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Profiles of bacterial assemblages from microplastics of tropical coastal environments

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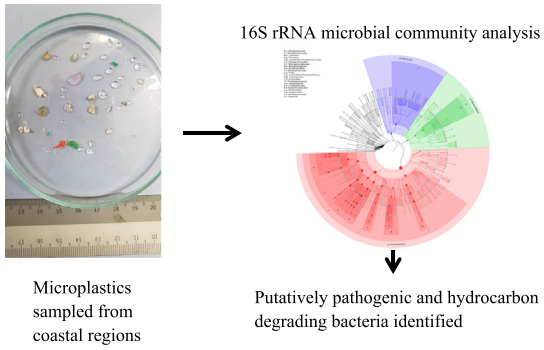
HIGHLIGHTS

- Microplastics are prevalent pollutants in tropical coastal ecosystems.
- Microplastic abundance influenced by anthropogenic activities
- Rich assemblage of microbial communities found on microplastic surfaces
- Putatively pathogenic and hydrocarbon degrading bacteria identified
- Microplastics act as a vector for the transport of harmful bacteria.

GRAPHICAL ABSTRACT



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ABSTRACT

Plastic waste is a global issue of an increasing concern in aquatic ecosystems. Microplastics form a large proportion of plastic pollution in marine environments. Although microplastics are prevalent, their distribution along the coasts of tropical regions is not well studied. Microplastic pieces (1–5 mm) were collected from two distinct regions along the coastlines of Singapore, from the northern coast in the Johor Strait and the southern coast in the Singapore Strait. Microplastics were present in concentrations ranging from 9.20–59.9 particles per kg of dry sand sediment. The majority of microplastics identified were foam particles (55%) and fragments (35%). Microplastics were significantly more abundant on heavily populated beaches compared to pristine beaches. High throughput sequencing was used to profile the communities of bacteria on the surfaces of microplastic particles. The structure of the microbial communities was primarily characterised by Proteobacteria and Bacteroidetes and were distinct across sites. Hydrocarbon-degrading genera such as *Erythrobacter* were dominant in areas with heavy shipping and pollution. Potential pathogenic genera such as *Vibrio* and *Pseudomonas* were also identified. This study highlights the diverse bacterial assemblages present on marine microplastic surfaces and the importance of understanding the bacterial plastisphere.

1. Introduction

An estimated 10% of the global annual production of plastics ends up in marine environments (Thompson, 2006). Since 2015, approximately 6300 million metric tons of plastic has been produced (Geyer et al., 2017). Microplastics are small plastic particles that end up in aquatic

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ecosystems. They are present in both freshwater (Wagner et al., 2014) and marine environments (Cole et al., 2011), in polluted as well as pristine waters (Browne et al., 2011; Lusher et al., 2015). Microplastics are durable, buoyant and strong (Subramanian, 2000). As a result, these particles are resistant to degradation and are able to exist in the marine environment for decades. Microplastics have been found on surface waters, in sediments and on beaches. Microplastics exist in the environment as primary and secondary microplastic particles. Primary microplastics exist as resin pellets from the manufacture of larger plastics and also in facial cleansers as microbeads (Zhang et al., 2015a, 2015b; Napper et al., 2015). Primary microplastics also include clothing fibres from washing machines. These fibres together with microbeads are able to escape the sewage filtration systems and are washed out into the ocean (Carr et al., 2016). Secondary microplastics are formed from the breakdown of larger plastic articles resulting from mechanical wear and tear, and ultra-violet (UV) degradation (Rillig, 2012).

The small size of microplastics results in marine organisms often mistaking these microplastics for food. The ingestion of microplastics has been observed in a wide range of biota, from microscopic organisms such as zooplankton (Desforges et al., 2015), small marine organisms such as barnacles, lugworms and mussels (Van Cauwenberghe et al., 2015), to large marine organisms such as pelagic fish (Romeo et al., 2015). Uptake of microplastic particles resulted in the increased bioaccumulation of persistent organic pollutants in lugworms (Besseling et al., 2012), tissue and cellular damage in blue mussels (Von Moos et al., 2012) and endocrine disruption in the medaka fish (Rochman et al., 2014). Such evidence indicates that microplastics threaten marine life and is a problem that should not be ignored. Understanding the distribution and abundance of microplastics is important for the management of microplastics on the national and global scale. The presence of microplastics has been reported continents worldwide, such as Africa (Heskett et al., 2012; Ryan et al., 2012), America (Costa et al., 2010; Rios et al., 2007; Heskett et al., 2011), Asia (Zurcher, 2009; Endo et al., 2005; Ismail et al., 2009), Australia (Gregory, 1977) and Europe (Turner and Holmes, 2011; Ashton et al., 2010; Holmes et al., 2012). In Asia, microplastic contamination in marine environments is heavily investigated in countries such as China (Li et al., 2015; Qiu et al., 2015; Su et al., 2016; Jabeen et al., 2017) and South Korea (Chae et al., 2015; Kang et al., 2015; Song et al., 2015; Kim et al., 2015), where microplastics have been examined in sediments, seawater and in marine organisms. The presence of microplastics from the coastlines of Singapore has been acknowledged in two reports to date (Ng and Obbard, 2006; Nor and Obbard, 2014). The updated distribution and abundance of microplastics in Singapore's marine environment is currently unknown.

Microplastics are able to exist in the marine ecosystem for several hundred years (Thompson et al., 2009). Compared to microplastics on land, microplastics in aquatic ecosystems take a much longer period of time to degrade due to the presence of salt and decreased temperatures (Barnes et al., 2009). As a result, they present a habitable environment for marine biota to colonise. The surfaces of microplastics from various oceans around the world have been investigated for attached marine organisms. Bacteria from the phyla Bacteroidetes and Proteobacteria (Oberbeckmann et al., 2014), diatoms such as *Cylindrotheca closterium* and *Striatella* sp. (Briand et al., 2012; Carpenter and Smith, 1972; Carson et al., 2013; Eich et al., 2015), dinoflagellates from the genera *Alexandrium*, *Coolia* and *Ostreopsis* (Masó et al., 2003) and cyanobacteria assemblages were found on microplastics collected from marine environments (Oberbeckmann et al., 2014).

By 2025, the cumulative amount of plastic pollution in marine environments is predicted to increase by an order of magnitude, rising to levels as high as 250 million metric tons (Jambeck et al., 2015). Given this expected increase in microplastic pollution over the next few decades, it is then crucial to understand the microbial communities that are present on the surfaces of these microplastics. The aim of this study was to profile the bacterial communities on microplastics collected from the coastal regions of Singapore and to identify the key bacterial groups present. We also aim to analyse spatial trends that are present in beach microplastics across pristine and populated locations.

2. Materials and methods

2.1. Sampling and analysis of microplastics

Microplastic samples were collected at three different beaches along the coastline of Singapore between April and July 2018. To investigate the relationship between microplastic abundance and human activities, three types of beaches were selected: pristine, moderately populated and heavily populated (Table 1). The pristine beach was located on Lazarus Island, a southern island of Singapore facing the Singapore Strait. The moderately populated beach was located on a seaside park, north of Singapore facing the West Johor Strait. The heavily populated beach was located beside a jetty of a sailing club, facing the East Johor Strait. Microplastic samples were obtained from sand sediments in 60 m transect lines from two beach zones. The high-strand line (HSL), which is located at the zone of vegetation and the low-strand line (LSL), which is located at the water-edge zone, are parallel to the shoreline and were chosen for sampling purposes (Fig. 1). Each transect line was split into three sections at 15 m intervals. 500 cm^3 of sand was collected from the top most 5 cm of sand sediment and poured into a bucket of seawater for density separation purposes. The seawater was sieved to ensure that no microplastic particles of sizes 1–5 mm were present before sand was added. Floating pieces on the surface of the seawater was filtered through a metal sieve of 1 mm mesh size. Particles were collected from the top of the metal sieve using a stainless steel spoon and collected in zip lock bags. Microplastics were sorted using forceps by eye and classified into five different categories: fragments, fibres, foam, pellets and film.

2.2. Preparation of samples

All seawater and freshwater was filter-sterilised through a sterile 0.22 μm filter and microscopically checked under 40× magnification to ensure that no organisms were present before use. All microplastic particles were thoroughly washed with Milli-Q water (Merck Millipore) to remove any attached debris and transferred to sterile 96-well plates using sterilised forceps. Seawater that was collected from the various sampling points was filtered with a sterile 0.22 μm syringe filter and added to the microplastics with the well plates. Microplastic particles were incubated in room temperature for one week under a 12:12 h light: dark cycle. After incubation, the filtered seawater surrounding the microplastic particles was used to wash the microplastic particles and resuspended for 5 min in the wells before transferring to sterile Eppendorf tubes. The filtered seawater was centrifuged at 10,000*g* to obtain a pellet for DNA extraction and sent to Novogene AIT Genomics, Singapore for high-throughput amplicon sequencing. The V3-V4 (515F-806R) hypervariable region of the 16S rRNA gene (Claesson et al., 2010) was chosen to resolve the identity of attached bacteria.

2.3. Sequencing analysis

Paired-end reads were merged using FLASH v1.2.7 (Magoč and Salzberg, 2011) and filtered for quality control using QIIME v1.7 (Caporaso et al., 2010). Tags were compared against the Gold reference

Table 1
Location of microplastic sampling sites.

Name of site	Type of beach	Latitude (N)	Longitude (E)
Lazarus island (LI1)	Pristine	1° 13′ 28.1″	103° 51′ 07.4″
Sembawang beach (S1b)	Moderately populated	1° 27′ 49.7″	103° 50′ 14.8″
Changi beach (S7b)	Heavily populated	1° 23′ 32.7″	103° 58′ 44.1″

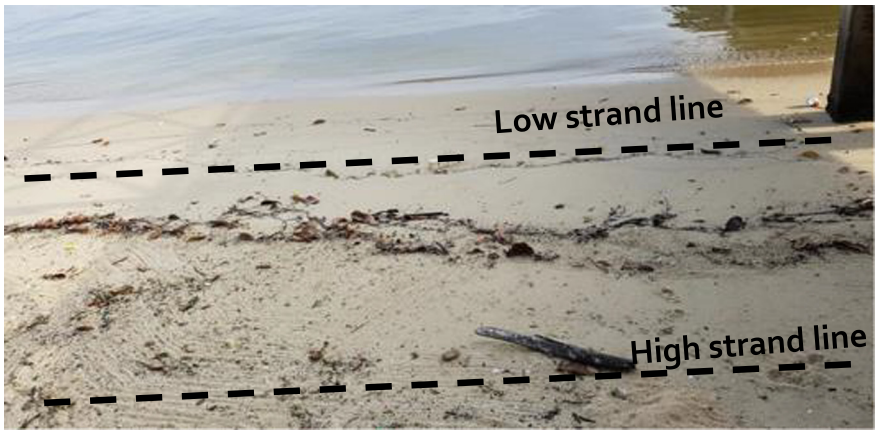

Fig. 1. Sampling site S7b. The high strand and low strand lines are indicated in the picture.

database using UCHIME to detect chimera sequences (Edgar et al., 2011). Chimera sequences were filtered and removed to obtain effective tags. UPARSE (Edgar, 2013) was used to assign sequences with effective tags to the same Operational Taxonomic Units (OTU) at 97% similarity. Representative sequences were annotated using MOTHUR (Schloss et al., 2009) against the small ribosomal subunit rRNA SILVA database (Quast et al., 2012) using a threshold of 0.8–1. MUSCLE was used to compare the phylogenetic relationships between representative sequences (Edgar, 2004).

2.4. Statistical analysis

OTUs were normalised for abundance for the calculation of diversity indices. All indices were calculated using QIIME v1.7 and visualised using R software v 2.15.3. Statistical analyses from this study were computed using the software program R. One-way analysis of variance (ANOVA) (Hinton, 2014) and Tukey's HSD test (Jaccard et al., 1984) was used to test for significant differences between the abundance of microplastics between sites. The mean abundances of microplastics collected from the HSL and LSL from each sampling site were compared using the Wilcoxon signed rank test (Rosner et al., 2006). Principal component analysis (PCA) was used to identify the relationship between the types of microplastic particles collected (Jolliffe, 2011) and permutational multivariate analysis of variance (PERMANOVA) was used to partition the Euclidean distance between the sites. All statistical analyses were performed using the R package Vegan version 2.5-2 (Oksanen et al., 2013).

3. Results

3.1. Microplastic abundance across sampling sites

Microplastics were found at all three sampling stations along the coast of Singapore. Fragments, fibres, foam, pellets and film were observed. A total of 275 microplastic pieces were collected, with 144 particles from S7b, 89 particles from S1b and 42 particles from LI1. The particle density was 59.9 particles/kg, 31.1 particles/kg and 9.16 particles/kg for sites S7b, S1b and LI1, respectively. The total abundance of microplastics was significantly different at the three sites ($p < 0.05$; One-way ANOVA). From S7b, 60 particles were found from the HSL and 84 particles were found from the LSL. From S1b, 29 particles were found from the HSL and 60 particles were found from the LSL. From LI1, 34 particles were found from the HSL and 8 particles were found from the LSL. No significant differences were observed when comparing the abundance of microplastics from the HSLs and LSLs of the three sites. The most abundant type of microplastic found at both S7b and S1b were foam pieces. Fragments were the most abundant type of microplastic found at LI1 (Table 2). Sampling site and abundance of microplastic type accounted for 98.56% of the total variance observed among the five types of microplastic particles observed from the PCA plot (Fig. 2). Microplastic pellets, fibres and film were grouped together, and there was a significant difference between the types of microplastics collected from the three sites ($p < 0.05$; PERMANOVA).

3.2. Analysis of bacterial communities

Bacterial communities colonizing the surfaces of microplastics were diverse. After filtering for quality and the removal of chimeras, an average of 443 OTUs were found, with 472, 430 and 427 OTUs identified from the stations S7b, S1b and LI1, respectively. There were 158 OTUs that were shared between the three sites. 91, 147 and 111 OTUs were unique to sites S7b, S1b and LI1, respectively (Fig. 3). Good's coverage was 99.9%, 99.9% and 100% for stations S7b, S1b and LI1, respectively. Stationary phases on rarefaction curves (data not shown) indicated that there was sufficient sequencing depth to account for most of the taxa present on the surfaces of microplastic particles. There were 426, 411 and 406 calculated observed taxa for stations S7b, S1b and LI1, respectively (Table 3). The Shannon-Weiner diversity index was 5.1, 5.93 and 6.85, species richness estimators Chao1 was 474, 417 and

Table 2
Average abundance of microplastic particles (per 500 cm^3) from high strand (HSL) and low strand lines (LSL) of all sampling sites. The total number of microplastic particles collected from each site is denoted by "n".

	S7b (populated) n = 144		S1b (moderate) n = 89		LI1 (pristine) n = 42	
	HSL	LSL	HSL	LSL	HSL	LSL
Fragments	7.00 ± 6.25	12.0 ± 11.5	5.00 ± 3.61	3.33 ± 1.53	3.67 ± 1.53	1.33 ± 0.58
Fibres	1.00 ± 1.73	1.00 ± 1.73	0	0.33 ± 0.58	1 ± 1.00	0
Foam	11.3 ± 3.51	14.7 ± 8.15	4.00 ± 2.00	15.7 ± 7.23	3.67 ± 1.15	0.67 ± 1.15
Pellets	0.33 ± 0.58	0.33 ± 0.58	0.67 ± 0.58	0.33 ± 0.58	3.00 ± 3.00	0.33 ± 0.58
Film	0.33 ± 0.58	0	0	0.33 ± 0.58	0	0.33 ± 0.58
Total	60	84	29	60	34	8

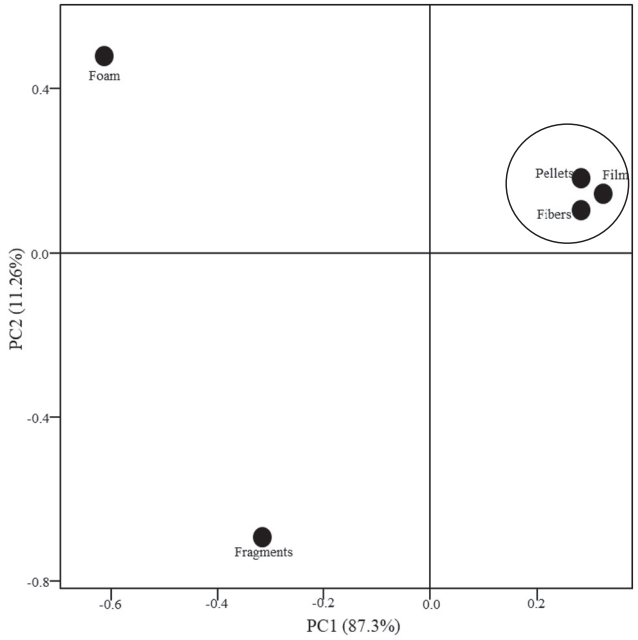

Fig. 2. Principal component analysis (PCA) plot demonstrating the relationship between foam, fragments, pellets, fibres and other types of microplastic particles observed from three sampling sites along the coast of Singapore.

433, and ACE was 487, 420 and 437 for the stations S7b, S1b and LI1, respectively (Table 3).

The structure of bacterial communities across the three sites was very different according to the PCoA analysis (figure not shown). At the phylum level, the structure of the bacterial communities differed distinctly (Fig. 4). Proteobacteria, Bacteroidetes and Firmicutes dominated microplastic surfaces across the three sites. Erythrobacteraceae (19%), Rhodospirillaceae (22%) and Rhodobacteraceae (21%) were the dominant families in S7b, S1b and LI1, respectively. *Erythrobacter* (21%), *Cohaesibacter* (12%) and *Hyphomonas* (10%) were the three

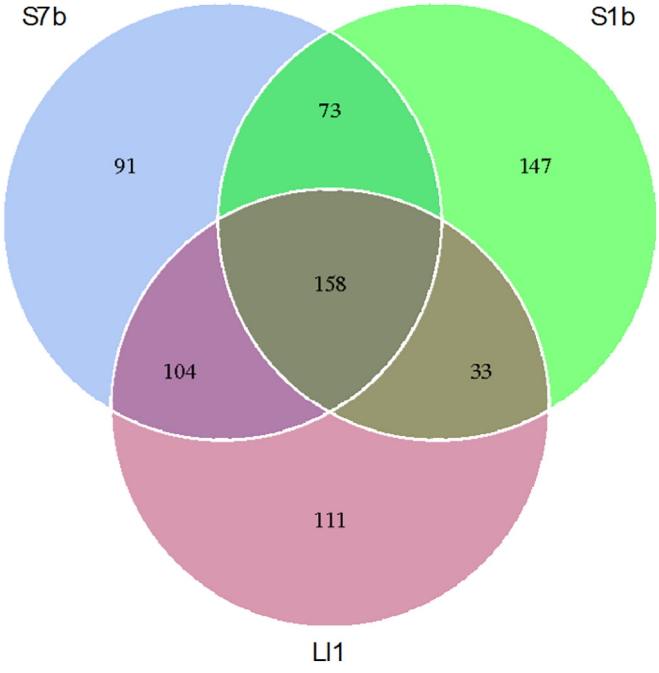

Fig. 3. Shared and unique operational taxonomic units (OTUs) across sampling sites S7b, S1b and LI1.

Table 3
Number of observed taxa, diversity index (Shannon-Weiner) and species richness (Chao1, Abundance based coverage estimator - ACE) estimators across locations.

Site	Number of observed taxa	Shannon-Weiner	Chao1	ACE
S7b	426	5.01	474	487
S1b	411	5.93	417	420
LI1	406	6.85	433	437

most abundant genera from site S7b. From S1b, *Arcobacter* (6%), *Albimonas* (5%) and *Bacteroides* (4%) were the three most abundant genera. *Brachymonas* (5%), *Pseudomonas* (5%) and *Sphingobium* (4%) were the three most abundant genera from site LI1. The genus *Clostridium* consisted of 1% of the total sequences at site LI1. In addition to site LI1, the genus *Pseudomonas* was also found at S7b and S1b at 0.8% and 0.9% of the total sequences, respectively. The dominant 35 genera among all samples were displayed in a species abundance heatmap (Fig. 5). From the genus *Pseudomonas*, five species were identified: *Pseudomonas alcaligenes*, *Pseudomonas azotoformans*, *Pseudomonas hussainii*, *Pseudomonas pachastrellae*, and *Pseudomonas veronii*. The genus *Vibrio* was also detected on microplastic particles, with *Vibrio fluvialis* present in <0.2% at all sites.

4. Discussion

4.1. Microplastics along different coastlines

Microplastics are known to be harmful pollutants having significant impacts on the marine environment. However, their distribution, characterisation and the attached organisms along tropical coastlines are not well understood. This is the first report on the presence of microbial community on microplastics in Southeast Asia in particularly in Singapore. From this study, foam pieces were the most abundant type of microplastic found from sites S7b and S1b, which were located on the northern coast of Singapore. The northern coast of Singapore faces the Johor Strait, which is an international strait separating Singapore and Peninsular Malaysia. The abundance of foam pieces were the greatest as many fish farms from the aquaculture industry along the Johor Strait use expanded polystyrene (EPS) floats. Sampling site LI1 faces the Singapore Strait, where there are also fish farms, although much fewer when compared to the Johor Strait. The increased occurrence of microplastic foam debris near aquaculture farms is not a surprise, as a high concentration of EPS microplastics has been observed near mussel farms in Brazil (Castro et al., 2016) and oyster farms in South Korea (Song et al., 2015).

The distribution of microplastics has been observed to vary according to environmental and anthropogenic factors. For instance, wind direction and tidal currents are said to be driving forces behind the spatial distribution of microplastics (Kim et al., 2015). Browne et al. (2010) postulated that there would be a greater accumulation of microplastics at downwind sites that experience onshore wind compared to sites that experience upwind. Upwelling of deep water has been linked to a lower abundance of microplastics, due to the dilution of surface water with deep water that had fewer microplastics (de Lucia et al., 2014; Desforges et al., 2014). In this study, the accumulation of microplastics appeared to be influenced by oceanographic conditions from the coastlines of Singapore. The Johor Strait is separated into the East Johor Strait (EJS) and West Johor Strait (WJS) by the causeway link bridge that connects between Singapore and Johor, Malaysia. As a result, the flow of water in the Johor Strait is obstructed, resulting in the accumulation of debris, especially during spring tides. In general, high abundance of microplastics was found in beach sediments (i.e. sites S7b and S1b). Conversely, a lower total abundance of microplastics on site LI1 was observed due to the unobstructed flow of water in the Singapore Strait. The accumulation of microplastic particles along the coastal shoreline is determined by the wind-derived surface current

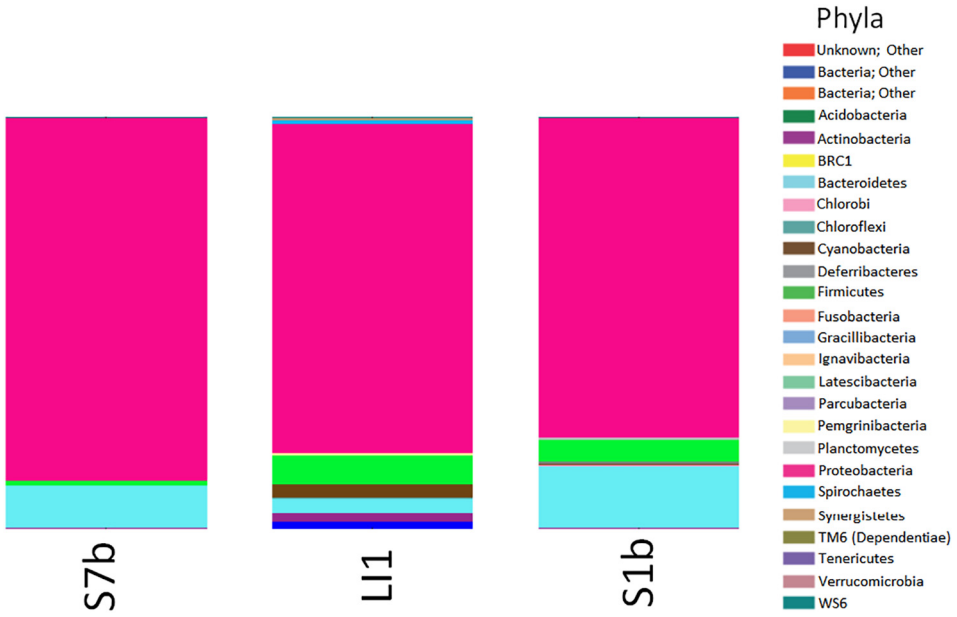

Fig. 4. Structure of bacterial community phyla across sampling sites S7b, S1b and LI1. Each colour corresponds to a single phylum depicted in the legend. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

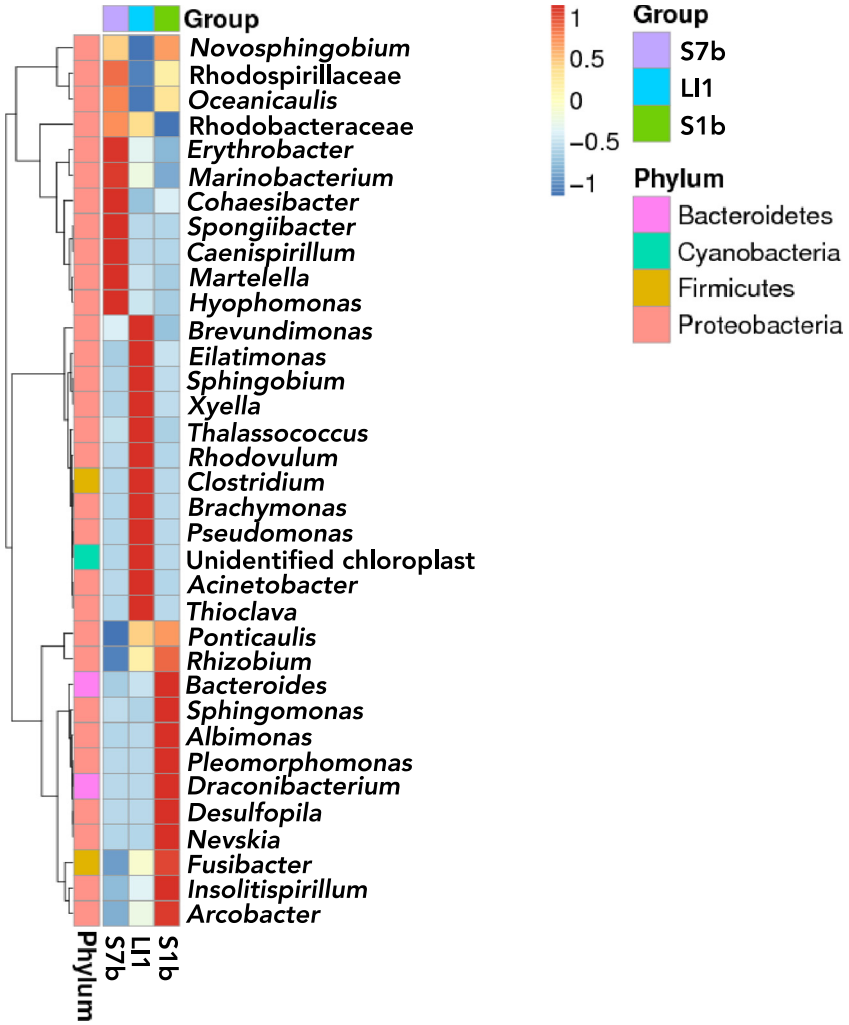

Fig. 5. Relative abundance species heatmap of the dominant 35 genera among samples. The values represent the distances between the raw mean of the standard deviation.

and tidal current. For instance, microplastics in estuaries were observed to readily move with the flow of water and were found to be deposited in areas with slow water flow (Dalrymple et al., 1992). In a port next to the Three Gorges Dam in China, microplastics were observed to accumulate due to the reduced water flow (Zhang et al., 2015a, 2015b). Large volumes of freshwater fluxes that create strong outward water flows were observed to result in the short retention time of surface waters and a moderate accumulation of microplastics in the North-eastern Pacific Ocean (Desforges et al., 2014).

This study showed that human activities are likely the essential factor contributing to the variability of the composition of microplastics. For instance, pristine beaches are characterised by limited or low human activities and are remote or present in protected areas. Moderately populated beaches are sites that are located on the outskirts of the country or in small villages. Heavily populated beaches are beaches that have extensive anthropogenic activities, such as jetties or harbours. The abundance of microplastics has been linked to the level of activity on land and sea (Anderson et al., 2016). There were a greater number of microplastics collected on beaches with a greater level of anthropogenic activity. S7b was located at the jetty of a sailing club, which was heavily used for recreational purposes. S1b was located at the edge of a nature park and was also a small fishing spot with moderate human traffic. Compared to site S1b, the level of anthropogenic activity at S7b was much greater, resulting in the larger number of microplastics collected. Sampling site LI1 was located on a southern island of Singapore, with little human activity. The low level of human activities surrounding site LI1 resulted in lesser microplastics when compared to other sites. A positive correlation between the concentration of microplastics and the level of anthropogenic activity has been established and reported in surface water trawls in the Laurentian Great Lakes (Browne et al., 2011; Eriksen et al., 2013) and estuarine rivers in the Chesapeake Bay of America (Yonkos et al., 2014) similar to the trend of observed in the current study. Many coastal regions also displayed similar relations. For example, in China, intensive anthropogenic activities at the Three Gorges Dam resulted in a high abundance of microplastics when compared to other estuarine parts of tributaries that had lesser human activities (Zhang et al., 2015a, 2015b). In the same study, a greater number of microplastics were collected from the Xiangxi River, China which flowed through a large area with a high density of human population.

4.2. Rich bacterial assemblages on microplastic surfaces

This study showed for the first time the bacterial community on microplastics in tropical region. The surfaces of microplastic particles were colonised by rich assemblages of bacteria, with bacterial community structures differing based on the site of sampling. Proteobacteria, Bacteroidetes and Firmicutes were the dominant phyla observed. This is consistent with previous studies characterising microbial communities on the surfaces of marine microplastics (Amaral-Zettler et al., 2015; Oberbeckmann et al., 2016). The differing composition of bacterial phyla is an indicator of the varying stages of biofilm formation. Proteobacteria is found to be a primary biofilm coloniser, while Bacteroidetes are secondary colonisers on anthropogenic substrates in marine ecosystems (Dang and Lovell, 2000). This indicates that bacterial biofilm communities on the surfaces of microplastics collected in this study were at the early stage of development. In addition, a fraction (~34%) of OTUs was shared among the three sampling sites, demonstrating a large proportion of site-specific OTUs and a distinct microbial community structure among the sites.

Important bacterial taxa capable of bioremediation were identified in this study. Species of *Erythrobacter*, the dominant bacterial genera of microplastics at site S7b, were capable of degrading polycyclic aromatic hydrocarbons (Zhuang et al., 2015). The increased levels of shipping have been associated with an increase in oil pollution (Mironov, 1968). *P. alcaligenes* found at site LI1 is a common bacterium found in soil and water (Tekorienė, 2008). It has been used in bioremediation purposes during oil spills, as it can degrade toxic polycyclic aromatic hydrocarbons (Subathra et al., 2013). *P. veronii* has been used in the bioremediation of contaminated soils and it shown to degrade a range of aromatic organic compounds including Toluene and Benzene (Onaca et al., 2007; Morales et al., 2016). It is likely that the Johor Strait, which has an increasing level of anthropogenic activities such as land reclamation and shipping, contributes to the increased eutrophication and oil pollution of the marine waters. As a result, the marine environment promotes the dominance of hydrocarbon-degrading bacteria as observed in this study. A similar case was seen in the Gulf of Mexico, where there was a shift in the bacterial community structure towards oil-degrading bacteria during the Deepwater Horizon oil spill (Kostka et al., 2011). Given the predicted increase in plastic waste contamination in oceans, the discovery of such bacteria provides important nature-friendly alternatives for the mitigation of these toxic pollutants.

In contrast, there were also putatively toxic bacteria identified on the surfaces of microplastics. It is well established that microplastics are small enough and has been mistaken for food by a wide range of marine life, from brown shrimp (Devriese et al., 2015), pelagic fish (Lusher et al., 2013) to humpback whales (Besseling et al., 2015). Although not dominant, the toxic bacterial genus *Vibrio* was also detected on microplastics from all sites (<0.2%). The young age of the biofilm could be a reason why marine pathogens are not in high abundances on the surfaces of microplastics. Species from this genus has been found toxic to marine animals like the brine shrimp (Puente et al., 1992) and the black tiger prawn (Manefield et al., 2000). Consumption of microplastics by marine organisms could lead to the accumulation of these marine pathogens within the food chain, transferring the bacteria to marine animals of different trophic levels. In addition, a *Vibrio* associated with coral bleaching and disease, *Photobacterium rosenbergii* (Thompson et al., 2005; Tait et al., 2010) was also found at site LI1. The proliferation and accumulation of this bacterium could be detrimental to the coral reefs in Singapore as the southern strait is characterised by multiple coral communities with great biodiversity that are under conservation (Pu, 2016). Marine *Vibrio* species are also a major cause of wound infections in humans, where many are life-threatening (Oliver, 2005).

The genus *Arcobacter* was a dominant genus from site LI1. Members of this genus are pathogenic and have been implicated as causative agents of gastrointestinal diseases (Kayman et al., 2012; Arguello et al., 2015). Although marine pathogens were not present in high abundances on microplastic surfaces, the long term colonisation of these bacteria should be considered. Furthermore, these plastics were collected from locations easily accessible to the public and in areas widely used for recreation. The identification of potentially pathogenic bacteria would be important for the mitigation of would infections and disease spreading.

5. Concluding remarks

This study demonstrated that microplastic abundance differed according to the levels of anthropogenic activities at the sampling site, highlighting the influence of anthropogenic activity on microplastic abundance. Furthermore, the structure of bacterial assemblages at each site was distinctly on the phylum level. Microplastics are evidently a rich habitat for the colonisation by wide range of bacterial taxa including bioremediating and putatively toxic bacteria. They present a surface rich in microbial life that present opportunities for the isolation of bioremediating bacteria such as *Erythrobacter*, which has shown to be able to degrade hydrocarbons. This demonstrates the potential for the discovery of useful organisms among waste matter. In contrast, the presence of putatively pathogens such as *Arcobacter* on microplastic surfaces also highlights the vulnerability of human health to pathogens and the importance of understanding the bacterial plastisphere. This is crucial as the first step to managing this urgent issue of microplastic

pollution would be to have a thorough comprehension of the problem and its associated implications.

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