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Effect of elevated pCO_2 on trace gas production during an ocean acidification mesocosm experiment

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Abstract. A mesocosm experiment was conducted in Wuyuan Bay (Xiamen), China, to investigate the effects of elevated pCO_2 on the phytoplankton species *Phaeodactylum tricornutum* (*P. tricornutum*), *Thalassiosira weissflogii* (*T. weissflogii*) and *Emiliania huxleyi* (*E. huxleyi*) and their production ability of dimethylsulfide (DMS), dimethylsulfoniopropionate (DMSP), as well as four halocarbon compounds, bromodichloromethane ($CHBrCl_2$), methyl bromide (CH_3Br), dibromomethane (CH_2Br_2) and iodomethane (CH_3I). Over a period of 5 weeks, *P. tricornuntum* outcompeted *T. weissflogii* and *E. huxleyi*, comprising more than 99 % of the final biomass. During the logarithmic growth phase (phase I), mean DMS concentration in high pCO_2 mesocosms (1000 µatm) was 28 % lower than that in low pCO_2 mesocosms (400 µatm). Elevated pCO_2 led to a delay in DMSP-consuming bacteria concentrations attached to *T. weissflogii* and *P. tricornutum* and finally resulted in the delay of DMS concentration in the high pCO_2 treatment. Unlike DMS, the elevated pCO_2 did not affect DMSP production ability of *T. weissflogii* or *P. tricornuntum* throughout the 5-week culture. A positive relationship was detected between CH_3I and *T. weissflogii* and *P. tricornuntum* during the experiment, and there was a 40 % reduction in mean CH_3I concentration in the high pCO_2 mesocosms. $CHBrCl_2$, CH_3Br, and CH_2Br_2 concentrations did not increase with elevated chlorophyll *a* (Chl *a*) concentrations compared with DMS(P) and CH_3I, and there were no major peaks both in the high pCO_2 or low pCO_2 mesocosms. In addition, no effect of elevated pCO_2 was identified for any of the three bromocarbons.

1 Introduction

Anthropogenic emissions have increased the fugacity of atmospheric carbon dioxide (pCO_2) from the pre-industrial value of 280 µatm to the present-day value of over 400 µatm, and these values will further increase to 800–1000 µatm by the end of this century (Gattuso et al., 2015). The dissolution of this excess CO_2 into the surface of the ocean directly affects the carbonate system and has lowered the pH by 0.1 units, from 8.21 to 8.10 over the last 250 years. Further decreases of 0.3–0.4 pH units are predicted by the end of this century (Doney et al., 2009; Orr et al., 2005; Gattuso et al., 2015), which is commonly referred to as ocean acidification. The physiological and ecological aspects of the phytoplankton response to this changing environment can potentially alter marine phytoplankton community composition, community biomass, and feedback to biogeochemical cycles (Boyd and Doney, 2002). These changes simultane-

ously have an impact on some volatile organic compounds produced by marine phytoplankton (Liss et al., 2014; Liu et al., 2017), including the climatically important trace gas dimethylsulfide (DMS) and a number of volatile halocarbon compounds.

DMS is the most important volatile sulfur compound produced from dimethylsulfoniopropionate (DMSP), which is ubiquitous in marine environments, mainly synthesized by marine microalgae (Stefels et al., 2007), a few angiosperms, some corals (Raina et al., 2016), and several heterotrophic bacteria (Curson et al., 2017) through complex biological interactions in marine ecosystems. Although it remains controversial, DMS and its by-products, such as methanesulfonic acid and non-sea-salt sulfate, are suspected of having a prominent part in climate feedback (Charlson et al., 1987; Quinn and Bates, 2011). The conversion of DMSP to DMS is facilitated by several enzymes, including DMSP lyase and acyl CoA transferase (Kirkwood et al., 2010; Todd et al., 2007); these enzymes are mainly found in phytoplankton, macroalgae, symbiodinium, bacteria and fungi (de Souza and Yoch, 1995; Stefels and Dijkhuizen, 1996; Steinke and Kirst, 1996; Chl *a* and Yoch, 1998; Yost and Mitchelmore, 2009). Several studies have shown a negative impact of decreasing pH on DMS-production capability (Hopkins et al., 2010; Avgoustidi et al., 2012; Archer et al., 2013; Webb et al., 2016), while others have found either no effect or a positive effect (Vogt et al., 2008; Hopkins and Archer, 2014). Several assumptions have been presented to explain these contrasting results and attributed the pH-induced variation in DMS-production capability to altered physiology of the algae cells or of bacterial DMSP degradation (Vogt et al., 2008; Hopkins et al., 2010, Avgoustidi et al., 2012; Archer et al., 2013; Hopkins and Archer, 2014; Webb et al., 2015).

Halocarbons also play a significant role in the global climate because they are linked to tropospheric and stratospheric ozone depletion and a synergistic effect of chlorine and bromine species has been reported, accounting for approximately 20 % of the polar stratospheric ozone depletion (Roy et al., 2011). In addition, iodocarbons can release atomic iodine quickly through photolysis in the atmospheric boundary layer and iodine atoms are very efficient in the catalytic removal of O_3, which governs the lifetime of many climate-relevant gases, including methane and DMS (Jenkins et al., 1991). Compared with DMS, limited attention was received about the effect of ocean acidification on halocarbon concentrations. Hopkins et al. (2010) and Webb et al. (2015) measured lower concentrations of several iodocarbons, while bromocarbons were unaffected by elevated pCO_2 in two acidification experiments. In addition, another mesocosm study did not elicit significant differences from any halocarbon compounds at up to 1400 µatm pCO_2 (Hopkins et al., 2013).

Taken together, the data indicate that the response of DMS and halocarbon release to elevated pCO_2 is complex and controversial. DMS and halocarbons play a significant role in the global climate and will perhaps act to a greater extent in the future. An intermediate step between laboratory and natural community field experiments was designed in this study to understand the response of the release of DMS and halocarbon to ocean acidification in Chinese coastal seas using isolates of non-axenic phytoplankton added to filtered natural water. We hypothesized that the response of DMS and halocarbon release to elevated pCO_2 in natural seawater can be better presented after minimizing the shifting composition of the natural phytoplankton and microbial communities.

2 Experimental method

2.1 Experimental setup

To investigate the response of DMS and halocarbon release to ocean acidification, a mesocosm experiment was carried out on a floating platform (set in seawater, about 150 m from the shore) at the Facility for Ocean Acidification Impacts Study of Xiamen University (FOANIC-XMU; 24.52° N, 117.18° E) (for full technical details of the mesocosms, see Liu et al., 2017). Six cylindrical transparent thermoplastic polyurethane bags with domes were deployed along the southern side of the platform. The width and depth of each mesocosm bag were 1.5 and 3 m, respectively. Filtered (0.01 µm ultrafiltration water purifier, MU801-4T, Midea, Guangdong, China) in situ seawater was pumped into the six bags simultaneously within 24 h. A known amount of NaCl solution was added to each bag to calculate the exact volume of seawater in the bags, according to a comparison of the salinity before and after adding salt (Czerny et al., 2013). The initial in situ pCO_2 was about 650 µatm. To set the low (400 µatm) and high pCO_2 (1000 µatm) levels, we added Na_2CO_3 solution and CO_2 saturated seawater to the mesocosm bags to alter total alkalinity and dissolved inorganic carbon (Gattuso et al., 2010; Riebesell et al., 2013). Subsequently, during the whole experimental process, air at the ambient (400 µatm) and elevated pCO_2 (1000 µatm) concentrations was continuously bubbled into the mesocosm bags using a CO_2 Enricher (CE-100B, Wuhan Ruihua Instrument & Equipment Ltd., Wuhan, China). Seawater taken from the coastal environment was first filtered to remove algae and their attached bacteria before usage in mesocosm bags. Bacterial abundance in the pre-filtered water was less than 10^3 cell mL^{-1}, which was 3 magnitudes lower than the bacterial abundance in the natural water and close to the detection limit of the flow cytometer. The trace gases, including DMS, bromodichloromethane ($CHBrCl_2$), methyl bromide (CH_3Br), dibromomethane (CH_2Br_2), and iodomethane (CH_3I) produced in the environment, did not affect the mesocosm trace gas concentrations after the bags were sealed.

2.2 Algal strains

Before being introduced into the mesocosms, the three phytoplankton species *Phaeodactylum tricornutum* (*P. tricornutum*), *Thalassiosira weissflogii* (*T. weissflogii*) and *Emiliania huxleyi* (*E. huxleyi*) were cultured in autoclaved, pre-filtered seawater from Wuyuan Bay at 16 °C (similar to the in situ temperature of Wuyuan Bay) without any addition of nutrients. Cultures were continuously aerated with filtered ambient air containing 400 µatm of CO_2 within plant chambers (HP1000G-D, Wuhan Ruihua Instrument & Equipment, China) at a constant bubbling rate of 300 mL min^{-1}. The culture medium was renewed every 24 h to maintain the cells of each phytoplankton species in exponential growth. When the experiment began, these three phytoplankton species were inoculated into the mesocosm bags, with an initial diatom/coccolithophorid cell ratio of 1 : 1. The initial concentrations of *P. tricornuntum*, *T. weissflogii*, and *E. huxleyi* inoculated into the mesocosm were 10, 10, and 20 cells mL^{-1}, respectively. *P. tricornuntum* and *T. weissflogii* were obtained from the Center for Collections of Marine Bacteria and Phytoplankton of the State Key Laboratory of Marine Environmental Science (Xiamen University). *P. tricornuntum* was originally isolated from the South China Sea in 2004 and *T. weissflogii* was isolated from Daya Bay in the coastal South China Sea. *E. huxleyi* was originally isolated in 1992 from the field station of the University of Bergen (Raunefjorden; 60°18′ N, 05°15′ E).

2.3 Sampling for DMS(P) and halocarbons

DMS(P) and halocarbon samples were taken from the above-mentioned mesocosm bags at 09:00; then all collected samples were transported into a dark cool box back to the laboratory onshore for analysis within 1 h. For the DMS analysis, a 2 mL sample was gently filtered through a 25 mm GF/F (glass fiber) filter and transferred to a purge and trap system linked to a Shimadzu GC-2014 gas chromatograph (Tokyo, Japan) equipped with a glass column packed with 10 % DEGS on Chromosorb W-AW-DMCS (3 m × 3 mm) and a flame photometric detector (Zhang et al., 2014). For total DMSP analysis, a 10 mL water sample was fixed using 50 µL of 50 % H_2SO_4 and sealed (Kiene and Slezak, 2006). After > 1-day preservation, DMSP samples were hydrolyzed for 24 h with a pellet of KOH (final pH > 13) to fully convert DMSP to DMS. Then, 2 mL of the hydrolyzed sample was carefully transferred to the purge and trap system mentioned above for extraction of DMS. For halocarbons, a 100 mL sample was purged at 40 °C with pure nitrogen at a flow rate of 100 mL min^{-1} for 12 min using another purge and trap system coupled to an Agilent 6890 gas chromatograph (Agilent Technologies, Palo Alto, CA, USA) equipped with an electron capture detector (ECD) as well as a 60 m DB-624 capillary column (0.53 mm ID; film thickness, 3 µm) (Yang et al., 2010). The analytical precision for duplicate measurements of DMS(P) and halocarbons was > 10 %.

2.4 Measurements of chlorophyll *a*

Chlorophyll *a* (Chl *a*) was measured in water samples (200–1000 mL) collected every 2 days at 09:00 by filtering onto Whatman GF/F filters (25 mm). The filters were placed in 5 mL 100 % methanol overnight at 4 °C and centrifuged at 5000 g for 10 min. The absorbance of the supernatant (2.5 mL) was measured from 250 to 800 nm using a scanning spectrophotometer (DU 800, Beckman Coulter Inc., Brea, CA, USA). Chl *a* concentration was calculated according to the equation reported by Porra (2002).

2.5 Enumeration of DMSP-consuming bacteria

The number of DMSP-consuming bacteria in the mesocosms was estimated using the most probable number methodology. The medium consisted of a mixture (1 : 1 v/v) of sterile artificial seawater and a mineral medium (Visscher et al., 1991), 3 mL of which was dispensed into 6 mL test tubes, which were closed by an over-sized cap, allowing gas exchange. Triplicate dilution series were set up. All test tubes contained 1 mmol L^{-1} DMSP as the sole organic carbon source and were kept at 30 °C in the dark. After 2 weeks, the presence/absence of bacteria in the tubes was verified by DAPI staining (Porter and Feig, 1980). Three tubes containing 3 mL ASW without substrate were used as controls.

2.6 Statistical analysis

One-way analysis of variance (ANOVA), Tukey's test, and the two-sample t test were carried out to demonstrate the differences between treatments. A p value < 0.05 was considered significant. Relationships between DMS(P), halocarbons and a range of other parameters were detected using Pearson's correlation analysis via SPSS 22.0 for Windows (SPSS Inc., Chicago, IL, USA).

3 Results and discussion

3.1 Temporal changes in pH, Chl *a*, *P. tricornuntum*, *T. weissflogii*, and *E. huxleyi* during the experiment

During the experiment, the seawater in each mesocosm was well mixed, and the temperature and salinity remained stable, with means of 16 °C and 29, respectively, in all mesocosm bags. We observed significant differences in pH levels between the two CO_2 treatments on days 0–11, but the differences disappeared with subsequent phytoplankton growth (Fig. 1). The phytoplankton growth process was divided into three phases in terms of variations in Chl *a* concentrations in the mesocosm experiments as described in Liu et al. (2017): (i) the logarithmic growth phase (phase I, days 0–13), (ii) a

Table 1. Dissolved inorganic carbon (DIC), pH, pCO_2 and nutrient concentrations in the mesocosm experiments. "–" means that the values were below the detection limit.

		pH	DIC ($\mu mol\,kg^{-1}$)	pCO_2 (μatm)	$NO_3^- + NO_2^-$ ($\mu mol\,L^{-1}$)	NH_4^+ ($\mu mol\,L^{-1}$)	PO_4^{3-} ($\mu mol\,L^{-1}$)	SiO_3^{2-} ($\mu mol\,L^{-1}$)
Day 0	Low pCO_2	8.0 ± 0.1	2181 ± 29	1170–1284	52–56	19–23	2.6 ± 0.2	38–40
	High pCO_2	7.5 ± 0.1	2333 ± 34	340–413	51–55	19–23	2.5 ± 0.2	38–39
Phase I	Low pCO_2	7.9–8.4	1825–2178	373–888	15–52	1.6–20	0.5–2.6	31–38
	High pCO_2	7.4–8.2	2029–2338	1295–1396	47–54	0.2–21	0.7–2.5	34–39
Phase II	Low pCO_2	8.4–8.5	1706–1745	46–749	−15.9	–	0.1–0.5	10–24
	High pCO_2	8.4–8.6	1740–1891	59–1164	1.1–25	–	−0.1	29–30
Phase III	Low pCO_2	8.5–8.8	1673–1706	30–43	–	–	–	10–16
	High pCO_2	8.6–8.7	1616–1740	34–110	–	–	−0.3	24–25

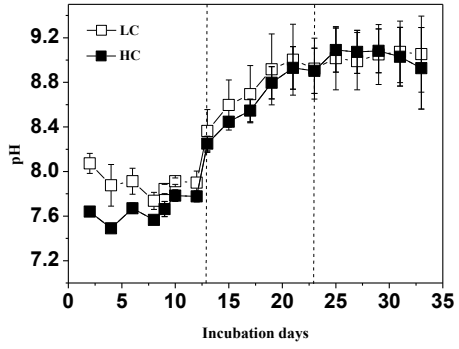

Figure 1. Temporal development of pH in the high pCO_2 (1000 µatm, solid squares) and low pCO_2 (400 µatm, white squares) mesocosms. Data are mean ± SD, $n = 3$ (triplicate independent mesocosm bags) (Origin 8.0).

plateau phase (phase II, days 13–23, bloom period), and (iii) a secondary plateau phase (phase III, days 23–33) attained after a decline in biomass from a maximum in phase II. The initial chemical parameters of the mesocosm experiment are shown in Table 1. The initial mean dissolved nitrate (including NO_3^- and NO_2^-), NH_4^+, PO_4^{3-} and silicate (SiO_3^{2-}) concentrations were 54, 20, 2.6 and 41 µmol L^{-1}, respectively, for the low pCO_2 treatment and 52, 21, 2.4 and 38 µmol L^{-1}, respectively, for the high pCO_2 treatment. The nutrient concentrations (NO_3^-, NO_2^-, NH_4^+ and phosphate) during phase I were consumed rapidly and their concentrations were below or close to the detection limit during phase II (Table 1). SiO_3^{2-} was detectable during the entire experimental period, and was unlikely to be a limiting factor for phytoplankton growth during the experiment. In addition, although dissolved inorganic nitrogen (NH_4^+, NO_3^-, and NO_2^-) and phosphate were depleted, Chl *a* concentration in both treatments (biomass dominated by *P. tricornuntum*) remained constant over days 12–22, and then declined over subsequent days. *T. weissflogii* was found throughout the entire period in each bag, but the maximum concentration was 8120 cells mL^{-1}, which was far less than the concentration of *P. tricornutum* with a maximum density of about 1.5 million cells mL^{-1} (Liu et al., 2017). It is possible that *P. tricornutum* outcompeted *T. weissflogii* because of its higher surface-to-volume ratio and/or species-specific physiology, which would enhance the efficiency of nutrient uptake and related metabolism (Alessandrade et al., 2007). *E. huxleyi* was only found in phase I and its maximal concentration reached 310 cells mL^{-1} according to the results of Liu et al. (2017). Previous studies have reported that the maximum specific growth rate of *T. weissflogii* and *P. tricornutum* is about 1.2 d^{-1} (Li et al., 2014; Sugie and Yoshimura, 2016), while that of *E. huxleyi* is about 0.8 d^{-1} (Xing et al., 2015). This might be the main reason why diatoms overwhelmingly outcompeted the coccolithophores during this experiment.

3.2 Impact of elevated pCO_2 on DMS and DMSP production

DMSP concentrations in the high pCO_2 and low pCO_2 treatments increased significantly along with the increase in Chl *a* concentrations and algal cells, and remained relatively constant over the following days. A significant positive relationship was observed between DMSP and phytoplankton in the experiment ($r = 0.961$, $p < 0.01$ for *P. tricornuntum*, $r = 0.617$, $p < 0.01$ for *T. weissflogii* in the low pCO_2 treatment, Table 2; $r = 0.954$, $p < 0.01$ for *P. tricornuntum*, $r = 0.743$, $p < 0.01$ for *T. weissflogii* in the high pCO_2 treatment, Table 3). DMS was maintained at a low level during phase I (mean of 1.03 nmol L^{-1} in the low pCO_2 and 0.74 nmol L^{-1} in the high pCO_2 treatments, respectively) compared with DMSP. DMS concentrations began to increase rapidly on day 15, peaked on day 25 in the low pCO_2 treatment (112.1 nmol L^{-1}) and on day 29 in the high pCO_2 treatment (101.9 nmol L^{-1}), respectively, and then decreased in the following days. A moderate positive relationship was observed between DMS and *P. tricornuntum* ($r = 0.560$, $p < 0.05$ in the low pCO_2 treatment; $r = 0.635$, $p < 0.01$ in the high pCO_2 treatment), while no relationship was observed be-

Table 2. Correlation between dimethylsulfide (DMS), dimethylsulfoniopropionate (DMSP), chlorophyll *a* (Chl *a*), bromodichloromethane ($CHBrCl_2$), methyl bromide (CH_3Br), dibromomethane (CH_2Br_2), iodomethane (CH_3I), DMSP-consuming bacteria, *Thalassiosira weissflogii* (*T. weissflogii*) and *Phaeodactylum tricornutum* (*P. tricornutum*) concentrations in the low pCO_2 treatments.

	DMS	DMSP	Chl *a*	$CHBrCl_2$	CH_3Br	CH_2Br_2	CH_3I	DMSP-consuming bacteria	*T. weissflogii*	*P. tricornutum*
DMS	1									
DMSP	0.701**	1								
Chl *a*	0.597**	0.792**	1							
$CHBrCl_2$	0.526	0.280	0.559	1						
CH_3Br	−0.413	−0.230	0.196	0.313	1					
CH_2Br_2	0.310	0.180	0.001	−0.136	−0.308	1				
CH_3I	0.694**	0.654**	0.717**	0.596*	−0.151	0.129	1			
DMSP-consuming bacteria	0.643**	0.520*	0.522*	0.394	−0.268	−0.038	0.762**	1		
T. weissflogii	0.410	0.617**	0.899**	0.301	0.322	0.028	0.680**	0.399	1	
P. tricornutum	0.560*	0.961**	0.821**	0.528	−0.032	0.162	0.588**	0.334	0.685**	1

* Correlation is significant at the 0.05 level (two-tailed). ** Correlation is significant at the 0.01 level (two-tailed).

Table 3. Correlation between dimethylsulfide (DMS), dimethylsulfoniopropionate (DMSP), chlorophyll a (Chl *a*), bromodichloromethane ($CHBrCl_2$), methyl bromide (CH_3Br), dibromomethane (CH_2Br_2), iodomethane (CH_3I), DMSP-consuming bacteria, *Thalassiosira weissflogii* (*T. weissflogii*) and *Phaeodactylum tricornutum* (*P. tricornutum*) concentrations in the high pCO_2 treatments.

	DMS	DMSP	Chl *a*	$CHBrCl_2$	CH_3Br	CH_2Br_2	CH_3I	DMSP-consuming bacteria	*T. weissflogii*	*P. tricornutum*
DMS	1									
DMSP	0.752**	1								
Chl *a*	0.318*	0.738**	1							
$CHBrCl_2$	0.324	0.094	0.326	1						
CH_3Br	−0.410	−0.349	0.065	0.076	1					
CH_2Br_2	0.540*	0.352	0.142	0.233	−0.377	1				
CH_3I	0.694**	0.816**	0.741**	0.690*	−0.407	0.316	1			
DMSP-consuming bacteria	0.544*	0.522	0.549*	0.532	−0.311	0.368	0.851*	1		
T. weissflogii	0.355	0.743**	0.930**	0.304	0.076	0.233	0.690**	0.567	1	
P. tricornutum	0.635**	0.954**	0.803**	0.143	−0.257	0.267	0.834**	0.559	0.820**	1

* Correlation is significant at the 0.05 level (two-tailed). ** Correlation is significant at the 0.01 level (two-tailed).

tween DMS and *T. weissflogii* (Tables 2 and 3) during the experiment. Similar to DMS, DMSP-consuming bacteria also maintained a low level during phase I (mean of 0.57×10^6 and 0.40×10^6 cells mL^{-1} in the low pCO_2 and high pCO_2 treatments, respectively). DMSP-consuming bacterial concentrations peaked on days 19 (11.65×10^6 cells mL^{-1}) and 21 (10.70×10^6 cells mL^{-1}) in the low pCO_2 and high pCO_2 treatments, respectively.

In this study, no difference in mean DMSP concentrations was observed between the two treatments, indicating that elevated pCO_2 had no significant influence on DMSP production in *P. tricornuntum* and *T. weissflogii*. However, significant reductions in mean DMS concentration (28 %) and DMSP-consuming bacteria (29 %) were detected during phase I in the high pCO_2 treatment compared with those in the low pCO_2 treatment, indicating that elevated pCO_2 inhibited DMSP-consuming bacteria and DMS production during the logarithmic growth phase. In addition, the peak DMS concentration in the high pCO_2 treatment was delayed 4 days relative to that in the low pCO_2 treatment during phase II (Fig. 2a). This result has been observed in previous mesocosm experiments and it was attributed to small-scale shifts in community composition and succession (Vogt et al., 2008; Webb et al., 2016). However, this phenomenon during the present study can be explained in another straightforward way. Previous studies have shown that marine bacteria play a key role in DMS production, and that the efficiency of bacteria converting DMSP to DMS may vary from 2 to 100 % depending on the nutrient status of the bacteria and the quantity of dissolved organic matter (Simó et al., 2002, 2009; Kiene et al., 1999, 2000). In addition, a significant positive relationship was observed between DMS and DMSP-consuming bacteria ($r = 0.643$, $p < 0.01$ in the low pCO_2 treatment; $r = 0.544$, $p < 0.01$ in the high pCO_2 treatment) during this experiment. All of these observations point to the importance of bacteria in DMS and DMSP dynamics. During the present mesocosm experiment, DMSP concentrations in the low pCO_2 treatment decreased slightly on day 23, while the slight decrease appeared on day 29 in the high pCO_2 treatment (Fig. 2b). In addition, the time that the DMSP concentration began to decrease was very close to the time when the highest DMS concentration occurred in both treatments. Similar to DMS, DMSP-consuming bacteria were also delayed in the

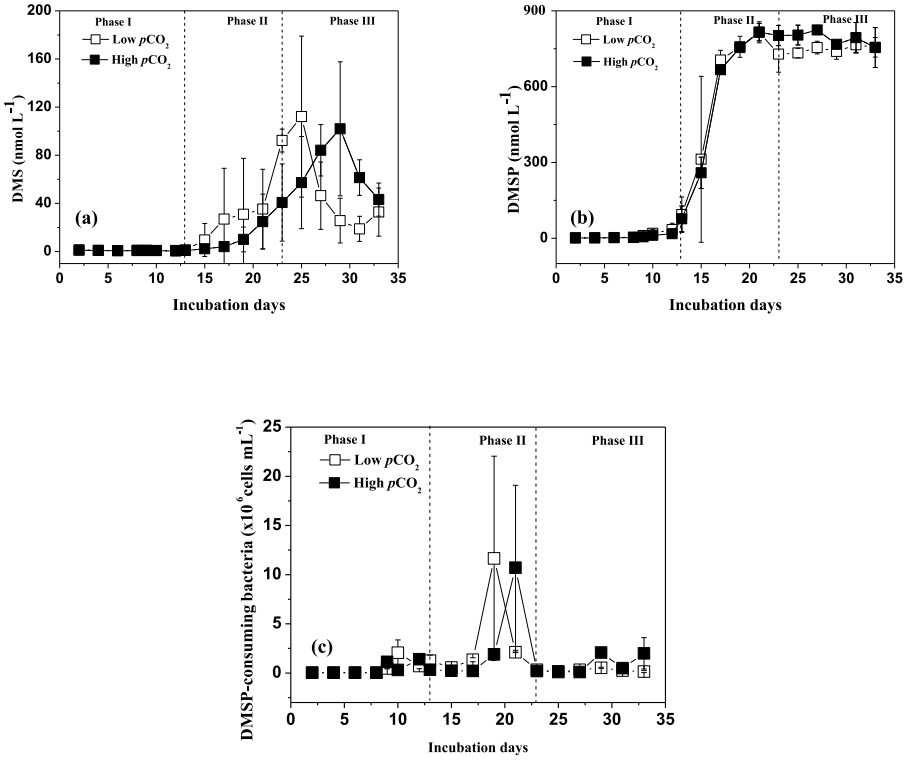

Figure 2. Temporal development in dimethylsulfide (DMS), dimethylsulfoniopropionate (DMSP) and DMSP-consuming bacteria concentrations in the high pCO_2 (1000 µatm, black squares) and low pCO_2 (400 µatm, white squares) mesocosms. Data are mean ± SD, $n = 3$ (triplicate independent mesocosm bags).

high pCO_2 mesocosm compared to those in the low pCO_2 mesocosm (Fig. 2c). Taken together, we inferred that the elevated pCO_2 first delayed growth of DMSP-consuming bacteria; then the delayed DMSP-consuming bacteria postponed the DMSP degradation process, and eventually delayed the DMS concentration in the high pCO_2 treatment. In addition, considering that algae and bacteria in natural seawater were removed through a filtering process before the experiment (Huang et al., 2018), we further concluded that the elevated pCO_2 controlled DMS concentrations mainly by affecting DMSP-consuming bacteria attached to *T. weissflogii* and *P. tricornuntum*.

3.3 Impact of elevated pCO_2 on halocarbon compounds

The temporal development in $CHBrCl_2$, CH_3Br, and CH_2Br_2 concentrations is shown in Fig. 3a, b, and c, respectively. The temporal changes in their concentrations were substantially different from those in DMS, DMSP, *P. tricornuntum* and *T. weissflogii*. The mean concentrations of $CHBrCl_2$, CH_3Br, and CH_2Br_2 for the entire experiment were 8.58, 7.85, and 5.13 pmol L^{-1} in the low pCO_2 treatment and 8.81, 9.73, and 6.27 pmol L^{-1} in the high pCO_2 treatment. The concentrations of $CHBrCl_2$, CH_3Br, and CH_2Br_2 did not increase with the Chl *a* concentration compared with those of DMS and DMSP, and no major peaks were detected in the mesocosms. In addition, no effect of elevated pCO_2 was identified for any of the three bromocarbons, which compared well with previous mesocosm findings (Hopkins et al., 2010, 2013; Webb et al., 2016). No clear correlation was observed between the three bromocarbons and any of the measured algal groups (Tables 2 and 3), indicating that *P. tricornuntum* and *T. weissflogii* did not primarily release these three bromocarbons during the mesocosm experiment. Previous studies reported that large-sized cyanobacteria, such as *Aphanizomenon flos-aquae*, could produce bromocarbons (Karlsson et al., 2008). Significant correlations between the abundance of cyanobacteria and several bromocarbons have been reported in the Arabian Sea (Roy et al., 2011). However, the filtration procedure led to the loss of cyanobacteria in the mesocosms and finally resulted in low bromocarbon concentrations during the experiment, although *P. tricornuntum* and *T. weissflogii* abundances were high.

The temporal dynamics of CH_3I in the high pCO_2 and low pCO_2 treatments are shown in Fig. 3d. The CH_3I concentrations in the low pCO_2 treatment varied from 0.38 to 12.61 pmol L^{-1}, with a mean of 4.76 pmol L^{-1}. The CH_3I concentrations in the high pCO_2 treatment ranged between 0.44 and 8.78 pmol L^{-1}, with a mean of 2.88 pmol L^{-1}.

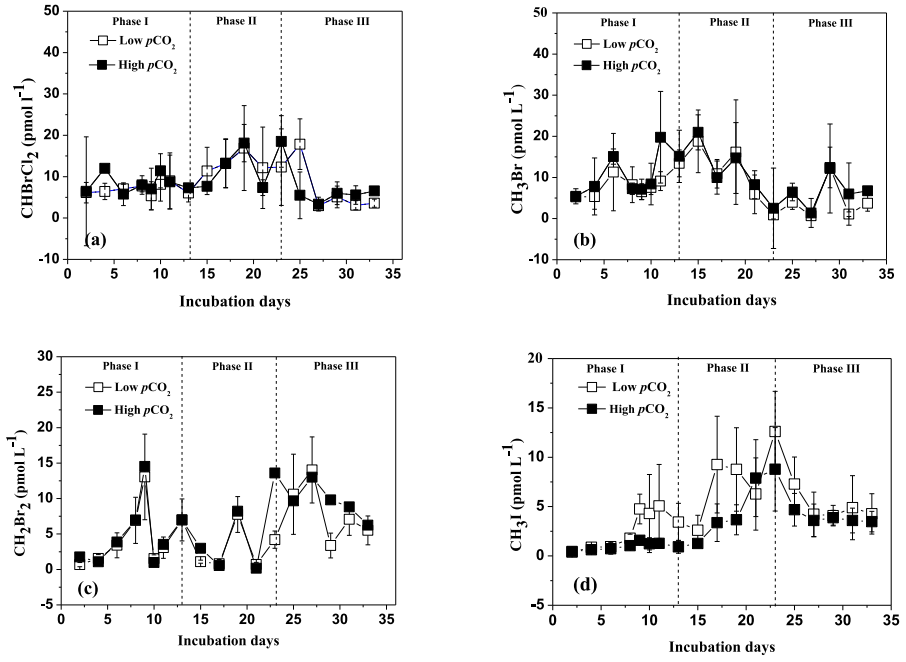

Figure 3. Temporal development in bromodichloromethane ($CHBrCl_2$), methyl bromide (CH_3Br), dibromomethane (CH_2Br_2), and iodomethane (CH_3I) concentrations in the high pCO_2 (1000 µatm, black squares) and low pCO_2 (400 µatm, white squares) mesocosms. Data are mean ± SD, $n = 3$ (triplicate independent mesocosm bags).

The maximum CH_3I concentrations in the high $pCO_2$and low pCO_2 treatments were both observed on day 23. The range of CH_3I concentrations during this experiment was similar to that measured in the mesocosm experiment (< 1–10 pmol L^{-1}) in Kongsfjorden conducted by Hopkins et al. (2013). In addition, the mean CH_3I concentration in the low pCO_2 treatment was similar to that measured in the East China Sea, with an average of 5.34 pmol L^{-1} in winter and 5.74 pmol L^{-1} in summer (Yuan et al., 2016). Meanwhile, a positive relationship was detected between CH_3I and Chl *a*, *P. tricornuntum* and *T. weissflogii* ($r = 0.588$, $p < 0.01$ in the low pCO_2 treatment; $r = 0.834$, $p < 0.01$ in the low pCO_2 treatment for *P. tricornuntum*; $r = 0.680$, $p < 0.01$ in the low pCO_2 treatment; $r = 0.690$, $p < 0.01$ in the high pCO_2 treatment for *Thalassiosira weissflogii*; $r = 0.717$, $p < 0.01$ in the low pCO_2 treatment; $r = 0.741$, $p < 0.01$ in the high pCO_2 treatment for Chl *a*). This result agrees with previous mesocosm (Hopkins et al., 2013) and laboratory experiments (Hughes et al., 2013; Manley and De La Cuesta, 1997) identifying diatoms as significant producers of CH_3I. Moreover, similar to DMS, the maximum CH_3I concentration also occurred after the maxima of *P. tricornuntum* and *T. weissflogii*, at about 4 days (Fig. 3d). This result was similar to the conclusions reported by Hopkins et al. (2010) and Wingenter et al. (2007) during two mesocosm experiments conducted in Norway. Their results confirmed that iodocarbon gases generally occur after the Chl *a* maxima. Furthermore, the mean CH_3I concentration measured in the high pCO_2 treatment was significantly lower (40 %) than that measured in the low pCO_2 treatment during the mesocosm experiment. This result is in accordance with Hopkins et al. (2010) and Webb et al. (2015), who also reported that elevated pCO_2 leads to a reduction in iodocarbon concentrations, but is in contrast to the findings of Hopkins et al. (2013) and Webb et al. (2016), who showed that elevated pCO_2 does not significantly affect the iodocarbon concentrations in the mesocosms. Considering that the phytoplankton species did not show significant differences in the high pCO_2 and low pCO_2 treatments during the experiment, this reduction in the high pCO_2 treatment was likely not caused by phytoplankton. Apart from direct biological production via methyl transferase enzyme activity by both phytoplankton and bacteria (Amachi et al., 2001), CH_3I is produced from the breakdown of higher molecular weight iodine-containing organic matter (Fenical, 1982) through photochemical reactions between organic matter and light (Richter and Wallace, 2004). Both bacterial methyl transferase enzyme activity and photochemical reaction could be responsible for the reduction of CH_3I concentrations in the high pCO_2 treatment, but further experiments are needed to verify this result.

4 Conclusions

In this study, the effects of increased levels of pCO_2 on marine DMS(P) and halocarbon release were studied in a controlled mesocosm facility. During the logarithmic growth phase, the elevated pCO_2 led to a reduction in mean DMSP-consuming bacteria (29 %) and DMS concentration (28 %) compared with those in the low pCO_2 treatment. In addition, a 4-day delay in DMS concentration was observed in the high pCO_2 treatment due to the effect of elevated pCO_2, and we attribute this delay in DMS concentration to the DMSP-consuming bacteria attached to *P. tricornuntum* and *T. weissflogii*. Due to the loss of main bromocarbon-producing species affected by the filtration procedure, three bromocarbon compounds measured in this study were not correlated with *P. tricornuntum* and *T. weissflogii*, and Chl *a*. In addition, elevated pCO_2 had no effect on any of the three bromocarbons. The temporal dynamics of CH_3I, combined with strong correlations with *P. tricornuntum* and *T. weissflogii*, and Chl *a*, indicate that *P. tricornuntum* and *T. weissflogii* play a critical role in controlling CH_3I concentrations. In addition, the production of CH_3I was sensitive to pCO_2, with a significant increase in CH_3I concentration at higher pCO_2. However, without additional empirical measurements, it is unclear whether this decrease was caused by bacterial methyl transferase enzyme activity or by photochemical degradation at higher pCO_2.

Data availability. The data in this research can be accessed by sending an e-mail to gpyang@mail.ouc.edu.cn.

Author contributions. GPY and KSG designed the experiments. SHZ, JY and QYD carried out the experiments and prepared the manuscript. HHZ and DWP revised the paper. SHZ and JY contributed equally to this work.

Competing interests. The authors declare that they have no conflict of interest.

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