

## RESEARCH LETTER – Environmental Microbiology

# Diversity of bacterioplankton in the surface seawaters of Drake Passage near the Chinese Antarctic station

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One sentence summary: Marine bacterioplankton diversity in the surface waters of Drake Passage.

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## ABSTRACT

The determination of relative abundances and distribution of different bacterial groups is a critical step toward understanding the functions of various bacteria and its surrounding environment. Few studies focus on the taxonomic composition and functional diversity of microbial communities in Drake Passage. In this study, marine bacterioplankton communities from surface seawaters at five locations in Drake Passage were examined by 16S rRNA gene sequence analyses. The results indicated that psychrophilic bacteria were the most abundant group in Drake Passage, and mainly made up of *Bacillus*, *Aeromonas*, *Psychrobacter*, *Pseudomonas* and *Halomonas*. Diversity analysis showed that surface seawater communities had no significant correlation with latitudinal gradient. Additionally, a clear difference among five surface seawater communities was evident, with 1.8% OTUs (only two) belonged to *Bacillus* consistent across five locations and 71% OTUs (80) existed in only one location. However, the few cosmopolitans had the largest population sizes. Our results support the hypothesis that the dominant bacterial groups appear to be analogous between geographical sites, but significant differences may be detected among rare bacterial groups. The microbial diversity of surface seawaters would be liable to be affected by environmental factors.

**Keywords:** Antarctic; Drake Passage; bacterial diversity; surface seawater; 16S rRNA

## INTRODUCTION

Antarctic environments are extraordinary in the harshness of their climates, such as drought, high ultraviolet (UV) radiation, light limitation, violent storms and extremely low temperatures (Tytgat et al. 2014). For withstanding the selective pressure, Antarctic insects and mammalian herbivores are generally absent and microorganisms play a critical role in the biogeochemical cycling of Antarctic ecosystem (Murray et al. 1998; Yerqau et al. 2009). According to different temperature limitation of cell growth, the psychrophilic microorganisms in Antarctic environments are mainly divided into psychrophiles and psychrotrophs, and both of them can survive at 0°C. The psychrophiles prefer

to thrive at temperature below 15°C, while the optimum temperature of psychrotrophs is 20–30°C (Morita 1975). The growth of microorganisms exposed to extremely low temperature is challenged by several factors including reduced enzymatic reaction rates, limited bioavailability of nutrients, and extreme pH or salinity. To thrive successfully in cold environments, the psychrophilic microorganisms have evolved a complex range of structural and functional adaptations (Margesin and Miteva 2011).

For two centuries, many animal and plant species do not exhibit geographic patterns like the latitudinal gradient of increasing species richness from polar to equatorial regions (Hillebrand 2004; Pommier et al. 2007). Due to small size, great abundance

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and easy dispersal, it is suggested that bacteria would also show little or no latitudinal gradient of diversity (Fuhrman *et al.* 2008). The geographical patterns lack a consensus explanation. Some studies show that geographical differences can be found in the structure and composition of marine bacterioplankton populations (Jamieson *et al.* 2012), while other studies demonstrate that the geographical parameters are not correlated with bacterioplankton distribution (Zubkov *et al.* 2002). In Antarctic surface seawaters, especially in Drake Passage, however, few studies focus on the relative investigations.

Drake Passage is located between the southern extension of the South American shelf and the Western Antarctic Peninsula shelf. Because of extreme environments, such as large waves, fierce storms and strong currents, sampling in Drake Passage is very difficult and therefore infrequent (Waller *et al.* 2011). Compared to other Antarctic environments, only limited information about the diversity and function of microbial communities in Drake Passage is available. In summer (2012) cruises in Drake Passage near Great Wall Station, we have investigated the diversity of marine bacterioplanktons, the dominant psychrophilic microorganisms and geographic pattern of five surface seawater communities with different locations. Our aims are to isolate the main psychrophilic microorganisms, describe and compare the bacterioplankton compositions with different geographical sites, demonstrate the correlation between microbial diversity and locations, and enhance understanding of diversity and activity of bacterioplankton communities in surface seawaters of Drake Passage near the Great Wall Station, Antarctic.

## MATERIALS AND METHODS

### Sample collection

Field measurements and sample collections were conducted in March 2012 during the 28th Chinese National Antarctic Research Expedition. Five surface seawater samples (5 m depth) with different locations (A1–A5) were collected from Drake Passage (Fig. 1) near the Great Wall Station (62°12′59″S, 58°57′52″W) in Antarctic. Bacteria existed in the surface seawater samples

were collected by filtration of 4 L of seawater onto 0.2 µm pore size filter (Pall, Lane Cove, Australia). All the samples were stored at –80°C until further processing.

### DNA extraction, 16S rRNA clone library construction, and restriction fragment length polymorphism

Genomic DNA was extracted in duplicate to avoid bias from five samples (A1–A5) using a QiAamp DNA stool Mini Kit (Qiagen, Germany). The PCRs were carried out in septuplicate 25 µL reactions with 50–80 ng of genomic DNA, 2.5 µL 10 × PCR buffer, 2 µL 10 mM dNTP, 0.2 µL Taq polymerase (Takara, Japan), 19.8 µL ddH<sub>2</sub>O, 0.5 µL 10 µM Bact 27F (5′-AGAGTTTGATCCTGGCTCAG-3′) and Bact 1492R (5′-GGTTACCTTGTACGACTT-3′). The amplification program consisted of an initial denaturation step at 95°C for 5 min, followed by 34 cycles of 95°C for 30 s, 55°C for 45 s and 72°C for 90 s, and a final extension period of 10 min at 72°C (Xing *et al.* 2013). Replicate PCR products were pooled, purified, cloned into PMD18-T vector (Takara, Japan) and transformed into Trans5α (Tiangen, China), respectively. About 200–300 positive colonies from each sample were chosen by chance. Products of the 27F–1492R 16S rRNA gene PCR amplification were digested with the restriction endonucleases BsuRI and Hin6I (Fermentas, Canada). The same restriction fragment length polymorphism (RFLP) patterns were clustered into operational taxonomic units (OTUs). Three clones of each OTU were chosen at random and plasmid inserts were sequenced bidirectionally with M13 primers (Xing *et al.* 2013). All experiments described above were repeated three times.

### Statistical and bioinformatics analysis

Bidirectional sequences were assembled with DNASTar and trimmed to remove vector and low-quality sequences using the PhredPhrap script. Chimeras were removed using Bellerophon software (Huber, Faulkner and Hugenholtz 2004), implemented at the Greengenes website (<http://greengenes.lbl.gov>) (DeSantis *et al.* 2006). The 16S rRNA gene sequences which passed the quality and chimera filters were used in the subsequent analyses. Each representative sequence of OTUs was submitted to



**Figure 1.** Location of sampling stations in Drake Passage near the Great Wall Station, Antarctic. Sampling coordinates: A1(64°00′S, 65°59′W), A2 (63°01′S, 65°02′W), A3 (62°59′S, 64°02′W), A4 (62°34′S, 61°58′W) and A5(62°00′S, 61°01′W).

**Table 1.** Clone library coverage and bacterial diversity indices for the 16S rRNA gene clone libraries constructed from five samples (A1–A5).

Samples	No. of OTUs	No. of clones	Coverage%	Chao1	ACE	Jackknife	Shannon	Simpson
A1	38	269	89.47	35.46	36.82	37.58	2.54	0.17
A2	32	256	87.50	27.54	29.33	31.00	2.21	0.19
A3	33	234	90.90	31.30	32.49	34.00	2.84	0.09
A4	14	184	92.86	11.00	11.58	12.00	1.29	0.44
A5	48	256	89.58	42.33	43.99	38.87	3.03	0.09

GenBank and granted an accession number. Taxonomy was assigned to each OTU using the Ribosomal Database Project (RDP) classifier with a minimum threshold of 80% (Pope et al. 2012) and BLAST method. The representative sequence for each OTU with <97% identity to any sequence in GenBank database was defined as previously undescribed OTUs (UOTUs) (Xing et al. 2013). Mothur was used to describe species diversity with a threshold of 97%. The richness indices included Chao1, the abundance-based coverage (ACE) and interpolated jackknife, and the diversity indices contained the Shannon–Weaver diversity index and Simpson reciprocal diversity (Schloss et al. 2009). Good's coverage and rarefaction analysis for the five libraries were also determined. Cluster analysis of the community composition was performed using PAST with a correlation matrix (Zeng et al. 2014).

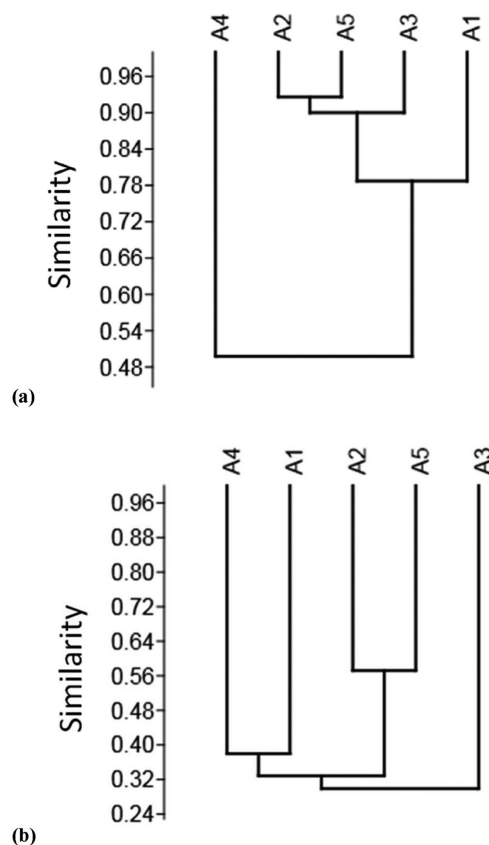
## RESULTS

### Sequence generation

A total of 1199 positive clones were picked from the five 16S rRNA clone libraries (A1–A5) and 112 OTUs were obtained through RFLP analysis. These near-full-length sequences (OTUs) were assigned to six different phyla or groups (including Proteobacteria, Firmicutes, Bacteroidetes, Actinobacteria, Verrucomicrobia and unclassified groups), and were deposited into the GenBank database with accession numbers KP975257–KP975368. Each of the 16S rRNA clone libraries contained 184–256 positive clones, with OTUs ranging from 14 to 48. Good's coverage estimations revealed that 87.5–92.86% of species were obtained in all of the five samples and the rarefaction curves tended to approach the saturation plateau (see Fig. S1, Supporting Information). The diversity indices showed that A5 and A4 communities appeared to have higher and lower richness as compared to other communities, respectively (Table 1).

### Bacterioplankton species diversity

The majority of OTUs (68%) showed  $\geq 97\%$  sequence similarity to known taxa in GenBank database. At the phylum level, cluster analysis of bacterial composition revealed a conservation of the community composition ( $>78\%$  similarity) in all of the libraries except the A4 library which was  $<50\%$  similar with other libraries (Fig. 2a). RFLP analysis revealed that the A1 library contained the maximum number of phyla (6), where Firmicutes, Proteobacteria and Actinobacteria were the most dominant groups and accounted for 97.4% of the OTU sequences (Fig. 3a). Both the A2 and A3 libraries showed relatively simple diversity wherein Proteobacteria and Firmicutes represented 91% and 98.7% of the OTU sequences, respectively. Although the number of phyla of A4 library was similar with A2 and A3 library, Firmicutes was the only dominant phylum in A4 library which accounted for 86.4% of the OTU sequences (Fig. 3a). Furthermore, Proteobacterial diversity analysis at the family level

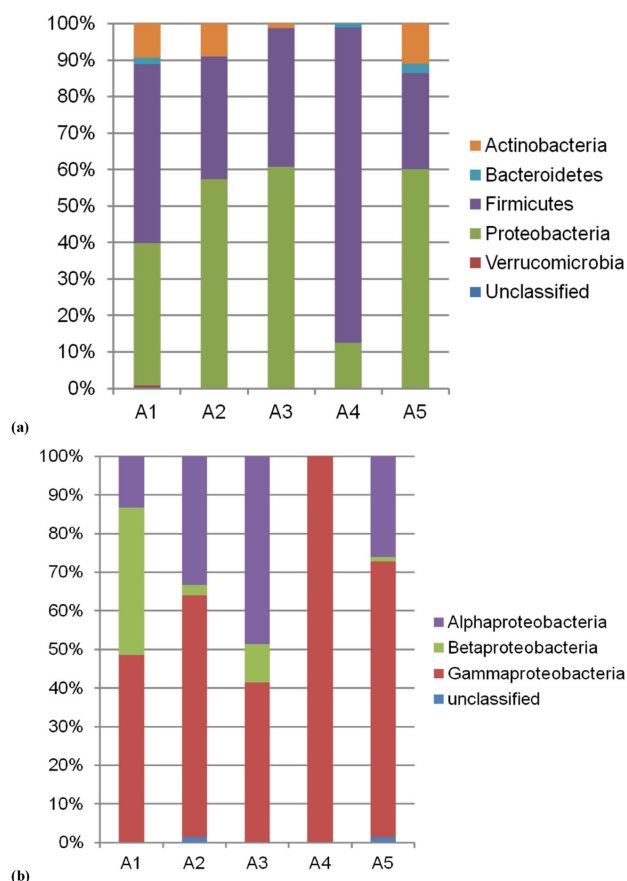


**Figure 2.** Sample sorting analysis. (a) Cluster analysis dendrogram showing percentage similarity of bacterial diversity at the phylum level in the five sampling sites based on Bray–Curtis resemblance of the relative abundance of bacterial groups. (b) Cluster analysis dendrogram showing percentage similarity of OTUs in the five sampling sites based on Bray–Curtis index.

indicated that *Gammaproteobacteria* was the principal contributor to the observed dissimilarity between A4 library and other libraries (Fig. 3b).

### Dominant bacterioplanktons and psychrophilic bacteria

The 10 most abundant OTUs within the five samples were determined to understand further the important bacteria. Dominant OTUs belonged to *Bacillus* (23.05–79.90%) were detected in all five libraries, and abundant OTU sequences related to *Aeromonas* (4.09–28.91%) and *Psychrobacter* (1.56–4.30%) were found in A1, A2, A4 and A5 library. In addition to these species, the most abundant OTUs associated with the A1 library were sequences related to *Pelomonas* (12.27%), *Curtobacterium* (7.81%), *Beijerinckia* (1.86%) and *Brevibacillus* (1.86%). The A2 library consisted mainly of sequences related to *Candidatus* (6.25%), *Rhodococcus*



**Figure 3.** Bacterial composition of the different communities. (a) Relative distribution of the bacterial phyla in the different locations. (b) Relative distribution of Proteobacteria in the different locations. Sequences that could not be classified into any known group were assigned as 'unclassified'.

(1.95%–5.86%), *Planktomarina* (3.91%), *Phyllobacterium* (1.56%) and *Pantoea* (1.56%); the A3 library consisted mainly of *Candidatus* (10.68%), *Swaminathan* (6.84%), *Stenotrophomonas* (6.41%), *Planktomarina* (4.27%), *Achromobacter* (2.99%), and two UOTUs belonged to *Gammaproteobacteria* (6.41%) and *Alphaproteobacteria* (3.85%), respectively; the most abundant sequences in the A4 library were those related to *Pseudomonas* (4.35%), *Fictibacillus* (2.17%) and *Elizabethkingia* (1.09%); for the A5 library, it was numerically contained sequences related to *Candidatus* (4.69%), *Rhodococcus* (4.69%), *Cobetia* (3.52%), *Planktomarina* (3.13%) and *Halomonas* (2.34–2.73%) (see Table S1, Supporting Information).

In the present work, *Gammaproteobacteria* which was recognized as the main psychrophilic bacteria in ocean environments dominated in all five libraries (Fig. 3b). Among them, *Aeromonas* and *Psychrobacter* were detected in five libraries (2.56–30.86% and 1.56–7.42%, respectively); *Pseudomonas* existed in the A1, A3 and A4 library (1.12, 0.85 and 4.35%, respectively); *Halomonas* was identified in A1, A3 and A5 library (0.74, 1.28 and 7.03%, respectively); *Acinetobacter*, *Cobetia* and *Marinomonas* were found in the A1 and A5 library (1.12 and 0.78%, 0.74 and 5.08%, 1.12 and 1.95%, respectively) (Table 2). Furthermore, *Bacillus* in Firmicutes which was also psychrophilic bacteria had been detected abundant in five surface seawater libraries (described above).

Thirty-six OTU sequences showed only 86–96% sequence similarity to known taxa in GenBank database (see Table S2, Supporting Information) and were defined as UOTUs. The major-

**Table 2.** The main psychrophilic bacteria present in five libraries (A1–A5)\*.

Group	A1	A2	A3	A4	A5
<i>Psychrobacter</i>	11/1	4/1	4/2	3/1	19/5
<i>Aeromonas</i>	15/2	79/3	6/1	12/4	39/3
<i>Pseudomonas</i>	3/1	0/0	2/1	8/1	0/0
<i>Halomonas</i>	2/1	0/0	3/2	0/0	18/4
<i>Acinetobacter</i>	3/1	0/0	0/0	0/0	2/1
<i>Cobetia</i>	2/1	0/0	0/0	0/0	13/3
<i>Marinomonas</i>	3/1	0/0	0/0	0/0	5/2

\*Numbers below the diagonal line represent the number of OTUs in five libraries, whereas numbers above the diagonal line indicated the number of clones in five libraries.

ity of UOTUs originated from A2 and A5 library. A5 library contained the maximum number of UOTUs (13) and the sequences mainly belonged to *Gammaproteobacteria* (6), *Alphaproteobacteria* (2), *Bacilli* (2) and *Actinobacteria* (2). A2 library contained 12 UOTUs which were mainly related to *Alphaproteobacteria* (7) and *Gammaproteobacteria* (2). Only one UOTU was identified in A4 library on the contrary. At the genus level, the sequences of five UOTUs (13.89%) had relatively high similarity with psychrophilic bacteria including *Psychrobacter* (4) and *Cobetia* (1), while the sequences of three UOTUs were similar with *Candidatus* (SAR11) (see Table S2, Supporting Information).

### Unique and shared OTUs among five bacterial communities of surface seawater in Drake Passage

Only 2 of the 112 identified OTUs (1.8%) were cosmopolitans, i.e. they were found at all libraries, belonging to *Bacillus*. In contrast, 80 OTUs (71%) were endemic, i.e. they were only found at one of surface seawater libraries, 18 OTUs (16%) were found in two of the libraries and only a small fraction (12) of all OTUs were found in three or four libraries (see Fig. S2a, Supporting Information). Comparing percentage similarity of OTUs composition in different samples using dendrogram indicated that five libraries were dissimilar to each other (less than 40%) except for A2 and A5 library with relatively high similarity (more than 56%) (Fig. 2b). However, the frequencies of the 80 endemic OTUs were mostly (65%) very low, with one or two representative sequences, and a few OTUs (28) contained from 3 to 15 sequences per library (see Fig. S2b, Supporting Information). Furthermore, the sequences of shared OTUs between five libraries mainly belonged to *Gammaproteobacteria*, *Alphaproteobacteria* and *Firmicutes*, and the percentage of sequences originated from shared OTUs in each library was very high, ranging from 66.24 to 91.58% (Table 3).

## DISCUSSION

### Taxonomy and comparison of bacterioplankton communities

Among the members of Proteobacteria, *Gammaproteobacteria*, *Alphaproteobacteria* and *Betaproteobacteria* dominated in all five communities of surface seawaters except the A4 community wherein only *Gammaproteobacteria* was abundant (Fig. 3b). This pattern of dominance has already been reported in the west of the Antarctic Peninsula (Murray and Grzymalski 2007) although the surface water of Scotia Sea, *Alphaproteobacteria* has been found to be the dominant group followed by

**Table 3.** Shared phyla/classes between five bacterial communities of surface seawater in Antarctic.

Phylum/class	Share OTUs	Clones <sup>#</sup>				
		A1	A2	A3	A4	A5
Bacteroidetes	1	3	0	0	2	0
Actinobacteria	4	23	20	3	0	23
Alphaproteobacteria	8	2	41	55	0	34
Betaproteobacteria	1	33	2	0	0	0
Gammaproteobacteria	11	40	83	28	9	78
Firmicutes	7	111	82	69	158	63
Total	32	212	228	155	169	198
Clone <sup>#</sup> /total clones (%)		78.81	89.06	66.24	91.85	77.34

<sup>#</sup>Number of clones belonging to the shared OTUs.

*Gammaproteobacteria* (Zinger et al. 2011). In a global distribution study, *Gammaproteobacteria* generally dominates in both pelagic and benthic ecosystems (Jamieson et al. 2012). Among the *Alphaproteobacteria*, SAR11 clade (*Candidatus* species) was abundant in A2, A3 and A5 community (see Table S1, Supporting Information), which was in accordance with a previous research which suggested that  $2.4 \times 10^{28}$  SAR11 cell existed globally in the oceans and half of them were located in the euphotic zone (Morris et al. 2002). However, Archaea was not detected in any communities in this study. According to previous research on Drake Passage, archaeal community richness was commonly lower in summer than in winter (Manganelli et al. 2009). The PCR primer in the present study which was mainly used to detect 16S rRNA genes of bacterial groups would be also difficult to discover the genes of Archaea. The specific primer of Archaea will be employed to identify the structure and diversity of Archaea in the future.

Bacteroidetes was only detected in A1, A4 and A5 community with low proportion (1.1–2.7%). This finding was in accordance with previous studies regarding the marine bacterioplankton diversity of the Scotia Arc with low chlorophyll *a* concentration (Jamieson et al. 2012). However, Zeng et al. (2014) demonstrated that Bacteroidetes was dominant in surface seawaters of Ardley Cove and Great Wall Cove, consistent with high concentrations of chlorophyll *a* and particulate organic carbon. Bacteroidetes members have the capability to degrade polymeric substances in the ocean, while *Gammaproteobacteria* and *Alphaproteobacteria* seem better adapted to use monomers rather than polymers (Cottrell and Kirchman 2000b; González et al. 2008). In this study, lower Bacteroidetes and higher *Gammaproteobacteria* and *Alphaproteobacteria* were found in five bacterial communities, suggesting the low concentration of polymeric substances in the surface seawater of Drake Passage. These may be the reasons that can partly explain the high similarity between A2 and A5 community (Fig. 2). Similar proportions of *Gammaproteobacteria* and *Alphaproteobacteria* in A2 and A5 community (Fig. 3b) may attribute to similar marine environments. The results above were also in agreement with a previous research, which suggested that bacterioplankton community structure could be used as an indicator of marine ecosystem status (Zeng et al. 2014).

Cluster analysis showed that A4 community had low similarity with other communities (Fig. 2a) and Firmicutes was the only abundant phylum in A4 community (Fig. 3a). Previously, Firmicutes was detected in coastal sediments with high proportion and Bacilli in Firmicutes had been identified as indicators of human fecal contaminations in watersheds (Zinger et al. 2011). Some investigations also suggested that coastal environments

including coastal waters and sediments were subjected to increasing nutrient, freshwater, organic matter and pollution originated from land (Rappé, Vergin and Giovannoni 2000; Halpern et al. 2008). According to the locations of sampling in this study, A4 was closest to the coast (Fig. 1). The taxonomic differences between A4 community and other communities might result from the influence of land.

### Psychrophilic bacteria

The last decade has been a growing interest in psychrophilic bacteria (Margesin and Miteva 2011). Various groups of bacteria belonging to  $\alpha$ -,  $\beta$ -,  $\gamma$ -proteobacteria and *Cytophaga-Flavobacterium-Bacterioides* phylum have been reported to survive in permanently cold environments, such as Arctic soils and sediments, Antarctic lakes and oceans (Gilbert et al. 2004; Männistö and Häggblom 2006; Zeng et al. 2014). For surviving in extremely cold environments, psychrophilic bacteria have often evolved specific biosynthetic pathways to overcome all the adversities (D'Amico et al. 2006), including maintenance of functional membranes, cold-adapted enzymes and cold-shock or heat-shock responses (Maiangwa et al. 2015). In polar ocean environments, psychrophilic bacteria are also halophilic and halotolerant (Oren 2015). In this study, psychrophilic bacteria were the main bacterioplankton groups in surface seawater communities of Drake Passage. Of the 10 most abundant bacterial OTUs, several were related to known psychrophilic bacteria wherein *Bacillus*, *Psychrobacter* and *Aeromonas* were dominant (see Table 3 and Table S1, Supporting Information). *Psychrobacter*, which is commonly observed in permanently cold environments (Jamieson et al. 2012), is also halotolerant (Juni and Heym 1986) and some species (such as *Psychrobacter* sp. strain G) can produce extracellular lipolytic enzymes with cold activity (Che et al. 2013). Previous investigations on *Bacillus* and *Aeromonas* in Antarctic disclosed that they were capable of producing cold-active glycosyl hydrolases, such as  $\beta$ -glucosidases, proteases and cellulases (Dong et al. 2013; Cristóbal et al. 2015).

Moreover, other psychrophilic bacteria which were detected in surface seawater communities also had the ability to surviving in cold ecosystems. *Pseudomonas* species are the most commonly reported psychrophilic bacteria (D'Amico et al. 2006). In addition to cold-active lipase, antifreeze proteins are also produced by *Pseudomonas* to deal with low temperature (Muryoi et al. 2004; Mohamad et al. 2013). Cold-active lipases have been reported from comparatively fewer species of *Halomonas* which are mainly halotolerant bacteria in surface seawaters (Kaye et al. 2004; Jadhav et al. 2013). *Cobetia* can produce a high amount of trans-unsaturated fatty acids at low growth temperature

(Yumoto et al. 2004), while *Acinetobacter* produce cold-active esterase and lipase (Zheng et al. 2011; Kim et al. 2012). Additionally, UOTUs analysis indicated that the sequences which had relatively high similarity with psychrophilic bacteria accounted for high percentage of all UOTUs (13.89%). This finding is in accordance with the survey on novel bacterial and fungal species and genera from various cold habitats, which demonstrates that psychrophilic bacteria represent a vast resource of novel microorganisms (Margesin and Miteva 2011).

The determination of the numbers and relative abundances of different bacterial groups is a critical step toward understanding the functions of various bacteria (Cottrell and Kirchman 2000a; Zeng et al. 2014). In the present work, psychrophilic bacteria were most abundant in surface seawater communities, suggesting that psychrophilic bacteria played a critical role in the biocycling of Drake Passage near the Great Wall Station, Antarctic. Although psychrotrophs and psychrophiles were not determined with respect to individual bacterial species, the results of this study increased the knowledge of psychrophilic bacteria in Drake Passage, the function and cold-adapted mechanism of specific psychrotrophs or psychrophiles need to be investigated further.

In addition to psychrophilic bacteria, some abundant OTUs recovered were related to *Rhodococcus* and *Stenotrophomonas*. Many investigations have demonstrated the resistance of *Rhodococcus* and *Stenotrophomonas* species to UV radiation in Antarctic (Gouvêa Taketani et al. 2013; Vasileva-Tonkova et al. 2014). Species of *Bacillus* which were main psychrophilic bacteria in surface seawater communities (described above) were also proved to be UV-resistant bacteria (Wang et al. 2011). Although Antarctic ozone hole and the consequent increase of UV radiation could be particularly deleterious for bacteria, aerobic bacteria in Antarctic surface seawater have high resistance and repair capabilities against UV radiation damage (Wang et al. 2011; Vasileva-Tonkova et al. 2014). Characterization of microbial diversity of surface seawaters in Antarctic would be of considerable relevance for assessing climatic effects on microbial communities.

### Latitudinal gradient and degree of shared/unique bacteria

To date, whether microbial diversity has correlation with latitudinal gradient is still uncertain. In this study, diversity for surface seawater communities did not correlate with latitude, i.e. microbial diversity across locations showed no apparent geographical pattern (Table 1). This finding is in accordance with the research on surface and deep marine bacterial communities in Antarctic and Arctic regions, which suggest that environmental factors rather than geographical isolation are the main determinant of the bacterial community composition in surface waters (Ghiglione et al. 2012; Zeng et al. 2014). On the contrary, other investigations on marine bacterioplankton show a significant latitudinal gradient in diversity, and correlations with environmental factors are much weaker (Pommier et al. 2007; Fuhrman et al. 2008). Although Pommier et al. (2007) showed latitudinal gradient in species diversity, sampling was restricted to coastal seawaters and high-latitude samples were only detected from the Northern Hemisphere. Sampling in the present work was also restricted to Drake Passage closed to Great Wall Station, and the number of sampling was relatively low. To conclusively determine the correlation between latitude and microbial diversity, more data need to be obtained from additional locations. Moreover, Ghiglione et al. (2012) revealed that the microbial diver-

sity of surface seawaters was vulnerable to environmental influences. Special environmental features of Drake Passage would be the main reason for microbial diversity of surface seawaters. Thus, the correlation between microbial diversity and environmental factors, such as primary production, temperature, chlorophyll concentration, water properties and anthropogenic factors (Ghiglione et al. 2012; Sul et al. 2013), need to be demonstrated further.

Although low degree of cosmopolitans and high degree of endemisms were observed in different communities of Drake Passage and little similarity at the OTU level was detected between the different communities, cosmopolitans had the largest population sizes. These findings were in accordance with previous study regarding the cosmopolitans/endemic microorganisms and different distribution of bacterial groups in the surface ocean (Bouman et al. 2006; Pommier et al. 2007), but contradicted the hypothesis that a majority of marine bacterioplanktons should be cosmopolitan, endemism should be rare and their global diversity should be low (Fenchel and Finlay 2004), i.e. marine bacterioplanktons should be ubiquitously distributed. Furthermore, two cosmopolitans (belonging to *Bacillus* described above) which were abundantly present in surface seawater communities were also detected in other marine bacterioplankton communities (Pommier et al. 2007). The finding was consistent with those of Zeng et al. (2014), who suggested that some cosmopolitans belonging to a few bacterial groups that were usually abundant in marine bacterioplankton communities may have similar ecological functions in similar marine environments but at different geographic locations.

## CONCLUSION

In this study, 16S rRNA-related technologies were used to reveal microbial diversity of marine bacterioplankton communities in Drake Passage near the Great Wall Station, Antarctic. The results showed that five communities of surface seawaters in Drake Passage consisted mainly of the same species: *Gammaproteobacteria*, which was in agreement with the investigations on pelagic and benthic ecosystems. At a finer phylogenetic resolution, psychrophilic bacteria, including *Bacillus*, *Aeromonas*, *Psychrobacter*, *Pseudomonas* and *Halomonas*, were the most abundant groups. As global marine bacterioplankton communities, a high degree of endemism and conversely few cosmopolitans were detected in surface seawaters communities of Drake Passage and cosmopolitans (*Bacillus* belonging to psychrophilic bacteria) had the largest population sizes. However, little similarity at the OTU level was detected among locations, and the microbial diversity of surface seawater communities did not correlate significantly with latitude. The environmental factors may be the main determinant of the bacterial community composition in surface waters of Drake Passage and need to be confirmed further.

## SUPPLEMENTARY DATA

Supplementary data are available at FEMSLE online.

## ACKNOWLEDGEMENTS

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**Conflict of interest.** None declared.

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