



Photodegradation and biodegradation of dissolved organic matter on the surface of the Greenland Ice Sheet 3

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11 Abstract

12 The surface (supraglacial) environment of the Greenland Ice Sheet (GrIS) is an active site for the storage, 13 transformation and transport of carbon, which is driven by extremely high levels of solar radiation throughout the 14 ablation season. Within the south west of the GrIS, blooms of Streptophyte micro-algae (hereafter 'glacier algae') 15 at abundances of $\sim 10^5$ cell mL⁻¹ dominate primary production in the surface ice and provide dissolved organic 16 matter (DOM) to the heterotrophic bacterial community. Glacier algae contain photoprotective secondary 17 phenolic pigment that comprises a large proportion of the cell (~4 % of the dry weight) and could represent a 18 substantial, additional carbon source for the heterotrophic community. The transformation and degradation of 19 DOM by solar radiation (photodegradation) and heterotrophic communities (biodegradation) represent two crucial 20 controls on DOM composition and quantity; however, the influence of these processes within the surface ice is 21 yet to be constrained. This study therefore assessed responses in the composition and quantity of two carbon 22 sources (glacier algae secondary pigment and surface ice DOM) following exposure to UV, PAR, UV+PAR 23 (photodegradation) and subsequent incubation with bacterial communities isolated from the ambient environment 24 (biodegradation). Our results indicate that exposure to predominantly UV radiation altered the composition of 25 glacier algal pigment and surface ice DOM; however, the quantity of DOM remained constant. Biodegradation 26 caused the greatest changes to both DOM composition and quantity, particularly in surface ice DOM. Secondary 27 pigment extracted from glacier algae was not a highly bioavailable source of carbon and did not support significant 28 growth of surface ice heterotrophic bacterial communities. Conversely, low molecular weight compounds in 29 surface ice DOM were rapidly utilised by heterotrophic bacteria supporting between a 3 and 9-fold increase in 30 bacterial abundance over a 30-day incubation. We found that photodegradation of glacier algal pigment and 31 surface ice DOM did not influence heterotrophic consumption. Photodegradation and biodegradation of DOM in 32 the surface ice habitat are likely intimately linked and act as fundamental controls on the composition and quantity 33 of DOM exported to downstream environments.

34 1 Introduction

35 Dissolved organic matter (DOM) is ubiquitous across all aquatic systems and comprises a chemically diverse

range of compounds (Baker and Spencer, 2004; Coble et al., 2014; Kellerman et al., 2018). DOM has multiple





37 functions within ecosystems including the provision of substrates for heterotrophic organisms; mobilising organic 38 and inorganic pollutants; and influencing the bioavailability of nutrients (Aiken, 2014; Baker and Spencer, 2004). 39 DOM originates from either autochthonous (i.e. in situ production) or allochthonous (i.e. terrestrial) sources with 40 varying levels of reactivity and composition. For example, autochthonous DOM typically comprises of low 41 molecular weight (LMW) compounds such as amino acids and carbohydrates, which are highly bioavailable 42 (Amado et al., 2015; Murphy et al., 2008; Stedmon and Markager, 2005). In contrast, allochthonous carbon 43 usually comprise of high molecular weight (HMW), aromatic compounds of a more recalcitrant nature (Amado 44 et al., 2015; Murphy et al., 2008). The composition and quantity of DOM fundamentally controls the flow of 45 carbon and energy through aquatic ecosystems, shaping the structure of the food web.

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47 The composition and quantity of DOM in aquatic ecosystems is primarily controlled by two processes: 48 photodegradation and biodegradation (Benner and Kaiser, 2011; Fasching et al., 2014; Hansen et al., 2016). 49 Chromophoric DOM (CDOM) comprises a proportion of total DOM that is highly reactive on exposure to solar 50 radiation (Coble, 2007). Consequently, high energy ultra-violet (UV) radiation can strongly influence carbon 51 cycling by degrading CDOM into a range of species including dissolved inorganic carbon, smaller organic carbon 52 compounds and reactive oxygen species (ROS; e.g. hydroxyl radicals) (Coble, 2007; Lindell et al., 1995; Stefan 53 et al., 2000; Tranvik and Bertilsson, 2001). DOM is a vast resource of biologically available organic carbon that 54 is consumed and transformed by heterotrophic bacteria (biodegradation) (Fellman et al., 2010). Carbon is utilised 55 by heterotrophic bacteria through two different processes: i) complete mineralisation of carbon to obtain energy 56 i.e. respiration; ii) incorporation into microbial biomass (Ducklow, 2000). Photodegradation of DOM can strongly 57 influence the interaction between heterotrophic communities and carbon within ecosystems exposed to high levels 58 of solar radiation (Anesio and Granéli, 2004; Stefan et al., 2000; Tranvik and Bertilsson, 2001; Tranvik and 59 Kokalj, 1998). The photodegradation of complex, recalcitrant DOM into more bioavailable compounds has been 60 found to stimulate bacterial production (Amado et al., 2015; Lindell et al., 1995; Zepp and Moran, 1997); however, 61 radiation can also remove LMW, bioavailable compounds from the DOM pool (Tranvik and Kokalj, 1998). 62 Additionally, the generation of ROS via photodegradation damages bacteria, reducing production (Holzinger and 63 Lütz, 2006; Ravanat et al., 2001). It is thought that the relative influence of photodegradation on bacterial 64 production is determined by the balance of these processes and relates to the source of DOM; i.e. photodegradation 65 tends to reduces bioavailability of algal-derived DOM but increases bioavailability of allochthonous DOM 66 (Amado et al., 2015). Thus, in ecosystems exposed to high levels of solar radiation, DOM composition and 67 quantity is controlled by two highly interlinked processes.

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69 The surface ice of the Greenland Ice Sheet (GrIS) hosts abundant and active algal and bacterial communities which influence both regional and global carbon cycling (Nicholes et al., 2019; Perini et al., 2019; Williamson et 70 71 al., 2018; Yallop et al., 2012). During the ablation season, the surface ice is exposed to extreme levels of photosynthetically active radiation (PAR; ~ 1700 μ mol photons m⁻² s⁻¹ on a cloudless day) and UV radiation. 72 73 Solar radiation drives high levels of carbon fixation $(0.35 - 1.12 \text{ mg C L}^{-1} \text{ d}^{-1})$ predominantly by blooms of highly 74 pigmented glacier algae (Musilova et al., 2017; Williamson et al., 2018; Yallop et al., 2012) that are particularly 75 prevalent in the so-called 'Dark Zone' in the south west of the ice sheet. Glacier algae are well-adapted to the 76 extreme light conditions and synthesise an abundant secondary phenolic pigment (purpurogallin carboxylic acid-





77 6-O-β-p-glucopyranoside) that exhibits maximal absorbance in UV-B wavelengths and thus protects the cells 78 from photo-damage (Remias et al., 2012; Williamson et al., 2020). This pigment comprises a relatively high 79 proportion of glacier algal cellular content (~ 4 % of the dry weight; Williamson et al. 2020) and likely reaches 80 high concentrations during bloom events when algal abundance peaks at 10⁴ cells mL⁻¹ (Williamson et al., 2018; Yallop et al., 2012). Glacier algal pigment, comprised predominantly of phenolic based compounds (Remias et 81 82 al., 2012), could therefore represent a vast source of organic carbon within the GrIS supraglacial environment if 83 released during cell lysis due to natural senescence or viral infection, providing an important energy source for 84 the diverse and active bacterial communities that numerically dominate surface ice (Hodson et al., 2008; Nicholes 85 et al., 2019; Stibal et al., 2015). These communities are thought to utilise predominantly algal-derived DOM to 86 achieve rates of bacterial production (BP) ranging $0.03 - 0.6 \ \mu g \ C \ L^{-1} \ h^{-1}$ (Nicholes et al., 2019; Yallop et al., 87 2012); approximately 30-times less than primary production (Nicholes et al., 2019; Yallop et al., 2012).

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89 Despite the presence of active autotrophic and heterotrophic communities, there remains several critical 90 knowledge gaps regarding carbon cycling within the high-light supraglacial surface ice environment. These 91 include the potential impact of photodegradation on surface ice DOM and subsequent heterotrophic utilisation; 92 the susceptibility of glacier algal secondary phenolic pigment to photodegradation (given its maximum absorbance 93 in UV-B wavelengths) and its bioavailability to heterotrophic bacteria; and the components of surface ice DOM 94 that are degraded by heterotrophic bacteria. Thus far, investigations into DOM cycling in glacial environments 95 have revealed that photodegradation produces a slight increase in bioavailable DOM in Antarctic snow samples 96 (Antony et al., 2018). However, DOM biodegradation was found to produce photoreactive compounds 97 highlighting the interlinked nature of these two processes (Antony et al., 2017, 2018). Here, we hypothesise that 98 photodegradation may alter the composition and bioavailability of organic carbon to heterotrophic bacterial 99 communities, subsequently impacting biodegradation pathways in surface ice. This investigation therefore aimed 100 to constrain changes in the composition and quantity of both ambient surface ice DOM and glacier algae secondary 101 phenolic pigment (representing a potentially abundant and refractory DOM source) following exposure to UV 102 and PAR radiation, and their subsequent bioavailability to surface ice bacterial communities.

103

104 2 Methodology

An incubation experiment was conducted to determine the degree to which glacier algal phenolic pigment (hereafter 'pigment') and surface ice dissolved organic matter (DOM) degrade when exposed to combinations of ultraviolet (UV) and photosynthetically active radiation (PAR) radiation. The bioavailability of pigment and surface ice DOM following photodegradation was subsequently assessed via incubations with a heterotrophic bacterial community isolated from surface ice samples.

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111 2.1 Surface ice preparation

Surface ice was obtained during the 2017 Black and Bloom field campaign (31st May to 1st July 2017) from the primary ice camp established within the GrIS ablation zone approximately 35 km from the south-western ice sheet margin (67 ° 04'43.3" N, 49 ° 20'29.7" W), adjacent to the S6 PROMICE weather station. The top 2cm of surface





115 ice containing a high algal coverage (~ 10^4 cells mL⁻¹) (Williamson et al., 2018) was sampled using a clean ice 116 saw and transferred into 5 WhirlPak bags. Each WhirlPak bag contained approximately 1.5L of frozen surface ice 117 and was transported back to the University of Bristol and stored at -20 °C. Prior to photodegradation, surface ice 118 was thawed over 24 hours at 3 °C and filtered through a 0.2 µm polyethersulfone (PES) filter (pre-flushed with 119 50 mL Milli-Q) to remove bacteria, fungi and glacier algae. The filtrate was homogenised and decanted into 250 120 mL pre-combusted Pyrex crystallising basins (n = 20).

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122 2.2 Glacier algal pigment preparation

123 Secondary phenolic pigment was extracted from glacier algal cells present in surface ice sampled from the primary 124 ice camp as outlined previously. Between 100 - 200 mL of sample (n = 45) was filtered onto combusted GF/F 125 filters, frozen and transported to the University of Bristol. Filters were freeze-dried for 24 hours and water-soluble 126 pigments extracted in 5 mL of Milli-Q water, following Remias et al., (2012) and Williamson et al., (2018). A 127 phase separation with n-hexane was performed to remove non-polar constituents from the raw extract, which was 128 subsequently stored frozen at -20 °C until being defrosted over 12 hours prior to use. Pigment was added to Milli-129 Q water to a 1:100 v/v dilution, homogenised and divided into 250 mL pre-combusted Pyrex crystallising basins 130 (n = 20).

131

132 2.3 Photodegradation

133 To stimulate photodegradation in the pigment and surface ice, both carbon sources were exposed to combinations 134 of UV and PAR over a 48-hour period. Short-wavelength, high-energy UV-radiation is widely reported as 135 responsible for inducing photodegradation in aquatic ecosystems (Amado et al., 2015; Bertilsson and Tranvik, 136 1998; Stefan et al., 2000; Tranvik and Bertilsson, 2001). Ultra-violet bulbs (25W, 220-240V, Exo Terra, Canada) and LED bulbs (Prolite, UK) were used to create 3 different light treatments: UV, PAR (432 µmol photons m⁻² s⁻ 137 ¹) or UV plus PAR (UV+PAR). Pigment and surface ice were exposed to UV, PAR and UV+PAR (n = 5 per light 138 139 treatment per carbon source) at 3 °C for 48 hours. Light exposure for 48 hours produced 840 kJ m⁻² of UV-A, 412 140 kJ m⁻² of UV-B and 16,456 kJ m⁻² of PAR, equivalent to approximately 2, 10 and 4 days of exposure on the 141 surface of the GrIS respectively (https://pvlighthouse.com.au/). To serve as a control, pigment and surface ice 142 samples were wrapped in foil and kept in total darkness during the exposure period ("DARK", n = 5). In addition, 143 a Milli-Q control (n = 5 per light treatment) was incubated alongside pigment and surface ice to detect any 144 contamination. Following photodegradation, dissolved organic matter composition (UV-Vis and fluorescence 145 spectroscopy) and quantity (dissolved organic carbon concentration) was assessed.

146

147 2.4 Biodegradation

To determine the bioavailability of photodegraded pigment and surface ice, carbon sources were inoculated with bacteria and incubated for 31 days. Bacterial cultures were established from surface ice from the primary ice camp, sampled as outlined previously. The surface ice was thawed at 3 °C over 48 hours, decanted into a precombusted 1000 mL beaker, covered with furnaced foil and sonicated for 2 minutes to facilitate cell detachment





(1)

from particles (Bradley et al., 2016). To isolate bacteria, surface ice was filtered through a combusted GF/D filter (Whatman, USA) and stored at 3 °C. Bacteria were inoculated to pigment, surface ice and Milli-Q control at a 10 % v/v final concentration in pre-combusted 30 mL amber glass vials, maintaining a headspace. Bacterial abundance at the start of the incubation averaged $3.7 \pm 0.2 \times 10^4$ cells mL⁻¹ and did not differ significantly across pigment, surface ice or Milli-Q control samples.

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To control for and examine the potential influence of nutrient limitation on carbon consumption and modification during incubations, half of all replicates received additions of inorganic nitrogen (NH₄NO₃) and phosphorus (KH₂PO₄) across all treatments at final concentrations of 30 μ M L⁻¹ and 10 μ M L⁻¹, respectively; representing 10times ambient concentrations reported from the surface of the GrIS (< 1 μ M P L⁻¹ Hawkings *et al.*, 2016; 1.3 μ M DIN L⁻¹ Wadham *et al.*, 2016). Incubations proceeded at 3 °C in the dark for a period of 31 days, with destructive sampling at days 0, 3, 6, 10, 17 and 31 to assess biodegradation impacts to DOM composition and quantity within incubations, relative to bacterial abundance and biovolume.

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166 2.5 UV-Vis spectroscopy

Analysis of CDOM via spectroscopy can provide information regarding DOM aromaticity, sources and reactivity
(Li and Hur, 2017). Accordingly, UV-Vis spectroscopy of the pigment and surface ice was conducted following
both photodegradation and biodegradation steps of our experiment. Absorbance spectra were obtained using a
Varian Cary 60 UV/Vis spectrophotometer (Agilent Technologies, USA) with scans run over wavelengths ranging
from 200 – 800 nm at 2 nm intervals. Absorption data is expressed as absorption coefficients, calculated following
Eq. (1):

173 $a(\lambda) = 2.303 A(\lambda)/l$

where a (λ) is absorption coefficient (m⁻¹), $A(\lambda)$ is the raw absorbance and 1 is the cuvette pathlength (m). Absorbance indices utilised are summarised in Table 1. Specific ultraviolet absorbance at 280 nm (SUVA₂₈₀) is a proxy for total aromaticity as electron transition occurs within this absorbance region for phenolic arenes, benzoic acids, aniline derivatives, polyenes and polycyclic aromatic hydrocarbons with two or more rings (Uyguner and Bekbolet, 2005). Although SUVA indices give an indication of the relative proportion of aromatic DOM, the relative reactivity of these compounds cannot be inferred (Weishaar et al., 2003). We therefore combined UV-Vis and fluorescence spectroscopy to provide information of composition and bioavailability of DOM.

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182 2.5.1 Fluorescence spectroscopy

A small fraction of CDOM, known as fluorescent DOM (FDOM), emits fluorescence energy when excited by photons at specific energies (Li and Hur, 2017). Fluorescence spectroscopy therefore characterises FDOM providing information on source, reactivity and composition (Aiken, 2014; Coble, 1996; Coble et al., 1990, 2014). To minimise the effects of temperature, samples were left to reach room temperature before measurements were undertaken. Fluorescence scans were conducted using a Varian Cary Eclipse Fluorescence Spectrophotometer (Agilent Technologies, USA) scanning over excitation wavelengths 250 – 450 nm at 5 nm intervals and 300 –





- 189 600 nm emission wavelengths at 2 nm intervals. Excitation- Emission Matrices (EEMs) were processed using the
- 190 StaRdom package (Pucher et al., 2019) in R (R Development Core Team, 2019). EEMs were blank corrected
- 191 using EEMs from daily Milli-Q scans, corrected for inner-filter effects using absorbance scans and Raman
- 192 normalised. Fluorescence indices derived from EEMs are summarised in Table 1. The fluorescence intensity of
- 193 commonly identified peaks in natural waters, summarised in Table 2, was identified in sample EEMs.
- 194





195Table 1: Absorbance and fluorescence indices utilised in this study. LMW= low molecular weight. Adapted from196Hansen et al., (2016)

| Indices | Calculation | Proxy | Reference | |
|---|---|--|-------------------------|--|
| Specific ultraviolet absorption (SUVA) E.g. SUVA ₂₅₄ , SUVA ₂₈₀ , SUVA ₃₆₅ (L mg ⁻¹ m ⁻¹) | Absorption coefficient at given wavelength in the ultraviolet region divided by DOC concentration | A higher number is generally associated with greater aromatic DOC content | (Weishaar et al., 2003) | |
| Specific visible absorption (SVA) E.g. SVA ₄₄₀ (L mg ⁻¹ m ⁻¹) | Absorption coefficient at 440 nm divided by DOC concentration | A higher number is generally associated with greater aromatic DOC content | (Chin et al., 1994) | |
| Absorption coefficient at 440 nm (A ₄₄₀) (m ⁻¹) | Absorption coefficient at 440 nm | Indicates the colour and is therefore a proxy for concentration of humic acid | (Fasching et al., 2014) | |
| Spectral slope λ300- 700 nm (S ₃₀₀₋₇₀₀) (nm ⁻¹) | Spectral slope within log-transformed spectra between 300 and 700 nm | Generally a higher value indicates LMW and/or decreasing aromaticity | (Helms et al., 2008) | |
| Humification index (HIX) | The area under the emission spectra 435- 480 nm divided by the peak area 300-345 nm + 435 – 480 nm, at excitation wavelength 254 nm | Gives an indication of the degree of humification. Higher values indicate an increasing degree of humification | (Ohno, 2002) | |
| Fluorescence index (FI) | The ratio of emission wavelengths at 470 nm and 520 nm, obtained at an excitation wavelength of 370 nm | Identified the relative contribution of terrestrial and microbial sources to the DOM pool. Increasing values suggests a microbial source | (McKnight et al., 2001) | |





| 198 Ta | able 2: Summary of commonly identified fluorescence peaks of aquatic DOM adapted from Fellman, Hood and |
|--------|--|
| 199 Sp | pencer, (2010). Peaks were originally identified by Coble et al., (1990), (2014); Coble, (1996); Coble, Del Castillo and |

Avril, (1998); Murphy et al., (2008). HMW = high molecular weight; LMW = low molecular weight.

| Peak name | Excitation (ex) and emission (em) maxima (nm) | Associated component | Possible sources |
|--------------|---|--|--|
| В | ex 270 - 275, em 304 - 312 | Tyrosine-like (proteinaceous) | Terrestrial, autochthonous production, microbial processing |
| Т | ex 270 - 280, em 330 - 368 | Tryptophan-like (proteinaceous) | Terrestrial, autochthonous production, microbial processing |
| М | ex 290 - 325, em 370 - 430 | UVA humic-like. LMW, common in marine environments and associated with biological activity | Terrestrial, autochthonous production, microbial processing |
| A | ex < 260, em 448 - 480 | UVC humic-like. Often HMW and aromatic | Terrestrial |
| С | ex 320 - 360, em 420 - 460 | UVC humic-like. Often HMW and aromatic | Terrestrial |

201

202 2.6 Dissolved organic carbon concentration

203 Dissolved organic carbon (DOC) concentration was measured following photodegradation and biodegradation 204 steps to determine the influence of these processes on the total quantity of carbon available. Samples were filtered 205 through a pre-flushed (3 times with 10 mL of Milli-Q) 0.22 µm polyethersulfone (PES) syringe filter (Whatman, England) into acid washed 30 mL HDPE Nalgene bottles and frozen until analysis. DOC concentrations were 206 207 quantified using a Shimadzu TOC-L Organic Carbon Analyser with a high-sensitivity catalyst. Non-purgeable 208 organic carbon (NPOC) was measured following the acidification of samples with hydrochloric acid and catalytic 209 combustion (680°C) of DOC to carbon dioxide, which is subsequently measured by infrared absorption. The limit 210 of detection (LoD) was 67 μ g L⁻¹ with a precision of ± 3 % and an accuracy of ± 2 % as defined by the comparison 211 of a gravimetrically diluted 500 mg L⁻¹ TOC certified stock standard to a concentration of 500 μ g L⁻¹ (Sigma 212 TraceCERT). Procedural blanks were analysed alongside samples to monitor for any contamination which may 213 have been introduced at any stage during the incubation and processing procedures. The DOC concentration 214 decreased by ~ 24 % in the control (Milli-Q inoculated with bacteria) and DOC concentrations in the pigment and 215 surface ice were therefore normalised against the control. The percent of biodegradable or bioavailable DOC





(2)

- 216 (%BDOC) was calculated as the difference in DOC concentration at the start and end of the 31 day biodegradation
- 217 incubation period (Fasching et al., 2014).
- 218

219 2.7 Bacterial enumeration and biomass

Bacterial enumeration was conducted at 0, 6, 15 and 30 days from 300 μ L of sample (n = 3) by epifluorescence microscopy following staining with 4', 6-diamidino-2-phenylindole (DAPI, Sigma) at a final concentration of 10 μ g mL⁻¹ (Porter and Feig, 1980). The staining, filtering and mounting procedure was conducted as outlined by Bradley *et al.* (2016). Bacterial cells were counted using a Leica DM 2000 epifluorescence microscope at 1000x magnification with attached MC120 HD microscope camera (Leica, Germany). A minimum of 300 cells or 30 randomly selected grids (each 10⁴ μ m²) were counted. Abundance in the pigment and surface ice was normalised to the control (Milli-Q inoculated with bacteria).

227

Imaging for the estimation of cell volumes was performed in parallel and measurements of cell diameter and height made using ImageJ software. Cell volumes were calculated following Eq. (2):

230
$$V = (w^2 * \pi/4) * (1 - w) + (\pi * w^3/6),$$

231 where $V(\mu m^3)$ is the cell volume, and w and l are cell width and length (in μm) (Fasching et al., 2014). Estimated cell volumes were converted to individual cell carbon content according to Bratbak and Dundas (1984). Microbial 232 233 biomass was then calculated as the product of bacterial abundance and the individual cell carbon content for each 234 sample. Bacterial growth efficiency (BGE) is an indicator of the use of DOM for bacterial growth and gives an 235 indication of the flow of carbon through the bacterial biomass (Anesio et al., 2005; Del Giorgio and Cole, 1998). 236 BGE was estimated as the change in biomass divided by the change in DOC concentration (assumed to represent 237 the DOC incorporated into the bacterial biomass plus respiration) over the 31-day incubation period. This assumes 238 carbon incorporated into the bacterial biomass was not utilised for respiration.

239

240 2.8 Data analysis

241 All statistical analyses and plotting of data were performed using R v.3.4.1 (R Core Team, 2019). Prior to 242 parametric analysis of datasets, Shapiro-Wilks Test combined with interrogation of frequency histograms was 243 used to determine normality. Three-way analysis of variance (ANOVA) with the fixed factors of carbon source 244 (i.e. pigment or surface ice; 2 levels); light (4 levels) and degradation type (i.e. photodegradation or 245 biodegradation; 2 levels) was used to determine significant differences in the absorbance and fluorescence indices. 246 Principal Component Analysis (PCA) was also used to summarise normalised and centred absorbance and 247 fluorescence indices utilising the 'factoextra' R package (Kassambara, 2020). Differences within DOC 248 concentration and bacterial abundance were described using a three-way ANOVA with the fixed factors of 'time' 249 (4 levels), 'light' (4 levels), nutrients (i.e. normal or +nutrients; 2 levels) for the pigment and surface ice.





251 3 Results

252 3.1 DOM composition

253 3.1.1 UV-Vis absorbance properties

254 Glacier algal pigment DOM that was not exposed to radiation (DARK) displayed two prominent peaks in absorption at λ_{285nm} and λ_{304nm} as well as a secondary peak at λ_{385nm} (Figure 1). These peaks were also evident in 255 256 pigment exposed to PAR and UV+PAR, which exhibited spectra highly comparable to DARK. In contrast, UV-257 irradiated pigment revealed marked differences in absorption with a conspicuous depression in the peaks at \$\lambda_{285nm}\$ and λ_{304nm} and 10 % greater absorption at λ_{250nm} and between $\lambda_{325-600nm}$. This was reflected in average specific 258 UV absorbance (SUVA) indices (Table 3) for UV-irradiated pigment which were 0.9 L m⁻¹ mg⁻¹ lower than DARK 259 260 for SUVA280 and between 0.8 - 1.0 L m⁻¹ mg⁻¹ higher for SUVA254 and SUVA365. For all light treatments, 261 absorption decreased with increasing wavelength across visible wavelengths (400-700 nm). Average absorption at 440 nm (A₄₄₀) was 16.9 ± 0.7 m⁻¹ in DARK and did not differ significantly across light treatments. 262

263

264 The inoculation of DARK pigment with bacteria (biodegradation) resulted in pronounced differences in the 265 absorbance spectra. For example, a conspicuous 33 % depression was evident in the peaks at λ_{285nm} and λ_{304nm} and the peak at λ_{385nm} was absent. In addition, a secondary peak at λ_{330nm} developed which was not evident in the 266 initial DARK spectra. SUVA254 and SUVA365 indices were significantly higher following biodegradation whereas 267 268 SUVA₂₈₀ was significantly lower (F_{3,32} = 21.8, p < 0.001; F_{3,32} = 20.0, p < 0.001; F_{3,32} = 36.3, p < 0.001respectively). Spectral differences across light treatments were also apparent following biodegradation with the 269 largest deviations in absorption occurring within UV wavelengths (200 - 400 nm). In particular, UV-irradiated 270 271 pigment retained the greatest absorption at λ_{285nm} and λ_{304nm} therefore SUVA₂₈₀ for this treatment was significantly 272 larger than DARK ($F_{3,32} = 1.7$, p < 0.01). All light treatments exhibited an ~ 20 % increase in A₄₄₀ following 273 biodegradation.





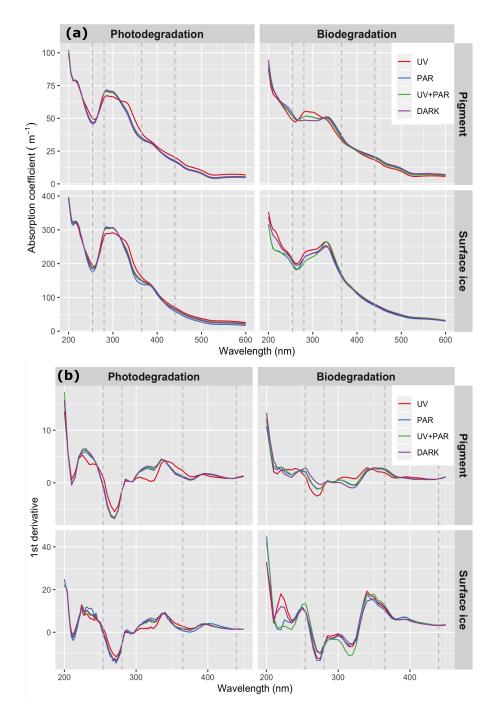


Figure 1: Average (a) and first derivative (b) of absorbance spectra across light treatments for the pigment and surface
 ice after exposure to light regimes (photodegradation) and following 31 days incubation with bacteria (biodegradation)
 (n=3). Dashed lines indicate the wavelengths at which specific UV absorbance (SUVA) was calculated (254 nm, 280 nm,
 365 nm) and the absorbance at 440 nm (A₄₄₀).





Table 3: Specific UV absorbance values (L m⁻¹ mg⁻¹) at 254 nm (SUVA254), 280 nm (SUVA280) and 365 nm (SUVA365) following photodegradation (Photo) and biodegradation (Bio) for the pigment and surface ice (mean ± SE, n=3). Highlighted values reflect trends on the absorbance spectra outlined previously. No significant differences were identified across light treatments per degradation type (i.e. photodegradation or biodegradation) per carbon source (pigment or surface ice), apart from SUVA₂₈₀ indices for pigment. Letters to denote homogenous subsets (lower case) are only displayed for this exception. Upper case letter denote significant differences between photodegradation and

287 biodegradation per light treatment per carbon source.

| DOM Light source treatment | | SUVA ₂₅₄ | | SUVA ₂₈₀ | | SUVA ₃₆₅ | |
|-------------------------------|----------|----------------------------|------------------------|---------------------------|------------------------------------|---------------------|----------------------|
| | | Photo | Bio | Photo | Bio | Photo | Bio |
| Pigment | UV | $9.8\pm0.2^{\rm A}$ | $12.5\pm0.7^{\rm \ A}$ | $12.9\pm0.2^{\rm A}$ | $^{a}14.2\pm0.7^{\rmA}$ | $7.7\pm0.1^{\rm A}$ | $8.6\pm0.7^{\rm B}$ |
| | PAR | $9.2\pm0.1^{\rm A}$ | $13.4\pm0.4^{\rm A}$ | $13.8\pm0.1^{\rm A}$ | $^{ac}13.4\pm0.3\ ^{A}$ | $7.0\pm0.1^{\rm A}$ | $9.2\pm0.5^{\rm B}$ |
| | UV + PAR | $9.1\pm0.3^{\rm A}$ | $10.9\pm0.3^{\rm A}$ | $13.7\pm0.3^{\rm A}$ | $^{bc}11.0\pm0.1^{B}$ | $6.8\pm0.4^{\rm A}$ | $7.4\pm0.3^{\rm B}$ |
| | Dark | $9.0\pm0.2^{\rm A}$ | $12.9\pm0.4^{\rm A}$ | $13.8\pm0.2^{\rm A}$ | $^{\text{c}}11.7\pm0.1^{\text{B}}$ | $6.7\pm0.2^{\rm A}$ | $8.9\pm0.6^{\rm B}$ |
| Surface ice | UV | $9.0\pm0.4^{\rm A}$ | $13.2\pm0.2^{\rm B}$ | $12.9 \pm 0.6^{\text{A}}$ | $14.5\pm0.3^{\rm A}$ | $7.4\pm0.5^{\rm A}$ | $10.5\pm0.3^{\rm A}$ |
| | PAR | $8.1 \pm 0.6^{\mathrm{A}}$ | $12.8\pm0.3^{\rm B}$ | $13.7\pm0.6^{\rm A}$ | $14.4\pm0.3^{\rm A}$ | $6.4\pm0.7^{\rm A}$ | $10.7\pm0.3^{\rm B}$ |
| | UV + PAR | $8.7\pm0.1^{\rm A}$ | $13.3\pm0.4^{\rm B}$ | $13.6\pm0.1^{\rm A}$ | $13.3\pm0.2^{\rm A}$ | $7.0\pm0.2^{\rm A}$ | $11.1\pm0.4^{\rm A}$ |
| | Dark | $8.4\pm0.2^{\rm A}$ | $14.1\pm0.1^{\rm B}$ | $13.8\pm0.2^{\rm A}$ | $14.8\pm0.8^{\rm A}$ | $6.8\pm0.2^{\rm A}$ | $11.2\pm0.3^{\rm A}$ |

²⁸⁸

DARK surface ice DOM exhibited absorption on average ~ 4 times greater than the DARK pigment DOM (Figure 1); however, distinct similarities in absorption were evident, particularly the corresponding peaks at λ_{285nm} , λ_{304nm} and λ_{385nm} . The average A₄₄₀ was 62.6 ± 2.4 m⁻¹ which was 3 times larger than the DARK pigment. Photodegraded surface ice exhibited spectral differences, with the most striking disparities in the UV and PAR treatments. In particular, surface ice exposed to UV radiation exhibited ~ 5 % less absorption at λ_{304nm} and an average SUVA₂₈₀ 1.1 L m⁻¹ mg⁻¹ lower than DARK (Table 3). Equally, PAR-irradiated surface ice exhibited lower absorption at λ_{250nm} and $\lambda_{350-370nm}$ and subsequently the average SUVA₂₅₄ was 5 % lower than DARK.

296

297 The biodegraded DARK surface ice absorption spectra exhibited similar trends to the pigment with a \sim 20 % 298 depression in peaks at λ_{285nm} and λ_{304nm} ; however, retained more defined peaks at these wavelengths compared to 299 the DARK pigment. In addition, a much more pronounced secondary peak at λ_{330nm} was visible in the DARK surface ice. Although SUVA254 in the DARK treatment increased significantly by 65 % following biodegradation 300 301 $(F_{3,32} = 21.8, p < 0.001)$, the other SUVA indices were not significantly different. Deviations in the spectra across 302 light treatments is largely confined between $\lambda_{200-350nm}$, with UV exhibiting the largest absorption over these 303 wavelengths and UV and UV+PAR the lowest. Absorbance across visible wavelengths was highly consistent 304 across light treatments and a ~ 20 % increase A440 was evident following biodegradation. 305

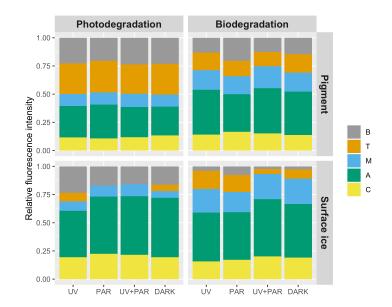




306 3.1.2 **Fluorescence properties**

307 Peaks commonly identified in the fluorescence spectra of natural waters (B, T, M, A, C) (Coble, 1996; Coble et 308 al., 2014) were all present in the DARK pigment treatment (Figure 2; Figure 3). We observed an approximate 309 50:50 ratio between peaks associated with fluorophores in proteinaceous (B and T) and humic-like (A, C and M) 310 DOM in the DARK treatment. Following photodegradation of the pigment, the relative intensity of all peaks was 311 comparable with DARK and only a slight increase in peak A was observed in the PAR treatment. Biodegradation 312 was observed to alter the fluorescence signature of the pigment with humic-like fluorescence increasing by almost 313 25 % in the DARK treatment. UV and UV+PAR-irradiated pigment resulted in very little difference in 314 fluorescence intensities compared to DARK. Only the PAR treatment exhibited noticeable changes with ~ 10 % greater fluorescence of peak B and a similar decrease in peak A compared to DARK. 315 316 317 In contrast to the pigment, DARK surface ice was dominated by fluorescence associated with humic-like DOM 318 (>75 %) consisting predominantly of peaks A and C. Following photodegradation, the relative intensity of peaks 319 deviated between light treatments. For example, the fluorescence intensities of humic-like peaks (A and C) was ~ 320 12 % lower in the UV treatment compared to DARK. In addition, PAR and UV+PAR exposed surface ice did not 321 contain peak T fluorescence but exhibited almost double the fluorescence associated with peak M. The 322 biodegradation of surface ice resulted in an ~ 10 % increase in fluorescence associated with humic-like DOM in 323 the DARK treatment. Reductions in proteinaceous fluorescence in DARK was particularly evident for peak B

- 324 which was almost undetectable following biodegradation (Figure 3). Overall, PAR and UV treatments retained
- 325 the largest proportion of proteinaceous peaks, predominantly due to increased fluorescence of peak T and M.
- 326



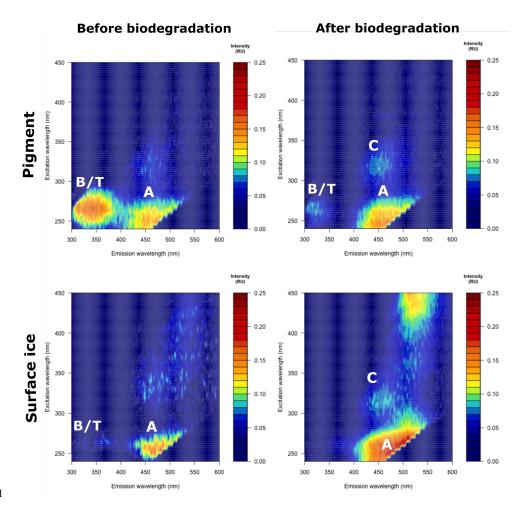
327

328 Figure 2: The mean relative fluorescence intensity (R.U.; n = 3) associated with commonly identified peaks (B, T, M, A 329 and C) in the fluorescence spectra of natural waters (Coble, 1996; Coble et al., 2014) (n=3). Peaks B and T are often

330 associated with protein







331

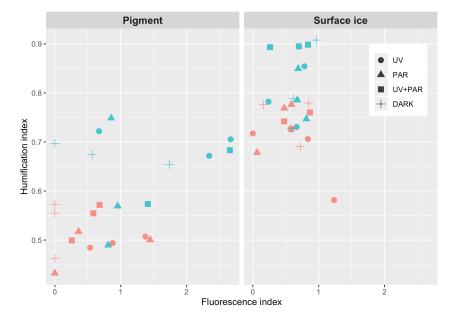
Figure 3: Excitation-Emission matrices (EEMs) for the DARK pigment and surface ice before and after
 biodegradation. Peaks identified are those typically identified in natural water fluorescence spectra (Birdwell and
 Engel, 2010; Coble, 1996; Coble et al., 2014). Peaks A and C are generally associated with fluorophores in humic-like
 DOM whereas peaks B and T are associated with proteinaceous DOM.

336

The average degree of humification (HIX) across all light treatments in the pigment was 0.51 ± 0.01 which was 337 338 significantly lower than the surface ice average HIX of 0.57 \pm 0.11 (F_{1,32} = 46.8, p < 0.001). Following 339 photodegradation, HIX was not significantly different across light treatments for either pigment or surface ice 340 (Figure 4). However, HIX increased significantly by 29 % and 12 % in the pigment and surface ice respectively 341 following biodegradation (pigment: $F_{1,32} = 46.8$, p < 0.001; surface ice $F_{1,32} = 46.8$, p < 0.01). The average 342 fluorescence index (FI) was not significantly different between the pigment (0.51 ± 0.15) and surface ice ($0.57 \pm$ 343 0.11). Following biodegradation, FI of the pigment increased significantly ($F_{1,32} = 3.5$, p < 0.05) whereas surface 344 ice FI remained relatively constant.







346

Figure 4: Humification index (HIX) against the fluorescence index (FI) for pigment and surface ice after photodegradation (red) and after biodegradation (blue) across all light treatments. Increasing HIX indicates the presence of more humic compounds. Low FI has been associated with terrestrially derived DOM and high FI with microbial DOM.

351

352 Principal component analysis (PCA) was utilised to summarise all absorbance and fluorescence indices and to 353 elucidate underlying trends of the dataset (Figure 5; Table 4). PC1 described 43 % of the variance in the data and 354 shows strong positive loadings for parameters associated with high molecular weight, aromatic compounds (peak M fluorescence intensity, SUVA₃₆₅ and peak A intensity; Table 4). PC2 accounted for 23 % of the variance and 355 represented Specific visible absorbance at λ 440 (SVA₄₄₀), spectral slope between 300 - 700 nm (S₃₀₀₋₇₀₀) and 356 357 SUVA254. There were no significant differences in PC1 or PC2 between light treatments; however, carbon source (i.e. pigment or surface ice) and type of degradation (i.e. photodegradation or biodegradation) were found to be 358 significant drivers of change in PC1 ($F_{1,46} = 31.8$, p < 0.001; $F_{1,46} = 35.6$, p < 0.001 respectively) and PC2 ($F_{1,46} = 35.6$, p < 0.001 respectively) 359 48.7, p < 0.001; F_{1,46} = 18.9, p < 0.001 respectively). 360 361





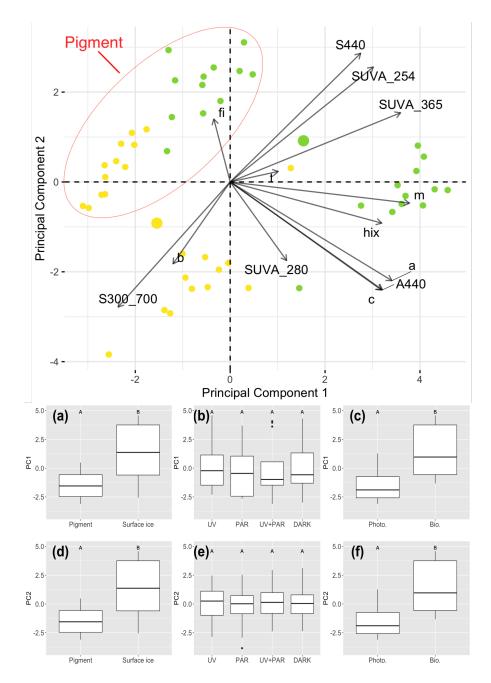


Figure 5: Principle component analysis (PCA) of the absorbance and fluorescence for photodegraded (yellow) or biodegraded (green) DOM. Points representing pigment DOM are circled in red and the remaining points represent surface ice DOM. PC1 accounts for 43 % and PC2 accounts for 23 % of the variability in the dataset. Absorbance indices include SUVA254, SUVA280, SUVA365, A440, spectral slope between 300 – 700 nm (S300_700) and fluorescence indices include fluorescence intensity of peaks B, T, M, A, C, humification index (HIX) and fluorescence index (FI). Boxplots of PC1 against carbon source (a), light (b) and degradation type (i.e. photodegradation or biodegradation; c) and PC2 against carbon source (d), light (e) and degradation type (f). Letters denote significant differences between groups (p < 0.05)</p>





| 372 | Table 4: Component loadings of PCA analysis of absorbance and fluorescence indices. The largest component loading |
|-----|--|
| 373 | is highlighted in grey. Absorbance indices include SUVA254, SUVA280, SUVA365, A440, spectral slope between 300 - |
| 374 | 700 nm (S300_700) and fluorescence indices include fluorescence intensity of peaks B, T, M, A, C, humification index |

374 375 (HIX) and fluorescence index (FI).

| | PC1 | PC2 | PC3 |
|--------------------------|--------|--------|--------|
| Proportion of variance | 42.7 % | 22.7 % | 10.1 % |
| Cumulative proportion | 42.7 % | 65.4 % | 75.5 % |
| Component loadings | | | |
| В | -0.12 | -0.26 | 0.28 |
| Т | 0.10 | 0.03 | 0.63 |
| Μ | 0.39 | -0.07 | 0.07 |
| Α | 0.35 | -0.31 | -0.04 |
| С | 0.33 | -0.34 | -0.01 |
| FI | -0.04 | 0.20 | -0.51 |
| HIX | 0.33 | -0.13 | -0.45 |
| S300-700 | -0.24 | -0.39 | -0.09 |
| SUVA ₂₅₄ | 0.31 | 0.36 | 0.05 |
| SUVA ₂₈₀ | 0.12 | -0.25 | 0.18 |
| SUVA ₃₆₅ | 0.37 | 0.22 | 0.09 |
| SVA440 | 0.28 | 0.40 | 0.07 |
| A440 | 0.33 | -0.34 | -0.07 |

376

377 **DOC** quantity 3.2

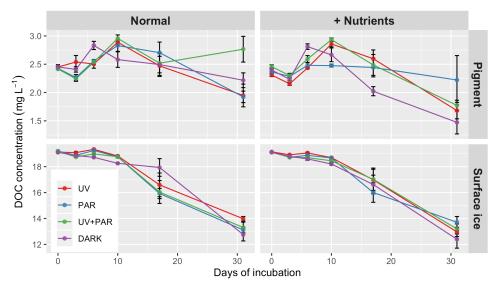
378 Average dissolved organic carbon (DOC) concentration of the DARK pigment was 2.5 \pm 0.04 mg $L^{\text{-1}}$ and 379 photodegradation did not significantly alter concentrations in the UV, PAR or UV+PAR treatments. During the 31-days of biodegradation, DOC concentrations in the DARK treatment exhibited high levels of variability and 380 by the end of the incubation period had decreased by ~ 0.25 mg L⁻¹, but this was not significant (Figure 6). 381 382 Concentrations across light treatments were equally variable decreasing by $\sim 1 \text{ mg } L^{-1}$ over 31 days; however, were not significantly different from DARK. The percent of biodegradable DOC (%BDOC) was ~ 10 % and was 383 384 not significantly different between UV and PAR exposed and DARK pigment (Appendix A; Table A1). The addition of nutrients (+Nutrients) to incubations did not affect the DOC concentration across any of the light 385 386 treatments; however, overall %BDOC in +Nutrients was significantly higher than the normal incubations ($F_{1,61}$ = 387 8.7, p < 0.01; Appendix A).



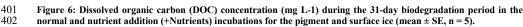


389 The average DOC concentration (19.1 \pm 0.03 mg L⁻¹) in the DARK surface ice was ~ 8 times greater than in the 390 pigment and no significant change in concentration was found across light treatments following photodegradation. 391 Nevertheless, DOC concentrations did decrease significantly during biodegradation incubations across all light 392 treatments ($F_{5,212} = 432$, p < 0.001). DOC concentrations in DARK were significantly lower than in other light 393 treatments at 6 days ($F_{3,36} = 41.4$, p < 0.01 for all) and 10 days ($F_{3,36} = 32.9$, p < 0.001 for all). The UV, PAR and 394 UV+PAR treatments followed similar trajectories during the incubation period; however, only the DOC 395 concentration in the UV treatment was significantly higher than in DARK at 31 days ($F_{3,36} = 4.7$, p < 0.01). The BDOC of surface ice was ~ 30 % and was significantly higher than the pigment ($F_{1,61} = 839$, p < 0.001); however, 396 397 there was no significant difference across light treatments (Appendix A). The DOC concentration in the normal treatment was not significantly different from the +Nutrients treatments following biodegradation. 398

399







403

404 3.3 Bacterial abundance and growth efficiency

405 Bacterial abundance in pigment incubations did not increase significantly over the 31-day incubation period across 406 any of the light treatments (Figure 7). Indeed, when normalised against the change in bacterial abundance in the 407 Milli-Q control, abundance actually decreased in the PAR, UV+PAR and DARK treatments during the incubation 408 period. In the +Nutrients treatment, abundance increased in the UV, PAR and DARK treatments to $0.7 \pm 0.2 \times 10^6$ 409 cells mL⁻¹; however, this was not significant. Average bacterial growth efficiency (BGE) for all pigment 410 treatments was < 4 % and substantial variability was observed across light and nutrient treatments (Appendix A). 411 412 In contrast to the pigment incubations, bacterial abundance across all surface ice treatments increased significantly 413 between 3 and 9-fold during the incubation period ($F_{3,61} = 18.4$, p < 0.001). At 17 days, the largest increases were

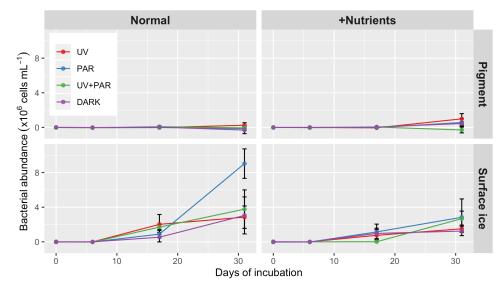
414 observed in the UV and UV+PAR treatments which supported an abundance of $2.0 \pm 1.1 \times 10^6$ cells mL⁻¹ and 1.7





415 $\pm 0.3 \times 10^{6}$ cells mL⁻¹ respectively. Rapid growth in PAR-irradiated surface ice was observed in the final 14 days 416 and as such the final abundance of $9.0 \pm 1.7 \times 10^{6}$ cells mL⁻¹ was significantly larger than DARK (F_{3,61} = 2.2, p < 417 0.05). Average abundance at the end of biodegradation across all light treatments was $4.7 \pm 1.5 \times 10^{6}$ cells mL⁻¹ 418 and was not significantly different in the +Nutrients treatment. Average BGE in the surface ice was $6.7 \pm 1.3 \%$ 419 which was significantly higher than the pigment (F_{1,31} = 4.7, p < 0.05). However, BGE was not significantly 420 different across light or nutrient treatments (Appendix A).

421



422

Figure 7: Bacterial abundance in pigment and surface ice coloured by light treatment across the nutrient and nutrient
 addition (+Nutrients) incubations (mean ± SE, n = 3)

425 4 Discussion

426 Active microbial communities store and transform carbon across the Greenland Ice Sheet (GrIS) supraglacial 427 environment. Glacier algae residing within the surface ice contain a dark coloured photoprotective pigment, which 428 comprises a large proportion of the cell (~ 4 % of the dry weight) (Remias et al., 2012; Williamson et al., 2020), 429 and may thus represent a vast source of carbon. Glacier algae are responsible for the majority of carbon fixation 430 within the surface ice (Williamson et al., 2018; Yallop et al., 2012), which is an essential autochthonous carbon 431 source for heterotrophic bacterial communities (Nicholes et al., 2019; Yallop et al., 2012). Despite the surface ice 432 receiving extremely high levels of irradiation, the role of photodegradation on carbon flows was vet to be 433 constrained. This study assessed responses in the composition and quantity of glacier algae secondary pigment 434 and surface ice DOM sources following exposure to UV, PAR, UV+PAR (photodegradation) and subsequent 435 incubation with bacterial communities isolated from the ambient environment (biodegradation). Our results 436 indicate that the composition of algal pigment and surface ice DOM is altered following exposure to radiation, 437 but that the quantity of DOC remains constant. Biodegradation caused the greatest changes to DOM composition 438 and DOC quantity, particularly for surface ice DOM sources.





440 4.1 Glacier algal phenolic pigment

441 The secondary phenolic pigment extracted from glacier algae exhibited absorbance that was highly comparable 442 with previous characterisations of this substance, displaying strong absorption particularly over UV-A and UV-B 443 wavelengths, which decreased across the visible spectrum (Remias et al., 2012; Williamson et al., 2020). Peaks 444 in absorption observed at λ_{285nm} , λ_{304nm} and λ_{385nm} likely reflect different moieties within the pigment structure 445 (Remias et al., 2012; Williamson et al., 2020). For example, peaks at λ_{304nm} and λ_{389nm} have previously been 446 identified as purpurogallin carboxylic acid- $6-O-\beta$ -D-glucopyranoside (C₁₈H₁₈O₁₂), which is formed from the 447 chemical oxidation of gallic acid or from a mixture of gallic acid and pyrogallol (Polewski et al., 2002; Remias et 448 al., 2012). Equally, a peak at λ_{278nm} is thought to be gallic acid glycoside and may represent an important 449 biosynthetic precursor to purpurogallin carboxylic acid (Remias et al., 2012). Given the similarity in absorption 450 peaks, it is likely these compounds are also present in the pigment utilised for this experiment. The chemical 451 composition and absorption of pigment likely reflects its primary role of protecting chloroplasts from damaging 452 UV and high energy blue visible radiation, while transmitting longer, less damaging wavelengths for 453 photosynthesis (Williamson et al., 2020).

454

455 We observed structural changes to light-sensitive (chromophoric) regions of the glacier algal pigment following 456 exposure to UV radiation; however, the quantity and bioavailability of compounds remained consistent across 457 light treatments. UV-irradiated pigment exhibited a depression in absorption associated with purpurogallin 458 carboxylic acid and gallic acid glycoside, suggesting that these compounds were subject to photodegradation. 459 Ward and Cory (2016) highlighted that carboxylic acids in Arctic algal mats and permafrost were highly 460 susceptible to photodegradation and form a variety of hydrocarbons. The concomitant increase in SUVA254 and 461 SUVA₃₆₅ may indicate the transformation into aromatic compounds, which absorb at λ_{254nm} and λ_{365nm} (Uyguner 462 and Bekbolet, 2005; Weishaar et al., 2003). Alternatively, UV radiation may preferentially degrade aliphatic, low molecular weight (LMW) DOM resulting in a greater proportion of aromatic DOM (Ward and Cory, 2016). This 463 464 is common in other aquatic environments and results in UV radiation effectively reducing the availability of LMW 465 DOM sources to heterotrophic communities (Amado et al., 2015; Ward and Cory, 2016). Despite compositional changes to pigment DOM following UV exposure, bulk DOM quantity remained constant across light treatments. 466 467 Photosensitive DOM (i.e. CDOM) accounts for only a fraction of the total DOM pool (Fleck et al., 2014), therefore 468 structural alterations can occur without altering the bulk DOM quantity (Cory et al., 2011; Spencer et al., 2007). 469 Given that pigment DOM fluorescence also remained consistent across light treatments, our data are consistent 470 with variation in pigment DOM composition but not quantity following exposure to potential photodegradation. 471

472 Biodegradation incubations revealed that certain components of glacier algal pigment may be transformed by the 473 heterotrophic bacterial community. Consistent with previous studies, SUVA254 and SUVA365 increased across 474 incubations, concomitant with decreasing contributions of proteinaceous fluorescence and suggestive of 475 preferential consumption of LMW aliphatic DOM by bacterial communities (Antony et al., 2018; Hansen et al., 476 2016; Kirchman, 2003). Most notably, reduced absorption associated with purpurogallin carboxylic acid and 477 gallic acid glycoside indicates that these compounds may comprise a proportion of the bioavailable substrates 478 consumed by the bacterial community. Carboxylic acids have been observed to be readily assimilated into 479 bacterial biomass, thus these compounds are considered largely bioavailable (Bertilsson and Tranvik, 1998).





480 Interestingly, irradiated pigment retained greater purpurogallin carboxylic acid and gallic acid glycoside 481 absorption compared to DARK treatments, highlighting that UV and PAR exposure either reduces the bioavailability of these compounds or produces more bioavailable compounds that are preferentially consumed 482 483 (Amado et al., 2015; Lindell et al., 1995; Zepp and Moran, 1997). The humificiation (HIX) of pigment and the 484 dominance of peak M indicated the production of LMW, humic DOM that is widely attributed to biological 485 activity (Coble, 1996; Murphy et al., 2008). This is corroborated by the increased FI following biodegradation 486 confirming a greater dominance of DOM of a microbial origin (McKnight et al., 2001). Overall, biodegradation incubations revealed the potential for bacterial communities to transform a small proportion of bioavailable carbon 487 488 (~ 10 %) sourced from glacier algal secondary pigment and demonstrated that UV degradation may influence 489 which DOM components are degraded.

490

491 Despite the marked changes in DOM composition following biodegradation, our results indicated that only ~ 3 % 492 of carbon was incorporated into bacterial biomass and bacterial abundance thus remained relatively constant 493 across all light treatments. This suggests that glacier algal pigment may be a low-quality carbon substrate for 494 surface ice bacterial communities and the overall quality of carbon was not changed by photodegradation. We 495 provide two explanations for this, both related to the polyphenolic nature of purpurogallin carboxylic acid and 496 gallic acid glycoside. Polyphenols represent a variety of chemical substances found in algae and higher plants that 497 have a range of ecological and physiological functions (Bhat et al., 1998; Cannell et al., 1988). Notably, 498 polyphenols have antimicrobial properties and play an essential role in protecting cells against bacterial and fungal pathogens (Cannell et al., 1988; Lima et al., 2016; Nguyen et al., 2013; Scalbert, 1991). A range of bacterial 499 500 species are susceptible to polyphenol inhibition (Scalbert, 1991; Taguri et al., 2006) and we propose that the 501 majority of the surface ice bacterial community are affected. Despite this, compositional changes to DOM outlined 502 previously may suggest that some resistant species reside within the surface ice environment. Bacterial 503 degradation or modification of polyphenols, as observed in our incubations, has been highlighted as an important 504 mechanism for overcoming inhibition, such as the ability of Achromobacter sp. to grow in a gallotannin media 505 (Bhat et al., 1998; Scalbert, 1991; Smith et al., 2005). It is possible that the inhibition of the majority of the 506 bacterial community by the polyphenolic nature of pigment may have resulted in low bacterial growth efficiency. 507

508 In addition to the potential inhibition of bacteria by antimicrobial properties of glacier algal phenolic pigment, 509 nutrient limitation may have also restricted bacterial growth. Nitrogen and phosphorus are essential 510 macronutrients obtained by bacteria from both inorganic and organic sources (Dodds, 2010; Sigee, 2004). Organic 511 sources include proteins, nucleic acids and amino acids, which are actively and passively released from cells via 512 extrapolymeric substances and cell lysis (Sigee, 2004). Both purpurogallin carboxylic acid and gallic acid 513 glycoside do not contain nitrogen or phosphorus and hence are easily synthesised in high light, low nitrogen 514 environments, such as supraglacial surface ice (Remias et al., 2009, 2012). Accordingly, organic nutrient sources 515 were likely very limited in the pigment incubations, potentially restricting bacterial activity, driving utilisation of 516 ~ 20 % of carbon. In contrast, incubations spiked with nitrogen and phosphorus (+Nutrients) exhibited much greater bacterial growth and a ~ 10 % increased BDOC, thus additional nutrients likely facilitated a greater 517 518 exploitation of carbon sources.





520 Although glacier algal secondary pigment could represent a substantial carbon source within the surface ice during 521 bloom events, the mechanism of pigment release remains unconstrained. Given the metabolic cost of producing 522 this secondary pigment and its essential role protecting the cell from photodamage, it is unlikely to be actively 523 excreted by glacier algae. Alternative mechanisms of release may include passive leakage or lysis of cells due to 524 natural senescence or viral/fungal attack (Dodds, 2010; Sigee, 2004; Zlotnik and Dubinsky, 1989); however, the 525 degree of leakage and mortality rate of glacier algae remains unconstrained. Overall, biodegradation incubations 526 revealed that glacier algal phenolic pigment is largely unavailable to heterotrophic bacterial communities from 527 the surface ice of the GrIS. Despite this, algal pigment may represent a viable carbon source for Archaea or fungi 528 within the surface ice community and further investigation is therefore required to reveal the fate of this carbon 529 source.

530

531 4.2 Surface ice DOM

532 To the best of our knowledge, this is the first spectroscopic characterisation of surface ice DOM from the Dark 533 Zone of the Greenland Ice Sheet. Our results highlight remarkable similarities in absorption characteristics 534 between surface ice and pigment DOM indicating the presence of purpurogallin carboxylic acid and gallic acid 535 glycoside in surface ice. This may be a result of natural glacier algal cell lysis; however, we also acknowledge 536 that algal cells may have lysed during experimental set up, releasing pigment and thus further in situ investigations 537 are required to clarify whether this is representative. Despite this, purpurogallin carboxylic acid and gallic acid 538 glycoside were some of the most strongly light absorbing compounds, therefore the release of even small 539 concentrations of pigment to the ambient environment could substantially alter the optical properties of surface 540 meltwater. Surface ice DOM exhibited predominantly humic-like fluorescence dominated by peaks A and C; both 541 of which are often associated with the presence of HMW, aromatic DOM of terrestrial plant or soil origin (Coble, 542 1996; Coble et al., 1990; Fellman et al., 2010). This is surprising given the high levels of primary production by 543 glacier algae reported from the surface ice (Williamson et al., 2018; Yallop et al., 2012) and the relatively low 544 input of carbon from allochthonous sources in our sampling region on the GrIS (Stibal et al., 2012). However, 545 peaks A and C have also been observed following bacterial degradation of autochthonous DOM (Stedmon and 546 Markager, 2005) and it is therefore possible that surface ice DOM had already undergone a degree of 547 biodegradation prior to sampling. Equally, the formation of humic-like DOM following photodegradation of algal-548 derived DOM is widely reported (Amado et al., 2015; Stefan et al., 2000; Tranvik and Kokalj, 1998). Carbon 549 transformation and cycling within the surface ice is thus highly dynamic, with rapid production and consumption 550 of bioavailable compounds via biotic and abiotic processes.

551

The exposure of surface ice to UV and PAR radiation resulted in a number of compositional changes to DOM. Purpurogallin carboxylic acid and gallic acid glycoside were susceptible to degradation on exposure to UV radiation and responsible for the major shifts in absorption and SUVA indices. An increased proteinaceous signature dominated by peak B in UV-irradiated surface ice indicated that UV radiation degraded high molecular weight (HMW) humic DOM into smaller, more bioavailable compounds. This is widely reported from other highlight aquatic environments and was found to stimulate bacterial production and growth (Amado et al., 2015; Anesio et al., 2005; Lindell et al., 1995; Zepp and Moran, 1997). Along with UV radiation, PAR was also found





559 to alter the chemical structure of surface ice DOM, with decreased SUVA254 and SUVA365 representing a lower 560 proportion of aromatic DOM compared to DARK treatment samples. A greater proportion of humic-like fluorescence, characterised by a lack of peak T and a dominant peak M, in PAR- and UV+PAR- irradiated surface 561 ice suggested that proteinaceous DOM is converted to LMW, humic-like DOM by PAR. It is likely that in the 562 563 UV+PAR treatment, these opposing processes (the degradation and formation of humic-like DOM) are occurring 564 simultaneously, with formation driven by PAR representing the dominant process. This contrasts with the findings 565 of Antony et al., (2018); however, may simply represent the difference in DOM composition between surface ice of the GrIS and snow in Antarctica. Although DOC concentrations were consistent across light treatments, we 566 567 have demonstrated that surface ice DOM undergoes structural and compositional changes following exposure to 568 UV and PAR.

569

570 Biodegradation incubations revealed that the heterotrophic bacteria community was able to extensively rework 571 surface ice DOM. The DARK surface ice exhibited increased SUVA indices, confirming that bacteria primarily 572 consume aliphatic, LMW compounds (Antony et al., 2018; Hansen et al., 2016; Kirchman, 2003). This was further 573 corroborated by an increase in peak M fluorescence and humification (HIX), highlighting preferential bacterial 574 consumption of proteinaceous surface ice DOM and production of LMW humic-like DOM (Murphy et al., 2008). 575 Although purpurogallin carboxylic acid and gallic acid glycoside were degraded across all treatments, absorption 576 was still evident demonstrating that these compounds were less rigorously degraded than in the pigment 577 incubations. This may indicate that degradation of these compounds is metabolically intensive and comparatively 578 less attractive in the presence of alternative carbon sources. The degradation of these compounds within surface 579 ice DOM supported substantial increases in bacterial abundance throughout incubations. It is likely that the greater 580 diversity of DOM compounds in surface ice provided a plethora of substrates that facilitated growth across a broader range of bacterial species within the community (Antony et al., 2017; Smith et al., 2018). BGE in surface 581 582 ice was highly comparable with that in glacier forefields (Bradley et al., 2016) and 3-times higher than within 583 supraglacial streams (Foreman et al., 2013). Bacteria are thus capable of assimilating a greater proportion of 584 bioavailable carbon from the surface ice compared to supraglacial streams.

585

586 Following the biodegradation of photodegraded surface ice, substantial variability in absorbance and fluorescence 587 across light treatments was observed, highlighting the impact of photodegradation on bacterial DOM 588 consumption. For example, UV-irradiated surface ice retained the greatest proportion of aromatic DOM, whereas PAR and UV+PAR retained the least. Additionally, UV- and PAR-irradiated surface ice exhibited a greater 589 590 proteinaceous signature than DARK, indicating that bioavailable DOM was not as readily consumed in these 591 incubations. Bacterial communities in surface ice are genetically diverse (Perini et al., 2019) and as such, are 592 likely capable of consuming a range of substrates (Fernández-Gómez et al., 2013; Kirchman, 2003). Thus, the 593 community may be consuming different DOM components across light treatments and it is possible that 594 genetically distinct communities develop as a result (Mahmoudi et al., 2017; Smith et al., 2018). We also observed 595 much greater increases in bacterial abundance in irradiated surface ice between 6 and 17 days of incubation 596 compared to DARK. Solar radiation has been observed to increase nitrogen, sulphur and phosphorus 597 bioavailability in organic compounds (Antony et al., 2018) and the formation of inorganic nitrogen on exposure 598 to UV radiation has been widely reported (Bushaw et al., 1996; Wang et al., 2000; Xie et al., 2012). Irradiated





599 surface ice may have contained a greater nutrient concentration that stimulated more rapid bacterial growth. 600 Despite this, the quantity of carbon consumed by bacteria did not differ across light treatments indicating that 601 consumption may be limited by a factor other than DOM composition, such as temperature; however, further 602 research is required to understand this. Our results therefore indicate that although photodegradation does alter 603 DOM composition, bacteria in the surface ice are adept at utilising a range of carbon sources to facilitate growth. 604

605 5 Conclusions

The results from this study reveal the complex interaction between photodegradation and biodegradation in 606 607 altering the composition and quantity of secondary phenolic pigment (purpurogallin carboxylic acid-6-O-β-Dglucopyranoside) extracted from glacier algae and surface ice DOM. Both carbon sources are susceptible to 608 609 photodegradation, particularly on exposure to UV radiation, which caused the largest compositional changes to 610 DOM. This is especially important given the potential for ozone holes over the Arctic and subsequent extreme 611 levels of UV radiation that may result (Manney et al., 2011). Our results indicate that glacier algae secondary 612 phenolic pigment contains components that can be degraded by surface ice bacterial communities; however, 613 degradation may be metabolically intensive and therefore pigment is likely not the primary source of carbon 614 within this system. We also hypothesise that glacier algal pigment may exhibit antimicrobial properties which 615 inhibit the growth of specific bacterial species. In contrast, surface ice DOM supported extensive bacterial growth 616 likely due to the wider variety of DOM compounds available. Despite compositional changes to both glacier algal 617 phenolic pigment and surface ice DOM following photodegradation, we did not observe any difference in 618 consumption by the bacteria community suggesting that the bioavailability of DOM was not influenced by 619 exposure to UV or PAR. Photodegradation and biodegradation of surface ice DOM are likely intimately linked 620 within the surface ice habitat and act as fundamental controls on the composition and quantity of DOM exported 621 to downstream environments.

622

623 Data availability

All data is available via the Polar Data Centre (<u>https://www.bas.ac.uk/data/uk-pdc/</u>). DOI TO BE MINTED
 AFTER REVIEW PROCESS.

626

627 Team list

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 Andrew Tedstone, Jason Box and Marek Stibal.

632

633 Author contribution

634 MN, CW and AA conceived and designed the study. AH aided MN with sampling during the incubation

experiment. Sample analysis and data presentation was conducted by MN with supervision from CW, AA, MT

and MY. MN wrote the manuscript with inputs from CW and AA, all authors reviewed the final manuscript.





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- 638 Competing interests
- 639 The authors declare that they have no conflict of interest.
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- 851 Appendices 6
- 852 Appendix A

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Table A1: Bioavailable DOC (BDOC; %) and bacterial growth efficiency (BGE; %) for the pigment and surface ice across light treatments and in the normal and +nutrient treatments (mean \pm SE, n=5 for BDOC and n=3 for BGE). Significant differences were only found in %BDOC for pigment across light treatments per nutrient treatment (i.e.

854 855 856 857 858 normal or +Nutrients) denoted lower case letters and between nutrient treatments per carbon source, denoted by upper

case letters.

| Carbon | Light | BD | OC (%) | BGE (%) | | |
|----------------|--------|-------------------------------|---------------------------|-------------|---------------|--|
| source | Light | Normal | + Nutrients | Normal | + Nutrients | |
| | UV | $^a21\pm8.1^A$ | $^{ab}27\pm6.0~^{A}$ | 2.9 ± 3.7 | 7.9 ± 4.1 | |
| D: (| PAR | a 21 \pm 4.2 $^{\rm A}$ | $^a6.4\pm17$ A | 1.9 ± 1.4 | 3.1 ± 1.1 | |
| Pigment | UV+PAR | ^b 0 ^A | $^{ab}28\pm3.0^{B}$ | 7.8 ± 2.7 | 2.4 ± 1.4 | |
| | DARK | $^{ab}9.3\pm6.2^{\mathrm{A}}$ | $^b39\pm8.6^{\mathrm{B}}$ | 0.1 ± 1.3 | 3.4 ± 2.5 | |
| Surface ice | UV | 27 ± 0.9 | 32 ± 1.8 | 2.3 ± 0.8 | 4.1 ± 1.2 | |
| | PAR | 33 ± 1.2 | 30 ± 2.3 | 11 ± 0.6 | 5.8 ± 2.8 | |
| | UV+PAR | 31 ± 2.3 | 31 ± 2.0 | 7.0 ± 2.3 | 13 ± 7.2 | |
| | DARK | 33 ± 2.5 | 35 ± 3.5 | 6.7 ± 2.5 | 3.5 ± 0.6 | |