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Effects of ocean acidification on pelagic carbon fluxes in a mesocosm experiment

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Abstract. About a quarter of anthropogenic CO2 emissions are currently taken up by the oceans, decreasing seawater pH. We performed a mesocosm experiment in the Baltic Sea in order to investigate the consequences of increasing CO2 levels on pelagic carbon fluxes. A gradient of different CO2 scenarios, ranging from ambient (∼370 µatm) to high (∼1200 µatm), were set up in mesocosm bags (∼55 m3). We determined standing stocks and temporal changes of total particulate carbon (TPC), dissolved organic carbon (DOC), dissolved inorganic carbon (DIC), and particulate organic carbon (POC) of specific plankton groups. We also measured carbon flux via CO2 exchange with the atmosphere and sedimentation (export), and biological rate measurements of primary production, bacterial production, and total respiration. The experiment lasted for 44 days and was divided into three different phases (I: t0–t16; II: t17–t30; III: t31–t43). Pools of TPC, DOC, and DIC were approximately 420, 7200, and 25 200 mmol C m−2 at the start of the experiment, and the initial CO2 additions increased the DIC pool by ∼7% in the highest CO2 treatment. Overall, there was a decrease in TPC and increase of DOC over the course of the experiment. The decrease in TPC was lower, and increase in DOC higher, in treatments with added CO2. During phase I the estimated gross primary production (GPP) was ∼100 mmol C m−2 day−1, from which 75–95% was respired, ∼1% ended up in the TPC (including export), and 5–25% was added to the DOC pool. During phase II, the respiration loss increased to ∼100% of GPP at the ambient CO2 concentration, whereas respiration was lower (85–95% of GPP) in the highest CO2 treatment. Bacterial production was ∼30% lower, on average, at the highest CO2 concentration than in the controls during phases II and III. This resulted in a higher accumulation of DOC and lower reduction in the TPC pool in the elevated CO2 treatments at the end of phase II extending throughout phase III. The “extra” organic carbon at high CO2 remained fixed in an increasing biomass of small-sized plankton and in the DOC pool, and did not transfer into large, sinking aggregates. Our re-
results revealed a clear effect of increasing CO₂ on the carbon budget and mineralization, in particular under nutrient limited conditions. Lower carbon loss processes (respiration and bacterial remineralization) at elevated CO₂ levels resulted in higher TPC and DOC pools than ambient CO₂ concentration. These results highlight the importance of addressing not only net changes in carbon standing stocks but also carbon fluxes and budgets to better disentangle the effects of ocean acidifica-

1 Introduction

Combustion of fossil fuels and change in land use have caused increasing atmospheric concentrations of carbon dioxide (CO₂). Ca. 25 % of the anthropogenic CO₂ is absorbed by the oceans, thereby decreasing surface water pH, a process termed ocean acidification (Le Quéré et al., 2009). Ocean acidification and its alterations of aquatic ecosystems have received considerable attention during the past decade, but there are many open questions, in particular related to consequences for plankton-mediated carbon fluxes.

Some studies on ocean acidification have reported increased carbon fixation (Egge et al., 2009; Engel et al., 2013), bacterial production (BP; Grossart et al., 2006), and bacterial degradation of polysaccharides (Piontek et al., 2010) at enhanced CO₂ levels, with potential consequences for carbon fluxes within pelagic ecosystems and export to the deep ocean, i.e., the biological carbon pump. Increasing carbon fixation in a high-CO₂ environment can translate into an enhanced sequestration of carbon (Riebesell et al., 2007), but this depends on numerous environmental factors, including phytoplankton community composition, aggregate formation, and nutrient availability. For example, if the community shifts towards smaller cell sizes and/or enhanced cycling of organic matter carbon, export from the upper water layers may decrease (Czerny et al., 2013a).

The effect of ocean acidification has mostly been studied in marine ecosystems under high phytoplankton biomass. Brackish water has lower buffering capacity than ocean water, and the pH fluctuates more. The limited number of studies of ocean acidification in brackish water and indications that ocean acidification effects are greatest under nutrient limitation (De Kluijver et al., 2010) motivated this mesocosm study in the Baltic Sea during low-nutrient summer months.

The Baltic Sea is functionally much like a large estuary, and budgets to better disentangle the effects of ocean acidifica-

K. Spilling et al.: Modified pelagic carbon fluxes

2 Materials and methods

2.1 Experimental setup

Six Kiel Off-Shore Mesocosms for Ocean Simulations (KOSMOS; with a volume of ca. 55 m³) were moored at Storfjärden, on the south west coast of Finland (59°51.5′ N; 23°15.5′ E) on 12 June 2012 (nine KOSMOS units were originally deployed, but three were lost due to leaks). A more detailed description of the setup can be found in Paul et al. (2015). The mesocosms extended from the surface down to 19 m depth and had a conical bottom end, which enabled quantitative collection of the settling material. Different CO₂ levels in the bags were achieved by adding filtered (50 µm), CO₂-saturated seawater. The CO₂-enriched water was evenly distributed over the upper 17 m of the water columns and added in four consecutive time steps (t0–t3). Two controls and four treatments were used, and for the controls, filtered seawater (without additional CO₂ enrichment) was added. The CO₂ fugacity gradient after all additions ranged from ambient (average throughout the experiment: ∼370 µatm CO₂) in the two control mesocosms (M1 and M5) up to ∼1200 µatm CO₂ in the highest treatment (M8). We used the average CO₂ throughout this experiment to denote the different treatments: 365 (M1), 368 (M5), 497 (M7), 821 (M6), 1007 (M3), and 1231 (M8) µatm CO₂. On t15, additional CO₂-saturated seawater was added to the upper 7 m in the same manner as the initial enrichment, to counteract outgassing of CO₂.

We sampled the mesocosms every morning, but some variables were determined only every second day. Depth-integrated water samples (0–17 m) were taken by using integrating water samplers (IWS, HYDRO-BIOS, Kiel). The water was collected into plastic carboys (10 L) and transferred to the laboratory for sub-sampling and subsequent determination of carbon stocks.

2.2 Primary variables

For more detailed descriptions of the primary variables and the different methods used during this CO₂ mesocosm campaign, we refer to other papers in this joint volume: i.e., total particulate carbon (TPC), dissolved organic carbon (DOC), and dissolved inorganic carbon (DIC) are described by Paul et al. (2015); micro- and nanophytoplankton enumeration by Bermúdez et al. (2016); picophytoplankton, heterotrophic
prokaryotes, and viruses by Crawfurd et al. (2016); zoo- 
oplankton community by Lischka et al. (2015); primary pro-
duction and respiration by Spilling et al. (2016a); BP by 
Hornick et al. (2016); and sedimentation by Boxhammer et 
al. (2016) and Paul et al. (2015).

Briefly, samples for TPC (500 mL) were GF/F-filtered and 
determined using an elemental analyzer (EuroAE). DOC was 
measured using an infrared absorption (LI-COR LI-7000 on 
an AIRICA system). The DIC concentrations were converted 
was determined by infrared absorption (LI-COR LI-7000 on 
an AIRICA system). The DIC concentrations were converted 
from µmol kg 

\[ \text{DOC} = \text{DIC} + \text{POC} \]

\[ \text{DOC} = \text{DIC} + \text{POC} \]

determined every second day using gas chromatography. Us-

\[ F_{\text{N}_2\text{O}} = I_1 - I_2 \]

\[ F_{\text{N}_2\text{O}} = I_1 - I_2 \]

where \( I_1 \) and \( I_2 \) are the bulk \( \text{N}_2\text{O} \) concentration at time \( t_1 \) and \( t_2 \), respectively; \( A \) is the surface area; and \( \Delta t \) is the time 
difference between \( t_1 \) and \( t_2 \).

The flux velocity was then calculated by

\[ k_{\text{CO}_2} = k_{\text{N}_2\text{O}} \left( S_{\text{CO}_2} / S_{\text{N}_2\text{O}} \right)^{0.5} \]

\[ k_{\text{CO}_2} = k_{\text{N}_2\text{O}} \left( S_{\text{CO}_2} / S_{\text{N}_2\text{O}} \right)^{0.5} \]

where \( S_{\text{CO}_2} \) and \( S_{\text{N}_2\text{O}} \) are the Schmidt numbers for \( \text{CO}_2 \) and \( \text{N}_2\text{O} \), respectively. The \( \text{CO}_2 \) flux across the water surface was calculated according to

\[ F_{\text{CO}_2} = k_{\text{CO}_2} \left( \text{CO}_2 - \text{CO}_2 \right) \]

\[ F_{\text{CO}_2} = k_{\text{CO}_2} \left( \text{CO}_2 - \text{CO}_2 \right) \]

where \( \text{CO}_2 \) is the water concentration of \( \text{CO}_2 \) and \( \text{CO}_2 \) is the equilibrium concentration of \( \text{CO}_2 \), \( \text{CO}_2 \) is preferen-
tially taken up by phytoplankton at the surface, where also 
the atmospheric exchange takes place. For this reason, we 
used the calculated \( \text{CO}_2 \) concentration (based on the inte-
grated \( \text{CO}_2 \) concentration and pH in the surface) from the 
upper 5 m as the input for Eq. (5).

In contrast to \( \text{N}_2\text{O} \), the \( \text{CO}_2 \) flux can be chemically en-
hanced by hydration reactions of \( \text{CO}_2 \) with hydroxide ions 
and water molecules in the boundary layer (Wanninkhof and 
Knox, 1996). Using the method outlined in Czerny et 
al. (2013b), we found an enhancement of up to 12 % on warm 
days, and this was included into our flux calculations.

2.4 Data treatment

The primary data generated in this study comprise carbon 
standing stock measurements of TPC, DOC, and DIC, as 
well as carbon estimates of meso- and microzooplankton, 
micro-, nano- and picophytoplankton, bacteria, and viruses.

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Flux measurements of atmospheric CO2 exchange and sedimentation of TPC as well as the biological rates of net primary production (NPPi), BP, and total respiration (TR) enabled us to make carbon budget.

Based on the primary variables (chlorophyll a (Chl a) and temperature), the experiment was divided into three distinct phases: phase I: t0–t16; phase II: t17–t30; and phase III: t31–t43, where, e.g., Chl a concentration was relatively high during phase I, decreased during phase II, and remained low during phase III (Paul et al., 2015). Measurements of pools and rates were averaged for the two first sampling points of each experimental phase (n = 2) and were normalized to square meters (m^2) knowing the total depth (17 m, excluding the sedimentation funnel) of the mesocosms. For phase III we used the average of the last two measurements as the end point (n = 2).

For fluxes and biological rates we used the average for the whole periods normalized to days (day^−1). The same was done for rates of change (ΔTPC, ΔDOC, and ΔDIC), which accounted for the difference between the start and end of each phase for all carbon pools (TPC_p, DOC_p, DIC_p). All error estimates were calculated as standard error (SE), and this was calculated using all measurements within each phase (e.g., calculating the ΔTPC SE using the difference between each TPC measurement). The three different phases of the experiments were of different length, and each variable had a slightly different sampling regime (every 1–3 days, with some measurements missing due to technical problems). The exact sample number (n) for each SE is presented in the Table legends 1–3. The SE for estimated rates was calculated from the square root of the sum of variance for all the variables (Eq. 5–10 below). The primary papers mentioned above (Sect. 2.2.) present detailed statistical analyses, and we only refer to those here.

NPP was measured directly, and we additionally estimated the net community production (NCP). This was done in two different ways, from the organic (NCP_o) and the inorganic (NCP_i) fractions of carbon. NCP_o was calculated from changes in the organic fraction plus the exported TPC (EXP_TP) according to

\[
NCP_o = EXP_TP + \Delta TPC + \Delta DOC. \tag{5}
\]

Direct measurements using 14C isotope incubations should in principal provide a higher value than summing up the difference in overall carbon balance (our NCP_o), as the latter would incorporate total respiration and not only autotrophic respiration. NCP_i was calculated through changes in the dissolved inorganic carbon pool, corrected for CO2 gas exchange with the atmosphere (CO2flux) according to

\[
NCP_i = CO2flux - \Delta DIC. \tag{6}
\]

In order to close the budget, we estimated GPP and DOC production (DOC_prod). GPP is defined as the photosynthetically fixed carbon without any loss processes (i.e., NPP + autotrophic respiration). GPP can be estimated based on changes in organic (GPP_o) or inorganic (GPP_i) carbon pools, and we used these two different approaches providing a GPP range:

\[
GPP_o = NCP_o + TR, \tag{7}
\]

\[
GPP_i = TR + CO2flux - \Delta DIC. \tag{8}
\]

During phase III, TR was not measured, and we estimated TR based on the ratios between NCP_o and BP to TR during phase II. The minimum production of DOC (DOC_minp) in the system was calculated assuming bacterial carbon uptake was taken from the DOC pool according to

\[
DOC_{minp} = \Delta DOC + BP. \tag{9}
\]

However, this could underestimate DOC_prod as a fraction of bacterial DOC uptake is respired. Without direct measurement of (heterotrophic prokaryote) bacterial respiration (BR), we estimated BR from TR. The share of active bacteria contributing to bacterial production is typically in the range of 10–30 % of the total bacterial community (Lignell et al., 2013). We used the fraction of bacterial biomass (BB) of total biomass (TB) as the maximum limit of BR (BR ≤ BB/TB) and hence calculated max DOC production (DOC_maxp) according to

\[
DOC_{maxp} = \Delta DOC + BP + (BB \times TR/TB). \tag{10}
\]

We assumed that carbon synthesized by bacteria was added to the TPC pool.

There are a number of uncertainties in these calculations, but this budgeting exercise provides an order-of-magnitude estimate of the flow of carbon within the system and enables comparison between the treatments. The average of the two controls (M1 and M5) and the two highest CO2 treatments (M3 and M8) were used to illustrate CO2 effects.

3 Results and discussion

3.1 Change in plankton community, from large to small forms over time

The overall size structure of the plankton community decreased over the course of the experiment. Figure 1 illustrates the carbon content in different plankton groups in the control mesocosms. During phase I, the phytoplankton abundances increased at first in all treatments before starting to decrease at the end of phase I (Paul et al., 2015). At the start of phase II (t17), the phytoplankton biomass was higher than at the start of the experiment (~ 130 mmol C m^−2 in the controls) but decreased throughout phases II and III. The fraction of pico-phytoplankton increased in all treatments, but some groups of picophytoplankton increased more in the high CO2 treatments (Crawford et al., 2016).
Nitrogen was the limiting nutrient throughout the entire experiment (Paul et al., 2015), and primary producers are generally N-limited in the main sub-basins of the Baltic Sea (Tamminen and Andersen, 2007). The surface-to-volume ratio increases with decreasing cell size, and consequently small cells have higher nutrient affinity and are better competitors for scarce nutrient sources than large cells (Reynolds, 2006). The prevailing N limitation was likely the reason for the decreasing size structure of the phytoplankton community.

Micro- and mesozooplankton standing stock was approximately half of the phytoplankton biomass initially but decreased rapidly in the control treatments during phase I (Fig. 1). In the CO\textsubscript{2}-enriched treatments, the zooplankton biomass also decreased but not to the same extent as in the control treatments (Spilling et al., 2016a). Overall, smaller species benefitted from the extra CO\textsubscript{2} addition, but there was no significant negative effect of high CO\textsubscript{2} on the mesozooplankton community (Lischka et al., 2015).

Bacterial biomass was the main fraction of the plankton carbon throughout the experiment. The bacterial numbers largely followed the phytoplankton biomass with an initial increase then decrease during phase I, increase during phase II, and slight decrease during phase III (Crawfurd et al., 2016). The bacterial community was controlled by mineral nutrient limitation, bacterial grazing, and viral lysis (Crawfurd et al., 2016), and bacterial growth is typically limited by N or a combination of N and C in the study area (Lignell et al., 2008, 2013).

The bacterial carbon pool was higher than the measured TPC. Part of the bacteria must have passed the GF/F filters (0.7 µm), and assuming pico- to mesoplankton was part of the TPC, > 50 % of the bacterial carbon was not contributing to the measured TPC. The conversion factor from cells to carbon is positively correlated to cell size, and there is consequently uncertainty related to the absolute carbon content of the bacterial pool (we used a constant conversion factor). However, bacteria are known to be the dominating carbon share in the Baltic Sea during the N-limited summer months (Lignell et al., 2013), and their relative dominance is in line with this.

Although there is some uncertainty in the carbon estimate (Jover et al., 2014), viruses make up (due to their numerical dominance) a significant fraction of the pelagic carbon pool. Of the different plankton fractions the virioplankton have been the least studied, but their role in the pelagic ecosystem is ecologically important (Suttle, 2007; Brussaard et al., 2008; Mojica et al., 2016). Viral lysis rates were equivalent to the grazing rates for phytoplankton and for bacteria in the current study (Crawfurd et al., 2016). As mortality agents, viruses are key drivers of the regenerative microbial food web (Suttle, 2007; Brussaard et al., 2008). Overall, the structure of the plankton community reflected the nutrient status of the system: the increasing N limitation favored development of smaller cells and increased dependence of the primary producers on regenerated nutrients.

### 3.2 The DIC pool and atmospheric exchange of CO\textsubscript{2}

The DIC pool was the largest carbon pool: three–four-fold higher than the DOC pool and roughly 60-fold higher than the TPC pool (Tables 1–3). After the addition of CO\textsubscript{2}, the DIC pool was ∼7 % higher in the highest CO\textsubscript{2} treatment than in the control mesocosms (Table 1). The gas exchange with the atmosphere was the most apparent flux affected by CO\textsubscript{2} addition (Tables 1–3). Seawater in the mesocosms with added CO\textsubscript{2} was supersaturated; hence CO\textsubscript{2} outgassed throughout the experiment. The control mesocosms were initially undersaturated; hence ingassing occurred during phases I and II (Fig. 2). In the first part of phase III, the control mesocosms reached equilibrium with the atmospheric fCO\textsubscript{2} (Fig. 2). The gas exchange had direct effects on the DIC concentration in the mesocosms (Fig. 3). From the measured gas exchange and change in DIC it is possible to calculate the biologically mediated carbon flux. In the mesocosms with ambient CO\textsubscript{2} concentration, the flux measurements indicated net heterotrophy throughout the experiment. The opposite pattern, net autotrophy, was indicated in the two mesocosms with the highest CO\textsubscript{2} addition (Fig. 3; see also Sect. 3.7.).

### 3.3 The DOC pool, DOC production, and remineralization

The DOC pool increased throughout the experiment in all mesocosm bags, albeit more in the treatments with elevated...
The standing stock of total particulate carbon (TPC<sub>pool</sub>), dissolved organic carbon (DOC<sub>pool</sub>), and dissolved inorganic carbon (DIC<sub>pool</sub>) at the start of phase I in mmol C m<sup>-2</sup> ± SE (n = 2). The DOC<sub>pool</sub> was missing some initial measurements and is the average for all mesocosms assuming that the DOC concentration was similar at the onset of the experiment. The net changes in TPC (∆TPC), DOC (∆DOC), and DIC (∆DIC) are average changes in the standing stocks during phase I in mmol C m<sup>-2</sup> day<sup>-1</sup> ± SE (n = 8). Flux measurements of atmospheric gas exchange (CO<sub>2</sub><sub>flux</sub>) and exported carbon (EXP<sub>TPC</sub>) plus biological rates – total respiration (TR), bacterial production (BP), and net primary production (NPP<sub>14C</sub>) – and net community production estimated based on organic carbon pools (NCP<sub>0</sub>) net primary production are all averages for the whole of phase I in mmol C m<sup>-2</sup> day<sup>-1</sup> ± SE (n = 13, 9, 16, 7, and 11 for CO<sub>2</sub><sub>flux</sub>, EXP<sub>TPC</sub>, TR, BP, and NPP<sub>14C</sub>, respectively). SE for NCP<sub>0</sub> was calculated from the square root of the sum of variance of the three variables used in Eq. (6). The NCP<sub>0</sub> was calculated from the net change in carbon pools plus carbon export, whereas NPP<sub>14C</sub> was measured carbon fixation using radio-labeled 14C over a 24 h incubation period in situ. TR was measured as O<sub>2</sub> consumption, and for comparison with carbon fixation we used a respiratory quotient (RQ) of 1. CO<sub>2</sub><sub>flux</sub> was only calculated for the period after full addition of CO<sub>2</sub> (t4–t16). A total budget of carbon fluxes for ambient and high CO<sub>2</sub> treatments is presented in Fig. 5.

### Table 1

<table>
<thead>
<tr>
<th>Phase I (t0–t16)</th>
<th>CO2 treatment (µatm f CO2)</th>
<th>M1</th>
<th>M5</th>
<th>M7</th>
<th>M6</th>
<th>M3</th>
<th>M8</th>
</tr>
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<tr>
<td></td>
<td></td>
<td>365</td>
<td>368</td>
<td>497</td>
<td>821</td>
<td>1007</td>
<td>1231</td>
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<tr>
<td>TPC&lt;sub&gt;pool&lt;/sub&gt;</td>
<td></td>
<td>417 ± 38</td>
<td>425 ± 39</td>
<td>472 ± 48</td>
<td>458 ± 38</td>
<td>431 ± 48</td>
<td>446 ± 57</td>
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<tr>
<td>DOC&lt;sub&gt;pool&lt;/sub&gt;</td>
<td></td>
<td>7172 ± 87</td>
<td>7172 ± 87</td>
<td>7172 ± 87</td>
<td>7172 ± 87</td>
<td>7172 ± 87</td>
<td>7172 ± 87</td>
</tr>
<tr>
<td>DIC&lt;sub&gt;pool&lt;/sub&gt;</td>
<td></td>
<td>25158 ± 9</td>
<td>25182 ± 10</td>
<td>25628 ± 8</td>
<td>26295 ± 22</td>
<td>26637 ± 36</td>
<td>26953 ± 48</td>
</tr>
<tr>
<td>∆TPC</td>
<td></td>
<td>−4.6 ± 15</td>
<td>−5.2 ± 13</td>
<td>−8.3 ± 13</td>
<td>−8.2 ± 17</td>
<td>−7.0 ± 13</td>
<td>−6.3 ± 20</td>
</tr>
<tr>
<td>∆DOC</td>
<td></td>
<td>15.5 ± 58</td>
<td>18.3 ± 30</td>
<td>18.5 ± 33</td>
<td>25.0 ± 36</td>
<td>18.5 ± 73</td>
<td>18.1 ± 63</td>
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<tr>
<td>∆DIC</td>
<td></td>
<td>5.5 ± 5.2</td>
<td>6.9 ± 9.2</td>
<td>−6.1 ± 11</td>
<td>−24 ± 14</td>
<td>−32 ± 20</td>
<td>−49 ± 42</td>
</tr>
<tr>
<td>CO&lt;sub&gt;2&lt;/sub&gt;&lt;sub&gt;flux&lt;/sub&gt;</td>
<td></td>
<td>4.4 ± 0.2</td>
<td>4.8 ± 0.3</td>
<td>−0.8 ± 0.5</td>
<td>−11 ± 1.0</td>
<td>−17 ± 1.4</td>
<td>−23 ± 2.0</td>
</tr>
<tr>
<td>EXP&lt;sub&gt;TPC&lt;/sub&gt;</td>
<td></td>
<td>6.6 ± 0.10</td>
<td>5.6 ± 0.04</td>
<td>5.4 ± 0.07</td>
<td>6.0 ± 0.07</td>
<td>5.6 ± 0.06</td>
<td>6.0 ± 0.05</td>
</tr>
<tr>
<td>TR</td>
<td></td>
<td>107 ± 9</td>
<td>82 ± 7</td>
<td>81 ± 6</td>
<td>80 ± 8</td>
<td>75 ± 8</td>
<td>74 ± 8</td>
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<tr>
<td>BP</td>
<td></td>
<td>27 ± 8</td>
<td>41 ± 6</td>
<td>43 ± 8</td>
<td>41 ± 4</td>
<td>36 ± 5</td>
<td>46 ± 9</td>
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<tr>
<td>NPP&lt;sub&gt;14C&lt;/sub&gt;</td>
<td></td>
<td>4.8 ± 0.8</td>
<td>11.4 ± 2.1</td>
<td>14.9 ± 3.6</td>
<td>12.3 ± 2.3</td>
<td>11.3 ± 2.4</td>
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<td>18.7 ± 20</td>
<td>15.6 ± 30</td>
<td>22.8 ± 28</td>
<td>17.1 ± 25</td>
<td>17.8 ± 28</td>
</tr>
</tbody>
</table>

### Table 2

The standing stock of total particulate carbon (TPC<sub>pool</sub>), dissolved organic carbon (DOC<sub>pool</sub>), and dissolved inorganic carbon (DIC<sub>pool</sub>) at the start of phase II in mmol C m<sup>-2</sup> ± SE (n = 2). The net changes in TPC (∆TPC), DOC (∆DOC), and DIC (∆DIC) are average changes in the standing stocks during phase II in mmol C m<sup>-2</sup> day<sup>-1</sup> ± SE (n = 7). Flux measurements of atmospheric gas exchange (CO<sub>2</sub><sub>flux</sub>) and exported carbon (EXP<sub>TPC</sub>) plus biological rates – total respiration (TR), bacterial production (BP), and measured (NPP<sub>14C</sub>) – and net community production estimated based on organic carbon pools (NCP<sub>0</sub>) are all averages for phase II in mmol C m<sup>-2</sup> day<sup>-1</sup> ± SE (n = 8, 7, 14, 5, and 14 for CO<sub>2</sub><sub>flux</sub>, EXP<sub>TPC</sub>, TR, BP, and NPP<sub>14C</sub>, respectively). See Table 1 legend for further details.

<table>
<thead>
<tr>
<th>Phase II (t17–t30)</th>
<th>CO2 treatment (µatm f CO2)</th>
<th>M1</th>
<th>M5</th>
<th>M7</th>
<th>M6</th>
<th>M3</th>
<th>M8</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>365</td>
<td>368</td>
<td>497</td>
<td>821</td>
<td>1007</td>
<td>1231</td>
</tr>
<tr>
<td>TPC&lt;sub&gt;pool&lt;/sub&gt;</td>
<td></td>
<td>339 ± 14</td>
<td>337 ± 20</td>
<td>331 ± 22</td>
<td>318 ± 9</td>
<td>312 ± 12</td>
<td>339 ± 23</td>
</tr>
<tr>
<td>DOC&lt;sub&gt;pool&lt;/sub&gt;</td>
<td></td>
<td>7435 ± 38</td>
<td>7483 ± 37</td>
<td>7487 ± 43</td>
<td>7597 ± 37</td>
<td>7487 ± 61</td>
<td>7479 ± 37</td>
</tr>
<tr>
<td>DIC&lt;sub&gt;pool&lt;/sub&gt;</td>
<td></td>
<td>25247 ± 34</td>
<td>25269 ± 34</td>
<td>25639 ± 8</td>
<td>26177 ± 25</td>
<td>26413 ± 28</td>
<td>26757 ± 45</td>
</tr>
<tr>
<td>∆TPC</td>
<td></td>
<td>−2.4 ± 5</td>
<td>−2.3 ± 8</td>
<td>−1.6 ± 14</td>
<td>0.3 ± 6</td>
<td>2.8 ± 4</td>
<td>3.2 ± 8</td>
</tr>
<tr>
<td>∆DOC</td>
<td></td>
<td>−0.6 ± 39</td>
<td>2.4 ± 30</td>
<td>3.6 ± 40</td>
<td>8.4 ± 31</td>
<td>11.3 ± 58</td>
<td>9.1 ± 36</td>
</tr>
<tr>
<td>∆DIC</td>
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<td>22.4 ± 12</td>
<td>17.6 ± 8.1</td>
<td>−0.4 ± 4.5</td>
<td>−10.5 ± 16</td>
<td>−14.2 ± 10</td>
<td>−23.1 ± 13</td>
</tr>
<tr>
<td>CO&lt;sub&gt;2&lt;/sub&gt;&lt;sub&gt;flux&lt;/sub&gt;</td>
<td></td>
<td>1.7 ± 0.3</td>
<td>1.2 ± 0.3</td>
<td>−2.6 ± 0.3</td>
<td>−10 ± 0.5</td>
<td>−14 ± 0.6</td>
<td>−19 ± 1.0</td>
</tr>
<tr>
<td>EXP&lt;sub&gt;TPC&lt;/sub&gt;</td>
<td></td>
<td>3.3 ± 0.08</td>
<td>2.6 ± 0.06</td>
<td>2.5 ± 0.08</td>
<td>2.6 ± 0.06</td>
<td>2.8 ± 0.07</td>
<td>2.9 ± 0.06</td>
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<tr>
<td>TR</td>
<td></td>
<td>140 ± 7</td>
<td>127 ± 5</td>
<td>103 ± 3</td>
<td>103 ± 4</td>
<td>101 ± 5</td>
<td>86 ± 4</td>
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<tr>
<td>BP</td>
<td></td>
<td>66 ± 17</td>
<td>57 ± 8</td>
<td>61 ± 7</td>
<td>57 ± 7</td>
<td>43 ± 6</td>
<td>47 ± 6</td>
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<tr>
<td>NPP&lt;sub&gt;14C&lt;/sub&gt;</td>
<td></td>
<td>3.8 ± 0.6</td>
<td>11.2 ± 1.9</td>
<td>10.8 ± 2.0</td>
<td>14.3 ± 2.8</td>
<td>10.4 ± 2.1</td>
<td>12.0 ± 2.5</td>
</tr>
<tr>
<td>NCP&lt;sub&gt;0&lt;/sub&gt;</td>
<td></td>
<td>0.3 ± 20</td>
<td>2.7 ± 15</td>
<td>4.5 ± 22</td>
<td>11.4 ± 16</td>
<td>16.9 ± 19</td>
<td>15.2 ± 16</td>
</tr>
</tbody>
</table>
Table 3. The standing stock of total particulate carbon (TPC<sub>pool</sub>), dissolved organic carbon (DOC<sub>pool</sub>), and dissolved inorganic carbon (DIC<sub>pool</sub>) at the start of phase III in mmol C m<sup>-2</sup>± SE (n = 2). The net change in TPC (ΔTPC), DOC (ΔDOC), and DIC (ΔDIC) are average changes in the standing stocks during phase III in mmol C m<sup>-2</sup> day<sup>-1</sup>± SE (n = 6), using the average of the last two sampling days as the end point. Flux measurements of atmospheric gas exchange (CO<sub>2</sub>flux) and exported carbon (EXP<sub>TPC</sub>) plus biological rates – BP and net community production estimated based on organic carbon pools (NCP<sub>O</sub>) – are all averages for phase III in mmol C m<sup>-2</sup> day<sup>-1</sup>± SE (n = 7, 6, and 7 for CO<sub>2</sub>flux, EXP<sub>TPC</sub>, and BP, respectively). See Table 1 legend for further details. During phase III we did not have direct measurements of net primary production (NPP<sub>14C</sub>) or TR.

<table>
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<tr>
<th>Phase III (t31–t43)</th>
<th>CO&lt;sub&gt;2&lt;/sub&gt; treatment (µatm fCO&lt;sub&gt;2&lt;/sub&gt;)</th>
<th>M1</th>
<th>M5</th>
<th>M7</th>
<th>M6</th>
<th>M3</th>
<th>M8</th>
</tr>
</thead>
<tbody>
<tr>
<td>TPC&lt;sub&gt;pool&lt;/sub&gt;</td>
<td>306 ± 12</td>
<td>365</td>
<td>368</td>
<td>309</td>
<td>323</td>
<td>351</td>
<td>384</td>
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<tr>
<td>DOC&lt;sub&gt;pool&lt;/sub&gt;</td>
<td>7426 ± 16</td>
<td>365</td>
<td>368</td>
<td>7485</td>
<td>7553</td>
<td>7593</td>
<td>7562</td>
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<tr>
<td>DIC&lt;sub&gt;pool&lt;/sub&gt;</td>
<td>25 557 ± 9</td>
<td>365</td>
<td>368</td>
<td>25 545</td>
<td>26 030</td>
<td>26 197</td>
<td>26 371</td>
</tr>
<tr>
<td>ΔTPC</td>
<td>−3.8 ± 10</td>
<td>365</td>
<td>368</td>
<td>0.3</td>
<td>3.3</td>
<td>3.3</td>
<td>−1.4</td>
</tr>
<tr>
<td>ΔDOC</td>
<td>9.8 ± 5</td>
<td>365</td>
<td>368</td>
<td>8.8</td>
<td>8.9</td>
<td>9.2</td>
<td>5.7</td>
</tr>
<tr>
<td>ΔDIC</td>
<td>4.3 ± 3.9</td>
<td>365</td>
<td>368</td>
<td>5.5</td>
<td>6.2</td>
<td>−12.3</td>
<td>16.3</td>
</tr>
<tr>
<td>CO&lt;sub&gt;2&lt;/sub&gt;flux</td>
<td>−0.3 ± 0.7</td>
<td>365</td>
<td>368</td>
<td>−0.8</td>
<td>−3.0</td>
<td>−7.3</td>
<td>−9.4</td>
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<tr>
<td>EXP&lt;sub&gt;TPC&lt;/sub&gt;</td>
<td>1.5 ± 0.07</td>
<td>365</td>
<td>368</td>
<td>1.4</td>
<td>0.4</td>
<td>1.9</td>
<td>1.6</td>
</tr>
<tr>
<td>BP</td>
<td>31 ± 6.8</td>
<td>365</td>
<td>368</td>
<td>37</td>
<td>38</td>
<td>27</td>
<td>17</td>
</tr>
<tr>
<td>NCP&lt;sub&gt;O&lt;/sub&gt;</td>
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<td>365</td>
<td>368</td>
<td>10.5</td>
<td>12.7</td>
<td>14.3</td>
<td>6.0</td>
</tr>
</tbody>
</table>

Figure 2. The calculated exchange of CO<sub>2</sub> between the mesocosms and the atmosphere. Positive values indicate net influx (ingassing), and negative values net outflux (outgassing) from the mesocosms. The flux was based on measurements of N<sub>2</sub>O as a tracer gas and calculated using Eqs. (2)–(5).

CO<sub>2</sub> concentration. The initial DOC standing stock in all treatments was approximately 7200 mmol C m<sup>-2</sup>. At the end of the experiment, the DOC pool was ∼2% higher in the two highest CO<sub>2</sub> treatments than in the controls (Fig. 4), and there is statistical support for this difference between CO<sub>2</sub> treatments (phase III, p = 0.05) (Paul et al., 2015). Interestingly, the data do not point to a substantially higher release of DOC at high CO<sub>2</sub> (Figs. 4 and 5). The bacterial production was notably lower during phase II in the high CO<sub>2</sub> treatments (Hornick et al., 2016) and of similar magnitude to the rate of change in DOC pool (Tables 2 and 3), indicating reduced bacterial uptake and remineralization of DOC. The combined results suggest that the increase in the DOC pool at high CO<sub>2</sub> was related to reduced DOC loss (uptake by bacteria), rather than increased release of DOC by the plankton community, at elevated CO<sub>2</sub> concentration.
Figure 4. Standing stocks of total particulate carbon (TPC) and dissolved organic carbon (DOC) at the last day of the experiment (n=43), plus the sum of exported TPC throughout the experiment; all values are in mmol C m$^{-2}$ ± SE (n = 2). The values are averages of the two controls (M1 and M5) and the two highest CO$_2$ treatments (M3 and M8). Red circles indicate statistically significant higher standing stocks in the high CO$_2$ treatments (further details in text). The size of the boxes indicates the relative size of the carbon standing stocks and export.

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Flux of TPC out of the mesocosms occurred during phase I with $\sim 6$ mmol C m$^{-2}$ day$^{-1}$. It decreased to $\sim 3$ mmol C m$^{-2}$ day$^{-1}$ during phase II and was $\sim 2$ mmol C m$^{-2}$ day$^{-1}$ during phase III (Tables 1–3). The exported carbon as the percent of average TPC standing stock similarly decreased from $\sim 1.3\%$ during phase I to 0.3–0.5% during phase III. The initial increase in the autotrophic biomass was likely the reason for relatively more of the carbon settling in the mesocosms in the beginning of the experiment, whereas the decreasing carbon export was most likely caused by the shift towards a plankton community depending on recycled nitrogen. The relatively high initial sedimentation reduced the overall suspended TPC and also the average plankton size in the community.

3.5 Biological rates: respiration

TR was always lower in the CO$_2$-enriched treatments (Tables 1–2). The average TR was 83 mmol C m$^{-2}$ day$^{-1}$ during phase I, and initially without any detectable treatment effect. The respiration rate started to be lower in the high CO$_2$ treatments than in the controls in the beginning of phase II. At the end of phase II there was a significant difference (p = 0.02; Spilling et al., 2016a) between the treatments (Table 2) and 40% lower respiration rate in the highest CO$_2$ treatment than in the controls (Spilling et al., 2016a).

Cytosol pH is close to neutral in most organisms, and reduced energetic cost for internal pH regulation (e.g., transport of H$^+$) and at lower external pH levels could be one factor reducing respiration (Smith and Raven, 1979). Hopkinson et al. (2010) found indirect evidence of decreased respiration and also proposed that increased CO$_2$ concentration (i.e., decreased pH) reduced metabolic cost of remaining intracellular homeostasis. Mitochondrial respiration in plant foliage decreases in high-CO$_2$ environments, possibly affected by respiratory enzymes or other metabolic processes (Anthor, 1991; Puhe and Ulrich, 2012). Most inorganic carbon in water is in the form of bicarbonate (HCO$_3^-$) at relevant pH, and many aquatic autotrophs have developed carbon-concentrating mechanisms (CCMs) (e.g., Singh et al., 2014) that could reduce the cost of growth (Raven, 1991). There are some studies that have pointed to savings of metabolic energy due to downregulation of carbon-concentrating mechanisms (Hopkinson et al., 2010) or overall photosynthetic apparatus (Sobrino et al., 2014) in phytoplankton at high CO$_2$ concentrations. Yet other studies of the total plankton community have pointed to no effect or increased respiration at elevated CO$_2$ concentration (Li and Gao, 2012; Tanaka et al., 2013), and the metabolic changes behind reduced respiration remain an open question. Membrane transport of H$^+$ is sensitive to changes in external pH, but the physiological impacts of increasing H$^+$ need further study to better address effects of ocean acidification (Taylor et al., 2012). An important aspect is also to consider the microenvironment surrounding plankton; exchange of nutrients and gases takes
Figure 5. Average carbon standing stocks and flow in the control mesocosms (M1 + M5) and high-CO$_2$ mesocosms (M3 + M8) during the three phases of the experiment. All carbon stocks (squares) – dissolved inorganic carbon (DIC), total particulate carbon (TPC), and dissolved organic carbon (DOC) – are averages from the start of the period in mmol C m$^{-2} \pm$ SE ($n$ = 2). Fluxes (arrows) and net changes ($\Delta$) are averages for the whole phase in mmol C m$^{-2}$ day$^{-1} \pm$ SE ($n$ present in Table legends 1–3). Solid black arrows indicate measured fluxes (Tables 1–3): TR, BP, and exported TPC (EXP$_{TPC}$). Dashed grey arrows are estimated by closing the budget: gross primary production (GPP) using Eqs. (7) and (8), and DOC production (DOC$_{prod}$) using Eqs. (9) and (10). Bacterial respiration was calculated using Eq. (10) and is a share of TR (indicated by the parenthesis). Aggregation was assumed to equal BP. Red circles indicate statistically significant higher values ($p < 0.05$, tests presented in the primary papers described in Sect. 2.2.). The size of the boxes indicates the relative size of the carbon standing stocks.

place through the boundary layer, which might have very different pH properties than bulk water measurements (Flynn et al., 2012).

3.6 Biological rates: bacterial production

BP became lower in the high CO$_2$ treatment in the latter part of the experiment. During phase I, BP ranged from 27 to 46 mmol C m$^{-2}$ day$^{-1}$ (Table 1). The difference in BP between treatments became apparent in phases II and III of the experiment. The average BP was 18 and 24% higher in the controls than in the highest CO$_2$ treatments during phases II and III, respectively (Tables 2 and 3).

The lower bacterial production accounted for $\sim$40% of the reduced respiration during phase II, and the reduced respiration described above could at least partly be explained by the lower bacterial activity. This raises an interesting question: what was the mechanism behind the reduced bacterial production/respiration in the high CO$_2$ treatment? There are examples of decreased bacterial production (Motegi et al., 2013) and respiration (Teira et al., 2012) at elevated CO$_2$ concentration. However, most previous studies have reported no change (Allgaier et al., 2008) or a higher bacterial production at elevated CO$_2$ concentration (Grossart et al., 2006; Piontek et al., 2010; Endres et al., 2014). The latter was also supported by the recent study of Bunse et al. (2016), de-
scribing upregulation of bacterial genes related to respiration, membrane transport, and protein metabolism at elevated CO₂ concentration; however, this effect was not evident when inorganic nutrients had been added (high Chl α treatment).

In this study, the lower bacterial activity in the high CO₂ treatments could either be due to limitation and/or inhibition of bacterial growth or driven by difference in loss processes. Bacterial grazing and viral lysis were higher in the high CO₂ treatments during periods of the experiment (Crawford et al., 2016) and would at least partly be the reason for the reduced bacterial production at high CO₂ concentration.

N limitation increased during the experiment (Paul et al., 2015), and mineral nutrient limitation of bacteria can lead to accumulation of DOC, i.e., reduced bacterial uptake (Thingstad et al., 1997), similar to our results. Bacterial N limitation is common in the area during summer (Lignell et al., 2013), however, this N limitation was not apparently different in the controls (Paul et al., 2015), and CO₂ did not affect N fixation (Paul et al., 2016a). In a scenario where the competition for N is fierce, the balance between bacteria and similar sized picophytoplankton could be tilted in favor of phytoplankton if they gain an advantage by having easier access to carbon, i.e., CO₂ (Hornick et al., 2016). We have not found evidence in the literature that bacterial production will be suppressed in the observed pH range inside the mesocosms, varying from approximately pH 8.1 in the control to pH 7.6 in the highest fCO₂ treatment (Paul et al., 2015), although enzyme activity seems to be affected even by moderate pH changes. For example, some studies report on an increase in protein-degrading enzyme leucine aminopeptidase activities at reduced pH (Grossart et al., 2006; Piontek et al., 2010; Endres et al., 2014), whereas others indicate a reduced activity of this enzyme (Yamada and Suzumura, 2010).

A range of other factors affect this enzyme, for example the nitrogen source and salinity (Stepanauskas et al., 1999), and any potential interaction effects with decreasing pH are not yet resolved. Any pH-induced changes in bacterial enzymatic activity could potentially affect bacterial production.

3.7 Biological rates: primary production

There was an effect of CO₂ concentration on the net community production based on the organic carbon fraction (NCPo). NCPo was higher during phase I than during the rest of the experiments and during this initial phase without any apparent CO₂ effect. There was no consistent difference between CO₂ treatments for NPP14C (p > 0.1), but NCPo increased with increasing CO₂ enrichment during phase II (phase II; linear regression p = 0.003; R² = 0.91). This was caused by the different development in the TPC and DOC pools. The pattern of GPP was similar to NCPo during phases I and II. During phase III there was no respiration or NPP14C measurements, and the estimated GPP is more uncertain. The NCPo and GPP indicated a smaller difference between treatments during phase III than phase II.

The measures of NPP14C and NCPo were of a similar magnitude (Tables 1–3). During phase I, NPP14C < NCPo (Table 1); this relationship reversed for most treatments during phase II, with the exception of the highest CO₂ levels (Table 2). The difference between NPP14C and NCPo suggests that observed reduction in respiration at elevated CO₂ could be mainly heterotrophic respiration. However, in terms of the NPP14C and NCPo, the uncertainty seems to be higher than the potential signal of heterotrophic respiration. This would also indicate that the NPP14C during phase I have been underestimated, in particular for the control mesocosm M1. During phase II, the NPP14C was higher than NCPo, except for the two highest CO₂ treatments, more in line with our assumption of NPP14C > NCPo. The systematic offset in NPP14C during phase I could be due to changed parameterization during incubation in small volumes (8 mL; Spilling et al., 2016a), for example increased loss due to grazing.

The results of the DIC pool and atmospheric exchange of CO₂ provide another way of estimating the net community production based on inorganic carbon (NCPi). There was some discrepancy between the NCPo and NCPi as the latter suggested net heterotrophy in the ambient CO₂ treatments, whereas the high CO₂ treatments were net autotrophic during all three phases of the experiment (Fig. 3). For the NCPi there was no indication of net heterotrophy at ambient CO₂ concentration. In terms of the absolute numbers, the NCPi estimate is probably more uncertain than NCPo. Calculating the CO₂ atmospheric exchange from the measurements of a tracer gas involves several calculation steps (Eq. 1–4), each adding uncertainty to the calculation. However, both estimations (NCPi and NCPo) indicate that increased CO₂ concentrations lead to higher overall community production, supporting our overall conclusion.

3.8 Budget

A carbon budget for the two control mesocosms and two highest CO₂ additions is presented in Fig. 5. During phase I the estimated GPP was ∼ 100 mmol C fixed m⁻² day⁻¹, from which 75–95 % was respired, ∼ 1 % ended up in the TPC (including export), and 5–25 % added to the DOC pool. The main difference between CO₂ treatments became apparent during phase II when the NCPo was higher in the elevated CO₂ treatments. The respiration loss increased to ∼ 100 % of GPP at the ambient CO₂ concentration, whereas respiration was lower (85–95 % of GPP) in the highest CO₂ treatment. Bacterial production was ∼ 30 % lower, on average, at the highest CO₂ concentration than in the controls during phase II. The share of NCPo of GPP ranged from 2 to 20 %, and the minimum flux to the DOC pool was 11 to 18 % of TPC.

The overall budget was calculated by using the direct measurements of changes in standing stocks and fluxes of export, respiration, and bacterial production rates. The most robust data are the direct measurements of carbon standing stocks.
and their development (e.g., ΔTPC). These are based on well-established analytical methods with relatively low SE of the carbon pools. However, the dynamic nature of these pools made the relative SE for the rate of change much higher, reflecting that the rate of change varied considerably within the different phases.

The rate variables, calculated based on conversion factors, have greater uncertainty, although their SEs were relatively low, caused by uncertainty in the conversion steps. For example, the RQ was set to 1, which is a good estimate for carbohydrate oxidation. For lipids and proteins the RQ is close to 0.7, but in a natural environment RQ is often > 1 (Berggren et al., 2012) and is affected by physiological state, e.g., nutrient limitation (Romero-Kutzner et al., 2015). Any temporal variability in the conversion factors would directly change the overall budget calculations, e.g., RQ affecting total respiration and gross primary production estimates. However, the budget provides an order-of-magnitude estimate of the carbon flow within the system. Some of the variables such as GPP were estimated using different approaches, providing a more robust comparison of the different treatments.

The primary effect of increasing CO₂ concentration was the higher standing stocks of TPC and DOC compared with ambient CO₂ concentration. The increasing DOC pool and relatively higher TPC pool were driven by reduced respiration and bacterial production at elevated CO₂ concentration. Decreasing respiration rate reduced the recycling of organic carbon back to the DIC pool. The lower respiration and bacterial production also indicate reduced remineralization of DOC. These two effects caused the higher TPC and DOC pools in the elevated CO₂ treatments. The results highlight the importance of looking beyond net changes in carbon standing stocks to understand how carbon fluxes are affected under increasing ocean acidification.

4 Data availability
The data presented in this paper can be found in Paul et al. (2016b) and Spilling et al. (2016b).

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