1 Ecological factors rather than barriers to dispersal shape genetic structure of algal
2 symbionts in horizontally-transmitting corals
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Abstract

Many reef-building corals acquire their algal symbionts (*Symbiodinium* sp.) from the local environment upon recruitment. This horizontal transmission strategy where hosts pair with locally available symbionts could serve to increase coral fitness across diverse environments, as long as the host maintains high promiscuity and symbionts adapt locally. Here, we tested this hypothesis in two coral host species by comparing host and symbiont genetic structures across different spatial scales in Micronesia. Each host species associated with two genetically distinct *Symbiodinium* lineages, confirming high promiscuity in broadly dispersing hosts. However, contrary to our initial expectation, symbiont genetic structure was independent of physical barriers to dispersal between islands, unlike genetic structure of their hosts that was nearly perfectly explained by oceanic currents. Instead, *Symbiodinium* consistently demonstrated genetic divergence among local reefs and between the two host species at each island, although not necessarily between distant islands. These observations indicate that *Symbiodinium* disperse much more broadly than previously thought and continuously adapt to specific hosts and reef environments across their range, following the classical Baas Becking's hypothesis: "Everything is everywhere, but the environment selects". Overall, our findings confirm horizontal transmission could be a mechanism for broadly dispersing coral species to enhance their local fitness by associating with locally adapted symbionts. Dramatic differences in factors driving the genetic structures of horizontally-transmitting corals and their *Symbiodinium* imply that viewing their combined genomes as a single evolving entity ('hologenome') would be misleading.

Introduction

Symbioses are ubiquitous in nature and the interactions between symbiotic partnerships

have been implicated in eukaryote evolutionary diversification (1-4) and in the origin of

eukaryotes (5). Many well-known symbioses involve the passing of symbionts from

parents to offspring (vertical transmission), fully aligning the evolutionary trajectories of

symbiotic partners and typically lead to their deep integration at biochemical and

genomic levels (i.e. Buchnera in aphids (6, 7)). The result of this symbiosis is essentially

a novel composite organism. In other types of symbioses, the association between

partners must be newly established in every generation (horizontal transmission), which

allows for the maintenance of each partner's species identity. In theory, this kind of

relationship should generate novel ecological opportunities for both symbiotic partners

through their mixing and matching across environments. For example, association with

ecologically specialized algal photobionts can lead to distinct ecological guilds of lichens

(8) or allow a fungal partner to expand its geographic range across a broader climatic

envelope (9). Similarly, in aphids, association with various horizontally transmitted

bacterial symbionts allows these insects to colonize novel host plants across climatic

zones (10). Considering these and other examples of ecological adaptation based on

varying symbiotic associations, it has been argued that the joint genomic content of

symbiotic systems should be studied as a single unit of evolution, the 'hologenome' (11,

12). However, the usefulness of this concept depends on whether the evolutionary

trajectories of both symbiotic partners are sufficiently aligned to present a unified target

of selection (13). Here, we explore this question in the symbiosis between a horizontally

transmitting reef-building coral and dinoflagellate algae of the genus *Symbiodinium* (14).

Association with *Symbiodinium* is obligatory for many coral hosts that rely on

algal photosynthesis for energy, while the algae benefit from protected and light-exposed

residence as well as inorganic nutrients and CO_2 concentration regulatory mechanisms

provided by the host (15-18). Given the obligatory nature of this symbiosis for the host, it

is somewhat surprising that in the majority of coral species (~85%) *Symbiodinium* are not

transmitted vertically, but rather must be acquired by the juvenile coral from its local

environment (19, 20). One possible explanation is that dispersal ranges of aposymbiotic

coral larvae typically extend over hundreds of kilometers (i.e. 21), while the

environmental variation corals must deal with exists on much smaller spatial scales: reef

environments with varying light, thermal and nutrient conditions can be separated by

meter-scale distances (i.e. 22). Under such circumstances, coral hosts would benefit from

the mixing and matching strategy, improving their fitness by associating with the locally

available, and putatively ecologically specialized, algal strains (23-25). Establishing the

relative roles of these symbiotic partners in adaptation to variable environments is

essential for better prediction of coral reefs' future under climate change (i.e. 26).

Although symbiont-free coral larvae show practically unrestricted flexibility in

symbiont uptake (27-30), it nevertheless results in strong specificity of the resulting

coral-*Symbiodinium* association: the majority of coral species are found hosting a single

Symbiodinium subclade (26, 31-38). This specificity putatively arises from within-host

competition between algal strains after initial uptake (32). Selection for a better match

with the host is therefore expected to be another major evolutionary force affecting

Symbiodinium populations (3), in addition to environmental specialization.

The third force that would influence the dynamics of coral-*Symbiodinium*

symbiosis is dispersal. It is reasonable to hypothesize that local environmental

specialization of the symbionts would be most easily achieved if the symbionts were

dispersal-limited compared to the coral host. Baums *et al.,* (26) investigated within-

subclade genetic variation of Caribbean *Symbiodinium* in the larger context of the

genetics of the host (*Acropora palmata*) and determined that *Symbiodinium* exhibited

stronger genetic structure than the coral host, suggesting limitation of symbiont dispersal

relative to the host.

To integrate these three evolutionary forces, we formulated a working hypothesis

for this study, the 'global host, local symbiont' hypothesis. It posits that (i) coral hosts

disperse widely and are able to establish symbiosis with diverse algal strains across

locations; (ii) *Symbiodinium* algae are poor dispersers, which results in strong divergence

among locations aligning with physical barriers and facilitates their local environmental

specialization; (iii) local *Symbiodinium* strains also diverge with respect to the host

species as a result of selective pressure towards higher host specificity. To validate all

three components of our hypothesis, we examined multi-locus genotypes (MLG) of clade

C *Symbiodinium* in two species of *Acropora* – *A. hyacinthus* and *A. digitifera* – collected

from the same reef locations across the Micronesian Pacific (Fig. 1). Our previous work

has shown that both host species exhibit extensive genetic connectivity and their genetic

structure is nearly perfectly explained by the patterns of regional surface currents (21).

By using two coral species that co-occur across the same locations as well as local reef

environments we aimed to disentangle the roles of environmental specialization, host

specialization, and physical barriers to dispersal in driving the fine-scale genetic structure

of *Symbiodinium*.

Figure 1: Geographic location of the Micronesian islands where *Acropora hyacinthus* and *A.*
digitifera coral samples were collected. Top: Map of the Micronesian Pacific with an inset of the
Pacific Ocean for reference. Islands where samples were collected and analyzed for *Symbiodnium*
genetics are designated with grey boxes. Detailed information on each sampling site is located in
Table 5. No *A. hyacinthus* were present in Guam and *A. digitifera* were not collected in Ngulu.
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Results

Two *Symbiodinium* clade C lineages

To enable standard population genetic analysis, we restricted our study to only corals that

hosted a single diploid *Symbiodinium* clone (i.e., yielded a unique diploid *Symbiodinium*

genotype across six analyzed microsatellite loci), which encompassed the majority (69%

A. digitifera and 64% *A. hyacinthus*) of our samples. Across the two coral species in

Micronesia (Fig. 1), two distinct *Symbiodinium* lineages were observed, which were most

clearly discriminated by two of the six microsatellite loci (Fig. S1). Sequencing of the

$psbA_{ncr}$ gene for a subset samples classified these lineages as C40 and C3 *sensu*

Lajeunesse et al. (39) and LaJeunesse and Thornhill (40) (Fig. 2). Corals of both species

from Palau and Ngulu hosted exclusively C40 *Symbiodinium* (Fig. 3A, pink bars). This

lineage was also prevalent in *A. digitifera* at one reef site on Yap and was rarely found in

A. digitifera across the rest of Micronesia. All other coral hosts of either species

associated with *Symbiodinium* C3 (Fig. 3A, turquoise bars). Both *Symbiodinium* lineages

possessed high genetic diversity, with a total of 70 unique alleles across six SSR loci

observed in C40 across three islands (Table 1A) and 130 unique alleles across the same

six SSR loci in C3 across five islands (Table 1B). Mean numbers of alleles per island for

each locus for C40 ranged from 3.00-4.67 with the highest numbers of private alleles in

Palau (N=7) (Table 1A). Mean allele numbers per island for each locus for C3 ranged

from 3.83-5.17 and numbers of private alleles ranged from 1-4 (Table 1B).

Table 1. Summary of allelic diversity measures for *Symbiodinium* C40 (A) and *Symbiodinium* C3
(B). Na: number of alleles, He: expected heterozygosity, Ho: observed heterozygosity, PA:
number of private alleles
A. *Symbiodinium* C40

	Na	He	Ho	PA
PAL	4.67	0.52	0.64	7
NGU	4.00	0.42	0.55	6
YAP	3.00	0.43	0.51	2

148   B. *Symbiodinium* C3

	Na	He	Ho	PA
YAP	4.33	0.47	0.56	1
GUA	3.83	0.42	0.46	3
CHU	5.17	0.58	0.51	3
POH	4.33	0.47	0.56	1
KOS	4.00	0.48	0.51	4

150 Figure 2. Phylogenetic analysis of psbA^{ncr} sequences from representative samples from this
151 study (labeled branch tips) along with publically available psbA^{ncr} sequences from known
152 *Symbiodinium* subclades identifies two lineages present (C3 and C40). Bootstrap support values
153 are shown at the partitions that define known subclades. Scale bar: replacements per nucleotide
154 site. Sequence accession numbers for reference sequences are given in Supplementary Table 1.
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Figure 3: Analyses of microsatellite loci data for *Symbiodinium* hosted by *Acropora hyacinthus*
and *Acropora digitifera* at thirteen sites across seven islands in Micronesia, using multilocus
genotyping data. A. STRUCTURE population assignment for *Symbiodinium* from two *Acropora*
host species across greater Micronesia at an optimal population number (K=2), corresponding to
C40 (pink) and C3 (turquoise) clade C subclades. Colors in the bottom panels correspond to host
species and shades of grey correspond to different sites within each island. B. Within-subclade
STRUCTURE analysis.
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***Symbiodinium* genetic structure**

All pairwise between-islands F_{ST} for *Symbiodinium* C40 were significant (Table 2A).

Symbiodinium C3 had one non-significant F_{ST} (Yap-Pohnpei) while all others were

significant and ranged from 0.058 (Guam-Chuuk) to 0.078 (Yap-Kosrae) (Table 2B).

Notably, *Symbiodinium* C3 differentiation did not show the isolation-by-distance pattern

observed in both coral hosts (Fig. 4). The correlation of F_{ST} with distance could not be

computed for *Symbiodinium* C40 due to few between-island comparisons available. For

Symbiodinium C3 F_{ST} values generally exceeded F_{ST} values for the host (Fig. 4A),

however, this result did not imply stronger genetic differentiation in the symbionts:

higher F_{ST} in the symbionts was a consequence of higher mean heterozygosity in

Symbiodinium markers (e.g. 41). Indeed, an alternative measure of genetic differentiation

controlling for mean heterozygosity - Jost's D (42) - demonstrated that *Symbiodinium* C3

genetic divergence was in fact intermediate between the two hosts (Fig. 4B).

Table 2. Summary of pairwise F_{ST} values between all islands for *Symbiodinium* C40 (A) and C3
(B). Permutations were run 9999 times. All significant comparisons are shaded in grey.
A. *Symbiodinium* C40

	PAL	NGU	YAP
PAL	0.000	***	0.004
NGU	0.279	0.000	***
YAP	0.056	0.326	0.000

183   B. *Symbiodinium* C3

	YAP	GUA	CHU	POH	KOS
YAP	0.000	***	***	0.059	***
GUA	0.062	0.000	***	***	***
CHU	0.066	0.058	0.000	***	***
POH	0.009	0.071	0.063	0.000	***
KOS	0.078	0.077	0.076	0.067	0.000

Figure 4: Comparison of two host species and *Symbiodinium* C3 differentiation. A. Pairwise genetic differentiation $[(F_{ST}/(1-F_{ST})]$ of two species of *Acropora* coral and *Symbiodinium* C3 across linear distances (km) demonstrating significant isolation by distance for the two host species but no correlation for the symbiont. B. Pairwise Jost's D for the same two host species and *Symbiodinium* C3 across linear distances (km) demonstrating no isolation by distance and no difference in overall divergence between the host and symbiont.

Host specificity and environmental specialization

Discriminant analysis of principal components (DAPC) strongly differentiated between host species for both *Symbiodinium* C40 and C3 (Table 3, Fig. 5A, B), suggesting that host specificity is an effective driver of symbiont diversity. In addition, DAPC analysis also demonstrated consistent differences among islands for each *Symbiodinium* type irrespective of host species: strong per-island assignment proportions were observed for C40 (Fig. 4C, 82-100%) and C3 (Fig. 5D, 51-98%), consistent with both STRUCTURE (Fig. 3) and F_{ST} results (Table 1). Moreover, nearly all pairwise F_{ST} values between different reef sites at the same island were significant for both *Symbiodinium* lineages (Table 4), suggesting environmental partitioning of symbionts. In accord with these results, of the two top eigenvalues in DAPC analyses within individual islands, one explained *Symbiodinium* genetic divergence by host species (host specificity) and the other corresponded to differences between reef sites (environmental specialization) (Fig.

6).

Table 3: Discriminant analysis of principle component (DAPC) model information including the
number of principle components ("PC") and discriminant functions ("DF") retained, the
proportion of conserved variance by the clustering model ("var"), and the overall assignment
proportions across the model ("assign"). A. DAPC information for *Symbiodinium* from different
host species, B. islands, and C. sites and host species within each island.
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214   Model Information

A. Host Species	PC	DF	var	assign
Symbiodinium C40	7	1	0.814	0.879
Symbiodinium C3	14	1	0.922	0.846
B. Islands	**PC**	**DF**	**var**	**assign**
Symbiodinium C40	16	4	0.970	0.981
Symbiodinium C3	19	4	0.966	0.796
C. Within Island	**PC**	**DF**	**var**	**assign**
Palau C40	14	3	0.984	0.735
Yap C3	7	3	0.844	0.778
Guam C3	3	3	0.647	0.860
Chuuk C3	12	3	0.933	0.927
Pohnpei C3	8	3	0.906	0.900
Kosrae C3	7	3	0.878	0.888

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216
217   Table 4. Summary of pairwise F_{ST} values for *Symbiodinium* C40 (A) and C3 (B) between all sites
218   pooled across host species. Permutations were run 9999 times. All significant comparisons are
219   shaded in grey.
220   A. *Symbiodinium* C40

	PAL1	PAL2	NGU	YAP2
PAL1	0.000	0.009	***	0.007
PAL2	0.031	0.000	***	0.007
NGU	0.283	0.303	0.000	***
YAP2	0.057	0.074	0.326	0.000

221   B. *Symbiodinium* C3

	YAP1	YAP2	GUA1	GUA2	CHU1	CHU2	POH1	POH2	KOS1	KOS2
YAP1	0.000	0.139	0.002	0.009	***	***	0.002	0.055	***	***
YAP2	0.011	0.000	***	0.003	***	***	0.027	0.064	***	***
GUA1	0.059	0.107	0.000	0.045	***	***	***	***	***	***
GUA2	0.045	0.062	0.025	0.000	0.002	***	***	0.008	***	***
CHU1	0.071	0.073	0.104	0.065	0.000	***	***	***	***	***
CHU2	0.079	0.112	0.070	0.086	0.068	0.000	***	***	***	***
POH1	0.053	0.028	0.126	0.111	0.085	0.126	0.000	***	***	***
POH2	0.018	0.018	0.093	0.039	0.067	0.092	0.063	0.000	***	***
KOS1	0.154	0.146	0.170	0.110	0.163	0.176	0.168	0.119	0.000	***
KOS2	0.092	0.121	0.116	0.131	0.129	0.090	0.136	0.100	0.183	0.000

Figure 5: Discriminant analysis of principal components (DAPC) of MLG data for *Symbiodinium* C40 and C3 hosted by *Acropora hyacinthus* and *Acropora digitifera* at thirteen sites across seven islands in Micronesia. A. DAPC analysis on two discriminant functions demonstrating strong host species assignments across all islands for *Symbiodinium* C40 and B. *Symbiodinium* C3. Numbers overlaying the curves indicate successfully assigned fraction of samples. C. DAPC scatter plot for individual samples from *Symbiodinium* C40 represented by colored dots clustered by islands. D. DAPC scatter plot for individual samples from *Symbiodinium* C3 represented by colored dots clustered by islands. Proportions of assignments are indicated in the clusters or in the legends. Information on the DAPC models can be found in Table 3.

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Figure 6: Discriminant analysis of principal components (DAPC) of MLG data for *Symbiodinium*
C40 and C3 hosted by *Acropora hyacinthus* and *Acropora digitifera* at twelve sites across six
islands (Ngulu not included) in Micronesia. DAPC analysis on two discriminant functions
demonstrating host species assignments and site assignments. DAPC scatter plots for individual
samples from within A. Palau for *Symbiodinium* C40. B. Yap for *Symbiodinium* C3, C. Chuuk for
Symbiodinium C3, D. Pohnpei for *Symbiodinium* C3, E. Kosrae for *Symbiodinium* C3, and F.
Guam for *Symbiodinium* C3 for *A. digitifera* hosts only (1 DF axis). Proportions of assignments
are indicated in the clusters. Information on the DAPC models can be found in Table 3.
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Discussion

Promiscuity of the coral host

Clade C *Symbiodinium* are the dominant symbiont type found in Indo-Pacific reef-

building corals (43), presumably because this clade is capable of greater rate of carbon

fixation (44) and increased carbon translocation to hosts, which positively influences host

fitness (growth) when compared to other clades (44-46). Clade C *Symbiodinium* are

considered to be the most derived lineage within the genus *Symbiodinium* and exhibit

significantly higher within-clade diversity when compared to other, more basal, clades

(14, 47, 48). Across the Micronesian Pacific (Fig. 1), both coral hosts associated

exclusively with clade C *Symbiodinium*, which was represented by two distinct lineages–

C40 and C3, putatively corresponding to different species (Fig. 2). This observation

confirms the first prediction of the 'global host, local symbiont' hypothesis: coral hosts

show considerable flexibility in their symbiotic association across their range and within

their habitat.

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Lack of dispersal limitation in Symbiodinium *across Micronesia*

Initially, we expected to find strong isolation by distance in *Symbiodinium*, since the

prevailing view of the *Symbiodinium* life cycle involves symbiotic existence in sedentary

hosts alternating with a free-living form that largely exists in the benthos where dispersal

by ocean currents must be limited (49-52). In contrast, we observed that genetic

differentiation between islands of *Symbiodinium* C3 across Micronesia did not exceed

$F_{ST} = 0.078$, which contrasts studies from other locations reporting symbiont F_{ST} as high

as 0.54 in clade A (53) and Φ_{ST} as high as 0.468 in clade C (54). This lack of physical

dispersal limitation is best demonstrated by comparing *Symbiodinium* C3 divergence to

divergence of their coral hosts, which has been shown to nearly perfectly follow

biophysical barriers (21). If *Symbiodinium* dispersal were limited by the same physical

barriers and to a greater extent, as our hypothesis posited, we would have observed

steeper increases in divergence with distance relative to the host; instead, no increase of

F_{ST} with distance was observed (Fig. 4A).   Moreover, after correcting for mean

heterozygosity, genetic divergence (Jost's D) in *Symbiodinium* C3 was found to be

intermediate between *A. hyacinthus* and *A. digitifera* (Fig. 4B), once again demonstrating

that symbiont dispersal is less limited than their hosts. This finding contradicts the second

prediction of our 'global host, local symbiont' hypothesis and is contrary to our

expectations based on earlier F_{ST}-based reports of stronger *Symbiodinium* differentiation

compared to hosts (3, 25, 26, 54).

Host specificity

The majority of reef-building coral species associate with a specific strain (termed

"clade" or "subclade") of *Symbiodinium* broadly defined based on ribosomal and/or

chloroplast markers (3, 36, 38, 55). Previous *Symbiodinium* multilocus genotyping

studies revealed that each of these strains harbors greater diversity, both in terms of

genetic and functional diversity (25, 54, 56). Our data indicate that the local association

of hosts and symbionts of the same genotypic cluster is due to pervasive evolution of host

specificity in *Symbiodinium* (Fig. 5 & 6). As our study includes two coral species, we

also observe that this specificity is not perfect: at every location there were symbionts

that would have been assigned to another coral host based on their multilocus genotype

(Fig. 6). This suggests that host specialization in *Symbodinium* arises in the face of

considerable exchange between symbiont communities hosted by different coral species

at the same location. However, to which extent this between-host exchange contributes to

gene flow is unclear since it remains unknown if *Symbidinium* undergo sexual

reproduction within or outside the host.

Environmental partitioning

The most ecologically relevant postulate of the 'global host, local symbiont' hypothesis is

that locally available symbionts are also locally adapted, giving rise to a locally adapted

holobiont. Recurrent genetic divergence of symbionts between reef sites within the same

island (Fig. 6) despite the lack of physical dispersal limitation across much larger

distances (Fig. 4) suggests that symbiont genetic divergence is likely due to poor survival

of immigrants rather than to physical barriers to migration. Given that hosts are available

at every site, this leaves other ecological parameters of local reef environment as the most

likely barrier-forming force, preventing survival of immigrants adapted to a different

environment– a situation termed "phenotype-environment mismatch" (57). Thus,

although our study did not directly test for local adaptation of *Symbiodinium* as per

Kawecki and Ebert (58), genetic partitioning of symbionts among different reef

environments across small spatial scales suggests that their local adaptation does indeed

occur, thereby supporting our hypothesis. Notably, similar to the situation with host

specificity, there are several *Symbiodinium* genotypes that appear to be successful

migrants between reef sites (particularly clearly visible for Kosrae, Fig. 6E), indicating

that environmental partitioning is also incomplete and arises in the face of considerable

gene flow.

Conclusions

Across Micronesia, both coral host species associated with two divergent *Symbiodinium*

lineages (putatively corresponding to species), indicating high host promiscuity in

symbiont association. In contrast, within each *Symbiodinium* lineage, strong associations

with particular host species were observed, suggesting that host-specificity is an

important driver of *Symbiodinium* diversification. Unexpectedly, *Symbiodinium* genetic

divergence did not correlate with physical distance between islands, contrary to our initial

prediction that symbionts would exhibit a more pronounced isolation-by-distance pattern

than their hosts due to stronger barriers to dispersal. Instead, *Symbiodinium* genetic

structure was driven by the combined effects of local (within-island) environment and

host identity, suggesting that *Symbiodinium* assemblages across Micronesia are

comprised by broadly dispersing lineages dynamically adapting to specific coral hosts

and reef environments across their range. Notably, this pattern perfectly follows Baas

Becking's hypothesis for microbial communities: "Everything is everywhere, but the

environment selects" (59), assuming that host species themselves contribute to this

'environment'. Although this observation contradicts the original formulation of our

'global host, local symbiont' hypothesis, it supports the view that coral hosts could derive

fitness benefits from associating with locally available *Symbiodinium*. Finally, dramatic

differences in factors that structure genetic diversity in the coral host and their algal

symbionts render the 'hologenome' concept irrelevant to horizontally-transmitting coral-

algal symbioses.

Materials and Methods

Sampling Locations and Methodology: This study comprised a subset of samples

previously analyzed for coral host genetics in Davies *et al.* (21) (Table 5, Fig. 1).

Twenty-five individuals of each coral host species (*Acropora hyacinthus* and *A.*

digitifera) were examined at two reef sites within seven islands, with the exception of

Ngulu (the only species collected was *A. hyacinthus*) and Guam (no *A. hyacinthus* were

found and only *A. digitifera* were collected), for a total of thirteen sites.

Table 5. Reef Site Collections. GPS coordinates, main island group, number of *A. digitifera* and
A. hyacinthus hosts genotyped. The numbers in brackets are individuals hosting a single
Symbiodinium MLG, which were included in all analyses presented here. Site letter corresponds
to island insets in Figure 1.

Site	Island	GPS	*A. digitifera*	*A. hyacinthus*
WC. West Channel Reef	Palau	7°31'55.7 N, 134°29'42.8 E	24 (20)	25 (17)
LH. Lighthouse Reef	Palau	7°16'62.4 N, 134°27'61.9 E	23 (15)	24 (16)
NG. Ngulu	Ngulu Atoll	8°18'12.0 N, 137°29'18.7 E	0[1]	39 (25)
ST. South Tip Reef	Yap	9°26'05.4 N, 138°02'10.4 E	25 (10)	25 (11)
GO. Goofnuw Channel	Yap	9°34'26.4 N, 138°12'19.2 E	24 (15)[m]	25 (20)
PB. Pago Bay	Guam	13°25'66.6 N, 144°47'94.3 E	26 (20)	0*
TG. Tanguisson	Guam	13°32'61.1 N, 144°48'52.6 E	21 (17)	0*
WP. West Polle	Chuuk	7°19'69.7 N, 151°33'21.1E	15 (6)[m]	24 (18)
SE. South East Pass	Chuuk	7°14'60.3 N, 152°01'29.1 E	21 (17)[m]	22 (16)
AN. Ant Atoll (East)	Pohnpei	6°47'42.3 N, 158°01'20.7 E	24 (16)	22 (13)
RO. Roj	Pohnpei	6°46'37.7 N, 158°12'24.1 E	24 (16)	23 (15)
CG. Coral Garden	Kosrae	5°18'47.2 N, 162°53'01.8 E	25 (15)[m]	24 (13)
HP. Hiroshi Point	Kosrae	5°15'88.0 N, 162°59'01.8 E	25 (23)[m]	25 (14)
TOTAL			**277 (190)**	**278 (178)**

* indicates that no individuals of this species were found
[1] indicates that individuals were not collected from this site but are likely present
[m] indicated sites where multiple *Symbiodinium* species were detected

Laboratory Procedures: Holobiont DNA was isolated following Davies *et al.* (60).

Microsatellite primers for this study consisted of six previously published clade C loci

(61, 62) and one novel locus mined using Msatcommander (63) from nucleotide EST data

for *Symbiodinium* sp. clade C3 in GenBank (64) (Table 6). Loci were multiplexed

according to annealing temperatures and fragment sizes. Each 20 µl polymerase chain

reaction (PCR) mixture contained 10 ng of DNA template, 0.1 µM of each forward

primer, 0.1 µM of each reverse primer, 0.2 mM dNTP, 1 µl 10X *ExTaq* buffer, 0.025 U

ExTaq Polymerase (Takara Biotechnology) and 0.0125 U *Pfu* Polymerase (Agilent

Technologies). Amplifications were performed using a DNA Engine Tetrad2 Thermal

Cycler (Bio-Rad, Hercules CA). Cycling began at 94°C for 5 min, followed by 35 cycles

of 94°C for 40 s, annealing temperature for 120 s, and 72°C for 60 s and a 10 minute

extension period at 72°C. Molecular weights were analyzed using the ABI 3130XL

capillary sequencer with an in-house ROX-labeled size standard. Data were binned by

repeat size and individuals failing to amplify at ≥3 loci were excluded from analyses.

Table 6: Summary of six polymorphic microsatellite loci used to assess genetic variation
Symbiodinium clade C hosted by *A. hyacinthus* and *A. digitifera* and their corresponding
multiplexing groups.

Multiplex Group	Locus (Repeat)	Primer Sequence 5'-3'	Repeat	Annealing Temperature	Source
A	*SgrSpl_30*	F: FAM-ccgaactacctttggtcaac R: aaaagacaaggacatctcgg	TA	53	Wham et al., 2014
B	*SgrSpl_78*	F: FAM-tgaaattcggtgttcattgt R:ctcagatgtttccgacgagt	TA	54	Wham et al., 2014
	Sgr_21	F: HEX-tgctgagtggcgtgtatatc R: tgatggtacttgatggtg	TCA	54	Wham et al., 2014
	Spl_33	F: HEX-acttgcaaagtccaagatcg R: gaacggtgaaaggaaaatga	CAT	54	Wham et al., 2014
C	*C784*	F: Hadp-ctccttaggactggactcgc R: agaagtcaaatcgtcaccatcg	ATC	60	This Study
D	*C105*	F: FAM-tttcgttgttggacattgttatg R: ggactgaaaggtgcttgagg	complex	55	Bay *et al.,* 2009

372 Fadp- labeled primers were indirectly labeled in each PCR reaction with an additional FAM labeled adapter
373 tag sequence: FAM: agcagcgaactcagtacaaca
374 Hadp- labeled primers were indirectly labeled in each PCR reaction with an additional FAM labeled
375 adapter tag sequence: HEX: tcgtcgcttgagtcatcgtta
376
377

Data Analysis: *Symbiodinium* in clade C microsatellite data were scored as diploid based
on available information on the ploidy of these organisms (3, 62, 65) Since each
individual host could potentially contain a population of genetically distinct
Symbiodinium individuals, multi-locus genotypes (MLG) were only considered in this
study if they contained two or fewer alleles across all loci, suggesting that all alelles
originate from a single, clonally replicated, genome (65), which was the case for a total of
190 out of 277 for *A. digitifera* hosts and 178 out of 278 for *A. hyacinthus* hosts. We first
applied a Bayesian approach implemented in STRUCTURE v2.3.3 (66). STRUCTURE uses a
Monte Carlo Markov chain (MCMC) clustering algorithm to assign individuals with
similar genotypes to populations. Mean and variance of log likelihood values of the
number of populations K (1-10) were inferred by STRUCTURE with 10^6 iterations (burn in
= 300,000 iterations) in ten replicate runs for each K. An admixture model was
implemented with no location prior. Following the recommendations of (67), the ad hoc
statistic ΔK was calculated based on the rate of change of the log-likelihood between
consecutive K values, which is implemented in the program STRUCTURE Harvester (68).
CLUMPP (69) and DISTRUCT (70) were used to produce graphics. We observed high
percent assignment to two different clusters among sympatric individuals. Following the
methodology of Wham and LaJeunesse (65), we investigated the relationship between
these cluster assignments and allele identities. From this analysis we found a strong
relationship between cluster assignments and allele identity, particularly at Sgr_21 and
Spl_33 (Supplement Fig. S1A, B), and it became clear that two distinct *Symbiodinium*
lineages were present. MLG data were then split into *Symbiodinium* lineages based on the
probability of species assignment conditioned on their cluster assignment (65).
Additional STRUCTURE runs were completed following descriptions above with these
subsequent differences: 1) location prior was implemented and 2) instead of using the ΔK
statistic, we presented the K that maximized the mean of the estimated probability of data
while   minimizing   the   standard   deviation.

405
406 Supplementary Figure 1: Bubble plot of the SSR allele frequencies of C3 (red) and C40 (blue) at
407 the two loci that showed the largest discrimination power, Sgr_21 (A) and Spl_33 (B). The size of
408 each bubble is proportional to the allele frequency within each *Symbiodinium* type.
409

Once data were partitioned by *Symbiodinium* lineages, genetic divergences among

islands and sites were investigated using F_{ST} (AMOVA, 9999 permutations in GENALEX

v6.5, (71)). Pairwise differentiations (F_{ST} and Jost's D) and pairwise island distances

were then correlated to test for isolation by distance (IBD) in *Symbiodinium* C3 (not

sufficient data for C40) and these IBD trends were compared to results from the host

species (72). Mean allelic diversities per island and numbers of private alleles per island

were also calculated in GENALEX v6.5.

To resolve differences between islands, between host species and between sites

and host species within each island, assignment of samples to genetic clusters using

discriminant analysis of principal components (DAPC) was performed in R (73) using the

ADEGENET package (74, 75). Here, *Symbiodinium* data were converted into principle

components and then a-scores were used to determine trade-offs between power of

discrimination and model over-fitting. Relationships were examined by DAPC, which

optimizes variation among clusters by minimizing variation within clusters, while

retaining the optimal number of principle components and maximum number of

discriminant functions. All information on DAPC model parameters and results are

contained in Table 3. Cluster assignment patterns were compared across islands, host

species, and among host species and sites within each island.

Sequencing Analysis of *Symbiodinium* psbA^{ncr}

In order to confirm the assignments of individuals to different *Symbiodinium* lineages, we

selected a small subset of the full sample set and analyzed the non-coding region of the

circular plastid (psbA^{ncr}). We amplified the psbA^{ncr} locus with the primers 7.4-Forw and

7.8-Rev following the methods described by LaJeunesse and Thornhill (40). The

amplified product was directly sequenced and the resulting sequences were aligned with

ClustalW2 (http://www.ebi.ac.uk/Tools/msa/clustalw2/) to clade C psbA^{ncr} sequences

from common *Symbiodinium* types found throughout the Indo-Pacific region

(Supplemental Table 1: JQ043587-JQ043676 from (40)). We reconstructed the

phylogeny of these samples using the default settings of Phylogeny.fr (76). The identities

of *Symbiodinium* types from our analysis were interpreted from their percent sequence

identity with these previously identified *Symbiodinium* types and their position on the

resulting phylogeny.

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References

1. Brucker RM & Bordenstein SR (2012) The roles of host evolutionary relationships (genus: Nasonia) and development in structuring microbial communities. *Evolution* 66(2):349-362.
2. Moran NA (2006) Symbiosis. *Curr Biol* 16(20):R866-871.
3. Thornhill DJ, Lewis AM, Wham DC, & LaJeunesse TC (2014) Host-specialist lineages dominate the adaptive radiation of reef coral endosymbionts. *Evolution* 68(2):352-367.
4. Brucker RM & Bordenstein SR (2012) Speciation by symbiosis. *Trends Ecol Evol* 27(8):443-451.
5. Mereschkowsky K (1910) Theorie der zwei Plasmaarten als Grundlage der Symbiogenesis, einer neuen Lehre von der Ent-stehung der Organismen. *Biol Centralbl* 30:353-367.
6. Nakabachi A, Ishida K, Hongoh Y, Ohkuma M, & Miyagishima SY (2014) Aphid gene of bacterial origin encodes a protein transported to an obligate endosymbiont. *Curr Biol* 24(14):R640-641.
7. Shigenobu S & Wilson AC (2011) Genomic revelations of a mutualism: the pea aphid and its obligate bacterial symbiont. *Cellular and molecular life sciences : CMLS* 68(8):1297-1309.
8. Peksa O & Skaloud P (2011) Do photobionts influence the ecology of lichens? A case study of environmental preferences in symbiotic green alga Asterochloris (Trebouxiophyceae). *Mol Ecol* 20(18):3936-3948.
9. Fernandez-Mendoza F*, et al.* (2011) Population structure of mycobionts and photobionts of the widespread lichen Cetraria aculeata. *Mol Ecol* 20(6):1208-1232.
10. Henry LM*, et al.* (2013) Horizontally transmitted symbionts and host colonization of ecological niches. *Curr Biol* 23(17):1713-1717.
11. Brucker RM & Bordenstein SR (2014) Response to Comment on "The hologenomic basis of speciation: Gut bacteria cause hybrid lethality in the genus Nasonia". *Science* 345(6200).
12. Zilber-Rosenberg I & Rosenberg E (2008) Role of microorganisms in the evolution of animals and plants: the hologenome theory of evolution. *Fems Microbiol Rev* 32(5):723-735.
13. Moran NA & Sloan DB (2015) The Hologenome Concept: Helpful or Hollow? *PLoS biology* 13(12):e1002311.
14. Lesser MP, Stat M, & Gates RD (2013) The endosymbiotic dinoflagellates (Symbiodinium sp.) of corals are parasites and mutualists. *Coral Reefs*:603-611.
15. Muscatine L (1990) The role of symbiotic algae in carbon and energy flux in reef corals. *Ecosystems of the World* 25:75-87.
16. Barott KL, Venn AA, Perez SO, Tambutte S, & Tresguerres M (2015) Coral host cells acidify symbiotic algal microenvironment to promote photosynthesis. *Proc Natl Acad Sci U S A* 112(2):607-612.
17. Muscatine L & Cernichiari E (1969) Assimilation of photosynthetic products of zooxanthellae by a reef coral. *The Biological Bulletin* 137(3):506-523.

500   18.   Trench RK & Blank RJ (1987) Symbiodinium microadriaticum Fredenthal, S.
501   Goreau sp. nov., S. Kawagut2 sp. nov., and S. pilosum sp. nov.: Gymnodinoid
502   dinoflagellate symbionts of marine invertebrates. *J Phycol* 23(3):469-481.
503   19.   Fadlallah YH (1983) Sexual reproduction, development and larval biology of
504   scleractinian corals. A review. *Coral Reefs* 2:129-150.
505   20.   Harrison PLW, C.C. (1990) *Reproduction, dispersal and recruitment of*
506   *scleractinian corals* (elsevier Science Publications Amsterdam).
507   21.   Davies SW, Treml EA, Kenkel CD, & Matz MV (2015) Exploring the role of
508   Micronesian islands in the maintenance of coral genetic diversity in the Pacific
509   Ocean. *Mol Ecol* 24(1):70-82.
510   22.   Gorospe KD & Karl SA (2011) Small-Scale Spatial Analysis of In Situ Sea
511   Temperature throughout a Single Coral Patch Reef. *Journal of Marine Biology*
512   2011:12.
513   23.   Byler KA, Carmi-Veal M, Fine M, & Goulet TL (2013) Multiple symbiont
514   acquisition strategies as an adaptive mechanism in the coral Stylophora pistillata.
515   *Plos One* 8(3):e59596.
516   24.   Rowan R & Knowlton N (1995) Intraspecific diversity and ecological zonation in
517   coral-algal symbiosis. *Proc Natl Acad Sci U S A* 92(7):2850-2853.
518   25.   Howells EJ*, et al.* (2012) Coral thermal tolerance shaped by local adaptation of
519   photosymbionts. *Nat Clim Change* 2:116-120.
520   26.   Baums IB, Devlin-Durante MK, & LaJeunesse TC (2014) New insights into the
521   dynamics between reef corals and their associated dinoflagellate endosymbionts
522   from population genetic studies. *Mol Ecol* 23(17):4203-4215.
523   27.   Abrego D, MJ VANO, & Willis BL (2009) Highly infectious symbiont dominates
524   initial uptake in coral juveniles. *Mol Ecol* 18(16):3518-3531.
525   28.   Gómez-Cabrera MdC, Ortiz JC, Loh WKW, Ward S, & Hoegh-Guldberg O
526   (2008) Acquisition of symbiotic dinoflagellates (Symbiodinium) by juveniles of
527   the coral Acropora longicyathus. *Coral Reefs* 27(1):219-226.
528   29.   Little AF, van Oppen MJ, & Willis BL (2004) Flexibility in algal endosymbioses
529   shapes growth in reef corals. *Science* 304(5676):1492-1494.
530   30.   Abrego D, van Oppen MJ, & Willis B (2009) Onset of algal endosymbiont
531   specificity varies among closely related species of Acropora corals during early
532   ontogeny. *Mol Ecol* 18(16):3532-3543.
533   31.   Ackerly DD, Schwilk DW, & Webb CO (2006) Niche evolution and adaptive
534   radiation: testing the order of trait divergence. *Ecology* 87(7 Suppl):S50-61.
535   32.   Coffroth MA, Santos SR, & Goulet TL (2001) Early ontogenetic expression of
536   specificity in a cnidarian–algal symbiosis. *Mar Ecol Prog Ser* 222:85-96.
537   33.   Finney JC*, et al.* (2010) The relative significance of host-habitat, depth, and
538   geography on the ecology, endemism, and speciation of coral endosymbionts in
539   the genus Symbiodinium. *Microbial ecology* 60(1):250-263.
540   34.   Lajeunesse TC (2005) "Species" radiations of symbiotic dinoflagellates in the
541   Atlantic and Indo-Pacific since the Miocene-Pliocene transition. *Mol Biol Evol*
542   22(3):570-581.
543   35.   LaJeunesse TC*, et al.* (2010) Host-symbiont recombination versus natural
544   selection in the response of coral-dinoflagellate symbioses to environmental

545   disturbance. *Proceedings. Biological sciences / The Royal Society*
546   277(1696):2925-2934.

547   36.   Rodriguez-Lanetty M, Krupp DA, & Weis VM (2004) Distinct ITS types of
548   Symbiodinium in Clade C correlate with cnidarian/dinoflagellate specificity
549   during onset of symbiosis. *Mar Ecol Prog Ser* 275(97-102).

550   37.   Thornhill DJ, Xiang Y, Fitt WK, & Santos SR (2009) Reef endemism, host
551   specificity and temporal stability in populations of symbiotic dinoflagellates from
552   two ecologically dominant Caribbean corals. *Plos One* 4(7):e6262.

553   38.   Weis VM, Reynolds WS, deBoer MD, & Krupp DA (2001) Host-symbiont
554   specificity during onset of symbiosis between the dinoflagellates Symbiodinium
555   spp. and planula larvae of the scleractinian coral Fungia scutaria. *Coral Reefs*
556   20(3):301-308.

557   39.   Polato NR, Vera JC, & Baums IB (2011) Gene discovery in the threatened
558   elkhorn coral: 454 sequencing of the Acropora palmata transcriptome. *Plos One*
559   6(12):e28634.

560   40.   LaJeunesse TC & Thornhill DJ (2011) Improved resolution of reef-coral
561   endosymbiont (Symbiodinium) species diversity, ecology, and evolution through
562   psbA non-coding region genotyping. *Plos One* 6(12):e29013.

563   41.   Jakobsson M, Edge MD, & Rosenberg NA (2013) The Relationship Between F-
564   ST and the Frequency of the Most Frequent Allele. *Genetics* 193(2):515-528.

565   42.   Jost L (2008) G(ST) and its relatives do not measure differentiation. *Mol Ecol*
566   17(18):4015-4026.

567   43.   Quigley KM*, et al.* (2014) Deep-Sequencing Method for Quantifying Background
568   Abundances of Symbiodinium Types: Exploring the Rare Symbiodinium
569   Biosphere in Reef-Building Corals. *Plos One* 9(4).

570   44.   Stat M, Morris E, & Gates RD (2008) Functional diversity in coral-dinoflagellate
571   symbiosis. *Proc Natl Acad Sci U S A* 105(27):9256-9261.

572   45.   Jones A & Berkelmans R (2010) Potential costs of acclimatization to a warmer
573   climate: growth of a reef coral with heat tolerant vs. sensitive symbiont types.
574   *Plos One* 5(5):e10437.

575   46.   Mieog JC*, et al.* (2009) The roles and interactions of symbiont, host and
576   environment in defining coral fitness. *Plos One* 4(7):e6364.

577   47.   Pochon X & Gates RD (2010) A new Symbiodinium clade (Dinophyceae) from
578   soritid foraminifera in Hawai'i. *Molecular phylogenetics and evolution* 56(1):492-
579   497.

580   48.   Pochon X, Montoya-Burgos JI, Stadelmann B, & Pawlowski J (2006) Molecular
581   phylogeny, evolutionary rates, and divergence timing of the symbiotic
582   dinoflagellate genus Symbiodinium. *Molecular phylogenetics and evolution*
583   38(1):20-30.

584   49.   Fitt WK, Chang SS, & Trench RK (1981) Motility Patterns of Different Strains of
585   the Symbiotic Dinoflagellate Symbiodinium (=Gymnodinium) Microadriaticum
586   (Freudenthal) in Culture. *Bulletin of Marine Science* 31(2):436-443.

587   50.   Fitt WK & Trench RK (1983) The Relation of Diel Patterns of Cell-Division to
588   Diel Patterns of Motility in the Symbiotic Dinoflagellate Symbiodinium-
589   Microadriaticum Freudenthal in Culture. *New Phytol* 94(3):421-432.

51.   Yacobovitch T, Benayahu Y, & Weis VM (2004) Motility of zooxanthellae
isolated from the Red Sea soft coral Heteroxenia fuscescens (Cnidaria). *J Exp*
Mar Biol Ecol 298(1):35-48.
52.   Littman RA, van Oppen MJH, & Willis BL (2008) Methods for sampling free-
living Symbiodinium (zooxanthellae) and their distribution and abundance at
Lizard Island (Great Barrier Reef). *J Exp Mar Biol Ecol* 364(1):48-53.
53.   Andras JP, Kirk NL, & Harvell CD (2011) Range-wide population genetic
structure of Symbiodinium associated with the Caribbean Sea fan coral, Gorgonia
ventalina. *Mol Ecol* 20(12):2525-2542.
54.   Howells EJ, van Oppen MJ, & Bay LK (2009) High genetic differentiation and
cross-shelf patterns of genetic diversity among Great Barrier Reef populations of
Symbiodinium. *Coral Reefs* 28(1):215-225.
55.   Fabina NS, Putnam HM, Franklin EC, Stat M, & Gates RD (2013) Symbiotic
specificity, association patterns, and function determine community responses to
global changes: defining critical research areas for coral-Symbiodinium
symbioses. *Global Change Biol* 19(11):3306-3316.
56.   Santos SR, Shearer TL, Hannes AR, & Coffroth MA (2004) Fine-scale diversity
and specificity in the most prevalent lineage of symbiotic dinoflagellates
(Symbiodinium, Dinophyceae) of the Caribbean. *Mol Ecol* 13(2):459-469.
57.   Marshall DJ, Monro K, Bode M, Keough MJ, & Swearer S (2010) Phenotype-
environment mismatches reduce connectivity in the sea. *Ecol Lett* 13(1):128-140.
58.   Kawecki TJ & Ebert D (2004) Conceptual issues in local adaptation. *Ecol Lett*
7(12):1225-1241.
59.   Baas Becking LGM (1934) Geobiologie of inleiding tot de milieukunde. *Den*
Haag [Netherlands]: W.P. Van Stockum & Zoon, N. V.
60.   Davies SW*, et al.* (2013) Novel polymorphic microsatellite markers for
population genetics of the endangered Caribbean star coral, Montastraea
faveolata. *Mar Biodivers* 43(2):167-172.
61.   Bay LK, Howells EJ, & van Oppen MJ (2009) Isolation, characterisation and
cross amplification of thirteen microsatellite loci for coral endo-symbiotic
dinoflagellates (Symbiodinium clade C). *Conserv Genet Resour* 1(1):199-203.
62.   Wham DC, Carmichael M, & LaJeunesse TC (2014) Microsatellite loci for
Symbiodinium goreaui and other Clade C Symbiodinium. *Conserv Genet Resour*
6(1):127-129.
63.   Faircloth BC (2008) MSATCOMMANDER: detection of microsatellite repeat
arrays and automated, locus-specific primer design. *Molecular ecology resources*
8(1):92-94.
64.   Leggat W, Hoegh-Guldberg O, Dove S, & Yellowlees D (2007) Analysis of an
EST library from the dinoflagellate (Symbiodinium sp.) symbiont of reef-building
corals. *J Phycol* 43(5):1010-1021.
65.   Traylor-Knowles N*, et al.* (2011) Production of a reference transcriptome and
transcriptomic database (PocilloporaBase) for the cauliflower coral, Pocillopora
damicornis. *BMC genomics* 12:585.
66.   Pritchard JK, Stephens M, & Donnelly P (2000) Inference of population structure
using multilocus genotype data. *Genetics* 155(2):945-959.

67.   Evanno G, Regnaut S, & Goudet J (2005) Detecting the number of clusters of
individuals using the software STRUCTURE: a simulation study. *Mol Ecol*
14(8):2611-2620.
68.   Earl DA & Vonholdt BM (2012) STRUCTURE HARVESTER: a website and
program for visualizing STRUCTURE output and implementing the Evanno
method. *Conserv Genet Resour* 4(2):359-361.
69.   Jakobsson M & Rosenberg NA (2007) CLUMPP: a cluster matching and
permutation program for dealing with label switching and multimodality in
analysis of population structure. *Bioinformatics* 23(14):1801-1806.
70.   Rosenberg NA (2004) DISTRUCT: a program for the graphical display of
population structure. *Mol Ecol Notes* 4(1):137-138.
71.   Peakall R & Smouse PE (2006) GENALEX 6: genetic analysis in Excel.
Population genetic software for teaching and research. *Mol Ecol Notes* 6(1):288-
295.
72.   Davies SW, Treml EA, Kenkel CD, & Matz MV (2015) Exploring the role of
Micronesian islands in the maintenance of coral genetic diversity in the Pacific
Ocean. *Mol Ecol* 24(1):70-82.
73.   R Development Core Team (2015) R: A language and environment for statistical
computing. (R Foundation for Statistical Computing, Vienna, Austria).
74.   Jombart T (2008) adegenet: a R package for the multivariate analysis of genetic
markers. *Bioinformatics* 24(11):1403-1405.
75.   Jombart T, Devillard S, & Balloux F (2010) Discriminant analysis of principal
components: a new method for the analysis of genetically structured populations.
BMC genetics 11:94.
76.   Dereeper A*, et al.* (2008) Phylogeny.fr: robust phylogenetic analysis for the non-
specialist. *Nucleic Acids Res* 36(Web Server issue):W465-469.
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664 Supplemental Table 1: Accession number and corresponding Clade C *Symbiodinium* lineage for
665 each unique sequence identifier from Figure 2.
666

Sequence ID	Accession Number	Lineage
1	JQ043642	C3
2	KF572372	C3
3	JQ043643	C3
4	JQ043641	C3
5	JQ043640	C3
6	JQ043644	C3
7	JQ043635	C3
8	JQ043638	C3
9	JQ043637	C3
10	JQ043636	C3
11	KF572331	C3
12	KF572332	C3
13	KF572318	C3
14	KF572319	C3
15	KF572373	C3
16	KF572374	C3
17	KF572358	C3
18	KF572368	C40
19	KF572359	C40
20	KF572367	C40
21	KF572366	C40
22	KF572360	C40
23	KF572357	C40
24	KF572363	C40
25	KF572365	C40
26	KF572364	C40
27	KF572370	C40
28	JQ043603	C31
29	JQ043599	C31
30	JQ043604	C31
31	JQ043671	C27
32	JQ043673	C27
33	JQ043670	C27
34	JQ043669	C27
35	JQ043676	C27

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