

I have reviewed the revised manuscript. It has improved but there remain a number of important issues that still need further attention before this manuscript can be published.

The title of the manuscript still emphasizes the “biogeochemical implications” which are actually fairly minor (see their abstract). The title also claims that it only studies lipids in the OMZ but that is not true. The term “diversity” for lipids seems odd, it is a biological term that should not be used in terms of chemical composition.

We changed the title to “Intact polar lipids in the water column of the Eastern Tropical North Pacific: Abundance and structural variety of non-phosphorus lipids”.

The authors have responded in an extensive way to my comments on the analytical methodology. It has become much more clear how the time-line of the analyses has been. They state that they have >10 years of experience with analysis of IPLs and I am not doubting their analytical capabilities at all. However, in the cases where they use rather unusual procedures (Soxhlet extraction of IPLs, re-analysis of IPL extracts after 7 years of storage at -20 degrees centigrade) they have to come up with evidence to back up their statements in the rebuttal and in the text (e.g. lines 195-197; “we believe”). Just the presence of labile IPLs does not mean that the distribution (i.e. relative percentage) has not changed (and it is the distribution that is the focus of the paper as explicitly mentioned in the rebuttal). The authors refer to Lengger et al. (2012) to support this statement. However, this paper uses only Bligh-Dyer extraction. Perhaps, they intended to refer to Lengger et al., *Organic Geochemistry* 47, 34 – 40 also published in 2012 but this paper shows that the extraction technique has a huge influence on the ratio between glyco- and phospholipids (see Figure 3 in that paper): Bligh Dyer extraction increases the relative amount of the phospholipid by a factor of ten or so. I therefore remain doubtful about the chosen methodology which in view of this is inappropriate.

We meant to cite Lengger et al., 2012 OGC, but mistakenly cited Lengger et al., 2012 GCA, we apologize for this mix-up. We agree with the reviewer that Bligh and Dyer extraction would be the choice method for IPL analysis, however, it is often the case that samples are re-analyzed after newer protocols have been developed and it is not possible anymore for us to perform a different extraction protocol for these samples.

We mention potential extraction issues due to the performed Soxhlet extraction in the revised methods section of the manuscript (lines 196-199) and hope that these now sufficiently address the reviewers concerns.

With respect to the storage issue: why don't the authors show a supplementary figure showing the composition of their IPL standard mixture over time? This would at least solve this issue convincingly with scientific data and would answer my questions in a reasonable way. With respect to the response factors of the standards: I do understand that these response factors are not useful for the community since they are specific for the instrument at that specific moment in time. However, it still would be very helpful to see the change in response factors over time for each individual standard. If the standards are so stable upon storage: why are they renewed every 3 years (which is only 40% of the time between extraction and analysis)?

We added a supplementary figure showing the fluctuations of relative and absolute responses of our different standard mixes over time (Suppl. Fig. 1). The response of each IPL varies over time as the machine is being tuned and cleaned, but there is no obvious indication for preferential degradation of any or all compounds, as absolute and relative responses go up and down (and up again) over the years.

We renew standards not primarily due to concerns of degradation, but mainly because they are either used up or new standards become commercially available. This is also why there is no fixed date when standards get renewed, but always ca. every 2 to 3 years.

A second major point that is not solved in this new version is the distinction between major and minor IPLs (see Figure 4). I reiterate my previous comment: “The whole distinction between major and minor IPLs is rather artificial. It becomes especially confusing when minor IPLs are normalized on

their sum which is a variable part of the IPLs as a whole. It is entirely unclear why this is done other than for “stamp collection” purposes. “.

As we stated in the first response to the reviewer, we visualize the minor lipids, because also minor lipids can be environmentally relevant (cf. ladderane lipids). If we would not zoom into the minor lipids in figure 4 as we do, then changes with depth and zonation would not be visible.

Nevertheless, we agree with the reviewer that scaling the minor lipids up to their sum is arbitrary and may be misleading. Therefore, we now decided to scale the minor lipids to their actual relative abundance to the total IPLs. See revised figure 4.

The text has now been changed to define major and minor IPLs (Lines 309-310) but this definition is rather confusing with the figure because it shows many IPL classes that are <10%. The bar plots of the minor compounds shows really weird things; sometimes there is only one IPL, sometimes none, and the most important thing is that it is normalized on something that is extremely variable (i.e. the sum of “minor” IPLs that varies between 0-20%). So, it is entirely confusing way of plotting the data. If the authors want to focus on these minor IPLs, why don't they use the scale of the plots shown on the left of this figure (IPL relative abundance normalized on the sum of all IPLs) but use a scale that runs from 0-2% or so. That would be a much more fair way to present the data and would also eliminate some of the weird things (i.e. “minor” IPLs dominated by one IPL because in these cases the “minor” IPLs represent <1% of the total).

As the reviewer suggested, we now plotted the minor lipids that they amount to their actual relative abundance compared to total IPLs, see revised figure 4.

This issue directly relates to the problem that the authors keep on insisting in their idea that relative abundances are more important than absolute abundances. The problem they generate in that way is directly evident from their Figure 4. At station 8 archaeal IPLs represent 50-80% of the IPLs whereas this is much lower in the shallower waters. Fig. 2e shows that in the shallower waters there are a comparable or perhaps even higher number of archaeal cells. However, in the shallow waters the IPL concentration is much higher. When absolute concentrations of archaeal IPLs would be taken into consideration this discrepancy would likely not exist. Therefore, I strongly urge the authors to look at their data also in terms of absolute concentrations. Can't they combine their measured absolute total concentrations of IPLs in 2010/2011 (which they now hardly use) with the %IPL determined in 2015 to arrive at concentration profiles for individual IPLs? That would allow a much more meaningful ecological interpretation of their extensive dataset. Of course, percentage data also provides some insight but the basic conclusion from Fig. 4 is now: the photic zone contains predominantly IPLs derived from phytoplankton whereas the IPLs in the OMZ are primarily derived from bacteria and archaea. This is hardly surprising; do we really need all these analyses to arrive at this conclusion?

As stated in the manuscript, the 2010/2011 analyses did not consider HPH-GDGT; therefore, we refrain from reporting total GDGT data from the Xie et al., 2012 paper as these only consider 1G-GDGT and 2G-GDGT.

Unfortunately, the reviewer still seems to misunderstand the main point of the paper if he/she believes it is simply to show that phytoplankton dominate the surface waters while bacteria and archaea dominate the deeper layers. Instead, the main point of the paper is to report on the types of lipids that are found with the different geochemical and biological zones. To us it was surprising that in deeper zones (within the OMZ and below) we find IPLs that were previously not assumed to be typical for bacteria.

Again, we can only re-iterate what we mentioned previously: We do not agree that showing absolute concentrations would gain any more insight into our main point. Furthermore, there are several papers that have reported on absolute concentrations of archaeal lipids in oxygen minimum zones (Pitcher et al., 2011, Schouten et al., 2012), and we thus do not see how our reporting of this would be novel.

I also still believe that correlating environmental parameters to relative abundances of IPLs is much less useful than to absolute concentrations. In any case, the statistical data treatment is not really used

in the discussion, so this section (Lines 406-429) can be easily eliminated.

We would like to keep the statistical evaluation of the data in the manuscript, otherwise we could not make statements about correlations of lipids with environmental parameters, which is surely of interest to many people in this field. Also, it is not true that we do not use the statistical data in the discussion, we do so in many instances in section 4.2.

The discussion has been shortened substantially but is still lengthy. It starts with a paragraph (lines 432-459) that only reiterates previous findings in this setting. Where these previous finding can be directly related to the IPL profiles they should be mentioned there and this paragraph can be skipped.

As this background information reports on previous findings we do believe that the discussion section is the appropriate placing of this relevant information.

There is also overlap in Lines 468-474. I am also puzzled by the fact that in section 4.1.3 IPLs from two completely different zones (core OMZ and deep oxycline, i.e. without and with oxygen) are discussed together.

We inserted a sentence in line 578 explaining why we discuss these two zones together because similar IPL distributions indicate similar biogeochemistries, even though oxygen is rising in the deep oxycline.

The discussion of the origin of the archaeal IPLs (Lines 558-570) is fairly limited. In the upper OMZ hardly any archaeal IPLs are detected (Figure 4) so this needs explanation.

As we report in line 458 (part of a paragraph the reviewer wanted us to delete) Podlaska et al., 2012 showed low archaeal abundances shallower than the upper OMZ, which matches our IPL data.

Also, the reason for linking them to Group II Euryarchaeota needs argumentation.

We revised the sentence where we linked the IPLs to Group II Euryarchaeota (line 572).

The conclusion (line 708-711) is simply wrong. Not only oxygen is the primary determinant but also light. Without light there would not be any production of IPLs by algae and cyanobacteria, quantitatively the most important IPLs in the water column of the studied area.

We now clarify in the text that not only oxygen, but also light drive IPL distribution (lines 265, 477, 657 and 715).

In summary, I strongly feel that this manuscript still needs quite some revision.

We again revised the methods section as well as the discussion and figure 4 according to the reviewers concerns. In addition, we added a supplemental figure showing the fluctuations of the IPL standard response factors over time.

Line 1: The title of the manuscript was changed

Line 33, 35, 143: 'oxygen minimum zone' was replaced with 'water column' to highlight that we are not only focusing on the OMZ.

Line 203: The methods section was revised to address the Soxhlet extraction issue.

Line 597: Sentence was rephrased according to the reviewer's request.

Line 603: Sentence was added according to the reviewer's request.

Lines 277, 687, 745 and 746: Next to high oxygen content also the presence of light in the surface waters is stressed here, according to the reviewer's request.

We modified Figure 4 and added Suppl. Figure 1 according to the reviewer's request.

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- Deleted: Biogeochemical implications of

1 **Intact polar lipids in the water column of the Eastern Tropical North Pacific: Abundance and**
2 **structural variety of non-phosphorus lipids**

3 Florence Schubotz ^{1*}, Sitan Xie ^{1,¶}, Julius S. Lipp ¹, Kai-Uwe Hinrichs ¹, Stuart G. Wakeham ²

4
5
6 ¹MARUM and Department of Geosciences, University of Bremen, 28359 Bremen, Germany

7 ²Skidaway Institute of Oceanography, Savannah, GA 31411, USA

8 [¶]Current address: Wai Gao Qiao Free Trade Zone, 200131 Shanghai, China

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10
11
12
13
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15
16
17 *Corresponding author. MARUM, University of Bremen, Leobener Str. 13, Room 1070, 28359 Bremen,
18 Germany. Tel: +49-421-218-65724. Fax: +49-421-218-65715. E-mail: schubotz@uni-bremen.de

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20 **Keywords:** intact polar lipids, phospholipids, glycolipids, betaine lipids, ether lipids, oxylipins,
21 phospholipid substitution, oxygen minimum zone

26 **Abstract**

27 Intact polar lipids (IPLs) are the main building blocks of cellular membranes and contain
28 chemotaxonomic, ecophysiological and metabolic information, making them valuable biomarkers in
29 microbial ecology and biogeochemistry. This study investigates IPLs in suspended particulate matter
30 (SPM) in the water column of the Eastern Tropical North Pacific Ocean (ETNP), one of the most extensive
31 open ocean oxygen minimum zones (OMZ) in the world with strong gradients of nutrients, temperature
32 and redox conditions. A wide structural variety in polar lipid head group composition and core structures
33 exists along physical and geochemical gradients within the water column, from the oxygenated photic
34 zone to the aphotic OMZ. We use this structural diversity in IPLs to evaluate the ecology and
35 ecophysiological adaptations that affect organisms inhabiting the water column, especially the mid-depth
36 OMZ in the context of biogeochemical cycles. Diacylglycerol phospholipids are present at all depths,
37 but exhibit highest relative abundance and compositional variety (including mixed acyl/ether core
38 structures) in the upper and core OMZ where prokaryotic biomass was enriched. Surface ocean SPM is
39 dominated by diacylglycerol glycolipids that are found in photosynthetic membranes. These and other
40 glycolipids with varying core structures composed of ceramides and hydroxylated fatty acids are also
41 detected with varying relative abundances in the OMZ and deep oxycline, signifying additional non-
42 phototrophic bacterial sources for these lipids. Betaine lipids (with zero or multiple hydroxylations in
43 the core structures) that are typically assigned to microalgae are found throughout the water column down
44 to the deep oxycline but do not show a depth-related trend in relative abundance. Archaeal IPLs
45 comprised of glycosidic and mixed glycosidic-phosphatidic glycerol dibiphytanyl glycerol tetraethers
46 (GDGTs) are most abundant in the upper OMZ where nitrate maxima point to ammonium oxidation, but

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49 increase in relative abundance in the core OMZ and deep oxycline. Abundant non-phosphorus
50 “substitute” lipids within the OMZ suggest that the indigenous microbes might be phosphorus limited (P
51 starved) at ambient phosphate concentrations of 1 to 3.5 μM , although specific microbial sources for many
52 of these lipids still remain unknown.

53 **1. Introduction**

54 Oxygen Minimum Zones (OMZ) are permanently oxygen-deficient regions in the ocean defined by
55 O₂ concentrations <20 μM. They occur in areas where coastal or open ocean upwelling of cold, nutrient-
56 rich waters drive elevated levels of primary production and the subsequent respiration of organic matter
57 exported out of productive surface waters consumes oxygen faster than it is replaced by ventilation or by
58 mid-depth lateral injections of oxygenated water. Low oxygen levels cause habitat compression,
59 whereby species intolerant to low levels of oxygen are restricted to oxygenated surface waters (Keeling
60 et al., 2010; Rush et al., 2012). But even these low levels of oxygen permit vertical migration of some
61 zooplankton taxa into hypoxic waters (e.g., Seibel, 2011; Wishner et al., 2013). Oxygen depletion
62 stimulates diverse microbial life capable of utilizing alternative electron acceptors for respiration under
63 microaerobic conditions (e.g., Ulloa et al., 2012; Tiano et al., 2014; Carolan et al., 2015; Kalvelage et al.,
64 2015; Duret et al., 2015). Important prokaryote-mediated processes within OMZs include denitrification
65 and the anaerobic oxidation of ammonium (anammox), which together may account for 30-50% of the
66 total nitrogen loss from the ocean to the atmosphere (Gruber, 2008; Lam and Kuypers, 2011). Modern
67 day OMZs comprise ~8% of global ocean volume (Karstensen et al., 2008; Paulmier and Ruiz-Pino, 2009;
68 Lam and Kuypers, 2011), but any expansion in the coming decades as a consequence of global warming
69 and increased stratification (Stramma et al., 2008; Keeling et al., 2010) would have profound effects on
70 marine ecology, oceanic productivity, global carbon and nitrogen cycles, the biological pump and
71 sequestration of carbon (Karstensen et al., 2008; Stramma et al., 2010; Wright et al., 2012). A better
72 understanding of the effect of low-O₂ on marine biogeochemistry and microbial ecology is thus warranted.

73 The Eastern Tropical North Pacific Ocean (ETNP), situated off the west coast of Mexico and Central
74 America, hosts one of the largest OMZs in the open ocean, extending halfway across the Pacific Ocean
75 and comprising ~41% of global OMZs (Lavin and Fiedler, 2006; Fiedler and Talley, 2006; Paulmier and
76 Ruiz-Pino, 2009). By comparison, OMZs of the Eastern Tropical South Pacific Ocean off Peru and Chile
77 and in the Arabian Sea are ~14% and ~8%, respectively, of global OMZs. In the ETNP, a sharp
78 permanent pycnocline develops where warm, saline surface waters lie on top of a shallow thermocline,
79 producing a highly stratified water column. Moderate primary production, dominated by picoplankton,
80 depends on oceanic upwelling and wind mixing of coastal waters but is generally limited by the lack of
81 micronutrient dissolved iron (Franck et al., 2005; Pennington et al., 2006). Remineralization, ~70% of
82 which is microbially mediated (Cavan et al., 2017), of particulate organic carbon exported out of surface
83 waters consumes oxygen at rates that cannot be balanced by ventilation across the pycnocline and by
84 sluggish lateral circulation, leading to O₂ levels <2 μM at depths between ~100 and ~800 m.
85 Abundances of micro- (Olson and Daly, 2013) and macro-zooplankton (Wishner et al., 2013; Williams et
86 al., 2014) that are high in surface waters are reduced in the OMZ, and those macrozooplankton that are
87 diel vertical migrators survive in the OMZ with reduced metabolic rates (Maas et al., 2014; Cass and Daly,
88 2015). Microbial abundances and activities for both heterotrophic and chemoautotrophic metabolisms
89 are high in both surface waters and within the OMZ, but again with reduced metabolic rates in the OMZ
90 (Podlaska et al., 2012). A strong nutricline indicates microbial nitrogen cycling involving co-occurring
91 nitrification, denitrification and anammox (Rush et al., 2012; Podlaska et al., 2012), perhaps contributing
92 up to 45% of the global pelagic denitrification (Codispoti and Richards, 1976). Microbial communities
93 are mainly comprised of proteobacteria, with increasing contributions of archaea in deeper waters. Yet, on

94 average ca. 50% of the prokaryotic communities within the OMZ of the ETNP remained uncharacterized
95 (Podlaska et al., 2012).

96 Intact polar lipids (IPLs) are the main building blocks of cellular membranes and may be used to
97 characterize abundance and physiology of aquatic microorganisms from all three domains of life. IPLs
98 represent a diverse range of molecular structures, including phosphatidyl, glycosidic, phospho-glycosidic,
99 and amino acid polar head groups linked to glyceryl-acyl and glyceryl-*O*-alkyl apolar moieties. IPL
100 distributions have been documented in surface waters of the Eastern Subtropical South Pacific (Van Mooy
101 and Fredricks, 2010), the Western North Atlantic Ocean (Van Mooy et al., 2006; 200; Pependorf et al.,
102 2011a), the South Pacific Ocean (Kharbush et al., 2016), the Mediterranean Sea (Popendorf, et al., 2011b),
103 the North Sea (Brandsma et al., 2012), lakes (Bale et al., 2016), the Western English Channel (White et
104 al., 2015) and throughout the water columns of stratified water bodies (Ertefai et al., 2008; Schubotz et
105 al., 2009; Wakeham et al., 2012; Pitcher et al., 2011; Xie et al., 2014; Basse et al., 2014; Sollai et al., 2015).
106 Surface waters are typically dominated by nine IPL classes. Three diacylglycerol glycolipids,
107 monoglycosyl (1G-), diglycosyl (2G-) and sulfoquinovosyl diacylglycerol (SQ-DAG), are main IPLs
108 found in all thylakoid membranes of phototrophs, including those of cyanobacteria (Siegenthaler et al.,
109 1998)¹. Three betaine lipids, diacylglyceryl homoserine (DGTS), hydroxymethyl-trimethyl- β -alanine
110 (DGTA) and carboxy-*N*-hydroxymethyl-choline (DGCC), are also generally abundant. Betaine lipids
111 are widely distributed in lower plants and green algae (Dembitsky, 1996) and are thus usually assigned to

¹ Elsewhere in the literature 1G-DAG, 2G-DAG, and SQ-DAG are also termed MGDG, DGDG and SQDG. However, we have opted to retain the 1G-DAG, 2-DAG, etc. nomenclature as other IPLs discussed throughout also contain monoglycosyl- and diglycosyl-moieties (e.g., 1G-GDGT and 2G-GDGT). Likewise, we retain the nomenclature PC-DAG, PE-DAG, and PG-DAG for phospholipids elsewhere termed PC, PE, PG.

112 eukaryotic algae in the ocean (Popendorf, et al., 2011a), but DGTS was recently also found in bacteria
113 when phosphorus is limited (Yao et al., 2015; Sebastian et al. 2016). Three common detected
114 phospholipids are diacylglycerol phosphatidyl choline (PC-DAG; often simply referred to elsewhere as
115 PC), phosphatidyl ethanolamine (PE-DAG, often PE), and phosphatidyl glycerol (PG-DAG, often PG),
116 all of which have mixed eukaryotic or bacterial sources in the upper water column (Sohlenkamp et al.,
117 2003; Popendorf, et al., 2011a). Microbial source assignments have been broadly confirmed by isotope
118 labeling studies (Popendorf, et al., 2011a). In oxygen-deficient subsurface waters IPL distributions are
119 more diverse and other phospholipids such as diacylglycerol phosphatidyl (*N*)-methylethanolamine
120 (PME-DAG), phosphatidyl (*N,N*)-dimethylethanolamine (PDME-DAG) and diphosphatidyl glycerol
121 (DPG) increase in abundance; these IPLs occur in a number of bacteria that may inhabit low oxygen
122 environments (Schubotz et al., 2009; Wakeham et al., 2012). Dietherglycerol phospholipids and
123 glycosidic ceramides with unidentified sources have also been detected (Schubotz et al., 2009; Wakeham
124 et al., 2012), the latter have been recently observed to be abundant in phosphorus-limited diatoms (Hunter
125 et al., 2018). IPLs that are unique to marine archaea are comprised of glycerol dialkyl glycerol tetraethers
126 (GDGT) core lipids with various glycosidic, diglycosidic and mixed phospho-glyco polar head groups
127 (e.g., Schouten et al., 2008; Pitcher et al., 2011; Zhu et al., 2016; Elling et al., 2017). Abundances of
128 archaeal IP-GDGTs vary considerably with depth, but are typically elevated in zones of water column
129 oxygen depletion, especially where ammonium oxidizing thaumarchaea are abundant (Pitcher et al., 2011;
130 Schouten et al., 2012; Sollai et al., 2015).

131 IPL can also be indicators of metabolic and physiologic status. Many organisms remodel their IPL
132 composition when faced with environmental stressors such as changes in pH, salinity, temperature or

133 availability of nutrients (Zhang and Rock, 2008; Van Mooy et al., 2009; Meador et al., 2014; Carini et al.,
134 2015; Elling et al., 2015). Replacing phospholipids with non-phosphorus containing substitute lipids is
135 an important mechanism when facing nutrient phosphate starvation in oligotrophic surface waters where
136 phosphate concentrations may be as low as nanomolar levels. Cyanobacteria replace PG-DAG with SQ-
137 DAG (Benning et al., 1993; Van Mooy et al., 2006) and microalgae and some bacteria replace PC-DAG
138 with DGTS (Geiger et al., 1999; Van Mooy et al., 2009; Popenorf, et al., 2011b) due to their similar ionic
139 charge at physiological pH. Heterotrophic marine bacteria can replace PE-DAG with either 1G-DAG or
140 DGTS (Carini et al., 2015; Sebastian et al., 2016; Yao et al., 2015). Notably, substitute lipids are also
141 biosynthesized under micromolar concentrations of phosphate (Bosak et al., 2016).

142 Here, we use IPL distributions in suspended particulate matter (SPM) to characterize eukaryotic,
143 bacterial and archaeal communities inhabiting the water column of the ETNP. This study is an extension
144 of that of Xie et al. (2014), which focused on the distribution of core and intact polar archaeal and bacterial
145 tetraether lipids at two stations investigated here (stations 1 and 8). The water column of the ETNP
146 comprises distinct biogeochemical zones based on oxygen concentrations and IPL distributions reflect the
147 localized ecology. Abundant non-phosphorus substitute lipids within the core of the OMZ suggest
148 phosphorus limitation of the source microorganisms even at micromolar concentrations of phosphate.
149 Overall our results provide deeper insight into the broad community composition and the physiologic state
150 of microorganisms inhabiting OMZs.

151

152 **2. Methods**

153 *2.1 Sample collection and CTD data*

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155 Suspended particulate matter (SPM) samples were collected at four stations (distance to shore:
156 400~600 km; Fig 1) along a northwest-southeast transect (Station 1: 13° 01.87'N, 104° 99.83'W; Station
157 2: 11° 99.96' N, 101° 22.82' W; Station 5: 10° 68.94' N, 96° 34.12' W; and Station 8: 8° 99.46'N,
158 90°00.18'W) in the ETNP during the R/V *Seward Johnson* cruise in November 2007 (R/V *Seward Johnson*
159 Cruise Scientists, 2007). Station 1 in the Tehuantepec Bowl is an area of relatively low primary
160 productivity (e.g., 0.05 mg Chl-*a*/m²; (Fiedler and Talley, 2006; Pennington et al., 2006) whereas Station
161 8 in the Costa Rica Dome is moderately productive (1 mg Chl-*a*/m²). All stations are characterized by a
162 strong thermocline/pycnocline/oxycline (at 20-50 m depths depending on location) and a profound and
163 thick OMZ (down to ~2 μM O₂ between ~300-800 m depth). Station 1 is a reoccupation of the Vertical
164 Transport and Exchange II/III site from the early 1980's (Lee and Cronin, 1984; Martin et al., 1987;
165 Wakeham and Canuel, 1988; Wakeham, 1987, 1989).

166 Seawater was filtered *in-situ* using submersible pumps (McLane Research Laboratories WTS-142
167 filtration systems) deployed on the conducting cable of the CTD/rosette that measured temperature,
168 conductivity, oxygen, fluorescence/chlorophyll-*a* and transmissivity during pump deployments and
169 during pumping. Filtered water volumes ranged between 130 and 1800 L (Suppl. Table 1). Pumps
170 were fitted with two-tier 142 mm diameter filter holders: a 53 μm mesh Nitex “prefiltration” screen to
171 remove larger eukaryotes and marine snow aggregates and a double-stacked tier of ashed glass fiber filters
172 (142 mm Gelman type A/E, nominal pore size 0.7 μm). IPL concentrations we report represent minimum
173 values to reflect potentially inefficient collection of 0.7 μm particles by GFFs. Since pore size of the
174 filters may also decrease during filtration the recovered material may vary dependent on filtration time.

175 Following pump recovery, GFF filters and Nitex screens were wrapped in pre-combusted foil and stored
176 frozen at -20°C until extraction.

177

178 *2.2 Elemental, pigment and nutrient analysis*

179 Particulate organic carbon (POC) and total particulate nitrogen (TN) were measured on 14 mm-
180 diameter subsamples of each glass fiber filter (GFF) prior to lipid extraction; therefore, POC and TN
181 concentrations reported here are only for <53 µm material. The plugs were acidified in HCl vapor in a
182 desiccator for 12 hours to remove inorganic carbon. Elemental analysis was performed with a
183 ThermoFinnigan Flash EA Series 1112 interfaced to a ThermoFinnigan Delta V isotope ratio mass
184 spectrometer at the Skidaway Institute Scientific Stable Isotope Laboratory. Organic carbon and
185 nitrogen contents were calibrated against internal laboratory chitin powder standards which in turn had
186 previously been cross-calibrated against USGS 40 and 41 international standards.

187 Chlorophyll-*a* (Chl-*a*) and pheopigment concentrations were measured on-board the ship (Olson and
188 Daly, 2013). Seawater samples (100 – 500 ml) from CTD casts were filtered onto Whatman GF/F filters
189 (0.7 µm) which were immediately extracted with 90% acetone. Fluorescence was measured with a
190 Turner Designs 10AU fluorometer and Chl-*a* concentrations were determined after Parsons et al (1984).
191 Post-cruise HPLC analysis of pigments in 100 – 500 ml seawater samples filtered onto Whatman GF/F
192 (0.7 µm) filters were conducted at the College of Charleston Grice Marine Laboratory, Charleston, SC on
193 a Hewlett Packard 1050 system (DiTullio and Geesey, 2002).

194 Seawater samples for nutrient analyses (NO_2^- , NO_3^{2-} , NH_4^+ and PO_4^{3-}) were collected directly from
195 Niskin bottles into acid-washed, 30-mL high-density polyethylene (HDP) bottles. After three rinses,

196 bottles were filled to the shoulder, sealed, and frozen (-20°C). All frozen samples were transported to
197 the Oceanic Nutrient Laboratory at USF for analysis using a Technicon Autoanalyzer II.

198

199 2.3 Lipid extraction and analysis of intact polar lipids

200 Lipids associated with the <53 µm SPM on the GFFs were Soxhlet-extracted shortly after the
201 expedition in 2008 using dichloromethane:methanol (DCM:MeOH; 9:1 v/v) for 8 h. Extracted lipids
202 were partitioned into DCM against 5% NaCl solution and dried over Na₂SO₄. Total lipid extracts (TLEs)
203 were stored at -20°C. Soxhlet extractions, rather than for example microwave assisted Blich-Dyer
204 extractions, were chosen at the time because it was the only feasible way to handle the double 142mm
205 filters. Extraction protocol surely can affect IPL distributions; as shown by Lengger et al. (2012) for
206 smaller sediment samples.

207 IPL analyses by high-performance liquid chromatography-mass spectrometry (HPLC-MS) were
208 carried out initially in 2010/2011 and again in 2015 as instrument protocols improved. In between these
209 analyses we did not observe a notable selective loss of IPL compounds, instead we were able to detect a
210 much larger suite of IPL structures due to improved detection and chromatographic separation techniques
211 (Wörmer et al., 2013). The confidence in these results are supported by the analysis of IPL standards
212 (Suppl. Table 2) that are stored at -20 °C over several years (fresh standard mixtures are typically prepared
213 every 2 to 3 years), which do not indicate degradation of any particular IPL over time (Suppl. Fig. 1).
214 The analysis in 2010/2011 focused on absolute concentrations of the major IPLs (for distinction between
215 major and minor IPLs see results section). Aliquots of the TLE were dissolved in DCM/methanol (5:1
216 v/v) for injection on a ThermoFinnigan Surveyor HPLC system coupled to a ThermoFinnigan LCQ

Deleted: More recent IPL analyses typically utilize less harsh modified Blich-Dyer extraction procedures, however, we believe that our finding labile IPLs, such as hexose-phosphate-hexose GDGTs, indicates that our results are not compromised (cf. Lengger et al., 2012).

222 DecaXP Plus ion-trap MS via electrospray interface (HPLC-ESI-IT-MS^b) using conditions described
223 previously (Sturt et al., 2004; Xie et al., 2014). Ten μ L of a known TLE aliquot spiked with C₁₉-PC as
224 internal standard was injected onto a LiChrosphere Diol-100 column (150 \times 2.1 mm, 5 μ m, Alltech,
225 Germany) equipped with a guard column of the same packing material. Absolute IPL concentrations
226 were determined in positive ionization mode with automated data-dependent fragmentation of the two
227 most abundant base peak ions. Acyl moieties of glycolipids and aminolipids were identified via HPLC-
228 IT-ESI-MS² experiments in positive ionization mode, whereas phospholipid side chain composition was
229 analyzed in negative ionization mode. Details of mass spectral interpretation, and identification of fatty
230 acid moieties are described in Sturt et al. (2004) and Schubotz et al. (2009) and are exemplified in Suppl.
231 Table 3. HPLC-MS analysis is not able to differentiate between double bonds or rings, therefore in the
232 subsequent text we will refer to double bond equivalents (DBE) to include both possibilities, similarly
233 absolute chain length cannot be determined as branched and straight chain alkyl chains cannot be
234 differentiated, therefore we report total carbon atom numbers for the alkyl side chains. Assignment of
235 the betaine lipid DGTS was according to the retention time of the commercially available standard DGTS
236 (Avanti Polar Lipids, USA). The isomer DGTA, which elutes at a different retention time due to its
237 structural difference (e.g., Brandsma et al., 2012) was not observed in the HPLC-MS chromatograms.
238 For all analyses, response factors of individual IPLs relative to the injection standard C₁₉-PC were
239 determined using dilution series of commercially available standards (Suppl. Table 2).

240 Subsequent analyses in 2015 were used to obtain sum formulas and IPL structures based on exact
241 masses in the MS1 and MS-MS experiments and to additionally provide data on minor lipids, which were
242 below detection limit during the 2010/2011 ion trap analyses (for distinction between major and minor

243 lipids see results section). For these measurements absolute quantities could not be determined since the
244 TLE had been used for other experiments and the information on TLE amounts used was unknown;
245 therefore, these analyses are used to describe relative abundances. Analyses were performed on a Bruker
246 maXis Plus ultra-high resolution quadrupole time-of-flight mass spectrometer (Q-TOF) with an ESI
247 source coupled to a Dionex Ultimate 3000RS UHPLC. Separation of IPLs was achieved using a Waters
248 Acquity UPLC BEH Amide column as described in Wörmer et al. (2013), which resulted in better
249 chromatographic separation of compounds and higher sensitivity compared to the 2010/2011 analyses.
250 Relative proportions of compounds were quantified taking the different response factors of IPL classes
251 into account. Peak areas in extracted mass chromatograms were corrected with absolute response factors
252 determined in dilution series of commercially available standards (Suppl. Table 2). Some ions assigned
253 to either PE-AEG and PC-AEG could not be quantified individually due to co-elution of these compounds
254 and were thus quantified as one group using the mean response factor of PE- and PC-DAG. For
255 compound classes for which no standards were available, (e.g., PI-DAG, OL and the unknown aminolipids
256 AL-I and AL-II) the relative responses could not be corrected for. Assuming these compounds may
257 ionize similarly as structurally related IPLs, values may be off by a factor of 0.2 to 1.4, which is the
258 maximum range of response factors observed for the standards.

259

260 *2.4 Statistical analysis*

261 Nonmetric multidimensional scaling (NMDS) analysis was used to illustrate the relationships
262 among objects hidden in a complex data matrix (Rabinowitz, 1975) and was performed in the free software
263 R (version 3.4.3, www.r-project.org/) with *metaMDS* (vegan library, version 2.4-6) as described by

264 Wakeham et al. (2012). The datasets of relative lipid distribution and variations in carbon number and
265 double bond equivalents were standardized by Hellinger transformation using the function *decostand*,
266 while for all other variables (environmental parameters, microbial groups) absolute numbers were used.
267 The compositional dissimilarity was calculated by Euclidean distance measure. The resulting plot shows
268 the distribution of lipids and sampling depths. Microbial groups and geochemical parameters were
269 overlaid by function *envfit*. Lower stress is related to high quality of solution, and stress values ≤ 0.1
270 indicate results of good quality (Rabinowitz, 1975). Non-parametric Spearman Rank Order Correlation
271 analysis was performed on combined data of environmental variables and IPL ratios and IPL relative
272 abundances of all four stations using SigmaPlot 11.0 (Systat Software Inc., San Jose, USA).

273

274 3. Results

275 3.1 Biogeochemical setting

276 All along the transect, the thin mixed layer (upper ~20 m) was warm, ~25–28 °C, with oxygen
277 concentrations approaching air saturation at ~200 μM (Fig. 2). The euphotic zone (1% of surface
278 photosynthetically active radiation) generally ranged between 50 and 80 m depth. The thermocline was
279 abrupt at ~20-50 m, where temperatures dropped to ~15–18 °C and oxygen decreased to ~20 μM .
280 Temperatures stabilized by ~250–300 m depth at ~10–12 °C and oxygen levels were <2 μM ; especially
281 at Station 8 there were spatially and temporally variable oxygen intrusions into the upper portion of the
282 OMZ. By ~600–800 m depth, a deep oxycline was observed where oxygen concentrations began to rise
283 again to ~40 μM at temperatures of ~4 °C by 1250 m. For the purposes of this discussion, the water
284 column of the ETNP was partitioned into four horizons based on oxygen content: an oxic epipelagic zone

285 down to the thermocline (0–50 m; $200 \mu\text{M} > \text{O}_2 > 20 \mu\text{M}$); an upper OMZ (Station 1 and 8: 50–300 m,
286 Station 5: 50 – 350 m, Station 2: 50–200 m; $20 \mu\text{M} > \text{O}_2 > 2 \mu\text{M}$); the core OMZ (Station 1 and 8: 300–
287 800 m, Station 5: 350 – 600 m Station 2: 200 – 600 m; $\text{O}_2 < 2 \mu\text{M}$); and a deep oxycline (Station 1 and 8
288 ≥ 800 m, Station 2 and 5 ≥ 600 m; $\text{O}_2 > 2 \mu\text{M}$) of rising O_2 levels (Fig. 1a). Note that sampling at stations
289 1 and 8 reached to 1250 m depth so SPM from >750 m depth best represents the deep oxycline.

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290 Chl- α was highest in surface waters with maximum values of $1.8 \mu\text{g/L}$ at 10 m at station 5, was
291 between 0.2 and $0.7 \mu\text{g/L}$ at station 1, 2 and 8 and decreased to values close to zero below 100 m at all
292 stations (Fig. 2; see also Fiedler and Talley, 2006, and Pennington et al., 2006, for additional results from
293 previous surveys). HPLC analysis of accessory pigments (Goericke et al., 2000; Ma et al., 2009) showed
294 that picoplankton, primarily *Prochlorococcus* (indicated by divinyl chlorophyll α), were an important
295 component of the photoautotrophic community, along with diatoms (fucoxanthin), especially *Rhizosolenia*
296 at the deep fluorescence maximum at stations 1 and 5 but *Chaetoceros* at station 8, and prymnesiophytes
297 (19'hexanoyloxyfucoxanthin and 19'butanoyloxyfucoxanthin; DiTullio and Geesey, 2002; Suppl. Table
298 4). High phaeopigment abundances (up to 90% of [Chl- α + phaeopigments]) attested to algal senescence
299 or grazing by macro- (Wishner et al., 2013; Williams et al. 2014) and micro-zooplankton (Olson and Daly,
300 2013) above and into the oxycline. Primary maxima in transmissivity corresponded with the peak Chl-
301 α concentrations and fluorescence maxima, but secondary transmissivity maxima between 300 and 400 m
302 at stations 1, 5, and 8 indicated elevated particle abundances in the core of the OMZ (Fig. 2).

303 Nitrite (NO_2^-) maxima in the OMZ at all stations coincided with nitrate (NO_3^{2-}) deficits (Fig. 3).
304 Ammonium (NH_4^+) concentrations changed little through the water column (Fig. 3). Phosphate (PO_4^{3-} ;
305 Fig. 3) and total dissolved nitrogen (TDN; not shown) were low (respectively, < 0.5 and $< 3 \mu\text{M}$) in the

307 upper 20 m of the oxic zone, but increased in the OMZ. High PO_4^{3-} (up to 3.4 μM) and high TDN (up
308 to 44.5 μM) were observed in the deep OMZ at stations 2, 5 and 8 (Fig. 3). N:P ratios were lower than
309 the Redfield ratio (16) at all sites and depths (Fig. 3); N:P minima were lowest in surface waters (2.6 to
310 10 in the upper 20 m) and at ~500 m within the core OMZ and the deep oxycline at station 1 (<9).

311 POC and TN concentrations (< 53 μm material) were highest in the euphotic zone (POC: 20 – 100
312 $\mu\text{g/L}$; TN: 4 – 15 $\mu\text{g/L}$), rapidly dropping to 5 $\mu\text{g/L}$ and 1 $\mu\text{g/L}$ below the upper OMZ, respectively (Fig.
313 2; Suppl. Fig. 2). Secondary maxima for POC (~10 $\mu\text{g/L}$) and TN (~2 $\mu\text{g/L}$) within the core of the OMZ
314 might reflect elevated microbial biomass there. Concentrations dropped in the deep oxycline to ≤ 3 $\mu\text{g/L}$
315 and ≤ 0.5 $\mu\text{g/L}$ for POC and TN, respectively.

316 Absolute IPL concentrations were determined by ion trap LCMS and varied between 250 and 1500
317 ng/L in the oxic zone and abruptly decreased more than 10-fold (to <20 ng/L) in the upper OMZ (Fig. 2).
318 Secondary maxima in IPL concentrations (15–40 ng/L) within the OMZ at all stations roughly coincided
319 with elevated numbers of prokaryotes (Fig. 2). IPL:POC ratios decreased with increasing depth (Fig. 2),
320 tracking trends of POC, TN and IPL concentrations.

321

322 3.2 Changes in IPL composition with water column depth in the ETNP

323 In total, 24 IPL classes were identified in the ETNP (Fig. 4, Suppl. Fig. 3). Eleven major and thirteen
324 minor IPL classes were detected in the QTOF analyses, which were classified according to their relative
325 abundance: if an individual IPL comprised more than 10% of total IPLs at any depth of the four stations
326 it was classified as a major IPL, compounds <10% were minor IPLs. Based on their head group
327 composition IPLs were grouped into glycolipids, phospholipids or aminolipids. Figure 3 shows changes

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330 in the relative abundances (as percentages of total IPLs, excluding isoprenoidal archaeal IPLs) of
331 glycolipids, phospholipids and aminolipids as well as several substitute lipid ratios, reflecting preferential
332 biosynthesis of non-phosphorus lipids to replace phospholipids under phosphate-limiting growth (cf. Van
333 Mooy et al., 2006; Popendorf, et al., 2011b; Carini et al., 2015; Bosak et al., 2016). Relative abundances
334 of non-isoprenoidal phospholipids were highest in the core OMZ between 400 and 600 m at all sites,
335 where they comprise up to 45–76% at stations 1, 2 and 5 and between 12 and 61% at station 8.
336 Phospholipid abundances were lower within the upper OMZ and oxic zone at all stations (between 4 and
337 55%) and in the deep oxycline at station 8 (<1%). Aminolipid content was highest in SPM from the
338 upper 55 m at station 5 and 8 (10 to 25%), the core OMZ at station 8 (15 to 34%) and the deep oxycline
339 at station 1 (17%). Lower aminolipid contents (2 to 11%) were observed in the oxic zone and the core
340 OMZ at stations 1 and 2, the upper OMZ at station 5 (0 to 11%) and the deep oxycline at station 8 (<2%).
341 Glycolipid abundance was >9% at all depths, with highest abundance (average 54%, max. 82%) within
342 the upper OMZ and oxic zone at all stations and the deep oxycline at station 8. Values down to 9% were
343 observed within the core OMZ.

344

345 3.2.1 Major lipids

346 The eleven major IPL classes included three IP-GDTs of archaeal origin: (1G-GDGT, 2G-GDGT and
347 HPH-GDGT); and eight IPLs assigned to either a bacterial or eukaryotic origin: three glycolipids (1G-
348 DAG, 2G-DAG, SQ-DAG), four phospholipids (PG-DAG, PE-DAG, PC-DAG, PE+PC-AEG) and one
349 aminolipid (DGTS). All major lipid classes were found at almost all depths at all four stations, but with
350 varying relative abundances (as % of total IPL; Fig. 4, Suppl. Table 1).

351 *Archaeal IP-GDGTs*: Relative abundances of archaeal IPL (IP-GDGTs) generally increased with
352 depth from non-detectable in surface waters to >50% of total IPLs at station 8 (bottom of core OMZ and
353 deep oxycline). Archaeal IP-GDGT abundances at stations 1 and 2 peaked at 30% (bottom of upper
354 OMZ, core OMZ and deep oxycline) but were generally <10% at station 5 (Fig. 4). At station 1 and 2,
355 1G-GDGT and 2G-GDGT were most abundant with variable amounts of HPH-GDGTs, whereas 1G-
356 GDGT and HPH-GDGT dominated archaeal IPLs at station 5 and 8 at most depths. Distributions of
357 glycosidic IPL-GDGTs obtained in the present investigation corroborate the absolute values reported by
358 (Xie et al., 2014) for stations 1 and 8: 1G-GDGT was more abundant than 2G-GDGT at station 8 when
359 compared to station 1. The core GDGTs of 1G-GDGTs and HPH-GDGTs are dominated by GDGT-0
360 and crenarchaeol (Suppl. Fig. 4), whereas 2G-GDGTs are dominated by GDGT-2 and a small amount of
361 crenarchaeol (Zhu et al., 2016)

362 *Diacylglycerol lipids*: The oxic zone and the upper OMZ were dominated (~50–80% of IPL) at all
363 sites by the diacylglycerol glycolipids, 1G-DAG, 2G-DAG and SQ-DAG (Fig. 4). In the core OMZ and
364 deep oxycline, relative amounts of 2G-DAG and SQ-DAG decreased to 4% and 12%, respectively. 1G-
365 DAG abundances were lowest in the core OMZ at all stations, but were up to 47% of total IPL in the deep
366 oxycline. Diacylglycerol phospholipids, PE-, PG- and PC-DAG, were the second most abundant IPLs.
367 Abundances of PE- and PG-DAG were highest within the upper and core OMZ, constituting >50% in the
368 core OMZ at station 1, >30% at stations 2 and 5, and 16% at station 8. PC-DAG, with average
369 abundances of 5% at stations 1, 2, 8 and 3% at station 5, did not exhibit depth-related trends. The third
370 most abundant diacylglycerol class was the betaine lipid DGTS, which was present throughout the water
371 column at average abundances of 7% at station 1, 2 and 8, and 5% at station 5.

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373 Major diacylglycerol lipids showed changes in average number of carbon atoms and double bond
374 equivalents (DBE) with depth (Fig. 5, Suppl. Table 5). The glycolipids and PC-DAG decreased in average
375 carbon number by up to three carbons and decreased in DBE by up to 2 at the top of the upper OMZ and
376 within the core OMZ compared to the oxic zone and the deep oxycline. Average carbon numbers for
377 PE- and PG-DAG and DGTS showed an inverse trend, both generally increasing up to two carbons
378 between the upper OMZ and the core OMZ. Changes in DBE were not as pronounced for PG-DAG and
379 DGTS, on average 1 to 2 DBE greater in surface waters than in deeper waters, while the number of DBE
380 increased on average with depth for PE-DAG.

381 *Acyl-ether glycerol lipids:* Mixed ether-ester glycerol core structures with either PE or PC head
382 groups were observed at all stations and all depths (generally 4-12%) except for the deep oxycline at
383 station 8.

384

385 3.2.2 Minor lipids

386 Thirteen minor IPL classes were identified, five of which were glycolipids, four phospholipids and
387 four aminolipids. All minor lipid classes were detected at each site except for OH-DGTS which was
388 absent at station 1. Some minor lipids were found at all depths, whereas others were restricted to specific
389 depth zones as defined by oxygen content (Fig. 4).

390 *Diacylglycerol lipids:* Two minor diacylglycerol glycolipids, 1G-OH-DAG and 3G-DAG, were
391 most abundant within the oxic zone and the upper OMZ, comprising between 2 to 15% of minor lipids on
392 average (0.1 to 0.6% of total IPLs), but were only sporadically found within the core OMZ and deep
393 oxycline. 1G-OH-DAG showed highest relative abundances at station 5, constituting up to 40% of minor

394 lipids. Four additional phospholipids with diacylglycerol core structures with the following head groups
395 were identified: diphosphatidylglycerol (DPG), phosphatidyl-(*N*)-methylethanolamine (PME),
396 phosphatidyl-(*N,N*)-dimethylethanolamine (PDME) and phosphatidyl inositol (PI). DPG, PME-DAG and
397 PDME-DAG had highest relative abundances (respectively 65, 56 and 35% of minor IPL) within the upper
398 and core OMZ, but at lower abundances within the oxic zone at all stations and in the deep oxycline at
399 stations 1, 2 and 5. PI-DAG was most abundant in the oxic zone and the upper OMZ (up to 25% of
400 minor IPL), but was also present in the core OMZ and the deep oxycline, except for station 8. Three
401 types of aminolipids were observed as minor lipids. OH-DGTS with up to three hydroxyl-groups
402 attached to the fatty acyl side chains (Suppl. Fig. 5) was observed at most depths at station 8 with an
403 average relative abundance of 23% among the minor lipids; it was also occasionally detected at stations 2
404 and 5 within the oxic zone and upper OMZ. Two additional aminolipids had an undefined head group
405 that exhibited fragmentation patterns characteristic of betaine lipids, but without established betaine head
406 group fragments (Suppl. Fig. 6b, c). The tentatively assigned sum formula for the head group of the first
407 unknown aminolipid (AL-I) at ca. 6.7 minutes LC retention time was $C_8H_{17}NO_3$ and for the second
408 unknown aminolipid (AL-II) at 10.5 minutes was $C_7H_{15}NO_3$. The head group sum formula for AL-II
409 matches that of DGCC, but the diagnostic head group fragment of *m/z* 252 was not detected, and
410 furthermore, AL-II did not elute at the expected earlier retention time for DGCC. AL-I and AL-II were
411 detected at most depths at all four stations, with average abundances of 1 to 6% of the minor lipids for
412 AL-I and comparably higher relative abundances ranging from 16 to 36% for AL-II.

413 *Acyl-ether glycerol lipid*: One minor compound that eluted slightly earlier than SQ-DAG had a
414 fragmentation pattern similar to SQ-DAG but with exact masses of the parent ion and MS-MS fragments

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417 in both positive and negative ion mode that suggested a mixed acyl-ether glycerol core lipid structure
418 (Suppl. Fig. 6d, e). Tentatively assigned as SQ-AEG, this IPL was observed at most depths at all four
419 stations with highest relative abundances of 5 to 60% of minor IPLs within the oxic zone.

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420 *Sphingolipids*: Two types of sphingolipids were identified, monoglycosyl ceramide (1G-CER), and
421 hydroxylated monoglycosyl ceramide (1G-OH-CER) with up to two hydroxyl groups attached to the
422 hydrophobic side chains (Suppl Fig. 5e). Both were observed at all depths at stations 1, 2, and 5 at
423 average relative abundances between 3 and 8% of minor IPLs, but neither was detected in the deeper part
424 of the core OMZ or deep oxycline at station 8.

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425 *Ornithine lipids*: Trace amounts (<4%) of ornithine lipids were detected in the core OMZ of stations
426 2 and 5.

427

428 3.2.3 Statistical relationships between environmental parameters and lipid distribution

429 Spearman Rank Order Correlation was used to evaluate relationships between relative lipid
430 abundance of lipid classes and environmental parameters (Table 1). The glycolipids 2G- and SQ-DAG
431 showed highly significant ($p < 0.001$) and positive correlations with depth, fluorescence, POC, TN,
432 temperature and Chl- α , significant positive correlations were also observed with oxygen. Both also
433 showed highly significant but negative correlations with phosphate and nitrate, and these overall trends
434 were mirrored in the SQ-DAG:PG-DAG ratio. Total glycolipids (GL) and 1G-DAG only showed
435 correlations with a few environmental parameters and total GL were only significantly positively
436 correlated with oxygen. Most aminolipids and phospholipids did not show significant correlations with
437 environmental parameters and any other correlations were neither strongly positive nor negative.

440 Relative abundances of total aminolipids and aminolipid (AL) to phospholipid (PL) ratios correlated
441 positively with ammonium. AL:PL also correlated positively with oxygen. Relative abundance of total
442 phospholipids and most individual phospholipids (PG-, PE-, PME-, and PDME-DAG) correlated
443 negatively with oxygen. The only phospholipid that significantly correlated with phosphate was PDME,
444 however, the positive correlation is not strong ($r^2 < 0.4$).

445 NMDS analysis revealed that all samples from the oxic zone had a negative loading on the NMDS2
446 axis along with environmental variables such as oxygen, fluorescence, TN, POC and Chl- α . IPLs with
447 a strong negative loading on the NMDS2 axis (< -0.2) were 1G-OH-DAG, SQ-AEG, 2G-DAG, SQ-DAG,
448 PI-DAG and OH-DGTS. Most samples from the core OMZ and deep oxycline had a positive loading on
449 the NMDS2 axis, together with depth, phosphate and nitrate. IPLs that showed a strong positive loading
450 on the NMDS2 axis (> 0.2) were PDME-DAG, 2G-GDGT, DPG, PME-DAG and HPH-GDGT. Almost
451 all environmental variables had low p -values (< 0.001), indicating highly significant fitted vectors with the
452 exception of temperature, salinity, ammonium and nitrate. Highest goodness of fit statistic was observed
453 with oxygen ($r^2 = 0.54$), followed by phosphate ($r^2 = 0.48$) and then fluorescence ($r^2 = 0.46$).

454

455 **4. Discussion**

456 The moderate primary productivity in surface waters of the ETNP, intense microbial degradation of
457 particulate organic matter exported to the thermocline, and restricted midwater oxygen replenishment
458 produce the strong, shallow (~20 m deep) oxycline and a ~500 m thick OMZ with dissolved oxygen
459 concentrations of $< 2 \mu\text{M}$, not unlike other oceanic OMZs (e.g., Ulloa et al., 2012). The ETNP is
460 dominated by picoplankton, and micro-grazers reported consuming most phytoplankton production

461 (Landry et al., 2011; Olsen and Daly, 2013). Peak macrozooplankton biomass was located at the
462 thermocline, near the upper boundary of the OMZ, but a secondary biomass peak of a different
463 zooplankton assemblage was present at the deep oxycline once O₂ concentrations rose to ~2 μM (Wishner
464 et al., 2013). Shallow-water, plankton-derived particulate organic carbon is the primary food source for
465 zooplankton in the mixed layer, upper oxycline and core OMZ, whereas deep POC, some of which might
466 have been produced by microbes in the OMZ, is important for deep oxycline zooplankton (Williams et al.,
467 2014). Microbial community structure and activities are typical of other OMZs (Taylor et al., 2001; Lin
468 et al., 2006; Woebken et al., 2007; Wakeham et al., 2007; 2012). Cell numbers of total prokaryotes were
469 highest in the euphotic layer and decreased with depth at the thermocline but rose again within the core
470 OMZ (Podlaska et al., 2012). Elevated rates of chemoautotrophy, measured by dark dissolved inorganic
471 carbon (DIC) assimilation, were observed at several depths in the OMZ and in the lower oxycline.
472 Transfer of chemoautotrophically-fixed carbon into zooplankton food webs is also evident (Williams et
473 al., 2014). Bacteria dominate the prokaryotic community at all stations. Nitrifying bacteria constituted
474 3-7% of total DAPI-positive prokaryotes in surface waters; sulfate-reducing bacteria (17 and 34% of total
475 prokaryotes), planctomycetes (up to 24% of total prokaryotes), and anammox bacteria (<1% of
476 prokaryotes) in the upper OMZ and deep oxycline might be associated with anoxic microzones within
477 particle aggregates even at low dissolved oxygen concentrations (Woebken et al., 2007; Carolan et al.,
478 2015). Archaeal cell abundances peaked at the start of the upper OMZ at all stations (up to 37% of total
479 prokaryotes at station 2), within the core OMZ at station 2 (up to 54% of total detected cells) and within
480 the deep oxycline at station 5 and 8 (around 25%; Fig. 2e). Crenarchaeota/thaumarchaeota represented
481 ~20% of prokaryotes throughout the water column, generally being highest in the lower OMZ and deep

482 oxycline, and at stations 2 and 5 just above the secondary Chl-*a* maxima at ~75 m. Euryarchaeota were
483 16-20% of total prokaryotes, especially in waters above the OMZ.

484 Total IPL concentrations that were over 50 times higher in the surface waters than at deeper depths
485 coincided with high Chl-*a* concentrations, reflecting the importance of phototrophic sources to the IPL
486 pool above the thermocline. Below the thermocline, IPL concentrations generally track trends in
487 microbial cell abundances, and elevated IPL concentrations in the upper and core OMZ coincide with
488 elevated nitrite concentrations. The rapid decrease in IPL concentrations below ~100 m probably results
489 from a combination of a dearth of potential source organisms and the decomposition of sinking detrital
490 lipids (Harvey et al., 1986; Matos and Pham-Thi, 2009). IPL concentration decreases below the euphotic
491 zone are well established (Van Mooy et al., 2006; Schubotz et al., 2009; Van Mooy and Fredricks, 2010;
492 Pendorf et al., 2011b; Wakeham et al., 2012). We believe that the diverse molecular compositions and
493 shifts in relative abundances of IPLs with changing geochemistry reflect a complex biological community
494 structure and their ecophysiological adaptation throughout the water column.

495

496 *4.1 Provenance of IPLs in the ETNP*

497 Variations in IPL distributions and head group and core lipid compositions reflect the biogeochemical
498 stratification of the water column. Below we discuss potential sources of and possible physiological
499 roles for IPLs in the different zones.

500

501 *4.1.1 Oxic zone*

502 The glycosyldiacylglycerides that dominate the IPL composition in oxic surface waters, 1G-DAG,

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504 2G-DAG and SQ-DAG, are major constituents of photosynthetic thylakoid and chloroplast membranes
505 (Wada and Murata, 1998; Siegenthaler, 1998) and are therefore generally assigned to photosynthetic algae
506 or cyanobacteria (Van Mooy et al., 2006; Pependorf et al., 2011b). These are also the likely predominant
507 sources in our study, however, notably 1G-DAG may also be synthesized by heterotrophic bacteria
508 (Pependorf et al., 2011a; Carini et al., 2015; Sebastian et al., 2016). In the oxic zone, 1G- and 2G-DAG
509 are predominantly comprised of C₁₆ and C₁₈ fatty acids with zero to 5 double bond equivalents
510 polyunsaturated acid (PUFA) combinations such as C_{16:4}/C_{18:3}, C_{16:4}/C_{18:4}, C_{18:3}/C_{16:2}, C_{18:4}/C_{14:0} and
511 C_{18:5}/C_{14:0} (Suppl. Table 5, Fig. 5). These are characteristic of eukaryotic algae (Brett and Müller-
512 Navarra, 1997; Okuyama et al., 1993), such as diatoms and prymnesiophytes that are the major eukaryotic
513 phytoplankton in the ETNP. SQ-DAG biosynthesized by cyanobacteria do not contain PUFA, but
514 instead predominantly contain combinations of C_{14:0}, C_{16:0}, and C_{16:1} fatty acids (e.g., Siegenthaler, 1998),
515 yielding shorter chain lengths and a lower average number of double bonds (0.5 to 1) than the other
516 glycolipids as observed at the ETNP (Fig. 5). Betaine lipids (DGTS) in surface waters of the ETNP are
517 comprised of C₁₄, C₁₆, C₁₈ and C₂₀ with multiple unsaturations or rings (on average 1.5 to 3 double bond
518 equivalents) and are also likely phytoplankton derived (Dembitsky, 1996; Pependorf et al., 2011a).

519 PC-DAG with fatty acyl combinations of C_{22:6} and C_{20:5} long-chain PUFA and C_{16:0} fatty acids (Suppl.
520 Table 5) in surface waters also point to primarily eukaryotic algal sources. PG-DAG is the only
521 phospholipid in cyanobacteria and thylakoid membranes of eukaryotic phototrophs (Wada and Murata,
522 1998). Heterotrophic bacteria are an additional source for PG-DAG since it can be a major phospholipid
523 in bacterial membranes (Goldfine, 1984). PE-DAG is a minor phospholipid in eukaryotic algae (e.g.,
524 Dembitsky et al., 1996) but is common in membranes of bacteria (Oliver and Colwell, 1973; Goldfine,

525 1984) and is biosynthesized by heterotrophic marine bacteria (Popendorf et al., 2011a). Lower average
526 number of double bond equivalents in PG- and PE-DAG (<2) in the upper water column of the ETNP are
527 consistent with a bacterial origin (Fig. 5).

528 Oxic ETNP waters contain PE- and PC-based phospholipids with mixed acyl and ether core lipids
529 (AEG), which are often referred to as 1-*O*-monoalkyl glycerol ethers (MAGE) if detected as core lipids.
530 PE-AEG have been described in some sulfate-reducing bacteria (Rütters et al., 2001), which in the oxic
531 zone or OMZ of the ETNP would require anoxic microzones in fecal pellets or aggregates (e.g., Bianchi
532 et al., 1992; Shanks and Reeder, 1993). In the ETNP, MAGE-based phospholipids were 1 to 30% of
533 total IPLs. MAGE, detected as core lipids in surface waters of the Southern Ocean and eastern South
534 Atlantic are thought to be breakdown products of IP-AEGs of aerobic bacterial origin (Hernandez-Sanchez
535 et al., 2014), but culturing experiments have yet to confirm this conclusion. Similarly, aerobic bacteria
536 (possibly cyanobacteria) are likely sources for SQ-AEG, since sulfoquinovosyl is a diagnostic headgroup
537 found in cyanobacteria, although, again, these lipids have not been reported in cultured cyanobacteria.
538 Other minor phospholipids in the euphotic zone include PI-DAG and DPG. They are minor components
539 in several marine algae (Dembitsky, 1996) and bacteria (Morita et al., 2010; Diervo et al., 1975;
540 Mileykovskaya and Dowhan, 2009). Bacteria may also be the source of the low detected levels of *N*-
541 methylated phospholipids PME-DAG and PDME-DAG (Goldfine and Ellis, 1964). 3G-DAG comprised
542 of C₁₄, C₁₆ and C₁₈ fatty acids with up to six double bond equivalents is another minor IPL detected in the
543 euphotic zone at all stations except for station 5. It has been found in some plants (Hölzl and Dörmann,
544 2007) and some anaerobic gram-positive bacteria (Exterkate and Veerkamp, 1969), which could both be
545 probable sources in the oxic euphotic zone of the ETNP.

546 The sphingolipid, 1G-CER, consists of a sphingosine backbone linked to a fatty acid via an amide
547 bond and was a minor component in the oxic zone (<5% of IPL) at all stations (Fig. 4). Glycosidic
548 ceramides occur in eukaryotic algae such as the coccolithophore *Emiliania huxleyi* (Vardi et al., 2009).
549 We also detected 1G-OH-CER with up to 2 hydroxylations in the core lipid structure (Suppl. Fig. 5).
550 Multiple-hydroxylated sphingoid bases are potential markers of viral infection and cell death in at least
551 some marine phytoplankton, notably *E. huxleyi* (Vardi et al., 2009). We did not, however, find mass
552 spectral evidence for the presence of viral polyhydroxylated 1G-CER, as described by Vardi et al. (2009)
553 and therefore rather suggest that eukaryotic algal cells are potential sources for the 1G-CER (Lynch and
554 Dunn et al., 2004) in surface waters of the ETNP. We also detected hydroxylated glycolipids (1G-OH-
555 DAG) and aminolipids (OH-DGTS) with up to two hydroxyl-groups or one hydroxyl group combined
556 with an epoxy or keto function attached to the acyl groups (Suppl. Fig. 5). The addition of hydroxyl
557 groups or general oxidation of fatty acids in plants, algae and yeast is a defense mechanism and response
558 to oxidative stress (Kato et al., 1984; Andreou et al., 2009). Hydroxy fatty acids, for example, are
559 intermediates in oxidative degradation of fatty acids (Lehninger, 1970), and since they are constituents of
560 structural biopolymers of many microorganisms (Ratledge and Wilkinson, 1988), they are present in
561 marine particulate matter (e.g., Wakeham, 1999), likely derived from membrane constituents of Gram-
562 negative bacteria, the most abundant bacteria in seawater (Rappé and Giovannoni, 2000).

563

564 4.1.2 Upper OMZ

565 Glycolipid abundance varied between 15 to 80% of total IPL within the upper OMZ below the
566 thermocline/oxycline. SQ-DAG and 2G-DAG exhibited strong decreases in relative and absolute

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569 abundance below 125 m at all stations consistent with the decrease in their phototrophic biomass.
570 Number of carbon atoms in the core lipid chains and number of double bond equivalents of glycolipids
571 showed considerable variations within the upper OMZ (Fig. 5), indicating a different assemblage of source
572 organisms compared to the oxic zone. Likewise, decreasing carbon numbers and double bond
573 equivalents for PC-DAG and DGTS combined with a dominance by C₁₄, C₁₆ and C₁₈ saturated and
574 monounsaturated fatty acids (Suppl. Table 5) supports a shift from eukaryotic to bacterial sources. This
575 suggests the diverse proteobacteria in the upper OMZ may biosynthesize non-phosphorus substitute IPLs.
576 1G-DAG or DGTS are known to replace phospholipids, primarily PE-DAG and PC-DAG under
577 phosphorus limited growth (Geske et al., 2012; Carini et al., 2015; Sebastian et al., 2016; Yao et al., 2015),
578 including at the phosphate concentrations of 2 to 2.5 μM in the upper OMZ. Sulfate-reducing
579 proteobacteria, which comprise up to 10% of the total bacteria in the ETNP (Podlaska et al., 2012) may
580 be candidate organisms for this phospholipid to glycolipid replacement (Bosak et al., 2016). Structures
581 of minor IPLs, AL-I and AL-II were not fully elucidated (see Suppl. Fig. 6) and their origins remain
582 uncertain. PME- and PDME-DAG, DPG, 1G-CER and 1G-OH-CER within the upper OMZ are
583 consistent with previous reports of their production by (unidentified) bacteria near redox boundaries in
584 other stratified water bodies (Schubotz et al., 2009; Wakeham et al., 2012).

585 Archaeal IPLs with glycosidic headgroups and tetraether core structures (1G- and 2G-GDGT)
586 comprised a greater proportion of the overall IPL pool within the upper OMZ than in surface waters.
587 Analysis of these same samples by Xie et al. (2014) first reported that concentrations of glycosidic GDGTs
588 peak in the ETNP roughly at depths where nitrite maxima are observed. IP-GDGTs with the hexose-
589 phosphate-hexose (HPH) headgroups and the core GDGT crenarchaeol (Suppl. Fig. 4) of thaumarchaeota

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592 (Schouten et al., 2008; Elling et al., 2017) were most abundant at depths of nitrate maxima at all ETNP
593 stations, as they are in other oxygen-deficient water columns (e.g., Pitcher et al., 2011; Lengger et al.,
594 2012; Schouten et al., 2012; Sollai et al., 2015), although they were present at greater depths in the ENT
595 as well. The microbial enumerations by Podlaska et al. (2012) had shown previously that
596 thaumarchaeota (referred to as crenarchaeota) and euryarchaeota constitute almost equal amounts to <10%
597 of total cell number in the upper OMZ of the ETNP. It is also possible that uncultured marine Group II
598 euryarchaeota are additional sources for glycosidic GDGTs as has been suggested previously (Lincoln et
599 al., 2014; Zhu et al., 2016).

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601 4.1.3 Core OMZ and deep oxycline

602 IPL distributions in the core OMZ and at the deep oxycline of the ETNP that were notably different
603 from the oxic zone and the upper OMZ are consistent with *in-situ* microbial origins. We choose to
604 discuss the core OMZ and deep oxycline together because, although oxygen concentrations are beginning
605 to rise in the deep oxycline, IPL compositions in both zones are similar and likely reflect similar
606 biogeochemical sources. Phospholipid abundance at all stations generally increased to over 50% (except
607 for station 8) at the expense of glycolipids. PE and PG-DAG are the most abundant phospholipids in the
608 core OMZ, along with PC-DAG and PE- and PC-AEG, DPG. PME and PDME-DAG are all common
609 lipids in α -, γ - and some β -proteobacteria (Oliver and Colwell, 1973; Goldfine, 1984) that are present in
610 the OMZ (Podlaska et al., 2012). Changes in phospholipids chain length and number of double bond
611 equivalents further support *in-situ* IPL production (Fig. 5). Fatty acid combinations for phospholipids
612 were dominated by saturated C_{14:0}, C_{15:0} and C_{16:0} and monounsaturated C_{16:0} C₁₇ and C_{18:0} (Suppl. Table

617 5); PUFA were generally of reduced abundance, and odd-numbered fatty acids increased in proportion.
618 In the case of PUFA, even though they may be biosynthesized by piezophilic aerobic deep-sea bacteria
619 (DeLong and Yayanos, 1986; Fang et al. 2003; Valentine and Valentine, 2004), either the microaerophilic
620 bacteria in the deep OMZ of the ETNP do not produce PUFA or these labile fatty acids are rapidly degraded
621 *in-situ* (DeBaar et al., 1983; Prahl et al., 1984; Neal et al., 1986).

622 Among glycolipids, 1G-DAG was most abundant at the deep OMZ/oxycline at stations 1 and 8; here
623 1G-DAG abundance actually increases over that of shallower depths. Carbon number and number of
624 double bond equivalents for glycolipids are again distinct from the surface waters, with on average 1 to 2
625 carbon atoms shorter chain lengths and 1 to 3 fewer double bonds (Fig. 5), supporting the notion that at
626 least some of these glycolipids are biosynthesized *in-situ* and not simply exported from the surface waters.
627 In particular, SQ-DAG in the core OMZ/oxycline contained odd-carbon numbered fatty acids (e.g.,
628 C_{15:0}/C_{16:0} and C_{14:0}/C_{15:0}) different from the cyanobacterial SQ-DAG in surface waters (Suppl. Table 5).
629 Some Gram-positive bacillus and firmicutes biosynthesize 1G, 2G- and SQ-DAG (Hözl and Dörmann,
630 2007) and 1G-, 2G- and SQ-DAG in deeply buried Wadden Sea sediments are attributed to anaerobic
631 bacteria (Seidel et al., 2012). However, Gram-positive bacteria are generally not abundant in seawater.

632 The core OMZ/deep oxycline are particularly enriched in archaeal GDGT, notably 1G-GDGT and
633 HPH-GDGT, with predominantly GDGT-0 and crenarchaeol as core lipids (Suppl. Fig. 4). At stations 1
634 and 8 where sampling penetrated below ~800 m depth, 1G-GDGT and HPH-GDGT constitute up to ~60%
635 and ~22%, respectively, of total IPL. Significantly, the elevated abundances of 1G-GDGT and HPH-
636 GDGT at the bottoms of the sampling depth profiles in the deep oxycline of stations 1 and 8 correspond
637 to depths at which ammonium concentrations are higher than shallower in the core OMZ (Fig. 2).

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639 Remineralization at the deep-oxycline might provide additional ammonium to drive thaumarchaeotal
640 ammonium oxidation and production of archaeal IPLs.

641

642 *4.2 Factors influencing IPL distribution in the ETNP*

643 *4.2.1 Factors affecting structural diversity of the core lipid composition*

644 IPL in the ETNP display considerable diversity not only in the headgroup but also core lipid types,
645 from diacylglycerol lipids with varying number of carbon atoms (likely chain lengths) and zero to multiple
646 double bond equivalents (likely reflecting the number of unsaturations), with or without hydroxylations
647 to mixed ether/ester glycerolipids, sphingolipids and ornithine lipids. Statistical analysis provides aids
648 in illuminating influences of environmental factors and microbial community structure on the lipid
649 composition in the water column of the ETNP. Changes in core alkyl lipid chain length and degree of
650 unsaturation are often associated with temperature (Neidleman, 1987), even at the range of temperatures
651 of the ETNP water column. However, NMDS analysis did not yield any strong correlations between
652 temperature and number of carbon atoms in the side chains or double bond equivalents of the major IPL
653 classes ($r^2 < 0.02$, Suppl. Table 6), nor with other environmental parameters ($r^2 < 0.3$, Suppl. Table 6).
654 Instead, changing biological sources may play a decisive role in determining number of carbon atoms and
655 double bond equivalents in the ETNP. For instance, long-chain PUFAs in surface waters are mainly
656 synthesized by phytoplankton, while in deeper waters some bacteria may biosynthesize these PUFAs.
657 The degree of hydroxylation in the acyl side chains also did not show any clear link to specific
658 environmental factors, although, both 1G-OH-CER and OH-DGTS had negative loadings on the NMDS-
659 2 axis indicating a higher abundance of these compounds in oxic samples. It is possible that hydroxylated

660 IPLs play a role during oxidative stress and/or are involved in other defense mechanisms (Kato et al.,
661 1984; Andreou et al., 2009).

662 Mixed ether-acyl lipids have been reported in various oceanic settings (Hernandez-Sanchez et al.,
663 2014). In our study, there was no noticeable correlation between PE- and PC-AEG and depth or oxygen
664 concentrations (Fig. 6). Ornithine lipids were strongly negatively loaded on the NMDS-1 axis, but none
665 of the measured environmental parameters could account for this negative loading (Fig. 6). Therefore,
666 it remains unclear what factor(s) ultimately determine their distribution. Likewise, there were no
667 significant correlations between the sphingolipid 1G-CER and any environmental parameter. Since
668 ether-acyl lipids, ornithine lipids and sphingolipids play many functional roles in biological systems, their
669 variable distribution within the water column reflect most likely the diversity of microbes inhabiting the
670 dynamic oxygen regime of the ETNP.

671

672 *4.2.2 Factors influencing head group composition*

673 NMDS analysis of normalized IPL composition and quantitative microbial data (abundance of α , β ,
674 γ , ϵ -proteobacteria, sulfate-reducing bacteria δ -proteobacteria, planctomycetes, crenarchaeota including
675 thaumarchaeota and euryarchaeota) did not yield any high goodness of fit statistic ($r^2 < 0.3$; Suppl. Table
676 6) that would clearly delineate specific prokaryotic sources for the various IPL. This absence of
677 statistical correlation would result if neither the IPL compositions of SPM nor the structure and lipid
678 composition of the prokaryotic community were sufficiently unique to strongly distinguish the
679 biogeochemical zones. Indeed, although there are depth-related differences in IPL composition of SPM
680 and prokaryotic community, there is considerable overlap. Therefore, instead of trying to elucidate

681 specific IPL sources, we here query the affect environmental factors such as temperature, nutrient or
682 oxygen concentrations may have on the IPL compositions in the ENTP, and by analogy to natural marine
683 settings in general. Most the major and minor glycolipids were loaded negatively on the NMDS2 axis,
684 as were oxygen, fluorescence, Chl- α , POC and TN (Fig. 6). A notable exception was 1G-DAG which
685 had only a slightly negative loading on the NMDS-2 axis. These relationships (loadings) roughly reflect
686 the vertical distribution of IPLs in the water column of the ETNP. Glycolipids, particularly 2G-DAG
687 and SQ-DAG, were most abundant in the euphotic oxic zone characterized by high oxygen concentration
688 and moderate primary productivity, dominated by phytoplankton, primarily cyanobacteria (high POC, TN
689 and elevated Chl- α and fluorescence). Spearman Rank Order Correlations confirm these observations,
690 including the lack of significant correlations between 1G-DAG and depth or any other environmental
691 parameter. One explanation is that 1G-DAG originates from assorted sources throughout the water
692 column independent of any single environmental variable. Similarly, PC-DAG, PG-DAG, and DGTS
693 did not correlate with any of the tested environmental variables, because their compositions are relatively
694 homogeneous across all biogeochemical zones. PE-, PME- and PDME-DAG, and DPG, on the other
695 hand, that became more prevalent within the core OMZ, and at deeper depths where oxygen concentrations
696 decrease and nutrient (NO_3^- and PO_4^{3-}) concentrations were elevated due to organic matter
697 remineralization, gave positive loadings with these environmental parameters on the NDMS2 axis.
698 Archaeal IPLs showed positive loadings on the NMDS2 axis, consistent with the increasing importance
699 of archaeal abundance with depth and at reduced oxygen concentrations.

700

701 *4.2.3 Links between substitute lipid ratios and nutrient concentrations*

702 SQ-DAG and PC-DAG are often the most abundant respective glycolipids and phospholipids in the
703 surface ocean (Popendorf et al., 2011a,b), including the Eastern Tropical South Pacific (Van Mooy and
704 Fredricks, 2010). The abundance of SQ-DAG in the surface waters of the ETNP (18-50% of total IPL)
705 is thus not unusual. In the ETNP, however, PC-DAG was comparably minor (3-13% of total IPL).
706 Instead, DGTS was abundant at some stations, up to ~20% of major IPL at station 5. SQ-DAG and
707 DGTS serve similar biochemical functions as the phospholipids PG-DAG and PC-DAG, respectively, due
708 to similar ionic charges at physiological pH. The former may be preferentially biosynthesized by
709 phytoplankton and some bacteria as substitute lipids for PG-DAG and PC-DAG when phosphate starved
710 (Benning, 1993; Van Mooy et al., 2006, 2009). Likewise, 1G-DAG, glycuronic acid diacylglycerol
711 (GADG) and ornithine lipids may substitute for PE-DAG in marine bacteria (e.g., chemoheterotrophic α -
712 proteobacteria of the SAR11 clade of *Pelagibacter* sp.: Carini et al., 2015; the sulfate reducing bacterium,
713 *Desulfovibrio alaskensis*: Bosak et al., 2016). In oligotrophic surface waters of the Sargasso Sea (PO_4^{3-}
714 <10 nM) ratios of SQ-DAG:PG-DAG and DGTS:PC-DAG are high (4 to 13) compared to the same ratios
715 (3) in the phosphate replete South Pacific ($\text{PO}_4^{3-} >100$ nM), consistent with cyanobacteria synthesizing
716 phosphorus-free substitute lipids to maintain growth in response to phosphorus deprivation (Van Mooy et
717 al., 2009). At the ETNP, SQ-DAG:PG-DAG ratios ranged between 1 and 10 within the upper 100-200
718 m along the transect and were <1 deeper into the OMZ (Fig. 3). DGTS:PC-DAG ratios in the ETNP
719 were quite variable, ranging between 0.4 and 2.4 at most depths, but with notable spikes (>30) within the
720 oxic zone at station 5, within the upper core OMZ at station 2 and 8 and in the lower portion of the core
721 OMZ at station 8. 1G-DAG:PE-DAG ratios were highly variable (0.2 to 945) and were highest within
722 the upper OMZ at station 2, 5 and 8 and within the deep oxycline at station 8, where 1G-DAG:PE ratios

723 range between 290 and 945 (Fig. 3). To test the substitute lipid hypothesis for the ETNP, we performed
724 a Spearman Rank Order Correlation analysis of known substitute lipid ratios as well as total aminolipid
725 (AL) to phospholipid (PL) and total glycolipid (GL) to PL ratios with nutrient concentrations and other
726 environmental parameters. Only SQ-DAG:PG-DAG was significantly correlated with phosphate (-0.56,
727 $p < 0.001$) but also correlated with other parameters, such as depth (-0.76, $p < 0.001$) and oxygen
728 concentration (0.58, $p < 0.001$). These correlations reflect the elevated SQ-DAG:PG-DAG ratios (2-8) in
729 the surface waters and upper OMZ (Fig. 3) and support the notion that SQ-DAG might serve as a substitute
730 lipid in both surface waters and the OMZ when phosphate concentrations are in the low micromolar range
731 (~ 0.1 - $0.4 \mu\text{M}$ in surface waters; ~ 2 - $3.5 \mu\text{M}$ in the OMZ). Other proposed substitute lipid ratios,
732 DGTS:PC-DAG (Van Mooy et al., 2009) and 1G-DAG:PE-DAG (Carini et al., 2015), did not correlate
733 with nutrient concentrations in the water column of the ETNP but rather showed highly variable
734 distributions. Similarly, AL:PL ratios did not exhibit strong relationships with any environmental
735 parameter, and GL:PL ratios showed similar but less pronounced trends as SQ-DAG:PG-DAG ratios.
736 Overall, we observed no correlation between these substitute lipid ratios and phosphate concentration in
737 the ETNP. We propose that non-phosphorus IPL within the OMZ of the ETNP originate from bacteria
738 growing under low micromolar concentrations of phosphate. Indeed, the culture experiments of Bosak
739 et al. (2016) demonstrated that the sulfate reducer, *Desulfovibrio alaskensis*, begins to replace most of its
740 membrane phospholipids with 1G-DAG, glycuronic acid diacylglycerol and ornithine lipids even at
741 phosphate concentrations as high as $20 \mu\text{M}$.

742

743 **5. Conclusions**

744 The water column of the ETNP is characterized by a diverse suite of intact polar lipids. IPL
745 distributions reflect the dynamic nature of the biological community in the ETNP, with light and oxygen
746 as primary determinants, from fully oxygenated euphotic surface waters to an aphotic strong oxygen
747 minimum zone at mid-depth. Highest concentrations of IPLs (250 – 1500 ng/L) in oxygenated surface
748 waters zone results from abundant phototrophic eukaryotic and cyanobacterial sources above the OMZ.
749 Secondary peaks in IPL concentration (12 – 56 ng/L) within the core of the OMZ mirror elevated
750 abundances of heterotrophic and chemoautotrophic bacteria and archaea under low oxygen conditions.
751 Glycolipids derived from photoautotrophs generally accounted for more than 50% of total IPLs in the
752 euphotic zone (< 200 m, oxic and upper OMZ zones), but bacterial phospholipids were more abundant
753 (avg. 40%) in the OMZ and deep oxycline layers. Archaeal GDGTs were abundant within the OMZ and
754 deep oxycline, consistent with elevated archaeal abundances there. Variations in major fatty acid
755 constituents within IPL classes with acyl core moieties show that biological source(s) for the different IPL
756 were distinct in each depth/oxygen-content horizon. Nevertheless, microbial sources for many of the
757 detected lipids remain unclear and therefore potentially unique ecophysiological adaptations these lipids
758 may represent remain to be explored.

759 The presence of the glycolipid, monoglycosyl diacylglycerol (1G-DAG), and the betaine lipid,
760 diacylglyceryl homoserine (DGTS), both with varying fatty acid compositions, within all biogeochemical
761 zones, and especially in the OMZ, indicates that these canonical phototrophic markers are not only
762 biosynthesized in surface waters, but may indeed be produced in the aphotic water column and by a much
763 larger host of organisms than previously thought. Since 1G-DAG and DGTS can be biosynthesized by
764 various bacteria to replace phospholipids under phosphorus limited growth, we suggest that they serve as

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766 non-phosphorus substitute lipids for some microorganisms in the OMZ. The presence of these substitute
767 lipids at micromolar concentrations of phosphate of the ETNP suggests that the paradigm of substitute
768 lipid biosynthesis being restricted to the PO_4^{3-} -depleted oligotrophic surface ocean may need to be re-
769 evaluated.

770

771 **Author contribution**

772 SGW collected the samples. SGW, FS and KUH designed the study. SX and FS measured and processed
773 the data. JSL and FS performed statistical analyses. FS and SGW wrote the paper with input from SX,
774 KUH and JSL.

775

776 **Competing interests**

777 The authors declare that they have no conflict of interest.

778

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794

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.102

1103 **Tables**

1104 **Table 1.** Spearman Rank Order Correlation coefficients (r) for data combined from all four stations. Only
1105 significant correlations, where $p < 0.05$ (highly significant $p < 0.001$, in bold), are presented.

	Glycolipids					Ammolipids					Phospholipids					
	% GL	% IG	% 2G	% SQ	GL:PL	SQ:PG	% AL	% DGTS	AL:PL	DGTS:PC	% PL	% PC	% PG	% PE	% PME	% PDME
Depth	-0.32		-0.7	-0.67	-0.41	-0.76										
Fluorescence			0.63	0.67		0.65										
POC			0.61	0.6		0.6										
TN			0.66	0.62		0.63										
Oxygen	0.57	0.3	0.48	0.35	0.55	0.58			0.36		-0.49		-0.38	-0.33	-0.46	-0.52
Temperature	0.3		0.52	0.63	0.39	0.69										
Chl a	0.35		0.72	0.71	0.42	0.78										-0.33
Phosphate			-0.62	-0.53	-0.4	-0.56										0.36
Nitrate			-0.53	-0.49		-0.38										
Nitrite		-0.33														0.3
Ammonium							0.41	0.42	0.35	0.4						
N:P			-0.3	-0.32												-0.36

Abbreviations: GL – glycolipids, IG – monoglycosyl, 2G – diglycosyl, SQ – sulfoquinovosyl, PL – phospholipids, AL – aminolipids, DGTS – diacylglyceryl trimethyl homoserine, PC – phosphatidyl choline, PG – phosphatidyl glycerol, PE – phosphatidyl ethanolamine, PME – phosphatidyl methyl-ethanolamine, PDME – phosphatidyl dimethyl-ethanolamine

1107 **Figures**

1108 **Figure 1.** a) Map of ETNP with R/V *Seward Johnson* (November 2007) cruise sampling stations
1109 investigated in this study.

1110
1111 **Figure 2.** Depth profiles of (a) oxygen and temperature, (b) chlorophyll- α and transmissivity, (c)
1112 particulate organic matter (POC) and C:N, (d) intact polar lipid (IPL) to POC ratio and IPL concentration,
1113 and (e) absolute cell abundance and relative proportions of archaeal cells (data from Podlaska et al. (2012)).
1114 C:N (SPM) is total carbon over total nitrogen of the solid phase collected by water filtration. Note that
1115 C:N, POC and IPL/POC are only analyzed for <53 μm particle fraction. Also depicted are the different
1116 geochemical zones in the water column.

1117
1118 **Figure 3.** Depth profiles of (a) nitrate, nitrite, and ammonium, (b) phosphate and N:P, (c) total non-
1119 archaeal (non-isoprenoidal) phospholipids, glycolipids and (d) aminolipids shown as percent of total intact
1120 polar lipids and ratios of non-phospholipids to phospholipids for DGTS to PC-DAG (e) SQ-DAG to PG-
1121 DAG, (e), and 1G-DAG to PE-DAG. Also depicted are the different geochemical zones in the water
1122 column.

1123
1124 **Figure 4.** Relative abundance of (a) major and (b) minor IPLs at sampled depths of stations 1, 2, 5, and 8
1125 in the ETNP. Major IPLs are defined as those comprising more than 10% of total IPLs (minor compounds
1126 comprised less than 10%) at more than one depth horizon at the four stations. Also depicted are the
1127 different geochemical zones in the water column.

1128

1129 **Figure 5.** Changes in average carbon atoms (CA) and number of double bond equivalents (DB) of the
1130 alkyl side chains of major IPLs detected at stations 1, 2, 5 and 8 in the ETNP.

1131

1132 **Figure 6.** Nonmetric multidimensional scaling (NMDS) ordination plot assessing the relationship between
1133 IPL biomarkers, sampling depths and geochemical parameters in the ETNP (stress=0.125). Squares
1134 represent the water depth of each sample and are color-coded according to the defined geochemical
1135 zonation. Filled circles stand for lipid distribution of major IPLs and open circles for minor IPLs on the
1136 ordination. Vector lines of geochemical parameters are weighted by their p-values with each NMDS axis.

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