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Keywords: *Symbiodinium*, *Montipora capitata*, Kāne‘ohe Bay, Symbiosis, Distribution, Coral

**ABSTRACT**

As environmental conditions continue to change, the symbiosis between Scleractinian corals and photosynthetic dinoflagellates becomes increasingly critical. Divergent clades within the genus *Symbiodinium* possess functional optima lending to different stress-tolerances among symbionts. However, the spatial variability of *Symbiodinium* across habitat types and environmental regimes is poorly understood at large scales, yet is essential for elucidating resilience in coral populations. To investigate symbiont distribution in a dominant reef-building coral, colonies of *Montipora capitata* were sampled across Kāne‘ohe Bay, O‘ahu, Hawai‘i, USA for symbiont community analysis and temporal monitoring. A total of 707 colonies were tagged and sampled from 16 patch reefs and 9 fringing reefs across Kāne‘ohe Bay at different reef habitats and depths. Symbiont dominance and the relative ratio of clade C to D in each sample were recovered by quantitative PCR. Clade dominance was more significantly associated with depth than spatial distribution wherein clade D dominated shallow environments and clade C was more prevalent at depths > 1 m. A similar distribution was observed in colony color morph where orange morphs dominated the shallow environment and brown morphs dominated depths > 4 m. Such comparable patterns suggest a potential interactive effect between the symbiont community and color morph in need of further investigation. This work reveals that essential symbioses in *M. capitata* in Kāne‘ohe Bay are strongly related to abiotic conditions that vary with depth, suggesting niche partitioning as a potential source of resilience in corals under climate change.

**INTRODUCTION**

Coral reefs are among the most biologically diverse ecosystems on the planet, providing essential services such as shoreline protection, serving as vital habitat for fish and other organisms and functioning as a tourist destination with economic value (Barbier et al. 2011). Calcification by hermatypic stony corals in the order Scleractinia builds critical habitat, made possible by the formation of a mutualistic endosymbiosis with photosynthetic dinoflagellates (*Symbiodinium* spp.). Through this symbiosis, the coral host gains the majority of its required nutrients as photosynthate from the symbiont, allowing for coral growth (Baker 2003, Berkelmans & Van Oppen 2006).

Scleractinian corals associate with a diverse array of symbionts.Nine clades (A-I) have been described in *Symbiodinium* based on the internal transcribed spacer (ITS) region on nuclear ribosomal DNA (Pochon & Gates 2010). Different symbiont types within each clade have characteristic levels of stress-tolerance and physiological optima (Boulotte et al. 2016). Clade D symbionts have shown higher levels of thermal tolerance and photoprotection, but growth rates and photosynthetic efficiency of clade D-dominated corals are often depressed relative to corals associating with other symbiont clades (Little et al. 2004, Rowan 2004). Conversely, many types of symbionts in clade C tend to be less thermally tolerant, yet are better able to supply photosynthate to the coral host’s tissues (Cantin et al. 2009). Clade D, therefore, potentially functions more as an opportunistic symbiont that dominates and stressful environments (Toller et al. 2001, Baker 2004, Cantin et al. 2009, Cooper et al. 2011, Stat et al. 2013).

Most coral species tend to associate with a single symbiont clade; some even with a single type within a clade (LaJeunesse et al. 2004, Goulet 2006). Other species are able to host multiple clades concurrently (Van Oppen et al. 2001, Rowan 2004). While colonies harboring multiple clades are typically dominated by one clade with background populations (Silverstein et al. 2012), the presence of heterogeneous mixtures of multiple symbionts suggests a potential for symbiont shuffling (change in relative abundance of *in hospite* *Symbiodinium*) or switching (uptake of novel *Symbiodinium*) in response to changing environmental conditions (Rowan et al. 1995, Mieog et al. 2007, Jones et al. 2008, Boulotte et al. 2016).

Because symbioses play a vital role in coral survivorship, the factors shaping the presence and dominance of symbionts must be readily understood. Little is known about the environmental factors controlling the spatial distribution of *Symbiodinium* within a species though evidence suggests that variability may be due to factors such as irradiance and thermal stress (Rowan et al. 1995, Abrego et al. 2009, Stat et al. 2015). *Symbiodinium* of clade C (C1b-c) have shown thermal sensitivity whereas thermal tolerance observed in clade D symbionts (D1) have led to a dominance of clade D in areas that experienced thermal stress and bleaching events (Baker et al. 2016), consistent with previous correlative studies of symbiont distribution and sea surface temperatures (Tonk et al. 2013). Similarly, clade C symbionts (C1c) in the Gulf of California performed better at depth in low light than did clade D symbionts (D1) which were more successful in shallow, high light environments, suggesting that irradiance plays a vital role in niche-partitioning of *Symbiodinium* (Iglesias-Prieto et al. 2004, Sampayo et al. 2007, Bongaerts et al. 2015). These patterns elucidate differences in host-symbiont relationships across spatial distributions and among habitat types, yet large-scale studies of these phenomena are absent.

*Montipora capitata* is a dominant reef-building species inKāne‘ohe Bay that can harbor both clade C and D symbionts (Stat et al. 2011, Cunning et al. 2016). The associations between the coral host and its symbiont community composition 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 not well described. In Kāne’ohe Bay, *M. capitata* occurs as two distinct color morphs (brown and orange), and while the cause of these color morphs is unknown, studies suggest that color development in coral results from fluorescent proteins (Matz et al. 1999, Lukyanov et al. 2000). It is unclear what functional differences exist among *M. capitata* color morphs, however around O‘ahu the brown and orange color morphs are suggested to possess a specific endosymbiosis with *Symbiodinium* of clades C and D respectively (LaJeunesse et al. 2004). *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 in a dominant reef-building coral.

Kāne‘ohe Bay is a unique environment with a strong history of anthropogenic and environmental disturbance (Smith et al. 1981, Jokiel 1991) which may drive symbiont distributions (Cooper et al. 2011, Stat et al. 2011). Higher temperatures exist in the bay due to restricted circulation, causing corals to exist in conditions projected not to be experienced for another century (Bahr et al. 2015). The tops of the shallow (0 - 17 m) patch and fringing reef systems of Kāne‘ohe Bay can be exposed during low tides (Bahr et al. 2015), likely contributing to thermal stress as well. Despite being comparatively shallow relative to other reef systems, habitats on a single reef can be considerably different due to dramatic turbidity increases with depth. Though seemingly intolerable physiognomies for coral survivorship characterize Kāne‘ohe Bay, there exists high coral coverage and rapid recovery rates (Bahr et al. 2015, Cunning et al. 2016). This study aimed to characterize the spatial variability of *Symbiodinium* clades C and D to investigate the variability in symbioses among the Kāne‘ohe Bay population of *M. capitata*.

**MATERIALS AND METHODS**

*Study Design and Location*

Individual colonies of *Montipora capitata* in Kāne‘ohe Bay were tagged for continued monitoring and sampled to measure the spatial variability of *Symbiodinium* clades C and D among corals in different habitats. Colonies at five patch reefs and three fringing reefs were tagged in each of the northern, central and southern regions of the bay, along a gradient of decreasing oceanic influence, with an additional submerged patch reef south of the Hawai‘i Institute of Marine Biology on Moku o Lo‘e (Fig. 1). 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 < 1 m depth. Along the windward and leeward slopes, colonies were tagged randomly at 1 - 13 m depth. 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 m 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 - 5 cm) 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 assess size and color morph of each colony (Fig. 2). Each coral fragment was subsampled for a tissue biopsy shortly after collection (never greater than 1.5 hours) and placed in 500 μL 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 resulted from clade-level primers and probes targeting specific actin loci in *Symbiodinium* clades C and D (Cunning & Baker 2013). All samples were assayed with primers of both clades C and D in duplicate 10 μL 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 (Cunning et al. 2016). 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 dissimilarity 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 tested the effects of depth and location (bay region, reef type and reef ID) 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 between 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 R v.3.2.2 (R Core Team 2016).

**RESULTS**

*Symbiont Community Composition*

Quantitative PCR on 707 colonies of *Montipora capitata* detected *Symbiodinium* clades C and D present both in heterogeneous mixtures and as a single clade exclusively. Across all samples, 53 % contained clade C only, 1.2 % contained clade D only and 45.8 % contained a mixture of 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. In striking dissimilarity, only 3.3 % of clade D-dominated colonies harbored clade D *Symbiodinium* exclusively (Fig. 3). 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 clade D often indicates a D-dominated colony (Fig. 4).

*Spatial Distribution*

There was a slight 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 (62.7 %) than in the central (56.4 %) and southern (53.9 %) regions of the bay. This relationship was not different for each reef type (p = 0.29). No significant differences in symbiont-dominance resulted between regions of the bay (p = 0.14) or reef types (p = 0.37) alone. However, the effect of reef type on both symbiont-dominance and colony color morph also depended on the influence of depth (p < 0.01, p < 0.05). When eliminating the influence of the submerged reef south of the Hawai‘i Institute of Marine Biology, bay area proved to be more influential on symbiont distribution, yet the relationship was still insignificant (p=0.06). The interaction between color morph and dominant symbiont clade was significantly related to the area of the bay when adjusting for the influence of colony depth (p < 0.01; Fig. 5). Brown colonies dominated by clade D were more abundant in the southern (n = 18) and central (n = 10) bay areas than they were in the northern (n = 5) region, though this pertains to a trivial number of colonies (n = 33).

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 > 1.29 m, while clade D dominated colonies at depths < 1.29 m. A higher probability of orange-dominance was observed in colonies at depths < 3.64 m, whereas dominance shifted to the brown color morph > 3.64 m. 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,* consistent with results showing a higher likelihood of a colony being brown and dominated by clade C with increasing depth. Orange colonies, however, were more likely to be dominated by clade D at depths < 2.75 m and clade C at depths > 2.75 m (p < 0.001; Fig 6).

**DISCUSSION**

Symbiont association in *Montipora capitata* across Kāne‘ohe Bay showed a strong depth-dependent distribution with shallow colonies being dominated by clade D and colonies at depths > 1.29 m being dominated by clade C (Fig 6). This was observed across all reefs throughout the bay, indicating that the factors driving symbiont dominance in Kāne‘ohe Bay exist along a vertical depth gradient rather than a latitudinal geographic distribution. No significant spatial differences were observed among reefs, reef types or regions of the bay, consistent with the lack of spatial variation across sites and regions found in previous reports (Stat et al. 2011). Depth partitioning is consistent with observations that habitat depth influences bathymetric zonation of coral symbionts between shallow, high irradiance environments and deep, low irradiance environments (Finney et al. 2010).

Quantitative PCR (qPCR) revealed that the symbiont composition of sample colonies (n = 707) existed as either heterogeneous mixtures of clades C and D or as one clade exclusively. The presence of symbiont mixtures in a coral suggests a potential for either symbiont shuffling or switching to lessen the impacts of changing environmental conditions (Mieog et al. 2007). Under stressful conditions (i.e. thermal anomalies), corals have been shown to use clade D symbionts to supplement an increase heterotrophy despite the smaller supply of nutrients that these symbionts provide relative to other clades (Stat et al. 2008). Mixtures could also be more advantageous for recovery from stress events. For instance, in *M. capitata* the presence of symbionts in clade D may support post-bleaching recovery (Baker 2003) while the presence of symbionts in clade C may aid in reversion to previous non-stressed communities once a shift back to more idealistic conditions occurs; however, a study of symbiont association over time showed no switching between clades C and D in this species (Cunning et al. 2016).

Clade C symbionts tend to be ideal given efficient carbon-delivery to the coral host (Little et al. 2004, Cantin et al. 2009). Conversely, clade D symbionts tend to be opportunistic and less beneficial to the coral host, yet may be functionally important as a thermally stress-resilient symbiont (Cantin et al. 2009, Cunning et al. 2014). In the 707 sample colonies, clade C was overwhelmingly widespread; found in 98.7 % of colonies, while clade D was found in 46.8 % of colonies. However, when clade D was present, it typically dominated the symbiont community (Fig 4). Of the nine colonies that exclusively harbored clade D, five colonies showed amplification of clade C in one of the technical qPCR replicates, suggesting a likelihood that clade C was present but in low abundance. Therefore, all *M. capitata* colonies may host some clade C *Symbiodinium* but the levels of association may be below the detection threshold of qPCR.

Physical conditions in Kāne‘ohe Bay can be quite variable, even within a narrow depth-range. Environmental conditions at depths < 1 m are often dramatically different than conditions at > 10 m, particularly in terms of turbidity and temperature. Current data shows insignificant variation among bay regions in terms of daily mean temperature and sedimentation (Ritson-Williams & Gates 2016a, Ritson-Williams & Gates 2016b). These comparable regimes on a horizontal spatial scale are consistent with the findings that symbiont distribution is relatively similar across the bay. Variation along a vertical gradient, given current knowledge of tolerance in coral symbionts, is a candidate for monitoring at reefs in each region of the bay to determine their likelihood of contributing to variability in *Symbiodinium*.

Light intensity declines as depth in the photic zone increases and has induced differences in photosynthetic responses by means of photoinhibition and photoprotection in corals dominated by clades C and D respectively (Salih et al. 2000, Rowan 2004). Response variance validates the hypothesis that different clades of *Symbiodinium* adapt to particular light intensities (Iglesias-Prieto et al. 2004). The putative implication of light intensity on *Symbiodinium* variability supports the notion that habitat partitioning of the symbiont community composition exists along depth-mediated light gradients (Iglesias-Prieto & Trench 1994). A transition depth exists between 1 and 2 m, at which *M. capitata* association switches from a dominance of clade D to clade C. As Kāne‘ohe Bay is quite turbid, this shallow depth threshold suggests that depth stratification of light intensity might be a common driver of distribution among symbiont association, though the threshold depth of transition would depend on local abiotic conditions.

*M. capitata* exists as two distinct color morphologies in Kāne‘ohe Bay (Fig 2). This division in color has been observed before and was correlated with differences in symbiont communities (LaJeunesse et al. 2004). Research investigating the production of color in this species is understudied, yet previous work on other coral species suggests an exploitation of phenotypic plasticity in fluorescent proteins (Kelmanson & Matz 2003). Similarly to *M. capitata*, *Lobophyllia hemprichii* can exist as an orange morph which has been proven to result from a change in color due to light irradiation levels stimulating green fluorescent proteins (Oswald et al. 2007). Consequently, it is hypothesized that orange morphs may serve a photoprotective purpose, contributing to the dominance of this color morph in shallow depths observed in *M. capitata*, though further investigation is needed.

Studies suggest that coral color may be indicative of physiological function. For example, at shallow depths a green morph of *Porites astreoides* was observed more frequently than the brown morph, possibly indicative of tolerance to high-light environments (Gleason 1993). Another study investigating sedimentation influence on *P. astreoides* noted brown colonies more efficiently shed sediment than did green colonies, ultimately preventing sediment-induced mortality (Gleason 1998). Correspondingly, a study on sedimentation influence on *Symbiodinium* revealed that clade C symbionts were found in higher sedimentation areas (Garren et al. 2006). Such phenomena may be pertinent to *M. capitata*,which exhibit a comparable pattern where brown morphs and clade C were found at depth where sedimentation is often greater and light intensity is often reduced.

As demonstrated by qPCR analysis of *M. capitata* fragments from colonies across Kāne‘ohe Bay, we showed that the spatial variability of *Symbiodinium* occurs most strongly as a function of depth. No significant spatial patterns arose from different reefs, reef types or areas of the bay when considering the dominance of one clade over another. Portions of the reefs in Kāne‘ohe Bay can be quite shallow (< 0.5 m) at low tide and are probably exposed to high temperatures during summer months. Corals associating with clade D, often existing as an orange color morph, dominate this highly fluctuating environment. Because clades C and D have different physiological tolerances and depth has shown to be the strongest driver symbiont distribution, biotic and abiotic conditions along a depth gradient should be targeted for future investigations that may assist in conservation strategies and understanding resistance among coral in changing environmental conditions.

**ACKNOWLEDGEMENTS**

We thank J. Levy, D. Fant and A. Wen for field assistance and the Hawai’i Department of Aquatic Resources for authorizing coral sample collection (CITE). We thank M. Patterson, J. Grabowski and L. Magee for mentorship. Funding for this project was provided by \_\_\_\_\_\_\_\_\_\_\_. This is HIMB contribution number \_\_\_\_\_\_\_ and SOEST contribution number \_\_\_\_\_\_\_\_\_.

**LITERATURE CITED**

**FIGURE CAPTIONS**

Fig. 1. Collection reef locations in Kāne‘ohe Bay, O‘ahu, Hawai‘i, USA

Fig. 2. *Montipora capitata* colonies of both color morphs: orange (left) and brown (right). Photo credit: Raphael Ritson-Williams

Fig. 3. Proportion of occurrence of *Symbiodinium* clades C and D in *Montipora capitata* colonies per dominant symbiont clade

Fig. 4. Percentage of clade D in all colonies of *Montipora capitata*. Bar colors indicate colony color morph

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

Fig. 6. (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