique procaryotique en soumettant des lignées clonales d'*Aiptasia* hébergeant une algue tolérante ou sensible à un test de stress thermique qui déclenche le blanchiment. J'ai découvert que la souche d'algue était l’agent primaire du microbiome procaryote de l'*Aiptasia*, et des taxons procaryotes pourraient être des indicateurs potentiels d'une résilience améliorée ou réduite au blanchiment. De plus, je propose qu'une variance soutenue de la communauté, par opposition à une variance accrue en fonction de la température, puisse être

caractéristique d'holobiontes cnidaires plus sensibles à la température. Mon travail est le premier à contrôler explicitement la lignée génétique de l'hôte *Aiptasia* dans la caractérisation de la dynamique de la communauté procaryote en cas de stress thermique, soulignant comment la dynamique des algues et des procaryotes peut aboutir à des trajectoires de blanchissement différentes.

Collectivement, ma thèse montre que l'hôte et son microbiome ne sont pas seulement une unité soumise à la sélection, mais aussi une unité qui réagit collectivement au changement climatique. En étudiant les coraux et les anémones de mer, l'approche holobionte de mon travail souligne que l'influence des micro-organismes sur l'écologie et l'évolution des organismes peut révéler de nouvelles perspectives sur les facteurs qui contribuent à la résilience climatique.

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Preface

Thesis format

My thesis follows a manuscript-based format, where each chapter consists of an individual manuscript that has been published or is intended for publication in a peer-reviewed, academic journal. Manuscripts have been slightly edited for inclusion in the current thesis. The manuscripts associated with each chapter are as follows:

Chapter 1: Glynn, V. M., Vollmer, S. V., Kline, D. I., & Barrett, R. D. H. 2023. Environmental and geographical factors structure cauliflower coral's algal symbioses across the Indo-Pacific. *Journal of Biogeography*, 50(4), 669–684. https://doi.org/10.1111/jbi.14560

Chapter 2: Glynn, V. M., Marangoni, L. F., Guglielmetti, M., Tapia, E. R., Ali, V., Quintero, H., Guerra, E. C. R., Yuval, M., Kline, D. I., Leray, M., Connolly, S. R., & Barrett, R. D. H. Environmentally-driven holobiont changes impact thermotolerance for Tropical Eastern Pacific corals. *Current Biology* submitted.

Chapter 3: Glynn, V. M., Cleves, P. A., & Barrett, R. D. H. Algal thermotolerance drives differences in prokaryotic microbiome dynamics for an emerging coral model system. In prep for *Proceedings of the Royal Society B*.

Contribution to original knowledge

All chapters constitute contributions to original knowledge. The following are, to the best of my knowledge, the most novel aspects of this thesis:

Chapter 1:

- I am the first to explicitly consider how geographical and environmental parameters structure the Symbiodiniaceae communities associated with any coral genus across its range.

Chapter 2:

- I am the first to run and report data from an acute thermal stress assay in the Tropical Eastern Pacific (TEP).
- I am the first to generate whole-genome sequencing data for *Pocillopora* corals in the TEP.
- I provide the most recent characterization of Panama's TEP coral algal symbiont communities, and the only characterization of prokaryotic communities to date.
- I am the first to propose that prokaryotic dysbiosis may only be observable in *Pocillopora* corals at temperatures of 7.5°C above the mean monthly maximum temperature (MMM).
- I am the first to incorporate oxidative metabolism dynamics when running the standardized acute thermal stress assay known as the Coral Bleaching Automated Stress System (CBASS), presenting a complementary view to more commonly used physiology metrics.
- I am the first to explicitly model how algal symbiont's impact coral host thermotolerance via changes in total antioxidant capacity.
- I am the first to present that corals experiencing warm seasonal temperature anomalies like those in the Red Sea, and cold and warm seasonal temperature anomalies like those in Panama's TEP, have a similar degree of thermotolerance.

Chapter 3:

- I am the first to explicitly control for host genetic background for any *Aiptasia* prokaryotic microbiome study.
- I am the first to present that the algal symbiont alone can result in divergent cnidarian prokaryotic communities.
- I am the first to posit that sustained community variance, as opposed to increased community variance as a function of temperature, may be characteristic of more thermally sensitive cnidarian holobionts.

Author contributions

The work encompassing this thesis has spanned various study organisms, institutions, and analytical approaches. Below are the contributions of all co-authors to each of my thesis chapters. To be concise, I refer to co-authors through their initials: Victoria Marie Glynn (VMG), Steve V. Vollmer (SVV), David I. Kline (DIK), Laura Fernandes de Barros Marangoni (LFBM), Maxime Guglielmetti (MG), Eunice R. Tapia (ERT), Viviane Ali (VA), Helio Quintero (HQ), E. Catalina Rodriguez Guerra (ECRG), Matan Yuval (MY), Matthieu Leray (ML), Sean R. Connolly (SRC), Phillip Cleves (PA), and Rowan D.H. Barrett (RDHB).

Chapter 1: As stated in the publication, VMG, SVV, DIK and RDHB conceived the ideas, VMG downloaded and analyzed the data, VMG led the writing with assistance of SVV, DIK and RDHB.

Chapter 2: VMG, LFBM, DIK, ML, SRC, and RDHB designed the study. VMG, LFBM, HQ, MY, DIK, ML, and SRC performed the acute thermal stress assay and data collection. VMG and LFBM led the laboratory analyses, with support from ERT, VA, HQ, ECRG, and ML. VMG led all the statistical analyses, with support from MG, and with guidance from SRC and RDHB. SRC and RDHB jointly supervised the overall research project. VMG wrote the manuscript with substantive contributions from LFBM, ML, SRC, and RDHB.

Chapter 3: VMG, PAC, and RDHB designed the study. VMG performed the experiment, lab work and statistical analyses, and wrote the manuscript. PAC and RDHB jointly supervised the research, supported statistical analyses, and contributed to writing.

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List of Abbreviations

Abbreviation	Meaning
AFU	Canal de Afuera
AIC	Akaike information criterion
AKP	Anna Karenina Principle
ANOVA	Analysis of variance
ASV	Amplicon sequence variant
ASW	Artificial seawater
BAD	Bahía Damas
BLAST	Basic Local Alignment Search Tool
BSA	Bovine serum albumin
CAP	Canonical analysis of principal coordinates
CBASS	Coral Bleaching Automated Stress System
CCS	Cumulative sum square
CO_2	Carbon dioxide
CON	Contadora
CT_{max}	Critical thermal maximum
DH2O	Deionized water
DIV	Intragenomic sequence variants
DNA	Deoxyribonucleic acid
DRC	Dose–response curve
ED50	Effective dose 50
ENSO	El Niño–Southern Oscillation
Fis	Inbreeding coefficient
Fst	Fixation index
Fstp	Nei's Fst corrected for sample size
FSW	Filtered sea water
GLS	Generalized least squares
Ho	Observed heterozygosity
HPC	High performance computing
Ht	Overall gene diversity
ITS2	Internal transcribed spacer 2
LED	Light-emitting diode
LPO	Lipid peroxidation
MDA	Malondialdehyde
MMM	Mean monthly maximum
MOG	Mogo Mogo
mtORF	Mitochondrial Open Reading Frame
NCBI	National Center for Biotechnology Information
nMDS	Non-metric multidimensional scaling
NOAA	National Oceanic and Atmospheric Administration
OTU	Operational taxonomic unit
PCoA	Principal Coordinate Analysis

PCR	Polymerase Chain Reaction
PERMANOVA	Permutational multivariate analysis of variance
rDNA	Nuclear ribosomal DNA
REML	Restricted Maximum Likelihood
RNA	Ribonucleic acid
ROS	Reactive oxygen species
SAB	Saboga
SCUBA	Self-Contained Underwater Breathing Apparatus
SNP	Single-nucleotide polymorphism
SRA	Sequence Read Archive
SST	Sea surface temperature
TAC	Total antioxidant capacity
TBA	Thiobarbituric
TBARS	Thiobarbituric Acid Reactive Substances
TEP	Tropical Eastern Pacific
TSB	Time since the last local mass bleaching event
UVA	Uva

Introduction

0.1 We contain multitudes – ecology and evolution from a microbial lens

Microorganisms have shaped the evolution of modern life and are central to the functioning of virtually every ecosystem on the planet. Cyanobacteria changed the Earth's chemistry by releasing oxygen into seawater over the course of millions of years such that it eventually became a key component of our atmosphere (Sessions et al. 2009). The movement of plants from water to land is now thought to have been facilitated when green algae acquired genes from soil bacteria via horizontal gene transfer to help them cope with conditions on land, such as desiccation (Cheng et al. 2019). For animals, the rise of eukaryotes is hypothesized to have emerged from the union of an archaea and bacteria, otherwise referred to as the endosymbiotic theory, leading to the creation of the mitochondria (Margulis and Fester 1991). Animals and microorganisms are inextricably linked, from the scale of a single individual to entire ecosystems. When humans first came to realize that we were outnumbered by our microbial counterparts, the focus turned to ecosystem cycling and disease. The field of microbiology has since come to appreciate both the diversity in form and function within microorganisms, and that many host-microbiome associations are mutually beneficial (McFall-Ngai et al. 2013, Visick et al. 2021). This realization has ushered a new research frontier where instead of viewing the host and its microbiome as adversaries on a battlefield, we now consider them as partners and focus on the establishment and breakdown of their symbiotic relationships.

The holobiont theory reconceptualizes interactions between hosts and their microorganisms by considering the host and its microbiome as a single unit under selection, reciprocally impacting each other's development, fitness, and evolution (Margulis and Fester 1991, Rosenberg and

Zilber-Rosenberg 2018, Roughgarden 2023). It is the latter component that has piqued my scientific curiosity within the context of environmental stress. If the holobiont theory considers the host and its microbiome as a single unit under selection, is this same unit collectively responding to climate change? Given the pace and severity of anthropogenic climate change, by including microbiome dynamics as another pathway by which organisms can respond to climate change, we can potentially reveal new pathways by which organisms cope with changing abiotic conditions.

When we consider the mechanisms by which animals cope with changes in their environment, these are often described in isolation, focusing on a single taxa's mechanisms in isolation. The literature has often presented three main mechanisms for organisms to respond to climate change: (1) dispersing to more favorable environments, (2) engaging in phenotypic plasticity, or (3) genetically adapting via natural selection. These exist on a gradient from fastest to slowest acting, thus organisms are likely engaging to some degree in all of these mechanisms simultaneously (Gienapp et al. 2008, Sears et al. 2011, Hardie and Hutchings 2010, Edelsparre et al. 2024, Basso et al. 2018, Radchuk et al. 2019). Dispersal refers to the ability of organisms to move across their environment, thereby increasing the range of environments that an organism can encounter. This has been widely documented in terms of range expansions under increasingly warmer temperatures, where the geographic ranges of marine and terrestrial ectotherms are related to their limits of thermotolerance, with marine species more strongly tracking thermal shifts than their terrestrial counterparts (Sunday et al. 2012, Lenoir et al. 2020, Moore et al. 2023).

However, what if moving to a more favorable environment is less available to an organism due to dispersal limitation? In addition to, or instead of, dispersal, organisms can respond to environmental stress via phenotypic plasticity. In the broadest sense, phenotypic plasticity refers to the ability of an organism's features, spanning from morphology to reproduction, to be modulated by the environment. The labile nature of an organism's phenotype has been reported in a diversity of taxa, with some examples being plants flowering earlier due to increasing springtime temperatures, increasing appendage sizes thereby improving thermoregulation, and longer breeding seasons for birds due to longer growing seasons (Ellwood et al. 2013, Ryding et al. 2022, Møller et al. 2010). Phenotypic shifts may or may not have a genetic basis, though these are often conceptually placed as a stepping stone for genetic change via natural selection (see Crispo 2007, Chevin et al. 2013, Fox et al. 2019). In this case, evolution occurs when over the course of many generations, there is a change in a population's allele frequencies, where certain mutations beneficial to an organism's survival are passed down to future progeny. We now come to appreciate that natural selection does not only occur on the order of millennia but can also be much faster acting, a particularly pertinent detail when studying molecular evolution in response to climate change (see Hendry et al. 2000, Schluter et al. 2010, Bonnet et al. 2022). Contemporary evolution has a rich literature that has only grown with advances in next-generation sequencing. Examples of contemporary evolution include the emergence of melanism in the peppered moth during the Industrial Revolution and strong signatures of directional selection in genes involved in DNA repair and immune function for dogs exposed to radiation in Chernobyl (Hof et al. 2016, Dillon et al. 2023). Even with all three of these mechanisms available, it is still unclear if organismal responses will be able to keep pace with climate change,

urging us to consider what additional mechanisms are available to organisms (Berteaux et al. 2004, Liang et al. 2018, Loarie et al. 2009, Jump et al. 2006).

It is important to underline that no organism is an island, and that all the previous examples involved a single organism's interactions with their surroundings. Interactions between conspecifics and other species have been recently built into this discourse, where there is increasing evidence that predation and competition can modulate single taxa's ability to persist and respond to climate change (Edelsparre et al. 2024, Bastille-Rousseau et al. 2018, Peers et al. 2020, Alexander et al. 2015, Ettinger and HilleRisLambers 2017). Host-microbiome interactions are one of these many species interactions. Given the ability of the microbiome to change over the course of an organism's lifetime, microbiome dynamics may play a particularly important role in how their associated hosts are responding to rapid climate change (Uhr et al. 2019, Wright et al. 2019, Kolodny and Schulenburg 2020). There is a growing body of evidence that microorganisms play critical roles in assisting their hosts persist under environmental change, from coral reef bleaching to *Arabidopsis thaliana* drought stress, with ensuing microbiome shifts linked to host resilience to climate change (Trivedi et al. 2022, Voolstra and Ziegler 2020). The question that remains is how microbial dynamics may complement or even drive more well-studied host-centric response mechanisms (Figure 0.1). Although a microbial perspective is often omitted from international climate change discussions (see Gewin 2023), microorganism's key roles in nutrient and biogeochemical cycling, high adaptive potential via their large population sizes, rapid asexual generation times, and potential for horizontal gene transfer, posit them as an important albeit overlooked component of organismal responses to climate change (Cavicchioli et al. 2019).

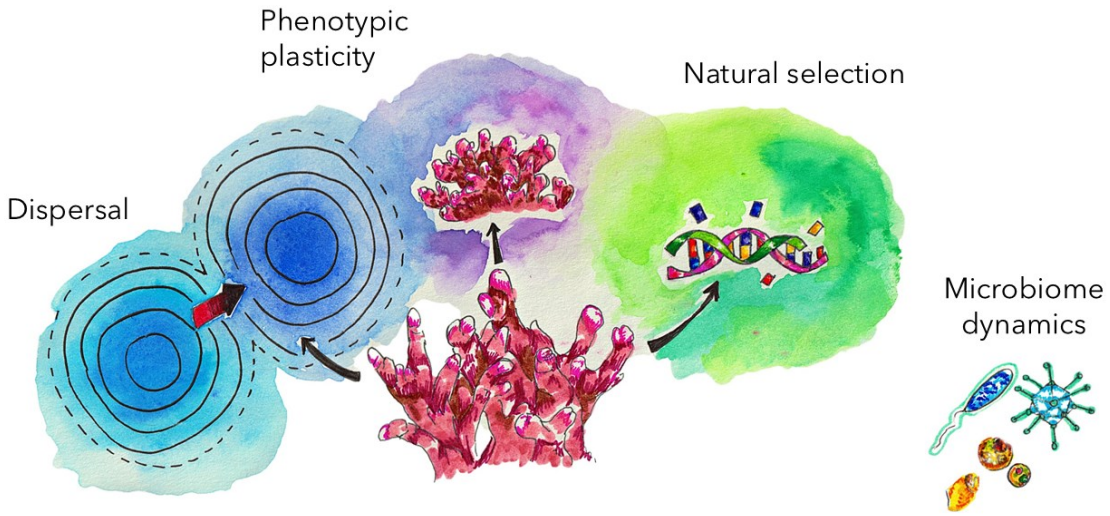

Figure 0.1. Overview of the literature's most frequently described pathways for organisms responding to climate change. The three traditional mechanisms are shown, each in their own, colored halo from left to right in the following order: (1) dispersal, (2) phenotypic plasticity, and (3) natural selection. For dispersal, the red arrow indicates movement between two environments, which are shown as two sets of different shades of blue concentric rings. For phenotypic plasticity, we see a change in colony morphology from the central coral figure to that in the purple halo. Lastly, for natural selection, the colored rectangles around the DNA strand represent changes at the nucleotide level. Microbiome dynamics are included separately without a halo to indicate that these are another potential response mechanism to climate change that is often poorly integrated with the three main mechanisms described in the literature.

Each holobiont can be considered an ecosystem within its own right, in that each host can be conceptualized as an environment containing a diversity of microorganisms, from pathogenic to putatively beneficial microorganisms, which interact with one another for space, energy, and resources, ultimately shaping overall holobiont health (see Rynkiewicz et al. 2015). Thus, if we adhere to the definition of an ecosystem as an assemblage of organisms and the biotic and abiotic environment in which they occur, a holobiont satisfies this definition (Begon and Townsend 2021). Thus, microbiomes may respond to changing conditions in the host in a variety of ways that parallel those of macro-organisms in their environments. For example, the transition from mature rainforests to agroforestry systems in the Amazon has been recently linked with a fungal to bacteria-driven microbiome shift belowground (Leite et al. 2023). There is evidence that the host's immune system, competitive interactions between species, and spatial structure, all play a role in maintaining a stable human gut microbe community (Coyte et al. 2015). Indeed, many core concepts within community ecology, such as Robert Paine's idea of a keystone species (Paine 1966), apply to microbiomes; simulations and experiments demonstrate that a few microbes with particular functional roles can significantly impact community structure, functioning, and overall health in soil, plant, and marine ecosystems, and the human microbiome (Amit and Bashan 2023, Banerjee et al. 2018). The holobiont theory therefore implies that we cannot fully grasp the impact of climate change on individual taxa or entire biomes if we do not consider this microbial filter. To begin to bridge this conceptual gap, it is critical that we study organisms as holobionts, as in doing so resilience pathways to climate change may emerge that otherwise would not if we considered hosts and microbiomes in isolation.

0.2 Corals as a model system for holobiont interactions under climate change

A model system to explore from a holobiont perspective the factors driving organisms' resilience to environmental stressors are coral reefs, as the emergence and subsequent decline of these ecosystems is tightly linked to their microbiome (Figure 0.2). Coral reefs are biodiversity hotspots in subtropical and tropical oceans, providing a home to over 25% of all marine life, and sustaining the livelihoods of over 500 million people (Ayre and Hughes 2004, Hoegh-Guldberg et al. 2000). Underpinning these incredibly diverse ecosystems are corals' obligate symbiotic relationship with photosynthetic algae in the family Symbiodiniaceae, where this single partner is responsible for approximately 90% of the host's energy requirements in most coral species (Grottoli et al. 2006, Jones et al. 2008). In exchange for photosynthetically derived glucose, the coral host provides its algal symbiont protection from external predators by residing in an intracellular compartment known as the symbiosome, and some additionally derived inorganic compounds such as carbon dioxide and ammonium (Yellowlees et al. 2008, Wilkerson and Trench 1986). This relationship has a more entrenched evolutionary history, as the adaptive radiation of reef-building corals and the subsequent formation of dominant reef structures coincides with the adaptive radiation of Symbiodiniaceae. The symbiotic relationship between corals and Symbiodiniaceae has been proposed to have contributed to the rapid growth, diversification and improved calcification of corals in the Late Triassic, a period of time where corals began to build the modern reef ecosystems we have today (Muscatine 1990, Cowen 1983, Cowen 1988, Lipps and Stanley 2016, Frankowiak et al. 2016, LaJeunesse et al. 2018, Bhattacharya et al. 2024). Coral reefs offer a unique case study to explore how host-microbiome dynamics impact the ecology and evolution of organisms, given the central role of Symbiodiniaceae in coral holobiont functioning and health.

Figure 0.2. Viewing coral reef ecosystems from a holobiont perspective, where the interconnected nature of the microbiome and host are visually represented.

As atmospheric carbon dioxide levels increase, corals face increasing extinction risk due to coral bleaching, with the fourth mass bleaching event declared in April 2024 (NOAA/NWS/CPC 2024). Coral bleaching is the process during which a coral's Symbiodiniaceae are lost due to thermal stress, often resulting in coral death (Hughes et al. 2018). Bleaching is an extremely destabilizing process for the coral host, as besides starving the host, bleaching can have longer term impacts on skeletal growth (Walker et al. 2023, Tanzil et al. 2009), calcification (Ross et al. 2022, Courtney et al. 2020), and fecundity (Johnston et al. 2020, Paxton et al. 2016), while also

making the host more susceptible to disease and mortality (Muller et al. 2018, Maynard et al. 2015, Jones et al. 2008, Suggett and Smith 2011). Since mass bleaching events were first reported in the 1980s, the scientific community has homed in on the dynamics that occur during this critical period, with an early appreciation of the role of algal symbionts in either alleviating or hampering recovery pathways (Glynn 1991, Buddemeier and Fautin 1993, Glynn et al. 2001). In particular, recent taxonomic revision of Symbiodiniaceae suggests that these coral symbionts do not belong to a single genus as initially thought but rather six or more (LaJeunesse et al. 2018). Symbiodiniaceae communities are highly diverse, differentially associating with different host species, and are structured by geographical and environmental factors alike, notably thermal regimes (LaJeunesse et al. 2018, Glynn et al. 2023, Tong et al. 2016, Kemp et al. 2015). Differences in host thermotolerance have been associated with a switch from *Cladocopium* spp. to *Durusdinium* spp. in both adult and juvenile corals (Naugle et al. 2021, Quigley et al. 2020, Manzello et al. 2019), and increased proportions of *Durusdinium* spp. at the beginning of thermal stress events are linked to bleaching resistance (Silverstein et al. 2015, Cunning and Baker 2020). Changes to the algal microbiome during bleaching can have long-term ramifications, where a combination of host selective mortality, host specificity, and algal community shuffling together can result in a drastic shift in the dominant Symbiodiniaceae genera (Claar et al. 2020, Quigley et al. 2022, Palacio-Castro et al. 2023). Coral algal dynamics represent both immediate and long-term consequences to host health, yet other holobiont components beyond this two-partner symbiosis can impact holobiont stability.

The coral microbiome extends beyond Symbiodiniaceae to also include bacteria, protists, viruses, archaea, endoliths, and fungi, making the coral polyp arguably one of the most diverse

ecosystems on this planet (Peixoto et al. 2021). These microorganisms have likewise been implicated in corals' ability to cope with environmental stress and to affect their bleaching susceptibility (Rodríguez-Román et al. 2006, Thornhill et al. 2006, Palumbi et al. 2014). Bacterial, viral, and archaeal communities can vary in response to stress and have been hypothesized to impact overall coral health, particularly within the context of disease as the presence of certain microorganisms has been linked to coral tissue loss and subsequent mortality (Meyer et al. 2019, Thurber et al. 2009, Zhang et al. 2015, Glasl et al. 2016, Correa et al. 2013, Kline and Vollmer 2011, Rosales et al. 2023). Bacteria are perhaps one of the most well-studied microbiome members besides Symbiodiniaceae, which like their algal counterparts have also shown signatures of co-phylogeny with their hosts (Pollock et al. 2018), are structured by environmental and biogeographical factors (Pantos et al. 2015, Speare et al. 2020), and certain members have been posited to be putatively beneficial to the host during bleaching (Doering et al. 2023, Gardner et al. 2019). Inoculating corals with bacterial cultures that have specific genetic and/or phenotypic characteristics can potentially reduce bleaching and pathogen presence, underscoring the microbiome's importance in maintaining coral health (Rosado et al. 2019, Santoro et al. 2021, Delgadillo-Ordoñez et al. 2024). However, how the microbiome is established and maintained, and is in communication with the host, is still an active area of research.

The microbiome's response mechanisms can impact the coral host's own acclimation and adaptation strategies. Acclimation refers to short-term phenotypic changes within the course of a single generation, often in response to transient environmental conditions. Adaptation refers to the accumulation of genetic changes across multiple generations, in response to more long-

lasting conditions. Both of these processes can occur simultaneously within corals. In terms of acclimation, some of the most well-studied mechanisms center on intracellular dynamics during coral bleaching. The most widely accepted cellular mechanism underpinning coral bleaching involves photoinhibition and damage to the algal chloroplast that results in an accumulation of reactive oxygen species (ROS); an increase in ROS in turn damages both algal and coral host tissues (see Weis 2008, Davy et al. 2012, Suggett and Smith 2020). For this reason, early studies focusing on host response mechanisms centered on physiology and oxidative metabolism. The fine-tuned balance between corals oxidative metabolism (e.g. ROS-triggered oxidative damage and total antioxidant capacity) and their physiological bleaching responses (e.g. chlorophyll *a* and host protein content) during thermal stress has been linked to both corals' baseline stress levels and also their ability to offset the impacts of environmental stress (see Marangoni et al. 2021, Marangoni et al. 2019, Liñán-Cabello et al. 2010, da Silva Fonseca et al. 2021, Luz et al. 2018).

In addition to these metabolically driven and intracellular processes, fast-acting genetic mechanisms such as transcriptional plasticity have emerged as a key acclimation response, where more resilient corals have a higher basal expression of key genes involved in processes such as protein folding and innate immune response prior to thermal stress (Barshis et al. 2013, Brener-Raffalli et al. 2022, Collins et al. 2021). Recent evidence further suggests that algal symbionts may be modulating gene expression patterns in the host, resulting in different bleaching outcomes (Strader and Quigley 2022, Cunning and Baker 2020). Finally, variation in coral thermal tolerance has been shown to be a heritable polygenic trait, implying that longer-term evolutionary responses might be possible if genetically based trait changes can keep pace with

the rate of environmental change (Drury et al. 2022, Rose et al. 2018, Bay and Palumbi 2014, Yetsko et al. 2020, Dixon et al. 2015, Smith et al. 2022). The responses of the host and its microbiome present parallel, and often integrated, pathways for resilience that need to be explored in unison, as it is unclear how these two components of the holobiont's response mechanisms are driving differences in thermotolerance, and in turn bleaching trajectories.

0.3 Panama's Tropical Eastern Pacific (TEP) as a natural laboratory for studies on coral holobiont's thermotolerance

Panama's Tropical Eastern Pacific (TEP) represents an ideal natural laboratory for studying corals' responses to environmental stress from a holobiont perspective, with seminal papers on the environmental and microbial underpinnings of coral bleaching having been based on work in the TEP. Some of the first evidence of the role of algal dynamics in differential bleaching and survivorship outcomes emerges from studying TEP reefs (Glynn et al. 2001, Baker et al. 2004). The TEP has also experienced three major bleaching events to date due to the El Niño-Southern Oscillation (ENSO) cycle, and yet these reefs have demonstrated remarkable recovery and reef accretion rates over the past century (Romero-Torres et al. 2020, Glynn et al. 2016, Glynn et al. 2001, Vargas-Ángel et al. 2001, Guzmán and Cortés 2001). In the TEP, there is a single ecologically dominant coral genus, *Pocillopora* spp., which is exposed to contrasting environmental conditions in Panama's TEP, allowing us to explore how the environment is shaping coral holobiont configurations (Romero-Torres et al. 2020, Manzello et al. 2008, Glynn 1983, Glynn 1993). *Pocillopora* corals experience intra-annual environmental variability due to a process known as upwelling. Upwelling is the process by which cold, nutrient-rich water displaces warmer, less nutrient-rich surface water. In Panama's TEP, corals in the Gulf of

Panama encounter drastic annual fluctuations in temperature, pH, oxygen, and nutrients, due to intense seasonal upwelling. Conversely, the nearby Gulf of Chiriquí experiences weak to no upwelling due to trade winds being blocked by the Cordillera Central mountain range (Figure 0.3; O'Dea et al. 2012, D'Croz and O'Dea 2007). There is some evidence to suggest that this region's upwelling may be impacting the population genetics, physiology, and microbial dynamics of *Pocillopora* corals (Glynn 1990, Maté 2003, Glynn and D'Croz 1990, Cunning et al. 2013, Combosch and Vollmer 2011, Toth et al. 2012, Palacio-Castro et al. 2023). These studies have been almost exclusively observational in nature (but see D'Croz and Maté 2004), thus future work should focus on experimentally disentangling the effects of host genetics, microbiome and environment in coral thermotolerance for TEP corals.

Figure 0.3. Map of Panama's TEP. Trade winds are shown as black arrows. The trade winds are orthographically blocked by the Cordillera Central mountain range, resulting in little to no upwelling in the Gulf of Chiriquí as compared to the Gulf of Panama. Background image is from the U.S. Central Intelligence Agency.

0.4 Leveraging emerging coral model organisms

Even with natural laboratories such as the TEP and carefully conducted experiments, corals remain a difficult study organism for host-microbiome studies. Due to the difficulty associated with manipulating coral symbioses in the laboratory, alternative model systems are needed to interrogate in high resolution the different links within their holobionts. For instance, host clonal lines will allow us to control for previously reported genotype-specific effects (Palacio-Castro et al. 2022) and having stably engineered microbiomes will allow us to ascertain the role of specific members of the microbiome; for the latter, this is a rapidly evolving discipline with some promising coral-based developments in the last few years (see Delgadillo-Ordoñez et al. 2024). An emerging model organism that allows us to overcome some key issues in coral holobiont research is the sea anemone *Aiptasia*, which is a cnidarian closely related to reef building corals (Baumgarten et al. 2015; Figure 0.4). *Aiptasia* are symbiotic with dinoflagellate algal strains similar to those found in corals. But unlike coral, they can be cultured indefinitely without Symbiodiniaceae (aposymbiotic state) and reinfected with algae originating from both corals and other *Aiptasia* (Grawunder et al. 2015, Baumgarten et al. 2015, Weis et al. 2008, Hambleton et al. 2014, Tran et al. 2024, Schoenberg et al. 1980) allowing us to directly engineer their microbiome. *Aiptasia* also experiences bleaching like corals, with a similar transcriptional and microbial response to thermal stress (Cleves et al. 2020, Mansfield et al. 2017, Cui et al. 2023). The bacterial microbiome has yet to be manipulated in *Aiptasia*, but we do know that the bacterial microbiome significantly differs between symbiotic and aposymbiotic individuals, and that there is increased community variance for these microbiome members during long-term thermal stress (Röthig et al. 2016, Ahmed et al. 2019, Aguirre et al. 2023). Lastly, the settlement cue for laboratory-spawned *Aiptasia* larvae has been recently identified, facilitating the creation

of gene knockout lines using CRISPR-Cas9 (Grawunder et al. 2015, Jones et al. 2018, Maegele et al. 2023). *Aiptasia* are already allowing us to address long-standing questions in coral biology, such as the basis of metabolic interactions in controlling in hospite algal populations (Xiang et al. 2020), the relative contribution of various cellular mechanisms underpinning bleaching (Bieri et al. 2016), nutrient exchange between the host and its algal symbionts (Rädecker et al. 2018), and symbiont establishment (Wolfowicz et al. 2016). *Aiptasia*'s various clonal lines and compatible Symbiodiniaceae strains will allow us to explore fine-scale microbial shifts during temperature stress, permitting us to place our findings in conversation with insights gained when studying corals in both natural and experimental settings.

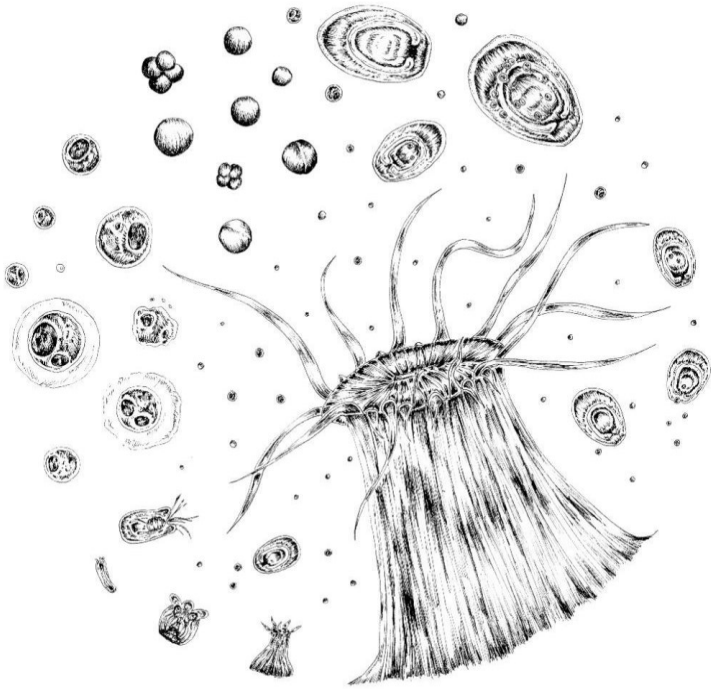

Figure 0.4. *Aiptasia* sea anemones as a model system for corals. In addition to associating with the same family of symbiotic algae as corals, Symbiodiniaceae, *Aiptasia*'s algal microbiome can be engineered so that animals can stably host non-native strains from corals and can be kept stably in a bleached state without any algal symbionts. Additionally, *Aiptasia*'s entire life cycle

has been successfully recapitulated in the lab, allowing us to create knock-out lines with gene-editing tools like CRISPR-Cas9.

0.5 Towards a mechanistic understanding of cnidarian holobionts under climate change

Coral biology finds itself at a critical transition, both in terms of the state of our planet and the experimental tools at our disposal to interrogate the factors driving divergent bleaching trajectories. It is precisely this realization that has inspired my dissertation. A holobiont approach urges us to consider where various host and microbiome response mechanisms intersect by employing a diversity of techniques. This ranges from whole-genome sequencing for population genetic analyses to metabolic characterization of the host under stress using biochemical assays, and combining laboratory-based experimental work with long-term monitoring of natural populations. Additionally, studying corals vis-à-vis emerging model systems such as *Aiptasia* will further inform our understanding of the mechanisms driving bleaching by providing the ability to monitor and engineer various components of the holobiont. Chapter 1 closely interrogates my thesis' focal coral taxa *Pocillopora* spp. across its entire range in the Indo-Pacific, leveraging publicly available data to ask how environmental and biogeographical approaches structure coral-algal symbioses. In Chapter 2, I focus on *Pocillopora* spp. corals in Panama's TEP, employing the previously described two-gulf upwelling system to discern the factors structuring coral holobiont configurations, and how these are driving differences in thermotolerance during an acute thermal stress assay. In Chapter 3, building upon insights gained in Chapter 2 regarding temperature-driven prokaryotic dysbiosis, I use *Aiptasia* to explore how algal symbiont's thermotolerance impacts bacterial community's stability under thermal stress. My dissertation's unique approach, moving from the field to the lab and crossing taxonomic

lines, offers novel insights into the factors driving coral thermal resistance, providing a glimmer of hope for the future of these rainforests under the sea.

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Chapter 1 | Environmental and geographical factors structure cauliflower coral's algal symbioses across the Indo-Pacific

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1.1 Abstract

Aim

The symbioses between corals and their dinoflagellate partners (Symbiodiniaceae) have been described as a flexible relationship whose dynamics could serve as a source of resilience for coral reef ecosystems. However, the factors that drive the establishment and maintenance of this co-evolutionary relationship remain unclear. We examined the environmental and geographic factors structuring the Symbiodiniaceae communities in a wide-ranging Indo-Pacific coral, the cauliflower coral (*Pocillopora* spp.), to begin to address this gap in the literature.

Location

Coral reefs in the Indo-Pacific, representing the following locations: Djibouti, Oman, Taiwan, and French Polynesia.

Taxon

Cauliflower coral (*Pocillopora* spp.), dinoflagellates (family Symbiodiniaceae).

Methods

We performed a meta-analysis by mining publicly available amplicon sequence data from the nuclear ribosomal DNA (rDNA) internal transcribed spacer 2 (ITS2), originating from *Pocillopora* spp.; this is the most widely used marker-gene for Symbiodiniaceae. We also compiled associated environmental data from these sequences, such as sea surface temperature (SST) and time since the last local mass bleaching event (TSB).

Results

Sea surface temperature (SST) was the most important factor driving Symbiodiniaceae community differences, with the largest effect size of the statistically significant factors. When focusing on individual Symbiodiniaceae genera, SST was likewise the most important factor. Our indicator species analysis revealed that samples that had recently bleached were characterized by roughly equal proportions of *Cladocopium* spp. and *Durusdinium* spp., while samples that had not recently bleached had a similar proportion of *Durusdinium* spp. as those that had recently bleached, but also showed a reduction of *Cladocopium* spp., with this deficiency made up by the presence of *Symbiodinium* spp.

Main conclusions

By evaluating the importance of thermal and geographic factors in driving the relationship between dinoflagellate partners and one of the Indo-Pacific's dominant reef building genera, we provide further support for the hypothesis that coral's Symbiodiniaceae communities could facilitate host resilience to thermal stress. Our work is in direct conversation with a larger body of biogeography literature that highlights how local environmental regimes can impact contemporary population structure, even in marine taxa with wide-range dispersal.

1.2 Introduction

Host-symbiont relationships are increasingly recognized as being important for contributing to host tolerance of environmental stress (Iltis et al., 2021; Dastogeer et al., 2022; Ainsworth et al., 2010). A classic example are reef-building corals (Order Scleractinia), which thrive in nutrient-poor, tropical and sub-tropical marine ecosystems due to an ancient, co-evolutionary relationship with photosynthetic dinoflagellates from the family Symbiodiniaceae (Campoy et al., 2020; Liu et al., 2018; Frankowiak et al., 2016). As atmospheric CO_2 levels increase due to anthropogenic climate change, corals face increasing extinction risk due to rising sea water temperatures driving mass coral bleaching events (Hughes et al., 2018; Carpenter et al., 2008), which destabilizes the coral-algal symbiosis (Hoegh-Guldberg, 1999). Changes in the symbiont communities associated with coral have been connected to ecological and performance shifts in the host-symbiont relationship, potentially assisting these corals in coping with repeat thermal stress events (Glynn et al., 2001; Rowan et al., 1997; Rodríguez-Román et al., 2006; Cunning et al., 2015). However, the specific environmental and geographic factors that structure the distribution of symbiont communities are not fully understood. Prior studies on the factors structuring marine invertebrate communities suggest that despite high potential for long distance dispersal with oceanic currents, regional differentiation can often arise in response to local environmental conditions (e.g. Hirschfeld et al., 2021; Lopes da Silva Ferrette et al., 2020; Lim et al., 2021; Coppard et al., 2021; Lessios et al., 2003; van der Ven et al., 2021; Wepfer et al., 2020; Cineas & Dolédec, 2022; Pappalardo et al., 2014). In particular, the Indo-Pacific has served as a key area of study for understanding how current species distributions can be structured by the complex interplay between contemporary environmental pressures and historical patterns of gene flow (see Benzie, 1999; Lessios et al., 2001; Crandall et al., 2019). However, there remains a knowledge gap

concerning where and why particular Symbiodiniaceae taxa are associated with particular coral genera. To date, coral studies have typically focused on the factors structuring these symbioses in either a single geographic location (Pollock et al., 2018; O'Brien et al., 2020; Ricci et al., 2022; Johnston et al., 2022a; Osman et al., 2020) or for a single Symbiodiniaceae genus at the regional level (Turnham et al., 2021). It is important to consider how environmental and geographic factors together are driving the establishment and maintenance of this symbiotic relationship, as the diversity, distribution, and stability of Symbiodiniaceae communities is central to coral's future in an increasingly warmer, high CO_2 world.

Generally, host-specificity results in an individual coral being in symbiosis with a single Symbiodiniaceae taxon (see Smith et al., 2017; van Oppen et al., 2001; LaJeunesse et al., 2004). Given the evolutionary distance between taxa, LaJeunesse et al. (2018) recently reclassified each as its own genus. While many coral species often associate with a single Symbiodiniaceae genus, two coral genera - *Orbicella* (Western Atlantic) and *Pocillopora* (Indo-Pacific) - regularly host multiple genera, suggesting more labile and potentially adaptive coral-symbiont associations (Kennedy et al., 2016; Kemp et al., 2015; Toller et al., 2001; Cunning et al., 2013; Ziegler et al., 2017). For example, *O. faveolata* has been shown to be most resistant to bleaching when harboring phylotype A3 (now *Symbiodinium* spp.), and during bleaching events there was an increased presence of this phylotype alongside the D1a phylotype (now *Durusdinium* spp.; Kemp et al., 2014). Within *Orbicella* spp., the length of thermal stress events can also dictate longer-term dynamics of *Durusdinium*, with D1a phylotypes being most retained after 14 days versus 7 or 10 days of experimentally induced heat stress (Cunning et al., 2018). Likewise, cauliflower coral (*Pocillopora* spp.) colonies in Panama (the easternmost part of this genus's range) were

shown to shift their communities from *Cladocopium* spp. to *Durusdinium* spp. during the 1997–98 El Niño–Southern Oscillation (ENSO) event (Glynn et al., 2001). *Pocillopora* colonies dominated by *Durusdinium* experienced less bleaching and mortality during the 1997-1998 ENSO thermal bleaching event compared to the 1982-83 ENSO event (Glynn et al., 2001). *Pocillopora* has also been observed to be less susceptible to bleaching during cold-water events when associated with *Durusdinium* spp. (LaJeunesse et al., 2010). More recently, *Pocillopora* spp. has been reported to acquire novel *Durusdinium* and *Cladocopium* species from the environment and maintain stable associations for up to 18 months after two subsequent bleaching events, suggesting that symbiont community changes could be an adaptive and flexible response to environmental stressors (Boulotte et al., 2016).

Together, data from *Orbicella* and *Pocillopora* corals presents that changes in coral symbiont genera can be linked to environmental stress, and that these changes to Symbiodiniaceae communities could provide benefits to the coral host. Although there is a considerable body of work that underscores the dynamic nature of coral-Symbiodiniaceae partnerships in the face of bleaching (Quigley et al., 2019; Baker et al., 2004; Rowan et al., 1997), other studies have highlighted the stability of Symbiodiniaceae communities or have suggested that many changes cannot be conclusively linked to environmental stressors (Epstein et al., 2019; McGinley et al., 2012; Manzello et al., 2018; Rouzé et al., 2019; Hoegh-Guldberg et al., 2002), urging us to consider additional factors that structure coral host-symbiont interactions.

In addition to thermal stress and bleaching events, Symbiodiniaceae communities can be structured by other abiotic and geographical factors, such as dispersal potential and adaptation to

local abiotic regimes. Previous research has shown that different oceanic basins possess divergent Symbiodiniaceae communities, both free living and in-hospite (Manning & Gates, 2008; LaJeunesse, 2005). For example, *O. annularis* in the Caribbean and Bahamas is predominantly associated with the genera *Breviolum, Cladocopium, and Durusdinium* (Kennedy et al., 2016), while *Pocillopora* in the Red Sea and Tropical Eastern Pacific is predominantly associated with the genera *Symbiodinium, Cladocopium, and Durusdinium* (LaJeunesse et al., 2004; Baker et al., 2017; Ziegler et al., 2017). Some Symbiodiniaceae taxa like *Cladocopium latusorum* are found in association with corals across the entire Indo-Pacific (Turnham et al., 2021). Additionally, host and local environmental regimes, such as sea surface temperature, appear to influence coral-Symbiodiniaceae partnerships (Tonk et al., 2013; Cooper et al., 2011; Osman et al., 2020), with particular genetic lineages more likely to associate with particular Symbiodiniaceae genera (Cunning et al., 2013). It has also been noted that *Symbiodinium* spp. and *Breviolum* spp. are most common at higher latitudes, while *Cladocopium* spp. is more common in tropical latitudes (Baker, 2003). The complex interplay between genera-specificity, dispersal, and environmental conditions represents a challenge for elucidating the factors that structure coral-algal symbioses across broad species ranges, particularly because most studies focus on local patterns at a single geographic location.

Pocillopora is a genus of reef-building corals that is widely distributed across the Indo-Pacific - ranging from the Red Sea to the Tropical Eastern Pacific (TEP) in Central and South America - and thus provides an excellent system to explore the factors that drive patterns of host-Symbiodiniaceae associations across large spatial scales and environmental regimes. *Pocillopora* corals are capable of withstanding considerable environmental heterogeneity compared to other

coral taxa (Hoegh-Guldberg, 2011). For example, *Pocillopora* corals in the Red Sea are found at extreme salinities up to 41 ppt (Paldor & Anati, 1979) and at temperatures above 30°C (Fine et al., 2013). In the TEP, *Pocillopora* corals experience seasonal upwelling conditions that trigger drastic annual fluctuations in abiotic conditions (O'Dea et al., 2012; D'Croz & O'Dea, 2007); for instance, corals in the Gulf of Panama experience a 10-degree shift in temperature across the non-upwelling and upwelling seasons, and as much as a 5-point drop in salinity, among other parameters (Manzello et al., 2008). To date, there has not been a study systematically exploring *Pocillopora*'s Symbiodiniaceae communities across its range. Given this taxon's symbiont flexibility during thermal stress events and the environment heterogeneity encompassed by its range, it represents an ideal system to address larger questions regarding the factors structuring coral-Symbiodiniaceae establishment and maintenance.

In this study, we mined publicly available Symbiodiniaceae nuclear ribosomal DNA (rDNA) internal transcribed spacer 2 (ITS2) sequences that spanned study locations across *Pocillopora*'s range to investigate the environmental and geographic factors structuring the Symbiodiniaceae communities in this wide-ranging Indo-Pacific coral. Given the evidence that bleaching disrupts symbiosis (Glynn, 1996; Brown, 1997; Hoegh-Guldberg, 1999; Douglas, 2003; Weis, 2008; Carpenter et al., 2008; Ainsworth et al., 2016; Hughes et al., 2018) and that migrant establishment may be lower in thermally-unsuitable locations relative to locally-adapted populations (Osman et al., 2020; Kelly et al., 2014; Nosil et al., 2009; Lessios et al., 2001; Fitzpatrick et al., 2015), we predicted that a region's thermal history, followed by geography, would most strongly drive host-symbiont associations. By focusing on a single cosmopolitan genus and its algal symbionts, we aim to identify and disentangle the various interconnected

factors responsible for the establishment and diversity of coral-Symbiodiniaceae symbioses, thus providing insights into how corals' symbiotic partnerships are structured and potentially impacted by environmental change.

1.3 Materials and Methods

1.3.1 Data mining

We downloaded all available Symbiodiniaceae ITS2 FASTQ sequence files in July 2021 from *Pocillopora* corals from NCBI's Sequence Read Archive (SRA) via the SRA Toolkit on Compute Canada (Baldwin, 2012). We also downloaded their associated metadata (i.e. publication source, species sampled, location sampled, coordinates of sampling location, time of year sampled, ITS2 primers used). We used NOAA's Coral Reef Watch Operational Daily Near-Real-Time Global 5-km Satellite Coral Bleaching Monitoring Products (NOAA Coral Reef Watch, 2000) to extrapolate sea surface temperature (SST) from the study locations, if this data was not already provided in the associated publication. Finally, we ascertained the time since the last local bleaching event (TSB) by referencing government monitoring program reports and scientific publications.

1.3.2 Sequence quality control and amplicon sequence variant (ASV) detection

Given the heterogeneous nature of the mined files, we used the R package 'DADA2' version 1.20 (Callahan et al., 2016; https://github.com/benjjneb/dada2) to filter and trim the mined ITS2 sequences and detect amplicon sequence variants **(**ASVs). We used an ASV approach rather than detecting and constructing operational taxonomic units (OTUs), because ASVs represent sequences that are stand-alone, reproducible, and informative, as a detected ASV is a sequence in

and of itself and is not contingent on the nature of the clustering approach used (see Callahan et al., 2017). We followed a standard DADA2 workflow: we trimmed and de-replicated sequences, removed chimeras, and generated a FASTA file with our detected ASVs. For sample inference, we took a pseudo-pooling approach as a compromise between processing time and improving the detection of low-frequency Symbiodiniaceae ASVs (c.f. Silverman et al., 2018). We ran our DADA2 R Script on the Compute Canada Cedar server.

1.3.3 Phylogenetic tree

We used FastTree 2 version 2.1.11 (Price et al., 2010) to construct an ITS2 phylogenetic tree, which implements the Shimodaira-Hasegawa test to compare alternative topologies with 1,000 resamples. For our tree, we first used Clustal Omega (Sievers & Higgins, 2021) on the Compute Canada Cedar server with default parameters to align our DADA2-generated FASTA sequences. We then used these aligned sequences to build our phylogenetic tree with FastTree 2, using a generalized time-reversible model.

1.3.4 Taxonomic assignment

We took two approaches to assign taxonomy to our ASVs using: (1) the SymPortal database (Hume et al., 2019) and (2) NCBI BLAST (Altschul et al., 1990; see details below). We selected the taxonomic assignment that most closely matched the phylogenetic tree presented in LaJeunesse et al. (2018), which is the most widely accepted phylogeny of Symbiodiniaceae, where each Symbiodiniaceae phylotype is its own clade on the tree; other recent Symbiodiniaceae phylogenetic trees have shown concordance with this tree (see Turnham et al., 2021; Teschima et al., 2019).

The SymPortal database (Hume et al., 2019) is a community-driven Symbiodiniaceae-specific database that uses the ITS2 marker and provides ITS "clade" and "type" assignments as it was built before this family's taxonomic reorganization. Yet these assignments represent ITS2-type profiles and will be referred to as such hereon. We downloaded the database and then used vsearch version 2.4.3 (Rognes et al., 2016; https://github.com/torognes/vsearch) and usearch version 11.0 (Edgar, 2010; http://www.drive5.com/usearch) to assign taxonomy to our ASV FASTA file generated in DADA2, requiring a pairwise identity of at least 0.6. As SymPortal is optimized for the SYM_VAR_5.8S2/SYM_VAR_REV primer pair (Hume et al., 2018; Hume et al., 2019) and our dataset included sequences generated using different primers, namely the ITSIntFor2 (LaJeunesse, 2002) and ITS2 pair (Coleman et al., 1994), or the ITS-DINO (Pochon et al., 2001) and ITS2Rev2 (Stat et al., 2009) pair, we also assigned taxonomy with NCBI BLAST. For NCBI BLAST, we set an E-value cut-off of $1x10^{-5}$ and a maximum of 5 target sequences. We manually annotated non-Symbiodiniaceae hits as no hits ("N") and established ITS2-type profiles based on the NCBI output reference entries, mirroring the SymPortal output. For ASVs that had multiple ITS2-type profiles as hits, we selected the one with the smallest E-value, least number of mismatches, and/or greatest percent alignment. If an ASV had two different ITS2-type profiles with the same E-value, number of mismatches, and percent alignment, we only assigned taxonomic resolution down to the genus level. Furthermore, as not all Symbiodiniaceae form symbioses with corals (c.f. Baker, 2003), if an ASV hit did not provide further taxonomic resolution past Symbiodiniaceae, it was also denoted as "N." We removed these uninformative ASVs before downstream analyses. The SymPortal taxonomic assignment can be found in Table A4 in the Supporting Information, and the NCBI taxonomic assignment in Table A5 in the Supporting Information.

1.3.5 ASV quality control and cumulative sum square (CSS) transformation

All statistical analyses were performed in R version 4.1.2 (R Core Team, 2021). Using the R package 'phyloseq' version 1.39.1 (McMurdie & Holmes, 2013; https://github.com/joey711/phyloseq), we integrated ASVs, taxonomy, and sample information into a single object. We then performed quality control, including removing taxa that had less than 1,000 reads, those that were observed less than once in at least 5% of the specimens, and removing any singleton ASVs. We performed a cumulative sum square (CSS) transformation, as opposed to rarefying Symbiodiniaceae reads, to avoid omitting data whose differences in library size and presence/absence of particular ASVs may be of biological importance (McMurdie & Holmes, 2014). CSS corrects for differences in library size by standardizing to the quartile where lower abundance taxa are well-represented (Paulson et al., 2013).

Given that the majority of our sequences (64% of mined SRA entries) were identified on NCBI as being from *P. damicornis*, we only analyzed this subset for downstream applications. We recognize that these sequences are not necessarily from *P. damicornis sensu lato*, as although some of the mined studies employed marker-based taxonomic assessment of the host, none implemented whole-genome sequencing. With increasing genetic resources, recent studies have come to highlight the complex genetics within this genus that often contradicts marker-based approaches (see Oury et al., 2022 using ultra-conserved elements). Therefore, in taking a more conservative approach, we have decided to refer to our analyzed sequences as coming from *Pocillopora* spp. Additionally, in generating diagnostic standardized residual and QQ-plots, some of our variables showed a multimodal distribution, even after log and square-root transformations, and thus we removed these outlier sequences to meet normality assumptions.

These removed sequences included specimens from the locations of Heron Island (Great Barrier Reef, Australia; n = 153 SRA entries) and New Caledonia (n = 70 SRA entries), specimens collected during the summer (n = 10 SRA entries), and specimens experiencing bleaching (n = 19 SRA entries). This pruned dataset was used for all subsequent analyses, which comprised a total of 101 SRA sample entries (see Table A2 in the Supporting Information for the entries used in downstream analyses and their associated data; the metadata can be found in Table A3).

1.3.6 ASV richness across abiotic parameters

To understand how Symbiodiniaceae diversity varied across abiotic parameters, we plotted taxa richness, the Shannon diversity index, and the inverse Simpson index across locations (categorized by region) and time since bleaching (TSB). For SST, we created scatterplots with 'ggplot2' package version 3.3.5 (Wickham, 2016). Given that there was heteroscedasticity in our residuals, even after transformation of the alpha diversity metrics, we fit linear models using generalized least squares (GLS) using the 'nlme' package version 3.1-153 (Pinheiro et al., 2021), where we allowed each level within our explanatory variable "location" to have different variances. For our GLS models, we nested locations within regions, and set SST and TSB as fixed effects. We performed post-hoc comparisons using the 'emmeans' package version 1.7.0 as this uses estimated marginal means to compare the effects of factors (Lenth, 2021), with effective degrees of freedom calculated with the Welch Satterthwaite approximation and implements the Benjamini and Hochberg p-value correction for multiple comparisons. All comparisons were tested at a 95% confidence level.

1.3.7 Symbiodiniaceae community composition

We created pie charts for each location's Symbiodiniaceae community using the 'plot_bar' argument from 'phyloseq' (McMurdie & Holmes, 2013) to further visualize differences across the Indo-Pacific; these pie charts were placed over a map of our study region. We also plotted Symbiodiniaceae ASV networks to ascertain how Symbiodiniaceae partnerships were structured across locations. We created connectivity networks via the 'plot_net' argument in 'phyloseq' (McMurdie & Holmes, 2013) using only the top 20 taxa by abundance, implementing the Fruchterman-Reingold layout algorithm (Fruchterman & Reingold, 1991) and using Bray-Curtis dissimilarity to calculate distances (Bray & Curtis, 1957).

We performed non-metric multidimensional scaling (nMDS) ordination with Bray-Curtis dissimilarities to visualize how Symbiodiniaceae community composition varied across our geographic parameters. We performed an nMDS with Bray-Curtis dissimilarities because this is a robust ordination approach that is able to handle missing ASVs (Buttigieg & Ramette, 2014). Bray-Curtis distances focus on compositional dissimilarity without making assumptions about the phylogenetic relationships between samples and can also process missing values. We created our ordination plots via 'ordinate' in the 'phyloseq' package (McMurdie & Holmes, 2013) and plotted 95% confidence ellipses. We performed a PERMANOVA with 999 permutations and Bray-Curtis distances via the 'adonis2' function in the R package 'vegan' version 2.5 (Oksanen et al., 2020) to determine which variables were driving significant differences in Symbiodiniaceae communities; post-hoc pairwise comparisons were performed with the 'pairwise.adonis2' function (Martinez Arbizu, 2020), implementing the Benjamini and Hochberg p-value correction for multiple comparisons. In the PERMANOVA, we nested locations within

regions, and set SST and TSB as fixed effects. We detected statistically significant heterogeneity of dispersions based on 'betadisper' in 'vegan' (Oksanen et al., 2020), and thus used PERMANOVA, which is more robust to heteroscedasticity than ANOSIM (see Anderson & Walsh, 2013).

We further explored how different Symbiodiniaceae ITS2-type profiles varied across our locations and environmental parameters by running each genus in its own PERMANOVA model, with 999 permutations and Bray-Curtis distances via the 'adonis2' function (Oksanen et al., 2020). Here, we nested locations within regions, and set SST and TSB as fixed effects in the model.

1.3.8 Mantel tests and indicator species analyses

We ran Mantel tests using the package 'vegan' (Oksanen et al., 2020) to determine if geographic distances and temperature differences could explain Symbiodiniaceae community dissimilarity. We calculated geographic distances from our sample location's coordinates using Haversine distances in the package 'geosphere' version 1.5 (Hijmans, 2019), as this takes into account the Earth's spherical shape. We used these calculated geographic distances for our Mantel tests, which we ran with 999 permutations and used Spearman correlation coefficients. For our temperature Mantel tests, we used the same parameters as for geographic distances, with the exception that we calculated differences across temperatures using Euclidean distances.

We performed an indicator species analysis (Dufrêne & Legendre, 1997) using the 'indicspecies' package's version 1.7.9 (Cáceres & Legendre, 2009) 'multipatt' command with 999

permutations and implementing the Benjamini and Hochberg p-value correction for multiple comparisons, to ascertain if certain Symbiodiniaceae taxa were significantly associated with certain locations or TSB.

1.4 Results

1.4.1 Overview of mined data

From NCBI's SRA, we downloaded 839 FASTQ files representing Symbiodiniaceae ITS2 sequences from *Pocillopora* corals. Our FASTQ files encompassed three different ITS2 primer pairs, 27 locations, and were referenced on NCBI as representing 4 *Pocillopora* species: *Pocillopora acuta, P. damicornis, P. meandrina*, and *P. verrucosa*. The majority of the sequences (79%) used one of two primer sets: the ITSIntFor2 (LaJeunesse, 2002) and ITS2 pair (Coleman et al., 1994), or the ITS-DINO (Pochon et al., 2001) and ITS2Rev2 (Stat et al., 2009) pair. As each primer set amplifies a slightly different length of the ITS2 region, combining these datasets could potentially cause the differences in length to be interpreted as mismatches by DADA2, and thus we only analyzed sequences amplified with the ITS-DINO and ITS2Rev2 primer pair (referred to as the "DINO" dataset hereon) because it represented the greatest geographic distribution and number of independent studies. We focused solely on entries identified as being from *P. damicornis* on NCBI for all our downstream analyses, as this was also the most abundant species present in the DINO primer set dataset, representing 63% of DINO sequences (see Table A1 in the Supporting Information to see all the mined DINO sequences' SRA numbers and associated data; the metadata can be found in Table A3). However, given the genetic delineation of species boundaries within of this genus is still being resolved (see Pinzón & LaJeunesse, 2011; Combosch & Vollmer, 2015, Johnston et al., 2017;

Johnston et al., 2022b; Oury et al., 2021; Oury et al., 2022), we will refer to these sequences as originating from *Pocillopora* spp. Furthermore, for downstream analyses, we used a subset of 101 SRA entries that met normality assumptions (see Table A2 in the Supporting Information for the entries used in downstream analyses and their associated data; the metadata can be found in Table A3).

1.4.2 Phylogenetic tree

The NCBI-based ITS2 taxonomic assignment resulted in a tree whose relationships best-represented the accepted phylogeny of Symbiodiniaceae (see LaJeunesse et al., 2018), whose most important feature is that each Symbiodiniaceae genus is a distinct phylogenetic clade on the tree (Figure 1.1b; see Table A5 in the Supporting Information). By comparison, the SymPortal-based taxonomic assignment did not group Symbiodiniaceae ITS2-type profiles into clades on our phylogenetic tree (Figure 1.1a; see Table A4 in the Supporting Information). Therefore, we decided to use the NCBI-based taxonomic assignment to assign Symbiodiniaceae genera ITS2-type profiles as we were interested in how environmental and geographic parameters impacted the entire Symbiodiniaceae community at the ASV-level with no additional classification. However, we also needed classification to the level of Symbiodiniaceae genera, which required us to classify the ASVs into generic groupings.

1.4.3 Patterns of diversity within Symbiodiniaceae communities

Symbiodiniaceae from Djibouti corals had the lowest median alpha diversity scores across richness, Shannon diversity, and inverse Simpson metrics, while Symbiodiniaceae from Oman corals had the highest median scores across all indices (Figure 1.2a). Corals from French

Polynesia (four islands in our dataset) had a Symbiodiniaceae community with a narrow spread around the median for all metrics, except for Tahiti's Shannon and inverse Simpson indices (Figure 1.2a). There was no apparent difference in the median scores for sequences originating from corals that had recently versus those that had not recently bleached, but across all alpha diversity metrics the range of diversity values was greatest for sequences originating from corals that had not bleached recently (Figure 1.2b, category "Long"). For SST, our scatterplots did not reveal a clear association between our three alpha diversity metrics and temperature (Figure 1.2c). Overall, our GLS models did not detect significant variation in median scores between sequences collected from corals representing distinct locations, regions, SST regimes, or TSB, except for the interaction between the Indian Ocean (region) and Oman (location) for Shannon diversity and inverse Simpson scores (Table A6-A8 in the Supporting Information).

1.4.4 Regional differences in Symbiodiniaceae communities

We observed broad differences in Symbiodiniaceae communities across regions (Figure 1.3). The farthest west location, Djibouti, was the only location with *Symbiodinium* spp. taxa (ITS2-type profiles A1 and A2) and was overall dominated by *Durusdinium* spp., ITS2 type profile D1 (Figure 1.3, location 1). Moving from west to east, specimens from Oman and Taiwan had Symbiodiniaceae communities predominantly composed of *Cladocopium* spp. (ITS2-type profiles C; Figure 1.3, locations 2-3, respectively). Specimens from French Polynesia, which were the furthest east (Figure 1.3, locations 4-7), were dominated by *Durusdinium* spp. (ITS2-type profile D). Network analysis supported these findings, as sequences from corals originating from Taiwan and Oman, which are in different oceanic basins, clustered with one another, although there was an isolated group of sequences from Oman which formed a separate cluster

(Figure 1.4a). Likewise, all sequences from French Polynesia (Mo'orea, Raiatea, Tahiti, and Taha'a), clustered with one another, and sequences from Djibouti did not cluster with other locations and instead formed two independent clusters (Figure 1.4a). nMDS plots also revealed concordant regional clustering of Symbiodiniaceae communities, where there was an overlap in the ellipses for sequences from Oman and Taiwan, while sequences from Djibouti formed their own separate, 95% confidence ellipse (Figure 1.4b). Sequences from French Polynesia also clustered with one another in ordination space (Figure 1.4b).

1.4.5 Geographic and environmental factors structuring Symbiodiniaceae communities

Our PERMANOVA analyses revealed that three variables were significantly associated with differences ($p < 0.05$) in ASVs across locations: SST ($p = 0.001$, pseudo-F-statistic $_{1, 83} = 61.384$, $R^2 = 0.238$), region (p = 0.001, pseudo-F-statistic $_{2, 83} = 51.626$, $R^2 = 0.401$), and TSB ($p = 0.031$, pseudo-F-statistic $_{1, 83} = 2.474$, $R^2 = 0.01$), as well as the interaction between region and location ($p = 0.003$, pseudo-F-statistic $_{3, 83} = 2.499$, $R^2 = 0.029$; Table A9 in the Supporting Information). Pairwise comparisons revealed that all locations significantly differed from each other except Taha'a versus Raiatea; all regions also significantly differed from one another (all $p < 0.05$; see Table A10-A11 in the Supporting Information). Mantel tests revealed that more distant specimens had more distinct Symbiodiniaceae communities (Mantel r statistic = 0.371, $p = 1x10^{-4}$, 9999 permutations). We found the same trend for SST, with specimens collected from regions with more distinct SST values possessing more divergent Symbiodiniaceae communities (Mantel r statistic = 0.409, $p = 1x10^{-4}$, 9999 permutations). The Mantel r statistic for SST comparisons was marginally larger than for geographic distances, 0.409 versus 0.371, respectively. In comparing effect sizes from our PERMANOVA, SST emerged as the strongest

driver of Symbiodiniaceae community composition across all statistically significant factors, followed by region (Table A9 in the Supporting Information).

Our PERMANOVAs for each major ITS2-type profile (A, C, and D) further revealed the factors structuring these symbioses. For all genera, on the basis of pseudo-F-statistics, SST most strongly impacted the presence/absence of specific ASVs, followed by region and then the interaction of region and location (all $p < 0.05$; see Table A12-A14 in the Supporting Information). Pairwise post-hoc analyses revealed that for *Symbiodinium* spp., detected ASVs were statistically distinct between the Indian Ocean and French Polynesia, and the Indian Ocean and Taiwan, while for *Cladocopium* spp. and *Durusdinium* spp., pairwise comparisons between all regions were statistically-significant (all $p < 0.05$; see Table A15-A20 in the Supporting Information for pairwise comparisons between locations and regions).

Indicator species analysis identified 79 ASVs that were differentially associated with TSB, while 328 and 267 ASVs were differentially associated with a given location and region, respectively (Table A21-A23 in the Supporting Information). When focusing on specific locations, all but one ASV (99.45%) from Taiwan were from *Cladocopium* spp., predominantly ITS2-type profile C1 (48.62%), with the sole remaining ASV being *Durusdinium* spp. ITS2-type profile D1 (Table A21 in the Supporting Information). For French Polynesia, all ASVs were *Durusdinium* spp., however the majority of the sequences could not be identified down to a specific ITS2-type profile, e.g. D1 (62.5%; Table A22 in the Supporting Information). For specimens from the Indian Ocean (Oman, Djibouti), the associations were more heterogeneous, with 5% of ASVs being *Symbiodinium* spp., 24% *Durusdinium* spp., and 71% *Cladocopium* spp. (Table A22 in the

Supporting Information). In comparing these two locations, Djibouti mostly had ASVs from *Durusdinium* spp. (81.82%), while Oman only had *Cladocopium* spp. (Table A21 in the Supporting Information). In recently bleached specimens, 48.84% of the ASVs were *Cladocopium* spp. and 51.16% were *Durusdinium* spp. For specimens that had not recently bleached, 13.89% of ASVs were *Symbiodinium* spp., 30.56% were *Cladocopium* spp., and 55.56% were *Durusdinium* spp. (Table A23 in the Supporting Information).

1.5 Discussion

This study represents the only meta-analysis to date that explicitly considers how geographic and environmental parameters structure the Symbiodiniaceae communities associated with a coral genus across its range. Our dataset captures the considerable diversity of thermal parameters, such as SST and TSB, which are found across *Pocillopora*'s range. We find support for our prediction that thermal regimes, here SST, most strongly structured *Pocillopora*-Symbiodiniaceae associations, and yet to a lesser extent, geographical isolation also explained community similarity patterns. Overall, our work underscores previous studies on *Pocillopora*'s diverse Symbiodiniaceae assemblages, while also placing potential mechanisms and consequences of this symbiont flexibility in conversation with previous work on the biogeographical factors impacting the distribution of Indo-Pacific marine taxa

1.5.1 Patterns of diversity in Symbiodiniaceae communities

Although alpha diversity metrics varied across locations, regions, SST, and TSB, based on our GLS models only the interaction between Oman and the Indian Ocean was significant for Shannon diversity and inverse Simpson indices; all other associations were not significant. This

is in line with the most notable pattern in the alpha diversity data, which was the strong difference between Oman and Djibouti within the Indian Ocean. Oman was the location with the largest values for Shannon diversity and inverse Simpson metrics in the dataset and also experienced the highest SST (30.8°C).

1.5.2 Symbiodiniaceae communities are structured by geography and thermal regime

Our results highlight the diverse Symbiodiniaceae community that is associated with *Pocillopora* spp. and reveal how these symbioses are structured across space and impacted by environmental parameters. *Cladocopium* spp., *Durusdinium* spp., and *Symbiodinium* spp. were most commonly associated with *Pocillopora* spp. within our dataset, in concordance with previous studies (LaJeunesse et al., 2004; Baker et al., 2017; Ziegler et al., 2017; Brener-Raffali et al., 2018). At the ASV-level, both geographic and environmental (SST and TSB) factors significantly influenced Symbiodiniaceae community dissimilarity, as revealed by our Mantel tests and PERMANOVA results. These findings suggest that local thermal regimes represent a key mechanism structuring Symbiodiniaceae communities.

While this study represents the first to investigate Symbiodiniaceae community composition across broad geographic scales for *Pocillopora* spp., previous work has revealed that differences in temperature, light availability, depth, and geographical separation can result in location-specific Symbiodiniaceae communities (c.f. Frade et al., 2008; Wicks et al., 2010; Cooper et al., 2011). Together, these results may reflect the dual processes of isolation by distance and isolation by adaptation (Nosil et al., 2009; Spurgin et al., 2014; Wang & Bradburd, 2014). For instance, prior studies with *Pocillopora* in the Arabian Peninsula have posited that

Symbiodiniaceae communities exhibit high host-specificity and site fidelity due to local adaptation to the region's high salinity and temperature regimes (Ziegler et al., 2017); other genera in this region exhibit similar host-symbiont interactions (Howells et al., 2020). Our results indicate that these patterns could be relatively widespread, with Symbiodiniaceae communities strongly associated with local SST, which was the variable with the largest effect size of the statistically significant factors in our PERMANOVAs. For example, despite being in distant regions of the Indo-Pacific, the communities found in Oman and Taiwan, which have similar SSTs (mean of 30.8°C and 28.63°C, respectively), were most similar to one another.

However, environmental conditions are not the only factor structuring these symbioses - our analyses also revealed a general pattern of isolation by distance across the Symbiodiniaceae communities. A recent *Pocillopora*-wide study in the Indo-Pacific proposed two newly defined Symbiodiniaceae taxa, *Cladocopium latusorum* and *C. pacificum*. These two taxa are genetically connected across their range but show greater genetic differentiation between populations from distant regions (Turnham et al., 2021). Symbiodiniaceae can disperse over long distances via sea surface currents (Chen et al., 2020; Pettay & LaJeunesse, 2013), and yet currents may also create hydrographic barriers preventing their movement (LaJeunesse et al., 2008). Our results suggest that long-distance dispersal does have limits, and that geographic distance and local SST regimes could act synergistically as a filter that determines the connectivity of Symbiodiniaceae communities across the disparate regions of *Pocillopora*'s range in the Indo-Pacific.

1.5.3 Bleaching events as a driver of Symbiodiniaceae community change

A switch from *Cladocopium* spp. to *Durusdinium* spp. has been reported to assist coral colonies experiencing thermal stress by significantly reducing bleaching-induced mortality (Glynn et al., 2001; Baker et al., 2004; Stat & Gates, 2010). Experimental work suggests that both *Symbiodinium* spp. and *Cladocopium* spp. show variable thermotolerance, with strain/species-level differences revealing thermotolerant and sensitive members alike (Fisher et al., 2012; Díaz-Almeyda et al., 2017). Long-term acclimation, or adaptation, of *Symbiodinium* spp. in the Red Sea has also been proposed, given this genus predominates under conditions that encompass a 6.0°C temperature gradient across seasons (Sawall et al., 2014). Our indicator species analyses present a community shift in relation to TSB, with *Symbiodinium* spp. no longer detected in recently bleached specimens, alongside a concordant increase in *Cladocopium* spp. The prevalence of *Durusdinium* spp. and *Cladocopium* spp. was comparable between specimens that had and had not recently bleached, albeit there was marginally less *Cladocopium* spp. found in specimens that had not recently bleached, purporting that perhaps the relative abundance of *Symbiodinium* spp. and *Cladocopium* spp. may be more indicative of responses to thermal stress within our system.

Our indicator species analysis findings are potentially consistent with the notion of coral symbiont shuffling as an adaptive response to thermal stress (see Buddemeier & Fautin, 1993; Cunning et al., 2015; Baker et al., 2004; Jones et al., 2008; Glynn et al., 2001). For instance, in the coral genus *Acropora*, there are tradeoffs in hosting *Durusdinium* spp. versus *Cladocopium* spp., with corals associated with *Durusdinium* spp. showing reduced growth rates but reduced temperature-induced bleaching (Little, 2004; Jones et al., 2008; Jones & Berkelmans 2010). It is

thought that this explains the pattern of Symbiodiniaceae communities reverting to their original composition once sea surface temperatures return to pre-bleaching conditions, which can take from several months to years (Lewis et al., 2019; Sampayo et al., 2008; Thornhill et al., 2006). We additionally present that the dynamics between *Cladocopium* spp. and *Symbiodinium* spp. may be another critical microbial interaction for *Pocillopora* corals under thermal stress, which has received much less attention to date (but see Sawall et al., 2014).

An important caveat is that none of the *Pocillopora* colonies in our analyzed dataset were sampled during a bleaching event, so it is also possible that the stress induced by recent periods of elevated SST were not sufficient to cause a shift in Symbiodiniaceae communities towards more thermotolerant strains/species, or that communities did shift but had reverted back under more benign conditions. It is also possible that the documented elevated SST was not sufficient to trigger thermal stress, perhaps because the Symbiodiniaceae communities were already locally adapted to conditions that would otherwise be denoted as stressful (Ziegler et al., 2017; Howells et al., 2020). Our results suggest that the traditional conceptualization of the benefits of switching to *Durusdinium* spp. may not accurately capture the potential of microorganisms to adapt to thermal stress events (see Abrego et al., 2008). Characterizing the thermotolerance of different Symbiodiniaceae species and strains will be greatly aided by further molecular analyses, with recent genome assemblies providing insights into genomic adaptations to thermal stress and symbiosis establishment (e.g. Shoguchi et al., 2021; Liu et al., 2018).

1.5.4. *Pocillopora*-Symbiodiniaceae associations complement previous work on the biogeographic factors structuring marine taxa

The influence of geographical and local environmental factors structuring *Pocillopora*-Symbiodiniaceae associations that we have reported here shows similarities with patterns that have been documented in a diversity of Indo-Pacific marine taxa (i.e. Benzie, 1999; Crandall et al., 2019; Hirschfeld et al., 2021; Lessios et al., 1999; van der Ver et al., 2021; DeBoer et al., 2014). In particular, there is consensus that current-assisted dispersal fails to fully explain contemporary species distributions, with regional environmental regimes being an important factor to consider. Our study adds new understanding by explicitly investigating the distribution of a core member of a microbiome within the context of its host range. In addition, we investigate the role of thermal regimes as a key environmental driver, whereas prior work has focused on factors such as salinity, habitat type (e.g., oceanic vs. benthopelagic), upwelling, or in some cases did not define specific factors but instead tested for 'regional differences' (e.g. Hirschfeld et al., 2021; Lessios et al., 2001; Crandall et al., 2019; but see Keith et al., 2013 where SST is explicitly considered). Although past studies of Symbiodiniaceae distributions have not explicitly considered thermal regimes, temperature has been hypothesized as being highly important in structuring marine host-microbiome interactions (see DeBoer et al., 2014 for *Tridacna* clams; Turnham et al., 2021 for *Pocillopora* corals). Given that climate change is causing SST to approach the thermal limits for many species, and the thermal sensitivity of many marine taxa (particularly corals), it is crucial to understand the influence of this factor for both the host and their microbiome.

1.5.5 Further work is needed to improve species delimitations within the *Pocillopora* genus

Although all sequences used for downstream analyses were identified on NCBI as being from "*Pocillopora damicornis*," we recognize that sequences on public repositories are heterogeneous, and that species-delineations within this genera are actively evolving (see Oury et al., 2022; Oury et al., 2021; Johnston et al., 2022b; Schmidt-Roach et al., 2013). None of the studies analyzed employed whole-genome sequencing to verify the identity of the host, with most implementing only single-marker data, most notably the mitochondrial open reading frame (mtORF), which is the most commonly used to distinguish between *Pocillopora* species given there is concordance between this marker and nuclear and morphometric datasets (Johnston et al., 2017; Pinzón et al., 2013; Pinzón & LaJeunesse, 2011). A few studies have implemented reduced-representation sequencing approaches (microsatellites, restriction-site associated DNA sequencing) to further improve genetic delineation of species within this genus, but the findings have yielded complex patterns of genetic differentiation and hybridization at both local and global scales (e.g. Aurelle et al., 2022; Oury et al., 2022; Oury et al., 2021; van Oppen et al., 2018; Combosch & Vollmer, 2015; Combosch & Vollmer, 2011). With whole genome approaches becoming more affordable, and the availability of many *Pocillopora* species' reference genomes (*P. acuta*: Vidal-Dupiol et al., 2020; *P. damicornis*: Cunning et al., 2018; *P. verrucosa*: Buitrago-López et al., 2020), we expect significant advances in our understanding of the genetic basis of thermal stress tolerance within *Pocillopora* (see Fuller et al., 2020 for this work in *Acropora*).

1.6 Conclusions

Our meta-analysis demonstrates the diversity of Symbiodiniaceae assemblages associated with cosmopolitan *Pocillopora* spp. and posits thermal regimes as a key factor driving variation in

community composition across this genus' range. Our work suggests that although isolation by adaptation to thermal regimes may be driving some differences across locations, there is also a signal of isolation by distance, indicating limits to connectivity across the Indo-Pacific. Additionally, time since the last mass bleaching event emerged as an important factor structuring Symbiodiniaceae communities, supporting previous work presenting Symbiodiniaceae community composition as a potentially adaptive response to local thermal regimes. Our work places coral-Symbiodiniaceae interactions in conversation with a robust corpus on the biogeographic factors structuring marine taxa's distributions, providing a framework for future Symbiodiniaceae community studies in *Pocillopora* corals that aim to characterize how the spatiotemporal patterns of diversity impact resilience to environmental stress.

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1.8 Figures

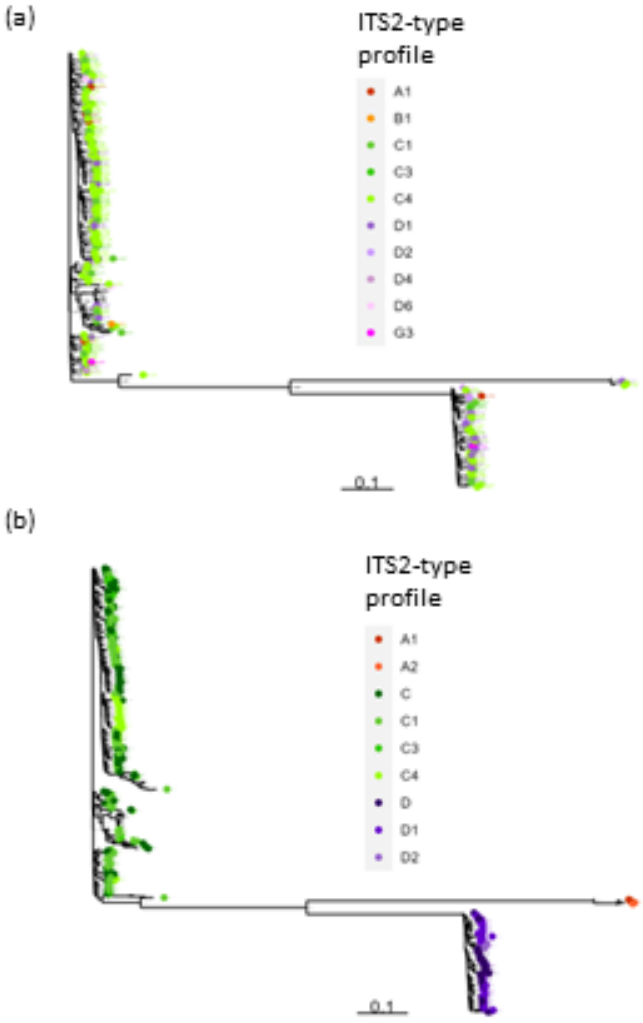

Figure 1.1. Symbiodiniaceae phylogenetic tree using ITS2 sequences derived from *Pocillopora* spp. The tree was made using FastTree 2 (Price et al., 2010) with 1,000 resamples. The scale bar represents substitutions per site. Symbiodiniaceae taxonomy is shown on the basis of ITS2-type profiles mirroring the SymPortal database's output (Hume et al., 2019). Yet based on recent taxonomic revision of the Symbiodiniaceae family, these profiles represent different genera and species (see LaJeunesse et al., 2018). Briefly, ITS2-type A profiles correspond to *Symbiodinium* spp., ITS2-type B profiles correspond to *Breviolum* spp., ITS2-type C profiles

correspond to *Cladocopium* spp., ITS2-type D profiles correspond to *Durusdinium* spp., and ITS2-type G profiles to *Gerakladium* spp. **(a):** Phylogenetic tree with the taxonomy assigned using SymPortal (Hume et al. 2019). **(b):** Phylogenetic tree with the taxonomy assigned using NCBI BLAST (Altschul et al., 1990).

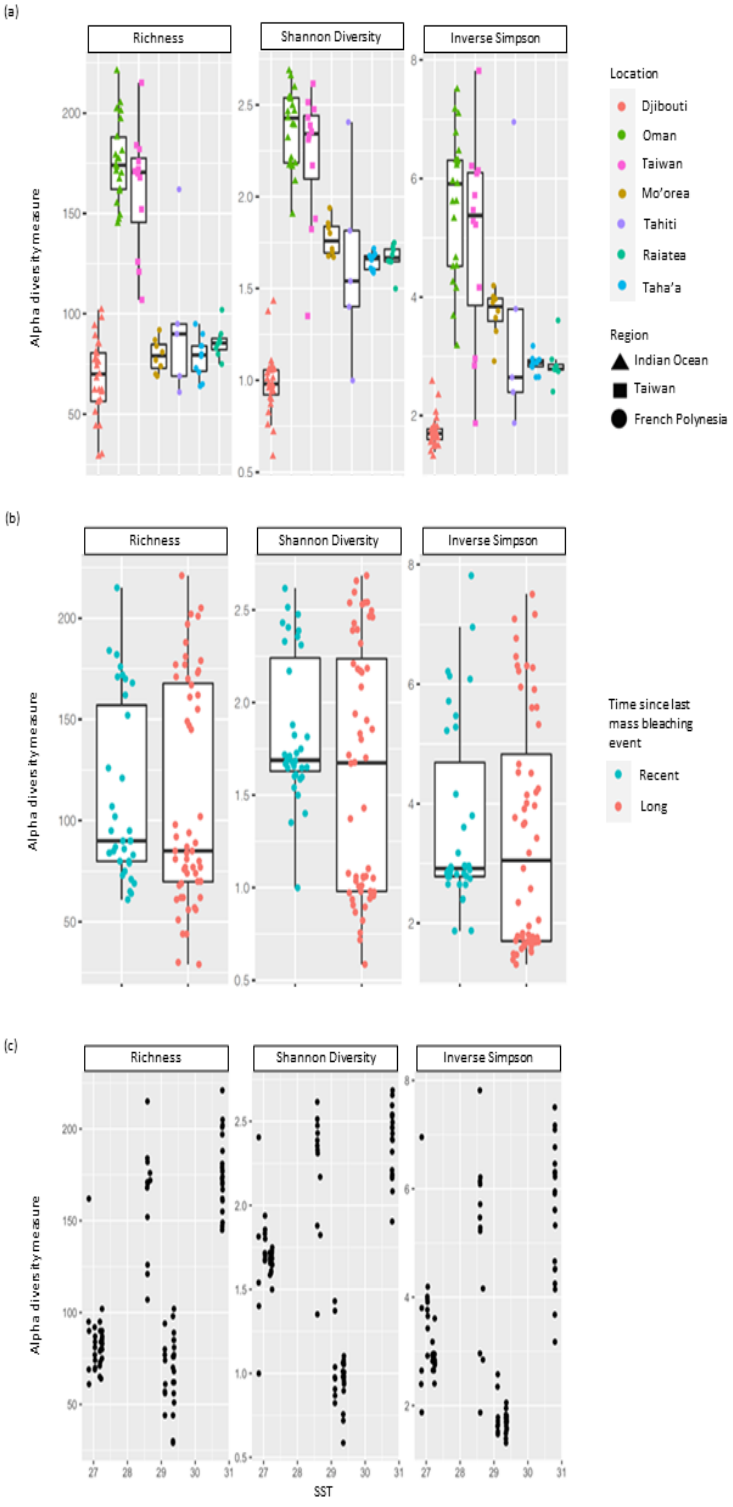

Figure 1.2. Symbiodiniaceae community diversity across locations, regions, time since last mass bleaching event (TSB), and sea surface temperature (SST). The locations are (from

west to east): Djibouti, Oman, Taiwan, Taha'a, Raiatea, Mo'orea, and Tahiti. The three regions (from west to east) are: the Indian Ocean, Taiwan, and French Polynesia. Three alpha diversity indices are shown: richness, Shannon diversity index, and inverse Simpson index (left to right on each plot). Differences across locations (as colors) and regions (as symbols) are shown in **(a)**, and **(b)** shows differences across TSB. **(c):** Scatterplots of sea surface temperature (SST) and richness, Shannon index, and inverse Simpson indices.

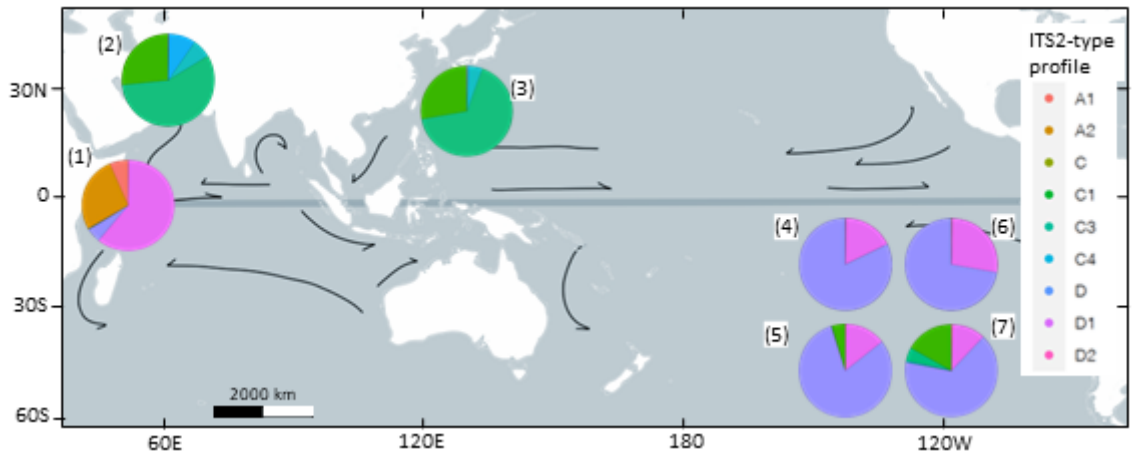

Figure 1.3. Symbiodiniaceae communities from *Pocillopora* spp. across the Indo-Pacific. Symbiodiniaceae communities across study locations. Pie charts represent community composition on the basis of ITS2-type profiles. Symbiodiniaceae taxonomy is shown on the basis of ITS2-type profiles mirroring the SymPortal database's output (Hume et al., 2019). Yet based on recent taxonomic revision of the Symbiodiniaceae family, these profiles represent different genera and species (see LaJeunesse et al., 2018). Briefly, ITS2-type A profiles correspond to *Symbiodinium* spp., ITS2-type B profiles correspond to *Breviolum* spp., ITS2-type C profiles correspond to *Cladocopium* spp., and ITS2-type D profiles correspond to *Durusdinium* spp. Major oceanic currents are shown as black arrows, with the equator shown as a thick dark gray line across the map. The map uses an equirectangular projection to best represent distances

across studied locations. Locations are as follows (from west to east): (1) Djibouti, (2) Oman, (3) Taiwan, (4) Taha'a, (5) Raiatea, (6) Mo'orea, and (7) Tahiti.

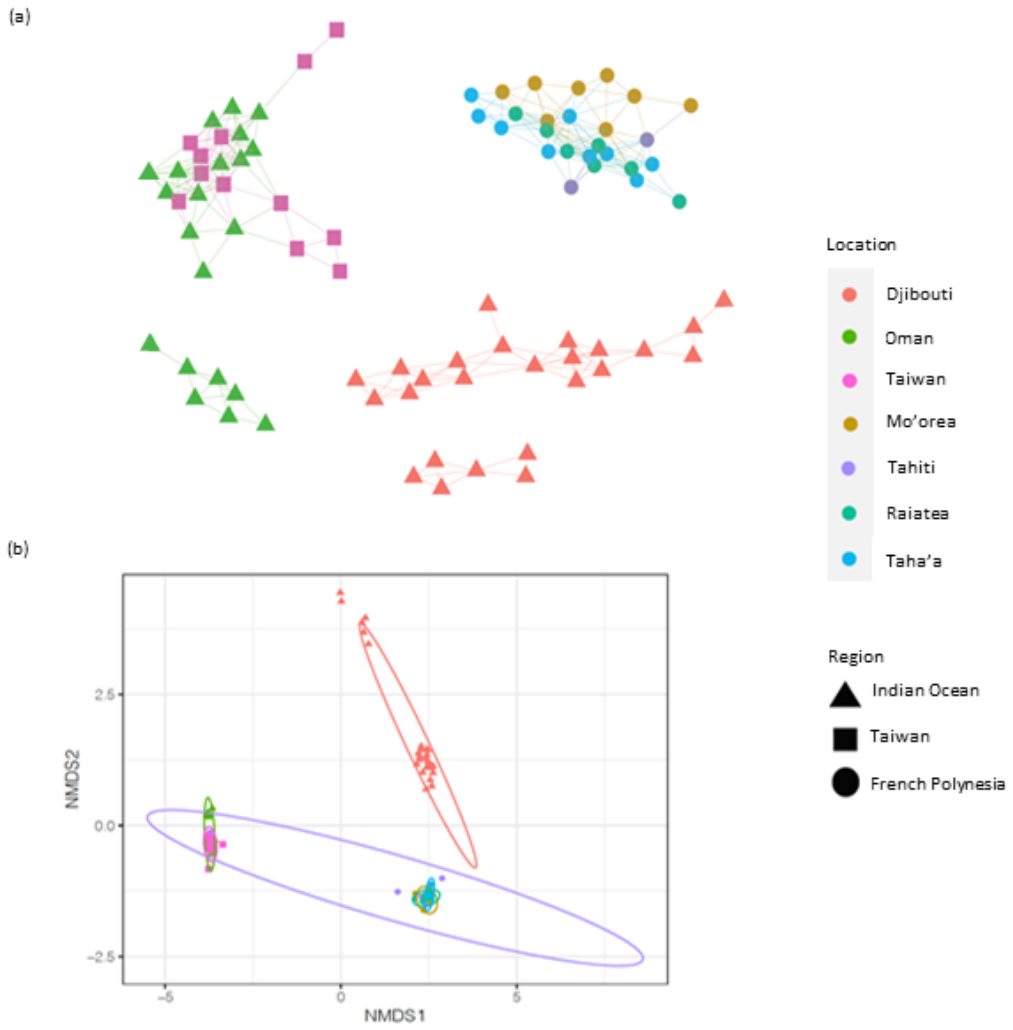

Figure 1.4. Regional differences in Symbiodiniaceae communities from *Pocillopora* spp. across the Indo-Pacific (a): Symbiodiniaceae networks across locations, where colors represent different locations and shapes are different regions. The locations are as follows (from west to east): Djibouti, Oman, Taiwan, Taha'a, Raiatea, Mo'orea, and Tahiti. The regions shown are (from west to east): the Indian Ocean, Taiwan, and French Polynesia. The network was created

via the Fruchterman-Reingold layout algorithm (Fruchterman & Reingold, 1991) with Bray-Curtis dissimilarities (Bray & Curtis, 1957) used as distances. **(b):** Non-metric multidimensional scaling (nMDS) ordination plots of Symbiodiniaceae across locations and regions, where colors represent different locations and shapes are different regions. Locations and regions are the same as in **(a)**. nMDS plots implement Bray-Curtis dissimilarities (Bray & Curtis, 1957) and show 95% confidence ellipses.

Connecting statement between Chapter 1 and 2

Pocillopora coral's diverse microbiome and large distribution make them an ideal coral genus to explore the factors that structure the coral microbiome. Focusing on a single member of this holobiont, algal symbionts in the family Symbiodiniaceae, we not only present the diversity in coral-algal associations across *Pocillopora* coral's Indo-Pacific range, but also how these are environmentally-responsive, with sea surface temperature most strongly affecting community composition, such that corals from locations most similar in temperature had more similar dinoflagellate communities (Figure 0.5). As highlighted in the Discussion of Chapter 1, the insights gained from taking a biogeographical approach to coral-microbiome interactions only further piqued research questions about what we did not observe. At the time of this study, there were no marker-gene data available for any *Pocillopora* coral community in the Tropical Eastern Pacific, despite the TEP being a region that has been historically important in coral-microbiome studies. Additionally, *Pocillopora* coral's species delineations are rapidly evolving, compounded by high levels of hybridization and phenotypic plasticity – this is why we did not define samples down to species. Lastly, it was interesting that when mining the data from NCBI, none of the articles had explicitly studied algal associations during an active bleaching event, only shortly after. Given the critical window represented during bleaching in terms of holobiont health and stability, honing into the dynamics at this time may yield some of the most pertinent insights into the factors underpinning coral thermotolerance.

Chapter 2 directly builds upon Chapter 1 by turning to the study of *Pocillopora* coral reefs in Panama's TEP and takes a more holistic approach to the study of coral holobionts. I studied

Pocillopora corals across this region's upwelling gradient, both in-situ and during an acute thermal stress experiment. In doing so, I move past the "single host-single microbe" model and consider the diversity of response mechanisms on behalf of both partners, from genetic evolution of the host and its physiological and biochemical responses to thermal stress, to directly pairing algal community dynamics with those of the prokaryotic community. My work is one of the first to present such a diversity of host and microbiome responses to environmental stress and as such further motivates taking a holobiont approach to coral thermotolerance.

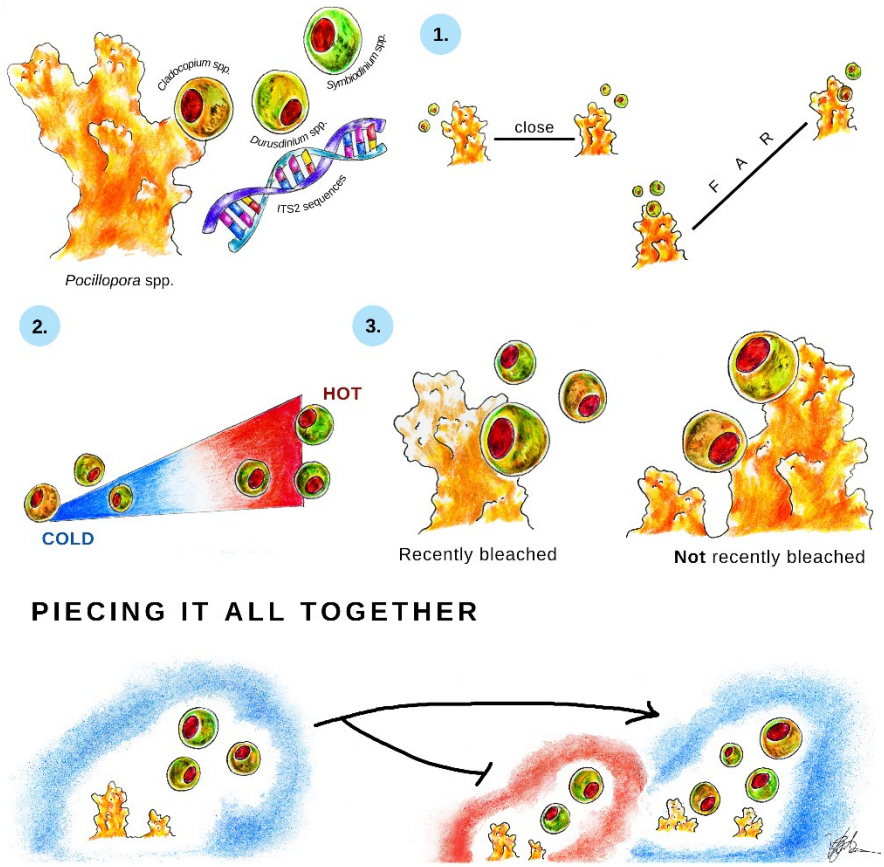

Figure 0.5. Visual overview of Chapter 1. When analyzing publicly available dinoflagellate marker-gene data from the nuclear ribosomal DNA internal transcribed spacer 2 (ITS2), *Pocillopora* corals across the Indo- Pacific were found to associate with three different dinoflagellate genera: *Cladocopium* spp., *Durusdinium* spp., and *Symbiodinium* spp. **(1)**

Although we found some evidence that geographic isolation could explain dinoflagellate community differences, thermal parameters most strongly structured coral-dinoflagellate associations across our study range. **(2**) Sea surface temperature was the factor that most significantly explained community composition, such that corals from locations most similar in temperature had more similar dinoflagellate communities. **(3)** Additionally, when considering time since the last mass bleaching event, corals that had more recently bleached (within the last 5 years) had similar proportions of *Cladocopium* spp. and *Durusdinium* spp. Meanwhile, corals that had not recently bleached were additionally associated with *Symbiodinium* spp.

Chapter 2 | Environmentally-driven holobiont changes impact thermotolerance for Tropical Eastern Pacific corals

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2.1 Abstract

Coral reefs support approximately 25% of all marine life, thus understanding the factors impacting their ability to withstand climate change is essential. Corals' response mechanisms encompass the host's own potential, as well as that of a highly diverse microbial community, collectively known as the holobiont. Research investigating how these co-evolved taxa affect each other during thermal stress has yielded new insights into both the vulnerability and resilience of coral reefs but the precise mechanisms underlying different bleaching trajectories are still poorly understood. Here, we implement a standardized acute thermal stress assay to investigate how seasonal upwelling in Panama's Tropical Eastern Pacific (TEP) influences host-

microbiome configurations in *Pocillopora* corals and to test holobionts' resistance to increasing water temperatures. We show that despite little genetic differentiation for the host, algal community shifts are modulated by both region and genetic lineage. This pattern with algal symbionts strongly contrasted with temperature-driven dysbiosis for the prokaryotic community. Host stress responses differed among regions during acute thermal stress. Regional variation in total antioxidant capacity was consistent with corals from the region with seasonal upwelling experiencing more stressful baseline conditions, which may contribute to these corals' higher predicted thermal thresholds as estimated via host protein concentrations. We contextualized the impact of algal microbiome shifts with our host physiology and oxidative metabolism data, which suggested that some of these shifts can have negative fitness consequences. By leveraging the natural laboratory created by Panama's TEP, we demonstrate that upwelling influences how holobionts are structured and their ability to withstand thermal stress, providing new insights into the factors driving coral thermal resistance.

2.2 Introduction

Understanding the mechanisms underlying organismal responses to environmental stress has been a long-standing pursuit in evolutionary biology, but anthropogenic climate change has made this interest an imperative. Most prior research on species persistence under climate change has investigated the ability of single taxa to respond to environmental stress via acclimation or adaptation, emphasizing how standing genetic variation and phenotypic plasticity together shape the evolutionary potential of organisms (Oostra et al. 2018, Richter et al. 2012, Bitter et al. 2019, Des Roches et al. 2020, Richardson et al. 2017). There is increasing evidence that species interactions such as facilitation, competition and predation can modulate how individual taxa

respond to environmental stress (Bastille-Rousseau et al. 2018, Peers et al. 2020, Alexander et al. 2015, Ettinger and HilleRisLambers 2017). Interactions that can have reciprocal impacts on the development, fitness, and evolution of multiple species are those occurring between a host and its microbiome (i.e., bacteria, archaea, microbial eukaryotes and viruses), collectively known as the holobiont (Margulis and Fester 1991, Rosenberg and Zilber-Rosenberg 2018, Roughgarden 2023). Although the importance of host-microbiome interactions for organismal health and functioning is well-recognized, much less is understood about how holobiont dynamics mediate responses to climate change.

Corals are a model system to explore the consequences of climate change on host-microbiome interactions because they associate with a highly diverse microbial community that has been implicated in their resilience to thermal stress (see Boilard et al. 2020, van Oppen and Blackall 2019, Bourne et al. 2016). Coral bleaching is a biological process in which environmental stressors disrupt the coral-algae symbiosis. As a result, corals become pale due to the loss of the algal symbionts residing within their tissues (Davy et al. 2012, Weis 2008). Some of these algal symbionts, which belong to the family Symbiodiniaceae, have been linked to differences in coral's thermal tolerance. For instance, differences in thermotolerance have been associated with a switch from *Cladocopium* spp. to *Durusdinium* spp. in both adult and juvenile corals (Naugle et al. 2021, Quigley et al. 2020, Manzello et al. 2019), and increased proportions of *Durusdinium* spp. at the beginning of thermal stress events are linked to bleaching resistance (Silverstein et al. 2015, Cunning and Baker 2020). Bleaching can also be impacted by interactions beyond these two focal taxa. Bacterial, viral, and archaeal communities can vary in response to stress and have been shown to influence coral health, particularly within the context of disease, as the presence

of certain microorganisms has been linked to coral tissue loss and subsequent mortality (Meyer et al. 2019, Thurber et al. 2009, Zhang et al. 2015, Glasl et al. 2016, Kline and Vollmer 2011). Inoculating corals with prokaryotic cultures that have specific genetic and/or phenotypic characteristics can reduce bleaching and pathogen presence, further underscoring the microbiome's importance in coral health (Rosado et al. 2019). Although there is a large body of work on microbial dynamics during bleaching, few studies simultaneously track physiological responses for the host (but see Grottoli et al. 2018, Marchioro et al. 2020), making it difficult to gauge the interconnectedness between host and microbiome response mechanisms.

Independent of its microbiome, the coral host can respond to increasing temperatures via both genetic adaptation and physiological plasticity. The latter has been the focus of previous research, given that it directly tests the proximate causes of coral bleaching. The most widely accepted cellular mechanism underpinning coral bleaching involves photoinhibition and damage to the algal chloroplast that results in an accumulation of reactive oxygen species (ROS); an increase in ROS in turn damages both algal and coral host tissues (see Weis 2008, Davy et al. 2012, Suggett and Smith 2019). The balance between oxidative metabolism (e.g. ROS-triggered oxidative damage and total antioxidant capacity) and physiological bleaching responses (e.g. chlorophyll *a* and host protein content) during thermal stress has been linked to coral's baseline stress levels and their ability to offset the impacts of environmental stress (Marangoni et al. 2021, Marangoni et al. 2019, Liñán-Cabello et al. 2010, da Silva Fonseca et al. 2021, Luz et al. 2018). In addition to these metabolically-driven intracellular processes, fast-acting genetic mechanisms such as transcriptional plasticity have emerged as a key acclimation response, where more resilient corals have a higher basal expression of key genes involved in processes such as

protein folding and innate immune response prior to thermal stress (Barshis et al. 2013, Brener-Raffalli et al. 2022, Collins et al. 2021). Recent evidence further suggests that algal symbionts modulate gene expression patterns in the host, resulting in different bleaching outcomes (Strader and Quigley 2022, Cunning and Baker 2020). Finally, variation in coral thermal tolerance has been shown to be a heritable polygenic trait, implying that longer-term evolutionary responses might be possible if genetically-based trait changes can keep pace with the rate of environmental change (Drury et al. 2022, Rose et al. 2018, Bay and Palumbi 2014, Yetsko et al. 2020, Dixon et al. 2015, Smith et al. 2022). It is currently unclear how this diverse suite of host response mechanisms interacts with microbial dynamics to yield divergent bleaching responses.

Insights about coral bleaching response mechanisms have predominantly emerged from a combination of correlative analyses of natural populations during bleaching events (e.g. Oliver and Palumbi 2011, Starko et al. 2023, Rodríguez-Casariego et al. 2020), and long-term thermal stress experiments on the order of weeks to months (e.g. D'Croz and Maté 2004, Kenkel et al. 2013, Gardner et al. 2017). Although these studies have provided foundational data on the drivers of coral bleaching resistance, the mechanisms underlying different bleaching trajectories are still poorly understood because the diversity of experimental approaches employed makes drawing inferences between studies a challenge. Standardized short-term assays offer a portable and cost-effective solution to this issue by facilitating comparisons of estimated thermal thresholds between regions, populations, and taxa. These assays also facilitate the exploration of various coral stress response mechanisms simultaneously, from microbiome dynamics to oxidative metabolism, improving our understanding of the mechanistic links within the coral holobiont, and in turn their consequences for thermotolerance (e.g. Voolstra et al. 2020).

Panama's Tropical Eastern Pacific (TEP) has long served as a natural laboratory to explore the factors driving coral holobiont's responses to climate change (Romero-Torres et al. 2020, Manzello et al. 2008, Leray et al. 2021), and represents an ideal location for coral thermotolerance studies employing standardized short-term assays. Across Panama's TEP, *Pocillopora* corals form the foundation of the reef framework (Glynn 1983, Glynn 1993). Corals from this genus experience strong, upwelling-mediated, intra-annual environmental variability in the Gulf of Panama, whereas they experience weak upwelling in the Gulf of Chiriquí. Upwelling is the process by which cold, nutrient-rich water displaces warmer, less nutrient-rich surface water. In the Gulf of Panama (and to a much lesser degree in the Gulf of Chiriquí), upwelling drives large annual fluctuations in temperature, pH, oxygen, and nutrients (Crawford et al. 2024, O'Dea et al. 2012, D'Croz and O'Dea 2007). There is considerable debate about whether the abiotic heterogeneity triggered by upwelling may influence the physiological and microbial mechanisms underlying differences in bleaching resilience (Chollett et al. 2010, Smith et al. 2017, Randall et al. 2020, Rodriguez-Ruano et al. 2023, Mayfield et al. 2013, Zhu et al. 2023). With only one study to date exploring these reef's experimental responses to thermal stress (D'Croz and Maté 2004), complementing observational data with a standardized acute thermal assay in Panama's TEP has the potential to further illuminate how host and microbiome stress response mechanisms are shaped by the region's upwelling regime and together are driving different bleaching trajectories, and how these compare with how corals in other reef regions respond to comparable thermal stress.

In this study we test how the different environmental regimes of the Gulfs of Panama and Chiriquí in Panama's TEP have shaped thermotolerance mechanisms for the coral holobiont. In leveraging an acute thermal stress assay known as the Coral Bleaching Automated Stress System (CBASS; following Voolstra et al. 2020), we present a comprehensive view of the holobiont's thermotolerance pathways by incorporating host genetics, algal and prokaryotic community dynamics, and host physiological and oxidative metabolism data. We expected a clear signature of local adaptation to each gulf, manifested through loci associated with functional responses to divergent abiotic conditions showing exceptional genetic differentiation, relative to the rest of the genome. During our acute thermal stress assay, we predicted that the most-thermally resistant colonies would show an algal shift from *Cladocopium* spp. to *Durusdinium* spp. at high temperatures, as *Durusdinium* spp. has previously been associated with more thermotolerant *Pocillopora* corals in the TEP (Palacio-Castro et al. 2023, Glynn et al. 2001). We also predicted that corals from the Gulf of Panama would experience less microbial dysbiosis during thermal stress, manifested via a lower variance in their community composition at higher temperatures, due to their exposure to a more seasonally variable thermal environment. Furthermore, we also expected that corals in the Gulf of Panama would have less drastic declines in physiological parameters such as host protein and chlorophyll *a* content, and a more effective biochemical apparatus to scavenge and neutralize ROS. By experimentally testing the responses of different holobiont configurations driven by upwelling, we aim to increase our understanding of the complex mechanisms by which the host and microbiome interact to govern corals' responses to environmental change.

2.3 Materials and methods

To explore how the upwelling regime in Panama's TEP influences *Pocillopora* corals' holobiont configurations and their functional consequences, we used both observational and experimental approaches to determine how coral-microbiome interactions were impacting thermotolerance (see Figure 2.1 for an overview). Specifically, we investigated how the TEP's seasonal upwelling regime impacts population genetic structure, microbiome dynamics, and host physiological and biochemical pathways during an acute thermal stress assay. To quantify genetic differentiation across the TEP and ascertain potential local adaptation to upwelling regimes, we conducted whole-genome shallow shotgun sequencing of coral colonies across the Gulf of Panama and the Gulf of Chiriquí. To determine whether and how different holobiont configurations were associated with thermotolerance, we ran an acute thermal stress assay known as the Coral Bleaching Automated Stress System (CBASS; following Voolstra et al. 2020) which subjected corals to a range of experimentally manipulated temperatures. Specifically, to determine algal and prokaryotic community dynamics during the CBASS experiments, we sequenced ITS2 and 16S marker genes, respectively. To assess differences in host physiological responses between upwelling regimes, we tested for differences between gulfs in their functional responses of host tissue protein and chlorophyll *a* concentrations to increasing temperatures. Lastly, to determine how the oxidative metabolism of the coral holobiont is impacted by upwelling, we quantified how total antioxidant capacity and lipid peroxidation vary as a function of temperature for each gulf. All corals were collected under permits issued by the Panamanian Ministry of the Environment (permit reference numbers SE/AO-4-19, ARB/ARG-093-2022, and ARB/ARG-090-2022). All scripts used in our analyses, alongside the physiology and oxidative metabolism data can be found at https://github.com/vmglynn/PanamaTEP_CBASS. All generated sequence

data is available on the NCBI Sequence Read Archive (SRA) under NCBI BioProject PRJNA1134702 and PRJNA1135493.

2.3.1 Field collections

In November-December 2020, we permanently marked 11-12 coral colonies in six different reef sites across Panama's Tropical Eastern Pacific. Three of these reefs were located in the Gulf of Panama, and the other three were located in the Gulf of Chiriquí. Colonies were selected as discernibly distinct coral colonies within 3-5 meters of a 50 m transect. Using Self Contained Underwater Breathing Apparatuses (SCUBA), we hammered into the reef matrix three PVC pipes to mark each colony, with a unique plastic cow tag attached at the end of one of them. We sampled these tagged corals for both population genetic analyses and our acute heat stress experiment. For the acute heat stress experiment, we collected 8 different coral branches from each colony, one for each of the temperature treatments. These were collected with SCUBA and removed using stainless steel bone cutters. Gloves were worn during the collection process. We selected branches approximately 10-12 cm long, and at least 2 cm in diameter. For the host population genetic analyses, we only collected a single branch, following the same protocol described above. This branch was further fragmented and placed into a 15 mL tube with 10 mL of DNA/RNA Shield (Zymo Research). We disinfected the bone cutters with >95% ethanol and wiped them with a clean Kim wipe in between coral colonies. We stored collected samples at 4°C for the duration of the field work, and then placed them at -80°C for long term storage prior to analyses.

2.3.2 Host population genetics

To determine the genetic landscape of corals across Panama's TEP, we extracted DNA from each in-situ sample using a modified phenol-chloroform protocol we optimized for corals. Briefly, we first lysed the coral branch, tissue, and skeleton together in DNA/RNA Shield (Zymo Research) using a combination of Lysing Matrix A and 1/4-inch ceramic spheres (MP Biomedicals). This was followed by enzymatic digestion using both proteinase K and RNAse A, and a standard phenol:chloroform:isoamyl phase separation. This protocol allowed for the production of high quantity and high molecular weight DNA. The resulting DNA was shipped to the McGill Genome Center (Montréal, Québec) where we performed shallow whole genome sequencing for all our coral samples. We aimed for 4M reads per sample with a pair-end read length of 150 bp. The center performed the library preparation and sequenced all samples on a single lane of an Illumina NovaSeq6000 S-Prime v1.5. The colony-region breakdown for analyzed samples can be found in Table B1.

To determine the genetic variation across our samples, we used SNP-by-genotyping with GenPipes (Bourgey et al. 2019) on the Digital Research Alliance of Canada's high performance computing (HPC) cluster. We implemented quality control and SNP filtering steps to align trimmed reads to our reference genome (Burrows and Wheeler 1994), Picard to mark fragment duplicates (Broad Institute 2019; https://broadinstitute.github.io/picard/), and the GATK Haplotype Caller (McKenna et al. 2010) to call SNPs. We used the *Pocillopora damicornis* coral genome as a reference genome (Cunning et al. 2018). Although recent work has determined that corals in Panama's TEP are not *P. damicornis* as previously believed, but part of the *P. verrucosa-P. grandis/P. meandrina* complex (Palacio-Castro et al. 2023, Connelly et al. 2023,

Johnston et al. 2017), the genome assembled by Cunning et al. 2018 was generated from an individual located in a plot adjacent to our Saboga reef transect in the Gulf of Panama; the *P. damicornis* reference genome on NCBI thus most likely forms part of the *P. verrucosa-P. grandis/P. meandrina* lineages and is an appropriate reference genome for this work. To determine the genetic lineages of our colonies, we amplified and Sanger sequenced the mitochondrial Open Reading Frame (mtORF), following Flot and Tiller 2007 and Gélin et al. 2017. Amplifying the mtORF is currently the most commonly implemented technique to distinguish between different *Pocillopora* spp. lineages (see Oury et al. 2023). Hereon, genetic lineages will be referred to by their mtORF lineage.

Prior to population genetic analyses, we engaged in quality control filtering using vcfstats (Danecek et al. 2011), and pruned loci potentially under linkage disequilibrium using PLINK (Purce et al. 2007). All statistical analyses were performed in R version 4.2.1 (R Core Team, 2022). After filtering, we retained 6,145 SNPs for downstream analyses. To determine the contribution of different ancestral source populations within our samples, we ran the program ADMIXTURE (Alexander and Lange 2011). To determine genetic differentiation metrics across all samples, we used the command 'basic.stats' from the package 'hierfstat' (Goudet 2005). For pairwise Fst calculations, we used the command 'genet.dist' with the Weir and Cockerham 1984 calculation from the package 'hierfstat' (Goudet 2005). To detect genetic markers involved in adaptation to contrasting upwelling regimes, we implemented the program 'pcadapt' (Luu et al. 2017). We used the principal component analysis approach in 'pcadapt' as it can handle admixed individuals and does not require pre-grouping individuals, while also implementing the robust Mahalanobis distance that can account for potential outlier loci (Luu et al. 2017). As our

population genetic analyses did not detect strong genetic differentiation across mtORF lineages, but instead high gene flow akin to between-gulf comparisons, we decided to run outlier analyses for both lineages together (see Figure B1). To detect putative outlier loci that may be underlying the adaptation to different upwelling regions, we implemented the package 'OutFLANK' (Whitlock and Lotterhos 2015; https://github.com/whitlock/OutFLANK). We chose to use 'OutFLANK' as it defines a null Fst distribution based on expected genomic signatures of diversifying and balancing selection. To account for Fst outliers driven by within-gulf microhabitat adaptation, we re-ran OutFLANK setting each reef as the population, as compared to setting each population as one of the two regions (Gulf of Panama, Gulf of Chiriquí). Any within-gulf outliers detected in our reef-based OutFLANK analysis were filtered from downstream outlier functional analysis. We defined outliers at a q-value cut-off of 0.05 and expected heterozygosity cut-off of 0.1.

To determine the potential functional roles of the identified outlier loci, we used snpEff (Cingolani et al. 2012) to annotate and determine the predicted effects of the identified variants. To do so, we built a custom snpEff database, using NCBI's RefSeq annotation for the *P. damicornis* genome (National Center for Biotechnology Information 2024; https://www.ncbi.nlm.nih.gov/genome/annotation_euk/Pocillopora_damicornis/100/). We selected loci that snpEff denoted as being missense variants and intron variants for further characterization, given these SNPs would most strongly impact downstream proteins. We defined a 2000 kb window around each of these SNPs using the UCSC Genome Browser (Karolchik et al. 2014). We then inputted this window into nucleotide BLAST (blastn) and compared our genomic windows to the nucleotide collection (Chen et al. 2015) to predict the

associated proteins containing outlier SNPs; we selected the resulting hit with the highest percent identity.

2.3.3 Acute thermal stress assay

To test the functional consequences of *Pocillopora* coral's host-microbiome interactions, we subjected all sampled corals to the Coral Bleaching Automated Stress System (CBASS). We selected this assay as it has been shown to correlate with thermal tolerance trends, ranging from microbiome dynamics to host physiological shifts, as detected from traditional, multi-week heat stress experiments (Klepac et al. 2024, Voolstra et al. 2020). Following Voolstra et al. 2020, we used eight, 10 L flow-through tanks representing independently controlled temperature treatments. Each tank's temperature was regulated by 200 W titanium heaters (Schego) and IceProbe Small Aquarium Chillers (Nova Tec), connected to a custom-built controller with a 12V power supply (Arduino Mega 2560). Full spectrum 165W aquarium LED lights (Galaxyhydro) provided ~ 600 mmol quanta m^{-2} s^{-1} to each tank on a 12 h:12 h light:dark cycle. Throughout the experiment, each tank received water at a rate of approximately 2 L hr^{-1}, with powerheads (SUNSUN JVP Series) and a reservoir pump (Jecod/Jebao DCT-4000) ensuring sufficient water flow. We also placed within each tank a HOBO Pendant Temperature Logger to record temperatures throughout the experiment at 5-minute intervals.

We programmed each tank to run one of eight temperature profiles. These temperature profiles represent the mean monthly maximum (MMM) temperature (28.5°C), and 1.5°C increments from the MMM up to MMM + 10.5°C. The 28.5°C tank served as our control and remained at this temperature throughout the experiment at each site. MMM was determined from the NOAA

Coral Reef Watch's 5 km global product (Liu et al. 2014; https://coralreefwatch.noaa.gov/product/5km/). Experiments began at 10:00 AM, with a three hour ramp up to temperature, a temperature hold for three hours, and a ramp down to MMM for two hours. For all tanks, there was an overnight hold at MMM. Sampling began at sunrise for all sites, which was approximately 7:00 AM. From each sample, we used bone cutters to cut small pieces of coral fragments and placed them in 1.5 mL of DNA/RNA Shield (Zymo Research) for downstream microbiome analyses. For physiological and oxidative stress analyses, we collected a single intact branch from the same sample which was first placed within a whirl-pak bag wrapped in aluminum foil before being stored in a liquid nitrogen dewar. We removed a single site from all downstream analyses, Contadora in the Gulf of Panama, due to poor temperature control for the 28.5°C treatment.

2.3.4 Microbiome characterization

To characterize microbial dynamics during the CBASS, we performed amplicon sequencing of the coral Symbiodiniaceae and prokaryotic community. We used the same phenol-chloroform protocol described above to extract DNA from the samples collected during the CBASS. We selected a subset of colonies and sites, representing two reefs per region, and four temperature treatments: 28.5°C (control), 30°C, 33°C, and 36°C; the precise sample breakdown can be found in Table B1. The resulting DNA was amplified for two markers, ITS2 rRNA for the dinoflagellate algal symbionts in the family Symbiodiniaceae and 16S rRNA for the prokaryotic community. For ITS2 amplification, we used the ITS-DINO (5'-GTGAATTGCAGAACTCCGTG-3'; Pochon et al. 2001) and ITS2Rev2 (5'-CCTCCGCTTACTTATATGCTT-3'; Stat et al. 2009) primer pairs. For 16S, we followed the

amplification protocol from the Earth Microbiome Project's protocol (Ul-Hasan et al. 2019; https://earthmicrobiome.org/protocols-and-standards/16s/) using their updated 515F (5'-GTGYCAGCMGCCGCGGTAA-3'; Parada et al. 2016) and 806R (5'-GGACTACNVGGGTWTCTAAT-3'; Apprill et al., 2015) primer pair. Precise PCR conditions can be found in Table B2-B3. Library prep was performed at the Naos Marine Laboratories at the Smithsonian Tropical Research Institute (Panamá, Republic of Panama) and sequenced on an Illumina MiSeq v2, with a pair-end read length of 250 bp.

We identified taxa from ITS2 reads using the SymPortal platform (Hume et al. 2019) as this database is specifically curated for coral-associated Symbiodiniaceae. SymPortal is a community-driven tool that is able to differentiate intra- and inter-genomic sources of genetic variation across Symbiodiniaceae, and thus defines putative taxa on the basis of intragenomic sequence variants (DIV) rather than amplicon sequence variants (ASVs) (Hume et al. 2019). As this platform was built prior to Symbiodiniaceae's taxonomic reorganization, the resulting taxa are assigned into ITS 'clades' and 'types.' As we wanted to see the dynamics of individual taxa over the course of our experiment, we did not use the aggregated type-profiles but instead the absolute sequence abundance DIV table. Our goal was to see broadscale shifts in genera so we summarized the taxonomic assignments down to the sub-clade level, e.g. C42ax = C42, *Cladocopium* spp. type 42, and did not use the more granular sub-species and sub-strain levels (Glynn et al. 2023, Pratomo et al. 2018, Oladi et al. 2021, Littman et al. 2010). These sub-clade classifications were used for downstream analyses in R version 4.2.1 (R Core Team, 2022), where we used the absolute abundance DIV table as our ASV table in the R package 'phyloseq' (McMurdie and Holmes 2013; https://github.com/joey711/phyloseq).

To test the factors significantly driving the observed algal microbiome trends, we modeled the relative proportion of ITS sub-clades as a function of temperature treatment, region, and mtORF as explanatory variables, using the generalized least squares (GLS) function 'gls' from the 'nlme' package in R version 4.2.1 (Pinheiro and Bates 1996, Lindstrom and Bates 1990, R Core Team 2022). We used GLS because preliminary analyses indicated heterogeneity of variances among temperatures, which can be explicitly modeled within a GLS framework. To determine community-level shifts during the CBASS, we performed a canonical analysis of principal coordinates (CAP) via the 'ordinate' function in 'phyloseq' (McMurdie and Holmes 2013), using Bray-Curtis dissimilarity to calculate distances (Bray and Curtis 1957). We opted for a distance-based redundancy analysis because we had a priori hypotheses about the factors driving community dissimilarity patterns. CAP implements a multivariate multiple linear regression to maximize the fit between principal component coordinates and explanatory variables. To help identify the impact of each explanatory variable in driving patterns within ordination space, we ran a PERMANOVA with 999 permutations using the 'adonis2' command from the package 'vegan' (Dixon 2003); post-hoc pairwise comparisons were performed with the 'pairwise.adonis2' function and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons (Martinez Abizu, 2020). To test the statistical significance of patterns of homogeneity of variance, we ran 'betadisper' with 999 permutations from the package 'vegan,' using Bray-Curtis distances (Dixon 2003). We then ran an ANOVA on the 'betadisper' group dispersion results to determine if the variance of each group's distance from the centroid was statistically significant. Post-hoc comparisons were performed with Tukey's Honest Significant Differences test which corrects for multiple testing at a 95% confidence level.

To detect differentially abundant microorganisms within particular locations and/or treatments, we performed an indicator species analysis (Dufrêne and Legendre 1997) using the package 'indicspecies' (Cáceres and Legendre 2009). Here, we used the 'multipatt' command with 999 permutations and implemented the Benjamini and Hochberg p-value correction for multiple comparisons. Given we had multiple temperature treatments, we first subsetted our phyloseq object to represent separate gulfs and mtORF lineages, and then ran 'multipatt' comparing Symbiodiniaceae communities across temperatures.

For 16S reads, we used the R package 'DADA2' version 1.20 (Callahan et al., 2016; http://github.com/benjjneb/dada2) to call amplicon sequence variants (ASVs). Here we used cutadapt in DADA2 to remove primer sequences (Martin 2011). We also assigned taxonomy using the SILVA 16S database release v138.1 (Quast et al. 2012), specifically formatted for the classification of ASVs derived from 'DADA2' (McLaren and Callahan 2021; https://zenodo.org/records/4587955). Using the R package 'phyloseq' (McMurdie and Holmes 2013; https://github.com/joey711/phyloseq), we integrated ASVs, taxonomy, and sample information into a single object. We then removed all ASVs assigned to chloroplasts, mitochondria, eukaryotes, or unassigned at the kingdom level. We used the package 'decontam' (Davis et al. 2018) to remove potential contaminants within ASV data, by implementing a statistical classification procedure on the basis of prevalence within our negative controls. We additionally removed singletons and performed an r-log transformation within the 'DESeq2' package (Love et al. 2014) prior to beta diversity analyses. Beta diversity analyses for 16S

follow the same pipelines as for the ITS2 analyses described previously (e.g. CAP, homogeneity of variances, and indicator species analyses).

2.3.5 Physiological measurements

We extracted chlorophyll *a* and coral host protein content following Hoogenboom et al. (2010). Briefly, we extracted coral tissue from the skeleton and placed this in 15 mL of 0.45 μM filtered sea water (FSW) using an airbrush. The resulting tissue slurry was then homogenized using a potter grinder. We determined chlorophyll *a* concentrations using the method adapted for microplate readers described by Schimidt et al. (2011). We centrifuged 2 mL of the homogenized tissue slurry at 8,000 x g for 10 min, after which the supernatant was discarded and the resulting algal symbionts were resuspended in 2 mL of 95% ethanol for chlorophyll *a* extraction. We assessed the protein content using the Bradford Protein Assay Kit (Thermo Scientific, USA) following the manufacturer's instructions which is based on the Bradford method (Bradford 1976). To determine absorbance measurements, we used a microplate reader (Elx 800, Biotek), and normalized data to surface area (cm^2) using the wax-dipping method (Veal et al. 2010).
To determine the factors driving changes in chlorophyll *a* and protein concentrations during the CBASS, we used nonlinear mixed effects models. Previous CBASS work has estimated thermal thresholds using Fv/Fm, which is a measure of photosynthetic efficiency. This has involved fitting separate log-logistic dose–response curves (DRCs) to each colony, from which an effective dose 50 (ED50) is calculated as the bleaching threshold and compared among sites for each species using one-way ANOVAs (Evensen et al. 2022). ED50 is the inflection point where Fv/Fm is 50% lower than the starting value. We wished to more comprehensively test and account for among-site effects, in order to better resolve differences in the functional form of the

thermal response among regions and mtORFs. To achieve this, we modeled the thermal functional response curve incorporating fixed effects of region and mtORF, and random effects of site. Specifically, we modeled the thermal response of each physiological response variable as a logistic function of temperature:

$$y_{m,r,s}(x) = \frac{\nu_{m,r,s}}{1 + e^{(\delta_{m,r,s} \times \left(log(x) - log(\alpha_{m,r,s})\right)}} \quad (1)$$

where $y_{m,r,s}(x)$ is the response of site *s*, within region *r*, and belonging to mtORF *m,* to temperature treatment *x*. Eqn. (1) has a sigmoid shape, declining from an asymptotic maximum value ν for the physiological response variable to a lower asymptote at zero. The parameter α is the temperature at which the physiological response has declined to 50% of that maximum value; we use this as our measure of threshold position – larger values of α imply that physiological condition is maintained at (i.e., more resistant to higher temperatures). The parameter δ regulates the steepness of this threshold, with larger values of δ implying steeper thresholds (i.e., the decline in performance from ν to zero is more concentrated around the threshold temperature α). For all parameters, our most general model allowed for differences depending on region *r* (upwelling or non-upwelling) and mtORF *m* (which we considered fixed effects of interest), and we also allowed random effects on the parameters of site within region. This allowed us to most effectively leverage the hierarchical structure in our data to resolve differences among regions and mtORFs. Although we initially also considered random effects on the parameters of colony within site, we removed these from our models to simplify the hierarchical structure of our data. This is because each colony has an associated mtORF lineage, and this was the most relevant source of colony-level differences. To fit our models to data, we used the 'nlme' package

(Pinheiro and Bates 1996, Lindstrom and Bates 1990) in the statistical program R version 4.2.1 (R Core Team, 2022).

Specifically, for each response variable, we first fit a full model with an interaction between gulf and mtORF lineage as fixed effects on each parameter, and random effects of reef site within region, on each of the three model parameters. We then systematically dropped fixed effects one at a time and compared model fits using likelihood ratio statistics to determine the best fixed-effects structure. We then repeated the same process to determine the random-effects structure. For all fixed-effects model selection fits, we used maximum likelihood (rather than Restricted Maximum Likelihood [REML]), to ensure comparability of likelihoods (Zuur et al. 2009). We also computed the Akaike information criterion (AIC) score for each of our fitted models, to determine whether the model selected by likelihood ratio tests was also the lowest AIC model.

2.3.6 Oxidative metabolism measurements

We prepared samples for oxidative metabolism analyses as previously described in Marangoni et al. (2019, 2020). Briefly, coral fragments (approximately 0.5 cm^2) were homogenized in ice using ultrasound, with specific buffer solutions tailored for each analysis. After homogenization, we centrifuged the holobiont samples at 13,000 x g and 4°C for 10 minutes. We normalized our results based on the total protein content in the sample, which was determined using a commercial reagent kit employing the Bradford assay (Sigma-Aldrich, St. Louis, MO, USA). We generated a protein standard curve using a bovine serum albumin (BSA) solution (2 mg/mL).
To measure oxidative damage to biomolecules, we quantified the amount of lipid peroxidation (LPO) within each sample. LPO is one of the most prevalent mechanisms of cellular injury and

has been extensively reported for corals and other marine organisms under oxidative stress (e.g. Lesser 2006 , Marangoni et al. 2020). To detect LPO, we used the Thiobarbituric Acid Reactive Substances (TBARS) method with the commercial kit "TBARS (TCA Method) Assay Kit" (Cayman Chemical, No 700870) following the manufacturer's instructions. The reaction between malondialdehyde (MDA) and Thiobarbituric Acid (TBA) under high temperatures (90-100°C) and acidic conditions creates an MDA-TBA adduct. We performed this reaction within each of our samples, and measured the resulting adduct calorimetrically at 540 nm using a microplate reader (ELx800, Biotek). We normalized our data by considering the total protein content in each well of the sample homogenates and expressed this as μM MDA mg protein^{-1}. Given the low amounts of tissue biomass for our LPO samples at 36°C, we only have data for the remaining three temperature treatments, here 28.5°C, 30°C, and 33°C (see Table B1 for the sample breakdown).

To assess each fragment's non-enzymatic total antioxidant capacity (TAC), we used the "OxiSelect^{TM} TAC Assay Kit" (Cell Biolabs Inc.) following the manufacturer's guidelines. This assay quantifies TAC through a single electron transfer mechanism (Huang et al. 2005), relying on the reduction of copper (II) to copper (I) by antioxidants. Following reduction, copper (I) ions react with a chromogenic reagent, yielding a maximum absorbance at 490 nm. We compared our sample's absorbance values with a uric acid standard curve, with absorbance directly proportional to the sample's reductive capacity. We conducted our measurements using a microplate reader (Elx-800, Biotek), and normalized our data based on the total protein content in each well of the sample homogenates, expressed as μM Copper Reducing Equivalents (CRE) mg protein^{-1}. For these analyses, we selected four separate temperature treatments: 28.5°C, 30°C,

33°C and 36°C (see Table B1 for the sample breakdown). These temperatures were selected based on our preliminary microbiome and physiology analyses, which suggested that the thermal threshold for corals in both regions was located within this range (see Results).

To analyze the decline in LPO and TAC concentrations during the CBASS, we used linear mixed effects models. We built our models using 'lm' from the base 'stats' package in R version 4.2.1 (R Core Team, 2022). So that the response variables' distributions approximated normal distributions, we log-transformed our LPO data and square-root transformed our TAC data. To explore if algal community dynamics could explain some of the variation in LPO and TAC during the CBASS, we additionally treated the relative proportion of the two algal clades (ratio of the relative reads mapping to *Cladocopium* spp. versus *Durusdinium* spp). within each sample as an ordinal fixed effect.

As we had only three temperature treatments for our LPO data, we lacked the power to model this metric as a continuous function of temperature. Instead, we treated temperature as a categorical variable; as this approach can accommodate non-monotonic responses to temperature. We first created a full model where LPO was a function of temperature, region, mtORF, and algal clade ratio all as fixed effects. We also found support for an interactive effect between the fixed effects of region and mtORF lineage during our preliminary modeling, so this was additionally considered. We systematically removed fixed effects and compared nested model fits using the likelihood ratio test to determine the final fixed effects structure. We also calculated each model fit's AIC score to confirm that the model selected on the basis of likelihood ratio tests was also the lowest AIC model. For TAC, we followed the same model

selection process, with a few modifications. First, as we had four temperature treatments, we were able to model TAC as a continuous function of temperature. Previous work suggests that TAC's responses to stress may be non-monotonic, as organisms may increase their TAC as stress increases from low levels but may decline at very high levels of stress as the organism's capacity to cope with oxidative stress becomes overwhelmed (Marangoni et al. 2019, Marangoni et al. 2022). Therefore, we modeled TAC as a quadratic function of temperature, rather than a sigmoid function.

2.4 Results

2.4.1 Signatures of local adaptation to upwelling amidst high gene flow for *Pocillopora* corals in Panama's TEP

Our population genetic analyses indicated that although there is negligible genetic differentiation across the two gulfs in Panama's TEP, there are signatures of potential local adaptation to each gulf's upwelling regimes. We found a mean Fst value of 0.0333 between gulfs, indicating a high degree of gene flow between locations (Table B4; Figure 2.2a). This lack of genetic differentiation was further supported by our ADMIXTURE analysis, where lack of clear divisions across gulfs suggests a high degree of admixture within and across our study sites (Figure 2.2b). It is important to note that when running the above analyses per mtORF lineage, here mtORF 1 and mtORF 3, and additionally running pcadapt to detect signatures of local adaptation, patterns of high gene flow remained (see Figure B1 and Table B4).

Given we did not have evidence of strong genetic differentiation across mtORFs, we detected putative outlier loci for both lineages together across gulfs. In doing so, we found evidence for

strong differentiation in a small number of outlier loci. Between gulf comparisons using the Fst-based approach OutFLANK detected 11 outlier loci at a q-value cut-off of 0.05 and expected heterozygosity cut-off of 0.1 (Figure 2.3; full list of loci can be found in Table B5). Analysis with snpEff revealed that two of these loci have a predicted impact on protein-coding regions, corresponding to a missense and intron variant, respectively. These variants are located in a predicted Rab-20-like protein (missense variant) and a predicted hemicentin-2-like protein (intron variant; Table B5). Rab-proteins have been linked to cnidarian host processes that differentiate healthy and dysfunctional cells, an important distinction during bleaching-induced dysbiosis (Chen et al. 2005, Yuyama et al. 2018). Hemicentin-2 is a known extracellular matrix protein with important roles in tissue development and has been recently suggested to be involved in cnidarian immune functioning under anthropogenic stress (Feitosa et al. 2012, Gianakas et al. 2022, Traylor-Knowles et al., 2021).

2.4.2 Thermal stress triggers Symbiodiniaceae community shifts for *Pocillopora* corals during the CBASS

Over the course of the CBASS, we observed marked differences across regions and mtORFs in terms of their relative abundance of different Symbiodiniaceae ITS sub-clades (Figure 2.4). When comparing mtORFs, we found that mtORF 1 was dominated by *Durusdinium* spp., with a sudden relative increase in *Cladocopium* spp. upon reaching 36°C. In contrast, *Cladocopium* spp. was dominant across the temperature treatments for mtORF 3 colonies. These trends were supported by our GLS model, which detected a significant interaction between temperature and region, and temperature and mtORF in driving differences in the relative abundance of ITS sub-clades ($p < 0.05$; see Table B6). Although we observed inter-colony variability in algal shifts,

these recapitulate the trends observed at the treatment level for mtORF 1 colonies (see Figure B2). For mtORF 3, we observe that many colonies have a more stable, *Cladocopium*-dominated community amidst heat stress in the Gulf of Panama, with the few colonies increasing their relative proportions of *Durusdinium* spp. doing so seemingly randomly with respect to temperature. In contrast, colonies in the Gulf of Chiriquí show a more consistent increase in the relative abundance of *Durusdinium* spp. at higher temperatures (see Figure B2).

When considering Symbiodiniaceae community composition shifts throughout the CBASS, our CAP analysis shows a clear difference between the 36°C treatment and the three other temperature treatments. This difference is most stark for mtORF 1 colonies in the Gulf of Chiriquí (Figure 2.5a). Observed differences in community composition were statistically significant ($p<0.05$) across temperatures ($p = 0.013$, pseudo-F-statistic$_{3,112} = 3.1948$, $R^2 = 0.03264$), regions ($p = 0.001$, pseudo-F-statistic$_{1,112} = 48.3366$, $R^2 = 0.16461$), mtORFs ($p = 0.001$, pseudo-F-statistic$_{1,112} = 100.8311$, $R^2 = 0.34339$), and the interaction between temperature and mtORF ($p = 0.001$, pseudo-F-statistic$_{3,112} = 5.0103$, $R^2 = 0.05119$) when performing PERMANOVAs (Table B7). Comparison of effect sizes on the basis of the pseudo-F-statistic revealed that mtORF was the strongest driver of Symbiodiniaceae communities across all statistically significant factors, followed by region (Table B7). Pairwise post-hoc analyses revealed that Symbiodiniaceae communities were distinct when comparing the highest temperature treatment, here 36°C, with 28.5°C and 33°C (see Table B8). We also detected significant differences in variance across temperature treatments, with post-hoc tests revealing that this was driven by samples representing 36°C being less variable as compared to all other temperature treatments (Table B9).

When considering each region and mtORF combination separately (e.g. mtORF 1 from the Gulf of Panama), indicator species analyses revealed 23 taxa that were differentially-associated with mtORF 1 from the Gulf of Chiriquí. All but one taxon was associated with the highest temperature treatment of 36°C, and all of these correspond to various *Cladocopium* spp. taxa. The only taxon not associated with 36°C was uniquely associated with the remaining three temperature treatments and was identified as being *Durusdinium* spp. (Table B10).

2.4.3 Temperature-induced microbial dysbiosis occurs for *Pocillopora* corals during the CBASS

Analysis of the prokaryotic microbiome revealed notable shifts in community composition between the baseline and the highest temperature treatment. Given the much higher taxonomic diversity of the coral prokaryotic community as compared to the Symbiodiniaceae community, we focused on aggregate community differences across ASVs as measured by statistics such as Bray-Curtis dissimilarity, rather than shifts in particular taxa. Our CAP analyses showed an increase in dispersion at the 36°C treatment as compared to the other three temperature treatments; this pattern was seen across all region-mtORF groupings (Figure 2.5b). Community dissimilarity trends were only statistically significant ($p < 0.05$) across regions ($p = 0.034$, pseudo-F-statistic$_{1,112} = 2.6340$, $R^2 = 0.02143$), with differences across temperatures, and the interaction between temperature and region, temperature and mtORF, region and mtORF, and the three-way interaction between temperature, region, and mtORF emerging as non-significant (Table B11). In testing for differences in homogeneity of variance, we detected significant

differences across temperature treatments, with post-hoc tests revealing that this was driven by samples representing 36°C being more variable as compared to all other temperature treatments (Table B12). In considering each region and mtORF combination separately (e.g. mtORF 1 from the Gulf of Panama), indicator species analyses did not identify any differentially-associated prokaryotic ASVs.

2.4.4 *Pocillopora* corals' physiological responses to thermal stress were mediated by region and mtORF lineages during the CBASS

Physiological responses during the CBASS, captured via both host protein and chlorophyll *a* concentrations, reveal that bleaching responses varied among regions and, in some cases, mtORF lineages. For host protein concentrations during the CBASS, our best-fitting non-linear model included a fixed effect of region for the 50% temperature threshold (α_r) and threshold steepness (δ_r), such that the protein content of corals in the Gulf of Panama was maintained at near-ambient levels under higher temperature conditions as compared to corals from the Gulf of Chiriquí (Figure 2.6a; Table B13). Random site-level variation in the maximum protein concentration (ν_s) and threshold steepness (δ_s) was also present. There was no evidence for a significant effect of mtORF lineage in host protein content over the course of the experiment. The 50% temperature threshold for the corals in the Gulf of Panama was approximately 1.2°C higher than for corals in the Gulf of Chiriquí, while the threshold steepness and maximum protein concentrations were highly variable across sites (Figure 2.6a; Table B14).

For chlorophyll *a* concentrations during the CBASS, the best-fitting non-linear model included a fixed effect of region on the maximum chlorophyll concentration (ν_r), and a fixed effect of the

interaction between region and mtORF on both the 50% temperature threshold ($\alpha_{r,m}$) and threshold steepness ($\delta_{r.m}$). This model showed that chlorophyll *a* concentrations were best maintained at near-ambient levels under high temperature conditions for mtORF 3 colonies across gulfs (Figure 2.6b, Table B15). Additionally, we found evidence of site-level variation only on the threshold steepness (δ_s). During our acute thermal stress assay, maximum chlorophyll *a* concentrations in the Gulf of Chiriquí were ~37% higher than for the Gulf of Panama (Figure 2.6b). There was also a markedly steeper threshold for mtORF 1 corals in the Gulf of Panama, which was also reflected in the estimated parameter values (Figure 2.6b; Table B16).

2.4.5 Levels of oxidative damage to lipids were strongly associated with region for *Pocillopora* corals during the CBASS

Oxidative metabolism dynamics, captured by lipid peroxidation (LPO) and total antioxidant capacity (TAC), provide further evidence that regional upwelling regimes impact *Pocillopora* corals' responses to temperature stress. LPO levels decreased from high values at ambient temperature to intermediate values at higher temperatures in the Gulf of Panama; whereas LPO levels increased from low to intermediate values as temperature increased in the Gulf of Chiriquí (Figure 2.6c). Together, this implies that corals in the Gulf of Panama experienced higher baseline levels of stress and yet were able to better counteract oxidative damage as temperature increased. This was reflected by our model selection, in which our best-fitting model only had an interaction effect between temperature treatment and region (Table B17-B18). Moreover, post-hoc comparisons revealed that the two regions only significantly differed in their LPO at the

baseline temperature treatment of 28.5°C, with all other within and between gulf comparisons across temperatures emerging as non-significant (Table B19).

For TAC, our best-fitting model was a second-order function solely driven by temperature; there was no evidence for a significant effect of region or mtORF for TAC during the experiment. In the model selection process, it is important to note that our selected model performed similarly to a model that additionally had a term that represented the relative proportion of *Cladocopium* spp. versus *Durusdinium* spp. For the latter, as TAC increased, the relative proportion of *Durusdinium* spp. also increased. The temperature and algal shifts model marginally outperformed the (1) temperature and mtORF model, and (2) the temperature and region model, further substantiating the importance of this interaction in modulating host redox metabolism. However, in comparing AIC and log-likelihood values and in choosing the most parsimonious model, the model with only temperature was selected (see Table B20-B22). Predicted responses for our best-fitted model showed a clear parabolic decrease for TAC throughout the experiment as the temperature increased up to 36°C (Figure 2.6d).

2.5 Discussion

Our study reveals a nuanced interplay of environment, host genetics, and microbiome in driving differences in coral thermotolerance. We found evidence that upwelling regime drives divergent selection on genes previously linked to coral's responses to thermal stress, and differences in how microbiome dynamics respond to thermal stress. Observational studies have documented shifts between *Cladocopium* spp. and *Durusdinium* spp. for *Pocillopora* corals in response to thermal stress in the Gulf of Chiriquí. By examining responses in this Gulf as well as the Gulf of

Panama, we additionally find that the shift to *Durusdinium* spp. is mediated by both mtORF and gulf of origin, with observed increases in *Cladocopium* spp. potentially resulting in negative fitness outcomes for the host (see Palacio-Castro et al. 2023, Glynn et al. 2001). In contrast to the algal community shifts across temperature treatments, we observed prokaryotic temperature-driven dysbiosis during our acute thermal stress assay, irrespective of gulf and mtORF. This is in line with previous studies on animal microbes under stress, suggesting that this component of the *Pocillopora* microbiome enters a disease-like state during our assay and that such signatures can be ascertained on shorter timescales than previously reported (Zaneveld et al. 2017, Wang et al. 2018, Bourne et al. 2008). In considering host response pathways, corals in the Gulf of Panama overall appear to experience less thermal stress during the CBASS, with mtORF 1 colonies across locations experiencing the most stress. This finding bolsters previous hypotheses positing that within the TEP, the increased temporal environmental variability caused by upwelling may produce more thermally-resistant corals. Furthermore, by presenting how specific coral lineages interact differently with members of their microbiome, we deepen our understanding of the factors that influence thermotolerance; the latter has seldom been considered when studying reefs experiencing upwelling (c.f. Randall et al. 2020, Rodriguez-Ruano et al. 2023, Mayfield et al. 2013). Additionally, by explicitly considering biochemical mechanisms for coping with oxidative stress, we identify a potential physiological pathway by which *Durusdinium* spp. enhances thermal resistance: by promoting greater antioxidant capacity in the host.

2.5.1 Upwelling is resulting in divergent selection on genes implicated in thermotolerance

Only two loci with protein-coding impacts were identified as being under divergent selection when comparing corals between the Gulf of Panama and the Gulf of Chiriquí, yet these variants

have been previously implicated in coral thermotolerance. The first variant is a predicted Rab-20 like protein, with this general family of proteins being linked to cnidarian host processes that differentiate healthy and dysfunctional cells. This is an important function during bleaching-induced dysbiosis because it is hypothesized that these proteins play a central role in the host's immune system by removing damaged symbionts (Chen et al. 2005, Yuyama et al. 2018, Traylor-Knowles et al. 2021). The second variant is a predicted hemicentin-2-like protein, a known extracellular matrix protein with important roles in tissue development that has been suggested to assist corals in the Red Sea in persisting under high summer temperatures (Feitosa et al. 2012, Gianakas et al. 2022). These two loci show strong differentiation between regions despite high gene flow, providing evidence that each gulf's thermal histories and upwelling regimes are shaping heritable differences in coral thermotolerance in the TEP. Prior to our experiment, corals in the Gulf of Chiriquí experienced substantial bleaching as a result of the 2015–2016 El Niño Southern Oscillation (ENSO) event, while colonies in the Gulf of Panama did not, as upwelling coincided with periods of high-water temperatures. Outside the thermal refugia that upwelling may provide, higher temperatures in the Gulf of Chiriquí seem to be hampering coral cover and subsequent recovery (Randall et al. 2020).

2.5.2 Divergent microbiome responses to thermal stress suggest contrasting roles in coral thermotolerance

During the CBASS, *Cladocopium* spp. and *Durusdinium* spp. were the only two algal genera identified, in line with previous work within this region (see Glynn et al. 2001, Palacio-Castro et al. 2023). There is a well-documented shift to *Durusdinium*-dominated communities under heat stress, due presumably to these symbionts best assisting the host during bleaching (Palacio-

Castro et al. 2023, Kemp et al. 2023, Cunning and Baker 2020, Claar et al. 2020; but see Turnham et al. 2023). For studies in Panama's TEP, these insights have been gained from solely studying seasonal-to-interannual variation in *Pocillopora* colonies in the Gulf of Chiriquí. We built upon this prior work by showing that during the CBASS, mtORF 3 colonies in the Gulf of Chiriquí had the greatest increases in *Durusdinium* spp., in line with Palacio-Castro et al. (2023). However, mtORF 3 corals in the Gulf of Panama had a more static *Cladocopium* spp. dominated community throughout the assay, reflecting a less labile algal microbiome that may be driven by strong mtORF lineage specificity. Conversely, mtORF 1 colonies from the onset of the CBASS were dominated by *Durusdinium* spp., and under thermal stress instead became *Cladocopium* spp. dominated, contrary to expectation. Our data represents the most recent characterization of Panama's TEP algal communities, thus it is plausible that given increasing seawater temperatures, previous predictions regarding *Durusdinium*-dominated microbiomes have already materialized. Therefore, the shift to *Cladocopium* spp. at our highest temperature treatment for mtORF 1 colonies may be capturing a selective loss of *Durusdinium* spp. When considering chlorophyll *a* dynamics, mtORF 1 colonies in the Gulf of Panama, which showed the greatest relative increases in *Cladocopium* spp. during the CBASS, were also the least thermally-tolerant based on their predicted temperature threshold and threshold steepness. The switch to *Cladocopium* spp. for mtORF 1 colonies may occur if *Durusdinium* spp. is unable to satisfy the host's energy requirement, which is a trade-off previously reported (Cantin et al. 2009, Allen-Waller et al. 2023). Thus, these colonies may associate with a symbiont that satisfies their energy requirements at the expense of lower conferred thermotolerance, as there are no further compatible symbionts in the system. mtORF 1 colonies may already find themselves at a local fitness optimum, and as a result, the speed and severity of climate change could mean that algal

shifts come at a fitness cost. Host-algal co-evolutionary responses may require longer timescales to match the requirements of current environmental conditions (Crespi et al. 2000, O'Brien et al. 2019).

Although we did not observe increases in community variance for the coral algal microbiome, there were temperature-driven community variance shifts for the prokaryotic community during the CBASS. The Anna Karenina Principle (AKP) proposes that increases in community variance for animal microbiomes under stress reflect a disease-like state, because the greater stochasticity indicates the inability of the host and/or microbiome to regulate their community composition (Zaneveld et al. 2017). Earlier AKP studies for cnidarians consider timescales on the order of months (Wang et al. 2018, Ahmed et al. 2019, Greene et al. 2023, Bourne et al. 2008).Thus, our findings are some of the first to show that drastic temperature-driven community dissimilarity shifts can occur on shorter-time scales and do not appear to be impacted by genetic lineage or region. This is in contrast with previous studies on *Pocillopora* spp. in the Great Barrier Reef that have documented a relatively stable prokaryotic microbiome during bleaching stress (Bergman et al. 2023, Bergman et al. 2021, Epstein et al. 2019). Yet these prior studies, which considered bleaching stress on the order of weeks to months, appear to represent less severe thermal stress than our CBASS experiments, e.g. with an MMM of approximately 28.2°C in the Great Barrier Reef (NOAA Coral Reef Watch 2024b), heat stress was ~4.3°C + MMM in Epstein et al. (2019) and ~5.3°C + MMM in Bergman et al. (2021). In contrast, with MMM across our sites in Panama's TEP being ~28.5°C, the prokaryotic shifts indicative of AKP in our experiment were not observed until the temperature anomaly reached ~7.5°C + MMM. This temperature is well above our estimated thermal physiological thresholds, suggesting that, at

least for this genus, more severe stress may be required to trigger prokaryotic dysbiosis than to trigger physiological breakdown.

The strong contrast that we observed between *Pocillopora* coral's algal and prokaryotic communities during the CBASS may reflect the larger role of these communities for holobiont functioning. Although bleaching is by definition triggered by algal-host dysbiosis, we see shifts in algal communities over the course of our assay without corresponding increases in algal community variance. Therefore, the observed high stochasticity of prokaryotic communities may indicate that these microbiome members are less likely than their algal counterparts to complement the host's existing response pathways to thermal stress (see Howe-Kerr et al. 2020, Díaz-Almeyda et al. 2022).

2.5.3 Region, mtORF lineage, and temperature shape host physiology and oxidative metabolism dynamics during thermal stress

The suite of physiological and oxidative metabolism metrics measured during the CBASS complement our microbial data and further substantiate how region and mtORF lineage are potentially shaping TEP *Pocillopora* thermotolerance. The host-derived metrics suggest that *Pocillopora* corals from the Gulf of Panama experience a more demanding environment to maintain their redox-balance (shown by the higher baseline levels of stress), in turn resulting in an overall improved ability to counteract oxidative stress damage (LPO) and physiologically resist thermal stress (protein). Although these parameters have been explored in unison for other coral populations during longer-term abiotic stress experiments, including during experimental simulations of upwelling (Marangoni et al. 2021, Marangoni et al. 2020, Marangoni et al. 2019,

Poquita-Du et al. 2020), we are the first to explore both sets of metrics within the context of an acute thermal stress assay. Although not commonly reported during experimental and in-situ explorations of thermotolerance, oxidative stress metrics provide an added perspective to understanding tolerable levels of bleaching stress. Our chlorophyll *a* model was the only model for which we found support for mtORF-driven differences in physiological condition. mtORF 1 colonies experienced sharper declines in this parameter, with this pattern being more pronounced for colonies from the Gulf of Panama. Our work provides new insights to coral gene-environment interactions by showing how seasonal upwelling can significantly shape coral holobiont configurations, and their physiological and biochemical responses to thermal stress (Lohr et al. 2019, Hackerott et al. 2023, Mayfield et al. 2018, Huffmyer et al. 2023).

Contrary to our expectations, our best model for TAC was solely driven by temperature, in contrast to the region and mtORF-specific patterns observed for other metrics. However, we did find moderate evidence for a model including a term encapsulating the relative proportion of *Cladocopium* spp. and *Durusdinium* spp. Here, higher proportions of *Durusdinium* spp. resulted in greater TAC values, which may be a potential mechanism by which *Durusdinium* spp. facilitates the acclimation of the coral holobiont under thermal stress (e.g. Kemp et al. 2023, Cunning and Baker 2020). This further supports the hypothesis that the increased dominance of *Durusdinium* spp. in mtORF 1 colonies is associated with acclimatization or adaptation to increasing sea surface temperatures (Palacio-Castro et al. 2023). Earlier experimental work has demonstrated that physiological resistance to bleaching is linked to the algal microbiome, such that *Durusdinium* spp. can increase the thermotolerance of their hosts by as much as 1.5°C (Berkelmans and van Oppen 2006, Silverstein et al. 2015). Our study offers a potential

mechanism by which this may occur, namely greater antioxidant capacity of the host in associating with *Durusdinium* spp. versus *Cladocopium* spp.

2.5.4 Comparative analyses of bleaching pathways are facilitated by the CBASS

Short-term assays such as the CBASS allow for reproducible, standardized, and accessible approaches to studying coral holobiont thermotolerance, providing insight into the factors driving divergent bleaching trajectories for reefs spanning the globe (see Reimer et al. 2024). Our findings qualitatively recapitulate those of other CBASS experiments, highlighting a shared set of coral thermotolerance response pathways. For instance, our two-gulf system emphasizes the importance of local abiotic regimes in shaping host and microbial dynamics under thermal stress, ranging from signatures of genetic adaptation to algal shifts, a similar conclusion also drawn in studies from the Red Sea, American Samoa and Australia (Voolstra et al. 2020, Klepac and Barshis 2020, Naugle et al. 2024). Two genetic lineages, here mtORF 1 and mtORF 3, also show nuanced differences in physiological responses during acute thermal stress. Nursery-based work in Florida has likewise presented genotype-specific responses during a CBASS experiment (Klepac et al. 2024). One of the added benefits in implementing a standardized assay is an improved ability to compare the predicted thermal thresholds across populations and regions. Our data suggests that the TEP's *Pocillopora* corals may have comparable bleaching resistance to those in the Red Sea. CBASS experiments in the Red Sea predicted that *Pocillopora verrucosa*'s (which putatively corresponds to mtORF 3 lineages) thermal thresholds range from 35.15°C to 36.73°C, as measured via Fv/Fm (Evensen et al. 2022). The Red Sea's MMM is approximately 29.9°C, therefore predicted thermal thresholds are ~5.3-6.8°C above the MMM (NOAA Coral Reef Watch 2024a). Our predicted thermal thresholds were 34.23°C for mtORF 3

colonies in the Gulf of Chiriquí (measured via chlorophyll *a*) and 34.95°C for the Gulf of Panama (measured via protein). The MMM for the Gulf of Chiriquí is 28.8°C and 28.2°C for the Gulf of Panama, meaning our estimated thermal thresholds are ~5.4-6.7 above the MMM (NOAA Coral Reef Watch 2024c, 2024d). This suggests that corals living in thermally-extreme environments like those in the Red Sea, and in regions with cold and warm anomalies like those in Panama's TEP, have a similar degree of thermotolerance. Further taxon- and region-specific trends will require follow-up CBASS experiments within and beyond the TEP, along with the consolidation of analytical approaches to studying physiological declines to enable more rigorous comparisons.

2.5.5 Panama's TEP as a natural laboratory for coral holobiont research

Panama's TEP has historically served as a natural laboratory for studies on coral thermotolerance, with some of the first evidence on the role of microbial dynamics in bleaching emerging from studying these reefs (see Glynn et al. 2001, Baker et al. 2004). Previous research in the TEP has been mostly observational in nature (Glynn et al. 1990, Maté 2003, Glynn and D'Croz 1990, Cunning et al. 2013, Combosch and Vollmer 2011, Toth et al. 2012; but see D'Croz and Maté 2004), which we have built upon by subjecting both gulfs to an acute thermal stress assay and in the process, exploring a diversity of host and microbiome mechanisms underlying thermotolerance. We find support for mtORF-specific responses to thermal stress during the CBASS, with mtORF 3 colonies across both gulfs showing the highest resistance to acute thermal stress, in contrast with previously reported long-term dynamics (Palacio-Castro et al. 2023). Importantly, by having physiological data for the host, we were able to ascertain potential fitness costs associated with increases in the relative abundance of *Cladocopium* spp.

for mtORF 1 colonies. In combining physiological and oxidative metabolism measurements, we support previous findings that corals in the Gulf of Panama are best able to cope with increasing thermal stress (Randall et al. 2020) and provide some of the first evidence that a more robust redox apparatus, here via TAC, can be linked to higher proportions of *Durusdinium* spp. at elevated temperatures. In leveraging the unique upwelling regime in Panama's TEP, our holobiont approach allows us to make inferences about how host and microbiome responses complement each other during bleaching, and how these configurations are shaped by the environment, providing a holistic view of the mechanisms that drives differences in coral thermotolerance.

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2.7 Figures

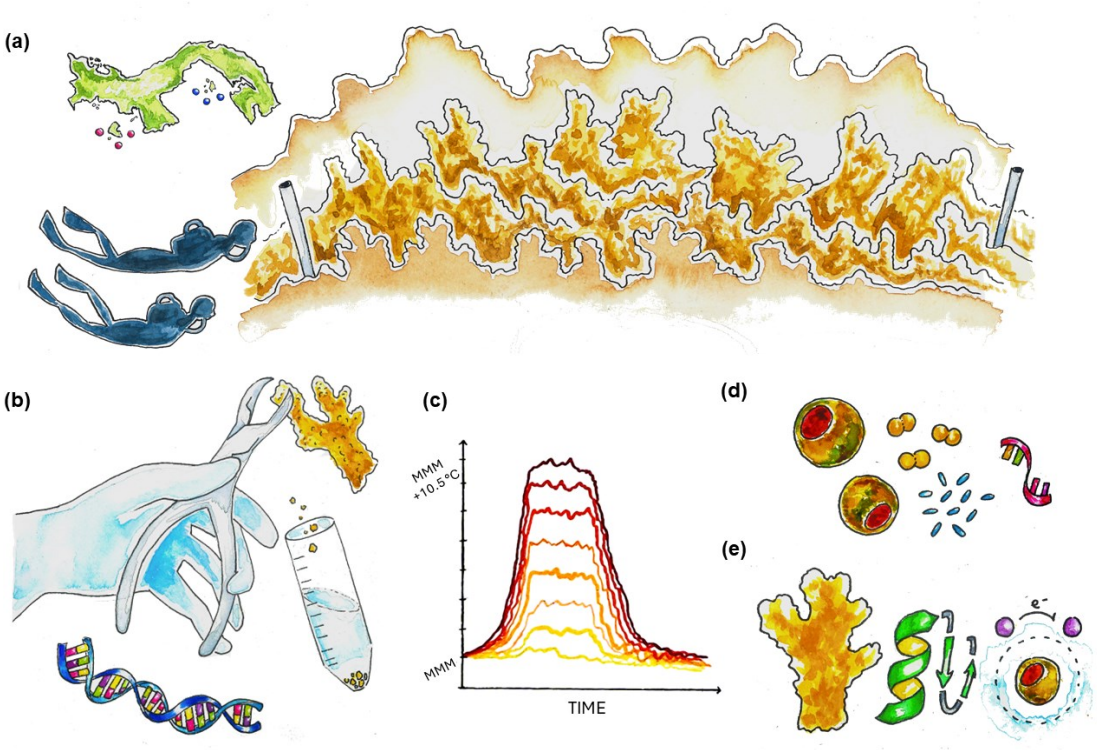


Figure 2.1. Overview of our experimental approach for studying *Pocillopora* coral's holobiont configurations and their consequences for thermotolerance across Panama's TEP. **(a)** Study sites in Panama's TEP (n = 3 per gulf, pink circles represent sites in the Gulf of Chiriquí, and blue circles represent sites in the Gulf of Panama), with a representation of each reef's 50 m transect. **(b)** Sampling *Pocillopora* corals for population genetic analyses. **(c)** The CBASS experiment's range of experimentally manipulated temperatures. MMM stands for mean monthly maximum temperature. **(d)** Coral microbiome dynamics during the CBASS using marker-gene sequencing approaches. **(e)** Host physiology and oxidative metabolism dynamics during the CBASS.

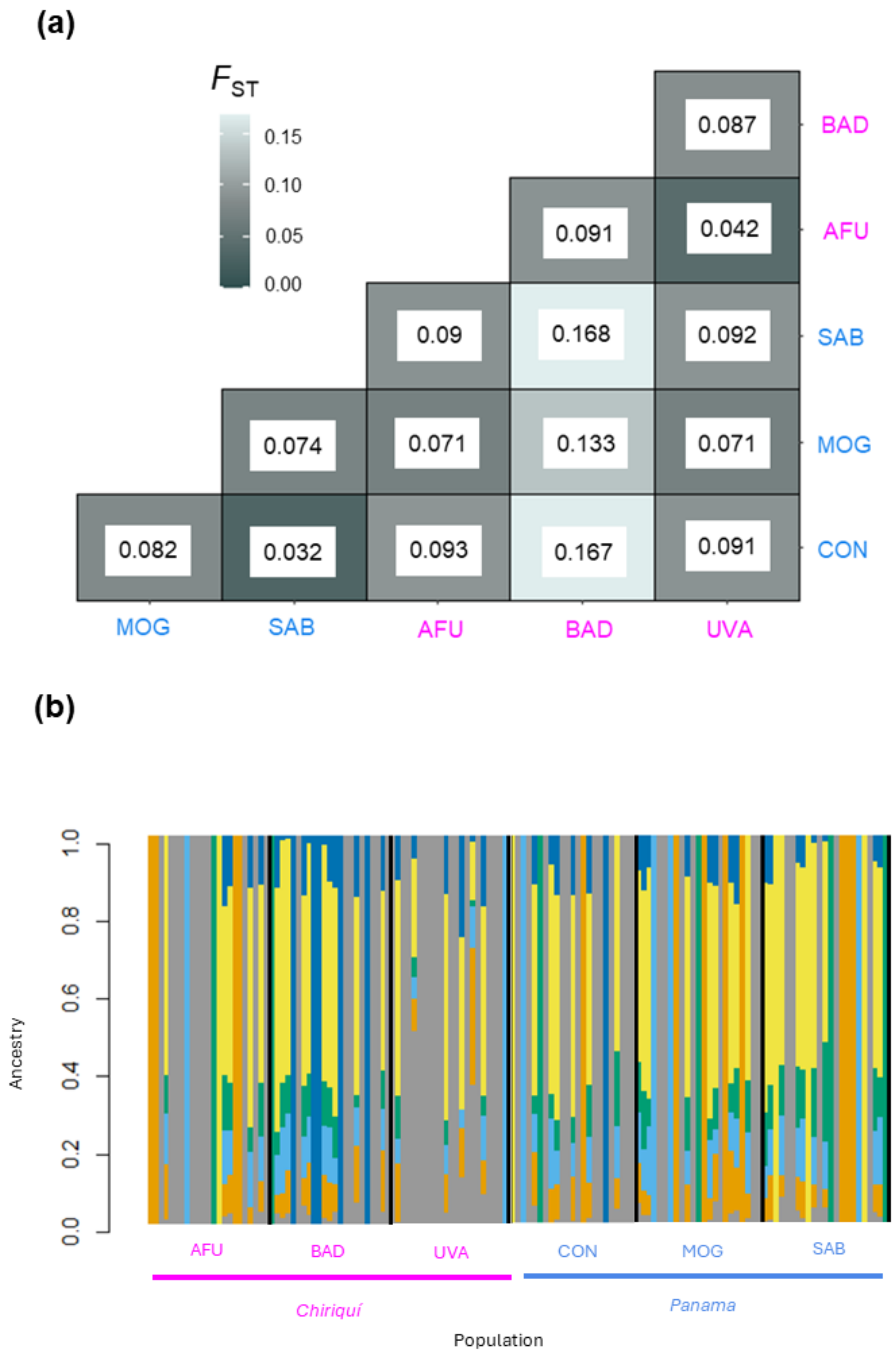


Figure 2.2. Population genetics of *Pocillopora* corals across Panama's TEP. Each reef site is denoted by its three-letter code. AFU = Canal de Afuera; BAD = Bahía Damas; UVA = Uvas; CON = Contadora; MOG = Mogo Mogo; SAB = Saboga. **(a)** Pairwise fixation index (Fst) values among the 137 *Pocillopora* coral colonies across six reefs in Panama's Tropical Eastern Pacific

(TEP). Fst calculations here are based on Weir and Cockerham's estimate (1984). **(b)** Ancestral populations across Panama's Tropical Eastern Pacific (TEP) as detected via ADMIXTURE (Alexander and Lange 2011). A total of six ancestral populations were identified, corresponding to six reefs across two different regions. Each line on the plot represents a single individual, where the colors within represent the different identified ancestral populations. Thick black lines delineate different reefs, which are further separated and color-coded by region, Gulf of Chiriquí and Gulf of Panama, respectively.

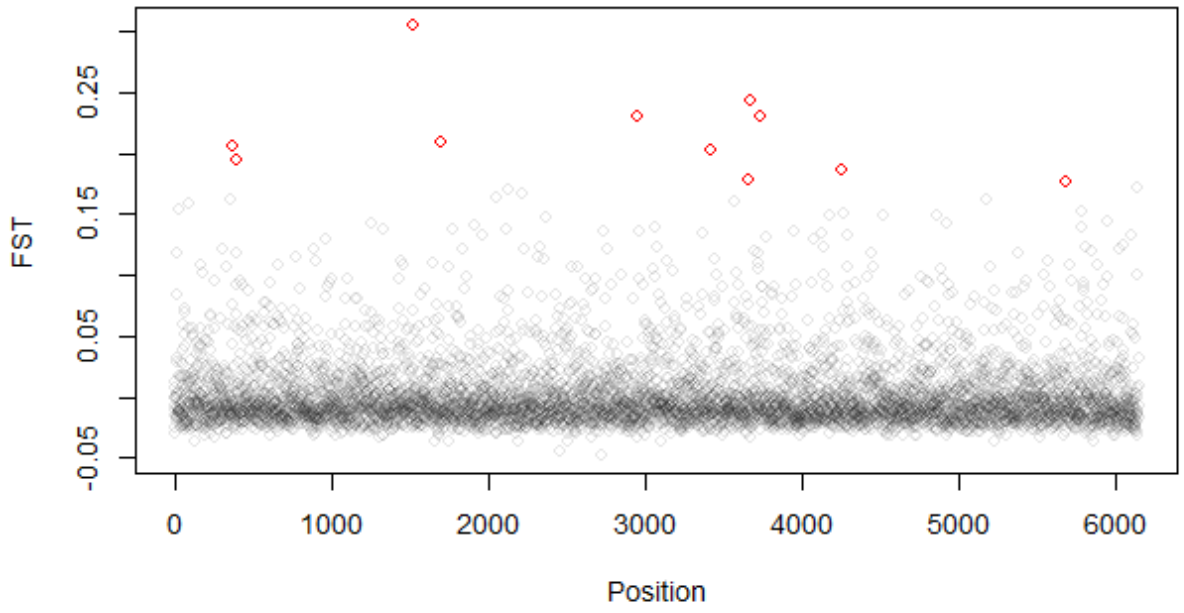


Figure 2.3. Loci under putative selection (outlier SNPs) across coral samples from Panama's Tropical Eastern Pacific (TEP) using OUTFLANK's fixation index (Fst) approach (Whitlock and Lotterhos 2015). Each point denotes a locus, with genomic position (x-axis) plotted against Fst (y-axis). Loci in red are considered outlier SNPs based on a q-value cut-off of 0.05 and an expected heterozygosity cut-off of 0.1.

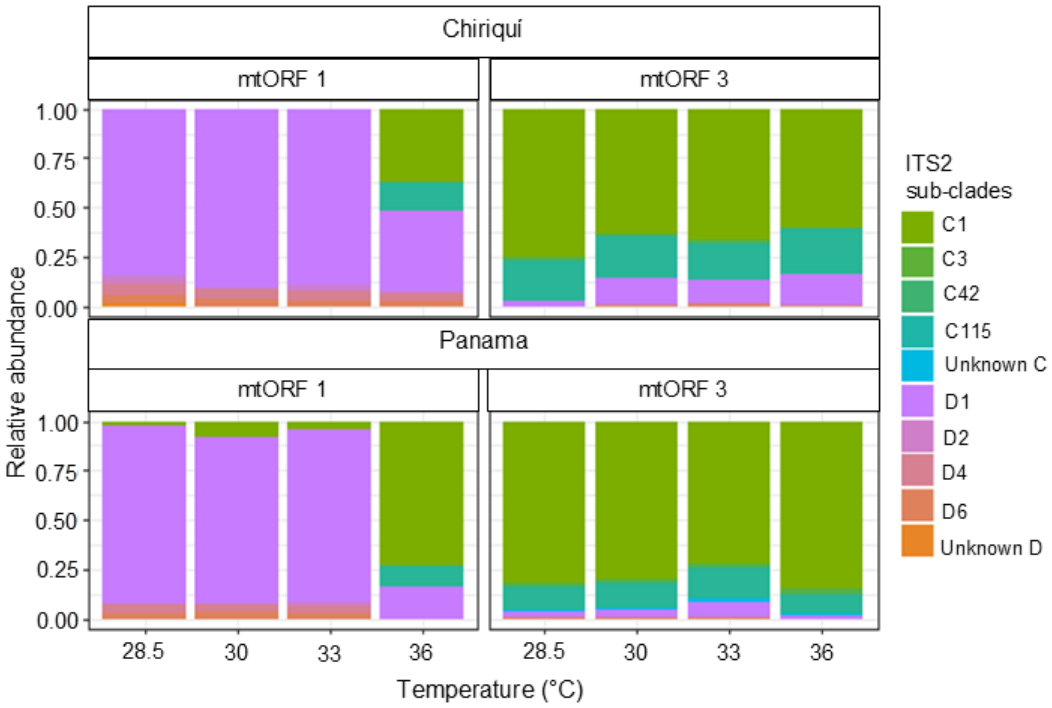
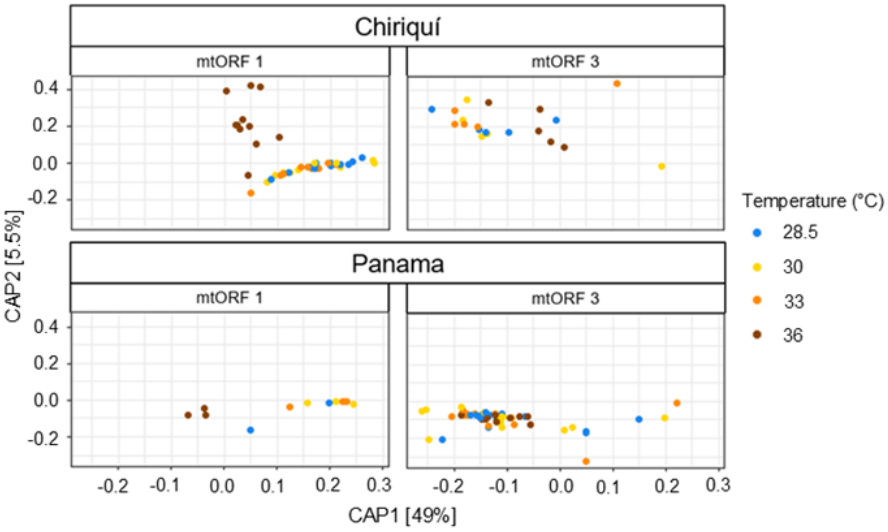


Figure 2.4. *Pocillopora* Symbiodiniaceae community shifts during the CBASS, across regions and mtORF lineages. Relative abundances of ITS2 sub-clades are shown on the x-axis and temperature treatments on the y-axis. Sub-clades starting with a "C" correspond to *Cladocopium* spp., and those starting with a "D" correspond to *Durusdinium* spp. ITS2 sequences that could not be identified beyond the genus level are denoted as "unknown C" or "unknown D," meaning these specific taxa were not found within the SymPortal database.

(a)



(b)

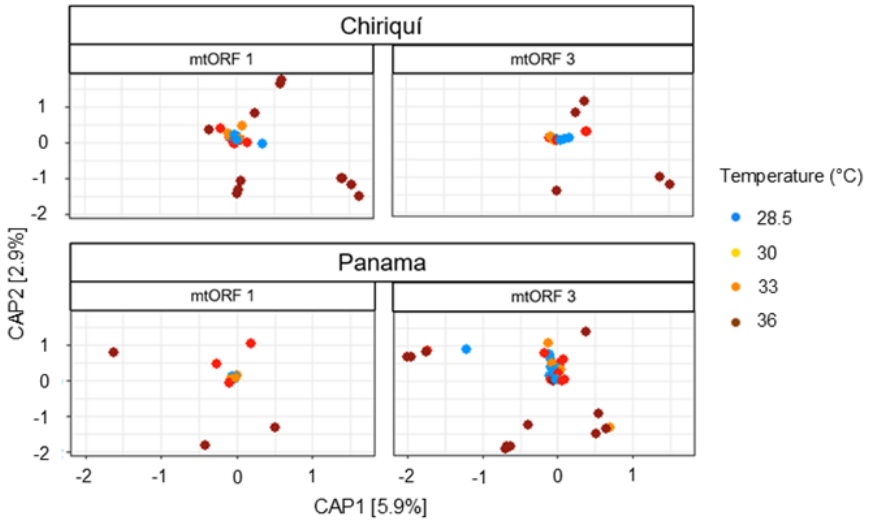


Figure 2.5. Canonical analysis of principal coordinates (CAP) plots for *Pocillopora* coral's microbial communities during the CBASS, based on Bray-Curtis dissimilarity in the relative abundances of DIVs for ITS2, and ASVs for 16S. (a) CAP plots for the Symbiodiniaceae communities. **(b)** CAP plots for the prokaryotic communities.

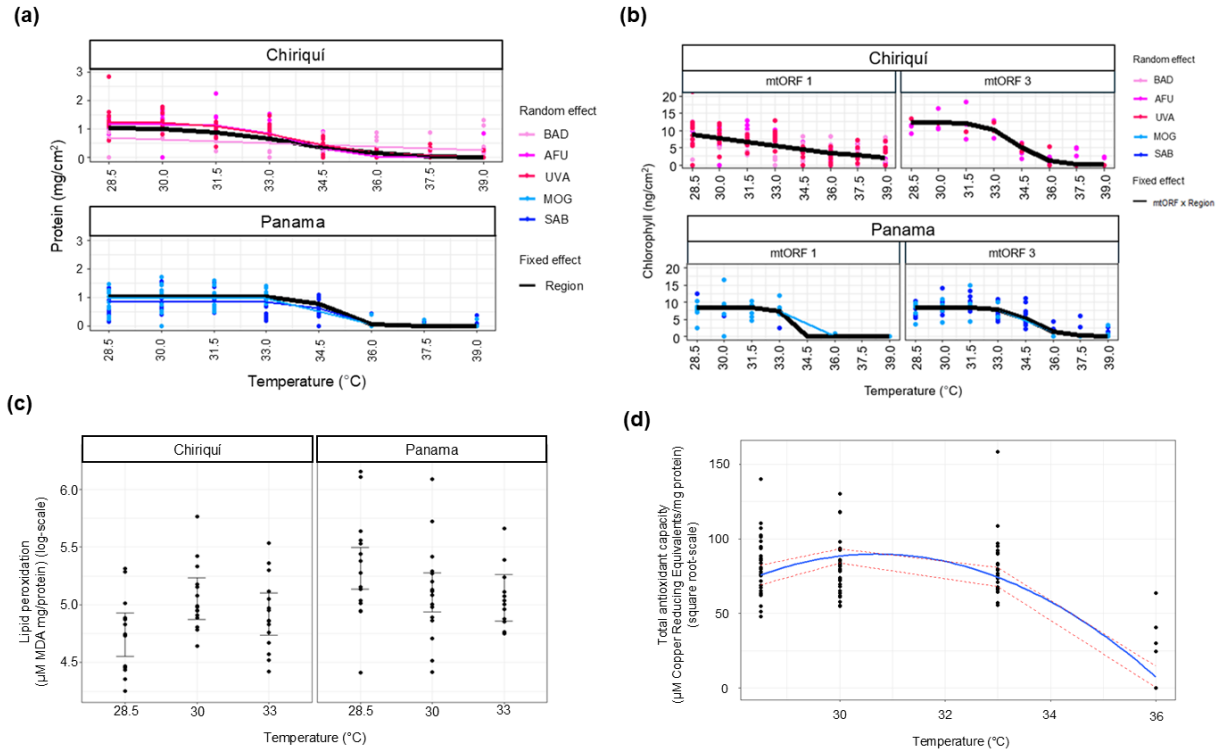


Figure 2.6. Physiological and oxidative metabolism dynamics for *Pocillopora* corals during the CBASS. Points represent predicted values**. (a)** Predicted changes in host protein concentrations. The estimated gulf-level average responses (i.e., incorporating fixed effects) are shown as a black line, and the site-level responses (i.e., incorporating random effects of site) are shown as different colored lines. **(b)** Predicted changes in chlorophyll *a* concentrations. The estimated average responses for the interaction of mtORF and region (i.e., incorporating fixed effects) are shown as a black line, and the site-level responses (i.e., incorporating random effects of site) are shown as different colored lines. **(c)** Predicted changes in lipid peroxidation (LPO; expressed on a logarithmic scale). Here three temperature treatments are examined, 28.5°C, 30°C, and 33°C, with 95% confidence intervals shown as a bar over each temperature treatment**. (d)** Predicted changes in total antioxidant capacity (TAC; expressed on a square-root scale). Here

four temperature treatments are examined, 28.5°C, 30°C, 33°C, and 36°C, with the 95% confidence interval shown as a red dotted line.

Connecting statement between Chapter 2 and 3

In Chapter 2, by leveraging Panama's TEP as a natural laboratory, I revealed a nuanced interplay between environment, host genetics, and microbiome dynamics in driving differences in coral thermotolerance (Figure 0.6). As a result of my analytical innovations, from modeling physiological declines with a random effect of site, to including a term in our oxidative stress models to capture algal symbiont shifts, I was able to not only identity potential mechanisms explaining differences in coral thermotolerance, but I also gained insights into the fitness costs associated with particular host-algal associations. Although we had hypothesized that our acute thermal stress assay would result in increases in community variance at elevated temperatures for all studied microbiome members, this was only observed for the prokaryotic community. The disparity between algal and prokaryotic dynamics was one of the most striking findings from our study. Prokaryotic dysbiosis, as captured by increased community variance, has been reported previously for animal microbiomes, corals included, facing environmental stress, but these patterns of dysbiosis are rarely reported for coral's algal symbionts. Perhaps algal shuffling precluded the increases in community variance, with these shifts hypothesized to impact host's thermotolerance. Given the central role of algal symbionts in host thermotolerance, a new question emerged at the end of Chapter 2: how do algal symbiont's drive differences in prokaryotic dysbiosis during bleaching?

As with most corals and as is the case for my studied *Pocillopora* corals, their algal symbionts are composed of various taxa, thus it is difficult to establish the relative role of each symbiont to overall host dynamics. Additionally, as Chapter 2 underscores, the coral host's genetic

background and environmental histories together impact holobiont structure and functioning under thermal stress, making it difficult to disentangle the relative contribution of various holobiont components. In Chapter 3, I turn to *Aiptasia* as a model system to help me overcome some of these challenges and elucidate connections that emerged from my work in the TEP between the algal and prokaryotic microbial communities. My goal was to gain insights into the role of algal symbionts in mediating overall microbiome stability and community composition, given their dual role in host homeostasis and bleaching.

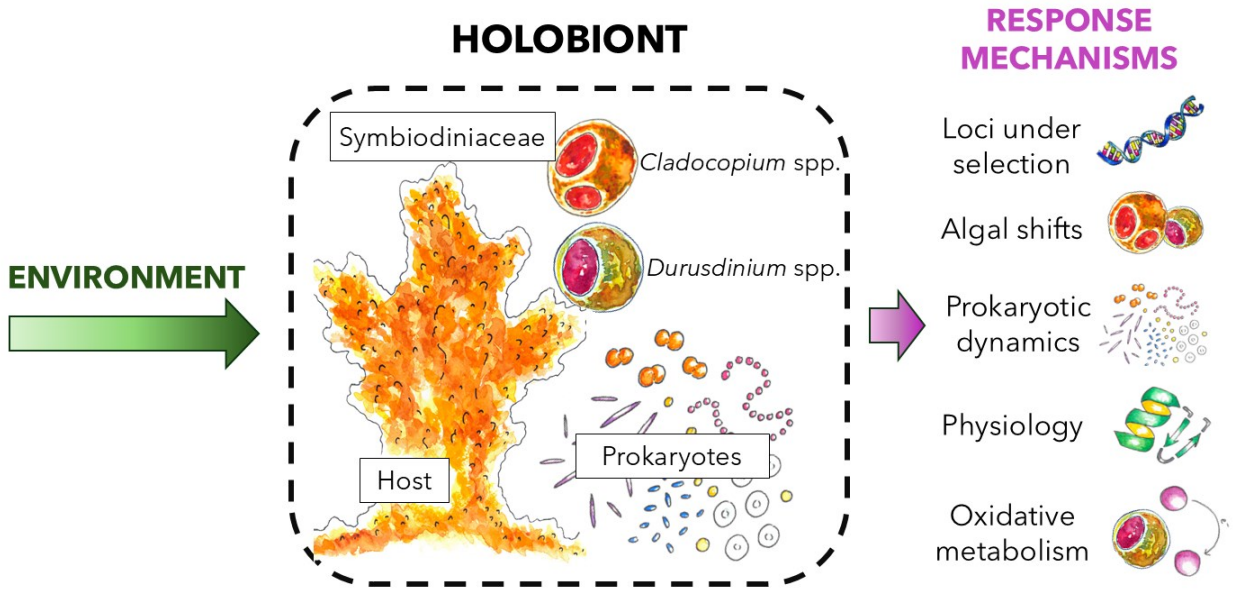


Figure 0.6. Visual overview of Chapter 2. In studying *Pocillopora* corals across Panama's TEP, we found that the region's upwelling regimes were shaping holobiont configurations (represented by the green arrow, titled "Environment"). Within these holobionts, we focused on three components: the coral host, the algal microbiome with members of the family Symbiodiniaceae and the prokaryotic microbiome. Within the algal microbiome, we only identified two genera in symbiosis with *Pocillopora* corals: *Cladocopium* spp. and *Durusdinium* spp. In studying these holobionts in-situ and during an acute thermal stress assay known as the

CBASS, we captured five response mechanisms to changing abiotic conditions (shown to the right of the purple arrow). These were: (1) divergent selection on loci with previously reported roles in bleaching, (2) algal shifts between *Cladocopium* spp. and *Durusdinium* spp. during thermal stress, (3) increases in prokaryotic community variance during thermal stress, and (4) changes to host physiology and (5) oxidative metabolism that significantly shaped coral's thermal thresholds and their ability to counteract increasing temperatures.

Chapter 3 | Algal thermotolerance drives differences in prokaryotic microbiome dynamics for an emerging coral model system

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3.1 Abstract

The coral microbiome is a highly complex entity, and interactions between microbiome members have been proposed as an important component of coral thermotolerance. Although there have been advances in probiotic development over the course of the last decade, engineering the coral microbiome is still a challenge. To overcome this issue, we used the emerging coral model system, *Aiptasia*, to explore how algal symbionts impact the structure and dynamics of the prokaryotic microbiome, and in turn their contributions to cnidarian thermotolerance. To do so, we generated clonal *Aiptasia* lines hosting either thermally sensitive or thermally tolerant algae and subjected them to an acute thermal stress assay to explore prokaryotic dynamics over the course of heat stress. We find that algal strain is the strongest driver of the *Aiptasia* prokaryotic microbiome and identify microbial taxa that may be potential indicators of both improved and reduced bleaching resistance. Additionally, we propose that sustained community variance with increasing thermal stress may be characteristic of more thermally sensitive cnidarian holobionts. Our study presents how algal and prokaryotic dynamics together result in different bleaching

trajectories and underscores the importance of interactions within the microbiome in driving organismal level responses to thermal stress.

3.2 Introduction

Climate change is increasing the frequency and severity of heat waves, greatly placing at risk coral reefs that support over 25% of all marine life (Wyatt et al. 2023, Donovan et al. 2021, Ayre and Hughes 2004, Hoegh-Guldberg et al. 1999). With 2023 being the hottest year on record and the fourth mass bleaching event declared in April 2024, it is imperative that we explore the mechanisms governing coral's thermal resistance (NOAA National Centers for Environmental Information 2024, NOAA/NWS/CPC 2024). The microbiome is a key element in coral thermotolerance, with algal symbionts in the family Symbiodiniaceae being central to the persistence and vulnerability of these organisms. This single microbiome member is predicted to supply up to 90% of the coral host's energy requirements and is hypothesized to have facilitated the emergence of coral reefs in warm, nutrient poor waters approximately 160 million years ago (Grottoli et al. 2006, Jones et al. 2008, LaJeunesse et al. 2018). Yet under thermal stress, these same symbionts are lost in a process known as coral bleaching, with ramifications for both the surrounding ecological community and human livelihoods (Graham et al. 2007, Stuart-Smith et al. 2018, Pratchett et al. 2008). Algal symbionts can support the coral host's own ability to withstand thermal stress, with *Durusdinium* spp. dominated corals reported to best survive thermal stress and *Durusdinium* spp. being linked to increasing host's thermal thresholds by as much as 1.5°C (Claar et al. 2020, Glynn et al. 2001, Berkelmans and van Oppen 2006, Silverstein et al. 2015). Algal symbionts evolved under heat stress have also been shown to increase the host's thermotolerance (Chan et al. 2023, Buerger et al. 2020). Although algal

symbionts have been an early focus of coral-microbiome interactions given their central role in bleaching and subsequent resistance, prokaryotic members have also emerged as ecologically-responsive members of the microbiome. Bleaching resistant colonies have been found to have different bacterial microbiome members as compared to more vulnerable conspecifics (Cárdenas et al. 2022, Xu et al. 2023, Ziegler et al. 2017), with the burgeoning field of coral probiotics beginning to present the ability of certain prokaryotic members in reducing bleaching severity (Delgadillo-Ordoñez et al. 2024, Santoro et al. 2021, Rosado et al. 2019). Disentangling the relative contribution of different algal and prokaryotic microbiome members, and the interactions between microbiome members, will elucidate the roles of different taxa to whole-animal responses to thermal stress.

Aiptasia is an ideal model system to explore the causal links between members of the coral microbiome, as these closely-related cnidarians can be stably engineered to host single algal strains, which is currently unachievable in corals. Aposymbiotic anemones can be reinfected with a variety of Symbiodiniaceae species including those from stony corals (Grawunder et al. 2015, Baumgarten et al. 2015, Weis et al. 2008, Hambleton et al. 2014), allowing for the creation of clonal lines differing in their hosted algal symbiont. By changing these algal symbionts, we see dramatic shifts in bleaching tolerance, suggesting a role of the microbiome in controlling the animal stress response (Cleves et al., unpublished). Additionally, *Aiptasia* are closely related to stony corals as these are both Class Anthozoa cnidarians but lack a calcareous skeleton. This feature facilitates tissue extractions, microscopy, and fluorescent analyses (Baumgarten et al. 2015, Lehnert et al. 2012). *Aiptasia*, like corals, also have a prokaryotic microbiome, but the role of these members in overall holobiont functioning is poorly understood, particularly within the

context of bleaching. Previous research has shown that aposymbiotic and symbiotic *Aiptasia* associate with different prokaryotic members, suggesting that algal symbionts may be impacting the community composition of other microbiome members (Röthig et al. 2016). Additionally, symbiotic state does impact *Aiptasia* bacterial community dynamics under thermal stress (Sydnor et al. 2023, Aguirre et al. 2023), with symbiotic *Aiptasia* of different clonal backgrounds having different prokaryotic communities (Ahmed et al. 2019). Yet prior studies have not explored how the thermal characteristics of algal symbionts influence overall community dynamics, and how these symbionts interact with prokaryotes, under the same clonal background. Doing so may reveal prokaryotic taxa associated with bleaching resilience at a resolution currently unavailable in corals, improving our understanding of the microbiome's role in coral thermotolerance.

In this study we explored how algal thermotolerance impacts *Aiptasia*'s prokaryotic community dynamics. To do so, we subjected *Aiptasia* clonal lines hosting either thermally sensitive or thermally tolerant algae to an acute thermal stress assay known to result in bleaching (Cleves et al. 2020) to explore prokaryotic dynamics over the course of heat stress. We predicted that different host-algae associations would result in divergent prokaryotic communities, as the algal symbiont's thermal characteristics would shape overall microbiome structure and functioning. Additionally, we expected that particular prokaryotic taxa would be uniquely associated with different time points in our assay, thus emerging as particular indicator species for bleaching severity. By leveraging *Aiptasia* as an emerging coral model system, we are able to experimentally manipulate the cnidarian microbiome to gain insights on how algal and prokaryotic dynamics together result in different bleaching trajectories.

3.3 Materials and Methods

3.3.1 Organisms and culture conditions

We generated all animals from a clonal population of CC7 *Aiptasia* animals, which naturally form symbioses with *Symbiodinium linucheae* (Bieri et al. 2016, Sunagawa et al. 2009). We first rendered these animals aposymbiotic, following the previously established combined cold-shock and diuron protocol (see Lehnert et al. 2012, Xiang et al. 2013). We then exposed the aposymbiotic CC7 animals to clonal, axenic strains of either Symbiodiniaceae strain SSA01 (*Symbiodinium linucheae*, ITS2 Clade A4) or SSB01 (*Breviolum minutum*; ITS2 Clade B1); these clonal strains have been described previously (Bieri et al. 2016, Xiang et al. 2013). The resulting animal lines will be referred to herein as CC7-SSA01 and CC7-SSB01. We grew *Aiptasia* under standard laboratory conditions (see below) for at least two years prior to our experiment to ensure that algal populations were in a steady state. We periodically sequenced cps23S (chloroplast rDNA), 18S (nuclear rDNA), and/or ITS2 (nuclear rDNA), to ensure animals remained in symbiosis with their axenic strains (Xiang et al. 2013). We maintained all animals at 27°C in artificial seawater (ASW), which we prepared by mixing Coral Pro Salt (Red Sea) with deionized water (dH2O), for a final salinity of 33.5 ppt. We kept animals under a 12 h:12 h light:dark cycle at an irradiance of ~25 μmol photons m^{-2} s^{-1} (Phillips Alto II 25 W white fluorescent bulbs) and fed them every 2-3 days with freshly hatched *Artemia nauplii*, with a subsequent water change at the end of feeding.

3.3.2 Heat stress experimental set-up

To explore prokaryotic shifts during thermal stress, we subjected CC7-SSA01 and CC7-SSB01 animals to the heat stress assay described in Cleves et al. 2020. Briefly, we placed 45 animals from each line in a polycarbonate tank with 1 L of ASW. For each line, we had a total of four tanks: three for our heat stress assay, and one to serve as our control. These animals were collected from our larger stocks and allowed to acclimate in our experimental incubators for 2 weeks at 27°C prior to the start of the experiment. At the end of the two-week acclimation period, we began our heat stress assay. Approximately three hours into their light cycle, 3 animals were pooled per line to serve as our t = 0h samples. Immediately after, three tanks per line were moved from their original incubator at 27°C to one at 34°C, with an approximate 5-hour ramp up to reach the final experimental temperature. We also prepared a tank with 1 L of ASW and a HOBO Pendant Temperature Logger to record water temperatures throughout the experiment at 5-minute intervals. One tank with a HOBO logger was kept with the control animals at 27°C, and another tank with a HOBO logger was moved from 27°C to 34°C alongside our heat stress treatment animals to track the increase in temperature. To account for tank effects, one animal from each of the three replicate heat stress tanks, for each line, was pooled at t = 0h, 3h, 12h, 24h, 48h, and 96h and placed in 1.5 mL of DNA/RNA Shield (Zymo Research) for downstream microbiome characterization. Three animals were also pooled from each control tank at the same sampling intervals as our heat stress treatment. Figure 3.1 provides an overview of our experimental design.

3.3.3 DNA extraction and 16S amplification

To characterize prokaryotic dynamics during heat stress, we performed amplicon sequencing of the *Aiptasia* prokaryotic community. From each sample, we extracted DNA using a modified phenol-chloroform protocol we optimized for cnidarians. Briefly, we first lysed whole animals in their stored DNA/RNA Shield (Zymo Research) using a combination of Lysing Matrix A and 1/4-inch ceramic spheres (MP Biomedicals). This was followed by enzymatic digestion using both proteinase K and RNAse A, and a standard phenol:chloroform:isoamyl phase separation. This protocol allowed for the production of high quantity and high molecular weight DNA. The resulting DNA was shipped to the McGill Genome Centre (Montréal, Québec) for amplicon sequencing of the 16S rRNA marker-gene using the Earth Microbiome Project's (Ul-Hasan et al. 2019; https://earthmicrobiome.org/protocols-and-standards/16s/) updated 515F (5'-GTGYCAGCMGCCGCGGTAA-3'; Parada et al. 2016) and 806R (5'-GGACTACNVGGGTWTCTAAT-3'; Apprill et al., 2015) primer pair. Amplicons were sequenced on an Illumina MiSeq v2, with a pair-end read length of 250 bp, aiming for approximately 100,000 reads per amplicon.

3.3.4 Characterizing prokaryotic dynamics under thermal stress

To determine prokaryotic taxonomy and community dynamics from our 16S reads, we used the R package 'DADA2' version 1.20 (Callahan et al., 2016; http://github.com/benjjneb/dada2) to call amplicon sequence variants (ASVs). Here, we used cutadapt in DADA2 to remove primer sequences (Martin 2011). We also assigned taxonomy using the SILVA 16S database release v138.1 (Quast et al. 2012), specifically formatted for the classification of ASVs derived from DADA2 (McLaren and Callahan 2021; https://zenodo.org/records/4587955). Using the R

package ‘phyloseq’ (McMurdie and Holmes 2013; https://github.com/joey711/phyloseq), we integrated ASVs, taxonomy, and sample information into a single object. We then removed all ASVs assigned to chloroplasts, mitochondria, eukaryotes, or unassigned at the kingdom level. We used the package ‘decontam’ (Davis et al. 2018) to remove potential contaminants within our ASV data, by implementing a statistical classification procedure on the basis of prevalence within our negative controls. We additionally removed singletons and performed an r-log transformation within the ‘DESeq2’ package (Love et al. 2014) prior to beta diversity analyses. All analyses were performed using R version 4.2.1 (R Core Team 2022).

To determine community-level shifts during thermal stress, we performed a Principal Coordinate Analysis (PCoA) via the ‘ordinate’ function in ‘phyloseq’ (McMurdie and Holmes 2013), using Bray-Curtis dissimilarity to calculate distances (Bray and Curtis 1957). To help identify the impact of each explanatory variable in driving patterns within ordination space, we ran a permutational multivariate analysis of variance (PERMANOVA) with 999 permutations using the ‘adonis2’ command from the package ‘vegan’ (Dixon 2003); post-hoc pairwise comparisons were performed with the ‘pairwise.adonis2’ function and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons (Martinez Abizu, 2020). To test the statistical significance of patterns of homogeneity of variance, we ran ‘betadisper’ with 999 permutations from the package ‘vegan,’ using Bray-Curtis distances (Dixon 2003). We then ran an ANOVA on the ‘betadisper’ group dispersion results to determine if the variance of each group’s distance from the centroid was statistically significant. Post-hoc comparisons were performed with Tukey’s Honest Significant Differences test, which corrects for multiple testing at a 95% confidence level.

To detect differentially abundant microorganisms across *Aiptasia* lines and time points, we performed an indicator species analysis (Dufrêne and Legendre 1997) using the package 'indicspecies' (Cáceres and Legendre 2009) and used a modified function from Setiawan et al. (2021) that groups our ASV table into higher order taxonomy, here down to the genus level. As a result, the input table for 'indicspecies' has collapsed the ASV counts into counts across different genera represented in our data. Using this genera table, we used the 'multipatt' command with 999 permutations and implemented the Benjamini and Hochberg p-value correction for multiple comparisons. As we were most interested in uniquely associated taxa during heat stress, we focused only on our heat stress samples in our analyses. Here, we analyzed each line separately to determine uniquely-associated taxa as a function of duration under heat stress.

To determine differences in *Aiptasia* prokaryotic communities across samples under heat stress, we calculated co-occurrence networks using 'phyloseq' (McMurdie and Holmes 2013). We used Bray-Curtis dissimilarity to define links between the nodes, here corresponding to individual samples, with a distance threshold of 0.1. We selected this threshold to recapitulate the two distinct clusters that emerged in our PCoA plots corresponding to each line (see Results). For each network, we calculated its density, transitivity, average path length, and maximal clique size, which are all indicators of community connectivity. To determine the likelihood of each network and its associated metrics, we created 1,000 random graphs using a Erdős–Rényi model and determined the proportion of graphs with a shorter path length than the original graph (Erdős and Rényi 2011). Here, randomly generated graphs have the same number of vertices and density as the original network whereas the location where the edges are drawn is allowed to vary. For

network-to-network metric comparisons, we used the random network's metric values to calculate our null distribution's mean and standard deviations. This was then used in a two-tailed z-score test to determine if metrics were statistically different between networks. For network-wide comparisons in the case of average path length, we calculated the average path length across our generated random graphs and determined the proportion of graphs with a path length smaller than in our observed networks.

3.4 Results

3.4.1 *Aiptasia* line and duration of thermal stress together drive differences in prokaryotic communities

Our PCoA plots reveal that CC7-SSA01 and CC7-SSB01 animals form two distinct clusters in ordination space for both the control and heat stress samples, with the duration of heat stress producing additional within-cluster structure among samples (Figure C1). Although PC1 separates our strains into two corresponding clusters, PC2 predominantly reflects changes that occur over time, where later time points such as 48h and 96h have negative values. When considering control and heat stress samples together, our PERMANOVA revealed that differences in community composition were only statistically significant ($p < 0.05$) across lines ($p = 0.001$, pseudo-F-statistic$_{19,42} = 86.6977$, $R^2 = 0.58981$) and time points ($p = 0.003$, pseudo-F-statistic$_{19,42} = 3.7001$, $R^2 = 0.12586$), but not the interaction between these two variables, which was marginally non-significant (see Table C1). Interestingly, differences in prokaryotic community composition between control and heat stress samples were also marginally non-significant, with interactions between treatment and line, and treatment and time also being non-significant (see Table C1). When considering control samples alone, we find that there is a

significant strain effect in driving community composition, but not time (Table C2-C3). Furthermore, when considering each line separately (CC7-SSA01 and CC7-SSB01), there is only an effect of time and not a treatment effect in shaping prokaryotic communities (Table C4-C5). It is important to be cautious in interpreting these results, as we had a smaller sample size for the control samples as compared to the heat stress samples, reducing our analysis' power to detect treatment effects.

When considering heat stressed animals alone, line ($p = 0.001$, pseudo-F-statistic$_{19,30} = 65.2872$, $R^2 = 0.61207$) and time ($p = 0.006$, pseudo-F-statistic$_{19,30} = 3.0417$, $R^2 = 0.14258$) separately emerge as significantly driving patterns in community similarity, with the interaction between time and line emerging as non-significant (Table C6). Comparison of effect sizes on the basis of the pseudo-F-statistic revealed that line was a stronger driver of prokaryotic communities than the duration of heat stress, as encapsulated by our time point variable (Table C6). Pairwise post-hoc comparisons for each line individually revealed that when comparing across time points, no two time points resulted in statistically distinct community compositions (Table C7-C8).

In analyzing heat stress samples alone, we detected significant differences in variance across lines and time points. First, in comparing CC7-SSA01 and CC7-SSB01 animals across all time points under heat stress, we find that the prokaryotic community of CC7-SSB01 was more variable than CC7-SSA01 (Table C9). In exploring line-specific trends further, although group variances are similar across time points for both CC7-SSA01 and CC7-SSB01 animals, there are significant differences in the location of each time point's centroid for both lines (Table C10-C11). For CC7-SSA01 animals, we see a significant increase in the distance from centroid from

0h to 3h, and a decrease in distance when comparing 3h to 12h, 24h, 48h, and 96h, respectively (Table C10). For CC7-SSB01 animals, although we did find statistically significant differences in centroid position across time points, post-hoc tests across timepoints revealed that there was only a marginally non-significant increase in distance from centroid from 24h to 96h (Table C11). It is important to note that CC7-SSA01 animals had fewer samples that successfully amplified rRNA 16S at time points 24h, 48h, and 96h, than CC7-SSB01 animals, potentially impacting our homogeneity of variance analyses. Lastly, in line with our PERMANOVA analyses, we did not find statistically significant differences in community variance or distance from centroid between control and heat stress animals across time points when analyzing heat stressed CC7-SSA01 and CC7-SSB01 animals separately (Table C12-C13).

3.4.2 Prokaryotic taxa are uniquely associated with *Aiptasia* lines over the duration of thermal stress

In considering each line separately during heat stress, our indicator species analyses revealed that different taxa were uniquely associated with CC7-SSA01 and CC7-SSB01 animals over the duration of heat stress. Only 6 taxa were uniquely associated with specific time points for CC7-SSA01 animals, as compared to 13 taxa uniquely associated with specific time points for CC7-SSB01 animals. For CC7-SSA01 animals, only a single taxon was uniquely associated with 0h, which was *Oleiphilus.* Three taxa were uniquely associated at 24h, corresponding to *Yangia*, *Blastopirellula*, and *Pseudoalteromonas*. Two taxa were uniquely associated with CC7-SSA01 animals at 96h, which corresponded to *Hyphomonas* and a member of the *Saprospiracea*e family that could not be identified down to the genus level (Table C14). For CC7-SSB01 animals, a single taxon was likewise uniquely associated with 0h, corresponding to *Maricaulis* (Table C9).

Five separate taxa were uniquely associated with CC7-SSB01 animals at 12h, corresponding to various members of the Gammaproteobacteria and Bacteroidia classes, such as *Pseudoalteromonas*, *Portibacter*, and *Thalassolituus*. A single taxon was uniquely associated with CC7-SSB01 animals at 24h, corresponding to the Pseudomonadales *P13-46* family that could not be identified down to the genus level, while six ASVs were uniquely associated with 96h. All these taxon correspond to the class Alphaproteobacteria, with only three taxon identified to the genus level, here corresponding to *Phaeobacter*, *Litorimicrobium*, and *Labrenzia*. The remaining three taxa were identified as members of the *Rhizobiaceae*, *Rhodobacteraceae*, and *Terasakiellaceae* families (Table C15).

3.4.3 Prokaryotic communities of CC7-SSB01 animals are more variable between samples

When comparing co-occurrence networks between lines under heat stress, the prokaryotic community of CC7-SSA01 animals was most similar between samples than for CC7-SSB01 animals, as seen by the longer path length between samples for CC7-SSB01 animals (Figure 3.3). This observation was further supported when calculating network metrics for the CC7-SSA01 and CC7-SSB01 plots, where the average path length was significantly longer ($p < 0.05$) between samples for CC7-SSB01 animals as compared to CC7-SSA01 animals. For our other metrics of interest, here network density, transitivity, and maximum clique size, these were not statistically distinct between the CC7-SSA01 and CC7-SSB01 plots (Table 3.1). Together, this indicates that although across lines we see similar trends in terms of the tendency of samples to closely cluster on the basis of prokaryotic community composition and overall similarity between samples, pairs of samples have more dissimilar prokaryotic communities for CC7-SSB01 animals as compared to CC7-SSA01 animals. Random graphs created using a Erdős–

Rényi model (Erdős and Rényi 1960), indicated that although the CC7-SSA01 plot did not have a path length that was significantly different from random graphs (44.6% of random graphs had a shorter average path length), the CC7-SSB01 plot had a longer path length than 100% of the random graphs. The average path length for CC7-SSB01 animals was statistically distinct from that of the randomly generated networks (Table 3.2). This can be interpreted as CC7-SSB01 samples being more dissimilar across time points, as compared to CC7-SSA01, which can also be confirmed by visual inspection of the networks (Figure 3.3).

3.5 Discussion

By directly comparing clonal *Aiptasia* lines that vary solely in their associated algal symbiont, our data indicates that algal symbiont's thermotolerance intrinsically shapes prokaryotic community dynamics. There are differences in the specific prokaryotic taxa associated with CC7-SSA01 and CC7-SSB01 animals under thermal stress. Prokaryotic taxa associated with CC7-SSB01 animals have been previously identified as differentially abundant in heat-stressed cnidarians and linked to coral diseases like stony coral tissue loss disease (c.f. Ahmed et al. 2019, Bourne et al. 2008, Huntley et al. 2022). Thus, our data suggests that the presence of these taxa is characteristic of an inherently more environmentally sensitive cnidarian holobiont. Future work should explore these taxa from the perspective of health indicators, and their potential correlations to overall bleaching and/or disease severity in corals. Lastly, our co-occurrence networks suggest that the prokaryotic communities of CC7-SSB01 animals were more dissimilar to one another across time points than for CC7-SSA01 animals. Although our PCoA plots did not show changes in prokaryotic community variance between timepoints for CC7-SSB01 animals under thermal stress, despite being the more thermally-sensitive line (Cleves et al., unpublished),

our network metrics posit that greater inter-sample variability may be indicating weaker host control on microbial dynamics (Zaneveld et al. 2017). Together, our findings underscore that algal symbionts may be impacting host thermotolerance beyond strictly metabolic interactions (Sproles et al. 2020, Rädecker et al. 2018, Cantin et al. 2009, Allen-Waller et al. 2023) by also indirectly shaping overall microbiome dynamics.

3.5.1 Hosted algal symbiont strongly structures the *Aiptasia* prokaryotic microbiome

Even under heat stress, hosted algal strain most strongly structured CC7 *Aiptasia*'s prokaryotic communities. Previous work in corals has presented how both species and abiotic conditions shape the microbiome, with strong host-specificity often resulting in less labile microbiomes than otherwise expected under bleaching stress (Glynn et al. 2023, Ziegler et al. 2019, Haydon et al. 2021). In explicitly controlling for host genetics by having clonal *Aiptasia* lines, we find that algal line, followed by duration of heat stress, were the main drivers of community composition. Additionally, in considering each line separately, post-hoc comparisons did not reveal significant differences in prokaryotic community composition between pairs of time points for either CC7-SSA01 or CC7-SSB01 animals, suggesting that these differences may have been capturing more global strain-specific changes. This was striking because all our *Aiptasia* lines were generated using axenic algal strains and the same reservoir of ASW was used to supply all tanks. This indicates that in addition to genetic background, algal symbionts may also shape the associated prokaryotic microbiome of their hosts (see Aguirre et al. 2023). Algal-prokaryotic interactions have been previously proposed as an important component of coral fitness (Matthews et al. 2020, Mohamed et al. 2023), and *Aiptasia* is positioned as an ideal system for future studies exploring

how these interactions, from a metabolic to oxidative metabolism standpoint, shape overall holobiont functioning and bleaching pathways.

We cannot exclude the possibility that the observed prokaryotic microbiome dynamics are capturing strain-specific rather than temperature-driven dynamics. Unfortunately, during our experiment, we did not have enough animals for our control tanks, reducing our analyses' ability to detect potential treatment effects. Even if strain differences alone are driving our prokaryotic community patterns under heat stress, it is interesting that these persisted during bleaching. Based on our initial findings, we are currently working on additional replication for our controls to increase our scope of inferences regarding treatment-specific effects during our assay.

3.5.2 Uniquely associated prokaryotes present potential cnidarian bleaching indicators

Different taxa were uniquely associated with our *Aiptasia* lines and time points, providing key candidates for health and bleaching indicators to be further validated. The taxa uniquely associated with the more heat-tolerant CC7-SSA01 animals have been implicated in coral nutrient cycling and with proposed antimicrobial properties, while the taxa uniquely associated with the more heat-sensitive CC7-SSB01 animals have been previously identified to negatively impacting overall host health and bleaching outcomes. The only ASV associated with CC7-SSA01 at t = 0h corresponds to *Oleiphilus.* Members of this genus have been previously described as key members of the coral mucus and coral juvenile microbiome (Frade et al. 2015, Quigley et al. 2020), with a known role as marine hydrocarbon degraders that assist the host in organic substrate cycling (Caughman et al. 2021). Later in the assay at 24h, we see that CC7-SSA01 animals were uniquely associated with *Pseudoalteromonas*, with species in this genus

demonstrating antimicrobial activity thought to play a protective role in coral holobiont's defenses against pathogens, which have been shown to increase under thermal stress (Shnit-Orland et al. 2012, Tout et al. 2015, Brodnicke et al. 2019). Additionally, we found *Yangia* was also uniquely associated with CC7-SSA01 animals at 24h. Members of this genus have been used previously in coral bacterial probiotics, given their hypothesized role in nitrogen cycling within the coral holobiont (Zhang et al. 2021). Yet by the latest time point of our heat stress assay, at 96h we found that a taxon corresponding to the order Saprospiraceae uniquely associated with CC7-SSA01. Members of this family have been previously shown to be enriched in heat stress samples in both corals and *Aiptasia*, and in corals with stony coral tissue loss disease (Savary et al., 2021 Sydnor et al. 2023, Huntley et al. 2022).

In contrast, the only taxon uniquely associated with CC7-SSB01 animals at 0h corresponds to *Maricaulis*, which has been identified as both a core microbiome member of *Aiptasia* (Wuerz et al. 2023) and enriched in lesions of corals with black band disease (Frias-Lopez et al. 2002). At 12h, we likewise see *Pseudoalteromonas* uniquely associated with CC7-SSB01 animals, but also *Thalassolituus* which has been shown to be enriched in bleached *Porites lobata* corals (Bui et al. 2024). At 96h, half of the taxa corresponded to members of the family Rhodobacteraceae. Although these have been identified as core members of the *Aiptasia* microbiome, for animals kept at baseline and elevated temperatures (Ahmed et al. 2019), they have also been proposed as potential bacterial indicators of thermally stressed *Porites lutea* corals (Pootakham et al. 2019). Future studies should strive to determine these taxa's functional potential, such as via metagenome assembled genomes to better characterize their role within the cnidarian holobiont (Robbins et al. 2021, Lima et al. 2023, Messer et al. 2024). With recent advances in coral

probiotic development, experimental inoculations can be developed with the taxa identified as being uniquely associated with our more heat-tolerant CC7-SSA01 animals to explore if bleaching severity can be mediated with bacterial symbionts as has been shown in corals (Rosado et al. 2019, Santoro et al. 2021).

3.5.3 *Aiptasia* hosting thermally sensitive algae have more dissimilar prokaryotic communities

Unlike previous studies exploring coral and *Aiptasia* prokaryotic dynamics under thermal stress, we did not see an increase in community variance for the prokaryotic community of thermally sensitive CC7-SSB01 animals as a function of the duration under heat stress. We expected to see such trends in line with the Anna Karenina Principle, which argues that animals under stress have a more variable microbiome community due to the inability of the host and/or microbiome to regulate community composition (Zaneveld et al. 2017). This pattern has been widely reported for corals and more recently for *Aiptasia* bacterial communities, emerging as a hallmark of prokaryotic dysbiosis (Wang et al. 2018, Ahmed et al. 2019, Greene et al. 2023, Bourne et al. 2008). Instead, we observed that the prokaryotic microbiome of CC7-SSB01 animals was more variable than that of CC7-SSA01 animals across time and therefore irrespective of the duration of heat stress. Thus, a more stochastic and potentially unstable prokaryotic community may represent a key characteristic of innately more thermally sensitive cnidarian holobionts. Replicating our heat stress assay with different *Aiptasia* clonal backgrounds and algal symbionts, alongside testing different stressors (e.g. nutrient, pH, salinity), will reveal how general this observation is.

3.6 Conclusion

In generating clonal *Aiptasia* lines associated with single algal symbiont strains, we show that algal symbionts impact the *Aiptasia* prokaryotic microbiome, in both their taxonomic composition and community variance. We revealed potential taxa that may be indicators of both improved and reduced bleaching resilience, and present that sustained community variance as opposed to increased variance as a function of the duration under heat stress, may be a characteristic of more thermally sensitive cnidarian holobionts. Few studies interrogate the connections between algal and prokaryotic microbiomes for cnidarians, which we highlight may represent an important microbiome interaction that impacts overall holobiont structure and thermotolerance. *Aiptasia* represents a tractable system for studies on coral thermotolerance, allowing us to control for and manipulate the cnidarian microbiome to distill the role of algal-prokaryotic interactions in coral bleaching resistance.

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3.8 Tables

Table 3.1. Network metric comparison between CC7-SSA01 and CC7-SSB01 co-occurrence networks. P-values were determined by generating 1000 random graphs using a Erdős–Rényi model, with the resulting metric values serving as our null distribution in two-tailed tests on the basis of z-scores. P-values represent metric comparisons between networks.

Metric	CC7-SSA01	CC7-SSB01	**P-value**
Density	0.744	0.464	0.973
Average path length	1.256	1.771	0.002
Transitivity	0.891	0.706	0.196
Maximum clique size	10	8	0.707

Table 3.2. Average path length comparison for CC7-SSA01 and CC7-SSB01 co-occurrence networks as compared to randomly generated graphs. P-values were determined by generating 1000 random graphs using a Erdős–Rényi model, with the resulting metric values serving as our null distribution in two-tailed tests on the basis of z-scores. P-values represent metric comparisons between networks.

Path length comparison	**P-value**
CC7-SSA01 – Observed vs Random	0.987
CC7-SSB01 – Observed vs Random	0.00001

3.9 Figures

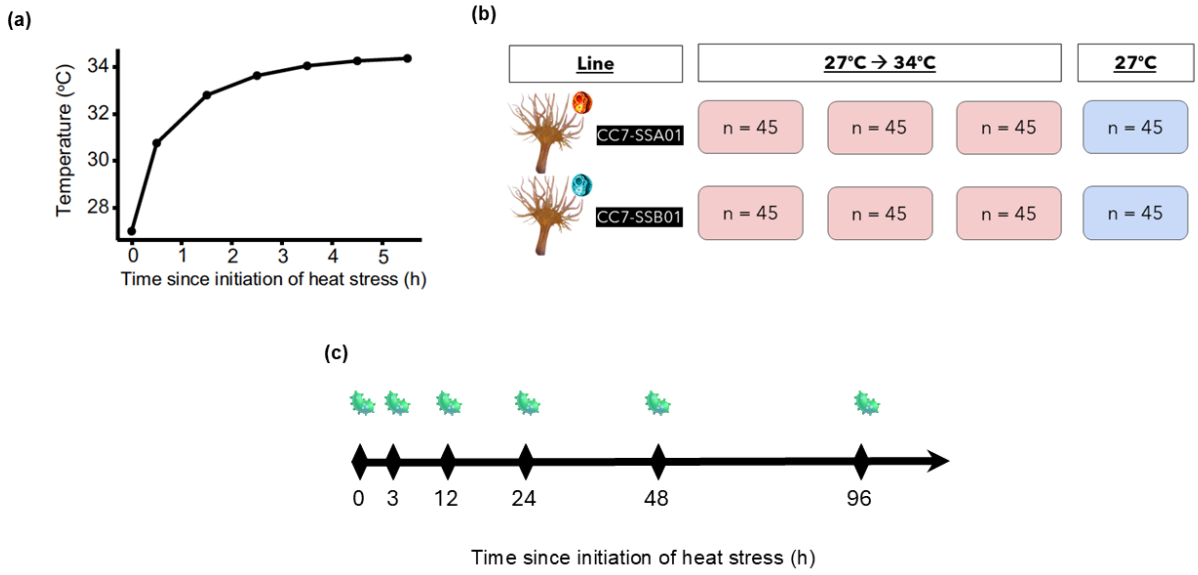

Figure 3.1. Overview of the experimental design for the *Aiptasia* prokaryotic heat stress experiment. The two *Aiptasia* lines used were CC7-SSB01 and CC7-SSA01. **(a)** Temperature ramp for the heat stress treatment. Animals were moved from their original incubators at 27°C to a 34°C incubator. This temperature increase occurred over the course of 5 hours**. (b)** Tank set-up for the experiment. To prevent overcrowding the animals, three separate tanks with 45 individuals each were subjected to our temperature ramp up. A single tank was kept at the animal's original housing temperature of 27°C as our control treatment. **(c)** Overview of sampling time points over the course of our heat stress assay. Note that given our temperature ramp-up, at t = 3h animals had not reached the final target temperature of 34°C.

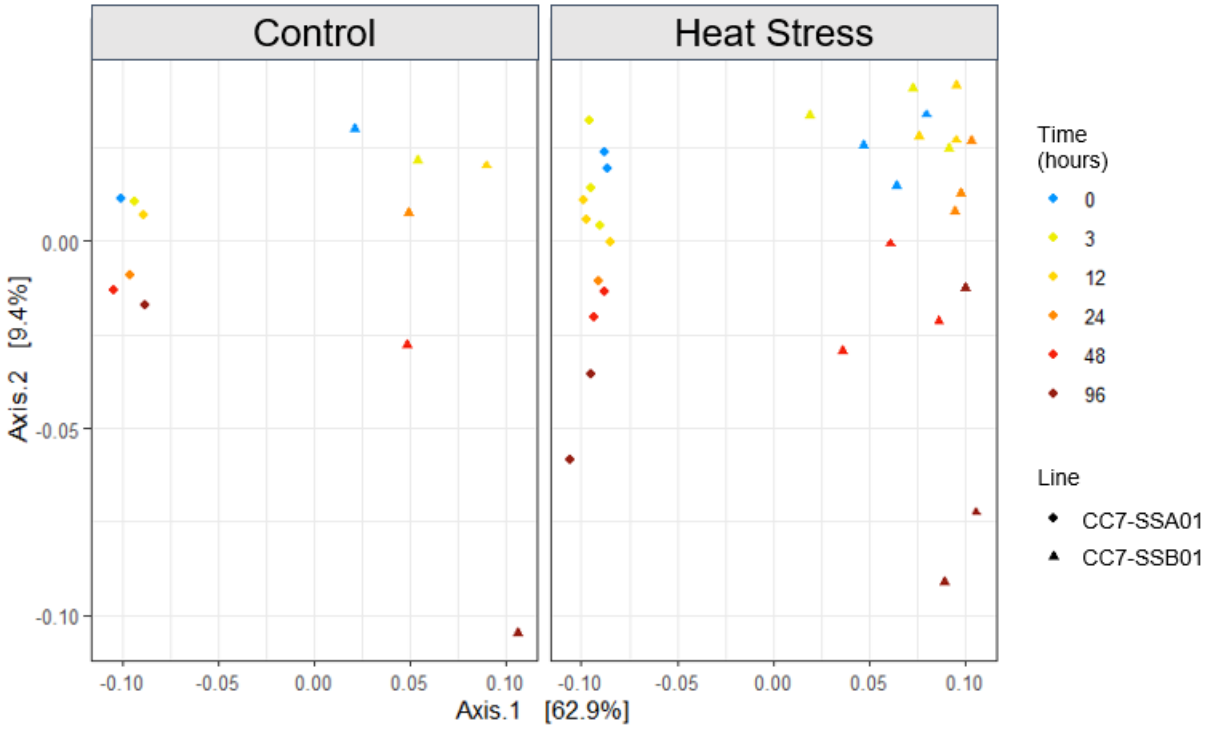

Figure 3.2. Principal coordinate analysis (PCoA) for *Aiptasia*'s prokaryotic communities over the course of heat stress, based on Bray-Curtis dissimilarity in the relative abundances of ASVs. Colors indicate different time points, while shapes represent one of the two *Aiptasia* lines used. Control and heat stressed samples are shown as separate panels.

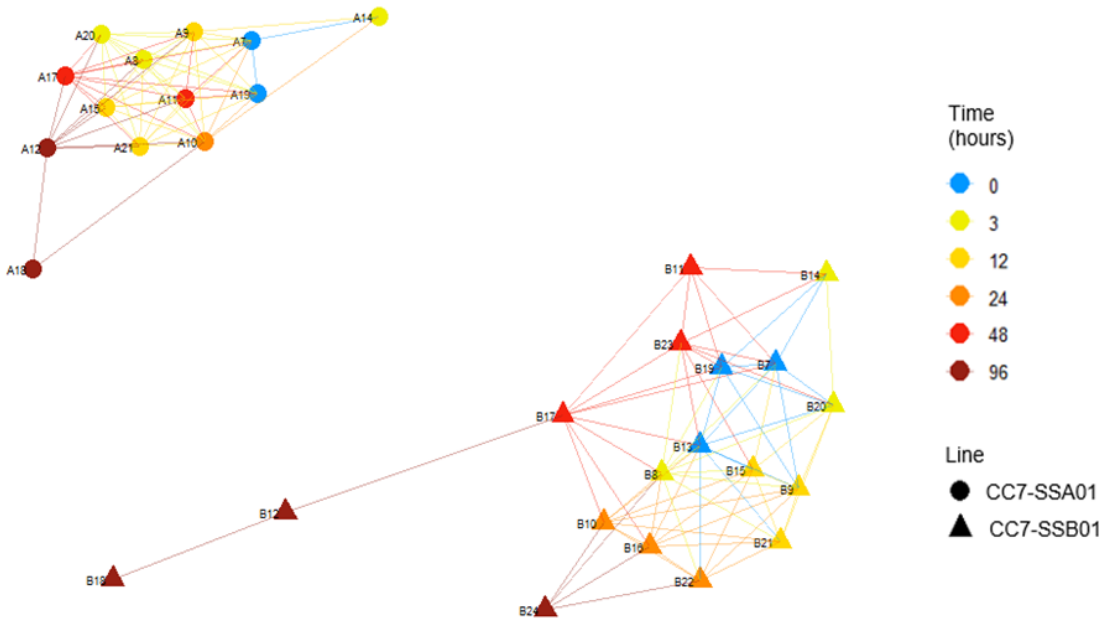

Figure 3.3. Co-occurrence networks for *Aiptasia* under heat stress. Plots implement Bray-Curtis dissimilarity to define links between the nodes, here corresponding to individual samples, with a distance threshold of 0.1. Colors indicate different time points, while shapes represent the two *Aiptasia* lines used.

Discussion

In his seminal 1990 paper on organismal responses to climate change, Dr. Robert D. Holt wrote:

Species may respond to climate change by shifting in abundance and distribution, by going extinct, or by evolving.

I would like to amend this statement to include an additional response mechanism – ***modifying their microbial associations***.

Corals are truly exemplary organisms in every sense of the word. They are the backbone of tropical and subtropical marine ecosystems and the surrounding communities that rely on them, from an economic to a cultural standpoint (Ayre and Hughes 2004, Hoegh-Guldberg et al. 2000). They also harbor extremely diverse microbial communities, making them an ideal candidate for studies on climate change resilience from a holobiont perspective (Peixoto et al. 2021). The coral microbiome has captured my intellectual curiosity due to its duality, hypothesized in playing a key role in the diversification of reef-building corals approximately 160 million years ago, while also contributing to their decline when faced with thermal stress (LaJeunesse et al. 2018, Bhattacharya et al. 2024, Hughes et al. 2018). Within the symbiosis discourse, I often hear phrases like “pathogenic” and “beneficial” when describing microbial associates, but I deem animal-microbiome interactions are more nuanced than this binary. We as humans like to place natural observations into boxes, which is a necessity when trying to draw parallels between systems and in defining mechanisms. But it is precisely this nuance that I wish to unearth, in this

thesis and beyond. When are interactions proposed to be beneficial, no longer beneficial? Are there microbiome members that play more of a prominent role than we have given them credit for? How are all these components working together and informing whole holobiont responses?

This latter question is gargantuan in that it extends past corals and other animals, and bleeds into all branches of the tree of life. My thesis aims to clear just a fraction of the tangled bramble that is the web of interactions within the coral holobiont. But in doing so, we strengthen previous inferences and pose potential mechanisms that merit further study. Over my three thesis chapters, I explore the factors that structure coral holobionts, from sea surface temperature to seasonal upwelling, and further interrogate the functional consequences of holobiont configurations during thermal stress. Together, my dissertation's overall goal is to gain insights on how host and microbiome dynamics together are shaping coral thermotolerance and governing their responses in a warmer, high carbon dioxide future.

An organism's surrounding environment strongly impacts their climate resilience, and corals are no exception. We see this at two different scales throughout this thesis: across *Pocillopora* coral's entire Indo-Pacific range (Chapter 1), and across gulfs in Panama's TEP (Chapter 2). Although we found evidence for isolation by distance across the Indo-Pacific, SST was the strongest driver of *Pocillopora* coral's algal symbiont communities. Chapter 1 was a meta-analysis where we did not have samples corresponding to an active bleaching event, thus the adaptive consequences of different algal communities could not be further validated. This is precisely what I build upon in Chapter 2, by ascertaining how abiotic differences across Panama's TEP are impacting the structure and in turn, the thermotolerance of *Pocillopora* coral

holobionts. Across Panama's TEP, I determined that corals experiencing seasonal upwelling were the most thermotolerant, substantiating our insights in Chapter 1 regarding the importance of abiotic regimes. But abiotic regimes can shape more than just the coral microbiome or the host's physiological/oxidative responses. As seen in Chapter 2, upwelling was found to drive the selection of loci with functions linked to enhanced coral thermotolerance. Besides the potential to offset bleaching during heat waves, we posit that upwelling can also impact coral thermotolerance on longer, evolutionary timescales.

Prior experimental work focusing on the impact of temperature variability on coral thermotolerance has explored this within the scope of diurnal and tidal variability (Voolstra et al. 2020, Klepac and Barshis 2020). We extend this notion by showing that persistent thermotolerance differences can be sustained when the variation in question is on the order of months, rather than days, and that these thermotolerance differences can have a genetic basis. Our findings provide further evidence that organisms living in variable environments may be better able to respond to environmental change, an observation that is likely generalizable to a broad range of biological systems (see Bernhardt et al. 2020).

An outstanding question within the realm of symbiosis research is how will climate change impact host-microbiome interactions? This is a complex question, as both the host and its microbiome have the ability to acclimate and/or adapt to changing abiotic conditions. Thus, disentangling these interactions within a single holobiont could encompass an ever-increasing list of response mechanisms. Much early work tackling this question has focused on disease. For instance, there is evidence that climate change is impacting the distribution of vectors, the range

over which diseases are transmitted, and even the efficiency of pathogen transfer, as in the case for tick-borne diseases like Lyme disease and mosquito-borne diseases like dengue (Pecl et al. 2017, Bhatt et al. 2013, Powell 2016, Crandall et al. 2024). Leveraging model systems can provide additional tools to disentangle the context-dependent nature of these interactions. For instance, for *Drosophila melanogaster*, interactions between different gut fly bacteria species mediate host health via life history trade-offs (Gould et al. 2018). Studying these interactions within natural populations remains difficult, given the diversity encapsulated by hosts and their microbiomes. However, standardized experimental approaches can begin to assist us in characterizing host-microbiome interactions in wild populations. As our CBASS experiment underscores (Chapter 2), by systematically exposing corals to temperatures above their MMM, we further support the notion that host-microbiome interactions are shaping organismal responses to climate change, here with regards to bleaching resistance.

How holobionts are responding to environmental stress can be conceptualized via one of two approaches: (1) via host-centric response mechanisms and (2) via microbiome-centric response mechanisms. In having both pieces of information, what is perhaps most interesting is where do these response mechanisms intersect (McFall-Ngai et al. 2012). From our work with the CBASS (Chapter 2), we find evidence that not only is upwelling shaping holobiont configurations, but that these different host-microbiome interactions result in different degrees of thermotolerance. This was most evident when considering coral-Symbiodiniaceae associations during our experiment. Different mtORF lineages not only had different baseline Symbiodiniaceae communities, but these shifted towards different communities during our assay. This speaks

more broadly to the role of host-specificity in shaping the microbiome, extending this notion to also encompass the host's role in driving microbiome shifts in response to abiotic stress.

Host physiological responses to climate change have been an early focus in climate change resilience studies. Approaches range from performance curves implementing organism's critical thermal maximum (CT_{max}), to measuring changes in respiration and nutrient assimilation rates (Chown et al. 2010, Herrando-Pérez et al. 2018, Crous 2019, Becklin et al. 2016). This has also been the case for studies on coral responses to thermal stress, where photosynthetic efficiency, symbiont density, and protein and chlorophyll *a* concentrations are commonly measured physiological variables as a function of increasing temperature (Krämer et al. 2022, McLachlan et al. 2022, Bove et al. 2022, Wall et al. 2018, van Woesik et al. 2022). Physiological responses have been the focus on previous CBASS studies (Voolstra et al. 2020, Evensen et al. 2021, Evensen et al. 2022), and yet the host's oxidative metabolism is less frequently explored in coral bleaching studies (but see Fernandes de Barros Marangoni et al. 2020, Marangoni et al. 2021, Marangoni et al. 2019, da Silva Fonseca et al. 2021). Besides being the first CBASS study to present oxidative metabolism dynamics under thermal stress (Chapter 2), our findings underscore that the host's biochemical responses via TAC and LPO provide a complimentary view to the insights gleaned from solely physiological characterization. Our physiological measurements capture how holobionts are resisting increasing temperatures, while oxidative metabolism measurements represent how holobionts are counteracting damage from increasing temperatures. More specifically, TAC and LPO provide information on how the accumulation of ROS results in damage to both algal and host tissues (Weis 2008, Davy et al. 2012, Suggett and Smith 2020). The production of ROS has been long reported as a signaling molecule for the immune system,

often linked to triggering a signaling-cascade of programmed cell death in eukaryotes and plants alike (Schieber and Chandel 2014, Kumar et al. 2020, Mahalingam and Fedoroff 2003, Ye et al. 2021). Given the conserved nature of ROS dynamics, future work on both corals and other taxa should consider explicitly measuring oxidative metabolism when interrogating host-microbiome interactions; for corals, previous studies linking host physiology with the microbiome have predominately leveraged transcriptomic datasets (Abbott et al. 2021, Kaniewska et al. 2015, Cunning and Baker 2020; but see Grottoli et al. 2018). In doing so, we were able to discern that a more robust redox apparatus, here via TAC, can be linked to higher proportions of *Durusdinium* spp. at elevated temperatures. However, recent work also argues for the importance of nutrient cycling, particularly carbon and nitrogen, in driving the establishment and maintenance of cnidarian-algal symbioses (see Rädecker et al. 2021, Rädecker et al. 2023). In taking a holobiont approach, we were able to characterize putative functional links between host-microbiome partnerships, which future work can further enrich by incorporating metabolomics and proteomics approaches.

In considering algal dynamics within corals more broadly, the literature has historically argued that observed shifts are adaptive at their core. This is under the premise that the host increases the relative abundance of certain algal taxa, as these members will confer greater thermotolerance to the host (Buddemeier and Fautin 1993, Cunning et al. 2015, Glynn et al. 2001, Baker et al. 2004). In Chapter 1, we functioned under this assumption, and thus concluded that changes in algal taxa for *Pocillopora* corals that had recently bleached represent a form of microbial accommodation to persist under environmental stress. Yet in Chapter 2, we provide a more concrete examination of potential fitness tradeoffs by integrating our physiological data.

We observe an algal shift from *Durusdinium* spp. to *Cladocopium* spp. for mtORF 1 corals, where instead of interpreting it as beneficial for the host, we interpreted it as a trade-off between enhanced nutrition and thermotolerance. These aforementioned dynamics are occurring on a considerably faster timescale (<24h) in Chapter 2 than Chapter 1 (months to many years) thus we cannot preclude potential photoacclimation for mtORF 1 associated algal symbionts, and their subsequent links and impacts on host physiology. Our holobiont approach in Chapter 2 therefore provides a framework for subsequent validation of potential trade-offs between algal dynamics and host physiology at various timescales.

Beyond host-microbiome interactions, interactions between microbiome members also have the potential to shape holobiont responses to thermal stress. As is the case for plants and the human gut, some of the most well-studied interactions are those between bacteria taxa. These interactions have been shown to strongly impact susceptibility to disease, nutrient cycling, and overall host fitness (Bäumler and Sperandio 2016, Moyano et al. 2017, Coyte and Rakoff-Nahoum 2019, Subramanian et al. 2014, Barratt et al. 2022). For corals, Symbiodiniaceae are arguably one of the most important microbiome members, given their role in satisfying up to 90% of the host's nutritional requirements (Grottoli et al. 2006, Jones et al. 2008). In this regard, Chapter 1 and Chapter 2 underscore the importance of algal symbionts in supporting and even driving host thermotolerance trends. Yet the contrast between algal and prokaryotic dynamics under thermal stress in Chapter 2 warranted further exploration to determine if interactions between these taxa can explain observed differences in bleaching sensitivity.

We concluded in Chapter 2 that the increased stochasticity of prokaryotes may reflect that algal symbionts are best positioned to support the host's response mechanisms, yet the inherent complexity when working with natural populations warrants caution. For instance, each coral colony in Chapter 2 corresponded to one of two mtORF lineages (mtORF 1 or mtORF 3), coming from one of six different reef sites across two gulfs in Panama's TEP, each experiencing different degrees of seasonal upwelling. Although our modeling allowed us to distill the relative contributions of these various parameters as they varied with thermal stress, there is likely unexplained variation we are not accounting for, e.g. microhabitat differences in nutrient, pH, and light availability, and genotype-specific responses. Laboratory model systems are a powerful tool to gain further insights into holobiont dynamics gleaned from natural systems. As such, in Chapter 3, we leveraged *Aiptasia* as a model system to control for genetic background and algal symbiont community composition, to more directly test how algal symbionts impact prokaryotic community dynamics under thermal stress.

A commonly cited hallmark of microbial dysbiosis under environmental stress is the Anna Karenina Principle (AKP), which proposes that increases in community variance for animal microbiomes under stress reflect a disease-like state. This is because increased stochasticity indicates the inability of the host and/or microbiome to regulate their community composition (Zaneveld et al. 2017). Support for this principle is commonly cited in microbiome studies, ranging from corals (Leinbach et al. 2023, Camp et al. 2020), to human microbiome-associated diseases (Ma 2020) and plants (Arnault et al. 2023). We find support for AKP in Chapter 2, and yet in Chapter 3, we were able to explore another factor that may be driving observed shifts in community variance: algal strain's thermotolerance. In controlling for hosted algal symbiont

strain, which is currently unachievable in corals, we found that more thermally sensitive cnidarians have an inherently more variable prokaryotic microbiome, providing a different perspective to AKP.

The prokaryotic dynamics in Chapter 2 may be capturing the increased stochasticity of natural communities, which are further amplified under thermal stress; by working with a model system in Chapter 3, we are controlling for some of the stochasticity we would otherwise expect. In our *Aiptasia* experiment, all animals were of the same clonal background and were laboratory stocks that had been at least two years under laboratory conditions. Additionally, *Aiptasia* are not stony corals but soft-bodied anemones, thus their prokaryotic community dynamics may be taxon specific, as perhaps reflected in the differences in community variance trends between Chapter 2 and 3. Lastly, there are inherent metabolic and proteomic differences between *Aiptasia* and corals that warrant caution in extrapolating our findings from Chapter 3. Of note, *Aiptasia* can be cultured indefinitely without an algal symbiont, which is currently impossible in corals given that at least 90% of their energy requirements are fulfilled by Symbiodiniaceae (Grottoli et al. 2006, Jones et al. 2008). Additionally, coral's calcium carbonate skeleton is energetically costly, requiring a unique genetic repertoire and various membrane proteins, which non-skeleton forming cnidarians like sea anemones lack (Tinoco et al. 2023, Schoepf et al. 2013). Although these differences exist, *Aiptasia* is still a well-positioned model system for coral-microbiome interactions during bleaching, as their transcriptomic response to thermal stress mirrors that of corals (see Cleves et al. 2020). By placing the findings of Chapters 2 and 3 in conversation with one another, we underscore the importance of combining studies of natural populations with model systems to leverage the strengths of each. In doing so, we can begin to reveal core

response mechanisms and guide more pointed explorations of coral thermotolerance mechanisms, while still gaining insights from observed ecological dynamics.

Conclusion

My thesis presents how by studying host and microbiome mechanisms together, we can begin to reveal their relative roles, and how their respective pathways drive differences in holobiont thermotolerance. This larger question required me to consider a diversity of timescales, from year-long observational data, to rapid bleaching assays spanning less than a day. But by the same token, the inherent complexity within the coral holobiont motivated me to use an emerging model organism to more directly determine the relative contributions of different microbiome members to overall holobiont functioning. My dissertation is pioneering in its integration of whole genome data, microbiome dynamics, and physiological and biochemical responses to thermal stress. My research provides foundational data for the TEP's *Pocillopora* corals, serving as an important point of comparison for long-term monitoring data and future CBASS studies within the region. Furthermore, my thesis motivates the use of *Aiptasia* as an emerging model cnidarian for studies on prokaryotic dynamics, positing some potential candidates for future probiotic development and validation. In studying corals and sea anemones, my work's holobiont approach emphasizes that by considering how microorganisms influence the ecology and evolution of organisms we can reveal novel perspectives into the factors that contribute to climate resilience.

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Appendices

Appendix A: Supplementary information for Chapter 1

Appendix B: Supplementary information for Chapter 2

Appendix C: Supplementary information for Chapter 3

Appendix A

Supplementary information for Chapter 1

Environmental and geographical factors structure cauliflower coral's algal symbioses across the Indo-Pacific

Content

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Table A1. Specimen information for downloaded *Pocillopora acuta*, *P. damicornis*, and *P. meandrina* derived ITS2 sequences from NCBI's Sequence Read Archive (SRA) using the ITS-DINO and ITS2Rev2 primer pair.

NCBI SRA	Loc	Yr	Spec	Exp_cond	Repro	Month	Season	S_region	L_region	Exact_date	Tbl_bin	T_bleach	DHW	DHW_cat	SST_a	Coord_X	Coord_Y	Primer	Pub
SRR7886695	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886696	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886697	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886698	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886699	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396

																			-019-0358-3.pdf?proof=t
SRR7886700	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886701	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886702	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886703	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886704	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886705	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/

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SRR7886706	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886707	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886708	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886709	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886710	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886711	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.lib

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SRR7886712	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886713	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886716	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886722	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886723	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886724	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-

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SRR7886725	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886726	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886727	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886728	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886729	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t

SRR7886730	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886731	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886732	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886733	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886734	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886735	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396

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SRR7886736	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886737	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886738	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886739	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886740	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886741	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/

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SRR7886742	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886743	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886744	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886745	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886746	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886747	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.lib

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SRR7886748	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886749	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886750	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886751	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886752	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886753	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-

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SRR7886754	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886755	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886756	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886757	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886758	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t

SRR7886759	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886760	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886761	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886762	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886763	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886764	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396

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SRR7886765	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886766	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886767	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886768	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886769	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886770	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/

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SRR7886771	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886772	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886773	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886774	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886775	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886776	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.lib

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SRR7886777	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886778	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886779	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886780	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886781	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886782	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-

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SRR7886783	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886784	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886785	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886786	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886787	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t

SRR7886788	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886789	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886791	Aus_GBR_Heron	2017	P_dam	Par	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886792	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886793	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886794	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396

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SRR7886795	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886796	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886797	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886798	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886799	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886800	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/

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SRR7886801	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886802	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886803	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886804	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886805	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886806	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.lib

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SRR7886807	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886808	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886809	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886810	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886811	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886812	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-

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SRR7886813	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886814	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886815	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886816	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886817	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t

SRR7886818	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886819	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886826	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886827	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886837	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886838	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396

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SRR7886847	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886848	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR7886849	Aus_GBR_Heron	2017	P_dam	Rec	B	Oct	Spring	Aus	WPac	NA	Long	15y	0	N	24.89	-23.45	151.92	ITS-DINO	https://www-nature-com.proxy3.library.mcgill.ca/articles/s41396-019-0358-3.pdf?proof=t
SRR5963023	NewCal	2014	P_dam	30C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.3	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963030	NewCal	2014	P_dam	30C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.3	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963031	NewCal	2014	P_dam	30C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.3	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963046	NewCal	2014	P_dam	27C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.3	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.

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SRR5963070	NewCal	2014	P_dam	27C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.3	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963071	NewCal	2014	P_dam	27C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.3	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963105	NewCal	2014	P_dam	Surface	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.3	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963022	NewCal	2014	P_dam	30C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.29	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963044	NewCal	2014	P_dam	27C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.29	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963045	NewCal	2014	P_dam	27C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.29	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963047	NewCal	2014	P_dam	27C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.29	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963094	NewCal	2014	P_dam	30C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.29	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.

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SRR5963095	NewCal	2014	P_dam	30C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.29	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963104	NewCal	2014	P_dam	Surface	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.29	166.43	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963048	NewCal	2014	P_dam	27C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.34	166.35	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963050	NewCal	2014	P_dam	27C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.34	166.35	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963051	NewCal	2014	P_dam	27C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.34	166.35	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963096	NewCal	2014	P_dam	30C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.34	166.35	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963097	NewCal	2014	P_dam	30C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.34	166.35	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963098	NewCal	2014	P_dam	30C	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.34	166.35	ITS-DINO	https://peercommunityjournal.org/articles/10.

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SRR5963103	NewCal	2014	P_dam	Surface	B	Nov	Spring	NewCal	WPac	NA	Long	15y	0	N	27.1	-22.34	166.35	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963042	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963043	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963049	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963099	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963100	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963101	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963102	Oman	2014	P_dam	Surface	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.

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SRR5963024	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963025	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963027	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963092	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963093	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963111	Oman	2014	P_dam	Surface	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963026	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963028	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.

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SRR5963029	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963106	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963107	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963108	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963109	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963110	Oman	2014	P_dam	Surface	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR7356901	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No
SRR7356909	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No
SRR7356922	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No
SRR7356929	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No

SRR7356950	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No
SRR7356938	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No
SRR7356937	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No
SRR7356996	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No
SRR7357011	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No
SRR7357017	Aus_GBR_Orp	2016	P_ac	Bleach	M	Jan	Summer	Aus	WPac	NA	Long	>15y	0.32	F	29.44	-18.601	146.489	ITS-DINO	No
SRR7356873	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR7356905	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR7356926	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR7356933	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR7356942	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR7356954	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR7356969	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR7356975	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR7356992	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR7357013	Aus_GBR_Orp	2015	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Long	>15y	0	N	28.38	-18.601	146.489	ITS-DINO	No
SRR8661812	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.111

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SRR8661821	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661820	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661819	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661818	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661817	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-

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SRR8661816	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661815	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661814	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661813	Aus_GBR_Heron	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.111

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SRR8661852	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661853	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661860	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661870	Aus_GBR_Heron	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Long	15y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661863	Aus_GBR_Heron	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Long	15y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-

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SRR8661864	Aus_GBR_Heron	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Long	15y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661865	Aus_GBR_Heron	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Long	15y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661899	Aus_GBR_Heron	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Long	15y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661895	Aus_GBR_Heron	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Long	15y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.111

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SRR8661894	Aus_GBR_Heron	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Long	15y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661893	Aus_GBR_Heron	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Long	15y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661892	Aus_GBR_Heron	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Long	15y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661938	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661937	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-

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SRR8661936	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661935	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661934	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661933	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.111

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SRR8661932	Aus_GBR_Heron	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Long	15y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR7356874	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR7356923	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR7356931	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR7356947	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR7356945	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR7356934	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR7356968	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR7356989	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR7356997	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR7357016	Aus_GBR_Orp	2016	P_ac	Bleach	M	Nov	Spring	Aus	WPac	NA	Recent	1y	0	N	28.04	-18.601	146.489	ITS-DINO	No
SRR8661792	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856

SRR8661793	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661794	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661795	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661796	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661797	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.lib

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SRR8661798	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661801	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661800	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661799	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856

SRR8661832	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661841	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661840	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661839	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661838	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.lib

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SRR8661837	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661836	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661835	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661834	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856

SRR8661833	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661858	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661857	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661856	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661855	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.lib

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SRR8661854	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661859	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661861	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661862	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856

SRR8661867	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661866	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661868	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661869	Aus_GBR_Orp	2017	P_ac	Rec	M	Apr	Fall	Aus	WPac	4/6/2017	Recent	1y	9.36	Many	28.09	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661882	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.lib

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SRR8661883	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661888	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661891	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661890	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856

SRR8661889	Aus_GBR_Orp	2017	P_ac	Ad	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661930	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661931	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR8661939	Aus_GBR_Orp	2017	P_ac	Lar	M	Apr	Fall	Aus	WPac	3Ap 2017-8 AM	Recent	1y	9.36	Many	28.86	-19.26	147.04	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/full/10.1111/1462-2920.14856
SRR7356883	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y

SRR7356899	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356902	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356903	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356906	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356910	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356921	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356924	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356932	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y

SRR7356925	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356949	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356948	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356944	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356943	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356939	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356936	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356935	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y

SRR7356953	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356967	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356970	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356990	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356991	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7357000	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356998	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356995	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y

SRR7357012	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7357018	Aus_GBR_Orp	2016	P_ac	Bleach	M	July	Winter	Aus	WPac	NA	Recent	6M	0	N	23.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7357015	Aus_GBR_Orp	2016	P_ac	Bleach	M	Sep	Spring	Aus	WPac	NA	Recent	6M	0	N	26.28	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7357014	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356976	Aus_GBR_Orp	2016	P_ac	Bleach	M	May	Fall	Aus	WPac	NA	Recent	6M	0	N	25.73	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356900	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356907	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356908	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y

SRR7356930	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356928	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356927	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356952	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356951	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356946	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356941	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356940	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y

SRR7356956	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356955	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356971	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356993	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356994	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7356999	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7357020	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y
SRR7357019	Aus_GBR_Orp	2016	P_ac	Bleach	M	March	Fall	Aus	WPac	NA	Bleaching	B	2.53	F	29.1	-18.601	146.489	ITS-DINO	https://link.springer.com/article/10.1007%2Fs00338-019-01783-y

SRR6489261	Panam	2016	P_me	Nat	SP	July	Winter	Panam	EPac	NA	Recent	6M	0	N	27.88	7.020917	-81.796194	ITS-DINO	https://peerj.com/articles/4816/
SRR6489262	Panam	2016	P_me	Nat	SP	July	Winter	Panam	EPac	NA	Recent	6M	0	N	27.88	7.020917	-81.796194	ITS-DINO	https://peerj.com/articles/4816/
SRR5970169	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794867	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970204	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303528	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970206	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303529	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970208	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.730353	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970210	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303531	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970223	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794868	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970230	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794869	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/

SRR5970262	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794864	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970264	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794866	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970266	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794865	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970278	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794863	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970282	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303535	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970284	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.5826139	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970286	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303533	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970288	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303534	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/

SRR5970290	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.582614	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970303	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303532	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970304	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.5826141	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970306	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.5826142	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970308	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.5826143	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970310	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.5826144	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970312	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.5826145	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970327	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.779487	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/

SRR5970329	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794861	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970331	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794872	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970333	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794871	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970335	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794862	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR3668232	Moorea	2013	P_me	Nat	B	July	Winter	FrPoly	EPac	NA	Long	10y	0	N	26	-17.480809	-149.805178	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/epdf/10.1111/1758-2229.12541
SRR3668236	Moorea	2013	P_me	Nat	B	July	Winter	FrPoly	EPac	NA	Long	10y	0	N	26	-17.480809	-149.805178	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/epdf/10.1111/1758-2229.12541
SRR3668239	Moorea	2013	P_me	Nat	B	July	Winter	FrPoly	EPac	NA	Long	10y	0	N	26	-17.480809	-149.805178	ITS-DINO	https://sfamjournals-onlinelibrary-

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SRR3668259	Moorea	2013	P_me	Nat	B	July	Winter	FrPoly	EPac	NA	Long	10y	0	N	26	-17.480809	-149.805178	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/epdf/10.1111/1758-2229.12541
SRR3668427	Moorea	2013	P_me	Nat	B	July	Winter	FrPoly	EPac	NA	Long	10y	0	N	26	-17.480809	-149.805178	ITS-DINO	https://sfamjournals-onlinelibrary-wiley-com.proxy3.library.mcgill.ca/doi/epdf/10.1111/1758-2229.12541
SRR5970158	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896945	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970221	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921449	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970225	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921447	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970227	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921448	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-

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SRR5970234	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921444	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970243	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921445	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970245	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921446	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970254	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896948	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970256	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896947	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970258	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896944	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970325	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896946	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970183	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.13	-22.2440644	166.418772	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970268	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.28	-22.1958808	166.339908	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970270	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.28	-22.1958807	166.339908	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970272	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.28	-22.1958806	166.339908	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970315	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.13	-22.2440643	166.418772	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970317	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.13	-22.2440639	166.418772	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970319	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.13	-22.244064	166.418772	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970321	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.13	-22.2440641	166.418772	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970323	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.13	-22.2440642	166.418772	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970336	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23	-22.2932946	166.470678	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970338	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23	-22.2932945	166.470678	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970340	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23	-22.2932944	166.470678	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970342	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23.28	-22.1958809	166.339908	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970344	NewCal	2013	P_dam	Nat	B	June	Winter	NewCal	WPac	21_June	Long	>15y	0	N	23	-22.2932947	166.470678	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970232	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894447	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970236	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.789445	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970238	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894449	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970241	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894451	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970250	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894445	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970252	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894444	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970259	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894448	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970280	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894446	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970178	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614178	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970176	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614177	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970174	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.676 7389	-151.45 5256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970172	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614179	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970181	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.676739	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970197	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614175	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970201	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614176	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970274	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.676 7397	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970276	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.676 7396	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970291	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.676 7395	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970294	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.676 7393	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970296	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.6767394	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970298	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.6767391	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970300	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.6767392	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970182	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574429	-149.619742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970193	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574427	-149.619742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970195	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.57443	-149.619742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970199	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574431	-149.619742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970247	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574426	-149.619742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970261	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574425	-149.619742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970263	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574428	-149.619742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970160	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9302	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970162	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9301	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970164	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9304	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970166	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9303	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970168	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9305	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970185	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9454389	120.748025	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970187	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.945439	120.748026	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970191	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.945392	120.748028	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970189	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.945391	120.748027	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970211	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.67	21.9938167	120.7063	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970213	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9306	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970215	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.67	21.9938169	120.7065	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970217	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.67	21.9938168	120.7064	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/

Table A2. Specimen information for *Pocillopora* spp. derived ITS2 sequences used for downstream analyses, all which used the ITS-DINO and ITS2Rev2 primer pair.

NCBI SRA	Loc	Yr	Spec	Exp_cond	Repro	Month	Season	S_region	L_region	Exact_date	Tbl_bin	T_bleach	DHW	DHW_cat	SST_a	Coord_X	Coord_Y	Primer	Pub
SRR5963042	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963043	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963049	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963099	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963100	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963101	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963102	Oman	2014	P_dam	Surface	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.28	Mod	30.8	23.5	58.75	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963024	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.

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SRR5963025	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963027	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963092	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963093	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963111	Oman	2014	P_dam	Surface	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	4.24	Mod	30.8	23.52	58.74	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963026	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963028	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963029	Oman	2014	P_dam	31C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963106	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.

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SRR5963107	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963108	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963109	Oman	2014	P_dam	34C	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5963110	Oman	2014	P_dam	Surface	B	June	Winter	IndianOc	IndianOc	NA	Long	15y	3.79	Mod	30.8	23.62	58.6	ITS-DINO	https://peercommunityjournal.org/articles/10.24072/pcjournal.79/
SRR5970169	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794867	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970204	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303528	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970206	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303529	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970208	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.730353	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/

SRR5970210	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303531	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970223	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794868	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970230	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794869	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970262	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794864	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970264	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794866	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970266	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794865	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970278	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794863	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970282	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303535	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970284	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.5826139	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970286	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303533	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970288	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303534	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970290	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.582614	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970303	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.11	11.7303532	43.2240806	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970304	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.582614	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970306	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.582614	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970308	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.582614	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970310	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.582614	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970312	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.35	11.582614	42.7960722	ITS-DINO	https://pubmed-ncbi-nlm-nih-

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SRR5970327	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.779487	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970329	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.7794861	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970331	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.779872	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970333	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.779871	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970335	Djib	2014	P_dam	Nat	B	Nov	Spring	IndianOc	IndianOc	23_Nov	Long	>15y	0	N	29.37	11.779862	42.9243472	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970158	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896945	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970221	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921449	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970225	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921447	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/

SRR5970227	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921448	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970234	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921444	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970243	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921445	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970245	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4921446	-149.868983	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970254	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896948	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970256	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896947	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970258	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896944	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970325	Moorea	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Long	10y	0	N	27.04	-17.4896946	-149.896847	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970232	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894447	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970236	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894445	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970238	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894449	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970241	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894451	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970250	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894445	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970252	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894444	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970259	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894448	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970280	Raia	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.25	-16.7894446	-151.391842	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970178	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614178	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970176	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614177	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-

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SRR5970174	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.6767389	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970172	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614179	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970181	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.676739	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970197	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614175	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970201	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.19	-16.614176	-151.542753	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970274	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.6767397	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970276	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.6767396	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970291	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.6767395	-151.455256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/

SRR5970294	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.676 7393	-151.45 5256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970296	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.676 7394	-151.45 5256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970298	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.676 7391	-151.45 5256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970300	Tahaa	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	27.22	-16.676 7392	-151.45 5256	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970182	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574 429	-149.61 9742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970193	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574 427	-149.61 9742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970195	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574 43	-149.61 9742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970199	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574 431	-149.61 9742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970247	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574 426	-149.61 9742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.libr

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SRR5970261	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574425	-149.619742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970263	Tahiti	2008	P_dam	Nat	B	June	Winter	FrPoly	EPac	NA	Recent	5y	0	N	26.86	-17.574428	-149.619742	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970160	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9302	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970162	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9301	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970164	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9304	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970166	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9303	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970168	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9305	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970185	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9454389	120.748025	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970187	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.945439	120.748026	ITS-DINO	https://pubmed-ncbi-nlm-nih-

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SRR5970191	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9454392	120.748028	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970189	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9454391	120.748027	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970211	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.67	21.9938167	120.7063	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970213	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.59	21.9306	120.744967	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970215	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.67	21.9938169	120.7065	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/
SRR5970217	Taiwan	2012	P_dam	Nat	B	Sep	Spring	Taiwan	NPac	24_Sep	Recent	5y	0	N	28.67	21.9938168	120.7064	ITS-DINO	https://pubmed-ncbi-nlm-nih-gov.proxy3.library.mcgill.ca/29463295/

Table A3. Specimen CSV metadata.

Column headers	
NCBI SRA	NCBI sequence read archive (SRA) accession number
Loc	Location
Yr	Year sampled
Spec	Species, as per the NCBI SRA entry
Exp_cond	Experimental condition, if applicable
Repro	Mode of reproduction
Month	Month sampled
Season	Season sampled, taking into account differences between Southern and Northern hemisphere
S_region	Smaller region categorization
L_region	Larger region categorization
Exact_date	Exact date sampled
Tbl_bin	Larger category, time since last bleaching event
T_bleach	Time since last bleaching event
DHW	Degree heating weeks when sampled
DHW_cat	Larger category, degree heating weeks when sampled
SST_a	Sea surface temperature when sampled, in Celsius
Coord_X	Longitude where sampled
Coord_Y	Latitide where sampled
Primer	ITS2 primer pair used
Pub	Original publication link, if applicable

Experimental conditions (Exp_cond)	
Rec	Coral recruit
Ad	Coral adult
Par	Coral parental colony
Bleach	Bleaching event
Nat	Natural conditions
Lar	Coral larvae
27C	Control temperature at 27°C
30C	Experimental heat stress at 30°C
31C	Control temperature at 31°C
34C	Experimental heat stress at 34°C
Surface	In-situ colony, collected from surface reef

Coral species (Spec)	
P_dam	*Pocillpora damicornis*
P_me	*Pocillpora meandrina*
P_ac	*Pocillpora acuta*

Location (Loc)	
Djib	Djibouti
Moorea	Mo'orea island
Tahaa	Taha'a island
Raia	Raiatea island
Tahiti	Tahiti island
Taiwan	Taiwan
Oman	Oman
NewCal	New Caledonia
Aus_GBR_Orp	Australia, Great Barrier Reef, Orpheus Island
Aus_GBR_Heron	Australia, Great Barrier Reef, Heron Island

Smaller region (S_region)	
Aus	Australia
NewCal	New Caledonia
FrPoly	French Polynesia
IndianOc	Indian Ocean
Taiwan	Taiwan

Larger region (L_region)	
WPac	Western Pacific
EPac	Eastern Pacific
NPac	Northern Pacific
IndianOc	Indian Ocean

Reproduction (Repro)	
B	Brooding
SP	Spawing
M	Mixture of brooding and spawning

Time since last mass bleaching event (T_bleach)	
15y	11 to 15 years since last mass bleaching event
10y	6 to 10 years since last mass bleaching event

5y	1 to 5 years since last mass bleaching event
1y	7 to 12 months since last mass bleaching event
6M	1 to 6 months since last mass bleaching event
B	Mass bleaching event ocurring during sampling period

Larger category, time since last mass bleaching event (Tbl_bin)	
Long	5+ years since last bleaching event
Recent	From 1 month - 5 years since last bleaching event
Bleaching	Currently bleaching

Larger category, degree heating weeks when sampled	
N	0 weeks
F	More than 0, less than 3 weeks
Mod	Over 3, less than 9 weeks
Many	Over 9 weeks

Primer	
ITS-DINO	ITS-DINO (Pochon et al., 2001) and ITS2Rev2 pair (Stat et al., 2009)
ITS2F	ITSIntFor2 (LaJeunesse, 2002) and ITS-2 pair (Coleman et al., 1994)
SYM_VAR	SYM_VAR_5.8S2 and SYM_VAR_REV pair (Hume et al., 2018)

Table A4. *Pocillopora* spp. derived ITS2 sequences' taxonomic assignment with SymPortal's database using vsearch and usearch. Only ASVs with Symbiodiniaceae hits are shown, with corresponding clade and phylotype descriptors. Symbiodiniaceae taxonomy is shown on the basis of ITS2-type profiles mirroring the SymPortal database's output, where "clade" and "type" delineations are shown. Yet based on recent taxonomic revision of the Symbiodiniaceae family, these profiles represent different genera and species. Briefly, ITS2-type A profiles correspond to *Symbiodinium* spp., ITS2-type B profiles correspond to *Breviolum* spp., ITS2-type C profiles correspond to *Cladocopium* spp., ITS2-type D profiles correspond to *Durusdinium* spp., and ITS2-type G profiles correspond to *Gerakladium* spp.

ASV	**ITSclade**	**ITStype**
asv135	A	A1
asv441	A	A1
asv649	A	A1
asv1212	A	A1
asv1847	A	A1
asv2260	A	A1
asv3045	A	A1
asv4205	A	A1
asv9973	A	A1

asv9651	A	A1
asv140	A	A1
asv702	A	A1
asv1100	A	A1
asv2151	A	A1
asv10527	A	A1
asv1582	A	A1
asv143	A	A1
asv569	A	A1
asv710	A	A1
asv1918	A	A1
asv2722	A	A1
asv464	A	A1
asv2440	A	A1
asv6849	A	A1
asv717	A	A1
asv24	A	A1
asv211	A	A1
asv214	A	A1
asv217	A	A1
asv437	A	A1
asv439	A	A1
asv503	A	A1
asv561	A	A1
asv582	A	A1
asv666	A	A1
asv707	A	A1
asv738	A	A1
asv887	A	A1
asv1157	A	A1
asv1473	A	A1
asv1557	A	A1
asv2062	A	A1
asv3049	A	A1
asv3124	A	A1
asv5589	A	A2
asv2785	A	A3
asv535	B	B1
asv5748	B	B1

asv8319	B	B1
asv171	C	C1
asv784	C	C1
asv929	C	C1
asv1314	C	C1
asv1841	C	C1
asv2222	C	C1
asv2231	C	C1
asv2386	C	C1
asv2519	C	C1
asv2520	C	C1
asv2964	C	C1
asv4503	C	C1
asv10448	C	C1
asv11805	C	C1
asv48	C	C1
asv82	C	C1
asv93	C	C1
asv102	C	C1
asv176	C	C1
asv258	C	C1
asv311	C	C1
asv332	C	C1
asv359	C	C1
asv426	C	C1
asv869	C	C1
asv910	C	C1
asv982	C	C1
asv1004	C	C1
asv1109	C	C1
asv1163	C	C1
asv1227	C	C1
asv1258	C	C1
asv1276	C	C1
asv1416	C	C1
asv1670	C	C1
asv1777	C	C1
asv1851	C	C1
asv1945	C	C1

asv2014	C	C1
asv2119	C	C1
asv2290	C	C1
asv2357	C	C1
asv3123	C	C1
asv3147	C	C1
asv4923	C	C1
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asv10449	C	C1
asv10496	C	C1
asv10503	C	C1
asv2585	C	C1
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asv494	C	C1
asv5498	C	C1
asv6423	C	C1
asv8772	C	C1
asv9638	C	C1
asv737	C	C1
asv1966	C	C1
asv1051	C	C1
asv1129	C	C1
asv1574	C	C1
asv2557	C	C1
asv2686	C	C1
asv19	C	C1
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asv204	C	C1
asv249	C	C1
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asv325	C	C1
asv354	C	C1
asv477	C	C1
asv663	C	C1

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asv1031	C	C1
asv1104	C	C1
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asv1259	C	C1
asv1406	C	C1
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asv3208	C	C1
asv3404	C	C1
asv5177	C	C1
asv5847	C	C1
asv7344	C	C1
asv339	C	C1
asv456	C	C1
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asv349	C	C1
asv121	C	C1
asv834	C	C1
asv1446	C	C1
asv1563	C	C1
asv1649	C	C1
asv1671	C	C1
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asv1791	C	C1
asv1906	C	C1
asv2007	C	C1
asv2203	C	C1
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asv3052	C	C1
asv3430	C	C1
asv3666	C	C1
asv4051	C	C1
asv4206	C	C1

asv5182	C	C1
asv5504	C	C1
asv1871	C	C1
asv10504	C	C1
asv139	C	C1
asv2503	C	C1
asv524	C	C1
asv11449	C	C1
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asv971	C	C1
asv1441	C	C1
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asv1740	C	C1
asv1822	C	C1
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asv10586	C	C1
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asv13	C	C1
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asv900	C	C1
asv1059	C	C1
asv1280	C	C1
asv1370	C	C1
asv1431	C	C1
asv1512	C	C1
asv1725	C	C1

asv1790	C	C1
asv1810	C	C1
asv1872	C	C1
asv1889	C	C1
asv1976	C	C1
asv2301	C	C1
asv2343	C	C1
asv2813	C	C1
asv2993	C	C1
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asv3241	C	C1
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asv3602	C	C1
asv3601	C	C1
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asv4158	C	C1
asv4442	C	C1
asv4563	C	C1
asv4564	C	C1
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asv5421	C	C1
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asv7890	C	C1
asv7893	C	C1
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asv9664	C	C1
asv9936	C	C1
asv9939	C	C1
asv9952	C	C1

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asv10443	C	C1
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asv10477	C	C1
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asv1546	C	C1
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asv1825	C	C3
asv2410	C	C3
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asv31	C	C3
asv45	C	C3
asv64	C	C3
asv291	C	C3
asv374	C	C3
asv422	C	C3
asv10006	C	C3
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asv3746	C	C3
asv1539	C	C3
asv2743	C	C3

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asv75	C	C4
asv80	C	C4
asv84	C	C4
asv83	C	C4
asv85	C	C4
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asv94	C	C4
asv104	C	C4
asv105	C	C4
asv106	C	C4
asv109	C	C4
asv119	C	C4
asv118	C	C4
asv122	C	C4
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asv225	C	C4
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asv230	C	C4

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asv237	C	C4
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asv365	C	C4
asv369	C	C4
asv375	C	C4
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asv382	C	C4
asv389	C	C4
asv386	C	C4

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asv397	C	C4
asv399	C	C4
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asv404	C	C4
asv406	C	C4
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asv612	C	C4
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asv618	C	C4
asv635	C	C4
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asv1248	C	C4
asv1272	C	C4
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asv1435	C	C4
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asv3469	C	C4
asv3472	C	C4
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asv3566	C	C4
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asv3951	C	C4
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asv2371	D	D1
asv3567	D	D1
asv5849	D	D1
asv9195	D	D1
asv9420	D	D1
asv10515	D	D1
asv10521	D	D1
asv144	D	D1
asv110	D	D1
asv8321	D	D1
asv8782	D	D1
asv9411	D	D1
asv9961	D	D1
asv10461	D	D1
asv10488	D	D1
asv1878	D	D1
asv3073	D	D1
asv1589	D	D1
asv3499	D	D1
asv7166	D	D1
asv9424	D	D1
asv9958	D	D1
asv10489	D	D1
asv81	D	D1
asv1362	D	D1
asv4259	D	D1
asv9960	D	D1
asv10517	D	D1
asv107	D	D1
asv4315	D	D1
asv9975	D	D1
asv10451	D	D1
asv10547	D	D1
asv2099	D	D1
asv3822	D	D1
asv61	D	D1
asv8550	D	D1
asv9957	D	D1

asv10522	D	D1
asv10536	D	D1
asv55	D	D1
asv90	D	D1
asv162	D	D1
asv229	D	D1
asv529	D	D1
asv742	D	D1
asv1116	D	D1
asv1545	D	D1
asv1860	D	D1
asv2241	D	D1
asv3011	D	D1
asv4778	D	D1
asv9639	D	D1
asv10482	D	D1
asv10499	D	D1
asv10512	D	D1
asv10523	D	D1
asv10526	D	D1
asv10565	D	D1
asv76	D	D1
asv268	D	D1
asv273	D	D1
asv2074	D	D1
asv2370	D	D1
asv2421	D	D1
asv2851	D	D1
asv9959	D	D1
asv10495	D	D1
asv10508	D	D1
asv10514	D	D1
asv205	D	D2
asv754	D	D2
asv1623	D	D2
asv5047	D	D2
asv8773	D	D2
asv9947	D	D2
asv10463	D	D2

asv10501	D	D2
asv10519	D	D2
asv49	D	D2
asv727	D	D2
asv1735	D	D2
asv3904	D	D2
asv4314	D	D2
asv7703	D	D2
asv8317	D	D2
asv8542	D	D2
asv9945	D	D2
asv282	D	D2
asv335	D	D2
asv2068	D	D2
asv2762	D	D2
asv301	D	D2
asv16	D	D2
asv490	D	D2
asv841	D	D2
asv1444	D	D2
asv2388	D	D2
asv2869	D	D2
asv3537	D	D2
asv10516	D	D2
asv10520	D	D2
asv23	D	D4
asv425	D	D4
asv491	D	D4
asv508	D	D4
asv509	D	D4
asv1364	D	D4
asv1397	D	D4
asv1432	D	D4
asv1586	D	D4
asv1842	D	D4
asv2173	D	D4
asv5046	D	D4
asv5418	D	D4
asv9404	D	D4

asv9962	D	D4
asv1888	D	D4
asv654	D	D4
asv849	D	D4
asv9637	D	D4
asv9660	D	D4
asv10511	D	D4
asv14	D	D6
asv175	D	D6
asv222	D	D6
asv322	D	D6
asv430	D	D6
asv516	D	D6
asv980	D	D6
asv1518	D	D6
asv1747	D	D6
asv1797	D	D6
asv2344	D	D6
asv2576	D	D6
asv6850	D	D6
asv9630	D	D6
asv9941	D	D6
asv9944	D	D6
asv9984	D	D6
asv5750	F	F3
asv7898	F	F5
asv2303	G	G3
asv4924	G	G3
asv9667	G	G3
asv6047	G	G3
asv384	G	G3
asv450	G	G3
asv461	G	G3
asv730	G	G3
asv866	G	G3
asv1262	G	G3
asv4047	G	G3

Table A5. *Pocillopora* spp. derived ITS2 sequences' taxonomic assignment with NCBI BLAST. **Only** ASVs with Symbiodiniaceae hits are shown, with corresponding clade and phylotype descriptors. Symbiodiniaceae taxonomy is shown on the basis of ITS2-type profiles mirroring the SymPortal database's output, where "clade" and "type" delineations are shown. Yet based on recent taxonomic revision of the Symbiodiniaceae family, these profiles represent different genera and species. Briefly, ITS2-type A profiles correspond to *Symbiodinium* spp., ITS2-type B profiles correspond to *Breviolum* spp., ITS2-type C profiles correspond to *Cladocopium* spp., ITS2-type D profiles correspond to *Durusdinium* spp., and ITS2-type G profiles to *Gerakladium* spp.

ASV	ITSclade	ITStype
asv1001	A	A2
asv1074	A	A1
asv1188	A	A1
asv1235	A	A2
asv1261	A	A1
asv1341	A	A2
asv137	A	A1
asv148	A	A1
asv1488	A	A2
asv149	A	A1
asv1617	A	A2
asv1660	A	A1
asv1689	A	A
asv1997	A	A1
asv2005	A	A1
asv221	A	A2
asv224	A	A2
asv228	A	A
asv2280	A	A2
asv2357	A	A1
asv2378	A	A1
asv25	A	A2
asv2553	A	A1
asv2754	A	A1
asv2830	A	A3
asv3083	A	A1
asv3798	A	A1
asv4369	A	A2
asv4370	A	A1
asv448	A	A1
asv449	A	A2

asv454	A	A2
asv492	A	A1
asv547	A	A2
asv604	A	A2
asv606	A	A2
asv618	A	A1
asv625	A	A1
asv640	A	A2
asv693	A	A1
asv756	A	A2
asv765	A	A2
asv779	A	A1
asv790	A	A1
asv793	A	A1
asv809	A	A2
asv831	A	A2
asv838	A	A2
asv860	A	A2
asv1	C	C1
asv1005	C	C
asv101	C	C
asv1019	C	C3
asv102	C	C
asv1023	C	C1
asv1033	C	C1
asv1037	C	C4
asv1039	C	C4
asv1042	C	C4
asv1046	C	C
asv105	C	C
asv1055	C	C
asv106	C	C1
asv1060	C	C
asv1067	C	C
asv107	C	C1
asv1078	C	C3
asv108	C	C1
asv1085	C	C1
asv1090	C	C

asv1093	C	C1
asv1098	C	C1
asv1108	C	C1
asv1110	C	C
asv112	C	C1
asv1124	C	C1
asv114	C	C
asv1144	C	C
asv1149	C	C
asv1153	C	C1
asv1156	C	C
asv1158	C	C3
asv1167	C	C1
asv117	C	C1
asv1172	C	C4
asv1175	C	C
asv1185	C	C
asv119	C	C
asv12	C	C1
asv120	C	C
asv1202	C	C
asv1205	C	C
asv1209	C	C
asv121	C	C4
asv1216	C	C
asv1227	C	C1
asv1228	C	C1
asv123	C	C
asv1236	C	C3
asv1239	C	C1
asv1247	C	C1
asv125	C	C
asv1252	C	C1
asv1256	C	C1
asv1265	C	C1
asv127	C	C1
asv128	C	C
asv1284	C	C
asv1285	C	C

asv1293	C	C
asv1295	C	C
asv1296	C	C
asv13	C	C
asv1302	C	C
asv1309	C	C
asv131	C	C
asv1310	C	C1
asv132	C	C1
asv133	C	C
asv134	C	C3
asv135	C	C
asv136	C	C
asv1360	C	C1
asv1363	C	C
asv1378	C	C3
asv138	C	C1
asv1389	C	C1
asv139	C	C
asv1405	C	C1
asv1408	C	C
asv1426	C	C
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asv15	C	C3
asv150	C	C4
asv1502	C	C4
asv1505	C	C
asv1511	C	C
asv1517	C	C
asv1519	C	C

asv152	C	C
asv1523	C	C1
asv153	C	C
asv154	C	C
asv1544	C	C4
asv1545	C	C1
asv155	C	C1
asv1561	C	C1
asv157	C	C3
asv159	C	C
asv1594	C	C1
asv1595	C	C
asv1599	C	C1
asv160	C	C4
asv1601	C	C3
asv161	C	C4
asv1610	C	C1
asv1616	C	C
asv163	C	C
asv1633	C	C
asv164	C	C
asv1653	C	C
asv1668	C	C4
asv167	C	C1
asv1678	C	C
asv1686	C	C1
asv1687	C	C
asv1690	C	C
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asv1715	C	C4
asv1719	C	C
asv1729	C	C1
asv173	C	C4
asv1737	C	C1

asv175	C	C1
asv176	C	C
asv1762	C	C1
asv1768	C	C1
asv177	C	C4
asv178	C	C
asv1784	C	C1
asv1786	C	C1
asv179	C	C
asv1792	C	C
asv1799	C	C4
asv18	C	C
asv180	C	C
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asv1858	C	C1
asv1863	C	C1
asv187	C	C1
asv1870	C	C1
asv1875	C	C1
asv188	C	C
asv1886	C	C3
asv1896	C	C1
asv1897	C	C1
asv19	C	C1
asv1903	C	C
asv1904	C	C1
asv1905	C	C
asv1906	C	C3
asv191	C	C
asv1913	C	C
asv192	C	C
asv1920	C	C1

asv1921	C	C4
asv193	C	C4
asv1938	C	C1
asv194	C	C
asv1952	C	C1
asv1960	C	C1
asv1969	C	C
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asv1982	C	C4
asv1983	C	C1
asv1990	C	C1
asv1995	C	C4
asv2	C	C
asv200	C	C4
asv2013	C	C
asv202	C	C1
asv2023	C	C
asv204	C	C1
asv2043	C	C4
asv2049	C	C3
asv2051	C	C
asv2052	C	C
asv206	C	C
asv2071	C	C
asv2075	C	C1
asv2076	C	C
asv209	C	C1
asv2095	C	C4
asv211	C	C
asv2117	C	C
asv215	C	C
asv2151	C	C
asv2157	C	C4
asv2158	C	C1
asv218	C	C4
asv2187	C	C
asv22	C	C
asv2226	C	C
asv223	C	C

asv2248	C	C1
asv2255	C	C
asv226	C	C
asv2268	C	C1
asv227	C	C1
asv229	C	C1
asv2309	C	C
asv232	C	C
asv2329	C	C1
asv233	C	C
asv2330	C	C
asv2339	C	C
asv2340	C	C4
asv2341	C	C
asv235	C	C
asv2356	C	C1
asv236	C	C
asv2367	C	C1
asv2368	C	C3
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asv239	C	C1
asv2399	C	C1
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asv2441	C	C
asv246	C	C1
asv248	C	C4
asv2486	C	C
asv2488	C	C
asv250	C	C
asv254	C	C
asv2552	C	C

asv2564	C	C
asv257	C	C
asv258	C	C3
asv26	C	C1
asv2600	C	C4
asv2608	C	C
asv2609	C	C
asv2610	C	C4
asv2622	C	C
asv2629	C	C
asv2631	C	C4
asv2632	C	C
asv264	C	C
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asv2662	C	C1
asv2663	C	C
asv2665	C	C
asv267	C	C
asv2682	C	C3
asv269	C	C
asv2698	C	C1
asv2699	C	C4
asv2701	C	C1
asv271	C	C
asv2717	C	C1
asv2718	C	C1
asv272	C	C
asv273	C	C3
asv2744	C	C
asv2755	C	C
asv276	C	C
asv280	C	C4
asv2804	C	C1
asv2805	C	C4
asv2806	C	C
asv281	C	C
asv2815	C	C1

asv2825	C	C1
asv2826	C	C
asv2827	C	C
asv283	C	C
asv284	C	C3
asv288	C	C4
asv2881	C	C1
asv29	C	C
asv290	C	C
asv2915	C	C1
asv2916	C	C3
asv2918	C	C4
asv2938	C	C3
asv295	C	C4
asv296	C	C
asv2965	C	C
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asv30	C	C4
asv300	C	C1
asv3003	C	C
asv301	C	C
asv302	C	C
asv3033	C	C
asv3049	C	C4
asv305	C	C4
asv3068	C	C1
asv31	C	C1
asv310	C	C
asv3104	C	C
asv3106	C	C1
asv3107	C	C
asv312	C	C
asv3134	C	C1
asv3135	C	C1
asv3138	C	C4
asv314	C	C4
asv3160	C	C1

asv317	C	C4
asv3180	C	C4
asv3181	C	C
asv3200	C	C1
asv3201	C	C4
asv321	C	C1
asv3217	C	C1
asv3219	C	C
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asv323	C	C
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asv3246	C	C
asv3247	C	C
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asv328	C	C1
asv33	C	C1
asv3304	C	C1
asv3306	C	C1
asv3307	C	C
asv332	C	C
asv3329	C	C1
asv3331	C	C4
asv334	C	C
asv335	C	C
asv3357	C	C4
asv3358	C	C4
asv336	C	C1
asv337	C	C
asv340	C	C4
asv341	C	C
asv3413	C	C
asv3414	C	C
asv343	C	C
asv3442	C	C1
asv3443	C	C1
asv3444	C	C4
asv347	C	C

asv3474	C	C
asv348	C	C4
asv35	C	C1
asv351	C	C1
asv3512	C	C1
asv3539	C	C
asv355	C	C
asv3577	C	C4
asv3578	C	C1
asv3580	C	C
asv3581	C	C4
asv3582	C	C4
asv3583	C	C3
asv3584	C	C
asv3608	C	C4
asv361	C	C
asv362	C	C
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asv3796	C	C4
asv3799	C	C1
asv38	C	C1
asv381	C	C1
asv3828	C	C1
asv3829	C	C1
asv383	C	C1

asv3830	C	C1
asv3831	C	C4
asv3832	C	C1
asv3871	C	C
asv388	C	C4
asv39	C	C
asv3925	C	C1
asv393	C	C3
asv395	C	C4
asv399	C	C1
asv4	C	C4
asv4005	C	C4
asv4006	C	C1
asv402	C	C1
asv404	C	C1
asv4048	C	C
asv4049	C	C1
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asv4097	C	C1
asv41	C	C
asv410	C	C3
asv411	C	C
asv414	C	C4
asv4154	C	C
asv4157	C	C4
asv4159	C	C1
asv42	C	C
asv4204	C	C
asv4208	C	C
asv4209	C	C
asv423	C	C3
asv424	C	C1
asv4253	C	C1
asv4254	C	C1
asv426	C	C4

asv427	C	C1
asv428	C	C4
asv43	C	C4
asv4307	C	C1
asv4308	C	C3
asv4310	C	C
asv4311	C	C
asv433	C	C
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asv460	C	C4
asv462	C	C4
asv468	C	C4
asv47	C	C4
asv471	C	C3
asv472	C	C
asv475	C	C3
asv476	C	C1
asv477	C	C
asv479	C	C4
asv48	C	C
asv486	C	C4
asv490	C	C3
asv491	C	C3
asv493	C	C

asv495	C	C
asv498	C	C1
asv499	C	C
asv50	C	C3
asv500	C	C3
asv505	C	C
asv507	C	C
asv51	C	C1
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asv52	C	C4
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asv540	C	C
asv543	C	C1
asv554	C	C
asv556	C	C1
asv56	C	C1
asv561	C	C
asv562	C	C1
asv563	C	C1
asv565	C	C
asv587	C	C1
asv60	C	C
asv605	C	C1
asv607	C	C1
asv609	C	C1
asv611	C	C
asv613	C	C1
asv63	C	C1
asv630	C	C
asv632	C	C
asv633	C	C
asv638	C	C

asv649	C	C1
asv653	C	C
asv654	C	C3
asv657	C	C
asv660	C	C4
asv661	C	C1
asv666	C	C
asv67	C	C
asv68	C	C
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asv699	C	C1
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asv703	C	C
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asv774	C	C
asv777	C	C1
asv78	C	C
asv784	C	C1
asv787	C	C
asv788	C	C
asv789	C	C

asv79	C	C1
asv792	C	C1
asv799	C	C1
asv8	C	C1
asv80	C	C
asv801	C	C
asv806	C	C
asv807	C	C1
asv808	C	C
asv818	C	C
asv82	C	C1
asv825	C	C1
asv827	C	C1
asv83	C	C
asv834	C	C
asv837	C	C
asv85	C	C
asv859	C	C1
asv86	C	C1
asv863	C	C
asv864	C	C4
asv87	C	C
asv873	C	C1
asv874	C	C
asv877	C	C1
asv88	C	C1
asv884	C	C1
asv887	C	C
asv89	C	C4
asv899	C	C1
asv9	C	C
asv90	C	C
asv902	C	C1
asv905	C	C1
asv911	C	C1
asv914	C	C
asv916	C	C1
asv92	C	C
asv922	C	C1

asv925	C	C
asv929	C	C
asv934	C	C1
asv94	C	C1
asv940	C	C1
asv943	C	C1
asv945	C	C4
asv946	C	C1
asv948	C	C1
asv950	C	C
asv956	C	C
asv961	C	C
asv967	C	C
asv968	C	C1
asv970	C	C
asv976	C	C
asv977	C	C4
asv985	C	C1
asv989	C	C1
asv992	C	C
asv999	C	C
asv1031	D	D
asv104	D	D
asv1049	D	D1
asv1050	D	D1
asv109	D	D
asv110	D	D
asv111	D	D1
asv1131	D	D
asv1171	D	D
asv1194	D	D1
asv1203	D	D1
asv1204	D	D1
asv1221	D	D
asv1258	D	D
asv1286	D	D1
asv129	D	D
asv1319	D	D
asv1342	D	D1

asv1354	D	D
asv1359	D	D1
asv1364	D	D1
asv1391	D	D
asv14	D	D1
asv142	D	D
asv1420	D	D1
asv145	D	D1
asv1460	D	D1
asv1465	D	D
asv1466	D	D
asv1471	D	D1
asv1475	D	D
asv1498	D	D
asv1532	D	D
asv1533	D	D1
asv156	D	D1
asv1581	D	D1
asv1589	D	D1
asv16	D	D1
asv1600	D	D1
asv1609	D	D1
asv166	D	D
asv1661	D	D
asv1667	D	D
asv1738	D	D
asv1749	D	D
asv1757	D	D
asv1763	D	D
asv1777	D	D1
asv1778	D	D
asv1785	D	D
asv1791	D	D
asv1805	D	D
asv183	D	D1
asv1852	D	D1
asv1853	D	D1
asv1864	D	D1
asv1874	D	D1

asv1879	D	D
asv1931	D	D
asv1948	D	D1
asv1973	D	D
asv201	D	D1
asv2026	D	D1
asv2032	D	D
asv2044	D	D
asv205	D	D
asv2063	D	D1
asv2105	D	D1
asv2124	D	D
asv2150	D	D1
asv2169	D	D
asv2213	D	D1
asv2290	D	D
asv23	D	D1
asv231	D	D1
asv2310	D	D1
asv2312	D	D
asv2328	D	D1
asv237	D	D
asv238	D	D
asv2401	D	D1
asv245	D	D2
asv2487	D	D
asv249	D	D
asv2523	D	D
asv2524	D	D1
asv2525	D	D1
asv259	D	D
asv2599	D	D1
asv260	D	D
asv2621	D	D1
asv2630	D	D1
asv2664	D	D1
asv27	D	D
asv270	D	D
asv2700	D	D1

asv279	D	D
asv2828	D	D2
asv2829	D	D
asv286	D	D
asv2862	D	D1
asv293	D	D
asv2937	D	D2
asv294	D	D1
asv297	D	D2
asv2985	D	D
asv2986	D	D1
asv3008	D	D1
asv3084	D	D
asv3105	D	D
asv3136	D	D
asv3137	D	D
asv318	D	D1
asv3248	D	D
asv327	D	D
asv3279	D	D
asv3305	D	D1
asv3328	D	D1
asv345	D	D1
asv357	D	D
asv3579	D	D
asv359	D	D2
asv3639	D	D1
asv3702	D	D
asv3797	D	D
asv390	D	D
asv3926	D	D1
asv396	D	D
asv40	D	D1
asv4003	D	D
asv4004	D	D1
asv415	D	D1
asv4155	D	D
asv4156	D	D
asv417	D	D

asv422	D	D
asv429	D	D
asv4309	D	D
asv431	D	D
asv437	D	D
asv4431	D	D1
asv4432	D	D1
asv447	D	D
asv453	D	D1
asv459	D	D1
asv463	D	D1
asv467	D	D
asv474	D	D1
asv49	D	D1
asv501	D	D1
asv504	D	D
asv529	D	D1
asv533	D	D1
asv538	D	D1
asv542	D	D1
asv55	D	D
asv553	D	D1
asv558	D	D
asv559	D	D1
asv567	D	D
asv571	D	D1
asv574	D	D1
asv575	D	D2
asv585	D	D1
asv598	D	D1
asv6	D	D
asv62	D	D
asv639	D	D1
asv66	D	D1
asv674	D	D
asv675	D	D
asv680	D	D1
asv682	D	D2
asv7	D	D1

asv702	D	D1
asv730	D	D1
asv738	D	D
asv74	D	D
asv767	D	D
asv780	D	D1
asv81	D	D
asv816	D	D1
asv820	D	D
asv822	D	D1
asv836	D	D1
asv84	D	D
asv848	D	D1
asv857	D	D1
asv862	D	D1
asv904	D	D
asv91	D	D
asv920	D	D1
asv95	D	D
asv952	D	D2
asv955	D	D
asv984	D	D
asv1059	G	G
asv1305	G	G
asv2311	G	G
asv2342	G	G3
asv3330	G	G
asv385	G	G
asv461	G	G
asv489	G	G
asv791	G	G
asv928	G	G

Table A6. Generalized least squares (GLS) model results of *Pocillopora* spp. derived ITS2 sequences' squared richness.

Model: Richness ~ S_region/Loc + SST_a + Tbl_bin

AIC: 695.5996

BIC: 762.1848

Log-likelihood: -317.7998

Variance function:

Structure: Different standard deviations per stratum

Formula: ~1 | Loc

	Value	Standard error	t-value	p-value
(Intercept)	-230.44070	1019.2544	-0.2260875	0.8218
S_regionIndianOc	-36.62356	85.2322	-0.4296916	0.6688
S_regionTaiwan	46.63350	66.8471	0.6976145	0.4878
SST_a	11.45306	37.6931	0.3038502	0.7622
Tbl_binRecent	18.21155	14.7878	1.2315271	0.2224
S_regionIndianOc:LocOman	90.59577	57.3935	1.5785027	0.1191
S_regionFrPoly:LocRaia	-13.86669	19.7166	-0.7033001	0.4843
S_regionFrPoly:LocTahaa	-20.81695	18.0428	-1.1537511	0.2526

Residual standard error: 23.04814

Degrees of freedom: 91 total; 68 residual

Table A7. Generalized least squares (GLS) model results of *Pocillopora* spp. derived ITS2 sequences' Shannon diversity indices.

Model: Shannon ~ S_region/Loc + SST_a + Tbl_bin

AIC: 79.68605

BIC: 146.2713

Log-likelihood: -9.843026

Variance function:

Structure: Different standard deviations per stratum

Formula: ~1 | Loc

	Value	Standard error	t-value	p-value
(Intercept)	13.018364	11.001708	1.183304	0.2408
S_regionIndianOc	0.145509	0.919986	0.158164	0.8748

S_regionTaiwan	1.313063	0.721539	1.819808	0.0732
SST_a	-0.415845	0.406855	-1.022097	0.3104
Tbl_binRecent	-0.216803	0.159618	-1.358267	0.1789
S_regionIndianOc:LocOman	2.021886	0.619498	3.263747	0.0017
S_regionFrPoly:LocRaia	0.194362	0.212819	0.913277	0.3643
S_regionFrPoly:LocTahaa	0.158328	0.194752	0.812973	0.4191

Residual standard error:
0.2487788
Degrees of freedom: 91 total;
68 residual

Table A8. Generalized least squares (GLS) model results of *Pocillopora* spp. derived ITS2 sequences' inverse Simpson indices.

Model: Inverse Simpson ~ S_region/Loc + SST_a + Tbl_bin

AIC: 281.1201

BIC: 347.7053

Log-likelihood: -110.56

Variance function:

Structure: Different standard deviations per stratum

Formula: ~1 | Loc

	Value	**Standard error**	**t-value**	**p-value**
(Intercept)	35.86945	48.38468	0.7413390	0.4610
S_regionIndianOc	0.67091	4.04603	0.1658198	0.8688
S_regionTaiwan	3.52021	3.17328	1.1093315	0.2712
SST_a	-1.18857	1.78932	-0.6642616	0.5088
Tbl_binRecent	-0.41047	0.70199	-0.5847217	0.5607
S_regionIndianOc:LocOman	5.66135	2.72451	2.0779356	0.0415
S_regionFrPoly:LocRaia	-0.20866	0.93596	-0.2229394	0.8243
S_regionFrPoly:LocTahaa	-0.25409	0.85651	-0.2966533	0.7676

Residual standard error: 1.09411

Degrees of freedom: 91 total; 68 residual

Table A9. Permutational multivariate analysis of variance (PERMANOVA) of *Pocillopora* spp. derived ITS2 sequences, using Bray-Curtis distances and 999 permutations.

Model: asv_css ~ S_region/Loc + SST_a + Tbl_bin

Variable	Degrees of freedom	Sum of squares	R^2	F-statistic	Pr (>F)
S_region	2	12.991	0.40081	51.6259	0.001
SST_a	1	7.723	0.23829	61.3842	0.001
Tbl_bin	1	0.311	0.00960	2.4742	0.031
S_region:Loc	3	0.943	0.02910	2.4986	0.003
Residuals	83	10.443	0.32220	N/A	N/A
Total	90	32.412	1	N/A	N/A

Table A10. Post-hoc analysis of pairwise permutational multivariate analysis of variance (PERMANOVA) across locations for *Pocillopora* spp. derived ITS2 sequences**.** We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons.

Oman vs Mo'orea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	4.776575	0.624263	44.8588365	0.001
Residual	27	2.874964	0.375737	N/A	N/A
Total	28	7.651538	1	N/A	N/A

Oman vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.399521	0.116339	4.081311	0.02
Residual	31	3.034599	0.883661	N/A	N/A
Total	32	3.43412	1	N/A	N/A

Oman vs Djibouti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	8.091838	0.515253	48.89492	0.001
Residual	46	7.612744	0.484747	N/A	N/A
Total	47	15.70458	1	N/A	N/A

Oman vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	5.698922	0.668645	58.51943	0.001
Residual	29	2.824169	0.331355	N/A	N/A
Total	30	8.523091	1	N/A	N/A

Oman vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	1.8377	0.326895	11.65563	0.001
Residual	24	3.783931	0.673105	N/A	N/A

Total	25	5.6216	1	N/A	N/A

Oman vs Raiatea	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	4.939131	0.650692	50.29557	0.001
Residual	27	2.651457	0.349308	N/A	N/A
Total	28	7.590588	1	N/A	N/A

Mo'orea vs Taiwan	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	4.284909	0.811218	77.3482	0.001
Residual	18	0.997158	0.188782	N/A	N/A
Total	19	5.282067	1	N/A	N/A

Mo'orea vs Djibouti	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	3.845420	0.408187	22.76089	0.001
Residual	33	5.575302	0.591813	N/A	N/A
Total	34	9.420722	1	N/A	N/A

Mo'orea vs Taha'a	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	0.255805	0.245369	5.202418	0.003
Residual	16	0.786727	0.754631	N/A	N/A
Total	17	1.042532	1	N/A	N/A

Mo'orea vs Tahiti	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	0.408775	0.189663	2.574605	0.006
Residual	11	1.746489	0.810337	N/A	N/A
Total	12	2.155264	1	N/A	N/A

Mo'orea vs Raiatea	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	0.234977	0.276772	5.357654	0.002
Residual	14	0.614015	0.723228	N/A	N/A
Total	15	0.848993	1	N/A	N/A

Taiwan vs Djibouti	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	6.259974	0.521886	40.38737	0.001
Residual	37	5.734938	0.478114	N/A	N/A
Total	38	11.99491	1	N/A	N/A

Taiwan vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	4.960935	0.839798	104.8421	0.001
Residual	20	0.946363	0.160202	N/A	N/A
Total	21	5.907298	1	N/A	N/A

Taiwan vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	1.815997	0.487893	14.29075	0.002
Residual	15	1.906125	0.512107	N/A	N/A
Total	16	3.722122	1	N/A	N/A

Taiwan vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	4.416149	0.850929	102.7475	0.001
Residual	18	0.773651	0.149071	N/A	N/A
Total	19	5.1898	1	N/A	N/A

Djibouti vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	4.558151	0.452078	28.87774	0.001
Residual	35	5.524508	0.547922	N/A	N/A
Total	36	10.08266	1	N/A	N/A

Djibouti vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	1.845761	0.221579	8.539562	0.001
Residual	30	6.48427	0.778421	N/A	N/A
Total	31	8.33003	1	N/A	N/A

Djibouti vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	3.999783	0.427712	24.66328	0.001
Residual	33	5.351796	0.572288	N/A	N/A
Total	34	9.351579	1	N/A	N/A

Taha'a vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.399488	0.19067	3.062667	0.005
Residual	13	1.695695	0.80933	N/A	N/A
Total	14	2.095183	1	N/A	N/A

Taha'a vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.064294	0.102458	1.82647	0.126
Residual	16	0.563221	0.897542	N/A	N/A

Total	17	0.627515	1	N/A	N/A

Tahiti vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.373161	0.1968	2.695216	0.011
Residual	11	1.522983	0.8032	N/A	N/A
Total	12	1.896143	1	N/A	N/A

Table A11. Post-hoc analysis of pairwise permutational multivariate analysis of variance (PERMANOVA) across regions for *Pocillopora* spp. derived ITS2 sequences. We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons.

Indian Ocean vs French Polynesia	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
S_region	1	9.087237	0.325359	37.13477	0.001
Residual	77	18.84264	0.674641	N/A	N/A
Total	78	27.92988	1	N/A	N/A

Indian Ocean vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
S_region	1	2.670352	0.140891	9.511799	0.001
Residual	58	16.28298	0.859109	N/A	N/A
Total	59	18.95333	1	N/A	N/A

French Polynesia vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
S_region	1	7.071941	0.655513	78.01771	0.001
Residual	41	3.716459	0.344487	N/A	N/A
Total	42	10.7884	1	N/A	N/A

Table A12. Permutational multivariate analysis of variance (PERMANOVA) for *Pocillopora* spp. derived ITS2 sequences corresponding to *Symbiodinium* spp. (ITS2-type A profiles), using Bray-Curtis distances and 999 permutations.

Model: asv_css_A ~ S_region/Loc + SST_a + Tbl_bin

Variable	Degrees of freedom	Sum of squares	R^2	F statistic	Pr (>F)
S_region	2	2.5064	0.11108	5.1774	0.001
SST_a	1	5.0493	0.22379	20.8606	0.001
Tbl_bin	1	0.2207	0.00978	0.9118	0.444
S_region:Loc	3	1.4738	0.06532	2.0296	0.014
Residuals	55	13.3128	0.59003	N/A	N/A
Total	62	22.5631	1.00000	N/A	N/A

Table A13. Permutational multivariate analysis of variance (PERMANOVA) for *Pocillopora* spp. derived ITS2 sequences corresponding to *Cladocopium* spp. (ITS2-type C profiles), using Bray-Curtis distances and 999 permutations.

Model: asv_css_C ~ S_region/Loc + SST_a + Tbl_bin

Variable	Degrees of freedom	Sum of squares	R^2	F statistic	Pr (>F)
S_region	2	7.2496	0.25521	25.7169	0.001
SST_a	1	7.8701	0.27706	55.8362	0.001
Tbl_bin	1	0.2128	0.00749	1.5097	0.180
S_region:Loc	3	1.3747	0.04840	3.2511	0.005
Residuals	83	11.6989	0.41184	N/A	N/A
Total	90	28.4061	1.00000	N/A	N/A

Table A14. Permutational multivariate analysis of variance (PERMANOVA) for *Pocillopora* spp. derived ITS2 sequences corresponding to *Durusdinium* spp. (ITS2-type D profiles), using Bray-Curtis distances and 999 permutations.

Model: asv_css_D ~ S_region/Loc + SST_a + Tbl_bin

Variable	Degrees of freedom	Sum of squares	R^2	F statistic	Pr (>F)
S_region	2	12.7427	0.40306	53.4274	0.001
SST_a	1	7.8263	0.24755	65.6281	0.001
Tbl_bin	1	0.3052	0.00965	2.5591	0.062
S_region:Loc	3	0.8427	0.02665	2.3554	0.016
Residuals	83	9.8980	0.31308	N/A	N/A
Total	90	31.6149	1.00000	N/A	N/A

Table A15. Post-hoc analysis of pairwise permutational multivariate analysis of variance (PERMANOVA) across locations for *Pocillopora* spp. derived ITS2 sequences corresponding to *Symbiodinium* spp. (ITS2-type A profiles). We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons.

Oman vs Mo'orea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.609514	0.207219	4.443506	0.013
Residual	17	2.331882	0.792781	N/A	N/A
Total	18	2.941396	1	N/A	N/A

Oman vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.100105	0.048429	0.91608	0.454
Residual	18	1.966956	0.951571	N/A	N/A
Total	19	2.067061	1	N/A	N/A

Oman vs Djibouti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	5.250893	0.364189	21.19343	0.001
Residual	37	9.167136	0.635811	N/A	N/A
Total	38	14.41803	1	N/A	N/A

Oman vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.165529	0.087479	1.629717	0.185
Residual	17	1.726674	0.912521	N/A	N/A
Total	18	1.892203	1	N/A	N/A

Oman vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.617114	0.384103	9.354715	0.003
Residual	15	0.989524	0.615897	N/A	N/A
Total	16	1.606638	1	N/A	N/A

Oman vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.955798	0.325863	8.21742	0.003
Residual	17	1.977331	0.674137	N/A	N/A
Total	18	2.933128	1	N/A	N/A

Mo'orea vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.366322	0.129326	1.336814	0.214
Residual	9	2.466239	0.870674	N/A	N/A
Total	10	2.832562	1	N/A	N/A

Mo'orea vs Djibouti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	1.53069	0.136704	4.433835	0.001
Residual	28	9.66642	0.863296	N/A	N/A
Total	29	11.19711	1	N/A	N/A

Mo'orea vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.325087	0.127433	1.168351	0.371
Residual	8	2.225957	0.872567	N/A	N/A
Total	9	2.551044	1	N/A	N/A

Mo'orea vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.399435	0.211538	1.609752	0.199
Residual	6	1.488807	0.788462	N/A	N/A
Total	7	1.888242	1	N/A	N/A

Mo'orea vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.280562	0.101757	0.906277	0.526
Residual	8	2.476614	0.898243	N/A	N/A
Total	9	2.757176	1	N/A	N/A

Taiwan vs Djibouti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	2.324016	0.199907	7.245769	0.001
Residual	29	9.301494	0.800093	N/A	N/A
Total	30	11.62551	1	N/A	N/A

Taiwan vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.036348	0.019157	0.175782	0.668
Residual	9	1.861031	0.980843	N/A	N/A
Total	10	1.897379	1	N/A	N/A

Taiwan vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.469227	0.294536	2.922541	0.042
Residual	7	1.123881	0.705464	N/A	N/A
Total	8	1.593108	1	N/A	N/A

Taiwan vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.594955	0.219813	2.535694	0.092
Residual	9	2.111688	0.780187	N/A	N/A
Total	10	2.706643	1	N/A	N/A

Djibouti vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	2.045281	0.184152	6.320111	0.001
Residual	28	9.061211	0.815848	N/A	N/A
Total	29	11.10649	1	N/A	N/A

Djibouti vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	1.58417	0.159884	4.948117	0.001
Residual	26	8.324061	0.840116	N/A	N/A
Total	27	9.908232	1	N/A	N/A

Djibouti vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	1.830594	0.16429	5.504441	0.001
Residual	28	9.311868	0.83571	N/A	N/A
Total	29	11.14246	1	N/A	N/A

Taha'a vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.353321	0.285646	2.399197	0.038
Residual	6	0.883599	0.714354	N/A	N/A
Total	7	1.23692	1	N/A	N/A

Taha'a vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.527428	0.219868	2.254679	0.131
Residual	8	1.871406	0.780132	N/A	N/A
Total	9	2.398833	1	N/A	N/A

Tahiti vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.593356	0.343455	3.138743	0.091
Residual	6	1.134256	0.656545	N/A	N/A
Total	7	1.727612	1	N/A	N/A

Table A16. Post-hoc analysis of pairwise permutational multivariate analysis of variance (PERMANOVA) across regions for *Pocillopora* spp. derived ITS2 sequences corresponding to *Symbiodinium* spp. (ITS2-type A profiles). We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons.

Indian Ocean vs French Polynesia	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
S_region	1	1.886525	0.090297	5.459268	0.003
Residual	55	19.006	0.909703	N/A	N/A
Total	56	20.89253	1	N/A	N/A

Indian Ocean vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
S_region	1	0.945361	0.057595	2.627923	0.024
Residual	43	15.46869	0.942405	N/A	N/A
Total	44	16.41405	1	N/A	N/A

French Polynesia vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
S_region	1	0.326265	0.054698	1.272976	0.291
Residual	22	5.638629	0.945302	N/A	N/A
Total	23	5.964894	1	N/A	N/A

Table A17. Post-hoc analysis of pairwise permutational multivariate analysis of variance (PERMANOVA) across locations for *Pocillopora* spp. derived ITS2 sequences corresponding to *Cladocopium* spp. (ITS2-type C profiles). We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons.

Oman vs Mo'orea	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	4.501036	0.58326	37.78853	0.001
Residual	27	3.216001	0.41674	N/A	N/A
Total	28	7.717037	1	N/A	N/A

Oman vs Taiwan	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	0.399832	0.1164	4.083759	0.016
Residual	31	3.035146	0.8836	N/A	N/A
Total	32	3.434979	1	N/A	N/A

Oman vs Djibouti	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	8.336763	0.553124	56.93672	0.001
Residual	46	6.735391	0.446876	N/A	N/A
Total	47	15.07215	1	N/A	N/A

Oman vs Taha'a	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	5.269272	0.604308	44.28923	0.001
Residual	29	3.450249	0.395692	N/A	N/A
Total	30	8.719520	1	N/A	N/A

Oman vs Tahiti	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	1.699050	0.301556	10.3621	0.001
Residual	24	3.935224	0.698444	N/A	N/A
Total	25	5.634274	1	N/A	N/A

Oman vs Raiatea	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	4.102718	0.520516	29.31051	0.001
Residual	27	3.779306	0.479484	N/A	N/A
Total	28	7.882025	1	N/A	N/A

Mo'orea vs Taiwan	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
Loc	1	4.068245	0.753009	54.87705	0.001
Residual	18	1.334408	0.246991	N/A	N/A
Total	19	5.402653	1	N/A	N/A

Mo'orea vs Djibouti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.220905	0.042033	1.447935	0.175
Residual	33	5.034653	0.957967	N/A	N/A
Total	34	5.255558	1	N/A	N/A

Mo'orea vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.327999	0.157881	2.999687	0.009
Residual	16	1.749511	0.842119	N/A	N/A
Total	17	2.07751	1	N/A	N/A

Mo'orea vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.419511	0.158068	2.06518	0.051
Residual	11	2.234486	0.841932	N/A	N/A
Total	12	2.653997	1	N/A	N/A

Mo'orea vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.142022	0.063957	0.956576	0.438
Residual	14	2.078568	0.936043	N/A	N/A
Total	15	2.220590	1	N/A	N/A

Taiwan vs Djibouti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	6.457582	0.570892	49.22547	0.001
Residual	37	4.853799	0.429108	N/A	N/A
Total	38	11.31138	1	N/A	N/A

Taiwan vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	4.623589	0.746674	58.94968	0.001
Residual	20	1.568656	0.253326	N/A	N/A
Total	21	6.192245	1	N/A	N/A

Taiwan vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	1.700060	0.452904	12.41747	0.001
Residual	15	2.053631	0.547096	N/A	N/A
Total	16	3.753692	1	N/A	N/A

Taiwan vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	3.729897	0.662785	35.37844	0.001
Residual	18	1.897713	0.337215	N/A	N/A
Total	19	5.62761	1	N/A	N/A

Djibouti vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.901526	0.146104	5.988616	0.001
Residual	35	5.268901	0.853896	N/A	N/A
Total	36	6.170427	1	N/A	N/A

Djibouti vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.415763	0.067389	2.16774	0.046
Residual	30	5.753876	0.932611	N/A	N/A
Total	31	6.16964	1	N/A	N/A

Djibouti vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.364649	0.061156	2.14961	0.05
Residual	33	5.597958	0.938844	N/A	N/A
Total	34	5.962608	1	N/A	N/A

Taha'a vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.613231	0.198974	3.229187	0.001
Residual	13	2.468734	0.801026	N/A	N/A
Total	14	3.081965	1	N/A	N/A

Taha'a vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.18615	0.074491	1.287779	0.183
Residual	16	2.312816	0.925509	N/A	N/A
Total	17	2.498965	1	N/A	N/A

Tahiti vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.276083	0.089816	1.085467	0.333
Residual	11	2.797791	0.910184	N/A	N/A
Total	12	3.073874	1	N/A	N/A

Table A18. Post-hoc analysis of pairwise permutational multivariate analysis of variance (PERMANOVA) across regions for *Pocillopora* spp. derived ITS2 sequences corresponding to *Cladocopium* spp. (ITS2-type C profiles). We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons.

Indian Ocean vs French Polynesia	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
S_region	1	2.780437	0.119025	10.40314	0.001
Residual	77	20.57972	0.880975	N/A	N/A
Total	78	23.36016	1	N/A	N/A

Indian Ocean vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
S_region	1	2.749984	0.149464	10.19233	0.001
Residual	58	15.64893	0.850536	N/A	N/A
Total	59	18.39891	1	N/A	N/A

French Polynesia vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
S_region	1	6.396736	0.512515	43.10509	0.001
Residual	41	6.084343	0.487485	N/A	N/A
Total	42	12.48108	1	N/A	N/A

Table A19. Post-hoc analysis of pairwise permutational multivariate analysis of variance (PERMANOVA) across locations for *Pocillopora* spp. derived ITS2 sequences corresponding to *Durusdinium* spp. (ITS2-type D profiles). We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons.

Oman vs Mo'orea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	5.030515	0.71524	67.81674	0.001
Residual	27	2.002808	0.28476	N/A	N/A
Total	28	7.033323	1	N/A	N/A

Oman vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.092216	0.032956	1.056455	0.336
Residual	31	2.705925	0.967044	N/A	N/A
Total	32	2.798141	1	N/A	N/A

Oman vs Djibouti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	8.15981	0.549554	56.12097	0.001
Residual	46	6.688253	0.450446	N/A	N/A
Total	47	14.84806	1	N/A	N/A

Oman vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	5.977133	0.753821	88.80068	0.001
Residual	29	1.951977	0.246179	N/A	N/A
Total	30	7.92911	1	N/A	N/A

Oman vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	2.056861	0.421283	17.47105	0.001
Residual	24	2.825512	0.578717	N/A	N/A
Total	25	4.882373	1	N/A	N/A

Oman vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	5.233413	0.752626	82.14639	0.001
Residual	27	1.720126	0.247374	N/A	N/A
Total	28	6.953539	1	N/A	N/A

Mo'orea vs Taiwan	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	4.074891	0.72575	47.63345	0.001
Residual	18	1.539843	0.27425	N/A	N/A
Total	19	5.614734	1	N/A	N/A

Mo'orea vs Djibouti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	3.818809	0.408823	22.82086	0.001
Residual	33	5.522171	0.591177	N/A	N/A
Total	34	9.34098	1	N/A	N/A

Mo'orea vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.255544	0.245376	5.202602	0.005
Residual	16	0.785895	0.754624	N/A	N/A
Total	17	1.041438	1	N/A	N/A

Mo'orea vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.359147	0.177921	2.380705	0.012
Residual	11	1.65943	0.822079	N/A	N/A
Total	12	2.018577	1	N/A	N/A

Mo'orea vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.22063	0.284803	5.575037	0.002
Residual	14	0.554044	0.715197	N/A	N/A
Total	15	0.774674	1	N/A	N/A

Taiwan vs Djibouti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	5.567784	0.472123	33.09213	0.001
Residual	37	6.225288	0.527877	N/A	N/A
Total	38	11.79307	1	N/A	N/A

Taiwan vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	4.706993	0.759682	63.22305	0.001
Residual	20	1.489012	0.240318	N/A	N/A
Total	21	6.196005	1	N/A	N/A

Taiwan vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	1.73715	0.423726	11.0293	0.002
Residual	15	2.362547	0.576274	N/A	N/A
Total	16	4.099697	1	N/A	N/A

Taiwan vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	4.243645	0.771459	60.7604	0.001
Residual	18	1.257161	0.228541	N/A	N/A
Total	19	5.500806	1	N/A	N/A

Djibouti vs Taha'a	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	4.502781	0.451446	28.80416	0.001
Residual	35	5.47134	0.548554	N/A	N/A
Total	36	9.974121	1	N/A	N/A

Djibouti vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	1.836256	0.22445	8.682231	0.001
Residual	30	6.344875	0.77555	N/A	N/A
Total	31	8.181131	1	N/A	N/A

Djibouti vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	3.993476	0.432524	25.15221	0.001
Residual	33	5.239489	0.567476	N/A	N/A
Total	34	9.232965	1	N/A	N/A

Taha'a vs Tahiti	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.324079	0.167684	2.619065	0.014
Residual	13	1.608599	0.832316	N/A	N/A
Total	14	1.932678	1	N/A	N/A

Taha'a vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.048805	0.088412	1.551795	0.192
Residual	16	0.503213	0.911588	N/A	N/A
Total	17	0.552018	1	N/A	N/A

Tahiti vs Raiatea	Degrees of freedom	Sum of squares	R^2	F model	Pr (>F)
Loc	1	0.338522	0.197358	2.70474	0.016
Residual	11	1.376748	0.802642	N/A	N/A
Total	12	1.71527	1	N/A	N/A

Table A20. Post-hoc analysis of pairwise permutational multivariate analysis of variance (PERMANOVA) across regions for *Pocillopora* spp. derived ITS2 sequences corresponding to *Durusdinium* spp. (ITS2-type D profiles). We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons.

Indian Ocean vs French Polynesia	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
S_region	1	9.452451	0.347477	41.00342	0.001
Residual	77	17.75068	0.652523	N/A	N/A
Total	78	27.20313	1	N/A	N/A

Indian Ocean vs Taiwan	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
S_region	1	2.037817	0.113166	7.401173	0.004
Residual	58	15.96954	0.886834	N/A	N/A
Total	59	18.00736	1	N/A	N/A

French Polynesia vs Taiwan	**Degrees of freedom**	**Sum of squares**	**R^2**	**F model**	**Pr (>F)**
S_region	1	6.757591	0.626766	68.85051	0.001
Residual	41	4.024098	0.373234	N/A	N/A
Total	42	10.78169	1	N/A	N/A

Table A21. Indicator species analysis for *Pocillopora* spp. derived ITS2 sequences across locations. Only ASVs with a $p < 0.05$ are shown, which are corrected for multiple testing via the Benjamini and Hochberg p-value correction. Symbiodiniaceae taxonomy is shown on the basis of ITS2-type profiles mirroring the SymPortal database's output, where "clade" and "type" delineations are shown. Yet based on recent taxonomic revision of the Symbiodiniaceae family, these profiles represent different genera and species. Briefly, ITS2-type A profiles correspond to *Symbiodinium* spp., ITS2-type B profiles correspond to *Breviolum* spp., ITS2-type C profiles correspond to Cladocopium spp., and ITS2-type D profiles correspond to *Durusdinium* spp.

ASV	ITSclade	ITStype	Djibouti	Mo'orea	Oman	Raiatea	Taha'a	Tahiti	Taiwan	Indices of combinations	Species indicator value	P-value
asv4	C	C4	0	0	1	1	0	0	1	56	0.995	0.002
asv8	C	C1	0	1	1	1	1	1	1	126	0.999	0.002
asv9	C	C	0	0	1	1	1	1	1	119	0.998	0.002
asv12	C	C1	0	0	1	0	0	1	1	59	0.998	0.002
asv13	C	C	0	0	1	0	0	1	1	59	0.882	0.002
asv15	C	C3	0	0	1	1	1	1	1	119	0.998	0.002
asv16	D	D1	0	1	0	1	1	1	0	90	0.983	0.004
asv17	C	C	0	0	1	0	0	1	1	59	0.827	0.002
asv19	C	C1	0	0	1	0	0	0	1	22	0.987	0.002
asv22	C	C	0	0	1	0	0	0	1	22	0.926	0.002
asv23	D	D1	1	1	0	1	1	1	1	124	0.999	0.002
asv24	C	C1	0	0	1	0	0	1	1	59	0.972	0.002
asv25	A	A2	1	0	0	0	0	0	0	1	0.943	0.002
asv26	C	C1	0	0	1	0	0	0	1	22	0.974	0.002
asv27	D	D	0	1	0	1	1	1	0	90	0.983	0.002
asv30	C	C4	0	0	1	0	0	0	1	22	0.986	0.002
asv33	C	C1	0	0	1	0	0	1	1	59	0.999	0.002
asv35	C	C1	0	0	1	0	0	0	1	22	0.979	0.002
asv37	C	C1	0	0	1	0	0	1	1	59	0.957	0.002
asv38	C	C1	0	0	1	0	0	0	1	22	0.982	0.002
asv39	C	C	0	0	0	0	0	0	1	7	0.887	0.002

asv40	D	D1	1	0	0	0	0	0	0	1	0.980	0.002
asv41	C	C	0	0	1	0	0	0	1	22	0.941	0.002
asv42	C	C	0	0	0	0	0	0	1	7	0.681	0.003
asv43	C	C4	1	0	1	0	0	1	1	79	0.804	0.012
asv44	C	C1	0	0	1	0	0	1	1	59	0.971	0.002
asv46	C	C1	0	0	1	0	0	0	1	22	0.971	0.002
asv47	C	C4	0	0	1	0	0	0	0	3	0.535	0.018
asv48	C	C	0	0	0	1	0	1	1	62	0.872	0.034
asv49	D	D1	1	1	0	1	0	1	0	69	0.959	0.002
asv51	C	C1	0	0	1	0	0	0	1	22	0.934	0.002
asv52	C	C4	0	0	1	0	0	1	0	21	0.679	0.003
asv54	C	C	0	0	1	0	0	0	1	22	0.970	0.002
asv55	D	D	0	1	0	1	1	1	0	90	0.999	0.002
asv60	C	C	0	0	0	0	0	0	1	7	0.912	0.002
asv62	D	D	0	1	0	1	1	1	0	90	0.999	0.002
asv66	D	D1	1	0	0	1	1	0	0	38	0.986	0.002
asv67	C	C	0	0	1	0	0	0	1	22	0.990	0.002
asv68	C	C	0	0	0	0	0	0	1	7	0.902	0.002
asv70	C	C	0	0	0	0	0	0	1	7	0.962	0.002
asv71	C	C1	0	0	1	0	0	0	1	22	0.881	0.002
asv73	C	C1	0	0	1	0	0	0	1	22	0.952	0.002
asv74	D	D	0	1	0	0	0	0	0	2	0.999	0.002
asv78	C	C	0	0	0	0	0	0	1	7	0.966	0.002
asv79	C	C1	0	0	1	0	0	1	1	59	0.956	0.002
asv80	C	C	0	0	0	0	0	0	1	7	0.722	0.002
asv81	D	D	0	1	0	1	1	1	0	90	1.000	0.002
asv82	C	C1	0	0	1	0	0	0	1	22	0.603	0.007
asv84	D	D	0	1	0	1	1	1	0	90	0.984	0.020

asv85	C	C	0	0	1	0	0	0	1	22	0.935	0.002
asv87	C	C	0	0	1	0	0	1	1	59	0.953	0.002
asv88	C	C1	0	0	1	0	0	0	1	22	0.976	0.002
asv89	C	C4	0	0	1	0	0	0	1	22	0.987	0.002
asv90	C	C	0	0	1	0	0	0	1	22	0.913	0.002
asv91	D	D	0	1	0	1	1	0	0	48	0.999	0.002
asv94	C	C1	0	0	1	0	0	0	1	22	0.951	0.002
asv95	D	D	0	1	0	0	0	1	0	17	0.911	0.002
asv101	C	C	0	0	0	0	0	0	1	7	0.645	0.002
asv105	C	C	0	0	0	0	0	0	1	7	0.996	0.002
asv106	C	C1	0	0	1	0	0	0	1	22	0.965	0.002
asv107	C	C1	0	0	1	0	0	0	1	22	0.916	0.002
asv108	C	C1	0	0	1	0	0	1	1	59	0.913	0.002
asv109	D	D	0	1	0	1	1	1	0	90	0.966	0.002
asv110	D	D	0	1	0	1	1	1	0	90	0.983	0.002
asv112	C	C1	0	0	1	0	0	0	1	22	0.982	0.002
asv117	C	C1	0	0	1	0	0	0	1	22	0.983	0.002
asv119	C	C	0	0	1	0	0	0	1	22	0.962	0.002
asv121	C	C4	0	0	1	0	0	0	0	3	0.617	0.004
asv123	C	C	0	0	1	0	0	0	1	22	0.935	0.002
asv125	C	C	0	0	1	0	0	1	1	59	0.798	0.002
asv127	C	C1	0	0	1	0	0	0	1	22	0.941	0.002
asv128	C	C	0	0	1	0	0	0	1	22	0.896	0.002
asv129	D	D	0	1	0	1	1	0	0	48	0.990	0.002
asv131	C	C	0	0	1	0	0	1	1	59	0.956	0.002
asv132	C	C1	0	0	1	0	0	0	1	22	0.836	0.002
asv133	C	C	0	0	1	0	0	0	1	22	0.991	0.002
asv134	C	C3	0	0	1	0	0	1	1	59	0.811	0.002

asv136	C	C	0	0	1	0	0	1	1	59	0.946	0.002
asv137	A	A1	1	0	0	0	0	0	0	1	0.839	0.002
asv138	C	C1	0	0	1	0	0	0	0	3	0.535	0.011
asv139	C	C	0	0	1	0	0	0	0	3	0.753	0.002
asv142	D	D	0	1	0	1	1	1	0	90	0.880	0.002
asv144	C	C1	0	0	1	0	0	0	1	22	0.813	0.002
asv145	D	D1	1	0	0	0	0	0	0	1	0.948	0.002
asv147	C	C1	0	0	1	0	0	0	0	3	0.528	0.034
asv148	A	A1	1	0	0	0	0	0	0	1	0.882	0.002
asv149	A	A1	1	0	0	0	0	0	0	1	0.860	0.002
asv150	C	C4	0	0	1	0	0	0	0	3	0.577	0.008
asv152	C	C	0	0	1	0	0	0	1	22	0.977	0.002
asv153	C	C	0	0	1	0	0	0	1	22	0.947	0.002
asv154	C	C	0	0	0	0	0	0	1	7	0.905	0.002
asv155	C	C1	0	0	1	0	0	0	1	22	0.862	0.002
asv156	D	D1	1	0	0	0	0	0	0	1	0.854	0.002
asv157	C	C3	0	0	1	0	0	0	1	22	0.833	0.002
asv159	C	C	0	0	0	0	0	0	1	7	0.947	0.002
asv160	C	C4	0	0	1	0	0	0	0	3	0.610	0.011
asv161	C	C4	0	0	1	0	0	0	0	3	0.614	0.012
asv163	C	C	0	0	1	0	0	0	1	22	0.944	0.002
asv164	C	C	0	0	0	0	0	0	1	7	0.986	0.002
asv166	D	D	0	1	0	1	1	0	0	48	0.996	0.002
asv167	C	C1	0	0	1	0	0	1	1	59	0.946	0.002
asv175	C	C1	0	0	1	0	0	1	1	59	0.607	0.017
asv176	C	C	0	0	1	0	0	0	1	22	0.980	0.002
asv177	C	C4	0	0	1	0	0	0	0	3	0.648	0.004
asv179	C	C	0	0	1	0	0	0	1	22	0.816	0.002

asv180	C	C	0	0	1	0	0	0	1	22	0.754	0.004
asv182	C	C1	0	0	1	0	0	1	1	59	0.778	0.003
asv185	C	C	0	0	1	0	0	1	1	59	0.827	0.003
asv187	C	C1	0	0	0	0	0	0	1	7	0.929	0.002
asv188	C	C	0	0	1	0	0	0	1	22	0.603	0.011
asv191	C	C	0	0	1	0	0	0	0	3	0.706	0.004
asv192	C	C	0	0	0	0	0	0	1	7	0.500	0.010
asv200	C	C4	0	0	0	0	0	0	1	7	0.898	0.002
asv201	D	D1	1	0	0	0	0	0	0	1	0.837	0.002
asv202	C	C1	0	0	1	0	0	0	1	22	0.822	0.002
asv205	D	D	0	1	0	1	1	0	0	48	0.994	0.002
asv209	C	C1	0	0	1	0	0	1	1	59	0.778	0.002
asv211	C	C	0	0	1	0	0	0	1	22	0.972	0.002
asv215	C	C	0	0	0	0	0	0	1	7	0.577	0.010
asv223	C	C	0	0	0	0	0	0	1	7	0.926	0.002
asv226	C	C	0	0	1	0	0	0	1	22	0.918	0.002
asv227	C	C1	0	0	1	0	0	0	1	22	0.835	0.002
asv229	C	C1	0	0	1	0	0	1	1	59	0.903	0.002
asv232	C	C	0	0	0	0	0	0	1	7	0.900	0.002
asv233	C	C	0	0	0	0	0	0	1	7	0.904	0.002
asv235	C	C	0	0	0	0	0	0	1	7	0.933	0.002
asv236	C	C	0	0	0	0	0	0	1	7	0.904	0.002
asv237	D	D	0	1	0	1	1	1	0	90	0.968	0.002
asv239	C	C1	0	0	1	0	0	0	1	22	0.968	0.002
asv240	C	C	0	0	1	0	0	0	1	22	0.889	0.002
asv243	C	C	0	0	0	0	0	0	1	7	0.897	0.002
asv245	D	D2	0	1	0	1	1	1	0	90	0.972	0.002
asv248	C	C4	0	0	1	0	0	0	0	3	0.557	0.020

asv249	D	D	0	1	0	0	0	1	0	17	0.996	0.002
asv260	D	D	0	1	0	1	1	1	0	90	0.980	0.002
asv264	C	C	0	0	1	0	0	1	1	59	0.761	0.002
asv265	C	C1	0	0	1	0	0	0	1	22	0.577	0.012
asv267	C	C	0	0	1	0	0	0	1	22	0.981	0.002
asv269	C	C	0	0	1	0	0	1	1	59	0.827	0.002
asv270	D	D	0	0	0	1	1	0	0	23	0.969	0.002
asv271	C	C	0	0	1	0	0	0	1	22	0.954	0.002
asv280	C	C4	0	0	1	0	0	0	0	3	0.436	0.043
asv283	C	C	0	0	1	0	0	1	1	59	0.843	0.002
asv286	D	D	0	0	0	1	1	0	0	23	0.996	0.002
asv288	C	C4	0	0	1	0	0	0	0	3	0.577	0.008
asv293	D	D	0	1	0	1	1	1	0	90	0.955	0.002
asv295	C	C4	0	0	1	0	0	0	0	3	0.577	0.007
asv297	D	D2	0	1	0	1	1	1	0	90	0.898	0.002
asv302	C	C	0	0	1	0	0	0	1	22	0.942	0.002
asv305	C	C4	0	0	1	0	0	0	0	3	0.689	0.004
asv312	C	C	0	0	1	0	0	0	1	22	0.946	0.002
asv317	C	C4	0	0	1	0	0	0	0	3	0.594	0.012
asv318	D	D1	0	1	0	0	0	0	0	2	0.620	0.007
asv321	C	C1	0	0	1	0	0	0	1	22	0.550	0.017
asv322	C	C1	0	0	1	0	0	0	1	22	0.870	0.002
asv323	C	C	0	0	1	0	0	0	1	22	0.814	0.002
asv327	D	D	0	1	0	1	1	1	0	90	0.964	0.002
asv328	C	C1	0	0	1	0	0	0	0	3	0.759	0.002
asv332	C	C	0	0	1	0	0	0	1	22	0.954	0.002
asv335	C	C	0	0	1	0	0	0	0	3	0.533	0.011
asv347	C	C	0	0	1	0	0	1	1	59	0.889	0.002

asv348	C	C4	0	0	1	0	0	0	0	3	0.750	0.002
asv351	C	C1	0	0	1	0	0	0	0	3	0.872	0.002
asv357	D	D	0	1	0	1	1	1	0	90	0.933	0.002
asv359	D	D2	1	1	0	1	1	1	0	105	0.937	0.002
asv368	C	C	0	0	1	0	0	0	1	22	0.862	0.002
asv371	C	C1	0	0	1	0	0	1	1	59	0.769	0.002
asv381	C	C1	0	0	1	0	0	0	1	22	0.816	0.002
asv383	C	C1	0	0	1	0	0	0	0	3	0.695	0.003
asv388	C	C4	0	0	1	0	0	0	0	3	0.577	0.007
asv393	C	C3	0	0	1	0	0	0	1	22	0.798	0.002
asv396	D	D	0	1	0	1	1	1	0	90	0.948	0.002
asv399	C	C1	0	0	1	0	0	0	1	22	0.953	0.002
asv402	C	C1	0	0	1	0	0	0	1	22	0.816	0.002
asv405	C	C1	0	0	1	0	0	1	1	59	0.707	0.002
asv406	C	C	0	0	1	0	0	0	1	22	0.846	0.002
asv414	C	C4	0	0	1	0	0	0	0	3	0.613	0.007
asv415	D	D1	0	1	0	0	0	1	0	17	0.827	0.002
asv417	D	D	0	1	0	1	1	1	0	90	0.983	0.002
asv426	C	C4	0	0	1	0	0	0	0	3	0.488	0.034
asv427	C	C1	0	0	1	0	0	0	1	22	0.577	0.010
asv428	C	C4	0	0	1	0	0	0	0	3	0.576	0.013
asv429	D	D	0	1	0	1	1	1	0	90	0.967	0.002
asv431	D	D	0	1	0	1	1	1	0	90	0.972	0.002
asv440	C	C1	0	0	1	0	0	0	1	22	0.927	0.002
asv444	C	C	0	0	0	0	0	0	1	7	0.876	0.002
asv446	C	C1	0	0	1	0	0	1	1	59	0.513	0.018
asv447	D	D	0	1	0	1	1	1	0	90	0.967	0.002
asv449	A	A2	1	0	0	0	0	0	0	1	0.882	0.002

asv450	C	C	0	0	1	0	0	0	0	3	0.614	0.008
asv453	D	D1	1	0	0	0	0	0	0	1	0.888	0.002
asv459	D	D1	1	0	0	0	0	0	0	1	0.918	0.002
asv460	C	C4	0	0	1	0	0	0	0	3	0.563	0.011
asv462	C	C4	0	0	1	0	0	0	0	3	0.577	0.008
asv463	D	D1	0	1	0	0	0	1	0	17	0.650	0.008
asv467	D	D	0	1	0	1	1	1	0	90	0.967	0.002
asv468	C	C4	0	0	1	0	0	0	0	3	0.577	0.008
asv474	D	D1	1	0	0	0	0	0	0	1	0.924	0.002
asv476	C	C1	0	0	1	0	0	0	1	22	0.969	0.002
asv477	C	C	0	0	1	0	0	0	0	3	0.716	0.003
asv479	C	C4	0	0	1	0	0	0	0	3	0.571	0.011
asv486	C	C4	0	0	1	0	0	0	0	3	0.617	0.010
asv498	C	C1	0	0	1	0	0	0	1	22	0.951	0.002
asv501	D	D1	1	0	0	0	0	0	0	1	0.901	0.002
asv505	C	C	0	0	1	0	0	1	1	59	0.688	0.007
asv516	C	C	0	0	1	0	0	0	0	3	0.814	0.002
asv519	C	C1	0	0	1	0	0	1	0	21	0.760	0.002
asv529	D	D1	1	0	0	0	0	0	0	1	0.914	0.002
asv531	C	C1	0	0	1	0	0	1	0	21	0.782	0.008
asv533	D	D1	0	1	0	0	0	0	0	2	0.961	0.002
asv535	C	C1	0	0	1	0	0	0	0	3	0.769	0.002
asv537	C	C4	0	0	1	0	0	1	1	59	0.946	0.002
asv543	C	C1	0	0	1	0	0	0	1	22	0.853	0.002
asv553	D	D1	1	0	0	0	0	0	0	1	0.914	0.002
asv556	C	C1	0	0	1	0	0	0	1	22	0.890	0.002
asv558	D	D	0	1	0	1	1	1	0	90	0.975	0.002
asv559	D	D1	0	1	0	1	1	0	0	48	0.985	0.002

asv563	C	C1	0	0	1	0	0	1	1	59	0.903	0.002
asv585	D	D1	0	1	0	0	0	1	0	17	0.452	0.046
asv598	D	D1	1	0	0	0	0	0	0	1	0.767	0.006
asv605	C	C1	0	0	1	0	0	0	1	22	0.953	0.002
asv607	C	C1	0	0	1	0	0	1	1	59	0.926	0.002
asv609	C	C1	0	0	1	0	0	1	1	59	0.946	0.002
asv611	C	C	0	0	1	0	0	0	1	22	0.962	0.002
asv613	C	C1	0	0	0	0	0	0	1	7	0.442	0.040
asv639	D	D1	1	1	0	0	0	1	0	32	0.842	0.002
asv654	C	C3	0	0	1	0	0	0	1	22	0.651	0.002
asv682	D	D2	1	1	0	1	1	1	0	105	0.927	0.002
asv703	C	C	0	0	1	0	0	0	0	3	0.488	0.039
asv730	D	D1	0	1	0	1	1	1	0	90	0.904	0.002
asv735	C	C	0	0	1	0	0	1	1	59	0.707	0.002
asv746	C	C1	0	0	1	0	0	0	1	22	0.928	0.002
asv753	C	C4	0	0	0	0	0	1	1	28	0.733	0.002
asv767	D	D	0	1	0	1	1	1	0	90	0.950	0.002
asv770	C	C	0	0	0	0	0	1	1	28	0.692	0.006
asv772	C	C1	0	0	1	0	0	0	1	22	0.843	0.002
asv780	D	D1	1	0	0	0	0	0	0	1	0.766	0.002
asv784	C	C1	0	0	1	0	0	0	0	3	0.613	0.006
asv788	C	C	0	0	1	0	0	1	1	59	0.827	0.002
asv816	D	D1	0	1	0	0	0	0	0	2	0.701	0.003
asv820	D	D	0	1	0	1	1	1	0	90	0.963	0.002
asv825	C	C1	0	0	1	0	0	1	1	59	0.669	0.007
asv827	C	C1	0	0	1	0	0	0	1	22	0.748	0.002
asv836	D	D1	0	1	0	1	0	1	0	49	0.535	0.034
asv848	D	D1	1	0	0	0	0	1	0	12	0.828	0.003

asv857	D	D1	0	1	0	0	0	0	0	2	0.700	0.004
asv859	C	C1	0	0	1	0	0	1	1	59	0.843	0.002
asv862	D	D1	0	1	0	1	1	1	0	90	0.967	0.002
asv863	C	C	0	0	1	0	0	1	1	59	0.956	0.002
asv899	C	C1	0	0	1	0	0	0	0	3	0.641	0.003
asv922	C	C1	0	0	1	0	0	1	1	59	0.743	0.002
asv940	C	C1	0	0	1	0	0	0	1	22	0.739	0.002
asv943	C	C1	0	0	0	0	0	0	1	7	0.589	0.004
asv946	C	C1	0	0	1	0	0	0	1	22	0.862	0.002
asv952	D	D2	1	0	0	1	0	0	0	10	0.866	0.002
asv955	D	D	0	1	0	1	1	1	0	90	0.960	0.002
asv1019	C	C3	0	0	1	0	0	0	1	22	0.492	0.031
asv1031	D	D	0	1	0	1	1	1	0	90	0.965	0.002
asv1037	C	C4	0	0	1	0	0	0	0	3	0.577	0.007
asv1039	C	C4	0	0	1	0	0	0	0	3	0.577	0.007
asv1050	D	D1	1	0	0	0	0	0	0	1	0.890	0.002
asv1085	C	C1	0	0	1	0	0	0	1	22	0.603	0.007
asv1093	C	C1	0	0	0	0	0	0	1	7	0.548	0.008
asv1108	C	C1	0	0	1	0	0	1	1	59	0.775	0.002
asv1124	C	C1	0	0	1	0	0	0	1	22	0.739	0.002
asv1131	D	D	0	0	0	1	0	1	0	24	0.516	0.022
asv1149	C	C	0	0	0	0	0	0	1	7	0.719	0.002
asv1156	C	C	0	0	1	0	0	1	1	59	0.843	0.002
asv1194	D	D1	1	0	0	0	0	0	0	1	0.885	0.002
asv1203	D	D1	1	0	0	0	0	0	0	1	0.893	0.002
asv1216	C	C	0	0	1	0	0	0	1	22	0.730	0.002
asv1247	C	C1	0	0	1	0	0	1	1	59	0.707	0.002
asv1252	C	C1	0	0	1	0	0	0	1	22	0.856	0.002

asv1256	C	C1	0	0	1	0	0	0	1	22	0.550	0.017
asv1258	D	D	0	1	0	1	1	1	0	90	0.964	0.002
asv1265	C	C1	0	0	1	0	0	0	0	3	0.519	0.030
asv1310	C	C1	0	0	1	0	0	0	1	22	0.853	0.002
asv1359	D	D1	0	0	0	1	1	0	0	23	0.848	0.002
asv1360	C	C1	0	0	1	0	0	0	1	22	0.821	0.002
asv1448	C	C1	0	0	1	0	0	1	1	59	0.863	0.002
asv1465	D	D	0	1	0	1	1	1	0	90	0.933	0.002
asv1471	D	D1	1	0	0	0	0	0	0	1	0.899	0.002
asv1475	D	D	0	1	0	1	1	1	0	90	0.963	0.002
asv1476	C	C	0	0	1	0	0	1	1	59	0.932	0.002
asv1544	C	C4	0	0	1	0	0	1	0	21	0.604	0.010
asv1594	C	C1	0	0	0	0	0	0	1	7	0.619	0.010
asv1600	D	D1	1	0	0	0	0	0	0	1	0.875	0.002
asv1601	C	C3	0	0	1	0	0	0	1	22	0.824	0.002
asv1686	C	C1	0	0	1	0	0	0	0	3	0.535	0.023
asv1693	C	C	0	0	1	0	0	0	0	3	0.535	0.012
asv1729	C	C1	0	0	1	0	0	0	1	22	0.754	0.003
asv1749	D	D	1	1	0	1	1	1	0	105	0.861	0.002
asv1777	D	D1	0	1	0	0	0	0	0	2	0.707	0.002
asv1778	D	D	0	1	0	1	1	1	0	90	0.957	0.002
asv1784	C	C1	0	0	1	0	0	1	1	59	0.607	0.009
asv1785	D	D	0	1	0	1	1	1	0	90	0.951	0.002
asv1799	C	C4	0	0	1	0	0	0	0	3	0.569	0.009
asv1810	C	C1	0	0	1	0	0	1	1	59	0.707	0.002
asv1863	C	C1	0	0	1	0	0	1	1	59	0.843	0.002
asv1864	D	D1	0	1	0	1	1	0	0	48	0.858	0.002
asv1886	C	C3	0	0	1	0	0	0	1	22	0.787	0.002

asv1897	C	C1	0	0	1	0	0	0	0	3	0.690	0.003
asv1931	D	D	0	1	0	1	1	1	0	90	0.944	0.002
asv1982	C	C4	0	0	1	0	0	0	0	3	0.577	0.006
asv2013	C	C	0	0	1	0	0	0	1	22	0.921	0.002
asv2051	C	C	0	0	1	0	0	0	0	3	0.488	0.029
asv2075	C	C1	0	0	1	0	0	0	1	22	0.718	0.003
asv2105	D	D1	1	0	0	0	0	0	0	1	0.873	0.002
asv2150	D	D1	0	1	0	1	1	1	0	90	0.835	0.002
asv2157	C	C4	0	0	1	0	0	0	1	22	0.739	0.002
asv2248	C	C1	0	0	1	0	0	0	1	22	0.778	0.002
asv2329	C	C1	0	0	1	0	0	1	1	59	0.669	0.004
asv2341	C	C	0	0	1	0	0	0	0	3	0.647	0.006
asv2356	C	C1	0	0	1	0	0	0	1	22	0.718	0.002
asv2486	C	C	0	0	1	0	0	0	1	22	0.696	0.003
asv2631	C	C4	0	0	1	0	0	0	0	3	0.488	0.040
asv2663	C	C	0	0	1	0	0	1	0	21	0.588	0.010
asv2701	C	C1	0	0	1	0	0	0	1	22	0.651	0.003
asv2718	C	C1	0	0	1	0	0	1	1	59	0.607	0.010
asv2804	C	C1	0	0	1	0	0	1	1	59	0.743	0.002
asv2805	C	C4	0	0	1	0	0	0	1	22	0.718	0.002
asv2828	D	D2	0	1	0	1	1	1	0	90	0.880	0.002
asv2916	C	C3	0	0	1	0	0	0	1	22	0.696	0.002
asv3104	C	C	0	0	1	0	0	0	0	3	0.690	0.002
asv3180	C	C4	0	0	1	1	0	0	1	56	0.541	0.019
asv3304	C	C1	0	0	1	0	0	0	1	22	0.603	0.008
asv3329	C	C1	0	0	1	0	0	0	0	3	0.657	0.003
asv3414	C	C	0	0	1	0	0	0	0	3	0.488	0.037

Table A22. Indicator species analysis for *Pocillopora* spp. derived ITS2 sequences across regions. Only ASVs with a $p < 0.05$ are shown, which are corrected for multiple testing via the Benjamini and Hochberg p-value correction. Symbiodiniaceae taxonomy is shown on the basis of ITS2-type profiles mirroring the SymPortal database's output, where "clade" and "type" delineations are shown. Yet based on recent taxonomic revision of the Symbiodiniaceae family, these profiles represent different genera and species. Briefly, ITS2-type A profiles correspond to *Symbiodinium* spp., ITS2-type B profiles correspond to *Breviolum* spp., ITS2-type C profiles correspond to *Cladocopium* spp., and ITS2-type D profiles correspond to *Durusdinium* spp.

ASV	ITSclade	ITStype	French Polynesia	Indian Ocean	Taiwan	Indices of combinations	Species indicator value	P-value
asv12	C	C1	0	1	1	6	0.9422	0.005
asv13	C	C	0	1	1	6	0.7149	0.004
asv16	D	D1	1	0	0	1	0.9829	0.002
asv17	C	C	0	0	1	3	0.8381	0.002
asv19	C	C1	0	1	1	6	0.9368	0.002
asv22	C	C	0	0	1	3	0.9616	0.002
asv24	C	C1	0	1	1	6	0.8590	0.002
asv25	A	A2	0	1	0	2	0.8897	0.002
asv26	C	C1	0	1	1	6	0.8703	0.002
asv27	D	D	1	0	0	1	0.9829	0.002
asv30	C	C4	0	1	1	6	0.8618	0.022
asv33	C	C1	0	0	1	3	0.8909	0.002
asv35	C	C1	0	0	1	3	0.8650	0.002
asv37	C	C1	0	1	1	6	0.7587	0.016
asv38	C	C1	0	0	1	3	0.7817	0.004
asv39	C	C	0	0	1	3	0.9279	0.002
asv40	D	D1	1	1	0	4	0.8929	0.009
asv41	C	C	0	0	1	3	0.8580	0.002
asv42	C	C	0	0	1	3	0.7023	0.002
asv43	C	C4	0	1	1	6	0.8323	0.002
asv44	C	C1	0	1	1	6	0.8260	0.002

asv46	C	C1	0	0	1	3	0.8759	0.002
asv49	D	D1	1	1	0	4	0.9051	0.005
asv51	C	C1	0	0	1	3	0.7690	0.002
asv54	C	C	0	1	1	6	0.7351	0.002
asv55	D	D	1	0	0	1	0.9978	0.002
asv60	C	C	0	0	1	3	0.9584	0.002
asv62	D	D	1	0	0	1	0.9966	0.002
asv66	D	D1	1	1	0	4	0.9274	0.002
asv67	C	C	0	0	1	3	0.9480	0.002
asv68	C	C	0	0	1	3	0.9579	0.002
asv70	C	C	0	0	1	3	0.9843	0.002
asv71	C	C1	0	0	1	3	0.8975	0.002
asv73	C	C1	0	1	1	6	0.7664	0.005
asv74	D	D	1	0	0	1	0.7613	0.015
asv78	C	C	0	0	1	3	0.9870	0.002
asv79	C	C1	0	1	1	6	0.7089	0.017
asv80	C	C	0	0	1	3	0.7448	0.002
asv81	D	D	1	0	0	1	0.9991	0.002
asv82	C	C1	0	0	1	3	0.6206	0.004
asv84	D	D	1	0	0	1	0.9830	0.002
asv85	C	C	0	0	1	3	0.9481	0.002
asv87	C	C	0	1	1	6	0.8176	0.005
asv88	C	C1	0	1	1	6	0.7623	0.002
asv89	C	C4	0	1	1	6	0.7936	0.002
asv90	C	C	0	0	1	3	0.7990	0.002
asv91	D	D	1	0	0	1	0.9323	0.002
asv94	C	C1	0	1	1	6	0.8059	0.002
asv95	D	D	1	0	0	1	0.8976	0.002

asv101	C	C	0	0	1	3	0.6455	0.002
asv105	C	C	0	0	1	3	0.9984	0.002
asv106	C	C1	0	1	1	6	0.8200	0.002
asv107	C	C1	0	1	1	6	0.6944	0.004
asv108	C	C1	0	1	1	6	0.7052	0.010
asv109	D	D	1	0	0	1	0.9655	0.002
asv110	D	D	1	0	0	1	0.9809	0.002
asv112	C	C1	0	0	1	3	0.8686	0.002
asv117	C	C1	0	1	1	6	0.7486	0.004
asv119	C	C	0	0	1	3	0.7661	0.002
asv123	C	C	0	0	1	3	0.7462	0.002
asv125	C	C	0	0	1	3	0.7231	0.004
asv127	C	C1	0	0	1	3	0.8602	0.002
asv128	C	C	0	0	1	3	0.8101	0.002
asv129	D	D	1	0	0	1	0.9792	0.002
asv131	C	C	0	1	1	6	0.7035	0.009
asv132	C	C1	0	0	1	3	0.7254	0.002
asv133	C	C	0	1	1	6	0.7933	0.002
asv134	C	C3	0	0	1	3	0.7652	0.004
asv136	C	C	0	0	1	3	0.9413	0.002
asv137	A	A1	0	1	0	2	0.6455	0.005
asv142	D	D	1	0	0	1	0.8792	0.002
asv144	C	C1	0	0	1	3	0.6464	0.002
asv145	D	D1	0	1	0	2	0.7720	0.004
asv148	A	A1	0	1	0	2	0.6769	0.007
asv149	A	A1	0	1	0	2	0.6454	0.005
asv152	C	C	0	1	1	6	0.7358	0.002
asv153	C	C	0	0	1	3	0.8143	0.002

asv154	C	C	0	0	1	3	0.9623	0.002
asv155	C	C1	0	0	1	3	0.7606	0.004
asv156	D	D1	0	1	0	2	0.7019	0.004
asv157	C	C3	0	0	1	3	0.7942	0.002
asv159	C	C	0	0	1	3	0.9550	0.002
asv163	C	C	0	1	1	6	0.7158	0.015
asv164	C	C	0	0	1	3	0.9940	0.002
asv166	D	D	1	0	0	1	0.9654	0.002
asv167	C	C1	0	0	1	3	0.8114	0.002
asv175	C	C1	0	0	1	3	0.5182	0.020
asv176	C	C	0	1	1	6	0.7708	0.002
asv179	C	C	0	0	1	3	0.8122	0.002
asv180	C	C	0	0	1	3	0.7357	0.002
asv182	C	C1	0	1	1	6	0.5722	0.026
asv185	C	C	0	1	1	6	0.6223	0.012
asv187	C	C1	0	0	1	3	0.9679	0.002
asv191	C	C	0	1	0	2	0.5523	0.040
asv192	C	C	0	0	1	3	0.5000	0.009
asv200	C	C4	0	0	1	3	0.9539	0.002
asv201	D	D1	0	1	0	2	0.7209	0.004
asv202	C	C1	0	0	1	3	0.6397	0.002
asv205	D	D	1	0	0	1	0.9809	0.002
asv209	C	C1	0	0	1	3	0.6458	0.002
asv211	C	C	0	0	1	3	0.9401	0.002
asv215	C	C	0	0	1	3	0.5774	0.004
asv223	C	C	0	0	1	3	0.9653	0.002
asv226	C	C	0	0	1	3	0.9552	0.002
asv227	C	C1	0	0	1	3	0.6779	0.002

asv229	C	C1	0	0	1	3	0.7826	0.002
asv232	C	C	0	0	1	3	0.9549	0.002
asv233	C	C	0	0	1	3	0.9544	0.002
asv235	C	C	0	0	1	3	0.9780	0.002
asv236	C	C	0	0	1	3	0.9558	0.002
asv237	D	D	1	0	0	1	0.9507	0.002
asv239	C	C1	0	1	1	6	0.7465	0.002
asv240	C	C	0	0	1	3	0.8321	0.002
asv243	C	C	0	0	1	3	0.9515	0.002
asv245	D	D2	1	0	0	1	0.9369	0.002
asv249	D	D	1	0	0	1	0.8600	0.002
asv260	D	D	1	0	0	1	0.9744	0.002
asv264	C	C	0	0	1	3	0.8305	0.002
asv267	C	C	0	1	1	6	0.7713	0.002
asv269	C	C	0	1	1	6	0.5909	0.025
asv270	D	D	1	0	0	1	0.8784	0.002
asv271	C	C	0	0	1	3	0.7466	0.002
asv283	C	C	0	0	1	3	0.8355	0.002
asv286	D	D	1	0	0	1	0.8597	0.002
asv293	D	D	1	0	0	1	0.9395	0.002
asv297	D	D2	1	0	0	1	0.8978	0.002
asv302	C	C	0	1	1	6	0.7175	0.012
asv312	C	C	0	1	1	6	0.7539	0.004
asv322	C	C1	0	0	1	3	0.7228	0.002
asv323	C	C	0	1	1	6	0.6148	0.010
asv327	D	D	1	0	0	1	0.9411	0.002
asv328	C	C1	0	1	1	6	0.5164	0.042
asv332	C	C	0	0	1	3	0.8595	0.002

asv347	C	C	0	1	1	6	0.7054	0.009
asv348	C	C4	0	1	0	2	0.5181	0.025
asv351	C	C1	0	1	1	6	0.6308	0.019
asv357	D	D	1	0	0	1	0.9321	0.002
asv359	D	D2	1	1	0	4	0.8186	0.005
asv368	C	C	0	1	1	6	0.6592	0.009
asv371	C	C1	0	0	1	3	0.7750	0.004
asv381	C	C1	0	0	1	3	0.7152	0.002
asv383	C	C1	0	1	1	6	0.5403	0.035
asv393	C	C3	0	0	1	3	0.7731	0.002
asv396	D	D	1	0	0	1	0.9243	0.002
asv399	C	C1	0	0	1	3	0.7200	0.002
asv402	C	C1	0	1	1	6	0.6055	0.021
asv404	C	C1	0	0	1	3	0.4411	0.025
asv405	C	C1	0	1	1	6	0.5377	0.034
asv406	C	C	0	1	1	6	0.6403	0.013
asv415	D	D1	1	0	0	1	0.7518	0.002
asv417	D	D	1	0	0	1	0.9626	0.002
asv429	D	D	1	0	0	1	0.9483	0.002
asv431	D	D	1	0	0	1	0.9594	0.002
asv440	C	C1	0	1	1	6	0.7508	0.002
asv444	C	C	0	0	1	3	0.9032	0.002
asv447	D	D	1	0	0	1	0.9476	0.002
asv449	A	A2	0	1	0	2	0.6613	0.007
asv453	D	D1	0	1	0	2	0.6880	0.002
asv459	D	D1	0	1	0	2	0.7051	0.002
asv463	D	D1	1	0	0	1	0.5690	0.015
asv467	D	D	1	0	0	1	0.9475	0.002

asv474	D	D1	1	1	0	4	0.7026	0.022
asv476	C	C1	0	1	1	6	0.7188	0.002
asv477	C	C	0	1	0	2	0.4675	0.039
asv493	C	C	0	0	1	3	0.4082	0.026
asv498	C	C1	0	0	1	3	0.8021	0.002
asv501	D	D1	0	1	0	2	0.6915	0.007
asv516	C	C	0	1	0	2	0.5379	0.022
asv519	C	C1	0	1	0	2	0.5100	0.025
asv529	D	D1	0	1	0	2	0.6894	0.005
asv533	D	D1	1	0	0	1	0.9158	0.002
asv535	C	C1	0	1	0	2	0.5367	0.016
asv537	C	C4	0	0	1	3	0.8428	0.002
asv543	C	C1	0	0	1	3	0.7830	0.002
asv553	D	D1	0	1	0	2	0.7330	0.002
asv556	C	C1	0	1	1	6	0.6679	0.005
asv558	D	D	1	0	0	1	0.9632	0.002
asv559	D	D1	1	0	0	1	0.9504	0.002
asv563	C	C1	0	1	1	6	0.6948	0.002
asv598	D	D1	0	1	0	2	0.5943	0.033
asv605	C	C1	0	0	1	3	0.8713	0.002
asv607	C	C1	0	0	1	3	0.8060	0.002
asv609	C	C1	0	0	1	3	0.8045	0.002
asv611	C	C	0	0	1	3	0.8145	0.002
asv613	C	C1	0	0	1	3	0.4719	0.015
asv639	D	D1	1	1	0	4	0.6747	0.021
asv654	C	C3	0	1	1	6	0.4830	0.027
asv682	D	D2	1	0	0	1	0.8425	0.002
asv730	D	D1	1	0	0	1	0.8715	0.002

asv735	C	C	0	0	1	3	0.6371	0.004
asv746	C	C1	0	1	1	6	0.7166	0.002
asv753	C	C4	0	0	1	3	0.8047	0.002
asv767	D	D	1	0	0	1	0.9497	0.002
asv770	C	C	0	0	1	3	0.7783	0.002
asv772	C	C1	0	0	1	3	0.8057	0.002
asv780	D	D1	0	1	0	2	0.5936	0.020
asv788	C	C	0	0	1	3	0.6366	0.010
asv806	C	C	0	0	1	3	0.4435	0.022
asv816	D	D1	1	0	0	1	0.4681	0.016
asv820	D	D	1	0	0	1	0.9383	0.002
asv825	C	C1	0	1	1	6	0.5058	0.046
asv827	C	C1	0	0	1	3	0.7269	0.002
asv836	D	D1	1	0	0	1	0.4399	0.029
asv859	C	C1	0	1	1	6	0.6472	0.010
asv862	D	D1	1	0	0	1	0.9672	0.002
asv863	C	C	0	0	1	3	0.7932	0.002
asv922	C	C1	0	0	1	3	0.7497	0.002
asv940	C	C1	0	0	1	3	0.7054	0.004
asv943	C	C1	0	0	1	3	0.6189	0.002
asv946	C	C1	0	1	1	6	0.6533	0.007
asv952	D	D2	1	1	0	4	0.7005	0.007
asv955	D	D	1	0	0	1	0.9348	0.002
asv1031	D	D	1	0	0	1	0.9448	0.002
asv1050	D	D1	0	1	0	2	0.7114	0.004
asv1093	C	C1	0	0	1	3	0.5970	0.002
asv1108	C	C1	0	1	1	6	0.5793	0.038
asv1124	C	C1	0	0	1	3	0.5619	0.017

asv1149	C	C	0	0	1	3	0.7692	0.002
asv1156	C	C	0	0	1	3	0.6697	0.007
asv1194	D	D1	0	1	0	2	0.6706	0.002
asv1203	D	D1	0	1	0	2	0.6735	0.002
asv1216	C	C	0	0	1	3	0.5743	0.017
asv1247	C	C1	0	1	1	6	0.5334	0.025
asv1252	C	C1	0	1	1	6	0.6583	0.009
asv1256	C	C1	0	0	1	3	0.4464	0.036
asv1258	D	D	1	0	0	1	0.9408	0.002
asv1310	C	C1	0	0	1	3	0.8558	0.002
asv1359	D	D1	1	0	0	1	0.6729	0.002
asv1360	C	C1	0	0	1	3	0.8270	0.002
asv1448	C	C1	0	1	1	6	0.6680	0.002
asv1465	D	D	1	0	0	1	0.9333	0.002
asv1471	D	D1	0	1	0	2	0.6862	0.002
asv1475	D	D	1	0	0	1	0.9423	0.002
asv1476	C	C	0	0	1	3	0.7708	0.002
asv1594	C	C1	0	0	1	3	0.6644	0.002
asv1600	D	D1	0	1	0	2	0.6670	0.002
asv1601	C	C3	0	0	1	3	0.7150	0.002
asv1729	C	C1	0	0	1	3	0.6350	0.002
asv1749	D	D	1	1	0	4	0.7378	0.004
asv1777	D	D1	1	0	0	1	0.4323	0.046
asv1778	D	D	1	0	0	1	0.9462	0.002
asv1784	C	C1	0	0	1	3	0.6283	0.002
asv1785	D	D	1	0	0	1	0.9278	0.002
asv1810	C	C1	0	0	1	3	0.5702	0.019
asv1863	C	C1	0	1	1	6	0.6430	0.005

asv1864	D	D1	1	0	0	1	0.7771	0.002
asv1886	C	C3	0	0	1	3	0.7059	0.002
asv1897	C	C1	0	1	0	2	0.4564	0.036
asv1931	D	D	1	0	0	1	0.9179	0.002
asv1952	C	C1	0	0	1	3	0.3620	0.050
asv2013	C	C	0	0	1	3	0.7256	0.002
asv2075	C	C1	0	1	1	6	0.5323	0.019
asv2105	D	D1	0	1	0	2	0.6834	0.002
asv2150	D	D1	1	0	0	1	0.8058	0.002
asv2157	C	C4	0	1	1	6	0.5477	0.021
asv2248	C	C1	0	1	1	6	0.5774	0.016
asv2329	C	C1	0	0	1	3	0.6871	0.002
asv2356	C	C1	0	0	1	3	0.6707	0.002
asv2486	C	C	0	1	1	6	0.5164	0.033
asv2701	C	C1	0	1	1	6	0.4830	0.047
asv2804	C	C1	0	1	1	6	0.5608	0.021
asv2805	C	C4	0	1	1	6	0.5323	0.021
asv2828	D	D2	1	0	0	1	0.8799	0.002
asv2916	C	C3	0	0	1	3	0.6903	0.002
asv3104	C	C	0	1	0	2	0.4564	0.034
asv3304	C	C1	0	0	1	3	0.4886	0.022
asv3329	C	C1	0	1	1	6	0.4830	0.040

Table A23. Indicator species analysis for *Pocillopora* spp. derived ITS2 sequences across time since last mass bleaching categories. Only ASVs with a $p < 0.05$ are shown, which are corrected for multiple testing via the Benjamini and Hochberg p-value correction. Symbiodiniaceae taxonomy is shown on the basis of ITS2-type profiles mirroring the SymPortal database's output, where "clade" and "type" delineations are shown. Yet based on recent taxonomic revision of the Symbiodiniaceae family, these profiles represent different genera and species. Briefly, ITS2-type A profiles correspond to *Symbiodinium* spp., ITS2-type B profiles correspond to *Breviolum* spp., ITS2-type C profiles correspond to *Cladocopium* spp., and ITS2-type D profiles correspond to *Durusdinium* spp.

ASV	ITSclade	ITStype	Long	Recent	Indices of combinations	Species indicator value	P-value
asv25	A	A2	1	0	1	0.8556	0.006
asv39	C	C	0	1	2	0.5464	0.046
asv40	D	D1	1	0	1	0.8960	0.008
asv42	C	C	0	1	2	0.4773	0.008
asv48	C	C	0	1	2	0.8614	0.012
asv55	D	D	0	1	2	0.8969	0.006
asv60	C	C	0	1	2	0.5297	0.047
asv68	C	C	0	1	2	0.5549	0.026
asv70	C	C	0	1	2	0.5879	0.008
asv78	C	C	0	1	2	0.5922	0.014
asv80	C	C	0	1	2	0.4209	0.043
asv81	D	D	0	1	2	0.7984	0.006
asv88	C	C1	1	0	1	0.6376	0.047
asv101	C	C	0	1	2	0.3780	0.023
asv105	C	C	0	1	2	0.6077	0.006
asv109	D	D	0	1	2	0.8003	0.006
asv129	D	D	0	1	2	0.8023	0.006
asv137	A	A1	1	0	1	0.5976	0.010
asv142	D	D	0	1	2	0.7599	0.006
asv145	D	D1	1	0	1	0.7401	0.006
asv148	A	A1	1	0	1	0.6547	0.006

asv149	A	A1	1	0	1	0.6123	0.010
asv154	C	C	0	1	2	0.5631	0.049
asv156	D	D1	1	0	1	0.6942	0.008
asv159	C	C	0	1	2	0.5842	0.006
asv160	C	C4	1	0	1	0.4009	0.045
asv164	C	C	0	1	2	0.5769	0.014
asv187	C	C1	0	1	2	0.5868	0.017
asv191	C	C	1	0	1	0.5142	0.049
asv200	C	C4	0	1	2	0.5688	0.019
asv201	D	D1	1	0	1	0.7067	0.006
asv205	D	D	0	1	2	0.7874	0.006
asv215	C	C	0	1	2	0.3381	0.041
asv223	C	C	0	1	2	0.5384	0.047
asv232	C	C	0	1	2	0.5704	0.023
asv235	C	C	0	1	2	0.5857	0.008
asv270	D	D	0	1	2	0.7728	0.006
asv286	D	D	0	1	2	0.8094	0.006
asv297	D	D2	0	1	2	0.6139	0.010
asv348	C	C4	1	0	1	0.4802	0.035
asv351	C	C1	1	0	1	0.5539	0.041
asv357	D	D	0	1	2	0.6617	0.012
asv396	D	D	0	1	2	0.7041	0.008
asv444	C	C	0	1	2	0.5523	0.026
asv449	A	A2	1	0	1	0.6123	0.008
asv453	D	D1	1	0	1	0.6648	0.008
asv459	D	D1	1	0	1	0.6529	0.008
asv474	D	D1	1	0	1	0.6613	0.047
asv477	C	C	1	0	1	0.4390	0.047

asv501	D	D1	1	0	1	0.6402	0.010
asv516	C	C	1	0	1	0.4989	0.014
asv519	C	C1	1	0	1	0.4713	0.026
asv529	D	D1	1	0	1	0.6523	0.010
asv535	C	C1	1	0	1	0.4968	0.008
asv553	D	D1	1	0	1	0.7053	0.006
asv558	D	D	0	1	2	0.7313	0.006
asv598	D	D1	1	0	1	0.5664	0.017
asv639	D	D1	1	0	1	0.6822	0.008
asv753	C	C4	0	1	2	0.5104	0.026
asv767	D	D	0	1	2	0.7344	0.006
asv780	D	D1	1	0	1	0.5660	0.014
asv862	D	D1	0	1	2	0.6652	0.010
asv952	D	D2	1	0	1	0.6641	0.008
asv1031	D	D	0	1	2	0.7035	0.008
asv1050	D	D1	1	0	1	0.6583	0.008
asv1131	D	D	0	1	2	0.3504	0.049
asv1194	D	D1	1	0	1	0.6218	0.010
asv1203	D	D1	1	0	1	0.6533	0.006
asv1359	D	D1	0	1	2	0.6339	0.006
asv1465	D	D	0	1	2	0.7456	0.006
asv1471	D	D1	1	0	1	0.6351	0.006
asv1600	D	D1	1	0	1	0.6347	0.008
asv1778	D	D	0	1	2	0.7450	0.006
asv1785	D	D	0	1	2	0.6959	0.006
asv1897	C	C1	1	0	1	0.4226	0.026
asv1931	D	D	0	1	2	0.7046	0.006
asv2105	D	D1	1	0	1	0.6324	0.006

asv2828	D	D2	0	1	2	0.6852	0.006
asv3104	C	C	1	0	1	0.4226	0.022

Appendix B

Supplementary information for Chapter 2

Environmentally-driven holobiont changes impact thermotolerance for Tropical Eastern Pacific corals

Content

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2 figures

Table B1. Sample breakdown for the various analyses. Region refers to the sample's gulf of origin, here Gulf of Panama = Panama, Gulf of Chiriquí = Chiriquí. Reefs are denoted by their three-letter code as follows: CON = Contadora; SAB = Saboga; MOG = Mogo Mogo; AFU = Canal de Afuera; BAD = Bahía Damas; UVA = Uvas. Cow tag refers to the colony's unique ID. The mtORF column denotes the mtORF lineage as follows: mtORF 1 = 1; mtORF 3 = 3; NA = unable to identify the mtORF lineage. Analyses are denoted as follows: Popgen = population genetics; Microbiome = microbiome analyses for both 16S and ITS2 marker-gene sequencing; Physio = physiology; Oxidative = oxidative metabolism.

Region	Reef	Cow tag	mtORF	Popgen	Microbiome	Physio	Oxidative
Panama	CON	700	1	X			
Panama	CON	701	3	X			
Panama	CON	702	3	X			
Panama	CON	703	3	X			
Panama	CON	704	1	X			
Panama	CON	705	3	X			
Panama	CON	706	1	X			
Panama	CON	707	3	X			
Panama	CON	708	3	X			
Panama	CON	709	3	X			
Panama	CON	710	3	X			
Panama	SAB	711	3	X	X	X	X
Panama	SAB	712	3	X	X	X	X
Panama	SAB	713	NA	X			
Panama	SAB	714	3	X	X	X	X
Panama	SAB	715	3	X	X	X	X
Panama	SAB	716	3	X	X	X	X
Panama	SAB	717	3	X			
Panama	SAB	718	3	X	X	X	X
Panama	SAB	719	3	X			
Panama	SAB	720	1	X	X	X	X
Panama	SAB	721	3	X	X	X	X
Panama	MOG	722	3	X	X	X	X
Panama	MOG	724	1	X	X	X	X
Panama	MOG	725	1	X	X	X	X
Panama	MOG	726	3	X	X	X	X
Panama	MOG	727	3	X	X	X	X
Panama	MOG	728	1	X	X	X	X
Panama	MOG	729	1	X			
Panama	MOG	730	1	X			
Panama	MOG	731	3	X	X	X	X
Panama	MOG	732	3	X	X	X	X

Chiriquí	AFU	733	1	X			
Chiriquí	AFU	734	1	X	X	X	X
Chiriquí	AFU	735	1	X			
Chiriquí	AFU	736	1	X	X	X	X
Chiriquí	AFU	737	1	X	X	X	X
Chiriquí	AFU	738	3	X	X	X	X
Chiriquí	AFU	739	1	X	X	X	X
Chiriquí	AFU	740	3	X	X	X	X
Chiriquí	AFU	741	3	X	X	X	X
Chiriquí	AFU	742	1	X			
Chiriquí	AFU	743	1	X	X	X	X
Chiriquí	BAD	744	1	X			
Chiriquí	BAD	746	1	X			
Chiriquí	BAD	747	1	X			
Chiriquí	BAD	748	1	X			
Chiriquí	BAD	749	1	X			
Chiriquí	BAD	750	1	X			
Chiriquí	BAD	751	1	X			
Chiriquí	BAD	752	1	X			
Chiriquí	BAD	753	1	X			
Chiriquí	BAD	754	1	X			
Chiriquí	UVA	755	NA	X			
Chiriquí	UVA	756	1	X	X	X	X
Chiriquí	UVA	757	3	X	X	X	X
Chiriquí	UVA	758	3	X	X	X	X
Chiriquí	UVA	759	1	X			
Chiriquí	UVA	760	1	X	X	X	X
Chiriquí	UVA	761	1	X	X	X	X
Chiriquí	UVA	762	1	X	X	X	X
Chiriquí	UVA	763	1	X	X	X	X
Chiriquí	UVA	764	1	X	X	X	X
Chiriquí	UVA	765	1	X			
Chiriquí	UVA	766	1	X			
Chiriquí	AFU	768	1	X			
Chiriquí	BAD	769	1	X			
Panama	SAB	772	3	X			
Panama	MOG	773	3	X			
Panama	CON	774	3	X			

Table B2. PCR thermocycler protocol for ITS2 rRNA amplification using the ITS-DINO (Pochon et al. 2001) and ITS2Rev2 (Stat et al. 2009) primer pair.

Temperature	Time	Repeat
94°C	3 minutes	
94°C	45 seconds	x35
50°C	1 minute	
72°C	1:30 minutes	
72°C	10 minutes	
10°C		

Table B3. PCR thermocycler protocol for 16S rRNA amplification using the updated 515F (Parada et al. 2016) and 808R (Apprill et al., 2015) primer pair from the Earth Microbiome Project (Ul-Hasan et al. 2019; https://earthmicrobiome.org/protocols-and-standards/16s/).

Temperature	Time	Repeat
95°C	3 minutes	
94°C	30 seconds	x40
52°C	30 seconds	
72°C	1:30 minutes	
72°C	7 minutes	
10°C		

Table B4. Global population genetic metric estimates for 137 *Pocillopora* coral colonies across our two gulfs in Panama's Tropical Eastern Pacific (TEP). The metrics shown are: observed heterozygosity (Ho), overall gene diversity (Ht), fixation index (Fst) following Nei (1987), Nei's Fst corrected for sample size (Fstp), and inbreeding coefficient (Fis). The first row shows values for between-gulf comparisons, and the second row shows values for between-mtORF comparisons.

	Ho	**Ht**	**Fst**	**Fstp**	**Fis**
Gulf	0.3929	0.4395	0.0333	0.0017	0.0752
mtORF	0.3674	0.4311	0.1261	0.1779	0.0249

Table B5. Functional annotations and characteristics of outlier SNPs detected as being putatively under selection by OUTFLANK (Whitlock and Lotterhos 2015). Variant type and impact were obtained from snpEff (Cingolani et al. 2012), and subsequent annotation was performed with nucleotide BLAST (blastn; Chen et al. 2015).

ID	**Chromosome**	**Position**	**SNP (ref./alt.)**	**Variant type (snpEff)**	**Variant impact (snpEff)**	**Annotation (blastn)**
NW_020843596.1:79068	NW_020843596.1	79068	G/T	Upstream gene variant	Modifier	PREDICTED: *Pocillopora damicornis* adhesion G protein-coupled receptor E1-like, mRNA
NW_020843604.1:16522	NW_020843604.1	16522	A/G	Intergenic region	Modifier	PREDICTED: *Pocillopora damicornis* uncharacterized LOC113667298 (LOC113667298), ncRNA
NW_020844150.1:1099	NW_020844150.1	1099	T/C	Intergenic region	Modifier	PREDICTED: *Stylophora pistillata* trace amine-associated receptor 1-like (LOC111346898), mRNA
NW_020844183.1:2479	NW_020844183.1	2479	A/T	Upstream gene variant	Modifier	PREDICTED: *Pocillopora damicornis* coiled-coil domain-containing protein 157-like

						(LOC113665569), partial mRNA
NW_020844825.1:12297	NW_020844825.1	12297	T/C	Intergenic region	Modifier	PREDICTED: *Pocillopora damicornis* tyrosine-protein kinase transmembrane receptor ROR2-like (LOC113671142), partial mRNA
NW_020845058.1:1199	NW_020845058.1	1199	C/T	Intergenic region	Modifier	PREDICTED: *Pocillopora damicornis* somatostatin receptor type 5-like (LOC113685845), transcript variant X1, mRNA
NW_020845258.1:5194	NW_020845258.1	5194	C/T	Missense variant	Moderate	PREDICTED: *Pocillopora damicornis* ras-related protein Rab-20-like (LOC113671341), mRNA
NW_020845264.1:311544	NW_020845264.1	311544	T/C	Upstream gene variant	Modifier	*Pocillopora damicornis* RNA-binding protein with serine-rich domain 1-like (LOC113671549), mRNA
NW_020845271.1:10758	NW_020845271.1	10758	T/C	Intron variant	Modifier	PREDICTED: *Pocillopora damicornis* hemicentin-2-like (LOC113671651), mRNA
NW_020845515.1:307337	NW_020845515.1	307337	A/G	Upstream gene variant	Modifier	PREDICTED: *Pocillopora damicornis* uncharacterized LOC113673174 (LOC113673174), mRNA
NW_020846227.1:337767	NW_020846227.1	337767	G/A	Downstream gene variant	Modifier	*Pocillopora damicornis* D(2)

						dopamine receptor A-like, mRNA

Table B6. Generalized least squares (GLS) model results of *Pocillopora* spp. ITS sub-clade relative abundances during the Coral Bleaching Automated Stress System (CBASS), across regions, temperatures, and mtORF lineages. In the GLS, the ratio of *Cladocopium* spp. to *Durusdinium* spp. is a function of the interaction between temperature, region and mtORF. Each temperature is allowed to have its own variance structure.

	Value	**Standard error**	**t-value**	**p-value**
(Intercept)	-2.078333	0.1538899	-13.505322	0.0000
Temperature	0.072155	0.0046797	15.418638	0.0000
Gulf of Panama	-1.135706	0.3658859	-3.103990	0.0024
mtORF 3	3.485324	0.2747633	12.684824	0.0000
Temperature x Gulf of Panama	0.040004	0.0109791	3.643606	0.0004
Temperature x mtORF 3	-0.088689	0.0083590	-10.610058	0.0000
Gulf of Panama x mtORF 3	0.618453	0.4551554	1.358772	0.1769
Temperature x Gulf of Panama x mtORF 3	-0.020947	0.0137268	-1.525988	0.1298

Table B7. Permutational multivariate analysis of variance (PERMANOVA) for *Pocillopora* spp. ITS2 intragenomic sequence variants (DIVs) during the Coral Bleaching Automated Stress System (CBASS), using Bray-Curtis distances and 999 permutations. The model has ITS2 DIVs as a function of the interaction between temperature, region and mtORF.

Variable	Degrees of freedom	Sum of squares	R^2	F statistic	Pr (>F)
Temperature	3	0.001092	0.03264	3.1948	0.013
Region	1	0.005507	0.16461	48.3366	0.001
mtORF	1	0.011488	0.34339	100.8311	0.001
Temperature x Region	3	0.000195	0.00584	0.5719	0.711
Temperature x mtORF	3	0.001713	0.05119	5.0103	0.001
Region x mtORF	1	0.000341	0.01020	2.9957	0.056
Temperature x Region x mtORF	3	0.000358	0.01071	1.0480	0.365
Residuals	112	0.012761	0.38142		
Total	127	0.033455	1.00000		

Table B8. Post-hoc analysis of the pairwise permutational multivariate analysis of variance (PERMANOVA) across temperatures for *Pocillopora* spp. Symbiodiniaceae communities during the Coral Bleaching Automated Stress System (CBASS). We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons.

28.5°C vs 33°C	Degrees of freedom	Sum of squares	R^2	F statistic	Pr (>F)
Temperature	1	0.0000381	0.00202	0.1256	0.939

Residual	62	0.0187984	0.99798		
Total	63	0.0188365	1.00000		

28.5°C vs 36°C	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Temperature	1	0.0008508	0.0637	4.218	0.025
Residual	62	0.0125051	0.9363		
Total	63	0.0133559	1.0000		

28.5°C vs 30°C	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Temperature	1	0.0000286	0.00147	0.094	0.957
Residual	64	0.0194426	0.99853		
Total	65	0.0194711	1.00000		

33°C vs 36°C	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Temperature	1	0.0005781	0.04283	2.6846	0.05
Residual	60	0.0129209	0.95717		

Total	61	0.0134991	1.00000		

33°C vs 30°C	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Temperature	1	0.0000157	0.00079	0.0492	0.983
Residual	62	0.0198584	0.99921		
Total	63	0.0198741	1.00000		

36°C vs 30°C	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Temperature	1	0.0006899	0.04839	3.1531	0.053
Residual	62	0.0135651	0.95161		
Total	63	0.0142550	1.00000		

Table B9. Analysis of *Pocillopora* spp. Symbiodiniaceae communities' homogeneity of multivariate dispersions across temperatures during the Coral Bleaching Automated Stress System (CBASS). We used Bray-Curtis distances and 999 permutations. Our group dispersion results were run in an ANOVA to determine if the variance of each group's distance from the centroid was statistically significant. Tukey's Honest Significant Differences test was used for post-hoc comparisons at a 95% confidence level, where the p-values shown have been adjusted for multiple comparisons.

Permutation test for homogeneity of multivariate dispersions

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Number of permutations	Pr (>F)
Groups	3	0.0009725	0.00032416	8.4304	999	0.001
Residuals	124	0.0047680	0.00003845			

Average distance to centroid

28.5°C	30.0°C	33.0°C	36.0°C
0.015575	0.016256	0.016886	0.009789

ANOVA

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Pr (>F)
Groups	3	0.0010008	0.00033359	10.803	2.343e-06
Residual	124	0.0038289	0.00003088		

Tukey's Honest Significant Differences test

Group	Differences	Lower	Upper	Adjusted p-value
30°C-28.5°C	0.0006811788	-0.002881354	0.004243712	0.9593972
33°C-28.5°C	0.0013108648	-0.002308672	0.004930402	0.7816485
36°C-28.5°C	-0.0057858521	-0.009405389	-0.002166315	0.0003368
33°C-30°C	0.0006296860	-0.002989851	0.004249223	0.9689230

36°C-30°C	-0.0064670310	-0.010086568	-0.002847494	0.0000485
36°C-33°C	-0.0070967170	-0.010772374	-0.003421060	0.0000100

Table B10. Indicator species analysis for the Symbiodiniaceae communities originating from *Pocillopora* spp. mtORF 1 colonies in the Gulf of Chiriquí during the Coral Bleaching Automated Stress System (CBASS). Only ITS sub-clades with a $p < 0.05$ are shown, which are corrected for multiple testing via the Benjamini and Hochberg p-value correction. Sub-clades starting with a "C" correspond to *Cladocopium* spp., and those starting with a "D" correspond to *Durusdinium* spp. Sub-clades starting with numbers, e.g. 92366_C, represent sequences not found on SymPortal and are thus given a unique number before their identified genus. DIV refers to intragenomic sequence variant. Temperatures shown are as follows: 28.5 = 28.5°C; 30 = 30°C; 33 = 33°C; 36 = 36°C.

DIV	**ITS sub-clades**	**Genera**	**28.5**	**30**	**33**	**36**	**Indices of combinations**	**Species indicator value**	**P-value**
DIV2	C42	*Cladocopium* spp.	0	0	0	1	4	0.982128289	0.0063125
DIV3	C1	*Cladocopium* spp.	0	0	0	1	4	0.985428774	0.0063125
DIV5	C42	*Cladocopium* spp.	0	0	0	1	4	0.983504895	0.0063125
DIV7	C1	*Cladocopium* spp.	0	0	0	1	4	1	0.0063125
DIV8	C1	*Cladocopium* spp.	0	0	0	1	4	1	0.0063125
DIV11	C3	*Cladocopium* spp.	0	0	0	1	4	1	0.0063125
DIV12	C1	*Cladocopium* spp.	0	0	0	1	4	0.979795897	0.0063125
DIV13	C42	*Cladocopium* spp.	0	0	0	1	4	0.985702203	0.0063125

DIV14	C115	*Cladocopium* spp.	0	0	0	1	4	0.986142517	0.0063125
DIV15	C45	*Cladocopium* spp.	0	0	0	1	4	0.674199862	0.01594737
DIV16	C1	*Cladocopium* spp.	0	0	0	1	4	0.641688948	0.02295455
DIV17	C42	*Cladocopium* spp.	0	0	0	1	4	0.674199862	0.01594737
DIV18	C42	*Cladocopium* spp.	0	0	0	1	4	0.992712032	0.0063125
DIV19	C42	*Cladocopium* spp.	0	0	0	1	4	0.891366897	0.0063125
DIV22	C1	*Cladocopium* spp.	0	0	0	1	4	0.852802865	0.0063125
DIV25	92271_C	*Cladocopium* spp.	0	0	0	1	4	0.738548946	0.0063125
DIV26	126_C	*Cladocopium* spp.	0	0	0	1	4	0.852802865	0.0063125
DIV27	115_C	*Cladocopium* spp.	0	0	0	1	4	0.674199862	0.0202
DIV30	33417_C	*Cladocopium* spp.	0	0	0	1	4	0.852802865	0.0063125
DIV31	92259_C	*Cladocopium* spp.	0	0	0	1	4	0.674199862	0.01188235
DIV33	92250_C	*Cladocopium* spp.	0	0	0	1	4	0.603022689	0.04391304

DIV35	92366_C	*Cladocopium* spp.	0	0	0	1	4	0.603022689	0.02295455
DIV96	D1	*Durusdinium* spp.	1	1	1	0	11	0.900132173	0.0063125

Table B11. Permutational multivariate analysis of variance (PERMANOVA) for *Pocillopora* spp. prokaryotic 16S amplicon sequence variants (ASV) during the Coral Bleaching Automated Stress System (CBASS), using Bray-Curtis distances and 999 permutations. The model has 16S ASVs as a function of the interaction between temperature, region and mtORF.

Variable	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Temperature	3	0.00690	0.00627	0.2570	0.999
Region	1	0.02357	0.02143	2.6340	0.034
mtORF	1	0.00448	0.00408	0.5010	0.763
Temperature x Region	3	0.04597	0.04179	1.7123	0.059
Temperature x mtORF	3	0.00754	0.00685	0.2809	0.996
Region x mtORF	1	0.00251	0.00229	0.2810	0.929
Temperature x Region x mtORF	3	0.00675	0.00613	0.2513	0.994
Residuals	112	1.00231	0.91116		
Total	127	1.10004	1.00000		

Table B12. Analysis of *Pocillopora* spp. prokaryotic communities' homogeneity of multivariate dispersions across temperatures during the Coral Bleaching Automated Stress System (CBASS). We used Bray-Curtis distances and 999 permutations. Group dispersion results were run in an ANOVA to determine if the variance of each group's distance from the centroid was statistically significant. Tukey's Honest Significant Differences test was used for post-hoc comparisons at a 95% confidence level, where the p-values shown have been adjusted for multiple comparisons.

Permutation test for homogeneity of multivariate dispersions

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Number of permutations	Pr (>F)
Groups	3	0.48455	0.161517	101.87	999	0.001
Residuals	124	0.19660	0.001585			

Average distance to centroid

28.5°C	30.0°C	33.0°C	36.0°C
0.01770	0.01870	0.03207	0.16632

ANOVA

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Pr (>F)
Groups	3	0.48914	0.163046	109.21	< 2.2e-16
Residual	124	0.18512	0.001493		

Tukey's Honest Significant Differences test

Group	Differences	Lower	Upper	Adjusted p-value
30°C-28.5°C	0.001000686	-0.02377100	0.02577237	0.9995811
33°C-28.5°C	0.014378593	-0.01078946	0.03954665	0.4479291
36°C-28.5°C	0.148628518	0.12346046	0.17379657	0.0000000
33°C-30°C	0.013377907	-0.01179015	0.03854596	0.5115752

36°C-30°C	0.147627831	0.12245977	0.17279589	0.0000000
36°C-33°C	0.134249925	0.10869164	0.15980821	0.0000000

Table B13. Akaike Information Criterion (AIC) and log-likelihood tests for our top six models of *Pocillopora* coral's protein concentrations during the Coral Bleaching Automated Stress System (CBASS). Each likelihood ratio test compares the model against the one above it.

Parameter						Degrees of freedom	AIC	Likelihood Ratio	P-value
Threshold location (a)		**Threshold steepness (d)**		**Maximum protein concentration (ν)**					
Fixed	Random	Fixed	Random	Fixed	Random				
Region	No	mtORF x Region	Site	mtORF x Region	Site	11	267.8205		
Region	No	Region	Site	No	Site	8	266.4547	4.634229	0.200625
No	No	Region	Site	mtORF x Region	Site	10	277.7896	7.33492	0.025541
No	No	No	Site	mtORF x Region	Site	9	276.7839	0.994294	0.318695
No	No	Region	Site	No	Site	7	275.6957	2.91176	0.233195
Region	No	No	Site	No	Site	7	268.2306		

Table B14. Model coefficients for host protein concentrations of *Pocillopora* corals during the Coral Bleaching Automated Stress System (CBASS). α = 50% temperature threshold; δ = threshold steepness; ν = maximum protein concentration. Parameter subscripts indicate how each varies according to region (e.g. Gulf of Panama = p) or to denote the intercept of a parameter. Rows denote the estimates for each reef site: BAD = Bahía Damas; SAB = Saboga; MOG = Mogo Mogo; AFU = Canal de Afuera; UVA = Uvas. Absolute values are calculated with reference to the parameter's intercept value.

Reef site	$\boldsymbol{\nu}$	$\boldsymbol{\delta_{\text{intercept}}}$	$\boldsymbol{\delta_{\text{p}}}$	$\boldsymbol{\alpha_{\text{intercept}}}$	$\boldsymbol{\alpha_{\text{p}}}$
BAD	0.9452581	6.229163	63.10046	33.72936	1.219967
SAB	0.8356587	25.405578	63.10046	33.72936	1.219967
MOG	0.9738917	27.357492	63.10046	33.72936	1.219967
AFU	1.1898177	44.899099	63.10046	33.72936	1.219967
UVA	1.2769188	28.016342	63.10046	33.72936	1.219967

Table B15. Akaike Information Criterion (AIC) and log-likelihood tests for our top six models of *Pocillopora* coral's chlorophyll *a* concentrations during the Coral Bleaching Automated Stress System (CBASS). Each likelihood ratio test compares the model against the one above it.

Parameter						Degrees of freedom	AIC	Likelihood Ratio	P-value
Threshold location (a)		**Threshold steepness (d)**		**Maximum chlorophyll *a* concentration (ν)**					
Fixed	Random	Fixed	Random	Fixed	Random				
mtORF x Region	No	mtORF x Region	Site	Region	No	12	1812.302		
mtORF x Region	No	No	Site	Region	No	9	1842.395	36.09252	7.16E-08
mtORF x Region	No	mtORF x Region	Site	No	No	11	1829.862	16.53239	0.000257062
No	No	mtORF x Region	Site	Region	No	9	1818.785	7.077612	0.029047985
No	No	No	Site	Region	No	6	1844.114	31.32896	7.25E-07
No	No	Region	Site	No	No	6	1843.763		

Table B16. Model coefficients for chlorophyll *a* concentrations of *Pocillopora* corals during the Coral Bleaching Automated Stress System (CBASS). α = 50% temperature threshold; δ = threshold steepness; ν = maximum protein concentration. Parameter subscripts indicate how each varies according to region (e.g. Gulf of Panama = p), mtORF lineage (e.g. mtORF 3 = 3), the interaction between two variables (e.g. mtORF lineage 3 and region = 3×p), or to denote the intercept of a parameter. Rows denote the estimates for each reef site: BAD = Bahía Damas; SAB = Saboga; MOG = Mogo Mogo; AFU = Canal de Afuera; UVA = Uvas. Absolute values are calculated with reference to the parameter's intercept value.

Reef site	$\nu_{intercept}$	ν_{p}	$\delta_{intercept}$	δ_{3}	δ_{p}	$\delta_{3}\times_{p}$	$\alpha_{intercept}$	α_{3}	α_{p}	$\alpha_{3}\times_{p}$
BAD	12.31379	-3.850346	8.063902	34.47371	136.9938	-134.2905	32.11737	2.105019	1.323442	-0.7420646
SAB	12.31379	-3.850346	8.064165	34.47371	136.9938	-134.2905	32.11737	2.105019	1.323442	-0.7420646
MOG	12.31379	-3.850346	8.064194	34.47371	136.9938	-134.2905	32.11737	2.105019	1.323442	-0.7420646
AFU	12.31379	-3.850346	8.064270	34.47371	136.9938	-134.2905	32.11737	2.105019	1.323442	-0.7420646
UVA	12.31379	-3.850346	8.064366	34.47371	136.9938	-134.2905	32.11737	2.105019	1.323442	-0.7420646

Table B17. Akaike Information Criterion (AIC) scores for our top models of *Pocillopora* coral's lipid peroxidation (LPO) concentrations during the CBASS. The term "Algae_prop" refers to the relative proportion of *Cladocopium* spp. versus *Durusdinium* spp. As a point of comparison, our intercept-only model is logLPO ~ 1.

Model	Degrees of freedom	AIC
logLPO ~ 1	2	84.65795
logLPO ~ Temperature x Region	7	74.10877
logLPO ~ Region	3	76.18086
logLPO ~ Region x Algae_prop	5	75.08119
logLPO ~ Temperature + Region	5	79.47314

Table B18. Likelihood ratio tests for our top models of *Pocillopora* coral's lipid peroxidation (LPO) concentrations during the CBASS. The term "Algae_prop" refers to the relative proportion of *Cladocopium* spp. versus *Durusdinium* spp.

Model	Number of degrees of freedom	Log-likelihood	Degrees of freedom	Chi-square test	Pr (>Chi-square test)
logLPO ~ Region	3	-35.090			
logLPO ~ Temperature x Region	7	-30.054	4	10.072	0.03923

Model	Number of degrees of freedom	Log-likelihood	Degrees of freedom	Chi-square test	Pr (>Chi-square test)
logLPO ~ Region	3	-35.090			
logLPO ~ Region x Algae_prop	5	-32.541	2	5.0997	0.07809

Model	Number of degrees of freedom	Log-likelihood	Degrees of freedom	Chi-square test	Pr (>Chi-square test)
logLPO ~ Region	3	-35.090			
logLPO ~ Temperature + Region	5	-34.737	2	0.7077	0.702

Table B19. Post-hoc comparisons of lipid peroxidation (LPO) in *Pocillopora* corals during the Coral Bleaching Automated Stress System (CBASS). We implemented the Bonferroni p-value correction due to multiple comparisons. Temperatures are shown in degrees Celsius.

Region	Temperature	Contrast	Estimate	Standard error	Degrees of freedom	T ratio	P-value
Chiriquí		30 vs 28.5	0.3136	0.131	82	2.393	0.1330
Chiriquí		33 vs 30	-0.1361	0.129	82	-1.057	1.0000
Panama		30 vs 28.5	-0.2071	0.125	82	-1.658	0.7084
Panama		33 vs 30	-0.0468	0.133	82	-0.352	1.0000
	28.5	Panama vs Chiriquí	0.5731	0.131	82	4.372	0.0003
	30	Panama vs Chiriquí	0.0524	0.125	82	0.419	1.0000
	33	Panama vs Chiriquí	0.1417	0.137	82	1.037	1.0000

Table B20. Akaike Information Criterion (AIC) scores for our top models of *Pocillopora* coral's total antioxidant capacity (TAC) during the Coral Bleaching Automated Stress System (CBASS). The term "Algae_prop" refers to the relative proportion of *Cladocopium* spp. versus *Durusdinium* spp. As a point of comparison, our intercept-only model is sqrtTAC ~ 1.

Model	Degrees of freedom	AIC
sqrtTAC ~ 1	2	1172.365
sqrtTAC ~ poly(Temp, 2)	4	1025.745
sqrtTAC ~ poly(Temp, 2) + Algae_prop	5	1024.500
sqrtTAC ~ poly(Temp, 2) + Region	5	1027.621
sqrtTAC ~ poly(Temp, 2) + mtORF	5	1027.376

Table B21. Likelihood ratio test for our top models of *Pocillopora* coral's total antioxidant capacity (TAC) during the Coral Bleaching Automated Stress System (CBASS). The term "Algae_prop" refers to the relative proportion of *Cladocopium* spp. versus *Durusdinium* spp.

Model	Number of degrees of freedom	Log-likelihood	Degrees of freedom	Chi-square test	Pr (>Chi-square test)
sqrtTAC ~ poly(Temp, 2)	4	-508.87			
sqrtTAC ~ poly(Temp, 2) + Algae_prop	5	-507.25	1	3.2455	0.07162

Model	Number of degrees of freedom	Log-likelihood	Degrees of freedom	Chi-square test	Pr (>Chi-square test)
sqrtTAC ~ poly(Temp, 2)	4	-508.87			
sqrtTAC ~ poly(Temp, 2) + Region	5	-508.81	1	0.1241	0.7247

Model	Number of degrees of freedom	Log-likelihood	Degrees of freedom	Chi-square test	Pr (>Chi-square test)
sqrtTAC ~ poly(Temp, 2)	4	-508.87			
sqrtTAC ~ poly(Temp, 2) + mtORF	5	-508.69	1	0.3688	0.5437

Model	Number of degrees of freedom	Log-likelihood	Degrees of freedom	Chi-square test	Pr (>Chi-square test)
sqrtTAC ~ poly(Temp, 2) + Region	5	-508.81			
sqrtTAC ~ poly(Temp, 2) + mtORF	5	-508.69	0	0.2447	< 2.2e-16

Model	Number of degrees of freedom	Log-likelihood	Degrees of freedom	Chi-square test	Pr (>Chi-square test)
sqrtTAC ~ poly(Temp, 2) + Region	5	-508.81			

sqrtTAC ~ poly(Temp, 2) + Algae_prop	5	-507.25	0	3.1215	< 2.2e-16

Model	**Number of degrees of freedom**	**Log-likelihood**	**Degrees of freedom**	**Chi-square test**	**Pr (>Chi-square test)**
sqrtTAC ~ poly(Temp, 2) + mtORF	5	-508.69			
sqrtTAC ~ poly(Temp, 2) + Algae_prop	5	-507.25	0	2.8768	< 2.2e-16

Table B22. Model results of *Pocillopora* coral's total antioxidant capacity (TAC) during the Coral Bleaching Automated Stress System (CBASS) as a function of temperature and the relative proportion of *Cladocopium* spp. versus *Durusdinium* spp, here "Algae_prop". This variable represents the relative reads mapping to *Cladocopium* spp. versus *Durusdinium* spp.

	Estimate	**Standard error**	**t-value**	**p-value**
(Intercept)	66.031	3.067	21.527	< 2e-16
poly(Temp, 2)1	-284.556	19.692	-14.450	< 2e-16
poly(Temp, 2)2	-174.592	20.007	-8.727	2.82e-14
Algae_prop	-7.517	4.217	-1.783	0.0774

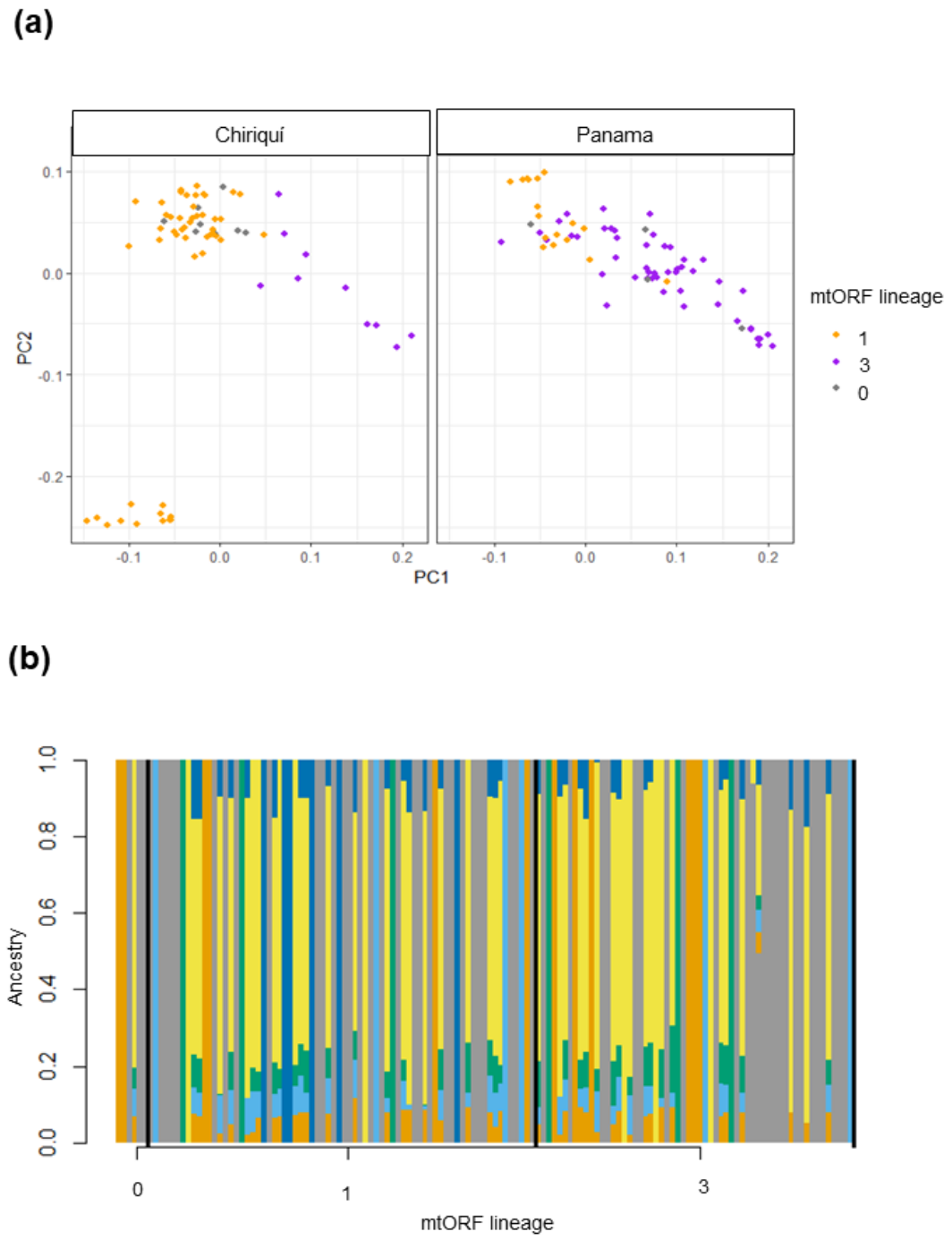

Figure B1. Population genetics of *Pocillopora* corals across mtORF lineages. Samples whose mtORF lineage could not be identified are denoted as "mtORF 0." **(a)** pcadapt plot (Luu et al. 2017) showing allele frequency differences across the mtORF lineages identified in Panama's TEP. **(b)** Ancestral populations across the mtORF lineages identified in Panama's Tropical Eastern Pacific (TEP) using ADMIXTURE (Alexander and Lange 2011). A total of six ancestral populations were identified and each line on the plot represents a single individual, where the colors within represent the different identified ancestral populations. Thick black lines delineate different mtORF lineages.

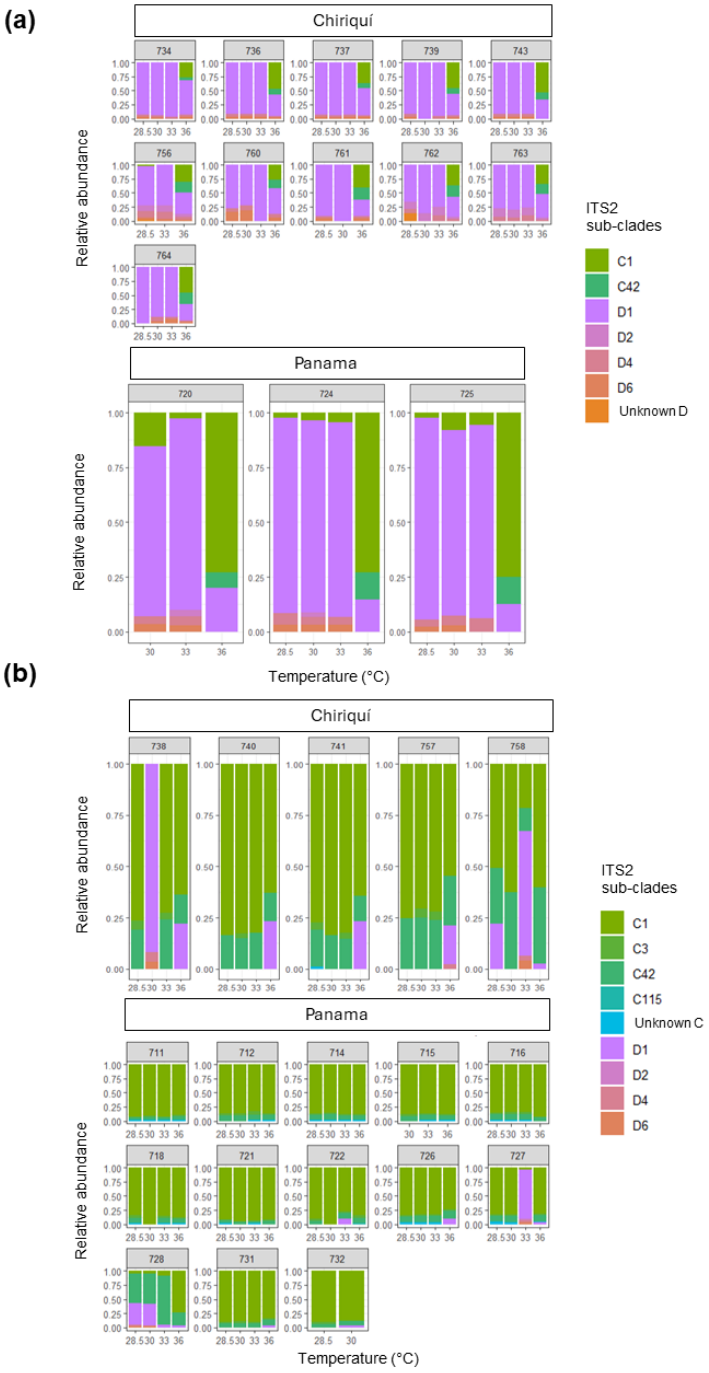

Figure B2. Individual *Pocillopora* colonies' Symbiodiniaceae community shifts during the Coral Bleaching Automated Stress System (CBASS), across regions and mtORF lineages. Relative abundances of ITS2 sub-clades are shown on the x-axis and temperature treatments on the y-axis. Corresponding colony cow tag numbers are shown above each individual plot. Sub-clades starting with a "C" correspond to *Cladocopium* spp., and those starting with a "D" correspond to *Durusdinium* spp. ITS2 sequences that could not be identified beyond the genus level are denoted as "unknown C" or "unknown D," meaning these specific taxa were not found within the SymPortal database. **(a)** Symbiodiniaceae community shifts for mtORF 1 colonies. **(b)** Symbiodiniaceae community shifts for mtORF 3 colonies.

Appendix C

Supplementary information for Chapter 3

Algal thermotolerance drives differences in prokaryotic microbiome dynamics for an emerging coral model system

Content

15 tables

Table C1. Permutational multivariate analysis of variance (PERMANOVA) for *Aiptasia*'s prokaryotic 16S amplicon sequence variants (ASV) during our acute thermal stress assay, for both heat stress and control samples together, using Bray-Curtis distances and 999 permutations**.** The model has 16S ASVs as a function of the interaction between treatment (control versus heat stress), line (CC7-SSA01 versus CC7-SSB01), and time point.

Variable	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Treatment	1	0.00835	0.01667	2.4508	0.073
Line	1	0.29552	0.58981	86.6977	0.001
Time	5	0.06306	0.12586	3.7001	0.003
Treatment x Line	1	0.00367	0.00733	1.0777	0.318
Treatment x Time	5	0.01449	0.02892	0.8503	0.607
Line x Time	5	0.02941	0.05869	1.7254	0.081
Treatment x Line x Time	5	0.02177	0.04346	1.2776	0.228
Residuals	19	0.06476	0.12926		
Total	42	0.50105	1.00000		

Table C2. Permutational multivariate analysis of variance (PERMANOVA) for *Aiptasia*'s prokaryotic 16S amplicon sequence variants (ASV) for only control samples across lines, using Bray-Curtis distances and 999 permutations. The model has 16S ASVs as a function of line (CC7-SSA01 versus CC7-SSB01).

Variable	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Line	1	0.076608	0.59336	14.592	0.006
Residuals	10	0.052501	0.40664		

Total	11	0.129109	1.00000		

Table C3. Permutational multivariate analysis of variance (PERMANOVA) for *Aiptasia*'s prokaryotic 16S amplicon sequence variants (ASV) for only control samples across time points, using Bray-Curtis distances and 999 permutations. The model has 16S ASVs as a function of time point.

Variable	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Line	5	0.02576	0.19952	0.2991	0.966
Residuals	6	0.10335	0.80048		
Total	11	0.12911	1.00000		

Table C4. Permutational multivariate analysis of variance (PERMANOVA) for *Aiptasia*'s prokaryotic 16S amplicon sequence variants (ASV) for only CC7-SSA01 animals, using Bray-Curtis distances and 999 permutations. The model has 16S ASVs as a function of the interaction between treatment (control versus heat stress) and time point.

Variable	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Treatment	1	0.001971	0.03021	0.7843	0.618
Time	5	0.026294	0.40304	2.0923	0.006
Treatment x Time	5	0.019380	0.29706	1.5421	0.107
Residuals	7	0.017594	0.26968		
Total	18	0.065240	1.00000		

Table C5. Permutational multivariate analysis of variance (PERMANOVA) for *Aiptasia*'s prokaryotic 16S amplicon sequence variants (ASV) for only CC7-SSB01 animals, using Bray-Curtis distances and 999 permutations. The model has 16S ASVs as a function of the interaction between treatment (control versus heat stress) and time point.

Variable	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Treatment	1	0.006237	0.04569	1.5866	0.139
Time	5	0.066389	0.48632	3.3779	0.001
Treatment x Time	5	0.016716	0.12245	0.8505	0.686
Residuals	12	0.047170	0.34554		
Total	23	0.136512	1.00000		

Table C6. Permutational multivariate analysis of variance (PERMANOVA) for *Aiptasia*'s prokaryotic 16S amplicon sequence variants (ASV) during our acute thermal stress assay, for only heat stress samples, using Bray-Curtis distances and 999 permutations. The model has 16S ASVs as a function of the interaction between line (CC7-SSA01 versus CC7-SSB01), and time point.

Variable	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Line	1	0.22254	0.61207	65.2872	0.001
Time	5	0.05184	0.14258	3.0417	0.006
Line x Time	5	0.02444	0.06722	1.4340	0.180
Residuals	19	0.06476	0.17813		
Total	30	0.36358	1.00000		

Table C7. Post-hoc analysis of the pairwise permutational multivariate analysis of variance (PERMANOVA) across time points for CC7-SSA01 *Aiptasia*'s prokaryotic communities during our acute thermal stress assay**.** We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons. Time points are on the basis of hours, e.g. 0h = 0 hours.

0h vs 3h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0022454	0.17096	0.6186	0.9
Residual	3	0.0108885	0.82904		
Total	4	0.0131339	1.00000		

0h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0025428	0.33539	1.5139	0.2
Residual	3	0.0050388	0.66461		
Total	4	0.0075817	1.00000		

0h vs 24h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0049322	0.83101	4.9174	0.3333
Residual	1	0.0010030	0.16899		
Total	2	0.0059352	1.00000		

0h vs 48h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0026782	0.56619	2.6103	0.3333
Residual	2	0.0020520	0.43381		

Total	3	0.0047302	1.00000		

0h vs 96h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0122407	0.82348	9.3303	0.3333
Residual	2	0.0026238	0.17652		
Total	3	0.0148645	1.00000		

3h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.002215	0.13726	0.6364	0.8
Residual	4	0.013921	0.86274		
Total	5	0.016136	1.00000		

24h vs 3h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0033343	0.25222	0.6746	0.75
Residual	2	0.0098855	0.74778		
Total	3	0.0132198	1.00000		

24h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0034665	0.46205	1.7178	0.25
Residual	2	0.0040358	0.53795		

Total	3	0.0075023	1.00000		

24h vs 48h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.003205	0.75341	3.0554	0.3333
Residual	1	0.001049	0.24659		
Total	2	0.004254	1.00000		

24h vs 96h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0052979	0.76573	3.2686	0.3333
Residual	1	0.0016208	0.23427		
Total	2	0.0069187	1.00000		

48h vs 3h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.004811	0.30555	1.3199	0.4
Residual	3	0.010934	0.69445		
Total	4	0.015745	1.00000		

48h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0031426	0.38197	1.8541	0.2
Residual	3	0.0050848	0.61803		

Total	4	0.0082275	1.00000		

48h vs 96h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0072675	0.73133	5.4442	0.3333
Residual	2	0.0026698	0.26867		
Total	3	0.0099373	1.00000		

96h vs 3h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0097304	0.45819	2.5369	0.1
Residual	3	0.0115064	0.54181		
Total	4	0.0212367	1.00000		

96h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0095316	0.62756	5.055	0.1
Residual	3	0.0056567	0.37244		
Total	4	0.0151882	1.00000		

Table C8. Post-hoc analysis of the pairwise permutational multivariate analysis of variance (PERMANOVA) across time points for CC7-SSB01 *Aiptasia*'s prokaryotic communities during our acute thermal stress assay. We used Bray-Curtis distances, 999 permutations, and implemented Benjamini and Hochberg p-value corrections due to multiple comparisons. Time points are on the basis of hours, e.g. 0h = 0 hours.

0h vs 3h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0023873	0.12738	0.5839	1
Residual	4	0.0163547	0.87262		
Total	5	0.0187420	1.00000		

0h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0063394	0.34095	2.0694	0.1
Residual	4	0.0122539	0.65905		
Total	5	0.0185934	1.00000		

0h vs 24h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0095031	0.46358	3.4568	0.1
Residual	4	0.0109963	0.53642		
Total	5	0.0204994	1.00000		

0h vs 48h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0060392	0.30984	1.7957	0.1
Residual	4	0.0134524	0.69016		

Total	5	0.0194917	1.00000		

0h vs 96h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.016882	0.47707	3.6492	0.1
Residual	4	0.018505	0.52293		
Total	5	0.035387	1.00000		

3h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0061267	0.27183	1.4932	0.1
Residual	4	0.0164125	0.72817		
Total	5	0.0225392	1.00000		

24h vs 3h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.010072	0.39927	2.6585	0.1
Residual	4	0.015155	0.60073		
Total	5	0.025227	1.00000		

24h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.0044709	0.28798	1.6178	0.2
Residual	4	0.0110541	0.71202		

Total	5	0.0155250	1.00000		

24h vs 48h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.013434	0.523	4.3857	0.1
Residual	4	0.012253	0.477		
Total	5	0.025687	1.000		

24h vs 96h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.011881	0.40709	2.7464	0.1
Residual	4	0.017305	0.59291		
Total	5	0.029186	1.00000		

48h vs 3h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.007074	0.28657	1.6067	0.2
Residual	4	0.017611	0.71343		
Total	5	0.024685	1.00000		

48h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.012959	0.48959	3.8369	0.1
Residual	4	0.013510	0.51041		

Total	5	0.026469	1.00000		

48h vs 96h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.011370	0.36523	2.3014	0.1
Residual	4	0.019761	0.63477		
Total	5	0.031131	1.00000		

96h vs 3h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.017862	0.44076	3.1525	0.1
Residual	4	0.022663	0.55924		
Total	5	0.040525	1.00000		

96h vs 12h	**Degrees of freedom**	**Sum of squares**	**R^2**	**F statistic**	**Pr (>F)**
Time	1	0.016383	0.46882	3.5304	0.1
Residual	4	0.018563	0.53118		
Total	5	0.034946	1.00000		

Table C9. Analysis of heat stressed *Aiptasia*'s prokaryotic communities' homogeneity of multivariate dispersions for CC7-SSA01 and CC7-SSB01 animals across all time points during our acute thermal stress assay. We used Bray-Curtis distances and 999 permutations. Our group dispersion results were run in an ANOVA to determine if the variance of each group's distance from the centroid was statistically significant. Tukey's Honest Significant Differences test was used for post-hoc comparisons at a 95% confidence level, where the p-values shown have been adjusted for multiple comparisons. Time points are on the basis of hours, e.g. 0h = 0 hours.

Permutation test for homogeneity of multivariate dispersions

	Degrees of freedom	**Sum of squares**	**Mean squared error**	**F statistic**	**Number of permutations**	**Pr (>F)**
Groups	1	0.0022604	0.00226044	6.5702	999	0.016
Residuals	29	0.0099773	0.00034405			

Average distance to centroid

CC7-SSA01	**CC7-SSB01**
0.05528	0.07228

ANOVA

	Degrees of freedom	**Sum of squares**	**Mean squared error**	**F statistic**	**Pr (>F)**
Groups	1	0.0021815	0.00218152	8.6812	0.006283
Residual	29	0.0072874	0.00025129		

Tukey's Honest Significant Differences test

Group	**Differences**	**Lower**	**Upper**	**Adjusted p-value**
CC7-SSB01 vs CC7-SSA01	0.01700012	0.005199533	0.02880072	0.0062834

Table C10. Analysis of heat stressed CC7-SSA01 *Aiptasia*'s prokaryotic communities' homogeneity of multivariate dispersions across time points during our acute thermal stress assay. We used Bray-Curtis distances and 999 permutations. Our group dispersion results were run in an ANOVA to determine if the variance of each group's distance from the centroid was statistically significant. Tukey's Honest Significant Differences test was used for post-hoc comparisons at a 95% confidence level, where the p-values shown have been adjusted for multiple comparisons. Time points are on the basis of hours, e.g. 0h = 0 hours.

Permutation test for homogeneity of multivariate dispersions

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Number of permutations	Pr (>F)
Groups	5	0.0030329	0.00060658	2.3448	999	0.107
Residuals	7	0.0018109	0.00025869			

Average distance to centroid

0h	3h	12h	24h	48h	96h
0.02239	0.05638	0.03646	0.00000	0.02290	0.02847

ANOVA

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Pr (>F)
Groups	5	0.0032347	0.00064695	11.463	0.002891
Residual	7	0.0003951	0.00005644		

Tukey's Honest Significant Differences test

Group	Differences	Lower	Upper	Adjusted p-value
3h vs 0h	0.0339893865	0.008002023	0.059976750	0.0131584
12h vs 0h	0.0140700044	-0.011917359	0.040057368	0.4015579
24h vs 0h	-0.0223943326	-0.057260039	0.012471374	0.2605829
48h vs 0h	0.0005073892	-0.027960341	0.028975120	0.9999997
96h vs 0h	0.0060735088	-0.022394222	0.034541239	0.9568628

12h vs 3h	-0.0199193822	-0.043163187	0.003324422	0.0967608
24h vs 3h	-0.0563837191	-0.089255423	-0.023512015	0.0028233
48h vs 3h	-0.0334819974	-0.059469361	-0.007494634	0.0142590
96h vs 3h	-0.0279158777	-0.053903241	-0.001928514	0.0357925
24h vs 12h	-0.0364643369	-0.069336041	-0.003592633	0.0306385
48h vs 12h	-0.0135626152	-0.039549979	0.012424748	0.4343045
96h vs 12h	-0.0079964955	-0.033983859	0.017990868	0.8397846
48h vs 24h	0.0229017217	-0.011963985	0.057767429	0.2441372
96h vs 24h	0.0284678414	-0.006397866	0.063333548	0.1168790
96h vs 48h	0.0055661197	-0.022901611	0.034033850	0.9696504

Table C11. Analysis of heat stressed CC7-SSB01 *Aiptasia*'s prokaryotic communities' homogeneity of multivariate dispersions across time points during our acute thermal stress assay. We used Bray-Curtis distances and 999 permutations. Our group dispersion results were run in an ANOVA to determine if the variance of each group's distance from the centroid was statistically significant. Tukey's Honest Significant Differences test was used for post-hoc comparisons at a 95% confidence level, where the p-values shown have been adjusted for multiple comparisons. Time points are on the basis of hours, e.g. 0h = 0 hours.

Permutation test for homogeneity of multivariate dispersions

	Degrees of freedom	**Sum of squares**	**Mean squared error**	**F statistic**	**Number of permutations**	**Pr (>F)**
Groups	5	0.0011007	0.00022013	0.8009	999	0.596
Residuals	12	0.0032981	0.00027484			

Average distance to centroid

0h	**3h**	**12h**	**24h**	**48h**	**96h**
0.04428	0.05832	0.04515	0.04037	0.04950	0.06295

ANOVA

	Degrees of freedom	**Sum of squares**	**Mean squared error**	**F statistic**	**Pr (>F)**

Groups	5	0.0011585	2.3170e-04	3.3033	0.04172
Residual	12	0.0008417	7.0142e-05		

Tukey's Honest Significant Differences test

Group	Differences	Lower	Upper	Adjusted p-value
3h vs 0h	0.0140411993	-0.0089278646	0.037010263	0.3698102
12h vs 0h	0.0008681386	-0.0221009253	0.023837203	0.9999940
24h vs 0h	-0.0039148532	-0.0268839172	0.019054211	0.9911031
48h vs 0h	0.0052149029	-0.0177541611	0.028183967	0.9689213
96h vs 0h	0.0186673570	-0.0043017069	0.041636421	0.1395401
12h vs 3h	-0.0179560525	-0.0409251165	0.005013011	0.1640043
24h vs 3h	0.0179560525	-0.0409251165	0.005013011	0.1640043
48h vs 3h	-0.0088262965	-0.0317953604	0.014142768	0.7846403
96h vs 3h	0.0046261577	-0.0183429063	0.027595222	0.9813519
24h vs 12h	-0.0047829918	-0.0277520558	0.018186072	0.9784627
48h vs 12h	0.0043467643	-0.0186222997	0.027315828	0.9858025
96h vs 12h	0.0177992184	-0.0051698455	0.040768282	0.1698751
48h vs 24h	0.0091297561	-0.0138393079	0.032098820	0.7616466
96h vs 24h	0.0225822102	-0.0003868537	0.045551274	0.0549611
96h vs 48h	0.0134524542	-0.0095166098	0.036421518	0.4117649

Table C12. Analysis of control and heat stressed CC7-SSA01 *Aiptasia*'s prokaryotic communities' homogeneity of multivariate dispersions, with time points pooled, during our acute thermal stress assay. We used Bray-Curtis distances and 999 permutations. Our group dispersion results were run in an ANOVA to determine if the variance of each group's distance from the centroid was statistically significant. Tukey's Honest Significant Differences test was used for post-hoc comparisons at a 95% confidence level, where the p-values shown have been adjusted for multiple comparisons. Time points are on the basis of hours, e.g. 0h = 0 hours.

Permutation test for homogeneity of multivariate dispersions

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Number of permutations	Pr (>F)
Groups	1	0.0000001	0.00000006	1e-04	999	0.988
Residuals	17	0.0076630	0.00045077			

Average distance to centroid

Control	Heat treatment
0.05565	0.05528

ANOVA

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Pr (>F)
Groups	1	0.0000006	5.7600e-07	0.002	0.9651
Residual	17	0.0049633	2.9196e-04		

Tukey's Honest Significant Differences test

Group	Differences	Lower	Upper	Adjusted p-value
Heat treatment vs Control	-0.0003745655	-0.01816689	0.01741776	0.9650904

Table C13. Analysis of control and heat stressed CC7-SSB01 *Aiptasia*'s prokaryotic communities' homogeneity of multivariate dispersions, with time points pooled, during our acute thermal stress assay. We used Bray-Curtis distances and 999 permutations. Our group dispersion results were run in an ANOVA to determine if the variance of each group's distance from the centroid was statistically significant. Tukey's Honest Significant Differences test was used for post-hoc comparisons at a 95% confidence level, where the p-values shown have been adjusted for multiple comparisons. Time points are on the basis of hours, e.g. 0h = 0 hours.

Permutation test for homogeneity of multivariate dispersions

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Number of permutations	Pr (>F)
Groups	1	0.0000829	0.00008286	0.1651	999	0.688
Residuals	22	0.0110378	0.00050172			

Average distance to centroid

Control	Heat treatment
0.06914	0.07228

ANOVA

	Degrees of freedom	Sum of squares	Mean squared error	F statistic	Pr (>F)
Groups	1	0.0000444	0.00004444	0.1292	0.7227
Residual	22	0.0075648	0.00034385		

Tukey's Honest Significant Differences test

Group	Differences	Lower	Upper	Adjusted p-value
Heat treatment vs Control	0.003142487	-0.01498602	0.021271	0.7226521

Table C14. Indicator species analysis for CC7-SSA01 *Aiptasia*'s prokaryotic communities across time points during our acute thermal stress assay. Only $p < 0.05$ are shown, which are corrected for multiple testing via the Benjamini and Hochberg p-value correction. Taxonomic information is shown down to the genus level, determined using the SILVA 16S database release v138.1 (Quast et al. 2012). Time points are on the basis of hours, e.g. 0h = 0 hours.

Group: 0h								
Taxon	Kingdom	Phylum	Class	Order	Family	Genus	Species indicator value	P-value
1	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	*Oleiphilaceae*	*Oleiphilus*	0.433	0.019

Group: 24h								
Taxon	Kingdom	Phylum	Class	Order	Family	Genus	Species indicator value	P-value
1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	*Rhodobacteraceae*	*Yangia*	0.642	0.034
2	Bacteria	Planctomycetota	Planctomycetes	Pirellulales	*Pirellulaceae*	*Blastopirellula*	0.461	0.021
3	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Pseudoalteromonadaceae*	*Pseudoalteromonas*	0.430	0.036

Group: 96h								
Taxon	Kingdom	Phylum	Class	Order	Family	Genus	Species indicator value	P-value
1	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	*Saprospiraceae*	NA	0.493	0.036
2	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	*Hyphomonadaceae*	*Hyphomonas*	0.457	0.015

Table C15. Indicator species analysis for CC7-SSB01 *Aiptasia*'s prokaryotic communities across time points during our acute thermal stress assay. Only $p < 0.05$ are shown, which are corrected for multiple testing via the Benjamini and Hochberg p-value correction. Taxonomic information is shown down to the genus level, determined using the SILVA 16S database release v138.1 (Quast et al. 2012). Time points are on the basis of hours, e.g. 0h = 0 hours.

Group: 0h								
Taxon	Kingdom	Phylum	Class	Order	Family	Genus	Species indicator value	P-value
1	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	*Hyphomonadaceae*	*Maricaulis*	0.447	0.024

Group: 12h								
Taxon	Kingdom	Phylum	Class	Order	Family	Genus	Species indicator value	P-value
1	Bacteria	Bacteroidota	Bacteroidia	Flavobacteriales	*Flavobacteriaceae*	*Tenacibaculum*	0.459	0.036
2	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	*Spongiibacteraceae*	*BD1-7 clade*	0.451	0.011
3	Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Pseudoalteromonadaceae*	*Pseudoalteromonas*	0.433	0.021
4	Bacteria	Bacteroidota	Bacteroidia	Chitinophagales	*Saprospiraceae*	*Portibacter*	0.433	0.011
5	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	*Saccharospirillaceae*	*Thalassolituus*	0.427	0.047

Group: 24h								
Taxon	Kingdom	Phylum	Class	Order	Family	Genus	Species indicator value	P-value
1	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	*P13-46*	NA	0.439	0.008

Group: 96h								
Taxon	Kingdom	Phylum	Class	Order	Family	Genus	Species indicator value	P-value
1	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	*Rhodobacteraceae*	*Phaeobacter*	0.548	0.040
2	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	*Rhodobacteraceae*	*Litorimicrobium*	0.523	0.009
3	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	*Rhizobiaceae*	*NA*	0.460	0.029
4	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	*Stappiaceae*	*Labrenzia*	0.450	0.009
5	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	*Rhodobacteraceae*	*NA*	0.447	0.009
6	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	*Terasakiellaceae*	*NA*	0.422	0.040

My courage always rises with every attempt to intimidate me.

- Jane Austen