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**Key Points:**
- Unlike the sea-ice melting system, enhanced bacterial production (BP) in the eastern Getz Ice Shelf (GtzIS) was uncoupled with phytoplankton biomass
- Dissolved organic carbon in glacier meltwater likely stimulates BP on the eastern GtzIS
- Warming-induced glacial melting may weaken carbon sequestration in the Antarctic Ocean by stimulating heterotrophic bacterial metabolism

## Glacial Ice Melting Stimulates Heterotrophic Prokaryotes Production on the Getz Ice Shelf in the Amundsen Sea, Antarctica

**Jun-Oh Min[1,2]** [ID], **Sung-Han Kim[3]**, **Jinyoung Jung[2]** [ID], **Ui-Jung Jung[3]** [ID], **Eun Jin Yang[2]** [ID], **SangHoon Lee[2]** [ID], and **Jung-Ho Hyun[1]** [ID]

[1]Department of Marine Sciences and Convergent Technology, Hanyang University, Ansan, Republic of Korea, [2]Division of Ocean Sciences, Korea Polar Research Institute, Incheon, Republic of Korea, [3]Marine Environmental Research Center, Korea Institute of Ocean Science & Technology, Busan, Republic of Korea

**Abstract** Extensive oceanographic data sets were combined with microbiological parameters to elucidate the tight coupling between glacial meltwater and heterotrophic bacterial production (BP) on the Getz Ice Shelf (GtzIS) in the Amundsen Sea. BP in the eastern GtzIS (EG; 85.8 pM Leu. h$^{-1}$), where basal glacier meltwater upwells, was significantly higher than BP measured in the western GtzIS (WG; 50.6 pM Leu. h$^{-1}$) and the Amundsen Sea Polynya (ASP; 27.8 pM Leu. h$^{-1}$). BP in the EG accounted for 49% of primary production, which was greater than that of the WG (10%) and ASP (9.2%). Enhanced BP in the eastern GtzIS was not coupled with phytoplankton biomass, but correlated significantly with the freshwater fraction containing meltwater-derived dissolved organic carbon (MW-DOC). These results suggest that warming-induced glacier melting weakens carbon sequestration efficiency in Antarctic coastal waters by stimulating heterotrophic metabolism that converts MW-DOC to $CO_2$.

**Plain Language Summary** The Getz Ice Shelf (GtzIS) in the Amundsen Sea, the third-largest ice shelf (34,018 km$^2$) on the West Antarctic Ice Sheet, is regarded as a hot spot for producing large amount of glacier meltwater (144.9 ± 14 Gt yr$^{-1}$). In general, the amount of dissolved organic carbon (DOC) from terrestrial sources is negligible in Antarctic waters, making DOC supplied by phytoplankton a major carbon source for heterotrophic bacteria growth. Although Antarctica's glacial ice shelves are presumably a large reservoir of organic carbon (ca. 5.5 Pg C), little is known about the effect of glacial melting on the supply of DOC available to heterotrophic bacteria. On the eastern GtzIS, where glacial meltwater upwells to the surface water column, heterotrophic bacteria production has no significant positive relationship with phytoplankton biomass, but is positively correlated with freshwater fraction. This suggests that DOC in glacial meltwater, rather than phytoplankton, provides DOC to support enhanced bacteria production. Our results imply that global warming–related increases in glacial meltwater may stimulate heterotrophic bacterial metabolism that respires DOC to $CO_2$, thereby reducing carbon sequestration efficiency in Antarctic coastal waters.

## 1. Introduction

Heterotrophic prokaryotes (hereafter bacteria) are a significant biological component that are almost exclusively responsible for the mineralization of dissolved organic carbon (DOC), the largest organic carbon pool in the ocean (Azam & Malfatti, 2007; Hansell & Carlson, 2015; Karl, 2007; D. L. Kirchman, 2008). DOC derived from various sources (Carlson & Hansell, 2015; Nagata, 2008) is either transferred to higher trophic levels or mineralized to $CO_2$ via bacterial production (BP) and respiration, respectively, within the microbial loop (Azam et al., 1983; del Giorgio et al., 1997; Duarte & Prairie, 2005; Ducklow et al., 1986. Consequently, the relative importance of heterotrophic bacteria in the microbial loop ultimately regulates the efficiency of the biologically mediated carbon sequestration process in the ocean (Chisholm et al., 2001; Karl, 2007; Legendre & Le Fèvre, 1995).

Antarctic glaciers store huge amounts of organic carbon (ca. 5.5 Pg C), and the amount of organic carbon discharged through subglacial Antarctic meltwater is estimated to be 0.33 Tg C year$^{-1}$ as particle organic carbon (POC) and 0.17 Tg C year$^{-1}$ as DOC (Wadham et al., 2019). Organic carbon in glacier meltwater consists of substantial amounts of bioavailable components (Hood et al., 2015; Musilova et al., 2017; Smith et al., 2017). Recent climate change and the consequent rise in water temperatures have stimulated the melting of glaciers, resulting in a total glacial mass loss of 252 Gt per year between 2009 and 2017 (Rignot et al., 2019). As the

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Southern Ocean accounts for approximately 20–50% of atmospheric $CO_2$ uptake in the global ocean (Arrigo et al., 2008; Takahashi et al., 2009), it is important to elucidate the metabolic response of heterotrophic bacteria to increased supplies of DOC derived from glacier meltwater to construct models of biogeochemical carbon cycles in the Southern Ocean (Ducklow et al., 2012; Lønborg et al., 2018, 2019; Paulsen et al., 2017).

The Getz Ice Shelf (GtzIS) in the Amundsen Sea is the third-largest ice shelf (34,018 km$^2$) on the West Antarctic Ice Sheet after the Ronne Ice Shelf (338,887 km$^2$) and the Ross West Ice Shelf (306,105 km$^2$) (Rignot et al., 2013). The GtzIS alone supports glaciers that hold enough ice to increase sea levels by 22 cm (Rignot et al., 2019). As a result of the inflow of warm Circumpolar Deep Water (CDW) into the west Antarctic shelf, including the Amundsen Sea (S. S. Jacobs et al., 2011; Jenkins et al., 2010), the GtzIS is now regarded as a hot spot that produces large amounts of glacier meltwater (144.9 ± 14 Gt yr$^{-1}$) (Morlighem et al., 2020; Rignot et al., 2013, 2019). Fresh and buoyant water released from a glacier cavity can drive regional and global ocean circulation (Jourdain et al., 2017; Nakayama et al., 2014; Raiswell et al., 2006; Silvano et al., 2018), while providing organic and inorganic substrates that stimulate biological production (Arrigo et al., 2017; Hood et al., 2015; Hopwood et al., 2018, 2020). Thus, increases in glacial meltwater can lead to changes in production and the community structure of phytoplankton (Arrigo et al., 2017; Alderkamp et al., 2012), as well as bacterial dynamics (Nicholes et al., 2019; Smith et al., 2017). Given that heterotrophic bacteria are a major consumers of DOC, enhanced bacterial metabolic activity associated with meltwaters may weaken carbon sequestration in Antarctic coastal waters (Ducklow et al., 2015; S. Lee et al., 2017). Despite the potential significance of meltwater-induced DOC release on bacterial dynamics, most microbiological oceanographic studies conducted in the water column of the Amundsen Sea Polynya (ASP) have been limited to bacterial dynamics coupled with various stages of phytoplankton blooms (Delmont et al., 2014; Hyun et al., 2016; J. G. Kim et al., 2014; S. J. Kim et al., 2019; B. Kim et al., 2022; Williams et al., 2016; Yager et al., 2012). Little information is available on the impact of glacier meltwater on the microbial metabolic activity in the Amundsen Sea, especially along the glacier ice shelves, largely due to an extensive sea-ice coverage making access difficult.

During an oceanographic research expedition to the Amundsen Sea in January and February 2016, we encountered a unique environmental condition in which most of the GtzIS was exposed to seawater (Figure 1). This provided us with direct opportunities to explore the bacterial dynamics associated with glacier meltwater input on the GtzIS. Here, we report that enhanced heterotrophic BP in front of the GtzIS was not coupled with phytoplankton that is supposedly the direct carbon source for heterotrophic bacteria in the Southern Ocean, but was directly related to glacier meltwater released from a basal part of the GtzIS affected by the intrusion of warm CDW. Our results are, to our knowledge, the first to demonstrate the importance of heterotrophic microbial processes in biogeochemical carbon cycles associated with glacier meltwater–induced DOC release along the west coast of Antarctica, where rapid glacial melting induced by climate change is occurring.

## 2. Materials and Methods

### 2.1. Study Area

The Amundsen Sea is located along Marie Byrd Land between the Bellingshausen Sea and the Ross Sea. The GtzIS extends 650 km along the Pacific sector of the Antarctic coastline between 115° W and 135° W, in the central and western Amundsen Sea (Figure 1). West Antarctica, including the Amundsen Sea and Bellingshausen Sea, has undergone rapid warming (Brown et al., 2019; Montes-Hugo et al., 2009) in recent decades, with the surface water temperature increasing by approximately 1.5°C since the 1950s (Turner et al., 2014). The estimated basal melt rate on the GtzIS was an area-averaged 4.15 m year$^{-1}$, resulting in a freshwater flux of 141.17 Gt year$^{-1}$ into the Southern Ocean (Wei et al., 2020). The glacier meltwaters discharged from the ice shelves in the Amundsen Sea during the summer of January 2011 and February 2012 reportedly extends more than 300 km offshore (I. Kim et al., 2016).

As a part of physical and biogeochemical processes studies in the Amundsen Sea, a multidisciplinary oceanographic survey was conducted onboard the RV Araon, a Korean research icebreaker, during the austral summer from January 14 to 16 February 2016. A temperature-salinity (T-S) diagram shows that the coastal waters of the Amundsen Sea can be divided into three main water masses: Antarctic Surface Water (AASW), Winter Water (WW), and modified Circumpolar Deep Water (mCDW) (S. S. Jacobs et al., 2011, Jenkins et al., 2010; Randall-Goodwin et al., 2015) (Figure S1 in Supporting Information S1). Water samples for microbiological
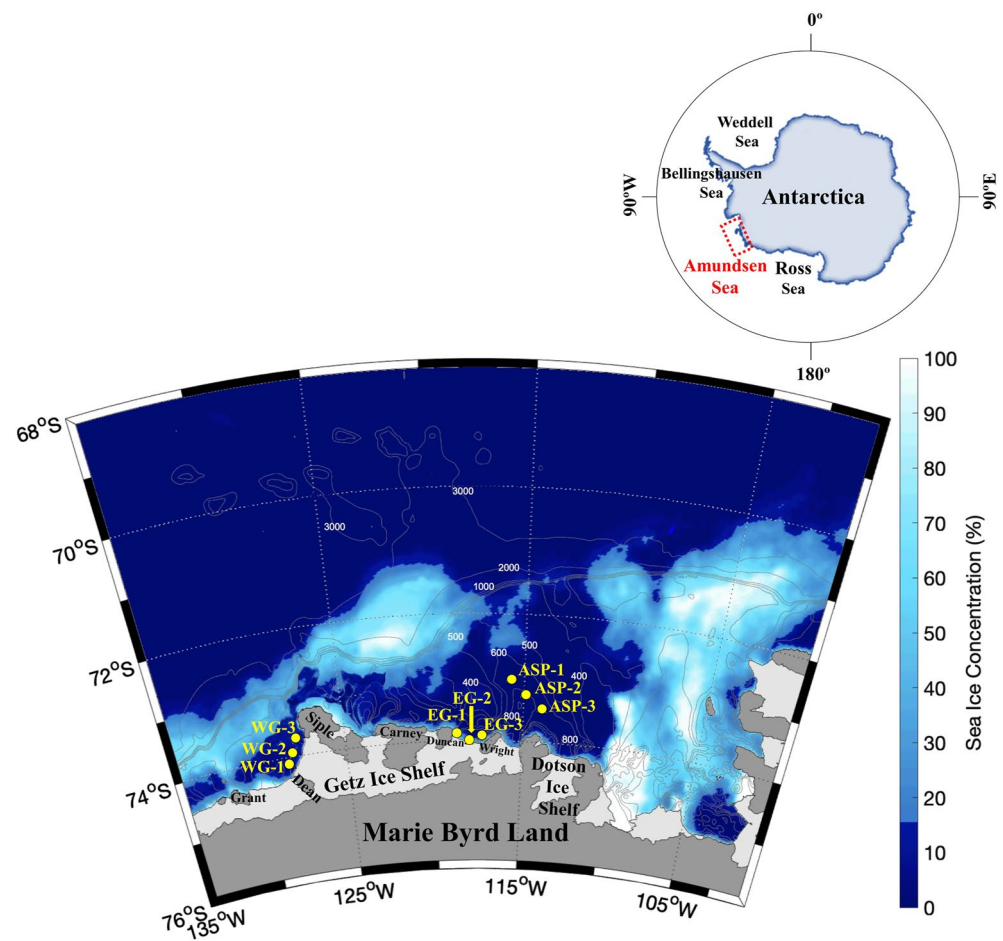
**Figure 1.** A map of the study area with the sampling locations in the Amundsen Sea during January 14 to 16 February 2016. The contours indicate bathymetric lines in meters.

analyses were collected at nine stations along the GtzIS and in the center of the ASP (Figure 1 and Table S1 in Supporting Information S1). A detailed description of the sample collection and handling procedure is presented in the Supporting Information (Text S1 in Supporting Information S1).

Sampling sites were grouped into three regions: eastern GtzIS (EG), western GtzIS (WG) and ASP, according to the distribution of potential temperature, salinity, chlorophyll-a (Chl-a) concentration, and freshwater fraction (FWF) (Table 1 and Figure S1 in Supporting Information S1). The EG site was characterized by a higher basal glacier melting rate because the bottom ice depth was deeper than the thermocline depth and an ice cavity was in direct contact with warmer mCDW, whereas a low basal melting rate was observed in the WG because the relatively cold water was in contact with the ice cavity, and the shallow ice-bottom depth prevents warm mCDW from entering the WG cavity (e.g., Wei et al., 2020).

The surface waters of the WG site were characterized by the lowest temperature and salinity and highest FWF (Figures 2h and 2i), whereas the EG site exhibited the highest temperature and an intermediate salinity ranging between the salinity values observed in the ASP and the WG (Figures 2a and 2b). The ASP sites were characterized by high Chl-a concentrations with relatively greater thermal stratification compared with the GtzIS sites (Figures 2o and 2r).

Based on a satellite image of the ice distribution and the sharp density gradient, the surface waters of the WG were largely affected by sea-ice meltwater (Figures 1 and 2j). In contrast, the vertically well-mixed water column with high temperature and low salinity at the EG site indicates that warm mCDW containing glacier meltwater upwells along the ice shelf, resulting in a moderately low salinity range (Figures 2a–2c).

**Table 1**
*Averaged (±1 SD) Physico-Chemical and Microbiological Parameters Within the Mixed Layer Depth in the Amundsen Sea*

| Oceanographic setting | Station | Depth (m) | Temp. (°C) | Sal. (psu) | Density (kg m$^{-3}$) | $Z_{eu}$ (m) | MLD (m) | FWF (%) | DOC (μM) | Chl-a (μg L$^{-1}$) | BA (×10$^7$ cells L$^{-1}$) | BP (pM Leu. h$^{-1}$) | BP:PP[a] (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Eastern Getz Ice Shelf | EG-1 | 674 | 0.28 (±0.02) | 33.9 (±0.03) | 27.2 (±0.03) | 28.7 | 95.0 | 2.25 (±0.11) | 49 (±2) | 0.67 (±0.14) | 43.2 (±3.32) | 73.5 (±14.1) | 49.8 |
| | EG-2 | 1119 | 0.30 (±0.10) | 33.9 (±0.03) | 27.2 (±0.03) | 28.0 | 53.4 | 2.50 (±0.10) | 52 (±1) | 0.63 (±0.18) | 41.4 (±10.5) | 79.9 (±17.6) | 39.5 |
| | EG-3 | 658 | 0.39 (±0.01) | 33.9 (±0.04) | 27.2 (±0.03) | 26.0 | 25.7 | 2.44 (±0.13) | 51 (±2) | 0.77 (±0.03) | 58.8 (±2.94) | 104 (±4.14) | 57.3 |
| | Average (±1 SD) | 817 (±262) | 0.32 (±0.07) | 33.9 (±0.01) | 27.2 (±0.01) | 27.6 (±1.40) | 58.0 (±34.9) | 2.40 (±0.13) | 51 (±2) | 0.69 (±0.07) | 47.8 (±9.56) | 85.8 (±16.1) | 48.9 (±8.94) |
| Western Getz Ice Shelf | WG-1 | 596 | −1.17 (±0.03) | 33.4 (±0.03) | 26.8 (±0.03) | 24.0 | 32.6 | 4.20 (±0.12) | 47 (±1) | 1.79 (±0.54) | 50.7 (±7.52) | 50.4 (±3.15) | 13.9 |
| | WG-2 | 780 | −1.11 (±0.05) | 33.5 (±0.02) | 27.0 (±0.02) | 19.0 | 24.7 | 4.11 (±0.09) | 46 (±2) | 3.86 (±0.02) | 49.3 (±1.89) | 46.4 (±2.67) | 7.11 |
| | WG-3 | 323 | −1.21 | 33.4 (±0.02) | 27.0 (±0.02) | 16.0 | 20.7 | 2.71 (±0.08) | 51 (±1) | 3.69 (±0.23) | 53.9 (±9.86) | 54.9 (±4.55) | 9.48 |
| | Average (±1SD) | 566 (±230) | −1.16 (±0.05) | 33.4 (±0.09) | 26.9 (±0.07) | 19.7 (±4.04) | 26.0 (±6.06) | 3.67 (±0.83) | 48 (±3) | 3.11 (±1.15) | 51.3 (±2.36) | 50.6 (±4.27) | 10.2 (±4.98) |
| Amundsen Sea Polynya | ASP-1 | 697 | 0.26 (±0.02) | 34.0 | 27.3 | 16.0 | 27.0 | 1.81 | 44 (±1) | 3.00 (±0.81) | 8.58 (±4.63) | 26.8 (±3.56) | 4.09 |
| | ASP-2 | 820 | −0.14 (±0.13) | 34.0 (±0.02) | 27.3 (±0.02) | 16.0 | 64.0 | 1.96 (±0.07) | 46 (±1) | 2.17 (±0.94) | 11.1 (±5.24) | 28.7 (±7.90) | 19.1 |
| | ASP-3 | 700 | −0.07 (±0.17) | 34.0 (±0.02) | 27.3 (±0.02) | 22.8 | 44.0 | 2.07 (±0.06) | 48 (±2) | 1.62 (±0.47) | 9.08 (±1.51) | 29.9 (±7.54) | 4.29 |
| | Average (±1SD) | 739 (±70) | −0.02 (±0.11) | 34.0 (±0.10) | 27.3 (±0.01) | 18.1 (±4.00) | 45.0 (±18.5) | 1.95 (±0.13) | 46 (±2) | 2.26 (±0.70) | 9.59 (±1.34) | 27.8 (±0.92) | 9.15 (±8.59) |

*Note.* $Z_{eu}$, euphotic depth; MLD, mixed layer depth; FWF, freshwater fraction; DOC, dissolved organic carbon; Chl-a, chlorophyll-a; BA, bacterial abundance; BP, bacterial production.

[a]BP:PP data were depth-integrated down to the MLD. Primary Production (PP) data from Lim et al. (2019).

## 3. Results and Discussion

### 3.1. Physico-Chemical Parameters

The FWF of the EG (range, 2.25%–2.44%; average, 2.40 ± 0.13%) displayed an intermediate range between those in the ASP (range, 1.81%–2.07%; average, 1.95 ± 0.13%) and WG (range, 2.71%–4.20%; average, 3.67 ± 0.83%) (Table 1). The warm mCDW intruding along the deep Dotson-Getz trough contacts the bottom of the ice shelf, thereby stimulating basal glacier melting in the EG (e.g., Wei et al., 2020). The vertically well-mixed water column with a deeper mixed-layer depth (MLD) (58 ± 34.9 m) at the EG (Figures 2c and Table 1) suggests that upwelling of mCDW containing buoyant basal glacier meltwater destabilizes the water column (S. Jacobs et al., 2012; Mankoff et al., 2012). In the WG, where the FWF was highest (Table 1), low potential temperatures ranging from −1.2 to −1.11°C (average, −1.16 ± 0.05°C) and salinity ranging between 33.4 and 33.5 psu (average, 33.4 ± 0.09 psu) were observed within MLD (Table 1). Satellite images showed that sea-ice covering >50% of the sea surface was distributed widely in the WG (Figure 1). These results indicate that sea ice–derived meltwater in the WG contributed to the high FWF. The salinity gradient caused by the addition of low-salinity meltwater discharged from the sea ice was responsible for the formation of a strong pycnocline at relatively depths within 30–50 m of the WG (Figure 2j). At the ASP site, the salinity ranged from 34.0 to 34.2 psu, and the temperature ranged from −1.64 to 0.28°C (Figures 2o and 2p). The water in the upper 100 m of the ASP exhibited the properties of AASW (S = <34.1 psu, T = −1.80 to >0°C) (Randall-Goodwin et al., 2015) that is fresher and warmer than the WW formed at 100–200 m due to sea-ice melting and surface heating by solar radiation.
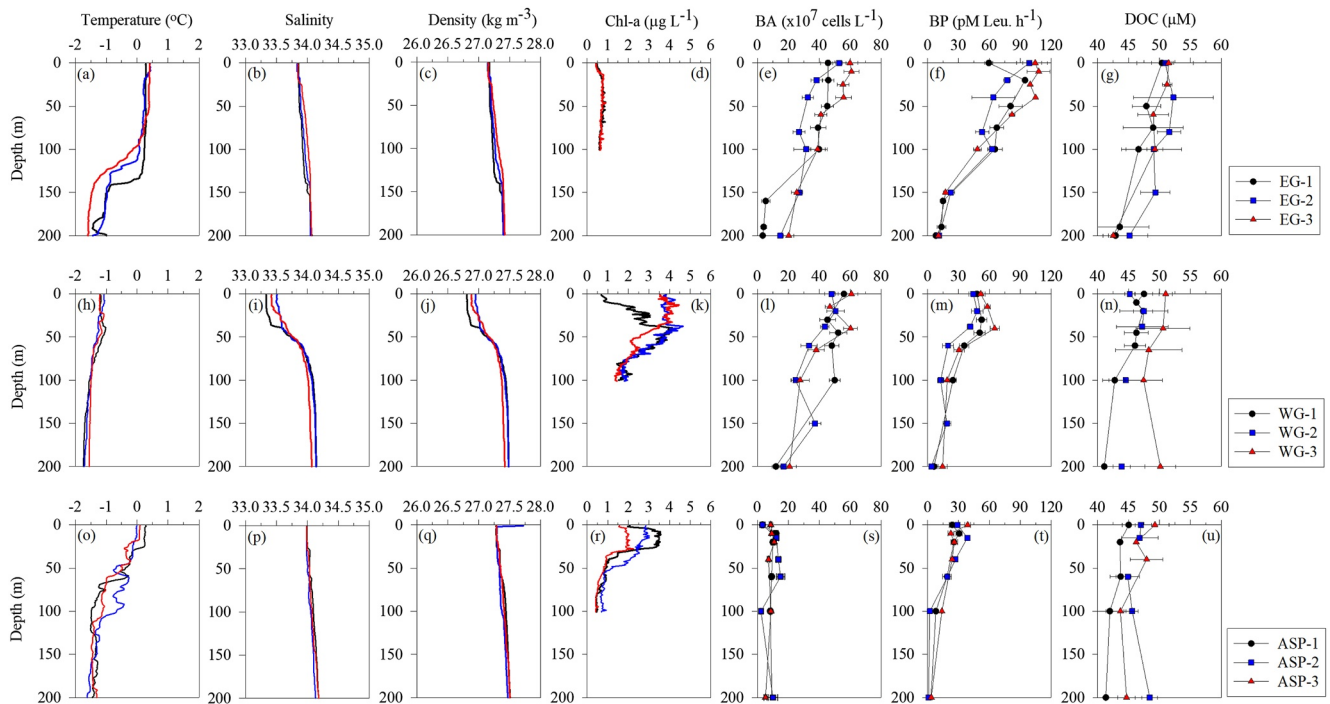
**Figure 2.** Vertical profiles of physico-chemical and microbiological parameters in the Amundsen Sea.

In the present study, the $NO_2^- + NO_3^-$ (11.75–31.98 μM; average, 22.74 ± 6.13 μM) and $PO_4^{3-}$ concentrations (0.94–2.20 μM; average, 1.67 ± 0.40 μM) (Table S1 in Supporting Information S1) appeared to be greater than the values reported in early summer from December 2013 to January 2014 ($NO_2^- + NO_3^-$, 3.4–34.6 μM; $PO_4^{3-}$, 0.8–2.3 μM) (B. K. Kim et al., 2018). The concentrations of DOC in the study area ranged from 41 to 52 μM (average, 47 ± 3 μM; Figures 2g, 2n and 2u), and were similar to those reported at MLD during the austral summer in the Ross Sea (average, 46 ± 2 to 56 ± 5 μM) (Carlson et al., 2000). The average DOC concentration at MLD was significantly higher in the EG (range, 49–52 μM; average, 51 ± 2 μM) than in the ASP (range, 44–48 μM; average, 46 ± 2 μM) and WG (range, 46–51; average, 48 ± 3 μM) (Table 1). Relatively higher DOC concentrations at the EG sites were likely associated with upwelling of buoyant basal glacier meltwater containing abundant DOC (average, 51 ± 2 μM) (Figure 2g and Figure S2b in Supporting Information S1).

### 3.2. Phytoplankton Biomass Associated With the Water Column Structure

Concentrations of Chl-a were higher in the WG (average, 3.11 ± 1.15 μg L$^{-1}$) than in the ASP (average, 2.26 ± 0.70 μg L$^{-1}$) and EG (average, 0.69 ± 0.07 μg L$^{-1}$) (Table 1). The significantly low Chl-a concentration in the EG (Kruskal−Wallis, $p < 0.01$) (Figure S2a in Supporting Information S1) was associated with the deep MLD, which resulted in a decrease in the residence time of phytoplankton in the euphotic layer. On the other hand, relatively high Chl-a concentrations in the WG were associated with the pycnocline formed by the salinity gradient in the shallow water column (30–50 m depth) due to the inflow of sea-ice meltwater (Figures 2i–2k), which increased the residence time of phytoplankton in the surface water column with sufficient light and nutrients to support high phytoplankton biomass. The Chl-a concentration in the ASP (average, 2.26 ± 0.70 μg L$^{-1}$) (Table 1 and Figure 2r) was lower than the values reported in December 2013 to January 2014 (average, 8.89 ± 1.11 μg L$^{-1}$) (Y. Lee et al., 2016) because phytoplankton blooms started further northeast of the ASP and the sampling sites at ASP along our sampling transect were not characterized by the blooms at the time of sampling (Fang et al., 2020).

### 3.3. Enhanced Bacterial Production Uncoupled With Phytoplankton in the Glacier Melting System

Unlike Chl-a, BP was significantly greater in the EG (range, 73.5–104 pM Leu. $h^{-1}$; average, 85.8 ± 16.1 pM Leu. $h^{-1}$) with deep mixed-layer depth (MLD) than in the WG (range, 46.4–54.9 pM Leu. $h^{-1}$; average, 50.6 ± 4.27 pM Leu. $h^{-1}$) and ASP (range, 26.8–29.9 pM Leu. $h^{-1}$; average, 27.8 ± 0.92 pM Leu. $h^{-1}$) (Kruskal–Wallis, $p < 0.01$; Figure S2d in Supporting Information S1). In Antarctic waters where terrestrial dissolved organic matter (DOM) input is negligible (Ducklow et al., 2007), DOM supplied by phytoplankton is a major source of carbon supporting heterotrophic bacterial growth (Ducklow et al., 2012; H. Kim and Ducklow, 2016; Morán et al., 2001; Ortega-Retuerta et al., 2008). Previous studies in the ASP revealed that BP is tightly coupled with phytoplankton biomass (Hyun et al., 2016; Williams et al., 2016). In the present study, the degree of coupling between BP and Chl-a varied according to spatial variations in oceanographic conditions (Figure 3a). BP was significantly correlated with Chl-a at the ASP sites ($r^2 = 0.47$, $n = 15$, $p < 0.01$) and WG sites ($r^2 = 0.27$, $n = 15$ $p < 0.05$). However, there was no significant correlation between BP and Chl-a in the EG ($p > 0.05$). In addition, BP at the EG site accounted for 48.9 ± 8.94% on average (range, 39.5%–49.8%) of primary production (PP) in MLD (Lim et al., 2019), which was higher than that estimated for the WG (average, 10.2 ± 4.98%; range, 7.11%–13.9%) and ASP (average, 9.15 ± 8.59%; range, 4.09%–19.1%) (Table 1).

Considering the median bacterial growth efficiency (BGE) of 11% (2%–28%) in the ASP (Williams et al., 2016), the unusually high BP:PP ratio (0.49 on average) in the EG implies that bacterial carbon demand (BCD = BP/ BGE; 105 ± 32.9 mmol C $m^{-2}$ $d^{-1}$; Table S2 in Supporting Information S1) to support metabolic activities (production and respiration) is greater than the organic carbon produced through PP (22.5 ± 11.78 mmol C $m^{-2}$ $d^{-1}$) (Lim et al., 2019). The positive relationship between BP and the FWF in the EG ($r^2 = 0.35$, $n = 16$, $p < 0.01$; Figure 3b), along with the absence of significant relationship between BP and Chl-a, strongly suggests that glacial meltwater rather than phytoplankton provides an extra source of DOC to support the high BP in the EG (Figure 4a). Indeed, the concentration of DOC was significantly greater in the EG, where warmer glacier meltwater upwells to the surface mixed layer, compared with the WG and ASP (Figure S2b in Supporting Information S1). Wadham et al. (2019) reported that the potential DOC flux for total organic carbon emissions from Antarctic subglacial meltwater is estimated to be approximately 0.17 Tg C $year^{-1}$, suggesting that significant amounts of fresh and labile DOC may be supplied to the surface mixed layer. Previous studies of the Greenland Ice Sheet have shown that DOC supplied through the export of meltwater is highly bioavailable and has a significant impact on microbial productivity and respiration (Bhatia et al., 2013; Lawson et al., 2014). Given that the Antarctic glacial ice shelves are considered a massive reservoir of organic carbon (ca. 5.5 Pg C) (Wadham et al., 2019), our results strongly imply that increases in glacial meltwater induced by global warming stimulate heterotrophic bacterial respiration that metabolizes DOM to $CO_2$, reducing the efficiency of carbon sequestration in Antarctic coastal waters.
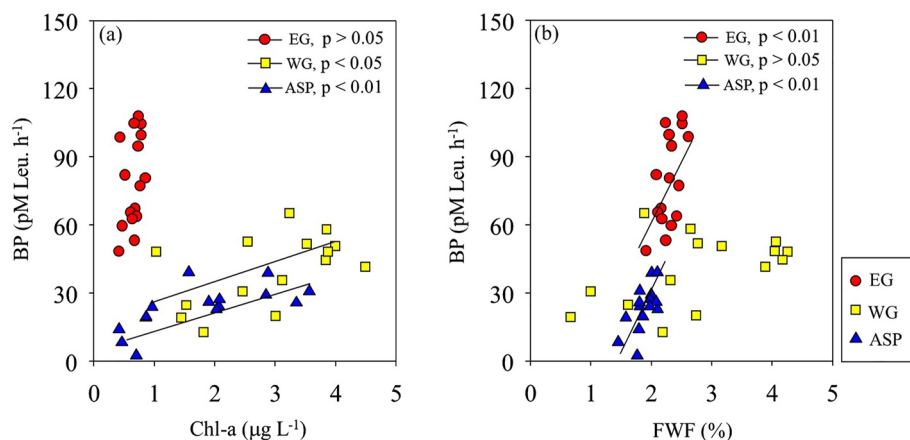


**Figure 3.** Relationships between bacterial production (BP) and chlorophyll-a (Chl-a) (a), and between BP and the freshwater fraction (b).
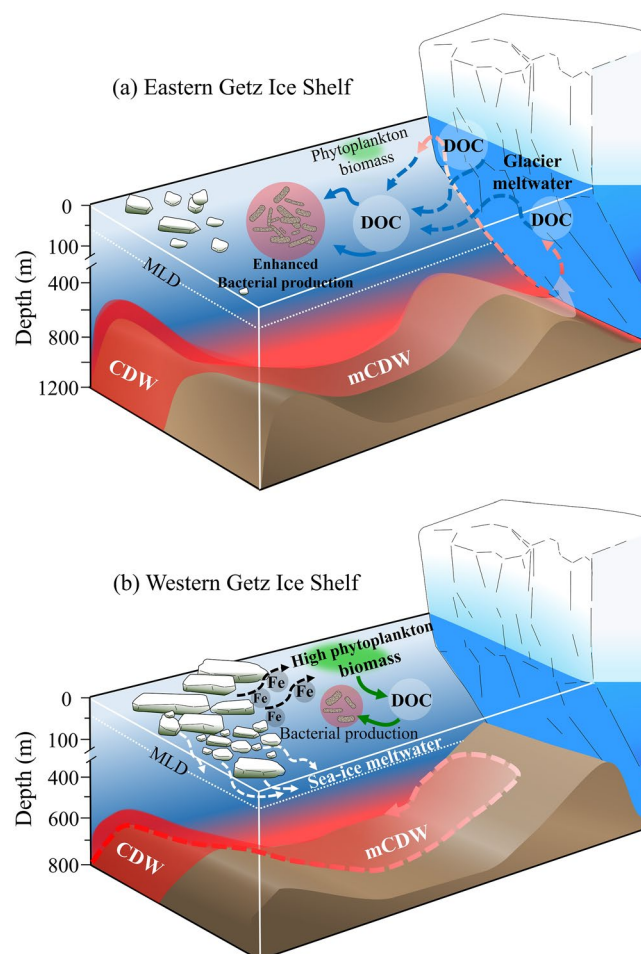
**Figure 4.** Schematic diagrams of bacterial responses to the dissolved organic carbon (DOC) derived from glacier meltwater in the eastern Getz (EG) Ice Shelf (panel a) and to the DOC derived from phytoplankton in the sea-ice melting system of the western Getz (WG) Ice Shelf (panel b) in the Amundsen Sea. Note that the EG region (glacier melting system) is characterized by an average deep-water depth of 817 m, which results in the direct contact of basal glacier with warmer modified circumpolar deep water (CDW), whereas the WG (sea-ice meltwater dominating system) features a relatively shallow water depth (566 m on average), which prevents warm CDW from melting the basal glacier. Consequently, the glacier-melting-dominated system (EG) features greatly enhanced bacterial production (BP) that is uncoupled with phytoplankton. In contrast, the sea-ice melting system (WG) a features high phytoplankton biomass resulting from shallow mixed-layer depth, and moderately enhanced BP coupled to phytoplankton.

### 3.4. Bacterial Production Coupled With Phytoplankton in the Sea-Ice Melting System

There was a positive relationship between BP and phytoplankton in the WG (Figure 3a), but no significant correlation with the FWF (Figure 3b). The tight coupling between BP and Chl-a in the WG indicates that iron-containing meltwater from sea ice stimulates phytoplankton growth in a relatively stratified surface water column (Grotti et al., 2005; Lannuzel et al., 2008, 2010; Wang et al., 2014), which provides DOC to support BP (Figure 4b). Similarly, the tight coupling between BP and Chl-a in the ASP is consistent with findings reported in previous studies showing that phytoplankton are a major source of DOC supporting BP (Figure 3a) (Hyun et al., 2016; Williams et al., 2016). The positive relationship between BP and FWF in the ASP indicates that BP is supported in part by DOC released from the surrounding sea-ice meltwater (Dinasquet et al., 2017; Sipler & Connelly, 2015) (Figure 3b). When sea-ice meltwater was experimentally added to sub-AASWs, the BP increased significantly and 63% of the DOC was consumed by bacteria (Kähler et al., 1997). These results suggest that DOC released from the surrounding sea-ice meltwater, together with phytoplankton, supports the metabolic activity of heterotrophic bacteria in the sea-ice melting system of the ASP (Figures 3a and 3b).

## 4. Summary

Given that the Antarctic glacial ice shelves retain a large amount of organic carbon (Wadham et al., 2019), the enhanced BP and high BP:PP ratio on the eastern GtzIS, where glacier meltwater upwells into the surface layer, have critical implications for the impact of warming-induced glacier meltwater on carbon cycles in Antarctic waters. An increase in glacial meltwater could stimulate heterotrophic bacterial respiration that metabolizes DOM to $CO_2$, ultimately weakening carbon sequestration in the Antarctic coastal waters. Our results raise additional questions about the glacial melting-induced supply of DOC and its effects on the net metabolic balance between heterotrophic and autotrophic processes in Antarctic coastal waters.

## Data Availability Statement

The primary production data in Table 1 are available from Lim et al. (2019). The physico-chemical and bacterial parameters used in this study were uploaded to the Korea Polar Data Center (https://dx.doi.org/doi:10.22663/KOPRI-KPDC-00001893.2). The data of the current manuscript is provided by Korea Polar Data Center.

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