**ABSTRACT**

**INTRODUCTION**

Coral reef habitats are among the most biologically diverse ecosystems on the planet. They provide essential services such as protecting the shoreline, serving as vital habitat for fish and other organisms and functioning as a tourist destination with economic value (Barbier 2011). The calcification by hermatypic stony corals in the order Scleractinia builds critical habitat, made possible by the formation of a mutualistic endosymbiosis with photosynthetic dinoflagellates in the genus *Symbiodinium*. Through this symbiosis, the coral host gains the majority of its required nutrients as photosynthate from the symbiont, which allows for coral growth and survival (Baker 2003; Berkelmans et al. 2006).

Scleractinian corals are known to associate with a diverse array of *Symbiodinium*.Nine clades (A-I) have been described in *Symbiodinium* based on the internal transcribed spacer (ITS) region on nuclear ribosomal DNA (Pochon et al. 2010). Though *Symbiodinium* can occupy nine clades, four clades (A-D) comprise the majority of symbionts found in corals (van Oppen et al. 2001). Clades A and B tend to be most common in Atlantic corals, while corals in the Pacific largely harbor clades C and D (LaJeunesse et al. 2004; Jones et al. 2008).

Each symbiont clade has characteristic levels of stress-tolerance and physiological optima (Boulotte et al. 2016). Clade D has shown higher levels of thermal tolerance and photoprotection but growth rates and photosynthetic efficiency of clade D-dominated corals are often depressed (Little et al. 2004; Rowan 2004). Conversely, clade C *Symbiodinium* tend to be less tolerant of thermal stress, yet are better able to supply photosynthate to the coral host’s tissues (Cantin et al. 2009). Thus, clade D potentially functions more as an opportunistic symbiont that dominates as a response to recent stress anomalies (Baker 2003; Cantin et al. 2009; Stat et al. 2013).

The majority of coral species tend to associate with a single symbiont clade (Goulet 2006; LaJeunesse et al. 2004), but other species are able to host multiple clades concurrently (Rowan 2004; van Oppen et al. 2001). Colonies harboring multiple clades are typically dominated by one clade over the other, yet the presence of heterogeneous mixtures of multiple symbionts suggests a potential for symbiont shuffling or switching in response to changing environmental conditions (Jones et al. 2008; Rowan et al. 1997).

Little is known about the environmental factors controlling the spatial distribution of *Symbiodinium*. Evidence suggests that variability may be due to factors such as depth, irradiance and thermal stress, though few studies have investigated this (Abrego 2009; Cooper et al. 2011; Rowan et al. 1997). Research is beginning to explore the patterns of symbiont association among host species, particularly when considering differences in habitat. *Acropora millepora* was found to associate with both *Symbiodinium* clades C and D on the Great Barrier Reef, with D proving more common in corals exposed to poor water quality (Cooper et al. 2011). *Acropora spp.* in American Samoa were more likely to associate with clade D if occupying habitats with a history of higher temperatures (Oliver and Palumbi 2009). Patterns are suggested for differences between inshore versus offshore reefs, across latitudinal gradients and even within the same reef environment, yet extensive studies of these phenomena are absent.

*Montipora capitata* is a dominant reef-building species inKāne’ohe Bay that can harbor both symbiont clades C and D (Cunning et al. 2016; Stat et al. 2011). The associations between the coral host and its symbiont community have proven relatively stable over time (Cunning et al. 2016), but the factors driving the distribution of clades C and D in *M. capitata* across different environmental regimes are still poorly understood. *M. capitata* is commonly found in a variety of habitat types in Kāne’ohe Bay, thus providing an excellent study species to explore the factors driving the relative abundance of multiple symbionts.

Kāne’ohe Bay is a unique environment with a strong history of disturbance (Jokiel 1991). Both from environmental and anthropogenic influences, these anomalies are potential drivers of symbiont distribution (Cooper 2011; Stat et al. 2011). The patch and fringing reef systems of Kāne’ohe Bay are quite shallow; some sections of the reef tops can be exposed during low tides (Bahr et al. 2015). Shallow depths and gradients of oceanic influence and freshwater input throughout the bay pose negative implications for stress, which has been observed in successive bleaching events in 2014 and 2015. Despite its seemingly intolerable physiognomies, there exists high coral coverage and rapid recovery rates in Kāne’ohe Bay. In light of these recent bleaching events, this study aimed to characterize the spatial patterns of *Symbiodinium* clades C and D to investigate the potential stress-response of the Kāne’ohe Bay population of *M. capitata*.

**METHODS**

*Study Design and Location*

Individual colonies of *M. capitata* were tagged and sampled to measure the spatial variability of *Symbiodinium* clades C and D found in colonies from different habitats. All corals were sampled from Kāne’ohe Bay, located on the east side of O’ahu, Hawai’i, USA. Corals were tagged with medium-sized yellow cattle tags throughout the bay. Colonies at five patch reefs and three fringing reefs were tagged in each of the northern, central and southern regions of the bay with an additional submerged patch reef south of the Hawai’i Institute of Marine Biology (HIMB). At each patch reef, 30 colonies were tagged; 10 colonies each from windward slope, top and leeward slope with depth recorded using a depth gauge. Given the lack of leeward slope on fringing reefs, 20 colonies were tagged at each site; 10 colonies each from the top and slope. At the tops of the patch reefs and the fringe sites most colonies were between 0 and 1 meter depth. Along the windward and leeward slopes, colonies were tagged randomly at a depth from 1 meter to 13 meters. Reefs lacking sufficient colonies from depths greater than 5 meters were re-visited and five additional colonies were sampled. Depth was later adjusted according to differences in mean sea level using NOAA’s daily tide tables for Moku o Lo’e, Kāne’ohe Bay at 6-minute intervals. In total, 16 patch reefs and 9 fringing reefs were sampled across Kāne’ohe Bay resulting in a sample size of 707 colonies. Tagging, photographing and sampling of colonies took place between 7 June 2016 and 12 August 2016.

*Sample Collection and Processing*

Ten weights with attached floats were randomly thrown from the surface across a distance of approximately 20 meters on each reef area (top and both slopes). The closest colony of *M. capitata* in proximityto each float was tagged and sampled. Each sample consisted of a small branch fragment (~4-5cm) taken from the tip of a branch located at the top of the colony. *In situ* photographs with an included scale bar and color standard were taken of each colony to later be used for color assignment of each colony (Fig. 1). The coral fragment was subsampled for a tissue biopsy shortly after collection (never greater than 1.5 hours), which was placed in 500μL DNA buffer (5M NaCl, 0.5M EDTA) with 1% sodium dodecyl sulfate (SDS). The remaining fragment was immediately frozen in liquid nitrogen and archived at -80°C in the laboratory. DNA was extracted from each sample biopsy following a modified CTAB-chloroform protocol (dx.doi.org/10.17504/protocols.io.dyq7vv).

*Symbiont Community Analysis*

Quantitative PCR (qPCR) was used to analyze the symbiont community of each collected sample. Sequences of *Symbiodinium* clades C and D resulted from clade-level primers and probes based on amplification of the internal transcribed spacer (ITS2) region (Cunning et al. 2013). All samples were assayed with primers of both clades C and D in duplicate 10μL reactions for 40 cycles on a StepOnePlus platform (Applied Biosystems). Parameters were set at a fluorescence threshold of 0.01 and a baseline interval of cycles 15-22. The StepOnePlus software produced the target symbiont ratio of clade C to D in each sample, normalized for fluorescence intensity and locus gene copy number. Symbiont clades detected in only one qPCR reaction were not considered as present in a colony. The proportion of clade C-dominance was calculated from the clade C to D ratio by the formula [(C:D)/(C:D+1)]. The resulting proportion of clade D-dominance was then calculated by the formula 1-[(C:D)/(C:D+1)]. Based on the proportion values of clades C and D, the dominant symbiont type was determined. If a colony harbored both symbiont clades, designated as a heterogeneous mixture, the clade present in higher proportion was noted as CD or DC accordingly.

*Data Analysis*

The differences in proportion of clades C and D present in colonies dominated by each clade and color morph were investigated using Chi-Squared analyses. Chi-Squared tests were then used to assess differences in dominant symbiont clade, colony color morph and heterogeneous symbiont mixtures between bay areas (northern, central and southern), reef types (patch vs. fringe) and each individually sampled reef. Bray-Curtis coefficient of similarity metrics were used to calculate differences in the dominant symbiont and color morph compositions of each reef, which were tested for spatial autocorrelation using Mantel Tests. To estimate the probability of occurrence of dominant symbiont and color morph as a function of depth, logistic regressions of generalized linear models were used. Depth was corrected for differences in mean sea level using daily tide tables for Moku o Lo’e, Kāne’ohe Bay at 6-minute intervals. Two-Way ANOVA tests were used to investigate the interactive effects of depth and location on the dominant symbiont and color morph. Spatial autocorrelation of dominant symbiont and color morph was tested using Mantel Tests after a MANCOVA adjusted for the influence of depth. The spatial autocorrelation of the interaction of dominant symbiont and color morph was tested using a Mantel Test after a Multinomial Logistic Regression was performed to discount the influence of depth on the spatial distribution of the interaction. A final Chi-Squared analysis was run on the interaction of colony color morph and dominant symbiont as a function of location (i.e. bay area). All analyses were performed in RStudio v.3.2.2.

**RESULTS**

*Symbiont Community Composition*

Quantitative PCR on 707 colonies of *M. capitata* detected *Symbiodinium* clades C and D present both in heterogeneous mixtures and as the only symbiont clade. Across all samples, 53% contained clade C only, 1.2% contained clade D only and 45.8% contained a mixture of both clades C and D. The dominant symbiont across all samples was clade C, being the dominant symbiont in 61% of colonies. In 86.6% of colonies dominated by clade C *Symbiodinium*, clade C was the only symbiont present. Conversely, only 3.3% of clade D-dominated colonies harbored only clade D *Symbiodinium* (Fig. 2). A significant relationship between color morph and dominant symbiont clade was observed wherein C-dominance was observed in 89% of brown colonies and 41% of orange colonies (p < 0.001). Clade D, when present in a colony, was almost always in abundance > 80%, demonstrating that presence of D often indicates a D-dominated colony (Fig. 3).

*Spatial Distribution*

There was a significant relationship between a colony’s color morph and the area of the bay it occupied (p < 0.05); reefs were more heavily dominated by the orange color morph in the northern bay than in the central and southern regions of the bay. This relationship was not different for each reef type (p = 0.29). No significant effects on symbiont-dominance resulted from location within the bay (p = 0.14) or reef type (p = 0.37) alone. When eliminating the influence of the submerged reef south of HIMB, bay area proved to be more influential on symbiont distribution, yet the relationship is still not significant (p=0.06). The interaction between color morph and dominant symbiont clade was significantly related to the area of the bay (p < 0.01). Brown colonies dominated by clade D were more abundant in the southern and central bay areas than they were in the northern region, though this pertains to an insignificant number of colonies (n = 9).

Depth proved to be the significant driving factor for symbiont-dominance (p < 0.001) and color morph (p < 0.001) among colonies of *M. capitata*. The probability of a colony harboring C as the dominant symbiont clade was higher at depths greater than 1 meter, while clade D dominated shallow colonies. A higher probability of orange-dominance was observed in colonies at depths shallower than 4 meters, where dominance shifted to the brown color morph. When considering the influence of depth on the interaction of colony color morph and dominant symbiont, brown colonies were always more likely to be dominated by clade C *Symbiodinium*. Orange colonies, however, were more likely to be dominated by clade D at depths less than 2.75 meters and clade C at depths greater than 2.75 meters (p < 0.001; Fig 4).

When considering the interaction of depth and reef type, a significant effect was had on both dominant symbiont (p < 0.01) and colony color morph (p < 0.05). A similar effect resulted from the interaction of depth and bay area on symbiont dominance (p < 0.05). Significant spatial autocorrelation of each sampled reef by the proportion of symbiont dominance among the sampled colonies on the reef was observed (p < 0.05). When adjusting for the influence of depth, there was no significant correlation among reefs (p = 0.26).

**DISCUSSION**

**ACKNOWLEDGEMENTS**

**FIGURE CAPTIONS**

Fig. 1. *Montipora capitata* colonies of both color morphs: orange (left) and brown (right). Photo credit: Raphael Ritson-Williams

Fig. 2. Proportion of occurrence of *Symbiodinium* clades C and D in *Montipora capitata* colonies per dominant symbiont clade.

Fig. 3. Proportion of clade D in all colonies of *Montipora capitata*. Bar colors indicate colony color morph

Fig. 4. (Top) Bars indicate the proportion of clade-dominance in all colonies grouped by 1m depth intervals. Line indicates the probability of clade D-dominance as a function of depth. (Middle) Bars indicate the proportion of occurrence of each color morph in all colonies grouped by 1m depth intervals. Line indicates the probability of occurrence of the orange color morph as a function of depth. (Bottom) Probability of clade D-dominance for all colonies of each color morph as a function of depth

Fig. 5. Distribution of *Symbiodinium* and color morph in *Montipora capitata* across Kāne’ohe Bay, O’ahu, Hawai’i, USA