Response to the Editor comments

A paragraph on the variability within the mesocosms was added in the revised version at the beginning of the discussion section.

It is effectively common to plot sd or se in the figures in biological oceanography papers. Note that it is defined exactly what are the error bars in the corresponding legends, and that we use appropriate statistics when we want to make comparison between samples or means. (In this ms we used non parametric statistics).

1 Heterotrophic bacterial production and metabolic balance

2 during the VAHINE mesocosm experiment in the New

3 Caledonia lagoon

4

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1 Abstract

1	Abstract
2	Studies investigating the fate of diazotrophs through the microbial food web is lacking
3	although N ₂ fixation can fuels up to 50% of new production in some oligotrophic oceans. In
4	particular, the role played by heterotrophic prokaryotes in this transfer is largely unknown. In
5	the frame of the VAHINE experiment, three replicate large-volume (~50 m ³) mesocosms
6	were deployed for 23 days in the new Caledonia lagoon and were intentionally fertilized on
7	day 4 with dissolved inorganic phosphorus (DIP) to stimulate N_2 fixation. We specifically
8	examined relationships between heterotrophic bacterial production (BP) and N ₂ fixation or
9	primary production, determined bacterial growth efficiency and established carbon budgets.
10	BP was statistically higher during the second phase of the experiment (P2: days 15-23), when
11	chlorophyll biomass started to increase compared to the first phase (P1: days 5-14).
12	Phosphatase alkaline activity increased drastically during the second phase of the experiment,
13	showing adaptations of microbial populations after utilization of the DIP added. Notably,
14	among autotrophs, Synechococcus abundances increased during P2, possibly related to its
15	capacity to assimilate leucine and to produce alkaline phosphatase, Bacterial growth
16	efficiency based on the carbon budget (27-43%), was notably higher than generally cited for
17	oligotrophic environments and discussed in links with the presence of abundant species of
18	Bacteria expressing proteorhodopsin, The main fate of gross primary production (particulate +
19	dissolved) was respiration (67 %), and export through sedimentation (17 %). BP was highly
20	correlated with particulate primary production and chlorophyll biomass during both phases of
21	the experiment but slightly correlated, and only during P2 phase, with N2 fixation rates.
22	Heterotrophic bacterial production was strongly stimulated after mineral N enrichment
23	experiments, suggesting N-limitation of heterotrophic bacteria all over the experiment. N2
24	fixation rates corresponded to 17-37 % of the nitrogen demand of heterotrophic bacteria. Our
25	results suggest that most of the <u>diazotroph derived nitrogen</u> <u>fuelled</u> the heterotrophic bacterial
26	community through indirect processes generating dissolved organic matter and detritus, like
27	mortality, lysis and grazing of both diazotrophs and non-diazotrophs.
28	

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Mis en forme : Indice

Supprimé: N_2 fixation fuels ~50 % of new primary production in the oligotrophic South Pacific Ocean. The VAHINE mesocosm experiment designed to track the fate of diazotroph derived nitrogen (DDN) in the New Caledonia lagoon. Here, we examined the temporal dynamics of heterotrophic bacterial production during this experiment.

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Supprimé: Heterotrophic bacterioplankton production (BP) and alkaline phosphatase activity (APA) were statistically higher during the second phase of the experiment (P2: days 15-23), when chlorophyll biomass started to increase compared to the first phase (P1: days 5-14).

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1 1 Introduction

2 In the South West Pacific ocean, the natural occurrence of abundant and diverse plankton taxa 3 capable of dinitrogen (N_2) fixation $(N_2$ -fixing or diazotrophic organisms) (e.g., Moisander et 4 al., 2010) can fuel ~50 % of new primary production. (Garcia et al., 2007; Bonnet et al., 5 2015c). However, little is known about the fate of the diazotroph-derived nitrogen (DDN) in 6 this environment (Bonnet et al., 2015b). In particular, the role played by the microbial food 7 web, and among them the heterotrophic bacteria in the transformation of DDN is largely 8 unknown. In the central gyre of the South Pacific, where N₂ fixation is lower than in the South 9 West Pacific, nitrogen is the first element limiting growth of both phytoplankton and heterotrophic bacterioplankton as observed in short-term nutrient enrichment experiments 10 (Bonnet et al., 2008; Van Wambeke et al., 2008a) or incubations with ¹⁵N- leucine or ¹⁵N-11 NH_4^+ , which significantly enhanced bicarbonate uptake (Halm et al., 2012). Such competition 12 13 for nitrogen influences dissolved organic carbon accumulation in the surface layers and 14 export. In the South West Pacific, however, the phytoplankton - heterotrophic bacterial coupling has mainly been investigated in the New Caledonia Lagoon. In this system, 15 16 phytoplankton and bacterial production show seasonal patterns, with maxima in December-January and annual bacterial production representing 21 to 34 % of particulate primary 17 18 production (Torreton et al, 2010), In the oligotrophic stations of the lagoon, based on a 19 bacterial growth efficiency of 10% or less, dissolved phytoplankton release was not sufficient 20 to sustain bacterial carbon demand (Rochelle-Newall et al., 2008). N-limitation of primary 21 production is expected based on year-round dissolved inorganic nitrogen (DIN) to dissolved 22 inorganic phosphorus (DIP) ratios and silicates to DIN ratios, respectively lower and higher 23 than Redfield ratios (Torréton et al., 2010). However, N_2 fixation is a recurrent feature in the 24 lagoon (Garcia et al., 2007; Biegala and Raimbault, 2008), and no information is available on 25 the potential role played by this process on the functioning of the microbial food web and how 26 it could influence the factors limiting heterotrophic bacterial production. As blooms of 27 diazotrophs are transient events, the production of varying sources and quality of organic 28 matter is expected, which may influence biogeochemical fluxes, in particular heterotrophic 29 bacterial production.

Through the VAHINE program (http://mio.pytheas.univ-amu.fr/?VAHINE-Project; Bonnet et al., 2015b), we experimentally investigated the fate of DDN in the planktonic food web and its potential impact on particle export. For this, we studied the development and the fate of a diazotroph bloom enhanced by intentional fertilization with DIP in large-volume (~50 m³) mesocosms deployed in the <u>oligotrophic part of the</u> New Caledonian lagoon, DIP being Supprimé: shown to be

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considered to control the nitrogen input by dinitrogen fixation in the SW Pacific upper surface 1 2 waters (Moutin et al., 2005, 2008). The VAHINE experiment provided a unique opportunity 3 to study such phytoplankton-heterotrophic bacteria interactions by simultaneously using biogeochemical techniques assessing stocks and fluxes in the same body of water for a period 4 5 of 3 weeks. In particular, our objectives were, i) to explore factors controlling heterotrophic 6 bacterial growth, ii) to examine the links between heterotrophic bacterial production and the 7 activity of N₂-fixing organisms and primary producers and iii) to study the fate of carbon 8 inside mesocosms and the balance of autotrophy versus heterotrophy. The factors controlling 9 heterotrophic bacterioplankton were studied using short-term nutrient enrichment experiments 10 and measurements of alkaline phosphatase activity. In oligotrophic systems, assimilation of organic nitrogen-containing molecules can also confer advantage for growth to some 11 12 cyanobacteria (Zubkov et al., 2004, Mary et al., 2008a). Thus we quantified fluxes of leucine 13 incorporation on a single cell basis, using flow sorting by cytometry (Talarmin et al., 2011).

14

15 2 Material and methods

16

17 **2.1 Mesocosm description and sampling strategy**

Three large mesocosms (\sim 50 m³) were deployed as open tubes with unfiltered, nutrient-poor, 18 19 waters of the_Nouméa lagoon close to the Boulari passage (22°29.073 S - 166°26.205 E) 20 located 28 km of the coast from January 13 to February 4, 2013 (Fig. 1). After 2 days for 21 stabilizing mixing and verticality of mesocosms, they were closed at their bottom, which 22 constituted the starting day of the experiment, and a sediment trap was screwed at the basis of 23 the bottom cone of each mesocosm and changed every morning by SCUBA divers. The 24 mesocosms design is based on Guieu et al. (2010) and the choice of the site in the lagoon, 25 deployment and sampling strategy are described in details in Bonnet el al. (2015b). The three 26 triplicate mesocosms were supplemented with 0.8 μ M KH₂PO₄ between day 4 and day 5 of 27 the experiment to alleviate potential P limitation and induce a bloom of naturally present 28 communities of N_2 fixing organisms. All samples for the parameters described below were 29 collected every morning for 23 days using a clean Teflon pumping system from three selected 30 depths (1 m, 6 m, 12 m) in each mesocosm (M1, M2 and M3) and in surrounding waters (i.e. 31 outside the mesocosms, hereafter called Nouméa lagoon waters). Seawater from each 32 mesocosm was first filled in a polypropylene 50 L tank for stocks measurements, 4.5 L 33 polycarbonate bottles for rates measurements and 10 L carboys for diversity. All carboys were 34 immediately transferred onto the R/V Alis anchored close to the mesocosms to serve as a lab

platform to ensure a quick processing of the samples. Subsampling procedure and analysis for 1 2 inorganic nutrients, chlorophyll a (Chl) and their associated phaeopigments, DIP turnover 3 time and N_2 fixation rates are detailed in a companion paper (Berthelot et al., 2015). Primary production (PP) is determined from short term (~ 4 h) incubations around noon using ^{14}C 4 labeling technique (see details in Berthelot et al., 2015) and a model of photosynthesis is then 5 6 applied which restitute daily fluxes (Moutin et al., 1999). Primary production (PP) was 7 determined from short term (~ 4 h) incubations around noon with H¹⁴CO₃ (see details in 8 Berthelot et al., 2015) and a model of photosynthesis applied to calculate daily fluxes (Moutin 9 et al., 1999). This model allows estimation of 24h-fluxes (dawn to dawn) from hourly rates, independent of starting time or duration of incubations, or of the geographic origin of the 10 samples or of the time of the year (i.e. systems with varying day-light periods). This model 11 avoids the general biases introduced by the large variety of incubation conditions used in the 12 Steemann-Nielsen (1952) ¹⁴C methodology (Regaudie-de-Gioux et al., 2014 and ref therein). 13 14 Another advantage of this model is that it allows estimation of both PP (24h dawn-to-dawn) and Gross Primary Production (GPP). For 24 h incubations, GPP is 1.72 x PP as determined 15 16 from the model (Figure 5 in Moutin et al., 1999). This constant is applicable as long as 24h-17 fluxes (dawn-to-dawn) are calculated using the same model.

18 19

20 **2.2 Heterotrophic bacterioplankton abundances**

21 Flow cytometry analyses were carried out at the PRECYM flow cytometry platform 22 (https://precym.mio.univ-amu.fr/). Samples were analyzed using a FACSCalibur (BD 23 Biosciences, San Jose, CA). For heterotrophic bacterial abundance (BA), 1.8 mL of seawater 24 was fixed with formaldehyde (2 % final concentration, 15 minutes incubation at RT), frozen 25 and stored in liquid N₂ until analysis in the laboratory. After thawing at room temperature, 0.3 26 mL of each sample was incubated with SYBR Green II (Molecular Probes, final conc. 0.05 % 27 [v/v]) for 15 minutes at room temperature in the dark) to stain nucleic acids (Marie et al. 1997). Cells were characterized by 2 main optical signals collected from the 488 nm laser: 28 side scatter (SSC, related to cell structure) and green fluorescence (530/40488 nm), related to 29 30 nucleic acids staining. For the calculation of heterotrophic prokaryotes abundances, 31 phytoplankton, in particular Prochlorococcus and Synechococcus, was gated out thanks to its 32 red autofluorescence induced by the chlorophyll (Sieracki et al., 1995). We discriminated 33 HNA (high nucleic acid) and LNA (low nucleic acid) cells and heterotrophic bacterial 34 abundance (HBA) was calculated as the sum of both categories. TruCount beads (BD

Biosciences) and 2 µm beads (Fluoresbrite YG, Polyscience) were added to the samples just before analysis. To determine the volume analyzed by the flow cytometer, the flow rate was estimated by weighing three tubes of samples before and after a 3 min run. The cell abundance was determined by dividing the number of cells by the volume analyzed determined both by the TruCount beads and flow rate. All data were collected in log scale and stored in list-mode using the CellQuest software (BD Biosciences). Data analysis was performed using the SUMMIT v4.3 software (Dako).

8

9 2.3 Heterotrophic bacterial production

Heterotrophic bacterial production (BP) was estimated daily using the ³H-leucine 10 incorporation technique (Kirchman, 1993), adapted from the centrifuge method (Smith and 11 12 Azam, 1992). For each sample, triplicate aliquots (1.5 mL) and one trichloroacetic acid (TCA) killed control were incubated with a mix of 6 nM hot leucine (L-[³H] leucine, Perkin Elmer® 13 specific activity ranging 106 Ci mmol⁻¹) and 14 nM cold leucine, at *in situ* surface 14 temperature (on-deck incubators equipped with 50 % light intensity screen and cooled with 15 16 circulating surface seawater), for 1 h. Linearity of leucine incorporation was checked 17 regularly by time series experiments. The live incubations were terminated with 5 % TCA 18 (final concentration). After three runs of centrifugation/aspiration of the supernatant (once 19 with the fixed sea water sample, once with a 5 % TCA rinse, once with an 80 % ethanol 20 rinse), the pellet was resuspended in Packard Ultima Gold MW Scintillation liquid®. 21 Radioactivity was counted using a Liquid Scintillation Analyzer Packard® 1600TR and the 22 ³H counting efficiency was corrected for quenching. Concentration kinetic experiments 23 showed that isotopic dilution factor ranged 1 to 1.56 and thus BP rates were calculated from 24 leucine incorporation rates using conversion factor adjusted from 1.5 to 2.4 kg C mol⁻¹ leucine. Daily rates were calculated assuming they are 24 times the hourly rate. 25

26 27

28 **2.4** Nutrient addition experiments

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The availability of phosphorus (P), nitrogen (N) and organic carbon (C) for heterotrophic bacteria was investigated by measuring changes in bacterial production following additions of DIP (0.25 μ M P), NO₃⁻ and NH₄⁺ (1 μ M each) or glucose (10 μ M C) (final concentrations). Two bioassays were realised, one right before (day 4) and one two weeks after (day 20) the DIP fertilization in M1 (samples from1 m depth). Eight combinations were tested (P, N, C, PN, PC, NC and PNC) including the non-enriched control T. Each bioassay condition was 1 tested in triplicate in 60 mL polycarbonate bottles incubated for 48 h under in situ-simulated

2 conditions in the on-deck incubator (described in section 2.3). After incubation, each bottle

3 was sub-sampled in order to measure BP using the leucine technique described in section 2.3.

4 5

2.5 Alkaline phosphatase activity

6 Total alkaline phosphatase activity (APA) was measured at the three depths in M1, M2 and 7 M3 and in Nouméa lagoon waters using the analog substrate methylumbelliferone phosphate 8 (MUF-P, 1 µM final concentration) (Hoppe, 1983). The linear increase in fluorescence of 9 seawater with added MUF was measured over the incubation time (up to 8h)), in the dark with 10 a TKO 100 Hoefer DNA fluorometer (single-wavelength with excitation/emission fixed at 365/460 nm but suitable for MUF). Concentration kinetics using a range from 25 to 2500 nM 11 12 MUF-P were run on some occasions to check that the 1 μ M concentration used for routine measurements was sufficient to saturate enzyme activity. Blanks were run by adding the 13 14 MUF-P to filtered boiled seawater and were shown to be insignificant. Calibration curves 15 were made with MUF standards.

16

17 **2.6** Statistical analyses

Non parametric Mann-Whitney and Kruskal-Wallis tests were used to compare differences of each parameter studied between mesocosms, periods of time, or effect of various amendments on BP in the nutrient addition experiments. Model I linear regressions and Pearson correlation coefficient were used to study Log-log relationships between BP and Chl or PP; and evolution of DOC and POC with time.

23

24 3 Results

25 Salinity and temperature measurements show that the water column was not stratified over the 26 course of the experiment, except the first two days, which were characterized by a slight stratification both inside and outside of the mesocosms (Bonnet et al., 2016). No vertical 27 28 stratification was observed in the mesocosms for bacterial production or alkaline phosphatase 29 activity (APA) (see <u>exemplary</u> data for M1 in Fig. <u>S1</u>) as for most of the parameters (Bonnet et al., 2015b; Turk-Kubo et al., 2015, Berthelot et al., 2015). For all description of 30 31 biogeochemical stocks and fluxes, we thus used the average of the three depths to plot the 32 temporal evolution within each mesocosm.

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34 **3.1 Chlorophyll stocks and net primary production**

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1	Based on the Chl and PP dynamics, two periods P1 (days 5-14) and P2 (days 15-23) were
2	identified after DIP fertilization, which were also identified by Berthelot et al. (2015) based
3	on biogeochemical characteristics and by Turk-Kubo et al. (2015) based on changes in
4	abundances of targeted diazotrophs. Diatom heterocyst-forming symbionts associated with
5	diatoms were abundant during P1 while a bloom of the unicellular N2-fixing cyanobacteria
6	from Group C (UCYN-C) occurred P2 (Leblanc et al., 2015; Turk-Kubo et al. 2015). Chl
7	stocks significantly increased during P2 compared to P1 in the three mesocosms (statistics are
8	presented in Table 1). Chl concentrations during P2 in all three mesocosms were significantly
9	higher than those in the Nouméa lagoon for the same period. PP showed the same trend as for
10	Chl, being higher during P2 in all three mesocosms (Fig. <u>3</u> , Table 1). However, the PP rates
11	and Chl concentrations reached during P2 were not identical between the three mesocosms:
12	M3 exhibited higher Chl concentrations during P2 (0.71 \pm 0.30 $\mu g \ L^{\text{-1}}$) than M2 (0.49 \pm 0.18
13	$\mu g~L^{\text{-1}})$ and M1 (0.42 \pm 0.14 $\mu g~L^{\text{-1}},~p<$ 0.001). This was equally true for PP rates (2.45 \pm
14	0.76 $\mu mol~C~L^{\text{-1}}~d^{\text{-1}}$ in M3 compared to 1.47 \pm 0.35 $\mu mol~C~L^{\text{-1}}~d^{\text{-1}}$ in M2 and 1.09 \pm 0.22
15	μ mol C L ⁻¹ d ⁻¹ in M1, p < 0.001). Significant increases of Chl and PP were also observed in
16	lagoon waters (reaching in P2 0.30 \pm 0.07 μg Chl L $^{-1}$ and 1.36 \pm 0.37 μmol C L $^{-1}$ d $^{-1},$
17	respectively, Table 1).
18	
19	3.2 Heterotrophic bacterioplankton abundance and production
20	Abundances of heterotrophic bacterioplankton (HBA) varied 10 fold, from 1.7 (day 9, M1, 1

m) to 12.8 x 10⁵ cells mL⁻¹ (M2, day 11, 6 m). Peaks of HBA were sporadic, like on day 11 in 21 22 M1,, but not repeated for the three depths sampled. They were possibly due to the presence of 23 a patchy distribution of aggregates that could have biased some of the results. These peaks are 24 occasional, and as they might reflect the reality of a patchy distribution, they were kept in the figures, statistics and estimates of means per day. Average HBA did not increase statistically 25 between phase P1 and P2 in M1 and M2 and increased slightly (p < 0.05) from (4.1 \pm 0.7) to 26 $(5.0 \pm 1.4) \times 10^5$ cells mL⁻¹ in M3 (Table 1, Fig. 3). Evolution of BP in the mesocosms was 27 close to that in lagoon waters during P1, except for a peak only detected on day 4 (the 28 29 morning before DIP fertilization) in M1 and M3, and at day 5 in M2. These peaks were not 30 related to any HBA, Chl or PP increase but were related to a steep increase in Rhodobacteraceae 16S ribosomal RNA genes (Pfreundt et al., 2016b). Just like PP, BP 31 32 significantly increased during P2 in all three mesocosms with higher values in M3 compared 33 to M1 and M2 during P2 (Kruskal-Wallis test, p < 0.05). This BP increase was also observed 34 in lagoon waters but with lower amplitude (Table 1). In the three mesocosms, the log-log

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1	relationship between BP and PP was significant only during P2 (r = 0.54 , p < 0.001), whereas	
2	that between BP and Chl was significant during P1 and P2 ($r = 0.4$, $p < 0.001$ and $r = 0.72$,	
3	p<0.001, respectively, Fig. <u>4</u>). In lagoon waters, the BP/PP ratio slightly increased (but	Supprimé: 5
4	significantly) between P1 and P2 (0.33 to 0.39, $p < 0.05$, Table 1). The BP/PP ratio	
5	significantly increased during P2 in M1 (0.48 to 0.65, $p < 0.001$), significantly decreased in	
6	M3 (0.50 to 0.35, $p < 0.05$) and remained stable in M2 (Table 1). Such differences probably	
7	depended on varying maximal values of PP in different mesocosms and the exact days when	
8	PP or BP started to increase. Thus we examined the trend of BP/PP ratio with PP, keeping in	
9	mind the risk of autocorrelation. BP/PP ratio decreased when PP increased, with higher	
10	intensities in the mesocoms compared to lagoon waters, and consistent for P1 or P2 (Table 2).	
11	The log-log relationship between N_2 fixation rates (nM d ⁻¹) and BP (mg C m ⁻³ d ⁻¹) was	
12	insignificant during P1 and significant during P2 ($\log_{(BP)} = 0.13 * \log(N_2 \text{ fix rates}) + 0.73, \text{ r}$	Supprimé:
13	= 0.21, p = 0.04, data not shown).	
14		
15	3.3 Alkaline phosphatase activity	
16	APA was homogeneous between the three depths sampled from the mesocosms (example for	
17	M1 on Fig. <u>\$1</u>), but this was not the case in the Nouméa lagoon, where activity was often	Supprimé: 3
18	higher at 1 m depth compared to the two other depths (data not shown). A slight but very	Supprimé:
19	reproducible decrease of APA occured on days 5 and 6 in all three mesocosms where DIP	
20	fertilization took place, and in lagoon waters only on day 5 (Fig 3). DIP was consumed more	Supprimé: 4
21	rapidly in M1, mirrored by higher APA and lower TDIP between day 9 and 18 in this	
22	mesocosm (Fig. 3). APA then increased very rapidly in M1 and M2 after day 17, but only	Supprimé: 4
23	after day 21 in M3. Such delays were in agreement with the evolution of DIP, which was less	
24	rapidly consumed in M3 compared to M1 and M2 (Berthelot et al., 2015). Consequently,	
25	although mean APA increased significantly in all three mesocosms between P1 and P2 (Table	
26	1), it was lower in M3 compared to M1 and M2 during P2 (3.1 vs 7.5-7.9 nmol MUF-P	
27	hydrolyzed L^{-1} h ⁻¹ , respectively, p < 0.01). Finally, APA also increased significantly between	
28	P1 and P2 in the lagoon waters, albeit to a lower extent as in the mesocosms (from 3 to 5	
29	nmol MUF-P hydrolyzed L ⁻¹ h ⁻¹ , Table 1). Noteworthy, APA in the lagoon waters exhibited	
30	the strongest increase between day 10 and 11 and stayed at this higher level until day 23, thus	
31	exhibiting different dynamics than in the mesocosms.	
32		

3.4 Enrichment experiments

1	In the two 48 h nutrient enrichment experiments performed on day 4 and on day 20, BP
2	increased 3-fold after nitrogen addition ($NH_4^+ + NO_3^-$) compared to the unamended controls.
3	This significant increase was observed irrespectively of whether these N sources were added
4	alone or in combination with DIP or glucose (N, NP, <u>NC</u> , <u>NPC</u> treatments, Fig. <u>5</u> , $p < 0.03$).
5	Only <u>PC</u> and <u>C</u> addition on day 4 led to significant BP increase without N addition ($p < 0.05$)
6	however, to a much lower extent than with all N combinations (factor 1.5 and 1.1,
7	respectively). On day 20, only N amendments led to significant BP increases after 48 h
8	incubations, compared to the unamended control (Fig. 5 , p < 0.03).

10 **3.5 Cell-specific leucine incorporation rates**

11 Among the different groups sorted by flow cytometry, significant cell-specific leucine incorporation rates into macromolecules were obtained for heterotrophic bacterioplankton. 12 LNA, HNA and hi-HNA cells had specific activities ranging from 4.6 to 86 x 10⁻²¹ mol cell⁻¹ 13 h^{-1} . Overall, cell specific leucine incorporation rates for LNA cells were lower than or equal to 14 15 rates for HNA cells, and rates for Hi-HNA cells were 1.2 - 4.8 times greater than rates for HNA cells (Table 3). All cell-specific rates increased when bulk activities increased. Among 16 17 autotrophic groups, significant leucine incorporation was detected for Prochlorococcus cells 18 (PRO) only on day 21 and day 23, due to the low volume available for sorting and a 19 significant decrease of PRO abundances in the samples to be sorted, when compared to the 20 abundances determined on samples analysed only three months after the experiment. We 21 checked on fresh Mediterranean samples that Prochlorococcus cells were clearly detectable 22 with the flow cytometer setting chosen, and could discard any instrument problem. We 23 assumed that the PRO cells lower detection was due to the long storage period of ³H-leucine 24 labelled samples until cell sorting (two years at -80°C) that could induce a loss of 25 fluorescence or cell damages. We obtained a maximum of 1200 PRO cells sorted. Thus, even 26 when the signal was significant, it was associated with a high standard deviation (40% on day 27 21, Table 3). On the opposite, Synechococcus cells (SYN) were well detected and their total 28 abundance matched with the total counts determined on samples analysed three months after 29 the experiment. Additional 651 nm and 355 nm laser excitations allowed us to distinguish two 30 different sub-groups, not clearly distinguishable using only 488 nm laser excitation, separated 31 mainly on the criterion of orange fluorescence (LO-SYN and HO-SYN) (Fig. 2), suggesting 32 different relative amounts of accessory pigments (Neveux et al., 2010). Leucine incorporation was detected in both SYN groups for all samples analysed. For a given sampling date, cell 33

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specific rates of both groups were almost equal, and increased on day 21 and 23 compared to 1 2 days 15 and 19. They were lower than LNA cell-specific rates (from ~20 % of the LNA rates 3 at day 15 to ~70 % at day 21). Cell-specific rates of LO-SYN and HO-SYN diverged only on 4 day 23 (Table 3). At this date, cell specific rates for LO-SYN were twice as high as for LNA cells, reaching 131 x 10^{-21} mol cell⁻¹ h⁻¹. Overall, the contribution of the two *Synechococcus* 5 groups to the bulk activity was very low: it ranged 0.2 to 0.7 % for LO-SYN or HO-SYN (i.e. 6 7 the contribution reached a max of 1.5 % for both SYN groups together), and 0.01-0.02 % for 8 PRO (when detected), respectively. Contribution of LNA cells to the bulk activity was 4-12 9 %. Thus, the most important contribution to the bulk leucine activity was due to HNA and Hi-10 HNA cells.

12 3.6 Carbon budget

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We used the advantage of a day to day sampling in an enclosed system to compute a carbon 13 14 budget that will allow to estimate the fate of phytoplankton-derived organic carbon and the 15 metabolic balance. This carbon budget was calculated using time-integrated data, and thus considered the whole data set. First, each time point was averaged for the three sampling 16 depths, and then time integration was calculated separately for each mesocosm assuming a 17 18 linear trend between 2 successive days. A mesocosm average was calculated based on the 19 time-integrated data obtained in each of the three mesocosms, with error bars representing the 20 standard deviation (sd) among the three mesocosms (Fig. 6a). Gross primary production 21 (GPP) is derived from PP assuming GPP=PP x 1.72 (Moutin et al., 1999) and represents the 22 whole photosynthetic source of organic matter, including both particulate and extracellular 23 release forms. The cumulated GPP at day 23 was $38 \pm 11 \ \mu M C$ (Fig. 6b). Carbon exported by 24 sedimentation into the traps (Cexp) was corrected in μ M C units based on a mean, constant water volume inside M1, M2, and M3 (see Berthelot et al., 2015 for details) and its cumulated 25 value reached 6.4 \pm 2.1 μ M C on day 23. For POC and DOC, for which data were more 26 27 irregular and showed outliers, we decided to calculate net variations of POC and DOC after a linear fit of the discrete data set between days 5 and 23 in each mesocosm (Table 4). POC 28 29 increased linearly in M1 and M3 (0.12 and 0.48 μ mol C L⁻¹ d⁻¹, r = 0.32 p < 0.03 and r = 0.70 p < 0.001, respectively) and showed no trend in M2. A significant increase of DOC was only 30 observed in M2 (Table 4). Due to the high sd resulting from variability in net variation of 31 POC and DOC versus time between the three mesocosms, the average accumulation of DOC 32 and POC estimated for the carbon budget was negligible (Fig. 6a), and the most important 33 measured fate of GPP was Cexp, representing 17 % of GPP (Fig. 6b). GPP - (net DOC + net 34

- 1 POC + Cexp) can be considered as community respiration (CR). CR was calculated and
 - reached $27 \pm 11 \,\mu\text{M}$ cumulated from day 5 to 23, i.e. 71 % of GPP.

4 Discussion

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3

5 4.1 Varibility within the triplicate mesocosms,

6 Overall, M3 exhibited maxium peaks of chlorophyll biomass reached, PP and BP rates 7 and these different responses were particularly seen during P2. A time lag of a few days in the 8 succession of the different planktonic populations was noticed, particularly for nitrogen fixers 9 (Turk Kubo et al. xxx), and DIP was consumed more rapidly in M1. However, slight 10 divergence in biological and chemical evolution among different replicated mesocosms is not uncommon, particularly after the first week of enclosure (Martinez-Martinez et al., 2006; 11 12 Pulido-Villena et al., 2014). Here, the divergence was probably resulting from a combination of bottom up (availability of DIP and nitrogen), and top down controls (grazing pressure and 13 14 viral lysis). The initial conditions prevailing before the DIP enrichment could be also at the 15 origin of the divergence. Indeed mesocosms were closed 3 days before the DIP addition, and many species of diazotrophs exhibit a patchy distribution (Bombar et al., 2015). In addition, 16 Hunt et al. (2016) noticed larger amounts of zooplankton individuals in M3 at the beginning 17 18 of the experiment, some of which, stressed by the mesocosms, might have died (some larger 19 amounts of 'swimmers' were recovered in the traps in M3), contributing to supplementary sources of N in M3. Nevertheless, overall the replicability among mesocosms was considered 20 21 sufficiently correct for most of the biogeochemical stocks, fluxes and abundances of 22 phytoplankton groups (Bonnet al al., 2016) and thus our results are discussed based on 23 averages.

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4.2 N limitation and coupling between BP and N₂ fixation

26 BP was significantly enhanced on a short-term scale (1 - 2 days) by $NO_3^- + NH_4^+$ but not DIP 27 or glucose amendments, indicating that BP was directly N-limited, and/or indirectly after 28 stimulation of N-limited phytoplankton (Fig. 4). In the New Caledonia lagoon, N-limitation 29 has previously been suggested based on a one-year survey of nutrient ratios (Torréton et al., 30 2010). N-limitation is a recurrent feature observed in the ultra-oligotrophic South Eastern 31 Pacific Gyre (Van Wambeke et al., 2008a; Halm et al., 2012), as assessed from short-term (1-32 3 days) enrichment experiments or incubations. As N2 fixation is assumed to be the only 33 process providing a source of new nitrogen to the mesocosms in this experiment, we

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1	examined the potential links between N ₂ fixation rates and BP. First, marine heterotrophic	
2	diazotrophs were detected at low abundances during the mesocosms experiment: γ -24774A11	
3	with ca 10^2 - 10^3 <i>nifH</i> gene copies L ⁻¹ (Turk-Kubo et al., 2015), and 16S tags corresponding to	
4	heterotrophic diazotrophs like <i>Bradyrhizobium</i> or <i>Mesorhizobium</i> were scarce (Pfreundt et al.,	
5	<u>2016b</u>). Therefore, N_2 fixation directly performed by heterotrophic bacteria probably	
6	accounted for a minor fraction of bulk N ₂ fixation during the mesocosm experiment. Second,	
7	as the log-log relationship between N_2 fixation rates and bacterial production was not	
8	significant during P1, and only slightly significant during P2 ($r = 0.21$, $p = 0.04$), the	
9	excretion of DON and NH4+ by diazotrophs likely did not supply much nitrogen for	
10	heterotrophic prokaryotes directly, particularly during P1 when the main organisms	
11	responsible for diazotrophy were diatom-symbiotic (Turk-Kubo et al., 2015). Assuming a C/N	
12	molar ratio of around 6.8 for heterotrophic prokaryotic biomass (Fukuda et al., 1998), N ₂	
13	fixation might have provided 17 to 30 % of the nitrogen demand of heterotrophic prokaryotes,	
14	depending on the phase and the mesocosm considered (Table 1). This proportion increases to	
15	30 - 37 % if we consider a C/N ratio of 8.2, which seems more appropriate in the Pacific	
16	Ocean (Fukuda et al., 1998). Thus, N ₂ fixation contributed to but was not sufficient to sustain	
17	100 % of the N requirements of heterotrophic bacteria during this study. Other potential	
18	sources were initial DON stocks, concentrations of which decreased slightly at the end of the	
19	experiment (Berthelot et al., 2015) and detritus. Indeed, there was a decay of larger	
20	phytoplankton cells after the closure of the mesocosms as discussed by Knapp et al. (2015)	
21	and Leblanc et al. (2015) following DIP availability (TDIP) as well as PP decreases (Berthelot	
22	et al., 2015) and Synechococcus 16S tags dropped substantially between day 2 and 4 (Pfreundt	
23	et al, <u>2016b</u>). Such detritus probably also contributed to sustain BP. NanoSIMS analyses were	
24	performed during a parallel experiment done at the height of a bloom of diazotrophic	
25	Cyanothece-like cyanobacteria (UCYN-C) on days 17-20 in M2 (Bonnet et al., 2015a). After	
26	24 h of ¹⁵ N ₂ -incubations, these authors reported significant ¹⁵ N-enrichment in picoplanktonic	
27	cells (0.2-2 μm fraction). This confirmed a rapid (one day) transfer of DDN (also $^{15}\text{N-}$	
28	enriched) to picophytoplankton, and potentially heterotrophic bacteria. However, such	
29	transfer likely occurred indirectly through DON after mortality and grazing processes, as	
30	shown by model simulations run during the VAHINE project (Gimenez et al., 2015).	
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- 31
- 32 4.3 Alkaline phosphatase activity and P acquisition

33 <u>A slight T_{DIP} decrease was noticed in the mesocosms before the DIP spike but not in the</u>

34 lagoon, suggesting a lower P availability inside and not outside the mesocosms. Therefore, N₂

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1 fixers might benefit from continuous and variable inputs of DIP sources in the lagoon waters 2 during that period. This is also confirmed by the low values of alkaline phosphatase activity in 3 the lagoon at the start of the experiment. Whether these sources were coming from the 4 benthos (Torréton et al., 2002), the atmosphere (soot emission can influence lagoon waters inside and outside the barrier reef, Mari et al., 2014) and/or currents (Fichez et al., 2010) is 5 6 beyond the scope of this study. Inside the mesocosms, when the DIP added was consumed, 7 the increase of APA observed could be due to i) a population switch towards phosphatase 8 producers, which can be heterotrophic bacteria and phytoplankton, and ii) increases in 9 specific activities due to enzymatic induction; or both. We used POP as a proxy of living biomass (Duhamel et al., 2007) to estimate specific activities (nmole MUF-P hydrolyzed per 10 unit POP per unit time) and found the same trend for specific activities and for bulk APA (i.e. 11 specific activity increased up to 10-fold). APA was produced by different phylogenetic groups 12 13 of heterotrophic bacteria, but also by cyanobacteria, as shown on a metatranscriptomic study 14 in the special issue (Pfreundt et al., 2016a), with the highest levels of alkaline phosphatase 15 transcripts originating from Synechococcus on days 14 and 20. Our results and those of 16 Pfreundt et al. (2016a) suggested a switch towards a microbial population that produced 17 phosphatase to escape P depletion after a transient P-replete period. Although T_{DP} decreased 18 and APA increased up to values analogous to those observed in P-limited areas (Moutin et al., 19 2002; Van Wambeke et al., 2002, respectively), heterotrophic bacteria stayed continuously N-20 limited but not P-limited. As discussed in Pfreundt et al. (2016a) and Pfreundt et al. (2016b), 21 some acquisition mechanisms of large P-containing organic molecules and reduction of 22 cellular P quota also helped microbial communities to resist P depletion during P2 phase.

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24 **4.4**. Cyanobacterial assimilation of leucine

BP was used in this study as a strict proxy of heterotrophic bacterial production. As we 25 26 incubated ³H leucine under light conditions, photoheterotrophic activity and the possibility 27 that some photosynthetic cyanobacteria incorporate leucine could biases BP estimates. 28 Whether light stimulation of bacterial production can be explained by direct (assimilation or 29 organic molecules by autotrophs), or indirect effects (stimulation of BP through release of 30 organic molecules or photo-labilization of organic matter), or both, is difficult to determine (Béjà and Suzuki, 2008). Assimilation of methionine, leucine, and ATP was shown to be 31 32 enhanced under light-incubation conditions in the North and South Atlantic Oceans and these 33 increases are generally attributed to stimulation of Prochlorococcus and SAR11 (Evans et al., 34 2015), but the spectrum of organic molecules tested is low. In the New Caledonia lagoon,

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1 incubation of samples under different light regimes influences estimates of BP determined by 2 the thymidine technique (Rochelle-Newall et al., 2008), but so far there is no information 3 available on the light effect on leucine uptake around New Caledonia. The capacity of both 4 marine Prochlorococcus and Synechococcus to assimilate some organic molecules is evident 5 from culture-studies, as well as flow cytometry cell sorting and gene studies (Béjà and 6 Suzuki, 2008). Assimilation of leucine by cyanobacteria can also occur in the dark (Talarmin 7 et al., 2011), but light clearly favours assimilation of leucine by cyanobacteria (Mary et al., 8 2008b). The polypropylene tubes used in this study to incubate BP attenuated the light 9 intensity by 40 % without spectral distortion in the visible range (Richardson and Porter, 10 2005). Under such conditions which were intermediary between simulated in situ light conditions and dark conditions, significant incorporation of leucine into macromolecules was 11 12 seen by flow cytometry sorting of *Synechococcus* cells. We could not unambiguously verify 13 leucine incorporation into Prochlorococcus cells due to technical reasons (low volumes and 14 long storage limitations). To conclude, although the relative contribution of cyanobacteria 15 (PRO + SYN) to the bulk (community) leucine assimilation into proteins was less than 2 %, and could not be responsible of a bias in BP estimates, we estimate significant potential for 16 leucine to be assimilated by cyanobacteria. Note that we used a 10 nM leucine concentration 17 18 for cell sorting, but in situ natural concentrations could be much lower. More studies are 19 needed, investigating the potential use of other organic molecules in lower, close to in-situ 20 concentrations. Mixotrophy may be the rule rather the exception in these experimental 21 systems (Moore, 2013; Evans et al., 2015).

22

23 **4.5** Phytoplankton-bacteria coupling and metabolic balance

Torréton et al. (2010) report mean Chl concentration around 0.3 μ g L⁻¹ over a seasonal cycle 24 performed at an oligotrophic station in the New Caledonia lagoon. These concentrations are 25 close to our reference conditions outside the mesocosms (lagoon waters), where means of Chl 26 values were 0.21 and 0.30 µg L⁻¹ during P1 and P2 phases. Under these oligotrophic 27 conditions, the seasonal variability of BP and PP in the Nouméa lagoon is much lower than in 28 29 temperate waters, only about 3-fold with an average BP/PP ratio of 0.21, and some rare peaks 30 reaching 0.6 (Torréton et al., 2010). This is in accordance with the range of BP/PP ratios 31 encountered in the lagoon waters during our study, with average values ranging 0.33 to 0.39 32 during phases P1 and P2, respectively. On the opposite, inside the mesocosms, average BP/PP 33 ratios were generally higher than in the lagoon waters whatever the phase or the mesocosm 34 considered. A negative trend of BP/PP with increasing PP was obtained, suggesting that a

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1 larger fraction of PP is channelled through the microbial food web when PP decreases, as 2 observed in the oligotrophic Mediterranean Sea (Conan et al., 1999). This is also the trend 3 when considering a large oceanic data set examined by Fouilland and Mostajir (2010). Indeed in their study, regression of $\log(BP)$ as a function of $\log(PP)$ resulted in a slope of 0.57, 4 5 inferring that BP increases less rapidly than PP when PP increases. Contrarily to the weak 6 (during P2) or absence of (during P1) correlation between BP and N2 fixation rates described 7 above, strong relationships between BP and Chl, and between BP and PP were obtained 8 during both phases (Fig. $\underline{4}$). This suggests that N₂ fixation stimulated autotrophic communities 9 during the VAHINE experiment, which may in turn have produced organic matter for heterotrophic prokaryotes. BP and PP are determined routinely, but to estimate the flux of PP 10 channelled through heterotrophic bacteria, or to infer metabolic balance between autotrophy 11 12 and heterotrophy, bacterial carbon demand (BCD) and gross primary production (GPP) must be also estimated. Such carbon fluxes are not directly estimated but are derived from PP and 13 14 BP using additional measurements of bacterial growth efficiency (or bacterial respiration) and 15 phytoplankton extracellular release of DOC. These parameters are less frequently acquired 16 due to time-consuming and difficult technologies (del Giorgio and Cole, 1998; Nagata, 2000), 17 which led to controversy on the metabolic balance in oligotrophic environments (Cole et al., 18 1988; Ducklow et al., 2002; Van Wambeke et al., 2008b; Fouilland and Mostajir, 2010; 19 Moran and Alonso-Saez, 2010). BCD is derived from BP by the use of bacterial growth efficiency (BGE) or respiration rates which are not often measured concomitantly with PP and 20 21 BP, and in many oligotrophic environments BCD/PP is higher than 1, or respiration exceeds 22 PP (del Giorgio et al., 1997). To explain this, different arguments are generally proposed. 23 First, other DOM sources than those deriving from phytoplankton (allochthonous sources) are used to sustain BCD. In Pacific lagoons, excretion of mucus by coral has been proposed as a 24 25 supplementary source of DOM for heterotrophic bacterioplankton (Torréton et al., 2002, Wild et al., 2004). Second, phasing between BP and PP peaks during seasonal blooms and 26 27 occasional presence of PP bursts (see for example Steinberg et al., 2001) are not always 28 detected due to inappropriate sampling frequency for BP and PP measurements. Daily and 29 parallel measurements of both BP and PP in the mesoscosms avoided such problems in this 30 study.

Assuming negligible effect of <u>a biofilm_development on the mesocosms walls (Knapp et al.</u> (2015) on the plankton C budget, the main fate of photosynthetically fixed organic carbon during the experiment was respiration (71 % of GPP) then sedimentation (17 % of GPP). The different responses between the triplicate mesocosms led to a great propagation of errors and

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Supprimé: We used the advantage of a day to day sampling in an enclosed system to compute a carbon budget that will allow to estimate the fate of phytoplankton-derived organic carbon and the metabolic balance. This carbon budget was calculated using timeintegrated data, and thus considered the whole data set. First, each time point was averaged for the three sampling depths, and then time integration was calculated separately for each mesocosm assuming a linear trend between 2 successive days. A mesocosm average was calculated based on the time-integrated data obtained in each of the three mesocosms, with error bars representing the standard deviation (sd) among the three mesocosms (Fig. 7a). Gross primary production (GPP) is derived from PP assuming GPP=PP * 1.72 (Moutin et al., 1999) and represents the whole photosynthetic source of organic matter, including both particulate and extracellular release forms. The cumulated GPP at day 23 was 38 \pm 11 μM C (Fig. 7b). Carbon exported by sedimentation into the traps (Cexp) was corrected in µM C units based on a mean, constant water volume inside M1, M2, and M3 (see Berthelot et al., 2015 for details) and its cumulated value reached 6.4 ± 2.1 µM C on day 23. For POC and DOC, for which data were more irregular and showed outliers, we decided to calculate net variations of POC and DOC after a linear fit of the discrete data set between days 5 and 23 in each mesocosm (Table 4). POC increased linearly in M1 and M3 (0.12 and 0.48 $\mu mol~C~L^{-1}~d^{-1},$ r=0.32~p<0.03 and $\dot{r} = 0.70 \text{ p} < 0.001$, respectively) and showed no trend in M2. A significant increase of DOC was only observed in M2 (Table 4).

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1	thus on the variability on CR/GPP ratio (70 \pm 36 %). CR being lower than GPP, the biological
2	system inside mesocosms was net autotrophic, with an upper error limit close to metabolic
3	balance between autotrophy and heterotrophy.
4	In the lagoon, as close to Grande Rade Bay, long residence times favored local degradation,
5	refractorisation of organic matter and not sedimentation (Mari et al., 2007). However, as these
6	authors discussed, modification of phytoplankton community composition in Grande Rade
7	Bay and the presence of metals could influence sticking properties of polymers. The
8	confinement of the seawater inside the mesocosms probably favored to some extent the
9	accumulation of UCYN-aggregates, as well as a possible reduction of grazing pressure (by a
10	factor of 1.6) in the mesocosms compared to those in the lagoon waters (Turk-Kubo et al.,
11	2015; Bonnet et al., 2015a; Hunt et al., 2016). However, UCYN-C formed large aggregates
12	(100-500 µm) embedded in an organic matrix that included TEP, which were largely
13	responsible for enhanced export flux through sedimentation observed during P2 (Berthelot et
14	al., 2015; Berman-Frank et al., 2016; Knapp et al., 2015). TEP evolution with time, however,
15	and the TEP-C to TOC ratio were similar in the lagoon waters, where wave turbulence and
16	tidal effects were present, and in the enclosed mesocosms, where these hydrodynamics were
17	reduced, and concentrations were similar (Berman-Frank et al., 2016). In an unconstrained
18	ordination analysis, Pfreundt et al. (2016b) described significant differences in bacterial
19	communities between M1 and the lagoon, but similar temporal dynamics. Direct comparisons
20	of our export results with findings from open ocean studies should be made cautiously as our
21	mesocosms were both shallower (15 m) than in typical oceanic export studies (> 100 m) and
22	exhibited reduced turbulence,
23	In order to calculate the fraction of GPP that channeled, directly or indirectly, through the
24	microbial food web, the bacterial carbon demand (BCD) must be estimated through additional
25	estimates of bacterial respiration (BR) or bacterial growth efficiency (BGE). In an
26	oligotrophic site inside the Nouméa lagoon, BGE was estimated at 10 % using incubated
27	samples where oxygen changes were followed with time in the dark (Briand et al., 2004).
28	However, as suggested by Aranguren-Gassis et al. (2012), using consistently low BGE

anguren-Gassis et al. (2012), usi ng derived from size fractionation experiments and long-duration incubations leads to probable BGE underestimation. In the lagoon, the use of a 10 % BGE would lead to BCD values higher than GPP (Rochelle-Newall et al., 2008). If we assume such low BGE in the mesocosms (10 %), cumulated BR from day 5 to 23 would rise to 93 \pm 6 μM C, which is not realistic

33 compared to CR estimated from the carbon budget. A more appropriate BGE of $27 \pm 9\%$ to

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34 $43\% \pm 11\%$ could be calculated, based on minimum and maximum ranges admitted for Supprimé: ¶

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1	BR/CR ratio (from 100 to 50 %, Lemée et al., 2002), and based on propagation of errors due
2	to the variability within triplicate mesocosms (Table S1). For sensitivity analysis of BR and
3	BGE calculation from the carbon budget, we examined whether the errors of different
4	methodological assumptions (conversion factors, analytical errors) were higher than those
5	arising from variability between triplicate mesocosms. We considered different errors based
6	on literature data for all the parameters used in computation of BR and BGE (i.e. GPP, Cexp,
7	DOC, POC, and BP). For GPP, we assumed GPP = 1.72 x PP, i.e. PP/GPP ratio = 58 %. In
8	the South Pacific Ocean, the mean average PP to GPP ratio (based on comparison between
9	oxygen and ¹⁴ C technique) was 47% (Van Wambeke et al., 2008b). If we consider that the
10	sum of dissolved and particulate PP in the lagoon (¹⁴ C technique, Rochelle-Newall et al.,
11	2008) is a good proxy of GPP, then an upper limit for this ratio is 65 % in the lagoon. We thus
12	applied a 15 % variability to the PP/GPP ratio, leading to GPP=1.36 x PP to 2.32 x PP, i.e.
13	approximately a 30 % variability on the conversion factor. For BP, we assumed a 25 % daily
14	variability of BP (Church et al., 2006, Van Wambeke et al., 2008c, Torréton et al., 2010). For
15	Cexp, DOC and POC, we assumed analytical errors of 10 %. We then used propagation of
16	errors to compute the error associated with BR and BGE (Table S1). For GPP, the errors
17	resulting from triplicate mesocosms or resulting from conversion factor and analytical errors
18	were the same. According to the propagation of errors, the error associated with GPP has the
19	largest effect on estimates of BR. The uncertainty of DOC, POC, and Cexp arising from
20	variability within the triplicate mesocosms is higher than the methodological error, whereas it
21	is the opposite for BP. Overall, the uncertainty of BGE estimates arising from variability
22	within triplicate mesocosms or methodology is similar (27 % \pm 9 % or 27 % \pm 10 % for BGE
23	based on BR= CR, 43 % ± 11 % or 43 % ± 12 % for BGE based on BR=CR/2)
24	The BGE values values determined from C budget could be potentially related to a beneficial
25	effect of photoheterotrophy, Indeed, in a companion metatranscriptomic study performed in
26	M1 (Pfreundt et al., 2016a), accumulation of proteorhodopsin transcripts was recurrently
27	detected among varying groups of bacteria notably Pelagibacteraceae, and SAR86 These
28	groups, belonging to the alpha- and gammaproteobacteria, respectively, were also abundant
29	community members as observed through 16S sequencing (Pfreundt et al., 2016b). Aerobic
30	anoxygenic phototrophic (AAP) bacterial abundances are reported to be particularly abundant
31	in the South Pacific Ocean (Lami et al. 2007), but to date, AAP abundances are not available
32	in the lagoon and they were not counted in this experiment. Nevertheless, Pfreundt et al.
33	(2016a) detected expression of the <i>pufM</i> gene, encoding a photoreaction centre protein of
34	AAP bacteria. Transcript abundances were an order of magnitude lower than for
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Supprimé: are more reliable than BR estimates based on Electron Transport System measurements (Aranguren-Gassis et al., 2012) and are in agreement with the

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Supprimé: Indeed, the BGE of a proteorhodopsin-containing strain (*Erythrobacter* sp.) was shown to increase during light periods in a continuous culture (Hauruseau et al., 2012).

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1 proteorhodopsin, and only observed for a group of Rhodocyclaceae on day 14 and much 2 weaker for *Rhodobacteraceae* on day 18. This suggests that AAP bacteria did not play a 3 major role in the investigated system and did not influence the above calculation to a large 4 extent. Dokdonia sp. strain MED134, proteorhodopsin containing flavobacteria, were shown 5 to increase the maximum number of cells reached when growing in the light compared to 6 darkness. However, if DOM was added initially, light vs dark responses changed depending 7 on DOM concentrations (Gomez-Consarnau et al., 2007). Other laboratory experiment, at the 8 opposite, showed no difference in growth rates or maximum cell yields of Pelagibacter 9 ubique cultures grown in natural seawater (in in a diurnal light regime or in complete darkness 10 (Giovannoni et al., 2005). The BGE of a bacteriochlorophyll-containing strain (Erythrobacter sp.) was shown to increase during light periods in a continuous culture (Hauruseau and 11 Koblížek, 2012). Thus the energy benefits of photoheterotrophy remain controversial, and 12 13 related to the difficulty to have true oligotrophic conditions in pure culture. Based on an 14 energy budget, Kirchman and Hanson (2013) suggested that the net energy gained by light is 15 mostly sufficient to meet maintenance cost of AAP but is not enough to meet that of proteorhodopsin-based phototoheterotrophic bacteria. Heterotrophic bacteria are limited by N 16 but also by energy in the South Pacific (Van Wambeke et al. 2008a); this could give an 17 18 advantage to photoheterotrophic prokaryotes for growth and their success in this area.

19 Assuming BGE values ranging from 27 to 43%, the BCD/GPP ratio would range from 63 to 20 99 %. A large part of the GPP is thus channelled through the microbial food web pathway 21 within 20 days. To examine potential links between phytoplankton release and BP, we 22 estimated a extracellular release of 35 %, as determined previously inside the Nouméa lagoon 23 (Rochelle-Newall et al., 2008). Such values are in agreement with higher percent extracellular 24 release that are generally obtained in nutrient limited environments (Nagata, 2000). According 25 to Rochelle-Newall et al. (2008), contemporaneous DOC excreted by phytoplankton was 26 sufficient to meet BCD only in the coastal part of the lagoon, but not in the offshore 27 oligotrophic part of the lagoon where the VAHINE experiment was performed, but these authors used a 10 % BGE. In the mesocosms, still based on a extracellular release 28 29 representing 35 % of GPP, DOC release was estimated at 13 µM C produced between 5-23 30 days. This is not sufficient to satisfy BCD cumulated for the same period (calculated as 24-38 μ M C) although we used BGE varying from 27 to 43 % as discussed above. Thus, 31 32 heterotrophic bacteria in the mesocosms used additional, not contemporaneous, sources of 33 organic matter derived from phytoplankton after transformation through the food web like 34 enzymatic hydrolysis of detritus, viral lysis, and/or sloppy feeding.

2 Conclusions

3 This study confirms that in the Nouméa lagoon, N_2 fixation is a relevant process to fuel the 4 microbial food web and to sustain a biological system which is net autotrophic or close to 5 metabolic balance. The relatively high BGE computed from the carbon budget (27-43 %) 6 could be related to light-harvesting systems developed by abundant bacterial 7 photoheterotrophs. The success of Synechococcus over Prochlorococcus descibed in 8 companion papers (Leblanc et al., 2015; Pfreundt et al., 2016b) might be attributed to their 9 ability to assimilate leucine, and possibly other amino acids, as well as reduction of their 10 cellular P demand through sulfolipid synthesis. The relative importance of mixotrophy in these oligotrophic system implies that it is important to i) find alternative techniques to dark 11 12 incubations to estimate bacterioplankton respiration, like with continuous measurements with 13 oxygen microprobes during alternate light and dark periods (Pringault et al., 2007) and ii) to 14 detect organisms responsible for the assimilation of a wide variety of organic molecules by cell sorting. From the carbon budget, a BCD to GPP ratio was estimated to range between 63 15 and 100 %, and thus a large part of the primary production is channelled through the 16 microbial food web. Bacterial production was strongly coupled with Chl biomass and/or PP, 17 18 rather than with N_2 fixation rates, suggesting that indirect routes through lysis, grazing and 19 mortality of phytoplankton were substantial for providing labile organic matter for 20 heterotrophic bacteria.

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Author contributions SB was the chief scientist responsible of the VAHINE program, she designed and executed the experiment in mesocosms. FV sampled for and analyzed BP and APA, TM sampled for and analyzed T_{DIP} and PP, AB performed the cell sorting, wrote the corresponding M&M section and made Fig. 2, HB contributed to the analyses of bacterial abundances by flow cytometry, MR sampled for and analyzed data, FV and UP equally wrote the manuscript and made the other figures. All the authors reviewed the manuscript.

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Supprimé: . Moreover, as indicated by the high expression of the sulfolipid biosynthesis gene *sqdB* (Pfreundt et al., 2015a), these cyanobacteria are able to

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Table 1 Averages ± standard deviations of some parameters during phases P1 (from day 5 to day 14) and P2 (from day 15 to day 23) in the three mesocosms M1, M2, M3 and in the lagoon waters, HBA: heterotrophic prokaryotic abundances, BP: heterotrophic prokaryotic 3 4 production, AOA: alkaline phosphatase activity, TDIP: turnover time of DIP. N2 fixation contribution to BP (N₂fix/BP ratio, in %) is based on a C/N of 6.8 for heterotrophic bacteria. 5 Mann - Whiney tests were performed to test significant differences between P1 and P2: * p < 6 7 0.05; ** 0.01 ; *** <math>p < 0.001.

8

	M1 P1	M1 P2	Lagoon P1	Jagoon P2		Supprimé: out
Chl ($\mu g L^{-1}$)	0.19 ± 0.05 ***	0.42 ± 0.14	0.21 ± 0.03 ***	0.30 ± 0.07		Supprimé: out
% pheopigments	24 ± 3 ***	28 ± 5	23 ± 6	26 ± 3	Ì	
HBA (x 10 ⁵ cells mL ⁻¹)	3.9 ± 1.9	4.5 ± 1.7	<u>5.5 ± 0.95</u>	<u>6.2 ± 1.2</u>		Supprimé: na
PP (μ mol C L ⁻¹ d ⁻¹)	0.71 ± 0.27 ***	1.09 ± 0.22	0.85 ± 0.17 ***	1.36 ± 0.37		Supprimé: na
BP (ng C $L^{-1} h^{-1}$)	157 ± 49 ***	348 ± 42	135 ± 24 ***	256 ± 60		
DOC μM C	59 ± 3	60 ± 2	60 ± 3	60 ± 2		
ΡΟϹ μΜ Ϲ	8 ± 3 *	9 ± 1	6.6 ± 1.1 **	7.6 ± 1.3		
APA (nmole MUF-P hydr $L^{-1} h^{-1}$)	1.5 ± 0.9 ***	8.0 ± 5.4	3.0 ± 2.3 **	5.0 ± 3.1		
TDIP (days)	16 ± 15 ***	0.5 ± 0.3	2.0 ± 0.9 ***	0.9 ± 0.4		
BP/PP ratio	0.48 ± 0.18 ***	0.65 ± 0.20	0.33 ± 0.11 *	0.39 ± 0.10		
N ₂ fix/BP ratio (%)	21 ± 11*	29 ± 16	22 ± 13 *	15 ± 8		
					1	
	M2 P1	M2_P2	M3_P1	M3_P2		
Chl (μg L ⁻¹)	0.22 ± 0.03 ***	0.49 ± 0.18	0.20 ± 0.04 ***	0.71 ± 0.30		
% pheopigments	23 ± 2 ***	28 ± 6	23 2	26 ± 15		
HBA (x 10^5 cells mL ⁻¹)	2.2 <u>±</u> 2.2	4.9 ± 1.8	4.1 ± 0.7 *	5.0 ± 1.4		
PP (μ mol C L ⁻¹ d ⁻¹)	0.75 ± 0.15 ***	1.47 ± 0.35	0.73 ± 0.15 ***	2.45 ± 0.76		
BP (ng C $L^{-1} h^{-1}$)	227 ± 114 ***	338 ± 116	168 ± 52 ***	422 ± 132		
DOC μΜ C	58 ± 3 **	61 ± 1	61 ± 3	60 ± 2		
ΡΟϹ μΜ Ϲ	10 ± 3	9 ± 1	9 ± 2 ***	13 ± 3		
APA (nmole MUF-P hydr $L^{-1} h^{-1}$)	1.0 ± 0.8 ***	7.6 ± 7.6	0.6 ± 0.5 ***	3.18 ± 2.61		
TDIP (days)	27 ± 19 ***	1.8 ± 2.0	25 ± 12 ***	3.0 ± 3.1		
BP/PP ratio	0.65 ± 0.41	0.47 ± 0.16	$0.50 \pm 0.24^*$	0.35 ± 0.08		
N ₂ fix/BP ratio (%)	17 ± 16 ***	30 ± 18	25 ± 15	22 ± 11		

9

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1 Table 2. Log - Log relationships between BP/PP ratio and PP (expressed in mgC $m^{-3} d^{-1}$). In

2 mesocosms, phase P1 and P2 are separated for the regressions. r: Pearson correlation

- 3 coefficient, p: probability.
- 4

_		equation	r	probability	
	phase P1	log <mark>(</mark> BP/PP <mark>)</mark> = - 0,87 log <mark>(</mark> PP <u>)</u> + 0,49	0,59	< 0.001	Supprimé:
	phase P2	log <u>(</u> BP/PP <u>)</u> = - 0,53 log <mark>(</mark> PP <u>)</u> + 0,33	0,6	< 0.001	Supprimé:
1	lagoon waters	log <mark>(</mark> BP/PP)= - 0,24 log <mark>(</mark> PP) -0,19	0,28	< 0,.01	
5					Supprimé:

1 Table 3 Specific leucine activities of main groups sorted. PRO : *Prochlorococcus*, LO-SYN

2 (low orange fluorescence Synechococcus-like cells), HO-SYN (high orange fluorescence

3 Synechococcus-like cells, PE (autotrophic pico-eukaryotes), LNA (low nucleic acid), HNA

4 (high nucleic acid), Hi-HNA (high size and high nucleic acid) heterotrophic bacteria and bulk

5 <u>activities</u> (total community leucine incorporation rates) corresponding to the same sample.

6 When tests of reproducibility have been done, the corresponding data is indicated with its

7 standard <u>deviation</u>. bdl: below detection limits, <u>lag: lagoon waters</u>

	PRO	LO SYN	HO SYN	PE	<u>LNA</u>	<u>HNA</u>	<u>Hi-HNA</u>	bulk
		pmole leu L ⁻¹ h ⁻¹						
d15 M1	bdl	4.6 ± 1.9	3.5 ± 0.3	19 ± 5	<u>20.6 ± 0.2</u>	<u>67 ± 1</u>	<u>79</u>	97 ± 3
d19 M1	bdl	5,4	3,5	17	<u>27</u>	<u>16</u>	<u>80</u>	126 ± 3
d21 Jag	69 ± 28	30 ± 4	25 ± 4	79 ± 12	<u>39</u>	<u>214</u>	<u>554</u>	186 ± 6
d23 M1	22	131	42	108	<u>56</u>	<u>113</u>	<u>356</u>	242 ± 7

Supprimé: error Supprimé: .

Tableau mis en forme

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Table 4. Linear regression fits on temporal trends of POC and DOC in M1, M2 and M3 from
days 5 to 23. DOC has been sampled only at 6 m depth in the 3 mesocosms. df: degree of
freedom, r: Pearson correlation coefficient, p: probability, ns: not significant. For POC trend,
some outliers have been suppressed from the regressions.

		Range µM	Outliers µM	slope	df	r	р
	POC M1	4.7-12.4	19.3	0.12	35	0.32	0.02
	POC M2	7.1-11.6	15.0, 15.0, 17.3	- <u>0.009</u>	28	0.03	ns
	POC M3	6.5-18.9	no	0,47	36	0.70	< 0.001
	DOC M1	54-64	no	0.071	13	0.15	ns
	DOC M2	53-62	no	0.25	13	0.48	0.04
	DOC M3	54-66	no	- <u>0.12</u>	14	0.22	ns
7							

4

33

2 Figure Legends

3 **Figure 1.** Position of mesocosms implemented in the southwest lagoon of New Caledonia.

5 Figure 2. Example (day 23 M3 1m) of flow cytometry cytogram dot plot of: a) naturally non-6 fluorescent bacterioplankton groups discriminated by their DNA content (SYBR green-7 induced fluorescence in arbitrary units (a.u.) versus cell size (side scatter), after 488 nm laser 8 excitation); b) phototrophic groups discriminated by their chlorophyll a content (related to the 9 red fluorescence intensity (a.u.) versus phycoerythrin related to the orange fluorescence 10 intensity (a.u.) after 488 nm laser excitation); c) low-orange (LO-SYN) and high-orange (HO-SYN) Synechococcus-like sub-groups separated by their chlorophyll a content (after 661 nm 11 12 laser excitation) versus their phycoerythrin content (after 488 nm laser excitation). 13

heterotrophic bacterial carbon demand (BCD) was calculated based on two hypotheses: BR =

14	Figure 3. Evolution of: a) chlorophyll a (Chl), b) heterotrophic bacterial abundance (HBA),	_	Supprimé: 4
15	c) primary production (PP), d) heterotrophic bacterial production (BP), e) alkaline		
16	phosphatase activity (APA) and f) DIP turnover time (TDIP) in the three mesocosms M1, M2,		
17	M3 and in the lagoon waters (lagoon). Each point is the mean of the three depths sampled,		
18	error bars are standard deviations. For lagoon HBA, only data from 1 m and 12 m depth are		
19	available occasionally and discrete data are presented instead	_	Supprimé: .
20			
21	Figure <u>4</u> . Log-log relationships between heterotrophic bacterial production (BP) and a)		Supprimé: 5
22	primary production (PP) or b) chlorophyll a (Chl).		
23			
24	Figure 5. Response of heterotrophic bacterial production to the enrichment experiments		Supprimé: 6
25	conducted on days 2 and 20. Asterisks show significant responses in comparison to the		
26	unamended control (Co) after Mann Whitney test (*: $p < 0.05$).		
27			
28	Figure 6 . Carbon budget of the mesocosms with time (µM C). a) Evolution of time-integrated		Supprimé: 7
29	gross primary production (GPP). Cexp: C export in sediment traps (Cexp), time-integrated net		
30	POC and net DOC are calculated assuming linear fits of these variables between days 5 and		
31	23 (see Table 3). b) Budget of time-integrated data on day 23. The difference GPP - (Cexp +		
32	net DOC + net POC) was assumed to be community respiration (resp). The range of		

100 % CR (BCD 1) or BR = 50 % CR (BCD 2). Standard errors are plotted from the sum of		Supprimé: DCB)
each category, using propagation of errors.	\sim	Supprimé: DCB	j
		Supprimé: Error bars)

1 Supplement of

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4

5 Material and Methods

6 Specific leucine assimilation assessment using cell sorting

7 On four occasions (day 15, M1, 6 m; day 19, M1, 6 m; day 21, lagoon waters, 1 m; day 23, M3, 1 m), additional seawater samples were incubated with ³H leucine for further cell sorting 8 9 of phytoplankton and heterotrophic bacteria: five polypropylene (Nunc) tubes (3 live samples, 10 2 killed controls) were filled with 4.5 mL of seawater and incubated with pure 3 H leucine (10 11 nM final conc.) for 1 h in the on-deck incubator as for bulk samples (section 2.3). Incubations 12 were stopped by addition of 0.5 mL of 20 %, 0.2 µm-filtered formalin, stored in the fridge for 15 minutes, and then stored in liquid N_2 until sorting. Two additional non-incubated tubes 13 (but fixed and stored in the same conditions) were used for total counts. Sorting of the 14 radiolabeled samples were performed with on a BD InfluxTM Mariner (BD Biosciences. San 15 Jose, CA) high speed cell sorter equipped with three laser lines: 488 nm (Sapphire, Coherent), 16 17 561 nm (Jive, Cobolt) and 355 nm (Xcyte, JDSU). All data were collected in log scale, stored 18 in list mode files and analyzed in real time for sorting using the BD FACSortware software 19 (BD Biosciences), or analyzed a posteriori using FlowJo v7.6.5 software (Tree Star). A solution of 0.5x PBS, 0.2 µm filtered, was used as sheath fluid. For heterotrophic prokaryote 20 21 analyses and sorting, (using a drop purity sort mode), cells were stained with SYBR Green II 22 as described above in section 2.2. Cells were characterized by two main optical signals 23 collected from the 488 nm laser: side scatter (SSC) and green fluorescence (530/40 488 nm), related to nucleic acid staining. Based on these criteria, low nucleic acid (LNA), high nucleic 24 25 acid (HNA), and HNA with high SSC (Hi-HNA) groups were determined (Fig. 2) and sorted 26 into different tubes. Like for determination of LNA and HNA abundances (section 2.2), 27 phototrophic cells were excluded thanks to their red fluorescence. To analyze and sort the 28 photosynthetic phytoplankton cells, the three laser lines were used. Red fluorescence 29 $(630LP_{488 \text{ nm}})$ related to chlorophyll *a* content, was used as trigger signal. Phytoplankton cells 30 were characterised by three other optical signals: forward scatter (FSC) related to cell size, side scatter (SSC), and the orange fluorescence (580/30488 nm) related to phycoerythrin. In 31 32 addition, the chlorophyll a red fluorescence was collected from the 355 nm and 561 nm Supprimé: 2.4.

 excitation (630LP_{355nm} and 630LP_{561nm}). The cytogram red fluorescence (induced by the 561 nm laser) vs orange fluorescence induced by the 488 nm laser evidenced two different subgroups of *Synechococcus* (one with Low and one with a High Orange fluorescence intensity, referred to as LO-SYN and HO-SYN, respectively, Fig. 2). Thus, four populations <
 μm were optically resolved and sorted simultaneously, directly into separate 2 mL Eppendorf centrifuge tubes, using the drop purity sort mode: *Prochlorococcus* (PRO), LO-SYN and HO-SYN, and pico-eukaryotes (PE).

8 Variable numbers of cells were sorted per sample depending on experiment and cell type, to 9 achieve sufficient signal and a good compromise with the volume available. The 10 phytoplankton collected cells ranged from 50 000-279 000 for the LO-SYN and HO-SYN groups, 16 000- 41 000 for the PE, to 1 600-10 000 for the PRO group. From the 1 mL SYBR 11 12 Green II stained aliquot, the three heterotrophic prokaryote groups were simultaneously 13 collected into separate 2 mL centrifuge plastic tubes, collecting a range of 100 000-250 000 14 cells for LNA and HNA groups, and 15000-53000 cells for Hi HNA group. After sorting, 1.5 mL of 5 % TCA was added into each tube and processed as for BP measurements. Bulk 15 16 activities were realized in triplicate by subsampling directly 1.0 to 1.5 mL of samples from the 17 5 mL tubes. In these tubes, 55 % TCA was added to give a final 5 % TCA concentration and 18 the three series of centrifugations were run as for the BP measurements. Formalin-killed 19 samples were also sorted in order to estimate blank values for each group. Dpm in the killed 20 control of a given group were subtracted from dpm in the corresponding incubated sample. 21 Blank values were independent of the number of sorted cells (on average 27 ± 9 dpm). We 22 checked that a linear increase of the dpm signal occurred with the number of sorted cells. The 23 coefficient of variation between triplicate sorts ranged 1-5 % when dpm signal were > 100024 dpm, but these values increased up to 30 % when the dpm signal were < 100 dpm due to 25 methodological limitations (limited volume available or lower activities). For this reason we 26 considered below detection limits all sorts where dpm values were less than twice the corresponding blank value. The radioactivity per cell was calculated and expressed in C units 27 $(10^{-21} \text{ mol leu cell}^{-1} \text{ h}^{-1})$. It was multiplied by the abundance of cells mL⁻¹ within in sorted 28 region to obtain the volumetric incorporation rate of each group, and the relative population 29 30 activity was calculated as the population fraction of the bulk (i.e. total community) activity. Considering a drop frequency set at 98500 per second and average sorting rates of 891 cells 31 per second for heterotrophic bacteria, the probability of free bacteria being sorted 32 simultaneously with an autotrophic cell in the same drop, leading to overestimation of leucine 33 assimilation rate per cell for autotrophic cells, was 0.9 % and thus considered negligible. The 34

effect of a long storage of the samples before cell sorting was checked by counting abundance
of cells mL⁻¹ directly on the Influx. For this, we used the additional non labeled tubes, ran
using similar procedure (sample preparation with control beads, and flow rate determination)
as described in section 2.2., except that we counted also Hi-HNA cells and the two categories

5 of Synechococcus.

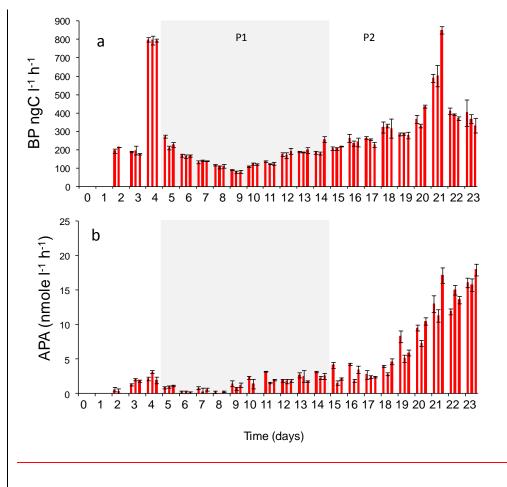
6

7 Figures

Figure <u>\$1</u>. Evolution of: a) bacterial production and b) alkaline phosphatase in the mesocosm
M1 at the three depths sampled. For each day 1 m, 6 m and 12 m are presented from left to
right. For the BP plot error bars are standard deviations within triplicate measurements. For
phosphatase activity, error bars are the standard errors of the slope of the linear regression
MUF production as a function of time. The vertical bar between day 4 and 5 indicates DIP
fertilization.

14

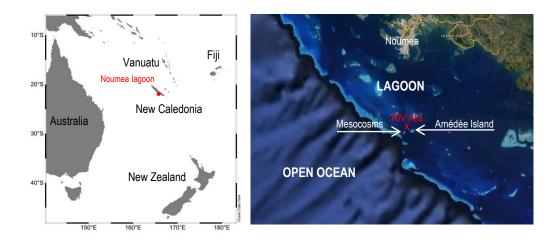
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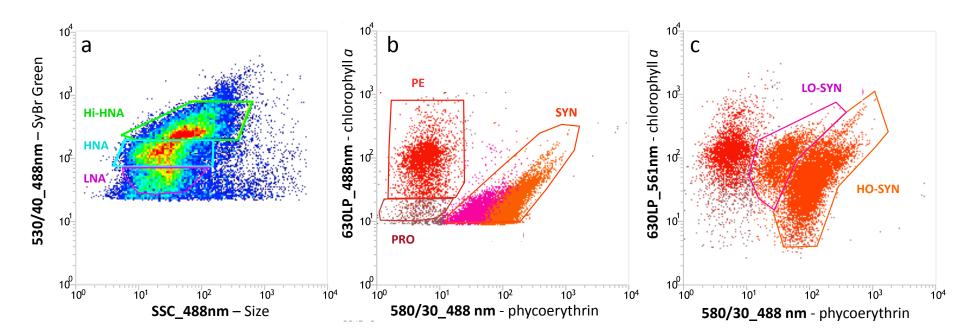


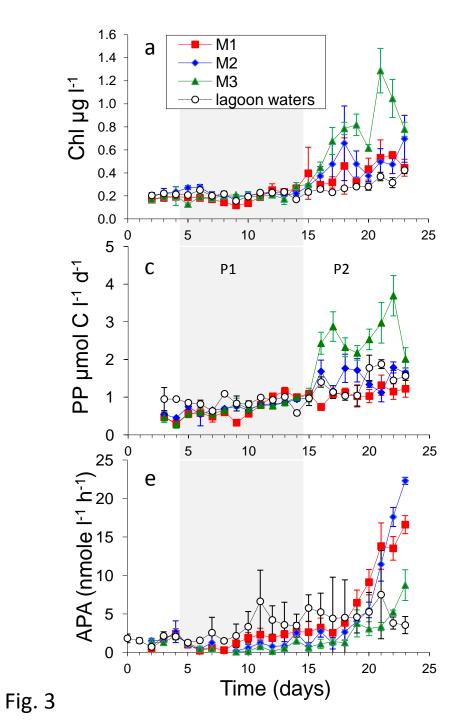
2 Tables

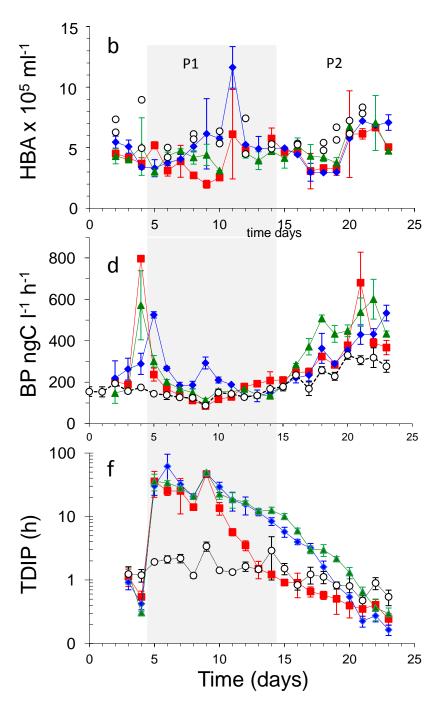
Table S1 : C budget. Time integrated measurements (average of the three mesocosms); sdmeso: standard deviation associated to the variability within the three mesocosms; sd-CF:
standard deviation reflecting the range of conversion factors or analytical methods and
assumptions. The errors considered for estimating sd-CF are discussed in the text: 30 % for
GPP, 25 % for BP and 10 % for Cexp, DOC and POC. The sd in italics are computed
assuming general laws of error propagation.

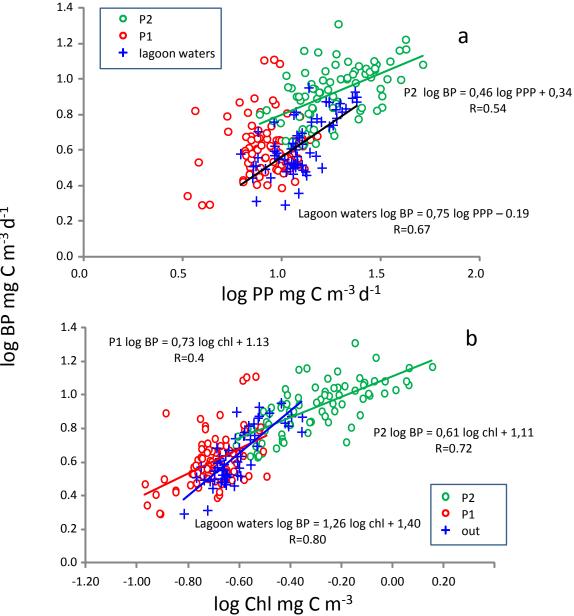
	<u>Time</u> integrated	<u>sd -</u>	<u>sd -CF</u>
-	measurements	meso	
	<u>μMC</u>	<u>μMC</u>	<u>μMC</u>
<u>GPP</u>	<u>38.1</u>	<u>11.2</u>	<u>11.4</u>
<u>Cexp</u>	<u>6.4</u>	<u>2.1</u>	<u>0.6</u>
<u>POC</u>	<u>3.1</u>	<u>5.4</u>	<u>0.3</u>
DOC	<u>1.3</u>	<u>3.6</u>	<u>0.1</u>
<u>BP</u>	<u>10.4</u>	<u>0.6</u>	<u>2.6</u>
resp 1=CR	<u>27.3</u>	<u>11.6</u>	<u>11.5</u>
<u>resp 2=CR/2</u>	<u>13.7</u>	<u>5.8</u>	<u>5.7</u>
	<u>%</u>	<u>%</u>	<u>%</u>
BGE1	<u>27 %</u>	<u>9 %</u>	<u>10 %</u>
BGE2	<u>43 %</u>	<u>11%</u>	<u>12 %</u>











log BP mg C m⁻³ d⁻¹

