Supplemental Information

Figure S1. Variations of DOM and nutrients in the treatment (solid lines) and seawater control (dashed lines) during the 364-day incubation. The chemicals shown here are: (A) dissolved organic carbon (DOC); (B) dissolved organic nitrogen (DON), ammonium, nitrite, and nitrate; (C) dissolved organic phosphorus (DOP) and phosphate. Error bars indicate standard deviation calculated from triplicate samples.

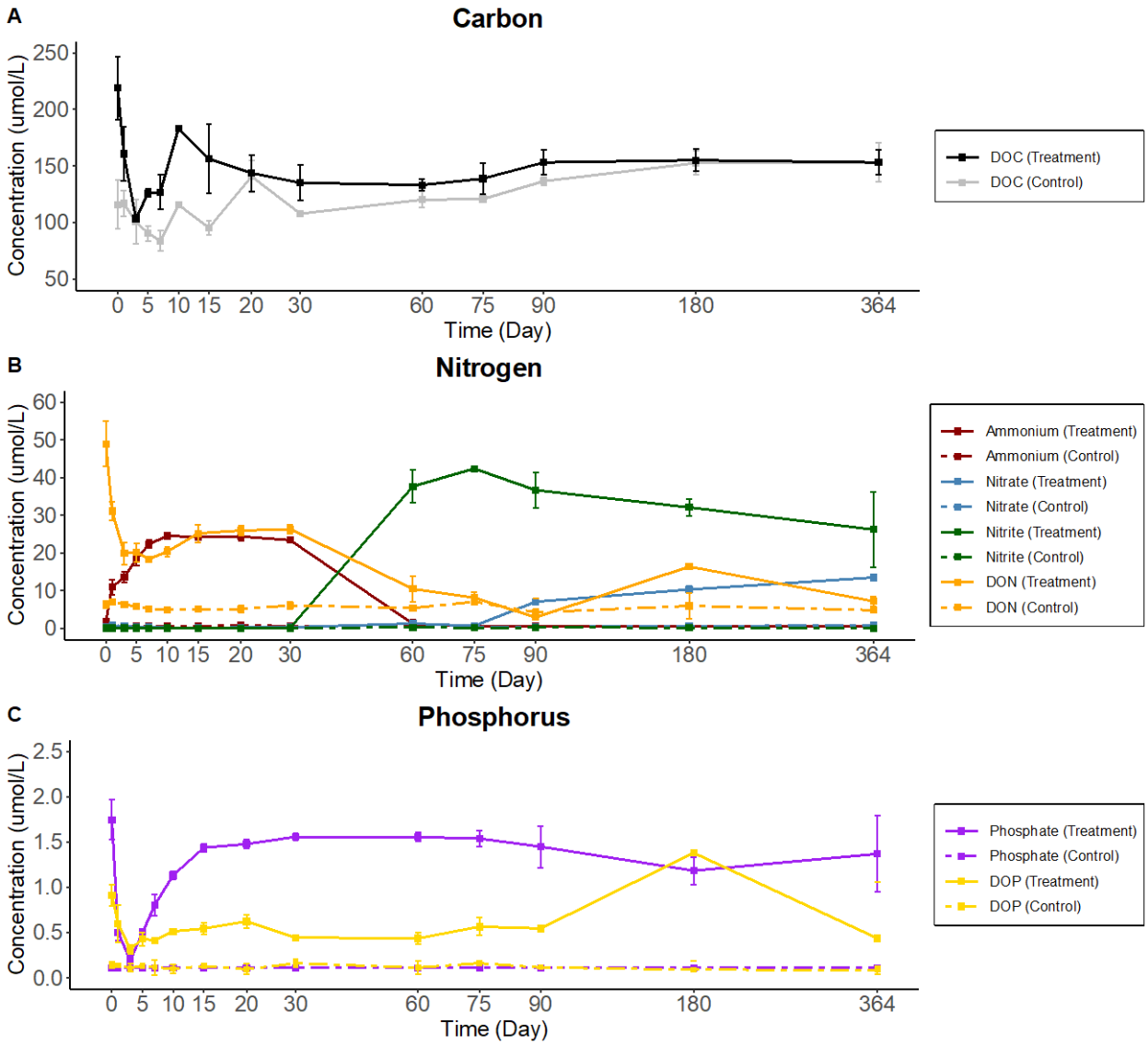
A
Carbon
Concentration (umol/L)
250
200
150
100
50
0 5 10 15 20 30 60 75 90 180 364
Time (Day)
DOC (Treatment)
DOC (Control)
B
Nitrogen
Concentration (umol/L)
60
50
40
30
20
10
0
0 5 10 15 20 30 60 75 90 180 364
Time (Day)
Ammonium (Treatment)
Ammonium (Control)
Nitrate (Treatment)
Nitrate (Control)
Nitrite (Treatment)
Nitrite (Control)
DON (Treatment)
DON (Control)
C
Phosphorus
Concentration (umol/L)
2.5
2.0
1.5
1.0
0.5
0.0
0 5 10 15 20 30 60 75 90 180 364
Time (Day)
Phosphate (Treatment)
Phosphate (Control)
DOP (Treatment)
DOP (Control)

Fig. S1

Subsample collection

Following incubation preparation, subsamples of 350 mL were collected on day 0, 1, 3, 5, 7, 10, 15, 22, 30, 60, 75, 90, 180, and 364 from both SDOM treatments (n = 3) and controls (n = 3). Of the 350 mL subsample, 300 mL was filtered through a 0.22μm polycarbonate filter and stored at -20 ˚C for subsequent DNA analysis. The filtrate from the same filter was stored at 4 ˚C for nutrient analysis. The other 50 mL were filtered with a pre-combusted Whatman® 0.7 μm GF/F filter and spiked with 50 μL 32% HCl for dissolved organic carbon (DOC) measurement.

Prokaryotic community analysis

Microbial DNA was extracted from 0.22 μm filters, using a modified phenol-chloroform protocol [1]. Briefly, thawed filter was placed in a Whirl-Pak bag, and 2 mL lysis buffer (0.1 M Tris-HCl, pH = 8.0; 0.1 M EDTA; 0.8 M sucrose) and 10 μL lysozyme (200 μg/μL) were added into the bag. The Whirl-Pak bag was incubated at 37 ˚C for 30 min, amended with 10 μL proteinase K (20 mg/mL) and 10 μL SDS (final concentration 1%), and further incubated at 37 ˚C overnight [2]. The solution was added 100 μL CTAB + NaCl (10%, 1.4 M) and incubated at 65 ˚C for 30 min. DNA was partitioned with phenol:chloroform:isoamyl alcohol (25:24:1, v/v) and chloroform:isoamyl alcohol (24:1, v/v) via centrifugation, and then precipitated by isopropanol. DNA precipitate was washed with cold ethanol (4˚C, 70%) and eluted with nuclease-free water.

The V4 region of microbial 16S rRNA gene was amplified with PCR using forward primer 515F (5'-GTGYCAGCMGCCGCGGTAA-3') [3] and reverse primer 806R (5'-GGACTACNVGGGTWTCTAAT-3') [4]. High-throughput DNA sequencing was performed on the Illumina MiSeq platform, and the raw sequences were treated using the QIIME 2 (version

2020.2) pipeline [5]. Operational taxonomic units (OTUs) were generated from raw reads by quality trimming, Dada2 denoising, and clustering, and their taxonomy were classified with SILVA database [6] by a machine learning software plugin scikit-learn [7].

Water chemical analysis

Chemical measurements were conducted following the same methods by Zhao et al. [8]. Briefly, DOC and total dissolved nitrogen (TDN) were analyzed using a Shimadzu TOC-V and aTNM-1 unit. All samples were run in triplicates and then averaged. Dissolved inorganic orthophosphate (PO_4^{3-}) was measured using EPA method 365.1 and the reaction of phosphate with ammonium molybdate and potassium antimony tartrate to form a blue-colored complex. Inorganic ammonium was quantified using the Bertholet reaction and the formation of a blue-colored compound after its reaction with sodium phenoxide. Nitrite and nitrate were measured using EPA method 353.2 and cadmium reduction of nitrate to nitrite. Nitrite is then quantified colormetrically upon its reaction with sulfanilamide and coupling to N-1-napthylethylenediamine dihydrochloride to form an azo dye. Concentration of dissolved organic nitrogen (DON) was calculated by subtracting inorganic nitrogen (NH^{4+}, NO^{3-} and NO^{2-}) from TDN.

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