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SPATIAL DIFFERENCES IN SUBTIDAL EPIBIOTIC COMMUNITY STRUCTURE IN MARINA AT KEPPEL BAY, SINGAPORE

K. M. Lam and **Peter A. Todd***
Experimental Marine Ecology Laboratory, Department of Biological Sciences, National University of Singapore
14 Science Drive 4, Singapore 117543, Republic of Singapore
*(*Corresponding author: dbspat@nus.edu.sg)*

ABSTRACT. — Urban structures in marine environments represent novel habitats for numerous species. Marinas are one such modified environment, exemplified by pontoons that can act as surrogate habitats for sessile epibiotic organisms. Because they float, pontoons are rather special structures where epibiota are not influenced by changes in depth associated with tidal variations. Baseline data for pontoon communities in Singapore are deficient, hence the present study surveyed subtidal epibiota growing on pontoons at Marina at Keppel Bay. Differences in community structure among three locations and between the interior and exterior of berths within the marina were investigated (six stations in total). It was hypothesised that dissimilarities in physicochemical parameters among survey stations could influence the composition of epibiotic assemblages. Forty-nine taxa were identified and these were generally similar to those found on local coral reefs. Dissimilarities in community structure were significant among locations but not between the interior and exterior of berths. Three major distinguishing taxa contributed to among-location differences (i.e., *Stereonephthya* sp., *Padina* sp., and *Halimeda* sp.). Light intensity and hydrodynamic conditions were identified as factors most likely influencing variation in taxa composition. This study shows how pontoons can support the settlement and growth of subtidal organisms, to some extent mitigating the negative impact associated with urbanisation and coastal modification.

KEY WORDS. — coastal modification, novel habitat, marina; pontoon; coral reef, Singapore

INTRODUCTION

Urbanisation and industrialisation have resulted in the establishment of artificial structures in numerous environments (Walker, 1988). The study of how these can act as surrogate habitats for organisms is an increasingly important priority for ecologists (McDonnell & Pickett, 1990; Pickett et al., 1997). Work to date has shown that they can both increase (Gilbert, 1989; Douglas & Lake, 1994; Bohninggaese, 1997) or decrease (Heck, 1979; McGuinness & Underwood, 1986) the number of species and/or the abundance of individuals in a community. However, as the relationship between diversity and habitat is a central issue in conservation biology (Dunning et al., 1992; Tilman et al., 1997; Chapin et al., 1998), much more research into the effects of urbanisation is required. This is especially true for marine systems, which are often overlooked in urban ecology studies.

During its transition into a developed nation, most of Singapore's natural coastline was highly modified. Marinas comprising man-made structures such as seawalls, pilings, and pontoons, are one example of anthropogenically altered marine environments. The semi-enclosed nature typical of marinas restricts hydrodynamic processes such as wave action and tidal flow (Hinwood, 1998). Modification of benthic substrata, and sediment accumulation resulting from the establishment of artificial structures, can also alter habitat complexity and subsequently marine communities (Turner et al., 1997). Despite the localised negative impacts of marinas on water quality, evidence has shown that they can also provide new and novel habitats, with distinct assemblages of marine epibiota compared to those found on natural substrata such as rocky reefs (Connell & Glasby, 1999; Glasby, 1999). Karlson (1978) suggested that the addition of artificial structures could affect the distribution and abundance of sessile biota. For example, the associated hard surfaces provide excellent colonisation opportunities for sessile epibiota such as ascidians, molluscs, and algae (Connell, 1999; Bacchiocchi & Airoldi, 2003; Bulleri & Chapman, 2004).

Since 1819, the original land area of Singapore has increased by more than 132 km^2 through land reclamation (Lok et al., 2010). Developments in the form of seawalls and marinas have dramatically changed the original coastal profile (Chou, 2006). Marina at Keppel Bay is one of the four main marinas situated on the southern coast of Singapore. To date, no published studies or surveys have been conducted on subtidal epibiotic communities on artificial structures at this site. The primary objective of the present study was to assess the taxon richness, abundance, and diversity of subtidal epibiotic communities that have naturally recruited on pontoon walls within the marina. Such an assessment of the biodiversity of subtidal epibiota from this survey can provide baseline data for subtidal organisms inhabiting the marinas of Singapore to be used as a reference for further comparative research. In addition, a better understanding of what lives on marine artificial structures can potentially help engineers design coastal infrastructure that increases, rather than reduces, biodiversity.

The secondary objective of this project was to investigate whether spatial differences affect subtidal epibiota by comparing communities among three locations within Marina at Keppel Bay as well as between the interior and exterior of berths. Pontoons are unique structures as they float and epibiota are not influenced by changes in water level associated with the rise and fall of the tides. However, features affecting variables such as light intensity can have significant effects on epibiotic diversity (Connell & Glasby, 1999; Irving & Connell, 2002). It was hypothesised that spatial variation in subtidal epibiotic communities existed within the marina and that these were likely to be driven by differences in micro-environmental parameters.

MATERIAL AND METHODS

Study site. — The study was conducted in Jun.2012 at Marina at Keppel Bay (01°15.90′N, 103°48.70′E) situated on the southern shore of Singapore Island. Previously an old shipyard, the marina currently has a berthing capacity of 168 boats, which are generally yachts and pleasure vessels. All floating pontoons surrounding the berths are made of concrete and constructed in two phases: in 2007 and in 2010. The construction of the marina was based on an 'open' concept, which allows water to flow through the entire marina. Green practices adopted by the marina ensure that sewage is not discharged into the water and exhaust pollution from the vessels is minimised.

Sampling locations and methods. — As the age of the substratum is an important determinant of the species and abundance of marine epibiota in a habitat (McGuinness, 1989; Underwood & Anderson, 1994), surveys were conducted only on pontoons which were built during the same phase, i.e., 2007. Three sampling locations (OUTER, CENTRAL and CLUB) were subsequently selected based on their accessibility and exposure to the open sea (Fig. 1). Locations that were not occupied by boats during the study period were selected (and, at other times, these berths are only used for temporary mooring). Situated at the outermost stretch of berths on the eastern side of the marina, 'OUTER' was more exposed to the open sea than 'CENTRAL' and 'CLUB'. In contrast, CENTRAL and CLUB were located within the central portion of the marina, where CLUB was directly opposite a clubhouse in the main building. At each location, sampling was conducted on the interior of the berth (berth station) and on a straight wall (wall station) that was outside the berth but nearby (within 5–10 m). In total, there were six sampling stations (OUTER-Berth, OUTER-Wall, CENTRAL-Berth, CENTRAL-Wall, CLUB-Berth, CLUB-Wall) within the marina.

Using a random number generator and a nylon measuring tape, the positions of six quadrats were established along a 10-m transect for each station. Sampling was conducted at a depth of 40 cm below the upper edge of the pontoon. 40 × 40 cm PVC quadrats (divided into 25 equal-sized squares) with additional extensions were constructed for attachment to the pontoons. Within each quadrat, the numbers of solitary organisms and surface area of encrusting organisms directly growing on the pontoon walls and were estimated in-situ. Photographs were taken with a Canon IXUS 220 HS camera in an underwater housing for verification of estimations. Organisms that could not be identified in-situ were extracted for subsequent identification in the laboratory.

Monitoring of physicochemical parameters. — Light intensity and temperature were recorded using HOBO Pendant® loggers deployed at each of the six stations. Each logger was attached to an aluminum plate (~ 2.5 × 100 × 0.5 cm) fixed to the side of the pontoon at 90 cm below the water's surface. Light intensity and temperature readings were simultaneously recorded at 30-min intervals for one month. As there was very little or no light before 0700 hours and after 1900 hours, only light intensity readings between 0700 hours and 1900 hours were analysed. As the loggers rapidly became fouled, they were cleaned weekly. To minimise the inaccuracy of data analysis due to encrusting organisms, only light intensity readings recorded one day after each round of cleaning were analysed. Salinity was measured using a RHS-10ATC refractometer at 1400 hours on the same days the loggers were cleaned.

Statistical analyses. — Community parameters in the form of taxon richness, abundance, and diversity among locations and between stations were examined. Abundance was obtained based on the number of solitary organisms while both solitary and encrusting epibiota were taken into account for richness. Two main biotic indices were used to compare epibiotic diversity among the stations. The diversity of countable, solitary epifauna was quantified using the Shannon-Wiener index (H′). A modified index known as Encrusting Diversity (ED) was used to determine the diversity of uncountable, encrusting organisms (Wilson, 1985). A two-way ANOVA was used to test for differences in community parameters among locations and between their respective berth and wall stations. Multi-dimensional scaling (MDS) based on Bray-Curtis dissimilarities in PRIMER (Plymouth Routines in Multivariate Ecological Research) was used to visually assess community differences among locations and stations. Data were square-root transformed prior to all multivariate analyses to allow rarer taxa a greater contribution to the outcome. A PERMANOVA (Permutational Multivariate Analysis of Variance) was used to analyse the variation among stations for significant differences ($p<0.05$). Based on the PERMANOVA results, a SIMPER (Similarity Percentages) routine was executed to identify which taxa contributed at least 10% of the dissimilarities between clusters.

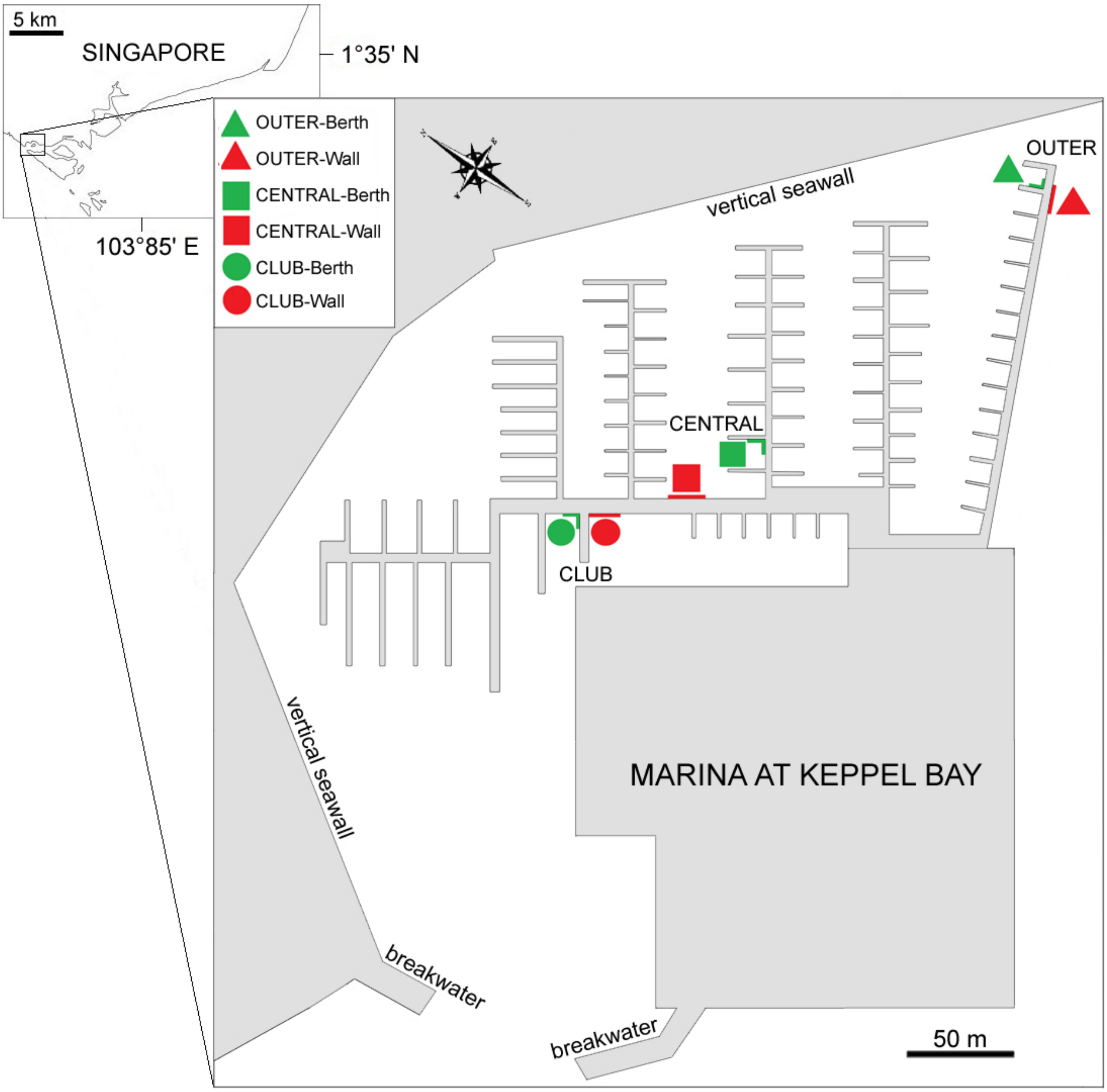

Fig. 1. Map of Marina at Keppel Bay indicating the three study locations (‘OUTER’, ‘CENTRAL’ and ‘CLUB’). At each of the locations, surveys were conducted on the interior (berth station) and exterior of the berth (wall station). Each red or green line represents a 10-m transect.

Variation in physicochemical parameters among the sampling stations was examined using SPSS 14.0. Two-way ANOVA was used to test for differences in temperature, light intensity, and salinity among locations and between stations. Light intensity data was log-transformed to homogenise variances prior to analysis.

RESULTS

Subtidal epibiota. — Forty-nine taxa were identified on the pontoon walls of all six stations (Table 1). Except for a few groups, almost all taxa were identified to genus level based on morphogenera and morphospecies characteristics. Taxon richness of both solitary and encrusting organisms was generally similar between the berth and wall stations of each location (Fig. 2A). However, abundances were markedly different as more solitary organisms, notably bivalves, vermetids, and ascidians were recorded in the wall than in the berth stations (Fig. 2B). From the ED and H′ values, the diversity of encrusting organisms was higher than that of solitary organisms in each station (Fig. 2C, D). Among the three locations, OUTER supported the highest richness, abundance, and diversity of solitary organisms, while the least richness and diversity of encrusting organisms was observed in CLUB. Even though CENTRAL harboured the lowest diversity of solitary organisms, it supported the highest diversity of encrusting organisms.

Table 1: Taxonomic list of subtidal epibiota in Marina at Keppel Bay. An asterisk (*) indicates the presence of the taxon in the survey station.

	OUTER		**CENTRAL**		**CLUB**	
Taxon	**Berth**	**Wall**	**Berth**	**Wall**	**Berth**	**Wall**
Rhodophyceae						
Crustose coralline algae	*	*	*	*	*	*
Amphiroa sp.	*	*	*	*	*	*
Phaeophyceae						
Lobophora sp.	*	*				*
Padina sp.	*	*		*	*	*
Sargassum sp.				*	*	*
Chlorophyceae						
Unidentified filamentous green algae	*	*	*	*	*	*
Bryopsis sp.	*	*	*	*	*	*
Halimeda sp.	*		*	*		*
Porifera						
Haliclona sp.	*	*	*	*	*	*
Iotrochota sp.	*	*	*	*	*	*
Lamellodysidea sp.	*	*				*
Mycale sp.	*	*	*	*	*	*
Hydrozoa						
Unidentified hydroids	*	*	*	*	*	*
Anthozoa						
Acropora sp.		*			*	
Goniopora sp.						*
Montipora sp.	*		*			*
Palythoa sp.	*					
Pectinia sp.	*					
Pocillopora damicornis	*	*	*	*	*	
Porites sp.	*		*			
Sarcophyton sp.	*					
Stereonephthya sp.	*	*	*	*	*	*
Tubastrea sp.	*		*		*	
Zoanthus sp.	*			*		*
Polychaeta						
Sabellastarte indica	*					
Polyplacophora						
Unidentified chiton	*					
Bivalvia						
Arca patriachalis				*		
Brachidontes sp.		*		*	*	*
Dendostrea sp.	*			*	*	*
Isognomon legumen	*	*	*	*	*	*
Leiosolenus sp.	*					
Limaria fragilis	*	*				
Malleus sp.	*				*	*
Modiolus sp.	*	*	*	*	*	*
Perna viridis	*	*	*		*	
Pinctada sp.					*	*
Septifer bilocularis	*	*			*	*
Gastropoda						
Diodora singaporensis	*					
Euplica scripta		*		*		
Siphonaria guamensis	*	*	*		*	*
Stomatia impertusa	*	*		*	*	*
Vermetus sp.	*	*	*	*	*	*
Echinodermata						
Colochirus quadrangularis		*		*	*	*
Ascidiacea						
Botrylloides sp.					*	
Clavelina moluccensis	*	*				
Didemnum sp.	*	*				*
Herdmania pallida	*	*	*	*	*	*
Microcosmus exasperatus	*	*	*	*	*	*
Phallusia philippinensis	*	*	*	*		*

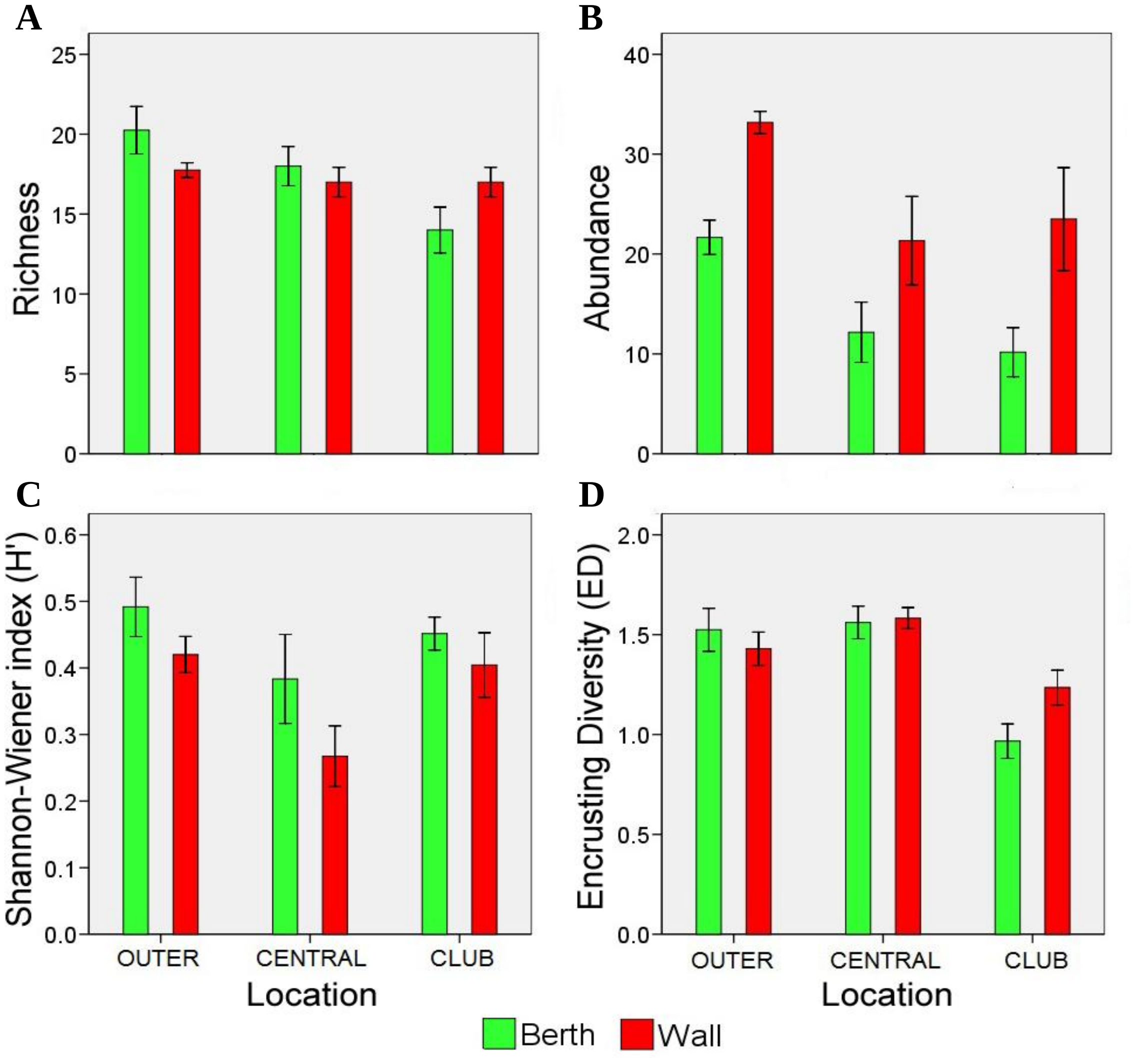

Fig. 2. Mean (± SE): A, taxon richness; B, abundance; C, Shannon-Wiener index (H′) for solitary organisms; D, Encrusting Diversity (ED) for colonial organisms—among locations and between stations.

The two-way ANOVA identified significant differences for all community parameters among locations (Table 2). Post-hoc pairwise comparisons indicated significantly higher richness of both solitary and colonial organisms in OUTER than in CLUB. OUTER also harboured a significantly greater abundance of solitary organisms than in CENTRAL and CLUB. There was a significantly higher diversity of solitary organisms in OUTER than in CENTRAL. However, the diversity of colonial organisms was significantly higher in CENTRAL compared to OUTER and CLUB.

Table 2. Two-way ANOVA comparing mean values of community parameters among locations (OUTER, CENTRAL, CLUB), between stations (berth station and wall station) and their interaction. **Bold** values indicate significant differences.

Factor	Variable	dF	F	Sig.
Location	Richness	2	4.820	**0.015**
	Abundance	2	6.880	**0.003**
	Shannon-Wiener index (H′)	2	4.620	**0.018**
	Encrusting Diversity (ED)	2	17.400	**< 0.001**
Station	Richness	1	0.033	0.858
	Abundance	1	17.600	**< 0.001**
	Shannon-Wiener index (H′)	1	4.510	**0.042**
	Encrusting Diversity (ED)	1	0.892	0.353
Location×Station	Richness	2	3.160	0.057
	Abundance	2	0.199	0.820
	Shannon-Wiener index (H′)	2	0.300	0.743
	Encrusting Diversity (ED)	2	2.400	0.108

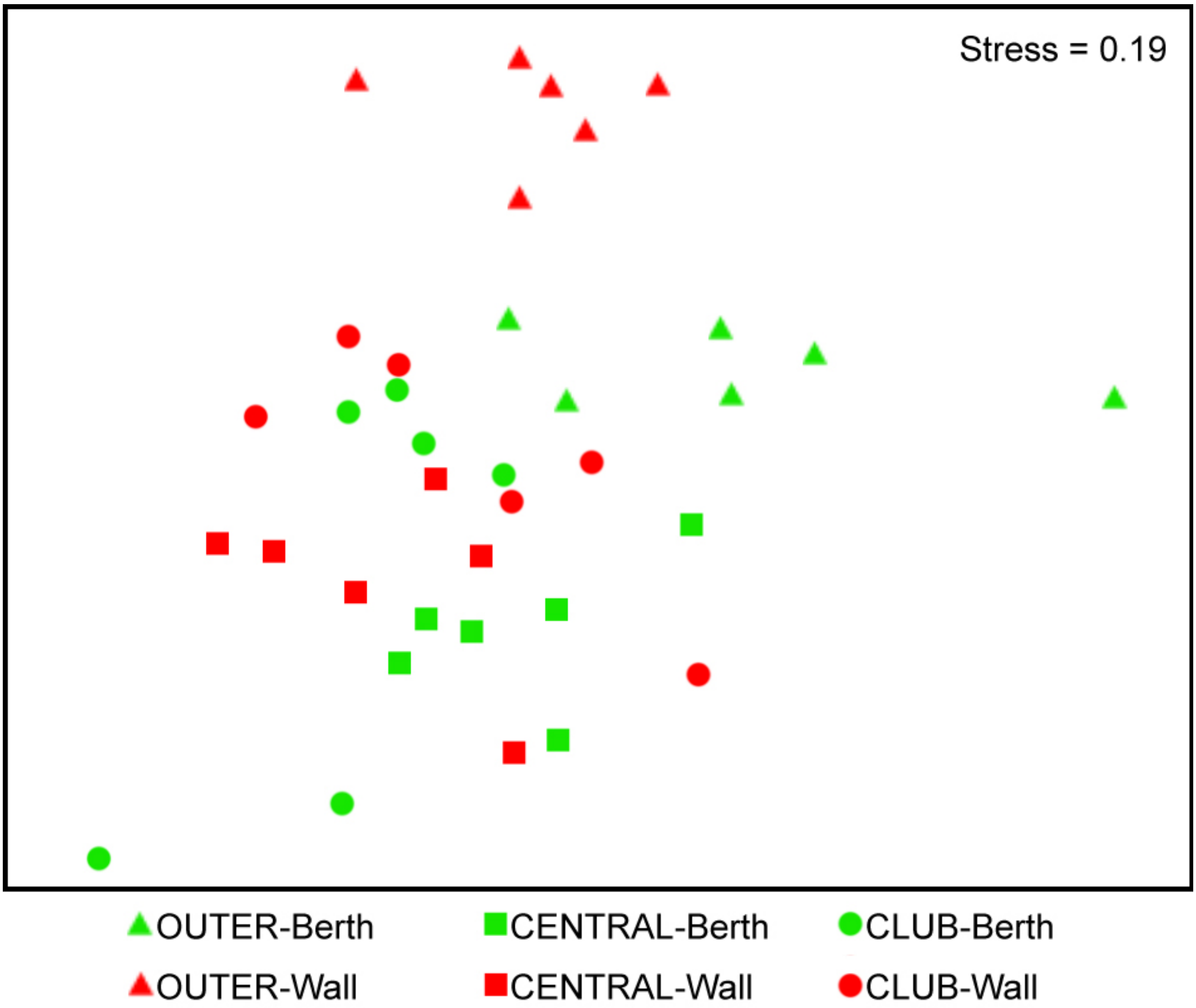

Fig. 3. MDS plot of epibiotic communities based on location and station. Each point represents one quadrat.

The MDS plot (Fig. 3) indicated differences in subtidal communities comprising solitary and colonial epibiota among locations and between stations. Points representing OUTER were well separated from the points representing CENTRAL and CLUB while there was a less distinct separation between CENTRAL and CLUB. Highly disparate clusters of points were observed between OUTER-Berth and OUTER-Wall. The separation between CENTRAL-Berth and CENTRAL-Wall was less distinct while there was no clear separation between CLUB-Berth and CLUB-Wall.

PERMANOVA showed that there were significant differences for location and the interaction term 'Location×Station' (Table 3). No significant differences were found between stations. These results suggest that location had a stronger influence on epibiotic communities than station. A significant difference in the interaction term indicates that patterns of differences between stations were dependent on the location. For post-hoc tests of the interaction, all pairwise comparisons were significantly different except for between CLUB-Berth and CLUB-Wall. Post-hoc tests for location revealed significant differences for all pairwise combinations.

SIMPER analysis revealed that *Stereonephthya* sp., *Halimeda* sp., and *Padina* sp. were characteristic taxa which contributed at least 10% to the average dissimilarity for all locations. Pairwise comparisons between locations showed

Table 3. PERMANOVA based on Bray-Curtis dissimilarities of subtidal epibiotic communities in response to location, station and their interaction. Data were square-root transformed prior to analysis. **Bold** values indicate significant differences.

Factor	dF	Mean Squares	F	Sig.
Location	2	4294	8.452	**0.001**
Station	1	2042	1.311	0.289
Location×Station	2	1557	3.065	**0.002**

that significant differences were present for certain taxa (Table 4). There were no significant differences for any characteristic taxa between OUTER and CLUB. OUTER hosted the smallest cover of *Stereonephthya* sp., *Halimeda* sp. and *Padina* sp. while CENTRAL supported the largest cover of these taxa (Fig. 4).

Physicochemical parameters. — No statistically significant differences were observed for mean salinity, light intensity, and temperature among locations and between berth and wall stations (Table 5). There was minimal variability in salinity and temperature (Fig. 5) among locations, however, OUTER and CENTRAL received the lowest and highest light intensity respectively. OUTER-Wall and CLUB-Wall received relatively lower light intensity than the other stations. Variation in light intensity at these two stations was also lower than at the other stations (Fig. 5C).

Table 4. SIMPER analysis showing taxa that contributed at least 10% to average dissimilarity in epibiotic communities between different locations. Average dissimilarity scores denote average Bray-Curtis dissimilarity values between pairwise comparisons. **Bold** values indicate significant differences. Ste=*Stereonephthya* sp., Ha=*Halimeda* sp., Pa=*Padina* sp.

Location		**CENTRAL**			**CLUB**		
OUTER	Taxon	Ste	Ha	Pa	Ste	Ha	Pa
	Average dissimilarity	5.834	4.066	4.381	5.912	4.186	4.012
	Sig.	**0.042**	**0.001**	**< 0.001**	0.083	0.975	0.558
CENTRAL	Taxon				Ste	Ha	Pa
	Average dissimilarity				7.714	4.186	4.012
	Sig.				0.973	**0.002**	**< 0.001**

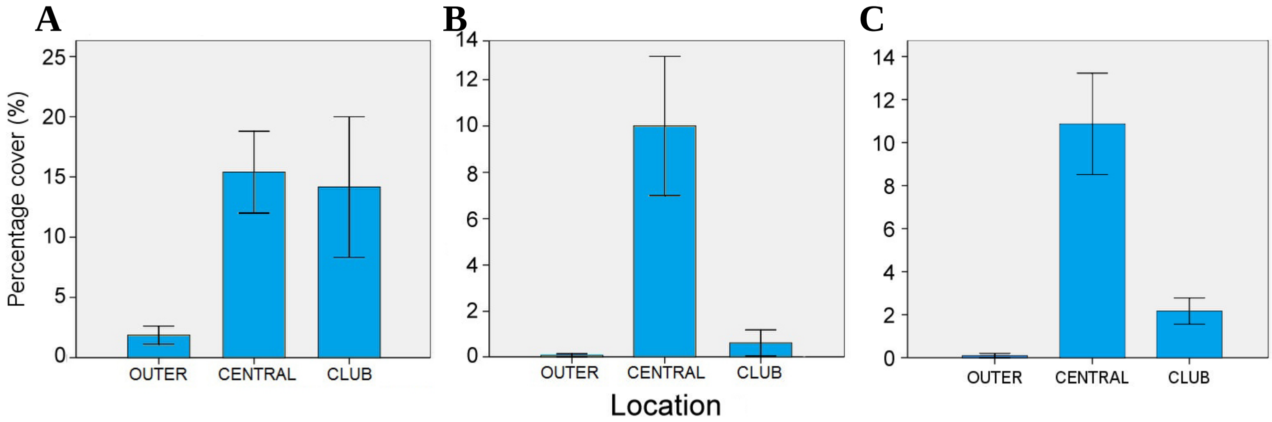

Fig. 4. Mean (± SE) percentage cover of: A, *Stereonephthya* sp.; B, *Halimeda* sp.;C, *Padina* sp., that contributed at least 10% to average dissimilarity in epibiotic communities based on Bray-Curtis dissimilarities among locations.

Table 5. Two-way ANOVA comparing the mean values of physicochemical parameters among locations (OUTER, CENTRAL, CLUB) and between stations (berth station and wall station). Data for light intensity were log-transformed to homogenise variances.

Factor	**Variable**	**dF**	**Mean Squares**	**F**	**Sig.**
Location	Salinity (‰)	2	1.233	1.762	0.193
	Temperature (^{o}C)	2	0.585	0.917	0.413
	Light intensity (lum ft$^{2-1}$)	2	0.238	2.666	0.090
Station	Salinity (‰)	1	0.033	0.048	0.829
	Temperature (^{o}C)	1	0.367	0.574	0.456
	Light intensity (lum ft$^{2-1}$)	1	0.229	2.565	0.122
Location×Station	Salinity (‰)	2	1.033	1.476	0.249
	Temperature (^{o}C)	2	0.077	0.121	0.887
	Light intensity (lum ft$^{2-1}$)	2	0.177	1.982	0.160

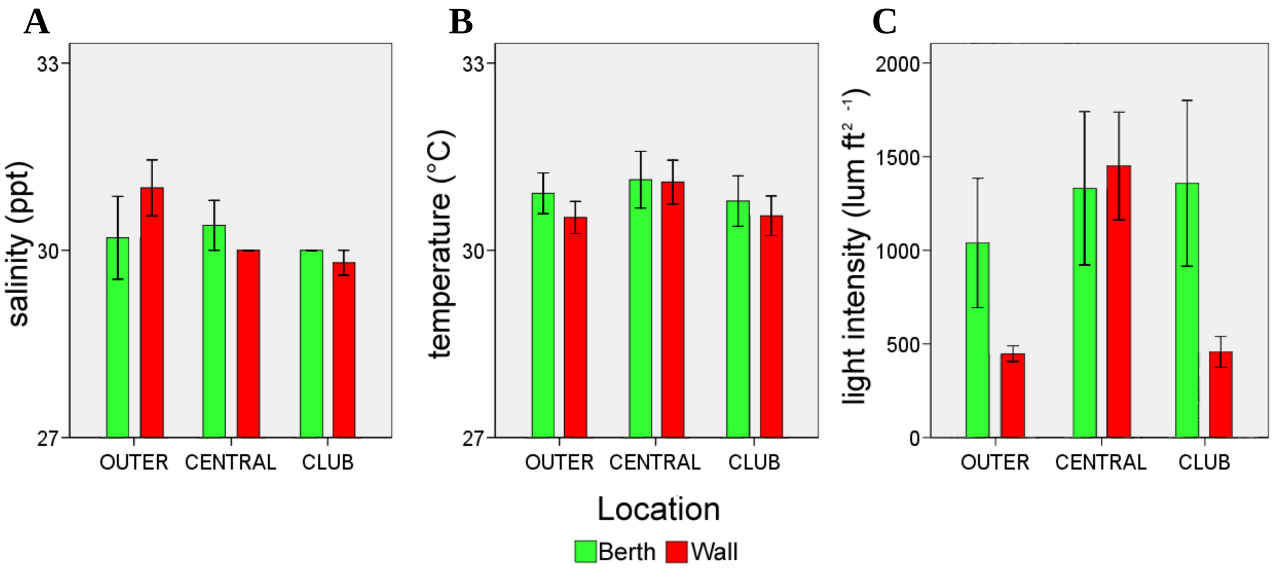

Fig. 5. Mean (± SE) of: A, salinity; B, temperature; and C, light intensity—among locations and between stations.

DISCUSSION

Urban marine structures such as seawalls and pontoons provide substrata that facilitate the growth of benthic communities (Relini et al., 2007). Marina at Keppel Bay is one of the few marinas in Singapore that adopts practices to minimise environmental impacts, and its design allows water flow throughout the entire marina. No quantitative surveys of subtidal epibiotic communities on artificial structures in the marina had been conducted prior to the present study. Our results indicate that the unique pontoon environment supported at least 49 taxa and that there existed variability in community composition among locations within the marina. However, differences between stations were less clear.

Based on the taxonomic list of subtidal epibiota recorded in all six stations, the assemblages of organisms growing on the pontoon walls were similar to those of a subtidal coral reef as opposed to other marine communities such as local rocky shores. Most of the organisms on the pontoon walls were permanently submerged underwater, with the exception of some mobile gastropods. Common genera of various marine fauna, such as corals (e.g., *Montipora* and *Stereonephthya*) and sponges (e.g., *Mycale* and *Haliclona*) found in the survey stations are also frequently encountered on the reefs of the Southern Islands of Singapore (Goh et al., 2008; Huang et al., 2009; Lim et al., 2012). The establishment of a community similar to that of a natural reef could be due to the settlement of various invertebrate larvae originating from the reefs of local offshore islands and the southwestern coast of the main island of Singapore (Chou & Tun, 2005). Thus, pontoon walls are able to provide suitable substrata for the recruitment and growth of assemblages similar to those found on coral reefs. In contrast, rocky shore communities are subjected to various environmental fluctuations associated with periodic emersion to the atmosphere (Thompson et al., 2002). Such communities also cannot thrive fully submerged due to subtidal predation and this probably restricts their development on the pontoon walls at Marina at Keppel Bay (Castilla & Paine, 1987).

From preliminary subtidal epibiota analyses, community parameters in the form of richness, abundance, and diversity were found to be different across the six sampling stations. Further multivariate analyses showed that the subtidal epibiotic communities were significantly different among locations but not between (Berth and Wall) stations. Three main taxa, i.e., *Stereonephthya* sp., *Halimeda* sp., and *Padina* sp. each contributed at least 10% to the overall differences in community structure among locations.

The percentage cover of *Padina* sp. and *Halimeda* sp. was significantly greater at CENTRAL compared to the other locations. Algae are sensitive to variations in shade (Meadows & Campbell, 1972; Buss, 1979) and are negatively affected by low light intensities due to reduced rates of photosynthesis (Levring, 1966; Kennelly, 1989). In Fig. 5C, it appears that, overall, CENTRAL received the greatest (and most variable) light intensity among the locations and this may partly explain the extensive cover of *Padina* sp. and *Halimeda* sp. However, light intensity at OUTER-Berth and CLUB-Berth was also relatively high and hence should not have limited *Padina* sp. and *Halimeda* sp., yet these species were very poorly represented. Hence, we suggest that some other (unrecorded) variable is influencing the distribution of *Padina* sp. and *Halimeda* sp. in the marina.

Even though the light intensity in OUTER-Wall and CLUB-Wall was (non-significantly) lower than that of the other four stations; taxon richness, abundance, and diversity were similar. For instance, richness in OUTER-Wall and CLUB-Wall was similar to that of CENTRAL (Wall and Berth). It is possible that hydrodynamics could account for some of the observed variability in subtidal epibiotic community structure. The construction of the marina allows water to flow throughout the entire area, but the flow around the three locations may still have been very different. Hydrodynamic conditions greatly influence the settlement and/or growth of marine organisms and can drive differences in assemblages (Eckman, 1983; Abelson & Denny, 1997). This could explain the higher abundances of solitary organisms on the wall station compared to the berth station at each location, as the berth stations were more enclosed and hence water circulation was probably restricted—potentially leading to reduced larval import and lower suspended food particle availability.

As OUTER was situated at the outermost stretch of berths on the eastern side of the marina, it was more exposed to the sea and periodic wave action (both natural waves and boat wakes). In contrast, CENTRAL and CLUB were situated in the middle of the marina facing a seawall, and were therefore sheltered from wave action. High wave action and associated drag forces can be damaging to arborescent soft corals owing to their lack of a solid, supporting skeleton (Fabricus & Klumpp, 1995). This may account for the relatively low percentage cover of *Stereonephthya* sp. at OUTER.

Our results indicate that differences in community structure were more evident among locations than between stations. These differences were probably influenced by variations in light intensity and hydrodynamic factors with other physical parameters and environmental conditions potentially contributing. The estimation of colonial and solitary organisms in this study did not take into account cryptic organisms such as polychaetes and brittle stars that often reside in other epifauna. Future studies should incorporate destructive samples to ensure that such cryptic species are accounted for (and biomass quantifications could be conducted at the same time). Sampling in more locations over a longer period of time would be beneficial as various organisms, such as some species of sponges and macroalgae, are only abundant at certain times of the year (Osman, 1977; Sutherland & Karlson, 1977). Future tests on factors structuring subtidal epibiotic communities will not only contribute to greater ecological understanding of epibiota and their growth on artificial structures, but also provide a deeper insight into how modified coastal environments can be managed to retain their biodiversity.

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