Faculty of Science and Engineering

School of Geography, Earth and Environmental Sciences

2021-01-23

Seasonal monitoring of lipid degradation processes in the western English Channel links bacterial 10S-DOX enzyme activity to free fatty acid production by phytoplankton

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http://hdl.handle.net/10026.1/16822

10.1016/j.marchem.2021.103928 Marine Chemistry Elsevier BV

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Abstract. In a few recent studies, the action of a bacterial dioxygenase (10S-DOX) on 27 palmitoleic acid was observed within some polar and estuarine settings. To add further 28 mechanistic information regarding the action of this enzyme in marine settings, we measured a 29 30 range of lipids (sterols, fatty acids and the chlorophyll phytyl side chain) and their biotic and abiotic degradation products in water samples collected in 2018 from two depths (5 m and 25 31 m) at the temperate oceanographic time series site L4, located in the western English Channel. 32 Lipid distributions indicated a dominance of diatoms and copepods during the spring bloom, 33 while a peak in dinoflagellate activity was evident in samples collected from late 34 summer/autumn, both outcomes being consistent with taxonomic data reported previously for 35 36 the same sampling site and interval. Monitoring of lipid oxidation products characteristic of different degradation pathways showed a relatively weak effect of photo- and autoxidation 37 processes, with these acting mainly on the more reactive lipids (i.e. chlorophyll and 38 39 polyunsaturated fatty acids). In contrast, monitoring of biotic degradation processes revealed significant quantities of 10S-hydroxyhexadec-8(E)-enoic acid in samples collected at the end 40 41 of April (reaching 40% of the residual parent palmitoleic acid), attributed to the involvement of bacterial 10-dioxygenase (10S-DOX) activity during the spring bloom. We propose that this 42 enzyme could be utilised by bacteria to detoxify free fatty acids released by wounded diatoms 43 44 in the presence of copepods

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Keywords: Biotic and abiotic degradation; 10S-DOX enzymatic activity; Bacteria; Wounded
diatoms.

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51 **1. Introduction**

Suspended particles sink very slowly through the water column and constitute most of the 52 standing stock of particulate matter in the oceans (Bacon et al., 1985; Wakeham and Lee, 1989). 53 54 These particles are composed of a heterogeneous mixture of biogenic, lithogenic, and authigenic components, with their relative proportions dependent on location and depth. 55 However, biogenic (mainly phytoplanktonic) material normally dominates particle composition 56 57 in the upper 100 m (Honjo et al., 1982). Suspended particles are also generally considered to contain more highly degraded organic matter (OM) than sinking particles due to their longer 58 residence times in the water column (Tanoue and Handa 1980). However, several previous 59 60 field-based studies have shown high abundances of relatively undegraded labile material in suspended particles (Lee et al., 1983; Wakeham et al., 1985; Wakeham and Canuel, 1988; 61 Sheridan et al., 2002). It is thus important to understand: (i) the mechanisms by which such 62 organic matter is degraded in the water column, and (ii) the relative importance of biotic vs. 63 abiotic processes responsible for this degradation. 64

Biotic degradation of algal material in the water column depends not only on zooplankton
grazing (Harvey et al., 1987), but also on the remineralization activity of the associated bacteria.
Indeed, particles are rapidly colonized by prokaryotes, and particle-attached communities are
often more metabolically active (Grossart et al., 2003; 2007) and phylogenetically diverse
(Ortega-Retueta et al., 2013; Ganesh et al., 2014) than free-living assemblages.

Although less widely studied than its biologically mediated (heterotrophic) counterpart, abiotic degradation by processes such as photooxidation and autoxidation (spontaneous free radical reaction of organic compounds with oxygen) is now understood to play a role in the fate of phytoplankton in the ocean (for a recent review, see Rontani and Belt, 2020). While, due to the presence of chlorophyll *a*, a very efficient photosensitizer (Foote, 1976), visible-lightinduced photosensitization involves mainly reaction with singlet oxygen (${}^{1}O_{2}$) and acts on the

unsaturated lipid components of algae, the mechanism by which autoxidation is initiated in
phytodetritus appears to be homolytic cleavage of photochemically-produced hydroperoxides
(Girotti, 1998; Rontani et al., 2003). Consequently, both photooxidation and autoxidation can
significantly affect the composition of lipids in suspended particles (Rontani and Belt, 2020).

Lipids, which constitute one of the three main classes of organic matter in algal material (Sun et al., 2002), are less labile than carbohydrates and proteins and are thus often used as biomarkers to determine the sources (Volkman, 1986, 2003) and the alteration state of specific organisms (Rontani et al, 2012; 2016).

In the present work, we monitored the biotic and abiotic degradation of lipids in 84 85 suspended particle material (SPM) collected in 2018 from the Western Channel Observatory (WCO, https://www.westernchannelobservatory.org.uk/) marine station L4, which is a highly 86 seasonal temperate shelf site (Widdicombe et al 2010, Atkinson et al 2015, Cornwell et al 2020). 87 88 A focus of the study was the action of a particular bacterial enzyme (10S-DOX), which was previously observed in Arctic sea ice and sinking particles (Amiraux et al., 2017; Rontani et al., 89 2018), and in estuaries of diverse latitudes (Galeron et al., 2018); however, the role of this 90 enzyme in the environment has hitherto remained unclear. Here, we hypothesised that this 91 enzyme could be employed by bacteria to detoxify free fatty acids released by wounded 92 93 diatoms, perhaps as a result of increased copepod activity (i.e. grazing).

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96 2. Experimental

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98 2.1. Site description

99 The oceanographic time-series and marine biodiversity reference site L4 (50° 15′N, 4° 13′W,
100 ca. 53 m water depth), is located in the Western English Channel, 13 km south southwest of

Plymouth, UK (Fig. 1). L4 is one of Europe's principal coastal time series sites and the 101 Plymouth Marine Laboratory has sampled its natural phytoplankton community since 1992. 102 The seasonal phytoplankton community at L4 has been well documented over many years (e.g. 103 104 Widdicombe et al. 2010, Atkinson et al. 2015, Tarran and Bruun 2015, Cornwell et al. 2020). Specifically, phytoplankton biomass at L4 typically comprises a background population of 105 flagellates, which increase steadily into summer (Atkinson et al 2015). A diatom bloom often 106 begins in April, with a bloom of *Phaeocystis* spp. (Prymnesiophyte) in some years 107 108 (Widdicombe et al 2010, Atkinson et al 2015). With the onset of summer stratification and nutrient limitation, Chl a levels often diminish around June as the diatom bloom is succeeded 109 by a peak of autotrophic dinoflagellates (Atkinson et al 2015). Coccolithophores increase in the 110 autumn of some years, but their contribution to biomass overall is relatively minor (Atkinson 111 112 et al. 2015).

The microzooplankton protist assemblages are dominated by ciliates and colourless dinoflagellates (defined here as heterotrophic). Ciliates typically peak at around the same time as the spring diatom bloom (Widdicombe et al 2010, Atkinson et al 2015, Cornwell et al 2020), whereas the stronger peak of dinoflagellates appears later (Atkinson et al 2015). The noncarnivorous holoplankton, which also includes copepods, starts to increase before the spring bloom and is often sustained until October (Atkinson et al 2015). In contrast, the carnivorous zooplankton typically peak during the autumn (Atkinson et al., 2015).

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121 *2.2 SPM sampling*

Water samples from 5 m and 25 m water depth were collected from the L4 station throughout
2018 (and some in 2019) on board the *R/V Plymouth Quest* (approximately monthly) using 10
L Niskin bottles mounted on to a conductivity, temperature and depth (CTD) rosette sampler.
The particulate fractions were collected under subdued light conditions from 2-4 L of water by

means of vacuum filtration on 47 mm glass microfibre filters (Whatman, GF/F, as supplied).
Water samples were processed immediately after collection and filtered materials kept frozen
(-20°C) until further analysis.

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130 *2.3. Lipid extraction*

Filtered water samples (GF/F filters) were reduced at room temperature with excess NaBH₄ (70 131 mg) after adding MeOH (25 mL, 30 min) to reduce labile hydroperoxides (resulting from photo-132 or autoxidation) to alcohols, which are more amenable to analysis by gas chromatography (GC). 133 Water (25 mL) and KOH (2.8 g) were then added and the resulting mixture saponified by 134 refluxing (2 h). After cooling, the mixture was acidified (HCl, 2 N) to pH 1 and extracted with 135 dichloromethane (DCM; 3×20 mL). The combined DCM extracts were dried over anhydrous 136 Na₂SO₄, filtered and concentrated by rotary evaporation at 40°C to give total lipid extracts 137 138 (TLEs). TLEs were then silvlated and analyzed by gas chromatography-electron impact quadrupole time-of-flight mass spectrometry (GC-QTOF). Analysis of blank filters showed the 139 140 presence of small amounts (< 10% of the values obtained from water samples) of cholesterol and saturated fatty acids, which were subtracted. 141

A different treatment was used to determine the proportion of free fatty acids (FFAs). The 142 samples were extracted three times with chloroform-MeOH-H2O (1:2:0.8, v:v:v) using 143 ultrasonication. The supernatant was separated by centrifugation at 3500G for 9 min. To initiate 144 phase separation, purified H₂O was added to the combined extracts to give a final volume ratio 145 of 1:1 (v:v). The upper aqueous phase was extracted three times with DCM and the combined 146 DCM extracts were filtered and the solvent removed via rotary evaporation. The residue 147 obtained after extraction was dissolved in 4 mL of DCM and separated into two equal 148 subsamples. After evaporation of the solvent, fatty acids were directly quantified by GC-QTOF 149 in the first subsample after silvlation, while the second subsample was saponified and treated 150

151 as described above. Comparison of the amounts of fatty acids present before and after 152 saponification enabled estimation of the percentage of FFAs. All the solvents (pesticide/glass 153 distilled grade) and reagents (Puriss grade) were obtained from Rathburn and Sigma-Aldrich, 154 respectively.

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156 2.4. Silylation

157 Dry TLEs and standards were derivatized by dissolving them in 300 μ L pyridine/bis-158 (trimethylsilyl)trifluoroacetamide (BSTFA; Supelco; 2:1, v/v) and silylated in a heating block 159 (50 °C, 1 h). After evaporation to dryness under a stream of N₂, the derivatized residue was 160 dissolved in ethyl acetate/BSTFA (2:1, v/v) (to avoid desilylation) and analysed by GC-QTOF. 161

162 2.5. Gas chromatography-EI quadrupole time-of-flight mass spectrometry

Accurate mass measurements were made in full scan mode using an Agilent 7890B/7200 163 164 GC/QTOF system (Agilent Technologies, Parc Technopolis - ZA Courtaboeuf, Les Ulis, France). A cross-linked 5% phenyl-methylpolysiloxane (Macherey-Nagel; OPTIMA-5MS 165 166 Accent, $30 \text{ m} \times 0.25 \text{ mm}$, 0.25 µm film thickness) capillary column was used. Analyses were performed with an injector operating in pulsed splitless mode set at 270°C. Oven temperature 167 was ramped from 70°C to 130°C at 20°C min⁻¹ and then to 300°C at 5°C min⁻¹. The pressure 168 of the carrier gas (He) was maintained at 0.69×10^5 Pa until the end of the temperature program. 169 Instrument temperatures were 300°C for transfer line and 230°C for the ion source. Nitrogen 170 (1.5 mL min⁻¹) was used as collision gas. Accurate mass spectra were recorded across the range 171 m/z 50–700 at 4 GHz with the collision gas opened. The QTOF-MS instrument provided a 172 typical resolution ranging from 8009 to 12252 from m/z 68.9955 to 501.9706. 173 Perfluorotributylamine (PFTBA) was used for daily MS calibration. Compounds were 174

identified by comparing their TOF mass spectra, accurate masses and retention times with those
of standards. Quantification of each compound involved extraction of specific accurate
fragment ions, peak integration and determination of individual response factors using external
standards and Mass Hunter (Agilent Technologies, Parc Technopolis – ZA Courtaboeuf, Les
Ulis, France) software.

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181 2.6. Standard compounds

Phytol (12), fatty acids, most of the sterols and 2,6,10,14-tetramethylpentadecanoic acid 182 (pristanic acid) (15) were purchased from Sigma-Aldrich (St. Quentin Fallavier, France). 3,6-183 Dihydroxycholest-4-ene (10) (employed for sterol photooxidation estimates) was obtained from 184 Maybridge Ltd. The synthesis of 3-methylidene-7,11,15-trimethylhexadecan-1,2-diol 185 (phytyldiol) (13) was described by Rontani and Aubert (2005). 4,8,12-Trimethyltridecanoic 186 187 acid (4,8,12-TMTD acid) (16) was synthesized from isophytol (19) (Interchim, Montluçon, France) by a previously described procedure (Rontani et al., 1991). 3,7,11,15-188 Tetramethylhexadecanoic acid (phytanic acid) (14) was produced in three steps from phytol 189 (12) as described previously (Rontani et al., 2003). Cholestane- 3β , 5α , 6β -triol (11) (employed 190 for sterol autoxidation estimates) was produced by oxidation of cholesterol (2) with 191 H₂O₂/KI/H₂SO₄ (Li and Li, 2013). (8-11)-Hydroperoxyhexadec-(8-10)-enoic acids (Z and E) 192 (30-35) were produced by Fe²⁺/ascorbate-induced autoxidation (Loidl-Stahlhofen and Spiteller, 193 1994) of palmitoleic acid (23). Subsequent reduction of these different hydroperoxides in 194 methanol with excess NaBH₄ afforded the corresponding hydroxyacids. A standard of *threo* 195 7,10-dihydroxyoctadec-8(E)-enoic acid containing 10% of threo 7,10-dihydroxyhexadec-8(E)-196 enoic acid (42) previously produced by *Pseudomonas aeruginosa* PR3 (Suh et al., 2011) was 197 obtained from Dr. H.R. Kim (School of Food Science and Biotechnology, Kyungpook National 198 University, Daegu, Korea). 199

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201 2.7. Estimation of autoxidative, photooxidative and 10S-DOX degradation

- The role played by autoxidation, photooxidation and 10*S*-DOX oxidation in the degradation of palmitoleic acid was estimated based on the profiles of isomeric allylic hydroxyacids obtained after NaBH₄-reduction as described previously by Rontani et al. (2018).
- 205
- 206 **3. Results**
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- 208 *3.1. Trophic environment at station L4 in 2018*

The main sterols in the filtered water samples: 24-norcholesta-5,22*E*-dien-3β-ol (24-norsterol) 209 (1), cholest-5-en-3β-ol (cholesterol) (2), cholesta-5,22*E*-dien-3β-ol (22-dehydrocholesterol) 210 (3), cholest-5,24-dien-3β-ol (desmosterol) (4), 24-methylcholesta-5,22E-dien-3β-ol (epi-211 brassicasterol) (5), 24-methylcholesta-5,24(28)-dien-3β-ol (24-methylenecholesterol) (6), 24-212 ethylcholest-5-en-3\beta-ol (sitosterol) (7), 24-ethylcholesta-5,22E-dien-3β-ol (fucosterol) (8) and 213 4α ,23,24-trimethyl- 5α -cholest-22*E*-en-3-ol (dinosterol) (9), were quantified to estimate the 214 nature and the amount of the algal material present in SPM samples across the 2018 time series. 215 216 At 5 m, sterol concentrations showed the occurrence of two peaks of phytoplanktonic biomass at the end of April and in September (Table 1, Fig. 2A). In April, the sterol profile was 217 218 characterized by the presence of high percentages of cholesterol (2) and 24-norsterol (1), while 219 in September, cholesterol (2), brassicasterol (5), 24-methylenecholesterol (6) and dinosterol (9) 220 were the most abundant. At 25 m, two peaks of phytoplanktonic biomass could be observed at the end of April and May (Table 2, Fig. 2B) with the percentages of cholesterol (2) and 24-221 222 norsterol (1) again relatively abundant during these two events. A relatively high abundance of brassicasterol (5) was also observed at 25 m in May. 223

At 25 m, the concentration of phytol (chlorophyll phytyl side-chain) (12) followed logically the same trend as that of the sterols (Table 2). In contrast, we observed a small lag between the date of the highest concentration of phytol (12) (08/13/18) and total sterols (09/17/18) at 5 m (Table 1). Concerning isoprenoid acids, a peak in phytanic acid (14) concentration was detected on 04/30/18 at both depths, while highest 4,8,12-TMTD acid (16) concentrations were observed in February and March at 5 m (Tables 1 and 2, Fig. 3).

We also quantified the main saturated (SFAs), monounsaturated (MUFAs) and polyunsaturated (PUFAs) fatty acids (Tables 3 and 4). While SFAs appeared to be dominant and the percentage of MUFAs relatively constant at both depths across the 2018 time series, PUFAs were highly variable at both depths. SFAs were dominated by $C_{16:0}$ (21) and $C_{14:0}$ (20), MUFAs by $C_{16:1\omega9}$ (palmitoleic acid) (22) and $C_{18:1\omega9}$ (oleic acid) (24), and PUFAs by $C_{20:5}$ (26) and $C_{22:6}$ (27). The bacterially-derived $C_{18:1\omega7}$ (*cis*-vaccenic acid) (25) and branched (*iso* and *anteiso*) $C_{15:0}$ acids (BrC_{15:0}) (28 and 29) were also detected.

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3.2. Biotic and abiotic degradation of lipid components of phytoplankton at station L4 in 2018
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240 3.2.1. Photooxidation

Due to the higher solar irradiance available, it is perhaps not surprising that photooxidation processes acted more intensively at 5 m than at 25 m, although only the most reactive lipids (e.g. chlorophyll) appeared to be strongly affected by this process (Tables 1 and 2, Fig. 4). Thus, chlorophyll photooxidation estimates were highly variable at 5 m (ranging from 8% to 100%) (Table 1, Fig. 4) yet relatively consistent and low at 25 m (10%–26%) (Table 2). The photooxidation of MUFAs (reaching 2.4% and 2.0% at 5 m and 25 m, respectively) was very limited at both depths (Fig. 5), while Δ^5 -sterols appeared to be essentially unaffected.

249 *3.2.2. Autoxidation*

3,7,11,15-tetramethylhexadec-3(*cis/trans*)-ene-1,2-diols (17) and 3,7,11,15-tetramethyl-250 hexadec-2(*cis/trans*)-ene-1,4-diols (18) resulting from autoxidation of the chlorophyll phytyl 251 side-chain could be identified in the different samples investigated, but were not quantified. 252 Similarly, the detection of *cis*-hydroxyhexadecenoic acids (40 and 41, see appendix) provides 253 evidence for autoxidation of palmitoleic acid (22), although this was relatively minor, reaching 254 255 only a maximum of 14% and 16% in January at 5 and 25 m, respectively (Fig. 5). In contrast, autoxidation products of Δ^5 -sterols (i.e. 3 β ,5 α ,6 β -steratriols; Rontani, 2012) were not detected 256 257 in any of the samples.

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259 *3.2.3. Biotic degradation*

A clear dominance of 10-hydroxyhexadec-8(E)-enoic acid (36) was observed within the 260 palmitoleic acid oxidation products in the sample collected on 04/30/18 at 25 m (Fig. 6B), and 261 attributed to the involvement of a bacterial 10-dioxygenase enzyme (10S-DOX). Similar 262 evidence for the involvement of this enzyme was also observed in the corresponding sample 263 collected at 5 m, but in this case 8-hydroxyhexadec-9(E)-enoic acid (38) was also dominant 264 (Fig. 6A). 10S-DOX degradation of palmitoleic acid (22) in these samples was estimated to be 265 27% and 25% at 5 m and 25 m, respectively (Fig. 5A and 5B). Analysis of samples collected 266 in 2019, albeit from 25 m water depth only, provides further indication of the seasonal nature 267 of this bacterial activity at the L4 station (10S-DOX degradation of palmitoleic acid reaching 268 6% in April; Rontani et al., unpublished data), although multi-annual studies are needed to 269 confirm this. 270

Quantification of the free fatty acid (FFA) content in the sample collected on 04/30/18 at 5 m showed a very high proportion of free palmitoleic (**22**) and C_{20:5} (**26**) acids (76% and 74%, respectively). Interestingly, *threo* 7,10-dihydroxyhexadec-8(*E*)-enoic acid (**42**) could also be

identified in these samples by comparison of its accurate mass spectrum and retention time with
those of a reference compound (Fig. S1). A slightly later eluting compound (Fig. S1), exhibiting
the same mass spectrum as *threo* 7,10-dihydroxyhexadec-8(*E*)-enoic acid (42), was identified
as a mixture of the *erythro* diastereoisomers of this diol (43). Such an elution order is in good
agreement with the results of Hansel and Evershed (2009).

- 279
- 280 **4. Discussion**

281 4.1. Trophic environment at station L4 in 2018

282 Sterols possess structural characteristics, such as double bond positions, nuclear methylation and patterns of side-chain alkylation, which are restricted to a few groups of organisms (for 283 reviews see Volkman, 1986; 2003; Rampen et al., 2010). These lipids are thus often used to 284 285 estimate phytoplanktonic diversity (e.g. Veron et al., 1998; Taipale et al., 2016). For example, 24-norsterol (1) has previously been identified as a characteristic sterol in diatoms, both in 286 culture of the centric diatom Thalassiosira antarctica (Rampen et al., 2007) and in the 287 environment (e.g. Suzuki et al., 2005). The relatively high proportions of 24-norsterol (1) 288 289 observed in our SPM samples collected on 04/30/18 at 5 m and 25 m (30% and 20% of total 290 sterols, respectively) (Tables 1 and 2), along with relatively high values of the diatom fatty acid 291 ratio (($C_{14:0} + C_{16:1007} + \Sigma C_{16}$ PUFAs)/ $C_{16:0}$) (Léveillé et al., 1997) and the diatom-specific C_{20:5} FA (Tables 3 and 4), thus suggest a strong contribution from diatoms during this period. Indeed, 292 our lipid data are consistent with previous taxonomic results of Cornwell et al. (2020), who 293 294 showed that diatom biomass increased strongly (more than fourfold) between weeks 16 and 18 of 2018 (corresponding to our 04/19/18 and 04/30/18 samples, respectively). In particulate 295 matter, the (MUFAs + PUFAs)/SFAs ratio varies generally from 0.6 during the initial and lag 296 297 phases of phytoplankton blooms to greater than 1.0 at high rates of organic production (Marty

et al., 1988; Mayzaud et al., 1989). The high values observed on 04/30/18 and 05/30/18 at 25 298 299 m (1.7 and 1.2, respectively), accompanied by elevated values of $C_{20:5}$ FA (Table 4), are thus also consistent with the occurrence of diatom blooms on these dates (Cornwell et al., 2020). 300 Interestingly, Widdicombe et al. (2010) previously observed a shift in phytoplankton 301 composition at the L4 station between late March and early May from a winter community 302 (dominated by centric and benthic diatoms) towards a community dominated by Chaetoceros 303 304 spp., Thalassiosira spp. (potential sources of 24-norsterol, Rampen et al., 2007) and 305 Skeletonema costatum.

On the basis of the relatively high abundance of brassicasterol (**5**) in the 25 m sample collected in May (Table 2, Fig. 2), a significant contribution of *Phaeocystis* could be inferred (Nichols et al., 1991), as is frequently the case at the L4 station during April/May (Widdicombe et al., 2010).

310 Dinoflagellates are important primary producers in the oceans (Kokke et al., 1982), differing from other classes of marine algae with respect to the dominance of 4α -methylsterols 311 among their sterols. Dinosterol (9), for example, which is the major sterol in several 312 dinoflagellates (Shimizu et al., 1976; Kokke et al., 1982), is often employed as tracer for the 313 contribution of these organisms in the marine environment (Robinson et al., 1984). The 314 significant proportion of this sterol in the 09/17/18 sample at 5 m (Fig. 2), along with relatively 315 elevated concentrations of the C_{22:6}FA (produced in high proportion by several dinoflagellates, 316 Peltomaa et al., 2019) (Table 3), thus suggests an important contribution of dinoflagellates to 317 this bloom event, consistent with the results of Cornwell et al. (2020), who identified a peak in 318 ellipsoid-shaped dinoflagellates between weeks 36 and 38 (Sept 2018) at 10 m water depth. 319

The lag between the highest concentrations of phytol (**12**) (08/13/18) and sterols (09/17/18) at 5 m (Table 1), can be attributed to the presence of a bloom of cyanobacteria (wellknown to contain very low proportions of sterols; Volkman, 2003) at the end of August, as also

supported by the observations of Cornwell et al. (2020), who showed the presence of a single
biomass maximum of *Synechoccocus* at the L4 station during the same period.

Pelagic crustaceans assimilate the chlorophyll phytyl chain when feeding herbivorously 325 (for a review see Rontani and Volkman, 2003). Phytanic acid (14), which arises from 326 hydrogenation and terminal oxidation of phytol (12), is an important lipid in species of *Calanus* 327 (Blumer and Cooper, 1967; Avigan and Blumer, 1968; Prahl et al., 1984). Classical oxidative 328 metabolism of this isoprenoid acid (Mize et al., 1969) affords pristanic (15) and 4,8,12-TMTD 329 330 (16) acids, which have also been detected in different *Calanus* species (Avigan and Blumer, 1968; Prahl et al., 1984). These three isoprenoid acids may also be produced during the 331 biodegradation of phytol (12) by marine bacteria (Rontani et al., 1999). The high concentrations 332 of phytanic acid (14) observed at the end of April at 5 m and 25 m (Fig. 3) therefore strongly 333 suggests the presence of a high proportion of copepods, evident also from a high proportion of 334 cholesterol (2) in these samples (Fig. 2). Indeed, herbivorous crustaceans use common dietary 335 algal sterols such as epi-brassicasterol (5) or 24-methylenecholesterol (6) to synthesize 336 337 cholesterol (2) via dealkylation and reduction (Grieneisen, 1994; Behmer and Nes, 2003). The 338 weak proportion of desmosterol (4) (an intermediate in the conversion of dietary phytosterols to cholesterol (2) by copepods; Goad 1978) observed in the April samples likely reflects the 339 highly efficient conversion of phytosterols to cholesterol (2) by copepods, with little 340 accumulation of desmosterol (4) (Cass et al., 2011). The presence of a high proportion of 341 copepods inferred from the sterol composition in April further aligns with the results of 342 Cornwell et al. (2020) who conducted a 1-year intensive study of the copepod Oithona similis 343 at the L4 station over the 2017–2018 season. Thus, increasing abundances of O. similis were 344 identified during the same period as the elevated cholesterol levels in our SPM samples (i.e. 345 between weeks 15 and 19 of 2018) (Cornwell et al., 2020), together with an increase in fecal 346 pellets in the phytoplankton community (phytoplankton net, 20 µm mesh size) (Widdicombe, 347

personal communication). Indeed, increased copepod grazing and feeding on diatoms are
common occurrences during the spring bloom at L4 (e.g. Bautista and Harris (1992), Harris et
al. (2000)).

In summary, biomarker analysis of the SPM samples provide valuable background 351 information about the trophic environment at L4 during 2018. Specifically, elevated 352 contributions from diatoms and *Phaeocystis* could be identified during the spring, along with 353 copepods. On the other hand, the late summer/autumn biomarker pool provides evidence for an 354 environment dominated by dinoflagellates, with some contribution from cyanobacteria. These 355 lipid data are also in very good agreement with recent and long-term studies of trophic 356 environments at L4 (e.g. Cornwell et al 2020, Atkinson et al 2015, Widdicombe et al 2010, 357 Eloire et al 2010). 358

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4.2. Biotic and abiotic degradation of lipid components of phytoplankton at station L4 in 2018
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362 *4.2.1. Photooxidation*

Due to the presence of chlorophylls, which are very efficient photosensitizers (Foote, 1976; 363 Knox and Dodge, 1985), unsaturated lipid components of phytoplankton are susceptible to Type 364 II photosensitized oxidation (i.e. involving singlet oxygen (¹O₂)) processes (Rontani and Belt, 365 2020). The efficiency of these processes is strongly dependent on: (i) the residence time of cells 366 within the euphotic layer (Zafiriou et al., 1984; Mayer et al., 2009), and (ii) the physiological 367 state of phytoplanktonic cells (Merzlyak and Hendry, 1994; Nelson, 1993). Indeed, ¹O₂ 368 production can exceed the quenching capacities of the photoprotective system (and thus induce 369 cell damage) only when the photosynthetic pathways are not operative as is the case of 370 371 senescent or highly stressed cells (Nelson, 1993).

Based on its high specificity and widespread occurrence in the environment (Cuny and 372 3-methylidene-7,11,15-trimethylhexadecan-1,2-diol 373 Rontani, 1999), (phytyldiol) (13) produced during Type II photosensitized oxidation of the chlorophyll phytyl side-chain 374 (Rontani et al., 1994), was proposed previously as a specific and stable tracer of chlorophyll 375 photodegradation (Cuny et al., 2002). The molar ratio phytyldiol (13)/phytol (12) is often 376 referred to as the Chlorophyll Phytyl side-chain Photodegradation Index (CPPI) and provides a 377 useful semi-quantitative estimate for photodegradation of all chlorophylls with a phytyl side-378 379 chain in the marine environment (Cuny et al., 2002). Interestingly, in our SPM samples, the highest chlorophyll photo-oxidation estimates at 5 m mirror the two bloom events and are 380 strongly anti-correlated to the concentration of phytol (12) (and therefore of chlorophyll) (Fig. 381 4) ($R^2 = 0.81$, n = 14), indicating that photooxidation processes act before and after the blooms 382 on old or senescent cells, but not on healthy cells during the blooms. 383

384 Unsaturated fatty acids, which generally predominate in the photosynthetic membranes of algae (Woods, 1974), may also be strongly affected by Type II photosensitized oxidation 385 386 processes in senescent phytoplanktonic cells (Rontani and Belt, 2020). The photodegradation 387 rates of these compounds logically increase with their degree of unsaturation (Rontani et al., 1998), rendering PUFAs, in particular, very reactive towards these processes (Frankel, 1998; 388 389 Rontani et al., 1998). Based on the correspondence between the lowest proportions of PUFAs 390 and the highest chlorophyll photooxidation estimates at 5 m (Fig. 4), the involvement of Type II photosensitized oxidation processes in PUFA degradation would be expected, yet no PUFA 391 photooxidation products were detected. This is possibly due to: (i) the instability of the 392 393 polyunsaturated hydroperoxides formed, or (ii) the involvement of intermolecular cross-linking reactions leading to the formation of compounds with macromolecular structures (Neff et al., 394 395 1988), which are not readily analyzed by gas chromatography. Exceptionally, for the sample collected on 01/22/18 at 5 m, where chlorophyll photooxidation % and the proportion of PUFAs 396

were both low (Fig. 4), PUFA degradation seems to result from autoxidation processes (seesection 4.2.2).

Type II photosensitized oxidation of Δ^9 MUFAs produces similar proportions of 9- and 399 10-hydroperoxides with an allylic *trans*-double bond (Frankel et al. 1979; Frankel, 1998), 400 which can subsequently undergo stereoselective radical allylic rearrangement to 11-trans and 401 8-trans hydroperoxides, respectively (Porter et al. 1995). In contrast, MUFA autoxidation 402 403 results mainly in the formation of 9-trans, 10-trans, 11-trans, 11-cis, 8-trans and 8-cis hydroperoxides (Frankel, 1998). Autoxidative processes can be readily characterised after 404 405 NaBH₄-reduction due to the formation of *cis* allylic hydroxyacids, which are specific products of these degradation processes (Porter et al., 1995; Frankel, 1998). The contribution of 406 hydroxyacids resulting from autoxidative processes may be distinguished from that arising from 407 photooxidative processes according to the proportions of *cis*-hydroxyacids detected and the 408 water temperature (Frankel, 1998; Marchand and Rontani, 2001). The results obtained here 409 410 showed only a very weak photooxidation of palmitoleic acid (22) (the main MUFA present in the samples) at both depths (Fig. 5). 411

Finally, as important unsaturated components of biological membranes, Δ^5 -sterols are 412 also susceptible to photooxidative degradation during the senescence of phytoplankton 413 (Rontani and Belt, 2020). However, their photodegradation is generally slower than that of 414 MUFAs due to steric hindrance between the sterol Δ^5 double bond and ${}^{1}O_{2}$ (Beutner et al., 415 2000). The failure to detect photooxidation products of Δ^5 -sterols is therefore consistent with 416 the very weak photodegradation of MUFAs (Tables 3 and 4). During the time series 417 investigated, Type II photosensitized oxidation thus seems to have acted most intensively only 418 on the more reactive lipids (i.e. chlorophyll and PUFAs). 419

420

421 *4.2.2. Autoxidation*

3,7,11,15-tetramethylhexadec-3(*cis/trans*)-ene-1,2-diols (17) and 3,7,11,15-tetramethyl-422 hexadec-2(cis/trans)-ene-1,4-diols (18) were previously proposed as indicators of radical-423 mediated oxidative degradation of the chlorophyll phytyl side-chain in the environment 424 425 (Rontani and Aubert, 2005), and were indeed detected in the current water column samples. Unfortunately, despite the high specificity and widespread occurrence of these diols in the 426 environment, the formation of several additional labile oxidation products during the 427 autoxidation of the phytyl side-chain (Rontani et al., 2003) prevented semi-quantitative 428 429 estimation of chlorophyll autoxidation.

Although more intense than photooxidation, autoxidation of palmitoleic acid (22) was 430 relatively low during the time series (Fig. 5). It may be noted that the autoxidation percentages 431 (ranging from 0 to 16%) are clearly in the low range previously observed in polar, tropical and 432 temperate regions (for a review see Rontani and Belt, 2020). Highest autoxidation (14.2 and 433 434 16.2% at 5 and 25 m, respectively) was observed in January (Fig. 5), suggesting that autoxidative processes also likely played an important role in the degradation of PUFAs at that 435 time (Fig. 4). Indeed, PUFAs such as $C_{20:5}$ (26) are autoxidized at a rate more than one order of 436 437 magnitude faster than MUFAs in senescent diatom cells (Rontani et al., 2014). It was proposed previously that the induction of autoxidative processes in phytodetritus derives likely from the 438 cleavage of photooxidative hydroperoxides (Girotti, 1998; Rontani et al., 2003) so it might be 439 expected that high rates of autoxidation would correspond to high rates of photooxidation. This 440 is clearly not the case in January, when the autoxidation state of MUFAs was the highest (Fig. 441 5) and chlorophyll photooxidation (%) was the lowest (Fig. 4), probably because the intensity 442 of autoxidative processes depends not only on the quantity of photochemically-produced 443 hydroperoxides present in the cells, but also on conditions favouring their homolytic cleavage 444 (e.g. the presence of LOXs or redox-active metal ions, heat or light; Sheldon and Kochi, 1976; 445 Schaich, 2005). 446

447 Autoxidation of Δ^5 -sterols is generally slower than that of MUFAs in senescent diatom 448 cells (Rontani et al., 2014). Since the extent of MUFA autoxidation was relatively low in the 449 SPM samples (Fig. 5), the very weak autoxidation of sterols was as expected. Therefore, as 450 seen for Type II photosensitized oxidation, autoxidation seems to have acted mainly on the 451 most reactive lipids (i.e. chlorophyll and PUFAs).

452

453 *4.2.3. Biotic degradation*

Type II photosensitized oxidation and free-radical induced oxidation of Δ^9 MUFAs such as 454 palmitoleic acid (22) produce (after NaBH₄-reduction of hydroperoxyacids) equal proportions 455 of the major 9-E and 10-E isomeric allylic hydroxyacids (36 and 37) (Frankel, 1998). The strong 456 predominance of 10-hydroxyhexadec-8(E)-enoic acid (36) observed in the SPM samples 457 collected on 04/30/18 (Fig. 6) can thus be attributed to the involvement of a specific biotic 458 459 oxidation process. A similar dominance of this isomer among palmitoleic acid (22) oxidation products was observed previously in sea ice and in sinking particles in the Canadian Arctic 460 (Amiraux et al., 2017; Rontani et al., 2018), and also in estuaries of diverse latitudes (Galeron 461 et al., 2018). Its occurrence has previously been attributed to the involvement of specific 462 bacterial dioxygenase activity and to a 10S-DOX enzyme, in particular. Indeed, a 10S-DOX 463 enzyme capable of converting palmitoleic acid (22) to 10(S)-hydroperoxyhexadec-8(E)-enoic 464 acid (30) (reduced to the corresponding hydroxyacid during NaBH₄-reduction) was previously 465 isolated from the bacteria Pseudomonas aeruginosa 42A2 (Guerrero et al., 1997; Busquets et 466 recently, found in other genera of marine bacteria, namely 467 al., 2004) and, more 468 Pseudoalteromonas, Shewanella and Aeromonas (Shoja Chaghervand, 2019). The involvement of 10S-DOX enzymatic activity in these SPM samples is further supported by detection of threo 469 470 7,10-dihydroxyhexadec-8(E)-enoic acid (42) (Fig. S1), formed from the specific action of 7S,10S-hydroperoxide diol synthase (linked to the 10S-DOX enzymatic activity) (Estupiñán et 471

al., 2014; 2015) on 10(*S*)-hydroperoxyhexadec-8(*E*)-enoic acid (**30**) (Fig. 7). It may be noted
that isomerization of the latter by hydroperoxide isomerases (Fig. 7), which are well known to
produce *erythro* allylic 1-4 diols (Jernerén et al., 2010), may explain the observed formation of
the *erythro* 7,10-dihydroxyhexadec-8(*E*)-enoic acids (**43**) (Fig. S1).

Martinez et al. (2010) previously suggested that fatty acids bind to bacterial 10S-DOX 476 via their carboxyl groups at a fixed position relative to the catalytic site. This enzyme, localized 477 in the periplasm (Martinez et al., 2013), should thus be mainly active on FFAs and therefore 478 479 contribute to the detoxification of these deleterious fatty acids (Monfort et al., 2000; Desbois and Smith, 2010) in the bacterial environment (Martínez et al., 2010). The very high proportions 480 481 of FFAs (and most notably of palmitoleic acid (22)) measured in the SPM samples exhibiting the highest 10S-DOX activity certainly supports this hypothesis. Further, the trophic level in 482 April 2018 was characterised by: (i) the dominance of diatoms (notably of *Thalassiosirales*) 483 484 and (ii) the presence of a very high copepod activity (see Section 4.1).

Interestingly, an oxylipin-based chemical defence against copepods was observed 485 previously in the diatom Thalassiosira rotula (Pohnert 2000; 2002), being initiated by 486 phospholipases acting immediately after cell damage. This lipase activity leads to the 487 preferential release of free MUFAs and PUFAs, the latter converted further by lipoxygenases 488 to reactive defensive metabolites such as the antiproliferative PolyUnsaturated Aldehydes 489 (PUAs) (Fig. 8), which are well-known to inhibit egg cleavage in copepods (Miralto et 490 al.,1999). In contrast, free MUFAs, which are not affected by lipoxygenases, are released intact 491 outside of wounded diatoms. These compounds (dominated by palmitoleic acid (22) in diatoms, 492 493 Pedersen et al., 1999) exhibit a strong bactericidal action towards marine Gram-negative pathogens (Desbois et al., 2009; Desbois and Smith, 2010). The strong 10S-DOX bacterial 494 495 activity observed in SPM samples in April (Fig. 5) can therefore be attributed to a detoxification strategy allowing bacteria associated to diatoms grazed by copepods to survive the release of 496

bactericidal free palmitoleic acid (**22**) (Fig. 8). 10(S)-Hydroperoxyhexadec-8(*E*)-enoic and *threo* 7,10-dihydroxyhexadec-8(*E*)-enoic acids (**30** and **42**) resulting from 10*S*-DOX and diol synthase activities, respectively, may be then transported from the periplasmic space of bacteria to the external medium (Martinez et al., 2013).

9- and 10-hydroperoxyacids with an allylic E double bond can undergo highly 501 stereoselective allylic rearrangement to 11-E and 8-E hydroperoxides, respectively (Fig. 7), the 502 extent of which increases with time (Porter et al., 1995). A lower proportion of the 8-E isomer 503 504 observed in the SPM sample collected on 04/30/18 from 25 m depth (10-E/8-E = 4.5 vs 10-E/8-EE = 1.2 at 5 m) (Fig. 6) thus suggests an involvement of the 10S-DOX activity at 25 m and an 505 aging of material collected from a shallower 5 m depth. The highest abundance of the copepod 506 O. similis at 25 m observed by Cornwell et al. (2020) likely indicates a strong alteration of 507 diatoms and thus an enhanced production of FFAs, which in turn supports an induction of the 508 bacterial 10S-DOX activity at this depth. The ascent of planktonic and bacterial material from 509 25 m to 5 m can be facilitated by the presence of a high proportion of Transparent Exopolymer 510 511 Particles (TEPs) in the shallower SPM, formed abiotically from dissolved precursors released 512 by phytoplankton and bacteria (Passow, 2000) and composed mainly of surface-active polysaccharides (Mopper et al., 1995). Due to their positive buoyancy, TEPs can provide a 513 514 means for the upward flux of bacteria and phytoplankton in the marine environment (Azetsu-515 Scott and Passow, 2004).

Allylic rearrangement of hydroperoxides in biological membranes is strongly sensitive to the hydrogen atom donor properties of their surrounding molecules (Porter et al., 1994; 1995). In algal membranes containing a high proportion of PUFAs, which are good hydrogen atom donors, allylic rearrangement should be weak (Fig. 7). In contrast, in bacterial periplasm containing only SFAs and MUFAs (both weak hydrogen atom donors), the rearrangement should be favoured (Fig. 7). The extent of the allylic rearrangement of the different

hydroperoxides present in each sample therefore reflects the composition of the organisms 522 523 (bacteria or phytoplankton) present. The strong allylic rearrangement of 10Shydroperoxyhexadec-8(E)-enoic acid (30) to 8-hydroperoxyhexadec-9(E)-enoic acid (32) 524 observed in the SPM sample collected at 5 m on 04/30/18 (Fig. 6A) thus provides further 525 evidence for 10S-DOX activity in the bacterial periplasm. Interestingly, in the same samples, 526 the rearrangement of 9-hydroperoxyhexadec-10(E)-enoic acid (31) (produced abiotically in 527 528 senescent algae) to the corresponding 11-hydroperoxyhexadec-9(E)-enoic acid (33) appeared 529 to be only very weak (Fig. 6A).

530

531 **5. Conclusions**

Selected lipids (sterols and fatty acids) and their biotic and abiotic oxidation products were quantified in SPM samples collected mainly in 2018 from two depths (5 m and 25 m) at the marine time series station L4 located in the western English Channel. The sterol and fatty acid composition was typical of mixed trophic communities at L4 throughout 2018, with a seasonal evolution from mainly diatoms and copepods in spring to dinoflagellates in late summer/autumn, consistent with recent and long-term taxonomic studies.

Abiotic lipid autoxidation and photodegradation were both found to be relatively minor, acting mainly on the most reactive lipids. A slightly greater influence of abiotic degradation, however, was found at 5 m compared to 25 m, likely due to higher irradiance and ascent of older planktonic/bacterial material from deeper to shallower waters.

In contrast, significant biotic degradation was evident in samples collected at the end of April. In particular, we observed a strong predominance of certain hydroxyacids linked to specific biotic oxidation process involving bacterial dioxygenase (10*S*-DOX) activity. This contribution from 10*S*-DOX in samples at the end of April was accompanied by a relatively high proportion of FFAs, likely resulting from a chemically-induced defense mechanism by

diatoms during times of increased zooplankton (copepod) activity. Since FFAs (dominated by palmitoleic acid in diatoms) exhibit a strong bactericidal action towards marine pathogens such as bacteria, the strong 10S-DOX bacterial activity observed in the April SPM samples points to a detoxification strategy by bacteria against the production of bactericidal free palmitoleic acid (22). We thus propose that this enzyme could be employed by bacteria to detoxify FFAs released by wounded diatoms in the presence of copepods.

553

554 Acknowledgements

We thank Louise Elizabeth Cornwell for providing us with some of the data from the Cornwell 555 et al (2020) study. We also thank the crew of the RV Plymouth Quest for collection of samples 556 used in this study. Financial support from the Centre National de la Recherche Scientifique 557 (CNRS) and the Aix-Marseille University is gratefully acknowledged. Thanks are also due to 558 559 the FEDER OCEANOMED (No. 1166-39417) for the funding of the GC-QTOF employed. Claire Widdicombe was funded through the UK Natural Environment Research Council's 560 561 National Capability Long-term Single Centre Science Programme, Climate Linked Atlantic Sector Science, grant number NE/R015953/1, and is a contribution to Theme 1.3 - Biological 562 Dynamics. We acknowledge Remi Amiraux for assistance with generating the schematic of 563 564 10S-DOX activity. We are also grateful to two anonymous reviewers for their useful and constructive comments. 565

566

APPENDIX



































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986

988 FIGURE CAPTIONS

989

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Figure 1. Map of the study area with location of the L4 station investigated.
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991

- **Figure 2.** Time series of sterol concentrations in SPM samples collected at 5 m (A) and 25 m
- 993 (B) from January to December 2018 at the L4 station.

994

Figure 3. Time series of acyclic isoprenoid acid concentrations in SPM samples collected at 5
m (A) and 25 m (B) from January to December 2018 at the L4 station.

997

- **Figure 4.** Time series of the proportion of the main classes of fatty acids (SFAs, MUFAs and
- 999 PUFAs) (A), phytol (12) concentration ($\mu g L^{-1}$) (B) and chlorophyll photooxidation estimate
- 1000 (%) (C) in SPM samples collected at 5 m from January to December 2018 at the L4 station.

1001

Figure 5. Time series of biotic and abiotic degradation percentage of palmitoleic acid (22) in
SPM samples collected at 5 m (A) and 25 m (B) from January to December 2018 and at 25 m
from January to December 2019 (C) at the L4 station.

1005

Figure 6. Partial ion chromatograms (m/z 199.1518, 213.1675, 329.1968 and 343.2125) showing the presence of palmitoleic acid (22) oxidation products in silylated TLEs in SPM samples collected at 5 m (A) and 25 m (B) on 04/30/18 at the L4 station.

- 1010 Figure 7. Formation and degradation pathways of 10*S*-hydroperoxyhexadec-8(*E*)-enoic acid1011 (30).
- 1012

- **Figure 8.** Conceptual scheme showing the defense system of diatoms during copepod grazing and the involvement of FFA detoxification in associated bacteria. (PUA = polyunsaturated aldehydes, 7,10-DS = 7,10-diol synthase, 10S-DOX = 10S-dioxygenase, 10S-HPHA = 10Shydroperoxyhexadecen-8(*E*)-enoic acid, 7,10-DiOHHA = 7,10-dihydroxyhexadecen-8(*E*)enoic acid).
- 1018

1019 Supplementary material

- 1020
- 1021 Figure S1. Partial ion chromatograms (*m/z* 225.1670, 315.2171, 327.1807 and 417.2808) of
- silylated TLE of the SPM sample collected on 04/30/18 at 25 m (A) and standard *threo* 7,10-
- 1023 dihydroxyhexadec-8(*E*)-enoic acid (42) TMS derivative (B).
- 1024









25 m











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25 m



A



B



Retention time (min)





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Table 1. Concentrations of sterols and acyclic isoprenoid compounds and chlorophyll photooxidation estimates in spm samples collected at station L4 during the time series 2018 at 5 m.

	01/25	02/18	03/25	04/19	04/30	05/14	05/30	06/25	07/16	08/13	09/17	10/17	11/26	12/10
24-Norcholesta-5,22 <i>E</i> -dien-3β-ol (24-norsterol) ^a	137.1	74.9	156.4	45.8	996.0	62.2	136.9	143.4	109.0	178.6	155.3	174.6	81.5	68.9
Cholesta-5,22 <i>E</i> -dien-3β-ol (22-dehydrocholesterol) ^a	46.9	98.1	152.4	29.4	249.5	40.9	103.7	58.6	203.8	269.1	442.3	192.8	127.8	96.9
Cholest-5-en-3β-ol (cholesterol) ^a	224.6	196.1	279.4	70.6	791.9	97.9	221.1	500.7	588.9	426.3	679.3	506.5	157.8	211.3
24-Methylcholesta-5,22 <i>E</i> -dien-3 β -ol (brassicasterol) ^a	109.2	185.8	312.3	55.9	323.7	51.7	273.6	278.8	323.0	349.3	932.4	340.7	158.1	119.7
Cholest-5,24-dien-3β-ol (desmosterol) ^a	41.3	77.6	198.7	27.4	128.1	50.8	92.1	368.4	196.2	99.6	348.7	116.0	61.8	79.3
24-Methylcholesta-5,24(28)-dien-3β-ol (24-	80.2	248.6	132.2	7.9	336.5	38.7	119.0	479.8	281.4	163.5	1173.6	159.9	103.0	60.7
methylenecholesterol) ^a														
24-Ethylcholest-5-en-3β-ol (sitosterol) ^a	48.5	23.1	39.6	4.1	47.2	5.6	36.9	60.6	97.8	74.3	156.6	82.7	31.1	45.2
24-Ethylcholesta-5,22E-dien-3β-ol (fucosterol) ^a	nde	13.8	55.5	nd	nd	5.0	23.2	38.3	57.1	nd	71.0	19.3	8.2	nd
4α,23,24-Trimethyl-5α-cholest-22 <i>E</i> -en-3-ol (dinosterol) ^a	10.7	nd	nd	1.2	42.8	17.9	35.0	30.3	38.3	52.0	827.0	29.1	12.1	12.2
Total sterols ^a	698.6	917.9	1326.6	242.2	2215.7	370.7	1041.4	1958.9	1895.6	1612.7	4786.2	1621.6	741.2	693.3
Phytol ^b	4.67	9.47	13.65	0.13	23.37	0.72	5.93	5.17	0.52	40.75	20.57	0.28	2.54	2.13
Phytyldiol ^b	0.11	0.13	0.10	0.02	0.60	0.07	0.07	0.17	0.04	0.37	0.12	0.14	0.06	0.04
Phytanic acid ^a	41.6	58.0	113.1	26.8	160.1	31.1	79.2	57.1	26.8	98.8	101.5	95.3	37.8	33.7
Pristanic acid ^a	2.3	7.7	16.7	5.4	25.9	5.1	5.8	9.8	3.6	14.3	13.1	6.0	2.2	2.3
4,8,12-TMTD acid ^a	5.5	46.2	82.2	11.7	16.1	9.0	10.4	7.5	4.5	19.6	23.8	20.0	6.9	7.1
CPPI ^c	0.018	0.011	0.006	0.115	0.021	0.078	0.009	0.026	0.060	0.007	0.005	0.392	0.019	0.016
Chlorophyll photooxidation estimate (%) ^d	28.5	18.6	10.3	86.7	31.7	75.0	15.5	37.9	65.3	12.7	8.2	99.8	29.3	25.5

 $a (ng L^{-1})$

 $^{b}(\mu g L^{-1})$

^c Chlorophyll Phytyl side-chain Photooxidation Index (molar ratio phytyldiol/phytol).

^d Estimated with the empirical equation: chlorophyll photodegradation $\% = (1 - [CPPI + 1]^{-18.5}) \times 100$ (Cuny et al. 2002).

^e Not detected

Table 2. Concentrations of sterols and acyclic isoprenoid compounds and chlorophyll photooxidation estimates in spm samples collected at station L4 during the time series 2018 at 25 m.

	01/25	02/18	03/25	04/19	04/30	05/14	05/30	06/25	07/16	08/13	09/17	10/17	11/26	12/10
24-Norcholesta-5,22 <i>E</i> -dien-3β-ol (24-norsterol) ^a	38.6	46.2	84.6	88.2	284.1	67.4	344.5	79.2	160.6	120.7	104.1	120.0	90.6	58.4
Cholesta-5,22 <i>E</i> -dien-3β-ol (22-dehydrocholesterol) ^a	51.9	51.7	69.1	82.0	173.5	62.7	312.2	102.1	251.3	190.5	161.8	132.7	200.8	87.9
Cholest-5-en-3β-ol (cholesterol) ^a	227.7	182.0	150.0	171.4	511.0	131.0	692.3	168.5	362.4	288.9	259.4	325.4	360.6	203.2
24-Methylcholesta-5,22 <i>E</i> -dien-3 β -ol (brassicasterol) ^a	100.0	78.2	65.8	70.2	130.2	53.5	803.2	121.5	208.7	249.9	91.1	125.0	201.0	84.8
Cholest-5,24-dien-3β-ol (desmosterol) ^a	23.6	20.8	25.2	184.3	195.6	140.8	227.5	40.9	66.2	106.5	36.8	45.1	94.9	18.3
24-Methylcholesta-5,24(28)-dien-3β-ol (24- methylenecholesterol) ^a	55.5	145.2	47.4	217.7	95.5	16.6	328.6	207.9	133.3	54.5	45.2	42.6	95.3	38.6
24-Ethylcholest-5-en-3β-ol (sitosterol) ^a	22.0	14.2	14.6	10.2	11.9	7.8	69.2	15.3	46.4	39.6	24.0	27.1	42.2	19.0
24-Ethylcholesta-5,22 <i>E</i> -dien-3β-ol (fucosterol) ^a	7.3	nde	5.7	2.4	2.1	1.8	20.1	9.6	16.3	6.4	nd	nd	9.3	nd
4α ,23,24-Trimethyl- 5α -cholest- $22E$ -en- 3 -ol (dinosterol) ^a	5.2	1.4	3.0	1.3	9.5	12.1	150.1	7.6	31.4	16.4	11.8	13.0	12.8	5.3
Total sterols ^a	545.0	539.7	465.4	871.5	1414.9	493.8	2948.8	753.5	1276.7	1072.4	735.9	836.8	1114.7	515.5
Phytol ^b	8.53	8.38	2.83	2.82	12.40	14.20	42.17	26.92	11.97	16.03	6.44	7.21	14.75	6.85
Phytyldiol ^b	0.06	0.12	0.06	0.04	0.16	0.18	0.34	0.48	0.16	0.12	0.08	0.14	0.10	0.10
Phytanic acid ^a	41.9	54.6	33.8	33.4	243.9	77.3	143.6	67.1	65.4	69.4	50.9	79.2	61.6	45.2
Pristanic acid ^a	2.5	3.5	1.5	8.6	54.4	10.1	17.6	14.1	12.2	6.6	12.2	10.8	6.8	4.0
4,8,12-TMTD acid ^a	6.5	7.3	6.9	30.5	55.3	60.1	21.0	19.2	18.9	32.5	14.9	26.6	13.8	10.8
CPPI (%) ^c	0.006	0.012	0.016	0.011	0.011	0.010	0.016	0.014	0.011	0.006	0.010	0.016	0.005	0.012
Chlorophyll photooxidation estimate (%) ^d	10.4	19.6	26.0	17.8	17.8	16.9	11.8	23.3	18.2	10.2	16.7	25.0	9.6	20.0

 $a (ng L^{-1})$

 $^{b}(\mu g L^{-1})$

^c Chlorophyll Phytyl side-chain Photooxidation Index (molar ratio phytyldiol/phytol).

^d Estimated with the empirical equation: chlorophyll photodegradation $\% = (1 - [CPPI + 1]^{-18.5}) \times 100$ (Cuny et al. 2002).

^e Not detected

	01/25	02/18	03/25	04/19	04/30	05/14	05/30	06/25	07/16	08/13	09/17	10/17	11/26	12/10
C _{12:0}	0.16	0.08	0.18	0.24	0.31	0.24	0.24	0.55	0.17	0.29	0.43	0.36	0.13	0.11
C _{14:0}	1.38	1.87	2.49	3.54	6.83	6.08	4.09	5.72	2.15	14.71	5.56	2.92	1.65	1.39
BrC _{15:0}	0.20	0.20	0.44	0.63	0.54	0.52	0.71	0.60	0.38	1.32	1.66	0.58	0.21	0.26
C _{15:0}	0.46	0.44	0.81	0.48	1.40	0.75	1.13	1.09	0.54	0.76	0.84	1.20	0.29	0.69
C _{16:4}	nd ^a	0.86	0.53	nd	1.36	nd	2.29	nd	nd	3.77	0.52	nd	0.30	nd
$C_{16:1007}$	1.06	1.95	2.80	2.15	8.39	9.03	1.82	4.69	1.99	6.56	6.58	1.78	1.62	0.90
C _{16:0}	4.80	4.17	6.95	9.27	11.18	15.88	9.33	10.23	6.58	25.69	16.72	9.19	3.35	6.97
C _{18:4}	nd	1.94	3.40	1.53	2.24	1.82	2.24	0.86	0.35	2.14	2.59	0.67	0.84	0.18
$C_{18,1009}$	0.84	1.78	3.04	2.25	2.62	3.70	2.66	3.16	1.14	8.10	3.15	2.13	0.79	0.79
C18:1@7	0.23	0.45	0.97	1.23	0.73	1.00	0.60	0.82	1.15	2.49	4.07	0.61	0.31	0.34
C _{18:0}	3.10	1.58	2.46	1.69	3.53	2.03	2.22	2.51	2.08	3.63	3.00	2.70	0.99	5.38
C _{20:5}	nd	3.68	1.91	0.94	4.34	2.02	2.34	1.54	0.75	2.20	1.88	nd	0.78	nd
C _{22:6}	nd	1.07	1.44	nd	2.46	nd	3.78	1.20	0.60	7.39	4.37	nd	0.45	nd
Total fatty acids	12.20	20.07	26.81	23.96	45.93	43.07	33.45	32.94	17.87	79.05	51.40	22.12	11.69	17.00
SFAs (%)	82.6	41.6	49.7	66.2	51.8	59.2	53.0	62.8	66.6	58.7	54.9	76.5	56.5	87.0
MUFAs (%)	17.4	20.8	23.1	23.5	25.6	31.9	15.2	26.3	23.9	21.7	26.9	20.4	23.3	11.9
PUFAs (%)	nd	37.6	21.2	10.3	22.8	8.9	31.8	10.9	9.5	19.6	12.2	3.1	20.2	1.1
Diatom fatty acid ratio ^b	0.5	1.1	0.8	0.6	1.5	1.0	0.9	1.0	0.6	1.0	0.8	0.5	1.1	0.3
(MUFAs+PUFAs)/SFAs	0.2	1.4	1.0	0.5	0.9	0.7	0.9	0.6	0.5	0.7	0.8	0.3	0.8	0.2

Table 3. Fatty acid concentrations ($\mu g L^{-1}$) in spm samples collected at station L4 during the time series 2018 at 5 m.

^a Not detected

 $^{\rm b} (C_{14:0} + C_{16:1 \varpi 7} + \Sigma C_{16} \text{ PUFAs}) / C_{16:0}$

° (Σ iso and anteiso C_{15:0})/C_{15:0}

	01/25	02/18	03/25	04/19	04/30	05/14	05/30	06/25	07/16	08/13	09/17	10/17	11/26	12/10
C _{12:0}	0.12	0.01	0.44	0.36	0.07	0.27	0.55	0.74	0.60	0.42	0.36	0.51	0.10	0.29
$C_{14.0}$	1.52	1.31	1.61	2.42	3.05	4.86	9.81	9.03	2.31	3.66	1.51	2.34	1.98	1.37
BrC _{15:0}	0.25	0.19	0.25	0.04	0.21	0.34	1.29	0.62	0.52	0.70	0.52	0.66	0.27	0.28
C _{15:0}	0.53	0.43	0.57	0.57	0.36	0.65	1.99	0.78	0.67	0.49	0.69	1.18	0.47	0.55
C _{16:4}	nd ^a	0.05	nd	nd	0.55	0.50	0.53	0.71	0.38	1.68	0.41	nd	0.42	0.28
$C_{16:1007}$	1.46	1.38	0.86	2.10	3.31	6.67	5.73	8.71	2.50	2.85	2.00	1.65	2.33	1.26
C _{16:0}	3.30	3.04	5.10	8.18	3.74	10.32	16.26	10.16	4.24	5.07	3.77	6.27	2.91	3.75
C _{18:4}	nd	0.53	0.21	0.75	1.13	1.43	5.19	1.99	0.57	1.45	0.39	0.75	0.97	0.47
$C_{18,100}$	0.84	0.99	0.49	1.30	1.80	2.23	7.63	3.40	0.82	1.56	1.43	1.53	0.86	0.89
C ₁₈ ·1@7	0.26	0.27	0.25	0.77	0.39	0.80	1.93	1.11	1.11	1.52	0.74	0.56	0.50	0.35
C _{18:0}	1.46	1.57	2.17	3.22	0.20	1.57	2.74	1.18	1.24	0.81	1.61	1.73	0.63	2.52
C _{20.5}	nd	1.85	0.16	0.50	3.59	2.69	5.96	3.92	1.19	1.88	1.17	0.81	1.07	0.39
C _{22:6}	nd	0.36	nd	nd	2.04	1.21	11.22	2.14	1.26	4.34	1.19	0.92	0.59	0.22
Total fatty acids	9.73	12.00	12.05	20.22	20.46	33.53	71.95	44.69	17.42	27.23	15.81	18.91	13.24	12.69
SFAs (%)	73.7	54.7	83.6	73.2	37.4	53.7	45.4	50.4	55.1	41.0	53.6	67.1	48.0	69.0
MUFAs (%)	26.3	22.0	13.3	20.7	26.9	28.9	21.3	29.6	25.4	21.7	26.4	19.8	27.9	19.7
PUFAs (%)	0	23.3	3.1	6.1	35.7	17.4	33.3	20.0	19.5	37.3	20.0	13.1	24.1	11.3
Diatom fatty acid ratio ^b	0.9	0.9	0.5	0.6	1.9	1.2	1.0	1.8	1.2	1.6	1.0	0.6	1.6	0.8
(MUFAs+PUFAs)/SFAs	0.4	0.8	0.2	0.4	1.7	0.9	1.2	1.0	0.8	1.4	0.9	0.5	1.1	0.5

Table 4. Fatty acid concentrations (μ g L⁻¹) in spm samples collected at station L4 during the time series 2018 at 25 m.

^a Not detected

 $^{\rm b} (C_{14:0} + C_{16:1 \omega 7} + \Sigma C_{16} \ PUFAs) / C_{16:0}$

^c (Σ *iso* and *anteiso* C_{15:0})/C_{15:0}