

1 **Identification and analysis of low molecular weight**
2 **dissolved organic carbon in subglacial basal ice**
3 **ecosystems by ion chromatography**

4
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19
20 **Abstract**

21 Determining the concentration and composition of dissolved organic carbon (DOC) in glacial
22 ecosystems is important for assessments of in situ microbial activity and contributions to
23 wider biogeochemical cycles. Nonetheless, there is limited knowledge of the abundance and
24 character of DOC in basal ice and the subglacial environment and a lack of quantitative data
25 on low molecular weight (LMW) DOC components which are believed to be highly
26 bioavailable to microorganisms. We investigated the abundance and composition of DOC in
27 basal ice via a molecular level DOC analysis. Spectrofluorometry and a novel ion
28 chromatographic method, which has been little utilised in glacial science for LMW-DOC
29 determinations, were employed to identify and quantify the major LMW fractions (free

30 amino acids, carbohydrates and carboxylic acids) in basal ice from four glaciers, each with a
31 different type of overridden material (i.e. the pre-entrainment sedimentary type such as
32 lacustrine material or paleosols). Basal ice from Joyce Glacier (Antarctica) was unique in that
33 98% of the LMW-DOC was derived from the extremely diverse free amino acids (FAA)
34 pool, comprising 14 FAAs. LMW-DOC concentrations in basal ice were dependent on the
35 bioavailability of the overridden organic carbon (OC), which in turn, was influenced by the
36 type of overridden material. Mean LMW-DOC concentrations in basal ice from Russell
37 Glacier (Greenland), Finsterwalderbreen (Svalbard) and Engabreen (Norway) were low (0 -
38 417 nM C), attributed to the relatively refractory nature of the OC in the overridden paleosols
39 and bedrock. In contrast, mean LMW-DOC concentrations were an order of magnitude
40 higher (4430 nM C) in basal ice from Joyce Glacier, a reflection of the high bioavailability of
41 the overridden lacustrine material (>17% of the sediment OC comprised extractable
42 carbohydrates, a proxy for bioavailable OC). We find that the overridden material may act as
43 a direct (via abiotic leaching) and indirect (via microbial cycling) source of DOC to the
44 subglacial environment and provides a range of LMW-DOC compounds that may stimulate
45 microbial activity in wet subglacial sediments.

46

47 **1. Introduction**

48 Basal ice forms part of the subglacial environment, which also includes subglacial sediments
49 and subglacial waters (Hodson et al., 2008). It hosts viable microbial communities that may
50 play a significant role in the organic carbon (OC) turnover in glaciated regions (Sharp et al.,
51 1999; Skidmore et al., 2000; Foght et al., 2004). Basal ice is typically defined as ice that has
52 acquired distinctive physical and/or chemical characteristics due to processes operating at or
53 near to the bed of an ice mass (Hubbard et al., 2009). Basal ice layers may comprise ice and
54 debris entrained from beneath the glacier and meteoric ice derived from the surface and
55 diagenetically modified by hydraulic, thermal and strain conditions at the glacier bed (Knight
56 et al., 1997). A range of processes can form basal ice, which we highlight briefly. For
57 instance, new basal ice may form from basal accretion of supercooled subglacial water, a
58 freeze-on (or adfreezing) mechanism (Lawson et al., 1998), or by regelation, the localised
59 melting and refreezing of ice at the glacier bed, e.g. around a bedrock obstacle, which
60 represents an important mechanism to entrain subglacial debris into the basal ice (Iverson and
61 Semmens, 1995). Sediment may also be incorporated into basal ice by folding (Hubbard and
62 Sharp, 1989), cavity/crevasse infilling, structural deformation, thrusting, traction/shearing

63 and metamorphism of existing ice at the glacier bed (Knight et al., 1997). Metamorphosis of
64 meteoric glacier ice can thicken basal ice layers (Sharp et al., 1994) and post-formational
65 tectonic deformation of basal ice can cause intermixing of glacier and basal ice (Waller et al.,
66 2000).

67

68 The chemical composition of basal ice reflects characteristics of the parent water prior to
69 being frozen (Knight, 1997). In temperate and polythermal glaciers, this may include
70 supraglacial inputs, whereas in cold-based glaciers where there is little surface meltwater
71 penetration, the majority of meltwater at the glacier bed likely derives from basal ice melting.
72 This water may flow at the base of the glacier, be held in porewaters in overridden water-
73 saturated sediment or represent refrozen water from pressure melting during the regelation
74 process. The parent water has potential to acquire dissolved compounds (including DOC and
75 LMW-DOC) via biogeochemical interactions with the overridden subglacial material. To
76 date, there has been only limited examination of the potential for different bedrock types and
77 overridden organic matter, such as paleosols and lacustrine material (Wadham et al., 2008;
78 Stibal et al., 2012), to act as a source of bioavailable DOC to basal ice, subglacial meltwaters
79 and runoff, either directly (via abiotic leaching or in situ abiotic processes such as dissolution
80 in water films around basal debris and in liquid water veins (Mader et al, 2006)) or indirectly
81 (via microbial cycling). Further knowledge is needed to determine the abundance and
82 composition of potentially bioavailable LMW-DOC in basal ice at the base of glaciers and ice
83 sheets and the implications this may have on subglacial DOC cycling.

84

85 OC cycling in the subglacial environment can be investigated by incubation experiments that
86 monitor DOC decline and/or biogenic gas (CO₂ and CH₄) production (Montross et al., 2012;
87 Stibal et al., 2012) and provide a direct measure of bioavailability. Analysis of marker
88 compounds in the DOC, such as free amino acids (FAAs) (Pautler et al., 2011), may provide
89 an indirect assessment of bioavailability. These analyses may be complemented by
90 fluorescence spectroscopy, where fluorescing components (fluorophores) are identified and
91 associated with particular DOC compounds, e.g. protein-like and humic-like components.
92 The protein-like compounds are more easily utilized by aquatic heterotrophs when compared
93 with the more aromatic humic-like components (Fellman et al., 2008) and are indicative of
94 recent microbial activity (Barker et al., 2006, 2010). More recently, glacial DOC has been

95 characterised at the molecular level by electrospray ionization (ESI) Fourier transform ion
96 cyclotron resonance (FT-ICR) mass spectrometry (MS) (Grannas et al., 2006; Bhatia et al.,
97 2010; Lawson et al., 2014a), and by solution-state ¹H nuclear magnetic resonance (NMR)
98 spectroscopy (Pautler et al., 2011; 2012). Both methods have provided unprecedented high
99 resolution mass spectral information on DOC, but are not fully quantitative. Ion
100 chromatography has been used to quantify a much smaller range of common LMW-DOC
101 compounds, including carboxylic acids in ice cores and snow from Greenland, Antarctica,
102 and alpine glaciers (Saigne et al., 1987; Maupetit and Delmas 1994; Tison et al., 1998). These
103 LMW-DOC compounds typically represent small fractions of the bulk DOC (Borch and
104 Kirchmann, 1997), yet are believed to be highly bioavailable to microorganisms owing to
105 their rapid turnover and uptake rates (Rich et al., 1997; Skoog and Benner, 1997). Ion
106 chromatography has yet to be widely employed to determine the molecular structure of
107 glacial LMW-DOC due to the trace analyte concentrations (Lawson et al., 2014b). Recent
108 advances in ion chromatography instrumentation and system optimisation (e.g. greater
109 column sensitivities, low flow rates, multiple eluents and gradient elution) enabled this study
110 to identify and quantify numerous LMW-DOC compounds at low (<70 nM C)
111 concentrations, and demonstrates a novel methodological approach to glacial LMW-DOC
112 analysis.

113

114 Here, we investigate the abundance and composition of LMW-DOC compounds (free amino
115 acids, carbohydrates and carboxylic acids) in debris-rich basal ice. We investigate four
116 different glaciers with distinct temperature regimes, overridden substrates, and hence,
117 contrasting sources of terrestrial organic matter. These glaciers were Joyce Glacier
118 (Antarctica – lacustrine organic matter, cold-based), Russell Glacier (Greenland Ice Sheet,
119 GrIS – paleosols, polythermal), Finsterwalderbreen (Svalbard – bedrock with high OC,
120 polythermal), and Engabreen (Norway – bedrock with low OC, temperate). We investigate
121 whether LMW-DOC abundance in basal ice is influenced by the magnitude and bioreactivity
122 of the OC in the overridden material.

123

124 **2. Sampling sites, basal ice description and sample collection**

125 **2.1. Joyce Glacier, Antarctica**

126 Joyce Glacier (67°06'S, 50°09'W, 90 km²) is situated in the Garwood Valley, Antarctica. A
127 large proglacial lake, dammed by an ice sheet grounded in the McMurdo Sound >23,000 ¹⁴C
128 yr BP (Péwé, 1960; Hendy, 2000), is thought to have previously occupied the valley (Hendy,
129 2000). Joyce Glacier is cold-based, meaning that it is completely frozen to the underlying
130 substrate. The bedrock lithology includes dolomite, granite and metamorphic rocks. Joyce
131 Glacier recently advanced over lake sediment (Stuiver et al., 1981) and hence, the basal
132 material is thought to contain labile OC and algal-derived organic matter of Holocene age.

133 **2.2. Russell Glacier, GrIS**

134 Russell Glacier (67°03'N, 50°10'W, >600 km²), situated on the west margin of the GrIS, is
135 polythermal-based. Warm ice, with a temperature at the pressure melting point, in the interior
136 is surrounded by a frozen layer beneath the thinner ice of the margins. Surface melting
137 delivers supraglacial meltwaters to the subglacial system from the onset of the spring thaw.
138 The bedrock is predominantly Archaean gneiss (Escher and Watt, 1976). Basal debris
139 contains overridden Quaternary deposits (including paleosols), and relatively fresh organic
140 matter (Knight et al., 2002), which was buried during the Holocene (Simpson et al., 2009).

141 **2.3. Finsterwalderbreen, Svalbard**

142 Finsterwalderbreen (77°28'N, 15°18'E, 44 km²) is located on the southern side of Van
143 Keulenfjorden, south Svalbard, and is a polythermal surge-type glacier. Finsterwalderbreen
144 last surged between 1898 and 1920 (Liestøl, 1969) which may have influenced the formation
145 of the basal ice as has been shown, for example, at Variegated Glacier (Sharp et al., 1994).
146 The glacier is currently retreating at a rate of 10-45 m a⁻¹ (Wadham et al., 2007). The bedrock
147 consists of Precambrian carbonates, sandstones, limestones and shales (Dallmann et al.,
148 1990). Shales exposed to water may provide a steady source of DOC (Schillawski and Petsch,
149 2008). The shale beneath Finsterwalderbreen contains up to 2.3 % OC (Wadham et al., 2004).

150 **2.4. Engabreen, Norway**

151 Engabreen (66°41'N, 13°46'E, 40 km²) is temperate and part of the western Svartisen ice cap,
152 northern Norway. Engabreen bedrock consists mostly of schist and gneiss, with calcite filled
153 cracks (Jansson et al., 1996), and contains relatively little OC. A combination of in-washed
154 material from the glacier surface and overridden soils of Holocene age may be the principal
155 OC sources (Stibal et al., 2012).

156 **2.5 Basal ice description and sample collection**

157 Joyce Glacier basal ice samples were collected in the austral summer of 2010 from recently
158 exposed, upthrust bands of debris-rich basal ice at the margin on the southern flank of the
159 glacier. Basal ice was sampled where the facies were composed of frozen debris and only
160 weakly exhibited layers that were >1 mm thick but < 1m thick, classified as solid banded
161 basal ice (Hubbard et al., 2009). We assume that the basal ice was formed under cold-based
162 conditions.

163

164 Debris-rich basal ice blocks from the Russell Glacier margin were collected in spring 2008.
165 Samples were collected from the southern corner of the glacier where it has previous
166 advanced into a dune and from within 1.5 m of the ice-bed contact. The basal ice samples
167 contained subglacial sediment that had been extruded up from the glacier bed via fissures
168 near the terminus. This comprised banded basal ice where the debris was generally restricted
169 to narrow sediment layers and large vein networks were clearly evident. As Russell Glacier is
170 polythermal, we assume that the basal ice was formed by a combination of regelation and
171 cold-based processes such as basal adfreezing onto the glacier sole.

172

173 Finsterwalderbreen was sampled in autumn 2008. Basal ice blocks were collected from the
174 terminus on the northern flank of the glacier from sections of dispersed banded basal ice
175 (referred to as DB basal ice), within 1.5 m of the ice-bed contact, and from surface outcrops
176 of frozen subglacial material, or thrust bands, with distinct debris layers (referred to as solid
177 banded (SB) basal ice). It is probable that the thrust bands were formed during the most
178 recent surge during two phases of thrusting; primary thrusting during the early surge phase in
179 the subglacial zone between temperate ice and cold ice, and secondary thrusting during the
180 surge termination due to ice flow compression, as envisaged for the similar polythermal
181 surge-type Kuannersuit Glacier (Larsen et al., 2010). Finsterwalderbreen DB and SB basal
182 ice are reported separately due to the very different mean debris concentrations (by mass); 20
183 $\pm 27\%$ (DB basal ice) and $86 \pm 6\%$ (SB basal ice, where the debris component was much
184 higher). As Finsterwalderbreen is polythermal, we assume that the basal ice was formed by a
185 combination of regelation and cold-based processes. Basal ice samples from
186 Finsterwalderbreen and Russell Glacier were collected from the same sites as the samples
187 that were analysed in Stibal et al., (2012) and hence, we use their ^{14}C ages (Table 2).

188

189 Debris-rich basal ice samples from Engabreen were collected in autumn 2009 from an
190 underground tunnel system excavated through bedrock beneath 210 m of sliding ice (Cohen,
191 2000). The basal ice stratigraphy comprises sediment-rich ice layers overlain by clean
192 sediment-free and bubble-free ice (Jansson et al., 1996). We collected samples from sections
193 of banded basal cryofacies from within 1.5 m of the ice-bed contact. Hot-water drilling was
194 first implemented to create a basal cavity and the ice subsequently extracted by chain-sawing
195 (described below). As Engabreen is temperate, we assume that the basal ice was formed
196 primarily by regelation (Jansson et al., 1996).

197

198 Basal ice blocks ($\sim 40 \text{ cm}^3$) were collected by chain-sawing in all sample locations. The
199 outermost $\sim 0.5 \text{ m}$ of the ice surface was removed before the blocks were cut. The blocks
200 were wrapped in pre-combusted foil and stored at $\leq -20 \text{ }^\circ\text{C}$, before being transported frozen to
201 the University of Bristol and subsequently stored at $\leq -20 \text{ }^\circ\text{C}$.

202

203 **3. Methodology**

204 **3.1. Basal icemelt and sediment sample preparation**

205 Subsamples of the basal ice were prepared for analysis by chipping $\sim 15 \text{ cm}^3$ chunks from the
206 main block using a flame sterilised chisel. The outer $\sim 10\text{-}30 \text{ mm}$ of the chips was removed by
207 rinsing with ultrapure ($\geq 18.2 \text{ M}\Omega\text{cm}$) deionized water (DI) (Millipore), and the remaining ice
208 was transferred into a pre-combusted glass beaker covered with foil. The ice was allowed to
209 melt inside a laminar flow cabinet (Telstar Mini-H) under ambient laboratory conditions,
210 which allowed any sediment to settle out of suspension. The icemelt was then decanted into
211 smaller pre-combusted beakers. Icemelt was filtered through Whatman polypropylene
212 Puradisc™ $0.45 \text{ }\mu\text{m}$ syringe filters. Water samples for subsequent OC analysis were stored in
213 clean pre-combusted borosilicate glass bottles (thrice rinsed with the sample before storage).
214 Five samples of filtered icemelt were taken from the $\sim 15 \text{ cm}^3$ chunks cut out of the Joyce
215 Glacier basal ice block, the Finsterwalderbreen DB ice block, and the Finsterwalderbreen SB
216 ice block. Slightly larger volumes of icemelt permitted six samples of filtered icemelt to be
217 collected from the Engabreen basal ice chunk, and seven from the Russell Glacier chunk. DI
218 procedural blanks ($n = 5$) were subject to identical processing as the samples from the
219 filtration stage onwards to monitor for possible contamination during processing and storage.
220 Sample concentrations were subsequently blank corrected (see Sect. 3.3.4).

221

222 Sub-samples from each ice block were also collected for free carboxylic acid (FCA)
223 determination. Ice was melted in an inert gas (O₂-free-N₂, OFN) atmosphere to limit potential
224 contamination during the melting process (Saigne et al., 1987). The OFN gas first travelled
225 through a hydrocarbon trap (HT200-4, Agilent) to remove any volatile OC compounds.
226 Icemelt was filtered through Whatman polypropylene Puradisc™ 0.45 µm syringe filters into
227 1.5 mL vials with PTFE caps (Chromacol). Samples were analysed within 24 hours of
228 melting to minimise losses due to the volatile nature of the FCA compounds. Procedural
229 blanks were collected in concert.

230

231 The subglacial sediment OC content was derived from analysis of the settled particles, which
232 were transferred from the beakers with clean, ethanol-rinsed metal spatulas and stored in
233 sterile 0.5 L Whirl-pak bags (Nasco). Every effort was made to collect as much of the finer
234 sediment as possible from the bottom and sides of the beakers. However, some fine sediment
235 may have remained in the beaker and were thus excluded from the OC determinations. We
236 were also unable to collect the fine particles that remained in suspension owing to the use of
237 syringe filters to filter the icemelt. The total mass of this finer sediment was small compared
238 to the mass of the settled sediment; therefore OC determinations were not unduly
239 compromised. Sediment and filtered samples were stored in the dark at ≤-20°C until
240 analytical processing.

241 **3.1.1 Basal ice debris concentration**

242 Basal ice debris concentrations (% by mass) were determined by mass subtraction. Basal ice
243 debris typically comprised sediment particles predominantly <2 mm plus some small gravel
244 in the Finsterwalderbreen SB samples. First, the melted basal ice samples (sediment +
245 icemelt) were weighed and the sediment extracted according to the procedure described
246 above. The sediment was dried in a hot air oven (105 °C) for a minimum of 12 hours and
247 weighed. The basal ice debris concentration was expressed as a percentage of a mass (of
248 sediment) to mass (total mass of ice and sediment) basis.

249 **3.2. Basal sediment analysis**

250 **3.2.1. Elemental analysis**

251 The subglacial sediments were first dried in a hot air oven (105 °C, 12 hours) and then
252 manually homogenized by grinding. Total carbon (TC) was measured on an EA1108
253 Elemental Analyser (EuroVector). Inorganic carbon (InC) was determined by a modified
254 Coulomat 702 Analyser (Strohlein Instruments). Total OC was calculated as the difference
255 between TC and InC. The precision of determinations was <5%. Samples were calibrated
256 using external reference standards at a detection limit of 0.1 mg g⁻¹ (or 0.01%).

257 **3.2.2. Carbohydrate sediment extractions**

258 Previous studies have estimated sediment OC bioavailability based on the concentration of
259 extractable carbohydrates (Biersmith and Benner, 1998; Pusceddu et al., 2009). We employed
260 this method to provide a conservative estimate and acknowledge that this is not a
261 comprehensive assessment of bioavailable OC in the subglacial material, as other
262 compounds, such as enzymatically hydrolysable amino acids, were not quantified.
263 Operationally-defined minimum estimates of extractable carbohydrate concentrations in basal
264 sediment were quantified by ion chromatography following an acid-extraction protocol to
265 convert any polysaccharides and sugar derivatives to lower molecular weight components
266 (Jensen et al., 2005). We followed the protocol described in (Stibal et al., 2010) and
267 conducted each extraction procedure in triplicate. Monosaccharide losses occurred during
268 hydrolysis, including the total loss of fructose, and were not compensated for (Borch and
269 Kirchmann, 1997; Jensen et al., 2005). This methodological limitation means that some of the
270 variability between samples will be due to procedural effects, rather than a true disparity
271 between sediment carbohydrate concentrations.

272 **3.2.3. Cell counts**

273 Cell counts were conducted to quantify the microbial abundance in basal sediment and
274 determine whether there is potential for subglacial microbial activity. We followed the
275 protocol described in (Stibal et al., 2012). For Joyce Glacier samples, the method followed
276 that of (Porter and Feig, 1980) (detailed in the Supplementary Methods).

277 **3.3 Analysis of basal icemelt**

278 **3.3.1. Bulk DOC**

279 DOC was determined by high temperature combustion (680°C) using a Shimadzu TOC-
280 V_{CSN}/TNM-1 Analyzer equipped with a high sensitivity catalyst. Precision and accuracy of
281 standard solutions (5-170 µM C) of potassium hydrogen phthalate (C₈H₅KO₄) (Merck) were
282 < ± 6%, and the limit of detection (LOD) was 5 µM C.

283 **3.3.2. Fluorescence spectroscopy**

284 Fluorescence spectra were determined on a HORIBA Jobin Yvon Fluorolog-3
285 spectrofluorometer equipped with excitation and emission monochromators, a Xenon lamp
286 (excitation source) and FluorEssence software. Synchronous scans were performed at 1 nm
287 increments with a 0.1 s integration period, 10 nm bandwidth and an 18 nm offset between
288 excitation and emission monochromators (Barker et al., 2006). The accuracy of the
289 monochromators was ± 0.5 nm. Synchronous scans of DI were run under identical scanning
290 conditions and subtracted from all sample spectra to correct for Raman scattering. All scans
291 were dark corrected and internally corrected for inner filter effects and variations in lamp
292 performance. Post-scan data correction followed the protocol described by (Barker et al.,
293 2006). Fluorophore recognition was based on values reported in the literature (Miano and
294 Senesi, 1992; Ferrari and Mingazzini, 1995; Coble, 1996; Yamashita and Tanoue, 2003) and
295 all spectra were normalized to the sample fluorescence peak spectral maximum.

296 **3.3.3. OC compound determination by ion chromatography**

297 Free amino acid (FAA), carbohydrate (FCHO) and carboxylic acid (FCA) determinations
298 were performed by an ICS-3000 dual-analysis reagent-free ion chromatography system,
299 employing electrolytic NaOH eluent generation (Dionex™, part of Thermo Fisher Scientific).
300 Precision and accuracy were monitored by periodically running certified external standards
301 (Dionex™), and internal standards during each sample run, at concentrations within the range
302 of sample concentrations (10 - 2000 nM C). The limit of quantification (LOQ) was defined as
303 the concentration of the lowest standard that could be significantly differentiated from the
304 next highest. The 28 basal ice samples and five DI blanks were analysed in small batches. To
305 limit any potential change in analyte abundance or composition over the course of the batch
306 analysis due to inorganic or organic activity within the sample vial, we typically ran 8-10
307 samples (plus standards and DI to flush the system) during each run. Prior to running the
308 samples we assessed the level of drift (which may account for instrumental drift plus changes

309 in LMW-DOC compounds) in a low level standard ($50 \mu\text{g L}^{-1}$) and found that *c.* 21 samples
310 could be run before significant drift (exceeding the precision of the instrument) was noted.
311 Due to the scarcity of sample volume we were unable to explore whether LMW-DOC
312 concentrations in each sample changed over the course of the sample run.

313

314 **FAA:** were separated via gradient anion exchange on an AminoPac PA10 column (2x250
315 mm) after passing through an AminoPac PA10 guard column (2x50 mm). Pulsed
316 electrochemical detection with an Au electrode was employed. A gradient mix of 0.25 M
317 NaOH, 1.0 M Na-acetate (NaOAC) and DI was used to elute 14 FAAs (lysine, alanine,
318 threonine, glycine, valine, serine/proline, isoleucine, leucine, methionine, phenylalanine,
319 cysteine, aspartic acid, glutamic acid and tyrosine) at a flow rate of 0.25 mL min^{-1} . Serine and
320 proline were reported together due to co-elution. Precision was typically *c.* $\pm 5\%$ for lysine,
321 alanine, threonine, glycine, valine, serine/proline, isoleucine, leucine, methionine, and
322 cysteine, and *c.* $\pm 10\%$ for phenylalanine, aspartic acid, glutamic acid and tyrosine. Accuracy
323 was $< \pm 7\%$ for all analytes (certified external standard, Fluka Analytical). The LOQ ranged
324 from 10-60 nM C.

325

326 **FCHO:** fucose, rhamnose, arabinose, galactose, glucose, xylose/mannose, fructose/sucrose,
327 ribose and lactose were separated isocratically at a flow rate of 0.35 mL min^{-1} on a CarboPac
328 PA20 column (3x150 mm) after passing through a CarboPac PA20 guard column (3x30 mm).
329 Xylose and mannose, and fructose and sucrose, were reported together due to co-elution.
330 Precision for fucose, rhamnose, arabinose, glucose and xylose/mannose was generally *c.* \pm
331 5% , and *c.* $\pm 10\%$ for galactose, fructose/sucrose, ribose and lactose. Accuracy of a certified
332 external standard (Dionex™) was $< \pm 7\%$ for all analytes. The LOQ ranged from 10-80 nM
333 C.

334

335 **FCA:** acetate, formate, propionate and butyrate were separated via gradient anion exchange
336 on an IonPac Hydroxide-Selective Anion Exchange AS11-HC column (2x250 mm) with an
337 AS11-HC guard column (2x50 mm) and Anion Self-Regenerating Suppressor (ASRS).
338 Electrolytic eluent generation was employed to allow analyte separation along a NaOH
339 gradient during the 30 minute run at a flow rate of 0.5 mL min^{-1} . Precision and accuracy of
340 the four FCAs in a certified reference standard (Supelco Analytics) was 5-8% (precision) and
341 3-4% (accuracy). The LOQ ranged from 90-130 nM C.

342 **3.3.4. Blank corrections**

343 Preparation of DI blanks is described in Sect. 3.1. Blank corrections were not required for
344 FAAs due to the negligible blank concentrations. Minimal corrections were required for
345 FCHOs (1.3 nM C), but larger corrections were required for DOC (5.85 μ M C) and FCAs
346 (23.06 nM C).

347

348 **4. Results**

349 **4.1. Basal sediment characteristics**

350 Basal ice debris concentrations (by mass) differed between glaciers. Finsterwalderbreen solid
351 banded (FSB) and Russell Glacier basal ice contained the highest concentration of debris (86
352 \pm 7% and 55 \pm 25%, Table 1), which are similar to percentages in GrIS banded ice (46-57%),
353 solid ice (61%) (Yde et al., 2010) and debris bands (71%) (Sugden et al., 1987). Debris
354 concentrations in basal ice from Engabreen (37 \pm 21%), Joyce Glacier (21 \pm 6%), and
355 Finsterwalderbreen dispersed banded (FDB) (20 \pm 27%) were lower than percentages in GrIS
356 and FSB ice.

357

358 We investigated possible correlations between DOC (and LMW-DOC) and the debris content
359 of the basal ice, which may provide information on DOC provenance and the potential for
360 DOC to leach from sediments into the basal ice. We acknowledge that if DOC is leached
361 from sediments the controlling variable will be the surface area, rather than the debris
362 concentration. However, a detailed investigation into the particle size distribution was beyond
363 the scope of this study. We thus conducted a preliminary analysis to determine if the
364 relationship with debris concentration differed for DOC and LMW-DOC. Significant positive
365 associations between debris concentration and DOC were only evident in Joyce Glacier ($R^2 =$
366 0.71, $p < 0.05$) and Russell Glacier ($R^2 = 0.72$, $p < 0.05$) basal ice (Figure 1a). No significant
367 associations between LMW-DOC and debris concentrations were observed (Figure 1b, $R^2 <$
368 0.1, $p < 0.05$).

369

370 The sediment OC content was low (<0.6%) in all basal ice samples (Table 2). Minor fractions
371 of extractable carbohydrate (<0.5% of the sediment OC) were measured in Engabreen,
372 Russell Glacier and Finsterwalderbreen sediments. A higher carbohydrate fraction (17% of
373 the sediment OC) was measured at Joyce Glacier (Table 2). We use this as a proxy for lability

374 (Biersmith and Benner, 1998; Pusceddu et al., 2009) and thus make the assumption that Joyce
375 Glacier sediment is bioavailable. Microbial cell abundance was comparable in all samples (1
376 $- 7 \times 10^5$ cells g^{-1} , Table 2).

377 **4.2. Subglacial DOC quantity and complexity**

378 DOC abundance and composition varied between the four glaciers. The highest mean DOC
379 concentrations were observed in basal ice from Joyce Glacier (272 ± 99 μM C) and
380 Engabreen (114 ± 106 μM C), with lower concentrations in Russell Glacier basal ice (53 ± 29
381 μM C), FDB (15 ± 10 μM C) and FSB (33 ± 33 μM C) (Table 1). The relatively large
382 standard deviations show that subglacial DOC concentrations are highly variable, even in
383 basal ice from the same glacier. Between 5 and 7 replicate samples were taken from each of
384 the ~ 15 cm^3 chunks cut out of the main ice blocks from each glacier (detailed in Sect. 3.1).
385 The variability in the DOC concentrations suggests that there is significant spatial
386 heterogeneity even at the level of the ~ 15 cm^3 basal ice chunks analysed from each glacier.

387
388 The composition of the subglacial DOC was investigated by spectrofluorescence and ion
389 chromatography. The synchronous fluorescence spectra of all basal ice samples illustrated the
390 dominance of three key fluorophores of a marine humic-like/fulvic acid type, at c. 340, 385
391 and 440 nm (excitation wavelengths, Figure 2, Table 3), and several unresolved fluorophores
392 at longer excitation wavelengths. Protein-like peaks (~ 279 nm excitation wavelength),
393 indicative of tyrosine-like compounds (Ferrari and Mingazzini, 1995; Yamashita and Tanoue,
394 2003), were only evident in Joyce Glacier and FSB basal ice (Table 3). Ion chromatographic
395 analyses provided a greater level of detail on the molecular composition of the DOC. LMW-
396 DOC compounds, with concentrations $>$ LOQ, accounted for $<3\%$ of the DOC in all basal ice
397 samples. Mean LMW-DOC concentrations in Engabreen, Finsterwalderbreen and Russell
398 Glacier basal ice were <420 nM C (Table 1). Mean LMW-DOC concentrations were an order
399 of magnitude higher (4430 nM C) in Joyce Glacier basal ice. As with DOC concentrations,
400 the variability in the LMW-DOC compound concentrations suggests high spatial
401 heterogeneity within the basal ice.

402
403 LMW-DOC was typically dominated by FCAs (Table 1), except in Joyce Glacier samples
404 which are subsequently discussed. Overall, acetate was the most common analyte (Figure 3),
405 being present in 60% of the samples that contained FCAs at concentrations $>$ LOQ. Basal ice

406 FCHO concentrations were typically < LOQ (<4% of the LMW-DOC, Table 1) and only
407 detected in Joyce Glacier samples, comprising glucose (16 - 49 nM C) and ribose (16 - 19 nM
408 C, data not shown). Joyce Glacier basal ice DOC was unique in that most (98%) of the
409 LMW-DOC was derived from the extremely diverse FAA pool (Figure 4). Mean FAA
410 concentration in Joyce Glacier basal ice (4353 ± 2643 nM C) was an order of magnitude
411 higher than mean FAA concentrations in Engabreen, Finsterwalderbreen and Russell Glacier
412 basal ice (0 – 51 nM C, Table 1). Some 14 FAAs were detected in Joyce Glacier basal ice,
413 including methionine, glutamic acid, aspartic acid and cysteine, which were not observed in
414 the other basal ice samples. Serine/proline, alanine and valine dominated the Joyce Glacier
415 FAA pool. FAAs accounted for 59% of the LMW-DOC in Russell Glacier basal and FSB ice,
416 primarily in the form of alanine and valine, respectively.

417

418 **5. Discussion**

419 The application of a novel methodological approach (within the field of glacial science) using
420 ion chromatography has allowed the identification and quantification of a range of LMW-
421 DOC compounds in debris-rich basal ice, including FCAs, FCHOs and FAAs, at
422 unprecedented low concentrations (<70 nM C). This represents, to our knowledge, the first
423 study to quantify LMW-DOC in basal ice from a range of glaciers and ice sheets. We
424 demonstrate that ion chromatographic systems that have been optimised for the detection of
425 trace level LMW-DOC concentrations, e.g. by using multiple eluents, low flow rates and
426 gradient elution, can be utilised as an additional quantitative technique to supplement
427 characterisations of glacial LMW-DOC by ESI FT-ICR MS (Grannas et al., 2006; Bhatia et
428 al., 2010; Lawson et al., 2014a) and solution-state ^1H NMR spectroscopy (Pautler et al.,
429 2011, 2012).

430 **5.1. The influence of debris type on sediment OC and basal ice DOC** 431 **concentrations**

432 We find little evidence that the type of overridden material (i.e. the pre-entrainment
433 sedimentary type such as lacustrine material or paleosols) and the mean sediment OC content
434 has a significant influence on the DOC content in basal ice. Indeed, the mean basal ice DOC
435 concentrations (Table 1) and mean sediment OC content (Table 2) were relatively similar in
436 all basal ice samples despite the differences in the types of overridden material. Furthermore,
437 the fact that the highest mean DOC concentration was observed in Joyce Glacier basal ice

438 (272 $\mu\text{M C}$) yet the corresponding sediment OC% was the lowest (0.01%) of all four sites
439 demonstrates the lack of a relationship between sediment OC% and basal ice DOC. This may
440 be due to the particular section of basal sediment that was sampled as, in the case of Joyce
441 Glacier, higher OC content has previously been observed in other Antarctic lacustrine
442 samples, such as subglacial sediment beneath Lower Wright Glacier (0.7% OC) (Stibal et al.,
443 2012), and Antarctic Dry Valley lacustrine sediments containing microbial mats (~9% OC)
444 (Squyres et al., 1991). This suggests a more diverse basal sediment matrix comprising algal
445 mats and organic lacustrine material that mixed with sand and/or other low-OC, mineral-
446 based material during basal ice formation beneath Joyce Glacier. However, we acknowledge
447 that some of the difference in sediment OC (and extractable carbohydrate concentrations)
448 may be due to the different analytical methods employed in this and previous studies. The
449 concentrations that we present may also be conservative as our methodological approach
450 meant that fine sediment fractions, which may be OC-rich, remained in suspension and were
451 not included in the OC determinations.

452

453 Key differences were, however, observed in the proportions of extractable carbohydrates (a
454 proxy for bioavailable compounds in the basal sediment) and LMW-DOC concentrations in
455 basal ice from the four sites. The LMW-DOC concentrations in Joyce Glacier basal ice,
456 which were an order of magnitude higher than LMW-DOC concentrations in samples from
457 the other three sites and predominantly due to high FAA concentrations, may have derived
458 from the relatively large pool of potentially-bioreactive extractable carbohydrates in Joyce
459 Glacier basal sediment (17% of the sediment OC, compared with <0.5 % of the sediment OC
460 in samples from Russell Glacier, Engabreen and Finsterwalderbreen). The bioreactive OC
461 pool in Joyce Glacier basal sediment may have been enhanced by the assimilation of
462 proglacial algal mats into overridden material during glacial advance, which likely enriched
463 the basal ice with lacustrine material and associated algal necromass (Pautler et al., 2012),
464 which may include autochthonous material produced by microorganisms prior to basal ice
465 formation. Indeed, lacustrine material is generally acknowledged as a source of reactive OC
466 to microorganisms (Meyers and Ishiwatari, 1993). The lower extractable carbohydrate
467 concentrations in basal sediment from Russell Glacier, Engabreen and Finsterwalderbreen
468 (compared with Joyce Glacier) are thought to reflect the more refractory nature of the
469 overridden material. OC in subglacial material beneath this sampled section of Russell
470 Glacier is thought to derive from a soil origin, based on relatively high concentrations of n-
471 alkanoic acids, steroids, and other soil-derived functional compounds that have been

472 identified in basal ice samples (Stibal et al. 2012). Due to this, and the relatively young age of
473 Russell Glacier sediment OC (<1900 ¹⁴C yrs BP), we expected the total and bioreactive OC
474 concentrations to be higher than 0.44% and 0.47% of the OC, respectively. For instance, OC
475 content in Greenland soils range from 0.1 - 44.8% in C horizons and peat soils (Horwath
476 Burnham and Slettern, 2010). The low OC and extractable carbohydrate concentrations in
477 Russell Glacier basal ice may reflect a heterogeneous sediment matrix that incorporates a
478 lower proportion of paleosols mixed with other low-OC, mineral-based material. However, as
479 discussed earlier, these differences in sediment OC concentrations may be due to the
480 conservative nature of our methodological approach that may have excluded the potentially
481 OC-rich fine sediment fractions. The low extractable carbohydrate concentration (0.04% of
482 the OC) in Finsterwalderbreen basal sediment is likely influenced by the predominance of
483 OC from kerogen in the overridden shale bedrock (Wadham et al., 2004) that has been
484 incorporated into the basal ice matrix. Kerogen is ancient carbon comprising stable carbon
485 macromolecules (Petsch et al., 2001) and has limited bioreactivity. Similarly, low bioreactive
486 OC in Engabreen basal sediment (0.17% of the OC comprised extractable carbohydrates) is
487 influenced by the subglacial substrate comprising overridden continental shield rock depleted
488 in reactive OC, the limited opportunity for material from supraglacial environments to be in-
489 washed, and the limited input of overridden paleosols (Stibal et al., 2012). A lack of organic
490 biomarkers (derived from algal and higher plant inputs) in Engabreen basal ice further
491 suggests that incorporation of organic material is probably limited (Stibal et al., 2012).
492 Alternatively, the lack of organic biomarkers may be due to debris entrainment by regelation
493 rather than freezing-on (adfreezing).

494

495 In summary, our data suggest that where glaciers and ice sheets override lacustrine
496 sediments, there is an injection of particulate and dissolved bioavailable compounds into the
497 basal ice at the glacier bed, which is less evident where the glacier overrode paleosols or
498 bedrock. This has implications for subglacial LMW-DOC cycling as this abiotic input of
499 LMW-DOC (via leaching) has the potential to stimulate microbial activity in wet sediments
500 in the subglacial environment. We go on to investigate the DOC and LMW-DOC signatures
501 in basal ice from these contrasting subglacial environments.

502 **5.2. Basal ice LMW-DOC signatures and provenance**

503 The presence of LMW-DOC compounds and the similarities in the types of compounds
504 detected in basal ice samples from the four sites may reflect common sources and pathways
505 of transformation of DOC in subglacial environments beneath glaciers and ice sheets. The
506 potential for interactions between basal sediment and subglacial icemelt suggest that inputs
507 from the overridden subglacial material may represent a key contribution to basal ice DOC.
508 The chemical composition of basal ice, including DOC compounds, should reflect
509 characteristics of the parent water prior to being frozen (Knight, 1997), where this water
510 might be either flowing at the base of the glacier, held in porewaters in overridden water-
511 saturated sediment, or refrozen water from pressure melting during the regelation process.
512 These water sources have extensive contact with the subglacial material and so have the
513 potential to acquire dissolved compounds via biogeochemical interactions. However, these
514 processes are highly site specific and where there are well-developed quick-flow components
515 and scoured bedrock channels, for instance, there will be less scope for fast-flowing waters to
516 acquire dissolved compounds from biogeochemical interactions with the overridden material.
517 DOC and LMW-DOC components in basal ice may also be acquired by in situ abiotic
518 processes, e.g. by reactions, such as dissolution, in water films around debris and in liquid
519 water veins (Mader et al, 2006). It is likely that certain organic compounds will remain
520 associated with the debris and others will dissociate to become DOC. To fully assess whether
521 DOC is largely terrestrially-derived and leached from sediments, we would need data on the
522 surface area of the debris and information on particle size distribution. As this was beyond
523 the scope of this study we instead used debris concentrations for a preliminary investigation.
524 We find that for sites where there is a bioavailable OC source in sediments (Joyce Glacier)
525 there is a significant relationship between DOC and debris concentration (Figure 1a). This
526 suggests that subglacial meltwater contact with subglacial sediment beneath Joyce Glacier,
527 which is cold-based and so has little supraglacial meltwater penetration to the glacier bed, is a
528 major control on DOC acquisition. We find several additional lines of evidence to support the
529 leaching of DOC from subglacial sediments, including the presence of fulvic acids that have
530 previously been associated with terrestrial material (> 440 nm fluorescence wavelengths) in
531 all basal ice samples (McKnight et al., 2001). The basal ice LMW-DOC compounds may also
532 be a leached relic of the overridden material that has been preserved in the ice when frozen.
533 However, the lack of significant association between LMW-DOC and debris concentration
534 (Figure 1b) is reflective of additional sources and sinks of these compounds in the basal ice
535 layer and/or in the parent water body from which basal ice formed. The LMW-DOC
536 signature in basal ice may also be influenced by in situ microbial production and

537 consumption, as illustrated in earlier work that has proposed a range of microbial processes to
538 be active in the subglacial environment, including in situ chemoautotrophic production
539 (Bhatia et al., 2006, 2013), chemoheterotrophic oxidation of OC substrates to protein-like
540 LMW-DOC compounds (Bhatia et al., 2010) and release of LMW-DOC from decaying cells.
541 It is probable that subglacial microbial activity cycles LMW-DOC both before and after the
542 formation of basal ice. For instance, microorganisms in subglacial sediment porewaters and
543 basal meltwaters flowing at the rock:water interface may actively utilise OC substrates and
544 energy sources derived from the overridden material. Via this activity, they may also go on to
545 produce simple LMW-DOC compounds which may subsequently be incorporated into basal
546 ice. The protein-like peaks that were observed in the spectrofluorescence spectra in Joyce
547 Glacier and FSB ice (Table 3) tentatively suggests that some of the LMW-DOC is of a
548 microbial provenance. Protein-like fluorescence is linked with recent biological activity (De
549 Souza Sierra et al., 1994) and is associated with active FAA production during microbial
550 metabolism (Yamashita and Tanoue, 2003). The finding that FSB samples contained larger
551 protein-like peaks and had higher mean FCA and FAA concentrations when compared with
552 FDB samples may be explained by the different basal ice formation processes at
553 Finsterwalderbreen. FSB debris, sampled from surface outcrops of frozen subglacial material,
554 or thrust bands, is expected to derive from further upglacier than FDB debris and likely
555 formed during the most recent surge *c.* 1898-1920 (Liestøl, 1969). This suggests that FSB
556 debris may have been glacier-covered for a much longer period than FDB debris. These
557 conditions may have led to enhanced leaching of LMW-DOC from the subglacial material
558 and/or greater production (vs. consumption) of LMW-DOC by in situ microorganisms. It is
559 also possible that LMW-DOC in basal ice from the polythermal and warm-based glaciers
560 sampled in this study (Finsterwalderbreen, Russell Glacier and Engabreen) could derive from
561 supraglacial inputs as glacially-overridden material is not the sole source of DOC in basal ice.

562
563 In this study, we were not able to categorically separate LMW-DOC derived from biotic and
564 abiotic processes as, at a molecular level, many LMW-DOC compounds are non-specific
565 biomarkers due to their pervasive occurrence in plants and microorganisms (Biersmith and
566 Benner, 1998). For example, valine, a common FAA in most basal ice samples, can be
567 synthesized in plants via several steps starting from pyruvic acid (e.g. described in Singh,
568 1999). Valine can also be microbially-synthesized from pyruvate (Blombach et al., 2007) and
569 produced by aerobic gram-positive microbes (Valle et al., 2008). Similarly, glucose can be
570 produced by photosynthesis (Kirchman et al., 2001) and chemoautotrophic bacterial activity

571 (Jansen et al., 1982). The key point is that the presence of numerous LMW-DOC compounds
572 in basal ice from all four glacial sites provides evidence that viable substrates for microbial
573 growth, whether derived from a terrestrial or microbial source, are available in subglacial
574 environments. These LMW-DOC compounds may help support microbial communities
575 within the present-day basal ice, e.g. beneath Russell Glacier, where recent work has shown
576 that the basal ice may be microbially-active in the current frozen state (Yde et al., 2010). The
577 microbial cell counts observed in all basal ice samples in this study (10^5 cells g^{-1} , Table 2) are
578 comparable to microbial populations ($10^5 - 10^8$ cells g^{-1}) reported in other subglacial
579 sediments that have been proven to be microbially-active (Sharp et al., 1999; Foght et al.,
580 2004; Kastovska et al., 2007; Yde et al., 2010; Montross et al., 2012).

581 **5.3. Implications for LMW-DOC cycling beneath glaciers with bioreactive** 582 **subglacial sediment**

583 The margin of Joyce Glacier rests upon ancient lake sediments and hence, represents a case
584 where a very labile organic matter source is overridden. This situation may have been
585 common in past periods of glaciation, when, for example, the Pleistocene ice sheets advanced
586 over regions with a high density of lakes, such as in northern Canada and Scandinavia
587 (Wadham et al., 2008). Hence, the potential for LMW-DOC incorporation in Joyce Glacier
588 basal ice and sediment may be applicable to these other types of lacustrine-based subglacial
589 ecosystems. In addition, the abundance of LMW-DOC in Joyce Glacier suggests that
590 overridden lacustrine material can be sequestered even if the glacier is cold-based. Contrary
591 to traditional assumptions that drainage in cold-based glaciers is entirely supraglacial, it is
592 possible that discrete subglacial channels exist where water is in contact with the substrate,
593 e.g. at Longyearbreen (Yde et al., 2008). This mechanism may enable the release of DOC to
594 downstream ecosystems. If the glacier was warm-based then the DOC could be flushed out
595 during the summer melt seasons and contribute to the net export of bioavailable DOC to
596 downstream environments. DOC in glacial runoff may derive from multiple sources;
597 terrestrial DOC derived from overridden material at the bed (Hood et al., 2009);
598 anthropogenic aerosol deposition on the glacier surface (Stubbins et al., 2012), and;
599 biological activity in both supraglacial (Anesio et al., 2009) and subglacial (Bhatia et al.,
600 2013) environments. The contribution from basal ice may be more significant in cold-based
601 glacier systems, e.g. in the Antarctic Dry Valleys, where daily radiation melting of the steep
602 ice cliffs may release solute from the debris-rich basal ice that is exposed on the cliffs. The

603 distributed drainage system beneath temperate and polythermal glaciers may also include a
604 constant source of water from basal ice melt and groundwater in contact with glacial till
605 (Paterson, 1999).

606

607 The dramatic difference in the DOC composition beneath glaciers resting on different OC
608 substrates that our data have highlighted may have implications for the rate and degree to
609 which this overridden OC can be cycled to biogenic gases in current subglacial environments,
610 which in turn, has relevance for the global carbon cycle (Wadham et al., 2008; Stibal et al.,
611 2012). While the DOC and LMW-DOC signatures of basal ice may arise from several
612 confounding factors which are difficult to disentangle, identifying the abundance and
613 composition of DOC in basal ice is an important first step to understanding LMW-DOC
614 cycling in subglacial environments.

615

616 **6. Conclusion**

617 We employ a combined spectrofluorometric and ion chromatographic methodological
618 approach to produce the first identification and quantification, at trace level concentrations, of
619 major LMW-DOC fractions (free amino acids, carbohydrates and carboxylic acids) in debris-
620 rich basal ice. We demonstrate that ion chromatographic systems that are optimised for trace
621 level LMW-DOC analyte detection can supplement traditional methods of LMW-DOC
622 characterisation as a quantitative technique. Our work adds to the growing body of research
623 addressing sources and reactivity of DOC in subglacial ecosystems and provides a
624 characterisation of LMW-DOC in basal ice from four different glacial environments with
625 distinctive basal debris types including lacustrine material (Joyce Glacier), overridden soils
626 and tundra (Russell Glacier), kerogen in bedrock (Finsterwalderbreen) and bedrock/soils
627 (Engabreen). We infer that terrestrial inputs from the overridden subglacial material represent
628 a key contribution to basal ice DOC. Our data show that LMW-DOC concentrations in basal
629 ice are dependent on the bioavailability of the overridden OC, which in turn, is influenced by
630 the type of overridden material. We find that where glaciers and ice sheets override lakes,
631 such as at Joyce Glacier, there is an injection of particulate and dissolved bioavailable
632 compounds into the basal ice at the glacier bed, which is less evident where glaciers overrode
633 paleosols or bedrock. There is also potential for the overridden substrate to act as an indirect
634 (via microbial cycling) source of DOC, as the leached LMW-DOC compounds may stimulate
635 microbial activity in wet sediments in the subglacial environment. This has implications for

636 the cycling of overridden OC to biogenic gases in subglacial environments and concurs with
637 recent findings that accelerated melting of glaciers and ice sheets could constitute a
638 significant source of DOC and other, potentially-bioavailable dissolved organic matter, to
639 glacially-fed ecosystems. The abundance of LMW-DOC in Joyce Glacier basal ice suggests
640 that overridden material may be sequestered even if the glacier is cold-based. Identifying the
641 abundance and composition of DOC in basal ice is an important first step to understanding
642 LMW-DOC cycling in subglacial environments, which has relevance for local carbon cycling
643 and wider ecosystem processes.

644 **Author Contributions**

645 JLW and MT conceived the project. ECL, JLW, GPL, MS and SF collected field data. ECL,
646 GPL, AEP, and MS undertook the lab analysis. PD, GPL and ECL assisted with the Dionex™
647 ICS-3000 ion chromatography system optimisation and method development. ECL, JLW and
648 MT wrote the paper with additional comments from the co-authors.

649

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871 Gunnlaugsson, H.P., Nielsen, O.B. Basal ice microbiology at the margin of the Greenland ice
872 sheet. *Annals of Glaciol.* 51, 71-79, 2010.

873 Table 1 Biogeochemical data for basal ice from Engabreen (E), Finsterwalderbreen (F),
 874 Russell Glacier (R) and Joyce Glacier (J). DB = dispersed banded and SB = solid banded.
 875 Values given are the mean concentrations for each analyte and the standard deviation is given
 876 in parentheses. LMW-DOC = free carbohydrates (FCHOs) + free amino acids (FAAs) + free
 877 carboxylic acids (FCAs). Only values > LOQ have been included.

878

Sample	% debris (by mass)	DOC ($\mu\text{M C}$)	LMW DOC (nM C)	FCHOs (nM C)	FAAs (nM C)	FCAs (nM C)
E (n = 6)	36.83 (20.96)	113.56 (106.60)	417.70 (213.07)	0.00	22.41 (24.24)	442.19 (164.00)
FDB (n = 5)	20.22 (26.74)	14.85 (9.91)	169.67 (183.90)	0.00	0.00	169.67 (183.90)
FSB (n = 5)	86.47 (6.58)	33.38 (33.30)	312.67 (502.64)	0.00	46.47 (48.99)	274.91 (549.83)
R (n = 7)	54.89 (24.51)	53.31 (28.89)	343.72 (689.83)	0.00	50.59 (62.97)	365.62 (817.56)
J (n = 5)	21.22 (6.41)	272.09 (99.38)	4429.83 (2625.95)	28.29 (15.83)	4353.30 (2643.59)	0.00

879 Table 2 Mean sediment characteristics. [§]sediment OC age from Stibal et al., (2012), method
 880 described in the online supporting information. ND = not determined. E = Engabreen, F =
 881 Finsterwalderbreen, R = Russell Glacier, J = Joyce Glacier. Standard deviation is given in
 882 parentheses.

Sample	¹⁴C age (years, BP)[§]	%OC	%InC	Extractable carbohydrates (µg/g)	Carbohydrate fraction (% of OC)[*]	Cell abundance (cell g⁻¹)
E (n = 5)	ND	0.19 (0.08)	0.24 (0.18)	3.26	0.17	6.80 x 10 ⁵
F (n = 5)	3750 (150)	0.57 (0.12)	1.80 (0.25)	2.34	0.04	1.68 x 10 ⁵
R (n=5)	1830 (50)	0.44 (0.09)	0.01 (0.00)	20.83	0.47	2.26 x 10 ⁵
J (n= 5)	ND	0.01 (0.02)	0.28 (0.05)	23.95	17.11	1.16 x 10 ⁵

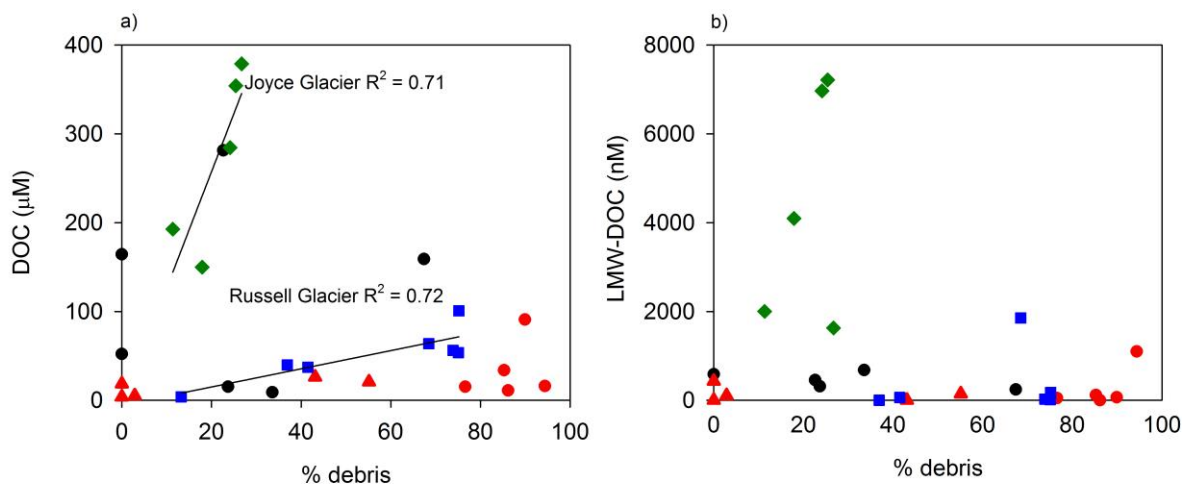
883 Table 3 Summary of the dominant fluorophores in basal ice from four contrasting glacial
 884 environments. The dominant fluorophores (denoted by *) have been identified according to
 885 previous characterisation of spectral compounds (see Barker et al., 2009 and references
 886 therein). DB = dispersed banded, SB = solid banded.

Sample	Fluorophore (peak excitation wavelength, nm)	Dominant fluorophore identification	n
Engabreen	342, 386*, 440, 483	Fulvic acid, marine humic-like	6
Finsterwalderbreen DB	342, 389*, 440	Fulvic acid, marine humic-like	5
Finsterwalderbreen SB	276, 336, 389*, 440	Fulvic acid, marine humic-like	5
Russell Glacier	335*, 385, 440, 483	Protein-like/marine humic-like	7
Joyce Glacier	279, 342, 386*, 440, 460, 551	Fulvic acid, marine humic-like	5

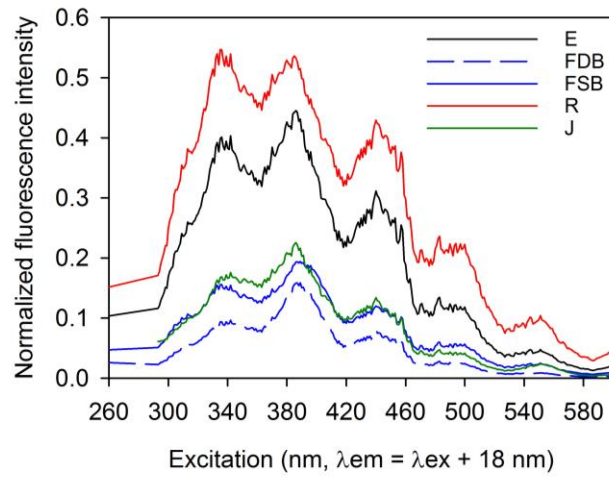
887 **Figures**

888

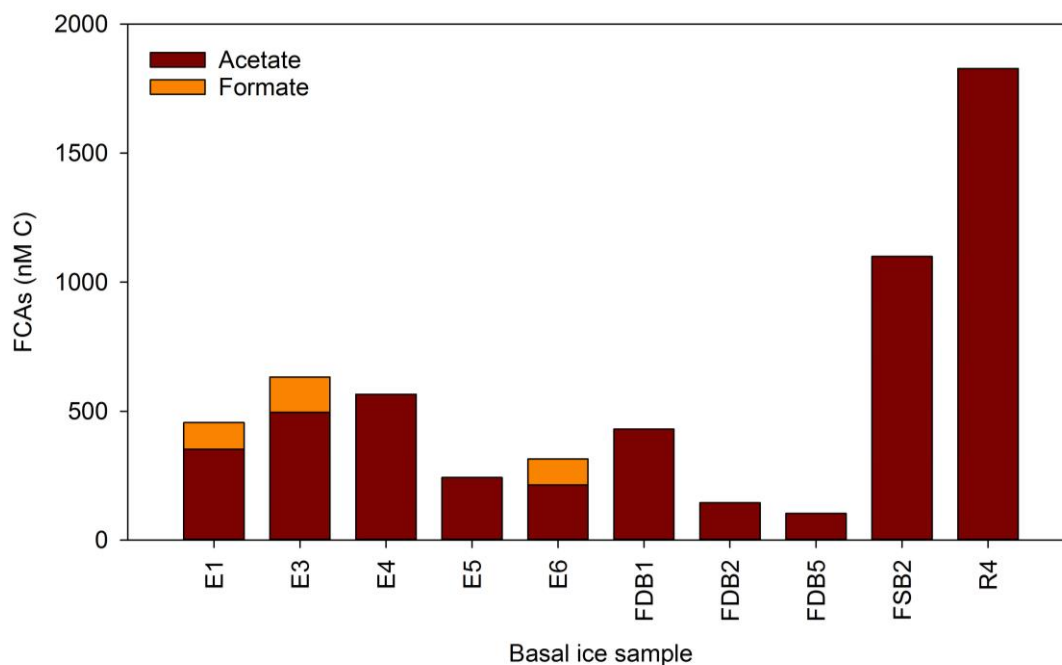
889 Figure 1 Associations between a) DOC and debris concentration, and b) LMW-DOC and
 890 debris concentration. Engabreen samples are given in black, Finsterwalderbreen in red (FDB
 891 (dispersed banded ice) as triangles and FSB (solid banded ice) as circles), Russell Glacier in
 892 blue and Joyce Glacier in green. $P < 0.05$ for all regression equations, only significant
 893 correlations are shown.



894 Figure 2 Mean normalized synchronous fluorescence spectra for basal ice samples. E =
895 Engabreen, F = Finsterwalderbreen, R = Russell Glacier, J = Joyce Glacier, DB = dispersed
896 banded, SB = solid banded.



897 Figure 3 FCA compositions in basal ice samples. E = Engabreen, F = Finsterwalderbreen, R
898 = Russell Glacier, DB = dispersed banded, SB = solid banded. Samples with zero
899 concentrations have been excluded from the plot and only values > LOQ have been included.



900 Figure 4 FAA composition in basal ice samples from a) Engabreen (E), Finsterwalderbreen
 901 (F), Russell Glacier (R) and Joyce Glacier (J), b) FAAs in Joyce Glacier basal ice, plotted
 902 separately due to an order of magnitude increase in concentrations. Samples with zero
 903 concentrations have been excluded from the plot and only values > LOQ have been included.
 904 S/P = serine and proline, reported together due to co-elution. SB = solid banded.

