Programmed cell death in diazotrophs and the fate of organic matter in the Western Tropical South Pacific Ocean during the OUTPACE cruise

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Abstract

The fate of diazotroph (N\textsubscript{2} fixers) derived carbon (C) and nitrogen (N) and their contribution to vertical export of C and N in the Western Tropical South Pacific Ocean was studied in OUTPACE (Oligotrophy to UlTra-oligotrophy PACific Experiment). Our specific objective during OUTPACE was to determine whether autocatalytic programmed cell death (PCD) is an important mechanism affecting diazotroph mortality and a factor regulating the vertical flux of organic matter and thus the fate of the blooms. We sampled at three long duration (LD) stations of 5 days each (LDA, LDB, and LDC) where drifting sediment traps were deployed at 150, 325 and 500 m depth. LDA and LDB were characterized by high chlorophyll a (Chl a) concentrations (0.2-0.6 µg L\textsuperscript{-1}) and dominated by dense biomass of Trichodesmium as well as UCYN-B and diatom-diazotroph associations \textit{(Rhizosolenia with Richelia-detected by microscopy and het-1 nifH copies)}. Station LDC was located at an ultra-oligotrophic area of the South Pacific gyre with extremely low Chl a concentration (~0.02 µg L\textsuperscript{-1}) with limited biomass of diazotrophs predominantly the unicellular UCYN-B. Our measurements of biomass from LDA and LDB yielded high activities of caspase-like and metacaspase proteases that are indicative of PCD in \textit{Trichodesmium} and other phytoplankton. Metacaspase activity, reported here for the first time from oceanic populations, was highest at the surface of both LDA and LDB, where we also obtained high concentrations of transparent exopolymeric particles (TEP). TEP was negatively correlated with dissolved inorganic phosphorus and positively coupled to both the DOC and POC pools reflecting the typically high production of TEP under nutrient stress and its role as a source of sticky carbon facilitating aggregation and rapid vertical sinking. Evidence for bloom decline was observed at both LDA and LDB. However, the physiological status and rates of decline of the blooms differed between the stations, influencing the amount of accumulated diazotrophic organic matter and mass flux observed in the traps during our experimental time frame. At LDA sediment traps contained the greatest export of particulate matter and significant numbers of both intact and decaying \textit{Trichodesmium}, UCYN-B, and het-1 compared to LDB where the bloom decline began only 2 days prior to leaving the station and to LDC where no evidence for bloom decline was seen. Substantiating previous findings from laboratory cultures linking PCD to carbon export in \textit{Trichodesmium}, our results from OUTPACE indicate that induction of PCD by nutrient limitation in high biomass blooms such as \textit{Trichodesmium} or diatom-diazotroph associations combined with high TEP production facilitates cellular aggregation and bloom termination, and expedites vertical flux to depth.
1. Introduction

The efficiency of the biological pump, essential in the transfer and sequestration of carbon to the deep ocean, depends on the balance between growth (production) and death. Moreover, the manner in which marine organisms die ultimately determine the flow of fixed organic matter within the aquatic environment and whether organic matter is incorporated into higher trophic levels, recycled within the microbial loop sustaining subsequent production, or sink out (and exported) to depth.

Important contributors to the biological pump are N$_2$ fixing (diazotrophic) prokaryotic organisms whose ability to fix atmospheric N$_2$ confers an inherent advantage in the nitrogen-limited surface waters of many regions. The oligotrophic waters of the Western Tropical South Pacific (WTSP) have been characterized by some of the highest recorded rates of N$_2$ fixation (151-700 µmol N m$^{-2}$ d$^{-1}$) (Garcia et al., 2007; Bonnet et al., 2005), and can reach up to 1200 µmol N m$^{-2}$ d$^{-1}$ (Bonnet et al., 2017b). These rates of N$_2$ fixation are accompanied with diazotrophic communities comprised of unicellular cyanobacteria lineages (UCYNA, B and C), diatom-diazotroph associations such as Richelia associated with Rhizosolenia, and diverse heterotrophic bacteria such as alpha and γ-proteobacteria. The most conspicuous of all diazotrophs, and predominating in terms of biomass, is the filamentous bloom-forming cyanobacteria Trichodesmium forming massive surface blooms that supply ∼ 60-80 Tg N yr$^{-1}$ of the 100-200 Tg N yr$^{-1}$ of the estimated marine N$_2$ fixation (Capone et al., 1997; Carpenter et al., 2004) with a large fraction fixed in the South West tropical Pacific (Dupouy et al., 2000; Dupouy et al., 2011; Tenorio et al., in review) that may, based-on NanoSIMS cell-specific measurements, contribute up to ~ 80 % of bulk N$_2$ fixation rates in the WTSP (Bonnet et al., 2017a).

How Trichodesmium or other diazotrophic blooms form and develop has been intensely investigated while little data is found regarding the fate of blooms. Trichodesmium blooms often collapse within 3-5 days, with mortality rates paralleling bloom development rates (Rodier and Le Borgne, 2008; Rodier and Le Borgne, 2010; Bergman et al., 2012). Cell mortality can occur due to grazing (O’Neil, 1998), viral lysis (Hewson et al., 2004; Ohki, 1999), and/or programmed cell death (PCD) an autocatalytic genetically controlled death (Berman-Frank et al., 2004). PCD is induced in response to oxidative and nutrient stress, as has been documented in both laboratory and natural populations of Trichodesmium (Berman-Frank et al., 2004; Berman-Frank et al., 2007) and in other phytoplankton (Bidle, 2015). The cellular and morphological features of PCD in Trichodesmium, include elevated gene expression and activity of metacaspases and caspase like-proteins important for initiation and execution of PCD; increased production of transparent exopolymeric particles (TEP) whose sticky matrix augments cell and particle aggregation; loss of buoyancy by gas-vesicle degradation resulting in rapid sinking rates (Bar-Zeev et al., 2013; Berman-Frank et al., 2004).

Simulating PCD in laboratory cultures of Trichodesmium in 2 m water columns (Bar-Zeev et al., 2013) led to a collapse of the Trichodesmium biomass and to greatly enhanced sinking of large
aggregates reaching rates of up to ~ 200 m d\(^{-1}\) that efficiently exported particulate organic carbon (POC) and particulate organic nitrogen (PON) to the bottom of the water column. Although the sinking rates and degree of export from this model system could not be extrapolated to the ocean, this study mechanistically linked autocatalytic PCD and bloom collapse to quantitative C and N export fluxes, suggesting that PCD may have an impact on the biological pump efficiency in the oceans (Bar-Zeev et al., 2013).

We further examined this issue in the open ocean and investigated the cellular processes mediating \textit{Trichodesmium} mortality in a large surface bloom from the New Caledonian lagoon (Spungin et al., 2016). Nutrient stress induced a PCD mediated crash of the \textit{Trichodesmium} bloom. The filaments and colonies were characterized by upregulated expression of metacaspase genes, downregulated expression of gas-vesicle genes, enhanced TEP production, and aggregation of the biomass (Spungin et al., 2016). However, due to experimental conditions we could not measure the subsequent export and vertical flux of the dying biomass in the open ocean. Moreover, while the existence and role of PCD and its mediation of biogeochemical cycling of organic matter has been investigated in \textit{Trichodesmium}, scarce information exists about PCD and other mortality pathways of other common marine diazotrophs.

The OUTPACE (Oligotrophy to UItra-oligotrophy PACific Experiment) cruise was conducted from 18 February to 3 April 2015 along a west to east gradient from the oligotrophic area north of New Caledonia to the ultraoligotrophic western South Pacific gyre (French Polynesia). The goal of the OUTPACE experiment was to study the diazotrophic blooms and their fate within the oligotrophic ocean in the Western Tropical South Pacific Ocean (Moutin et al., 2017). Our specific objective was to determine whether PCD was an important mechanism affecting diazotroph mortality and a factor regulating the fate of the blooms by mediation of vertical flux of organic matter. The strategy and experimental approach of the OUTPACE transect enabled sampling at three long duration (LD) stations of 5 days each (referred to as stations LDA, LDB, and LDC) and provided 5-day snapshots into diazotroph physiology, dynamics, and mortality processes. We specifically probed for the induction and operation of PCD and examined the relationship of PCD to the fate of organic matter and vertical flux from diazotrophs by the deployment of 3 sediment traps at 150, 325 and 500 m depths.
2. Methods

2.1. Sampling site and sampling conditions

Sampling was conducted on a transect during austral summer (18 Feb-5 Apr, 2015), on board of the R/V L’Atalante (Moutin et al., 2017). Samples were collected from three long duration stations (LD-A, LD-B and LD-C) where the ship remained for 5 days at each location and 15 short duration (SD1-15) stations (approximately eight hours duration). The cruise transect was divided into two geographic regions. The first region (Melanesian archipelago, MA) included SD1-12, LD-A and LD-B stations (160º E - 178º E and 170º - 175º W). The second region (subtropical gyre, GY) included SD 13-15 and LD-C stations (160º W - 169º W).

2.2. Chlorophyll a

Samples for determination of (Chl a) concentrations were collected by filtering 550 ml sea water on GF/F filters (Whatman, UK). Filters were frozen and stored in liquid nitrogen, Chl a was extracted in Methanol and measured fluorometrically (Turner Designs Trilogy Optical kit) (Le Bouteiller et al., 1992). Satellite derived surface Chl a concentrations at the LD stations were used from before and after the cruise sampling at the LD stations. Satellite Chl a data are added as supplementary video files (Supplementary videos S1, S2, S3).

2.3. Caspase and metacaspase activities

Biomass was collected on 25 mm, 0.2 µm pore-size polycarbonate filters and resuspended in 0.6-1 ml Lauber buffer [50 mM HEPES (pH 7.3), 100 mM NaCl, 10 % sucrose, 0.1 % (3-cholamidopropyl)-dimethylammonio-1-propanesulfonate, and 10 mM dithiothreitol] and sonicated on ice (four cycles of 30 seconds each) using an ultracell disruptor (Sonic Dismembrator, Fisher Scientific, Waltham, MA, USA). Cell extracts were centrifuged (10,000 x g, 2 min, room temperature), and the supernatant was collected for caspase and metacaspase activity measurements. Caspase specific activity (normalized to total protein concentration) was determined by measuring the kinetics of cleavage for the fluorogenic caspase substrate (Z-IETD-AFC) at a 50 mM final concentration (using Ex 400 nm, Em 505 nm; Synergy4 BioTek, Winooski, VT, USA), as previously described in Bar-Zeev et al. (2013).

Metacaspase specific activity (normalized to total protein concentration) was determined by measuring the kinetics of cleavage for the fluorogenic metacaspase substrate (Av-Val-Arg-Pro-Arg-AMC), (Klemenčič et al., 2015;Tsiatsiani et al., 2011) at a 50 mM final concentration (using Ex 380 nm, Em 460 nm; Synergy4 BioTek, Winooski, VT, USA) (Klemenčič et al., 2015;Tsiatsiani et al., 2011). Relative fluorescence units were converted to protein-normalized substrate cleavage rates using AFC and AMC standards (Sigma) for caspase and metacaspase activities, respectively. Total protein concentrations were determined by Pierce™ BCA protein assay kit (Thermo Scientific product #23225).
2.4. Phosphate analysis

Seawater for PO$_4^{3-}$ analysis were collected in 20 mL high-density polyethylene HCL-rinsed bottles and poisoned with HgCl$_2$ to a final concentration of 20 μg L$^{-1}$, stored at 4 °C until analysis. Phosphate (PO$_4^{3-}$, DIP) was determined by a standard colorimetric technique using a segmented flow analyzer according to Aminot and Kérouel (2007) on a SEAL Analytical AA3 HR system 20 (SEAL Analytica, Serlabo Technologies, Entraigues Sur La Sorgue, France). Quantification limits for phosphate were 0.05 μmol L$^{-1}$.

2.5. Particulate organic carbon (POC) and nitrogen (PON)

Samples were filtered through pre-combusted (4 h, 450 °C) GF/F filters (Whatman GF/F, 25 mm), dried overnight at 60 °C and stored in a desiccator until further analysis. POC and PON were determined using a CHN analyzer Perkin Elmer (Waltham, MA, USA) 2400 Series II CHNS/O Elemental Analyzer after carbonate removal from the filters using overnight fuming with concentrated HCl vapor.

2.6. Dissolved organic carbon (DOC) and Total organic carbon (TOC)

Samples were collected from the Niskin bottles in combusted glass bottles and were immediately filtered through 2 precombusted (24 h, 450 °C) glass fiber filters (Whatman GF/F, 25 mm). Filtered samples were collected into glass precombusted ampoules that were sealed immediately after filtration. Samples were acidified with Orthophosphoric acid (H$_3$PO$_4$) and analyzed by high temperature catalytic oxidation (HTCO) (Sugimura and Suzuki, 1988; Cauwet, 1994) on a Shimadzu TOC-L analyzer. TOC was determined as POC+DOC.

2.7. Transparent exopolymeric particles (TEP)

Water samples (100 mL) were gently (< 150 mbar) filtered through a 0.45 μm polycarbonate filter (GE Water & Process Technologies). Filters were then stained with a solution of 0.02 % Alcian blue (AB) and 0.06 % acetic acid (pH of 2.5), and the excess dye was removed by a quick deionized water rinse. Filters were then immersed in sulfuric acid (80 %) for 2 h, and the absorbance (787 nm) was measured spectrophotometrically (CARY 100, Varian). AB was calibrated using a purified polysaccharide gum xanthan (GX) (Passow and Allardredge, 1995). TEP concentrations (μg GX equivalents L$^{-1}$) were measured according to Passow and Alldredge (1995). To estimate the role of TEP in C cycling, the total amount of TEP-C was calculated using the TEP concentrations at each depth, and the conversion of GX equivalents to carbon applying the revised factor of 0.63 based on empirical experiments from both natural samples from different oceanic areas and phytoplankton cultures (Engel, 2004).
2.8. Diazotrophic abundance

The full description of DNA extraction, primer design and qPCR analyses are described in detail in this issue (Stenegren et al., 2017). Briefly, 2.5 L of water from 6-7 depths with surface irradiance light intensity (100, 75, 54, 36, 10, 1, and 0.1 %) were sampled and filtered onto a 25 mm diameter Supor filter (Pall Corporation, PallNorden, AB Lund Sweden) with a pore size 0.2 μm filters. Filters were stored frozen in pre-sterilized bead beater tubes (Biospec Bartlesville Ok, USA) containing 30 mL of 0.1 mm and 0.5 mm glass bead mixture. DNA was extracted from the filters using a modified protocol of the QiaGen DNAeasy plant kit (Moisander et al., 2008) and eluted in 70 μL. With the re-eluted DNA extracts ready, samples were analyzed using the qPCR instrument StepOnePlus (Applied Biosystems) and fast mode. Previously designed TaqMAN assays and oligonucleotides and standards were prepared in advance and followed previously described methods for the following cyanobacterial diazotrophs: *Trichodesmium*, UCYN-A1, UCYN-A2, UCYN-B, *Richelia* symbionts of diatoms (het-1, het-2, het-3) (Stenegren et al., 2017; Church et al., 2005; Foster et al., 2007; Moisander et al., 2010; Thompson et al., 2012).

2.9. Microscopy

Samples for microscopy were collected in parallel from the same depth profiles for nucleic acid as described in Stenegren et al. (2017). Briefly, 2 profiles were collected on day 1 and 3 at each LD station and immediately filtered onto a 47 mm diameter Poretics (Millipore, Merck Millipore, Solna, Sweden) membrane filter with a pore size of 5 μm using a peristaltic pump. After filtration samples were fixed with a 1 % paraformaldehyde (v/v) for 30 min. prior to storing at -20 °C. The filters were later mounted onto an oversized slide, and examined under an Olympus BX60 microscope equipped with blue (460-490 nm) and green (545-580 nm) excitation wavelengths. Three areas (0.94 mm²) per filter were counted separately and values were averaged. When abundances were low, the entire filter (area=1734 mm²) was observed and cells enumerated. Due to poor fluorescence, only *Trichodesmium* colonies and free-filaments could be accurately enumerated by microscopy, and in addition the larger cell diameter *Trichodesmium (Katagynemene pelagica)* was counted separately as these were often present albeit at lower densities. Other cyanobacterial diazotrophs (e.g. *Crocosphaera* watsonii-like cells, the *Richelia* symbionts of diatoms were present but with poor fluorescence and could only be qualitatively noted.

2.10. Particulate matter from sediment traps

Particulate matter export was quantified with three PPS5 sediment traps (1 m² surface collection, Technicap, France) deployed for 5 days at 150, 330 and 520 m at each LD station. Particle export was recovered in polyethylene flasks screwed on a rotary disk which allowed flasks to be changed automatically every 24-h to obtain a daily material recovery. The flasks were previously filled with a
buffered solution of formaldehyde (final conc. 2 %) and were stored at 4 °C until analysis to prevent degradation of the collected material. The flask corresponding to the fifth day of sampling on the rotary disk was not filled with formaldehyde to collect ‘fresh particulate matter’ for further diazotroph quantification. Exported particulate matter was weighed and analyzed on EA-IRMS (Integra2, Sercon Ltd) to quantify exported PC and PN.

### 2.11. Diazotroph abundance in the traps

Triplicate aliquots of 2-4 mL from the flask dedicated for diazotroph quantification were filtered onto 0.2 µm Supor filters, flash frozen in liquid nitrogen and stored in at -80 °C until analyses. Nucleic acids were extracted from the filters as described in Moisander et al. (2008) with a 30 second reduction in the agitation step in a Fast Prep cell disruptor (Thermo, Model FP120; Qbiogene, Inc. Cedex, Frame) and an elution volume of 70 µl. Diazotroph abundance for *Trichodesmium* spp., UCYN-B, UCYN-A1, het-1, and het-2 were quantified by qPCR analyses on the *nifH* gene using previously described oligonucleotides and assays (Foster et al., 2007; Church et al., 2005). The qPCR was conducted in a StepOnePlus system (applied Biosystems, Life Technologies, Stockholm Sweden) with the following parameters: 50 °C for 2 min, 95°C for 10 min, and 45 cycles of 95°C for 15s followed by 60°C for 1 min. Gene copy numbers were calculated from the mean cycle threshold (Ct) value of three replicates and the standard curve for the appropriate primer and probe set. For each primer and probe set, duplicate standard curves were made from 10-fold dilution series ranging from 108 to 1 gene copies per reaction. The standard curves were made from linearized plasmids of the target *nifH* or from synthesized gBLocks gene fragments (IDT technologies, Cralville, Iowa USA). Regression analyses of the results (number of cycles=Ct) of the standard curves were analyzed in Excel. 2 µl of 5 KDa filtered nuclease free water was used for the no template controls (NTCs). No *nifH* copies were detected for any target in the NTC. In some samples only 1 or 2 of the 3 replicates produced an amplification signal; these were noted as detectable but not quantifiable (dnq). A 4th replicate was used to estimate the reaction efficiency for the *Trichodesmium* and UCYN-B targets as previously described in (Short et al., 2004). Seven and two samples were below 95 % in reaction efficiency for *Trichodesmium* and UCYN-B, respectively. The detection limit for the qPCR assays is 1-10 copies.

### 2.12. Statistics

A Pearson correlation coefficient test was applied to examine the association between two variables after linear regressions or log transformation of the data. Statistical analyses were carried out with XLSTAT, a Microsoft Office Excel based software.
3. Results and discussion

3.1. Diazotrophic characteristics and abundance in the LD stations

The sampling strategy of the transect was planned so that changes in abundance and fate of diazotrophs could be followed in “long duration” stations where measurements were taken from the same water mass (and location) over 5 days and drifting sediment traps were deployed (Moutin et al., 2017). Although rates for the different parameters were obtained for 5 days, this period is still a “snapshot” in time with the processes measured influenced by preceding events and also continuing after the ship departed. Specifically, production of photosynthetic biomass (as determined from satellite-derived Chl a) and development of surface phytoplankton blooms, including cyanobacterial diazotrophs, displayed specific characteristics for each of the long duration stations. We first examined the satellite-derived surface Chl a concentrations by looking at changes around the long duration (LD) stations before and after our 5 day sampling at each station [daily surface Chl a (mg m⁻³)] (Supplementary videos S1, S2, S3).

At LDA, satellite data confirmed high concentrations of Chl a indicative of intense surface blooms (~ 0.55 µg L⁻¹) between 8.02.15 to 19.02.15 which began to gradually decline with over 60 % Chl a reduction until day 1 at the station (Supplementary video S1, Fig. 1a). By the time we reached LDA on 25.02.15 (day 1) Chl a concentrations averaged ~ 0.2 µg L⁻¹ Chl a at the surface (Fig. 1a) and remained steady for the next 5 days with Chl a values of 0.23 µg L⁻¹ measured on day 5 (Fig 1a). When looking for biomass at depth the DCM recorded at ~ 80 m depth was characterized by Chl a concentrations increasing from 0.34 to 0.48 µg L⁻¹ between day 3 and 5 respectively (Fig. 1d). While the Chl a values of the surface biomass decreased for approximately one week prior to our sampling at station, the Chl a concentrations measured at depth increased during the corresponding time.

In contrast to LDA, the satellite data from LDB confirmed the presence of a surface bloom/s for over one month prior to our arrival at the station on 15.3.15 (day 1) (Supplementary video S2, Fig. 1b). This bloom was characterized by high surface Chl a concentrations (~ 0.6 µg L⁻¹, Supplementary video S2) and on day 1 at the station surface Chl a was 0.58 µg L⁻¹ (Fig. 1b). Surface Chl a then decreased over the next days at the station with a 50 % reduction of Chl a concentration from the sea surface (5m) on day 5 (0.35 µg L⁻¹) (Fig. 1e). Thus, it appears that our 5 sampling days at LDB were tracking a surface bloom that had only began to decline after day 3 and continued to decrease (~ 0.1 µg L⁻¹) also after we have left (Fig.1b). On day 1 of sampling, the DCM at LDB was relatively shallow, at 40 m with Chl a values of 0.5 µg L⁻¹. By day 5 the DCM had deepened to 80 m (de Verneil et al., 2017).

LDC was located in a region of extreme oligotrophy within the Cook Islands territorial waters (GY waters). This station was characterized historically (~ 4 weeks before arrival) by extremely low Chl a concentrations at the surface (~ 0.02 µg L⁻¹, Supplementary video S3) that were an order of
magnitude lower than average Chl a measured at LDA and LDB. These values remained low with no significant variability for the 5 days at station or later (Fig. 1f) (Supplementary video S3, Fig. 1c).

Similar to the results from LDA, the DCM at LDC was found near the bottom of the photic layer at ~135 m, with Chl a concentrations about 10-fold higher than those measured at surface with ~ 0.2 µg L⁻¹ (Fig. 1f).

Chl a is an indirect proxy of photosynthetic biomass and we thus needed to ascertain who the dominant players (specifically targeting diazotrophic populations) were at each of the LD stations. Moreover, At LDA and LDB diazotrophic composition and abundance as determined by qPCR analysis were quite similar. At LDA Trichodesmium was the most abundant diazotroph, ranging between 6x10⁴ - 1x10⁶ nifH copies L⁻¹ in the upper water column (0-70 m). UCYN-B (genetically identical to Crocosphaera watsonii) co-occurred with Trichodesmium between 35 and 70 m, and het1 specifically identifying the diatom-diazotroph association (DDA) between the diatom Rhizosolenia and the heterocystous diazotroph Richelia, was observed only at the surface waters at 4 m. UCYN-B and het-1 abundances were relatively lower than Trichodesmium abundances with 2x10⁵ nifH copies L⁻¹ and 3x10⁵ nifH copies L⁻¹ respectively (Stenegren et al., 2017). Microscopic observations from LDA indicated that near the surface Rhizosolenia populations were already showing signs of decay since the silicified cell-wall frustules were broken and free filaments of Richelia were observed (Fig. 2e-f) (Stenegren et al., 2017). DDAs are significant N₂ fixers in the oligotrophic oceans. Although their abundance in the WTSP is usually low, they are common and highly abundant in the New Caledonian lagoon significantly impacting C sequestration and rapid sinking (Turk-Kubo et al., 2015).

At LDB, Trichodesmium was also the most abundant diazotroph with nifH copies L⁻¹ ranging between 1x10⁴ - 5x10⁵ within the top 60 m (Stenegren et al., 2017). Microscopical analyses confirmed high abundance of free filaments of Trichodesmium at LDB, while colonies were rarely observed (Stenegren et al., 2017). Observations of poor cell integrity were reported for most collected samples, with filaments at various stages of degradation and colonies under possible stress (Fig. 2a-d). In addition to Trichodesmium, UCYN-B was the second most abundant diazotroph ranging between 1x10⁴ and 2x10⁵ nifH copies L⁻¹. Other unicellular diazotrophs of the UCYN groups (UCYN-A1 and UCYN-A2) were the least detected diazotrophs (Stenegren et al., 2017). Of the three heterocystous cyanobacterial symbiont lineages (het-1, het-2, het-3), het-1 was the most dominant (1x10³ - 4x10⁴ nifH copies L⁻¹), (Stenegren et al., 2017). Microscopic analyses from LDB demonstrated the co-occurrence of degrading diatom cells, mainly belonging to Rhizosolenia (Stenegren et al., 2017) (Fig. 2e-f).

In contrast to LDA and LDB, at LDC, the highest nifH copy numbers (up to 6x10⁵ nifH copies L⁻¹) at 60 m depth were from the unicellular diazotrophs UCYN-B (Stenegren et al., 2017) Trichodesmium was only detected at 60 m and with very low copy numbers of nifH (~7x10² nifH copies L⁻¹) (Stenegren et al., 2017).
Corresponding to the physiological status of the bloom, higher N$_2$ fixation rates (45.0 nmol N L$^{-1}$ d$^{-1}$) were measured in the surface waters (5m) of LDB in comparison with those measured at LDA and LDC (19.3 nmol N L$^{-1}$ d$^{-1}$ in LDA and below the detection limit at LDC at 5m), (Caffin et al., 2017).

3.2. Diazotrophic bloom demise in the LD stations

Of the 3 long duration stations we examined, LDA and LDB had a higher biomass of diazotrophs during the 5 days of sampling and as shown (section 3.1). Furthermore, while our analyses examining bloom dynamics show these stations experiencing different stages of decline from the satellite-derived Chl $\alpha$ concentrations, both LDA and LDB were still characterized by high (and visible to the eye at surface) biomass on the first sampling day at each station (day 1) as determined by qPCR and microscopy (Stenegren et al., this issue). This is different from LDC where biomass was extremely limited, and no clear evidence was obtained for any specific bloom or bloom demise. We therefore show results mostly from LDA and LDB and focus specifically on the evidence for PCD and diazotroph decline in areas with high biomass and surface blooms.

Although the mortality of phytoplankton at sea can be difficult to discern as it results from several processes (grazing, viral lysis, PCD), not necessarily acting independently of one another, we here focused on evidence for PCD and whether the influence of zooplankton grazing on the diazotrophs and especially on *Trichodesmium* at LDA and LDB impacted bloom dynamics. At LDA and LDB total zooplankton population was generally low. Total zooplankton population at LDA ranged between 911-1900 individuals m$^{-3}$ and in LDB between 1209-2188 individuals m$^{-3}$ on day 1 and day 5 respectively. *Trichodesmium* is toxic and inedible to most zooplankton excluding three species of harpacticoid zooplankton (O’Neil and Roman, 1994). During our sampling days at these stations, *Macrosettella gracilis* a specific grazer of *Trichodesmium* comprised less than 1 % of the total zooplankton community with another grazer *Miracia efferata* comprising less than 0.1 % of total zooplankton community. *Oculosetella gracilis* was not found at these stations. The low number of harpacticoid zooplankton specifically grazing on *Trichodesmium* found in the LDA and LDB station, refutes the possibility that grazing caused the massive demise of the bloom. Moreover, the toxicity of *Trichodesmium* to many grazers (Rodier and Le Borgne, 2008; Kerbrat et al., 2011) could critically limit the amount of *Trichodesmium*-derived recycled matter within the upper mixed layer. Virus abundance and activity were not enumerated in this study, so we cannot estimate their influence on mortality.

Previous studies demonstrated that limited availability of Fe and P induce PCD in *Trichodesmium*. At LDA and LDB, Fe concentrations were relatively high, possibly due to island effects (de Verneil et al., 2017), that could have created favorable conditions for diazotrophs that require high Fe for the energy expensive processes of N$_2$ fixation and photosynthesis and thus could enhance the potential for increased growth rates and the formation of dense surface blooms.
Phosphorus availability, or lack of phosphorus, can also induce PCD (Berman-Frank et al., 2004; Spungin et al., 2016). \( \text{PO}_4^{3-} \) concentrations at the surface (0-40m) of LDA and LDB stations were extremely low around 0.05 \( \mu \text{mol L}^{-1} \) (de Verneil et al., 2017), possibly consumed by the high biomass and high growth rates of the bloom causing nutrient stress and bloom mortality. \( \text{PO}_4^{3-} \) concentrations observed at LDC were above the quantification limit with average values of 0.2 \( \mu \text{mol L}^{-1} \) in the 0-150 m depths (data not shown). These limited P concentrations may curtail the extent of growth, induce PCD, and pose an upper limit on biomass formation.

Here we compared, for the first time in oceanic populations, two PCD indices, caspase and metacaspase activities, to examine the presence/operation of PCD in the predominant phytoplankton (and diazotroph) populations along the transect. We specifically show the results from LDA and LDB where biomass and activities were detectable. Classic caspases are absent in phytoplankton, including in cyanobacteria, and are unique to metazoans and several viruses (Minina et al., 2017). In diverse phytoplankton the presence of a C14 caspase domain suffices to demonstrate caspase-like proteolytic activity that occurs upon PCD induction when the caspase specific substrate IETD-AFC is added. Cyanobacteria and many diazotrophs do contain genes that are similar to caspases, the metacaspases-cysteine proteases that share structural properties with caspases, specifically a histidine-cysteine catalytic dyad in the predicted active site (Tsiatsiani et al., 2011). While the specific role and functions of these genes are unknown, preliminary investigations have indicated that when PCD is induced some of these genes are upregulated (Bidle and Bender, 2008; Spungin et al., 2016). Of the abundant diazotrophic populations at LDA and LDB 12 metacaspases have previously been identified in *Trichodesmium* (Asplund-Samuelsson et al., 2012; Asplund-Samuelsson, 2015; Jiang et al., 2010; Spungin et al., 2016). Phylogenetic analysis of a wide diversity of truncated metacaspase proteins, containing the conserved and characteristic caspase super family (CASc; cl00042) domain structure, revealed metacaspase genes in both *Richelia* (het-1) from the diatom-diazotroph association and *Crocosphaera watsonii* (a cultivated unicellular cyanobacterium) which is genetically identical to the UCYN-B *nifH* sequences (Spungin et al., unpublished data).

We compared between metacaspase and caspase-like activities for the > 0.2 \( \mu \text{m} \) fraction sampled assuming that the greatest activity would be due to the principle organisms contributing to the biomass – i.e the diazotrophic cyanobacteria. Caspase activity and metacaspase activity were specifically measured during all LD stations (days 1,3,5) at 5 depths between 0-200 m. Caspase activity at the surface waters (50 m) at LDA, as determined by the cleavage of IETD-AFC substrate, was between 2.3±0.1-2.8±0.1 pM hydrolyzed mg protein\(^{-1}\) on days 1 and 3 respectively (Fig. 3a). The highest activity was measured on day 5 at 50 m with 5.1±0.1 pM hydrolyzed mg protein\(^{-1}\). Similar trends were obtained at LDA for metacaspase activity as measured by the cleavage of the VRPR-AMC substrate, containing an Arg residue at the P1 position, specific for metacaspase cleavage, (Tsiatsiani et al., 2011; Klemenčič et al., 2015). High and similar metacaspase activities were measured on days 1...
and 3 (50 m) with 32±4 and 35±0.2 pM hydrolyzed mg protein$^{-1}$ respectively (Fig. 3a). The highest metacaspase activity was measured on day 5 at 50 m with 59±1 pM hydrolyzed mg protein$^{-1}$ at 50 m decreasing with depth (Fig. 3b).

Caspase activity at LDB, was similar at all sampling days, with highest activity at the surface, ranging from 3±0.1 to 4.5±0.2 pM hydrolyzed mg protein$^{-1}$ min$^{-1}$ at 7 m depth and then decreasing with depth (Fig. 3d). At day 3 caspase activity at LDB increased at the surface with 4.5±0.2 pM hydrolyzed mg protein$^{-1}$ min$^{-1}$ and then declined by day 5 back to 3±0.1 pM hydrolyzed mg protein$^{-1}$ min$^{-1}$. The decrease in activity at the surface between day 3 and 5 was accompanied by an increase in caspase activity measured in the DCM between day 3 and 5 (Fig. 3d). Caspase activity at the DCM at day 3 (35 m) was 1±0.4 pM hydrolyzed mg protein$^{-1}$ min$^{-1}$ and by day 5 increased to 3±0.1 pM hydrolyzed mg protein$^{-1}$ min$^{-1}$ at the 70 m depth of the DCM. Thus, at LDB, caspase activity increased from day 1 to 5 and with depth, with higher activities that initially were recorded at surface and then at depth coupled with the decline of the bloom (Fig. 3d). Similar trends were obtained at LDB for metacaspase activity with the 11.1±pM hydrolyzed mg protein$^{-1}$ min$^{-1}$ at the surface (7 m) on day 1. A 4-fold increase in activity was measured at the surface on day 3 with 40.1±5 pM hydrolyzed mg protein$^{-1}$ min$^{-1}$ (Fig. 3e). Similar high activities were measured also on day 5 (Fig. 3e). However, the increase in activity was also pronounced at depth of ~ 70 m and not only at the surface. Metacaspase activity at day 5 was the highest with 40.3±0.5 and 44.6±5 pM hydrolyzed mg protein$^{-1}$ min$^{-1}$ at 7 and 70 m respectively (Fig 3e). The relatively low metacaspase activity at day 1, corresponds with the physiological stage of the bloom, which we believe was just prior to enhanced mortality and death. Metacaspase activity increased corresponding with the pronounced decline in Chl a from day 1 to day 5 (Fig. 1b).

Metacaspase activities were generally 10-fold higher than caspase activity rates obtained (Fig 3). Metacaspase and caspase activities are significantly and positively correlated at LDA and LDB ($r=0.8$, $p<0.05$ and $r=0.8$ $p<0.001$ for LDA and LDB respectively) (Fig. 3c and 3f). Both findings (i.e. higher metacaspase activity and tight correlation between metacaspase and caspases) were demonstrated specifically in cultures and natural populations of *Trichodesmium* undergoing PCD (Spungin et al., unpublished). *Trichodesmium* metacaspases are substrate specific, and activity is enhanced as PCD progresses (Spungin et al. unpublished). We do not know what protein is responsible for the caspase-specific activities and what drivers regulate it. Yet, the tight correlation between both activities specifically for *Trichodesmium*, and here at LDA and LDB suggest that both activities occur in the cell when PCD is induced. To date, we are not aware of any previous studies examining metacaspase or caspase activity (or the existence of PCD) in diatom-diazotroph associations such as *Rhizosolenia* and *Richelia*. 


3.3. TEP dynamics and carbon pools

Transparent exopolymERIC particles, that are formed both biotically and abiotically in the ocean, link between the particulate and dissolved carbon fractions and act to augment the coagulation of colloidal precursors from the dissolved organic matter and from biotic debris and to increase vertical carbon flux (Passow, 2002; Verdugo and Santschi, 2010). TEP production also increases upon PCD induction – specifically in large bloom forming organisms such as Trichodesmium (Berman-Frank et al., 2007; Bar-Zeew et al., 2013).

At LDA, TEP concentrations at 50 m depth were highest at day 1 with measured concentrations of 562±7 µg GX L⁻¹ (Table. 1) that appear to correspond with the declining physiological status of the cells that were sampled at that time (Fig. 2a-d). TEP concentrations during days 3 and 5 decreased to less than 350 µg GX L⁻¹, and it is possible that most of the TEP had been formed and sank prior to our measurements in the LDA.

At LDB, TEP concentrations at day 1 and 3 were similar with ~400 µg GX L⁻¹ at the surface (7 m) while concentrations decreased about 2-fold with depth, averaging at 220±56 and 253±32 µg GX L⁻¹ (35-200 m) for day 1 and 3 respectively (Fig. 4a, Table 2). A significant (>150 %) increase in TEP concentrations was observed on day 5 compared to previous days, with TEP values of 597±69 µg GX L⁻¹ at the surface (7m) (Fig 4b, Table 2). Although TEP concentrations were elevated at surface, the difference in averaged TEP concentrations observed at the deeper depths (35-200 m) between day 3 (157±28 µg GX L⁻¹) and day 5 (253±32 GX L⁻¹) indicated that TEP from the surface was either breaking down or sinking to depth (Fig. 4a, Table 2). Our measured TEP concentrations correspond with values and trends reported from other marine environments (Engel, 2004; Bar-Zeew et al., 2009) and specifically with TEP concentrations measured from the New Caledonian lagoon (Berman-Frank et al., 2016).

TEP is produced by many phytoplankton including cyanobacteria under conditions uncoupling growth from photosynthesis (i.e. nutrient but not carbon limitation) (Berman-Frank and Dubinsky, 1999; Passow, 2002; Berman-Frank et al., 2007). Decreasing availability of dissolved nutrients such as nitrate and phosphate has been correlated with increased TEP concentrations in both cultured phytoplankton and natural marine systems (Bar-Zeew et al., 2013; Brussaard et al., 2005; Engel et al., 2002; Urbani et al., 2005). TEP production in Trichodesmium is enhanced as a function of nutrient stress (Berman-Frank et al., 2007) yet, Crocosphaera watsonii (similar to UCYN-B) (>4 µm cell size) also produces large amounts of extracellular polysaccharides (EPS) during exponential growth (Sohm et al., 2011).

In the New Caledonian coral lagoon TEP concentrations were negatively correlated with ambient concentrations of dissolved inorganic phosphorus (DIP) (Berman-Frank et al., 2016). Here, at LDB a significant negative correlation of TEP with DIP was also observed (Fig. 4b, p<0.001),...
suggesting that lack of phosphorus set a limit to continued biomass increase and stimulated TEP production in the nutrient-stressed cells. TEP production was also positively correlated with metacaspase activity at all days (Fig. 4c, p<0.05) further indicating that biomass undergoing PCD produced more TEP. In the diatom Rhizosolenia setigera TEP concentrations increased during the stationary- decline phase (Fukao et al., 2010) and could also affect buoyancy. PCD in Trichodesmium leading to elevated production of TEP and aggregation has been previously shown in Trichodesmium cultures (Berman-Frank et al., 2007; Bar-Zeev et al., 2013) and here in oceanic populations as the bloom declined (Fig. 4c) (Spungin et al., 2016).

TEP concentrations at LDB were positively correlated to TOC, POC, and DOC (Fig. 4d-f) confirming the integral part of TEP in the cycling of carbon at this station. Assuming a carbon content of 63 % (w/w), (Engel, 2004) we estimate that TEP contributes to the organic carbon pool in the order of ~ 80-400 µg C L^{-1} (Table 1 and Table 2) with the percentage of TEP-C from TOC ranging between 0.08-42 % and 11-32 % at LDA and LDB respectively (Table 1 and 2, taking into account spatial and temporal differences). Thus, at LDB, surface TEP-C increased from 22 % at day 3 to 32 % of the TOC content at day 5. Yet, for the same time period a 2-fold increase of TEP was measured at 200 m (11 % to 21 %). These results reflect the bloom status at LDB. During bloom development; organic C and N are incorporated to the cells and little biotic TEP production occurs while stationary growth (as long as photosynthesis continues) stimulates TEP production (Berman-Frank and Dubinsky, 1999). When mortality exceeds growth, the presence of large amounts of sticky TEP provide “hot spots” or substrates for bacterial activity and facilitate aggregation of particles and enhanced sinking rates of aggregates as previously observed for Trichodesmium (Bar-Zeev et al., 2013).

3.4. Linking PCD-induced bloom demise to particulate C and N export

Measurements of elevated rates metacaspase and caspase activities and changes in TEP concentrations are not sufficient to link PCD and vertical export of organic matter as was previously shown in laboratory cultures of Trichodesmium (Bar-Zeev et al., 2013). To see whether PCD-induced mortality led to enhanced carbon flux at sea we now examined mass flux and specific evidence for diazotrophic contributions from the drifting sediment traps (150, 330 and 520 m) at LDA and LDB stations.

Mass flux was measured at LDA, increasing over time with maximum mass flux rates at the 150 m trap with 123 dry weight (DW) m^{-2} d^{-1} on day 4. The highest mass flux was 40 and 27 DW m^{-2} d^{-1} from the deeper sediment traps (325 and 500 m traps respectively). Particulate C (PC) and particulate nitrogen (PN) showed similar trends as the mass flux. At LDA, PC varied between 3.2-30 mg sample^{-1} and PN ranged from 0.3-3.17 mg sample^{-1} at the 150 m trap. At LDB PC varied from 1.6 to 6.1 mg sample^{-1} and total particulate nitrogen ranged from 0.24 to 0.78 mg sample^{-1}. The total sediment flux in the traps deployed at LDB ranged between 6.4 and 33.5 mg m^{-2} d^{-1}, with an average of 18.9 mg m^{-2}.
d^{-1}. Excluding the deepest trap at 500 m where the high flux occurred at day 2, in the other traps the highest export flux rate occurred at the last day at the station (day 5).

Analyses of the community found in the sediment traps, determined by qPCR from the accumulated matter on day 5 at the station, confirmed that *Trichodesmium*, UCYN-B and het-1 were the most abundant diazotrophs in the sediment traps at LDA and LDB stations (Caffin et al., 2017), correlating to the dominant diazotrophs found at the surface of the ocean (measured on day 1). *Trichodesmium* and Richelia-Rhizosolenia association (het-1) were the major contributors to diazotroph export at LDA and LDB and UCYN-B and het-1 were the major contributors at LDC (Caffin et al., 2017). At LDA *Trichodesmium* was found in the deeper depth traps with 2.6 x 10^7 and 1.4 x 10^7 nifH copies L^{-1} at the 325 and 500 traps respectively. UCYN-B was detected in all traps with the highest abundance in deeper depth traps with values of 4.2 x 10^6 and 2.8 x 10^6 nifH copies L^{-1} at the 325 and 500 traps respectively. Het-1 was specifically found only in the 325 m trap with 2.0 x 10^7 nifH copies L^{-1} (Fig. 5a). In LDB traps, *Trichodesmium*, UCYN-B and het-1 were not detected at the sediment trap at 150 m, rather in the deeper traps. At depth *Trichodesmium* counts were 9 x 10^5 at 325 m trap and 5 x 10^6 nifH copies L^{-1} for the 500 m trap (Fig. 5b). UCYN-B was 3.6 x 10^7 and 10 x 10^6 nifH copies L^{-1} at 325 and 500 m traps respectively, and 6 x 10^6 and 1 x 10^7 nifH copies L^{-1} of het-1 (Fig. 5b).

While the average size of *Trichodesmium* and the association between Rhizosolenia and Richelia is relatively large for microphytoplankton, the small unicellular UCYN-B (< 4 µm) were also found in the sediment traps, including the deeper (500 m) traps. UCYN-B is often associated with larger phytoplankton such as the diatom *Climacodium frauenfeldianum* (Bench et al., 2013) or in colonial phenotypes (> 10 µm fraction) as has been observed in the northern tropical Pacific (ALOHA) (Foster et al., 2013). The only other detection of UCYN-B in sediment traps was during the VAHINE mesocosm experiment in the New Caledonian lagoon where sediment traps were deployed at shallower depths (15 m) (Bonnet et al., 2015) and in high abundance in a floating sediment trap deployed at 75 m for 24 h is the North Pacific Subtropical Gyre (Sohm et al., 2011). Thus our data substantiates earlier conclusions that UCYN, which form large aggregates (increasing actual size and sinking velocities), can efficiently contribute to export in oligotrophic systems (Bonnet et al., 2015).

Increase in aggregate size could also occur with depth, possibly due to the high concentrations of TEP produced at the surface layer, sinking in the water column, providing a nutrient source and enhancing aggregation (Berman-Frank et al., 2016) which could also increase in size with depth due to TEP.

While this process was previously shown during a mesocosm experiment (Bonnet et al., 2015), it is now shown to be applicable also in the open-ocean system.

Sinking rates of aggregates in the water depends on many factors such as fluid viscosity, particle source material, morphology, density, and other variable particle characteristics. Sinking velocities of diatoms embedded in aggregates are generally fast (50-200 m d^{-1}) (Asper, 1987; Alldredge, 1998) compared with those of individually sinking cells (1-10 m d^{-1}) (Culver and Smith, 1989) allowing...
aggregated particles to sink out of the photic zone to depth. Assuming a sinking rate of

Trichodesmium-based aggregates of 150-200 m d\(^{-1}\) (Bar-Zeev et al., 2013), we would need to shift the
time frame by 1 day to see whether PCD measured from the surface waters is coupled with changes in
organic matter reflected in the 150 m sediment traps. Thus, at LDA, examining metacaspase activities
from the surface with mass flux and particulate matter obtained 24 h later yielded a significant positive
correlation between these two parameters (Fig. 5c).

LDA had the highest export fluxes and particulate matter found in its traps relative to LDB and
LDC. Diazotrophs contributed ~ 36 % to PC export to the 325 m trap at LDA, with Trichodesmium
comprising the bulk of diazotrophs (Caffin et al., 2017) In contrast, at LDB, we found lower flux rates
in the traps and lower organic material with Trichodesmium contributing the bulk of diazotroph
biomass at the 150 m trap. We believe that at LDB the decline phase began only halfway through our
sampling and thus the resulting export efficiency we obtained for the 5 days at station was relatively
low compared to the total amount of surface biomass. Moreover, considering export rates, and the
experimental time frame, most of the diazotrophic population may have been directly exported to the
traps only after we left the station (i.e. time frame > 5 days). This situation is different from the bloom
at LDA, where enhanced mortality, biomass deterioration, and bloom crash were initiated 1-2 weeks
before our arrival and sampling at the station. Thus, at LDA, elevated mass flux and higher
concentrations of organic matter were obtained from all three depths of the deployed traps.

4. Conclusion and implications

Our specific objective in this study was to examine whether diazotroph mortality mediated by
PCD can lead to higher fluxes of organic matter sinking to depth. The OUTPACE cruise provided this
opportunity in two out of three long-duration (5 day) stations where large surface blooms of
diazotrophs principally comprised of Trichodesmium, UCYN-B and diatom-diazotroph associations
Rhizosolenia and Richelia were encountered. Probing the biomass for characteristic indices of PCD
demonstrated high metacaspase activities, positively and significantly correlated to caspase-like
activities at both LDA and LDB, and reported here for the first time (metacaspase activity) in oceanic
populations of Richelia and Trichodesmium. We further show that TEP, facilitating aggregation of
biomass and enhancing sinking velocities, was high at both locations and changed with depth as
biomass declined. Moreover, we were able to specifically link for the first time in the open ocean
between blooms mediated by PCD and vertical fluxes through the deployment of sediment traps.

Yet, our results also delineate the natural variability of biological oceanic populations. The two
stations, LDA and LDB were characterized by biomass at physiologically different stages with the
biomass at LDA displaying more pronounced mortality that had begun prior to our arrival at station. In
contrast, satellite data indicated that at LDB, the surface Trichodesmium bloom was sustained for at
least a month prior to arrival and remained high for the first 3 days of our sampling before declining
by 40 % at day 5. As sediment trap material was examined during a short time frame of only 5 days at
each LD station, we assume that a proportion of the sinking diazotrophs and organic matter were not yet collected in the traps and had either sunk before trap deployment or would sink after we left the stations. Thus, these different historical conditions which influence physiological status at each location also impacted the specific results we obtained and emphasized a-priori the importance of comprehensive spatial and temporal sampling that would facilitate a more holistic understanding of the dynamics and consequences of bloom formation and fate in the oceans.

Author contributions

IBF, DS, and SB conceived and designed the investigation linking PCD to vertical flux within the OUTPACE project. NB, MS, AC, MPP, NL, CD and RAF participated, collected and performed analyses of samples, DS analysed samples and data. DS and IBF wrote the manuscript with contributions from all co-authors.

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References


Berman-Frank, I., and Dubinsky, Z.: Balanced growth in aquatic plants: Myth or reality? Phytoplankton use the imbalance between carbon assimilation and biomass production to their strategic advantage, Bioscience, 49, 29-37, 1999.


Bonnet, S., Caffin, M., Berthelot, H., Grosso, O., Guieu, C., and Moutin, T.: Contribution of dissolved and particulate fractions to the Hot Spot of N₂ fixation in the Western Tropical South Pacific Ocean (OUTPACE cruise), Biogeosciences, in review, 2017a.


Figure legends

Figure 1- Temporal dynamics of surface chlorophyll-a concentrations in the long duration (LD) stations (a) LDA (b) LDB and (c) LDC station. Chlorophyll a was measured over 5 days at each station (marked in gray). Satellite data of daily surface chlorophyll a (mg m\(^{-3}\)) around the long duration stations of OUTPACE was used to predict changes in photosynthetic biomass before and after our measurements at the station (marked as dashed lines). Satellite data movies are added as supplementary data (Supplementary videos S1, S2, S3). Chlorophyll a profiles in (d) LDA (e) LDB and (f) LDC. Measurements of Chl a were taken on days 1 (black dot), 3 (white triangle) and 5 (grey square) at the LDB station at 5 depths between surface and 200 m depths.

Figure 2- (a-d) Microscopic images of *Trichodesmium* from LDA and LDB. Observations of poor cell integrity were reported for collected samples, with filaments at various stages of degradation and colony under possible stress. (e) Confocal and (d) processed IMARIS images of *Rhizosolenia-Richelia* symbioses (het-1) at 6m (75 % surface incidence). Green fluorescence indicate the chloroplast of the diatoms, and red fluorescence are the *Richelia* filaments; Microscopic observations indicate that near the surface *Rhizosolenia* populations were already showing signs of decay since the silicified cell-wall frustules were broken and free filaments of *Richelia* were observed. Images by Andrea Caputo.

Figure 3- PCD indices from LDA and LDB (a) Caspase activity from LDA (pM hydrolyzed mg protein\(^{-1}\) min\(^{-1}\)) assessed by cleavage of the canonical fluorogenic substrate, z-IETD-AFC. (b) Metacaspase activity from LDA (pM hydrolyzed mg protein\(^{-1}\) min\(^{-1}\)) assessed by cleavage of the canonical fluorogenic substrate, VRPR-AMC. (c) Relationship between caspase activity and metacaspase activity from LDA (R\(^2\)=0.7, n=15, p<0.001). (d) Caspase activity rats in LDB station (pM hydrolyzed mg protein\(^{-1}\) min\(^{-1}\)), (e) Metacaspase activity in LDB station (pmol hydrolyzed mg protein\(^{-1}\) min\(^{-1}\)), (f) Relationship between caspase activity and metacaspase activity in LDB station (R\(^2\)=0.6, n=15, p<0.001). Caspase and metacaspase activites at LDA and LDB stations were measured on days: 1(black dot), 3 (white triangle) and 5 (grey square) between surface and 200 m. Error bars represent ± 1 standard deviation (n=3).

Figure 4- (a) Depth profiles of TEP concentrations (µg GX L\(^{-1}\)) at LDB station. Measurements were taken on days 1, 3 and 5 at the station at surface-200 m depths. (b) The relationships between the concentration of transparent exopolymeric particles (TEP), (µg GX L\(^{-1}\)) and dissolved inorganic phosphorus DIP (µmol L\(^{-1}\)) for days 1, 3 and 5 at the LDB station (R\(^2\)=0.5, n=15, p<0.001). Relationships between the concentration of transparent exopolymeric particles (TEP), (µg GX L\(^{-1}\)) and (c) metacaspase activity (pmol hydrolyzed mg protein\(^{-1}\) min\(^{-1}\)) for days 1, 3 and 5 at the LDB (R\(^2\)=0.4, n=15, p<0.05); (d) and with dissolved organic carbon (DOC), (µM) for days 1, 3 and 5 at the LDB.
station ($R^2=0.58$, $n=15$, $p<0.001$) (e) and with particulate organic carbon (POC) ($\mu$M) for days 1, 3 and
5 at the LDB station ($R^2=0.85$, $n=8$, $p<0.001$ for day 1 and $R^2=0.97$, $n=5$ $p<0.01$ for day 3 and 5) (f)
and with total organic carbon (TOC) ($\mu$M) for days 1, 3 and 5 at the LDB station ($R^2=0.65$, $n=15$,
$p<0.0001$). Measurements were taken on days 1 (black dot), 3 (white triangle) and 5 (grey square) at
LDB at 5 depths between surface and 200 m depths. Error bars for TEP represent ± 1 standard
deviation ($n=3$).

**Figure 5** (a) Diazotrophic abundance ($nifH$ copies L$^{-1}$) of *Trichodesmium* (dark grey bars); UCYN-B
(white bars); and het-1 (light grey bars) recovered in sediment traps at the long duration stations (A)
Diazotrophic abundance ($nifH$ copies L$^{-1}$) observed in the traps at LDA station (b) Diazotrophic
abundance ($nifH$ copies L$^{-1}$) observed in the traps at LDB station. Abundance was measured from the
accumulated material on day 5 at each station. Sediment traps were deployed at the LD station at 150
m, 325 m, and 500 m. Error bars represent ± 1 standard deviation ($n=3$). (e) Relationship between
metacaspase activity (pmol hydrolyzed mg protein$^{-1}$ min$^{-1}$) measured at the surface waters of LDA
station and mass flux rates (mg m$^{-2}$ h$^{-1}$) (green circle), particulate carbon (PC, mg sample$^{-1}$) (green
triangle) and particulate nitrogen (PN, mg sample$^{-1}$) (green square) measured in the sediment trap
deployed at 150 m. A 1-day shift between metacaspase activities at the surface showed a significant
positive correlation with mass flux and particulate matter obtained in the sediment trap at LDA station
at 150 m.
Table 1- Temporal changes in the relative composition (w/w) and distribution of TEP, TEP-C and organic carbon and nitrogen fractions within the water column during days 1, 3 and 5 in the LDA station at different depth ranging between surface (10 m) to 200 m.

<table>
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<tr>
<th>Day at LDA station</th>
<th>Depth (m)</th>
<th>TEP (µg GX L⁻¹)</th>
<th>TEP-C</th>
<th>%TEP-C</th>
<th>POC (µM)</th>
<th>TOC (µM)</th>
<th>POC/PON</th>
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Abbreviations: TEP, transparent exopolymeric particle; TEP-C, TEP carbon; POC, particulate organic C; TOC, total organic C; ND- no data.

Table 2- Temporal changes in the relative composition (w/w) and distribution of TEP, TEP-C and organic carbon and nitrogen fractions within the water column during days 1, 3 and 5 in the LDB station at different depth ranging between surface (7 m) to 200 m.

<table>
<thead>
<tr>
<th>Day at LDB station</th>
<th>Depth (m)</th>
<th>TEP (µg GX L⁻¹)</th>
<th>TEP-C</th>
<th>%TEP-C</th>
<th>POC (µM)</th>
<th>TOC (µM)</th>
<th>POC/PON</th>
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</tbody>
</table>

Abbreviations: TEP, transparent exopolymeric particle; TEP-C, TEP carbon; POC, particulate organic C; TOC, total organic C; ND- no data.
Figures

Figure 1

![Figure 1](image-url)
**Figure 2**

(a) 

(b) 

(c) 

(d) 

(e) 

(f)
Figure 3

- Caspase activity (pM hydrolyzed mg prot\(^{-1}\) min\(^{-1}\))
- Metacaspase activity (pM hydrolyzed mg prot\(^{-1}\) min\(^{-1}\))
- Depth (m)

(a) Day 1
(b) Day 3
(c) Day 5
(d) LDA
(e) LDB
(f) Caspase activity (pM hydrolyzed mg prot\(^{-1}\) min\(^{-1}\))
Figure 4

![Graphs showing relationships between various parameters](image-url)
Figure 5

(a) Trichodesmium
UCYN-B
Nel-I

Depth (m)
150
325
500

10^1 10^2 10^3 10^4
nIH copies L^-1

(b) Trichodesmium
UCYN-B
Nel-I

150
325
500

10^1 10^2 10^3 10^4
nIH copies L^-1

(c) Mass Flux (umol mg^-1)

Metacaspase activity (surface)
(pM hydrolyzed mg protein^-1 min^-1)

PC
PN
LDA

10
0
20
40
60
80
10

0
50
100
150
200
250

0
10
20
30
40
50
60
70