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Author(s): Xiao, Yihua; Hoikkala, Laura; Kasurinen, Ville; Tirola, Marja; Kortelainen, Pirkko;
Vähätalo, Anssi

Title: The effect of iron on the biodegradation of natural dissolved organic matter

Year: 2016

Version:

Please cite the original version:

Xiao, Y., Hoikkala, L., Kasurinen, V., Tirola, M., Kortelainen, P., & Vähätalo, A. (2016).
The effect of iron on the biodegradation of natural dissolved organic matter. *Journal
of Geophysical Research G: Biogeosciences*, 121(10), 2544-2561.
<https://doi.org/10.1002/2016JG003394>

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1 **Iron affects the biodegradation of natural dissolved organic matter**

2
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15 **Key Points:**

- 16 • The association of Fe with DOM can stimulate bacterial growth and the biodegradation
17 of DOM
- 18 • Insoluble Fe-precipitates on the bacterial cells can inhibit bacterial growth on DOM
- 19 • Fe associated with DOM reduces the bioavailability of P, which decreases bacterial
20 growth on DOM

21 **Abstract**

22 Iron (Fe) may alter the biodegradation of dissolved organic matter (DOM), by associating
23 with (DOM), phosphorus (P) and microbes. We isolated DOM and a bacterial community from

24 boreal lake water and examined bacterial growth on DOM in laboratory experiments. Fe was
25 introduced either together with DOM (DOM-Fe) or into bacterial suspension, which led to the
26 formation of insoluble Fe-precipitates on bacterial surfaces (Fe coating). In the latter case, the
27 density of planktonic bacteria was an order of magnitude lower than that in the corresponding
28 treatment without introduced Fe. The association of Fe with DOM decreased bacterial growth,
29 respiration, and growth efficiency compared with DOM alone at the ambient concentration of
30 dissolved P ($0.16 \mu\text{mol L}^{-1}$), indicating that DOM-associated Fe limited the bioavailability of P.
31 Under a high concentration ($21 \mu\text{mol L}^{-1}$) of P, bacterial biomass and respiration were similar or
32 several times higher in the treatment where DOM was associated with Fe than in a corresponding
33 treatment without Fe. Based on the next generation sequencing of 16S rRNA genes, *Caulobacter*
34 dominated bacterial communities grown on DOM-Fe. This study demonstrated that association
35 of Fe with a bacterial surface or P reduce bacterial growth and the consumption of DOM. In
36 contrast, DOM-Fe is bioavailable and bound Fe can even stimulate bacterial growth on DOM
37 when P is not limiting.

38

39 **1 Introduction**

40 Dissolved organic matter (DOM) contains a large pool of reactive organic carbon forming a
41 major source of energy and nutrients for heterotrophic bacteria. Iron (Fe) is the most abundant
42 element on Earth and interferes with the biogeochemical cycles of many important elements such
43 as carbon and phosphorus (P) [Cotner and Heath, 1990; Sarkkola *et al.*, 2013; Kritzberg *et al.*,
44 2014; Weyhenmeyer *et al.*, 2014]. Global carbon cycling has been a topical issue during the last
45 decades. Nevertheless, the links between carbon and other key elements in biogeochemical
46 cycles have remained poorly quantified. Iron can have a more important role in carbon cycling in

47 boreal zone than presently understood. For example, it plays a key role in carbon sequestration in
48 boreal lake sediments [Kortelainen *et al.*, 2004; von Wachenfeldt and Tranvik, 2008; Einola *et*
49 *al.*, 2011]. Recently, the concentrations of both dissolved organic carbon (DOC) and Fe have
50 increased in boreal rivers and streams [Kritzberg and Engström, 2012; Sarkkola *et al.*, 2013;
51 Weyhenmeyer *et al.*, 2014] causing pressure to better understand links between DOC and Fe in
52 the present and future conditions. To best of our knowledge, the role of Fe in the degradation of
53 DOM has not been examined, although Fe can alter the biodegradation of organic matter (OM)
54 in many ways, as exemplified below.

55 Insoluble Fe(oxy)hydroxides, like other mineral surfaces, can bind OM [Hedges and Oades,
56 1997; Baldock and Skjemstad, 2000; Kaiser and Guggenberger, 2000; 2007; Chan *et al.*, 2011;
57 Bennett *et al.*, 2014]. The adsorption of OM on mineral surfaces reduces the availability of OM
58 for osmotrophic microbes (archaea, bacteria, and fungi), and can result in the long-term
59 preservation of OM [Keil *et al.*, 1994; Hedges and Keil, 1995; White and Knowles, 2000;
60 Rothman and Forney, 2007; Lalonde *et al.*, 2012].

61 Fe can form coordination complexes with DOM [Leenheer *et al.*, 1998; Sjöstedt *et al.*, 2013].
62 For example, the potential binding sites of Fe in a hypothetical average molecule of Suwannee
63 River fulvic acid (SRFA) include four carboxylic groups, one quinoid structure, two phenolic
64 groups, and four carbonyls associated with esters and ketones [Leenheer *et al.*, 1998; Sjöstedt *et*
65 *al.*, 2013]. According to the proton donating carboxyl and phenolic groups, SFRA contains 14.3
66 $\mu\text{mol} [\text{mg C}]^{-1}$ of potential binding sites for Fe [Leenheer *et al.*, 1998; Ritchie and Perdue, 2003;
67 Sjöstedt *et al.*, 2013; Xiao *et al.*, 2013]. Not all the potential binding sites are occupied by Fe in
68 freshwaters, but loadings of up to ca. 2 $\mu\text{mol Fe} [\text{mg C}]^{-1}$ have been reported [Neubauer *et al.*,
69 2013a]. In the environment, DOM consists of thousands of molecules, which range from

70 dissolved single compounds to colloids [*Gustafsson and Gschwend, 1997; Wagner et al., 2015*].
71 Similarly, the species of Fe range from simple ions to colloids [*Boyd and Ellwood, 2010;*
72 *Sjöstedt et al., 2013*). Due to poor solubility of many inorganic Fe species, the association of Fe
73 with DOM is crucial for the solubility of Fe [*Shapiro, 1964; Gustafsson and Gschwend, 1997;*
74 *Boyd and Ellwood, 2010*). These associations ranging from monomeric Fe-DOM complexes to
75 colloidal assemblages of DOM and Fe are called collectively as “DOM-Fe” in this study. The
76 biodegradation of organic component in DOM-Fe is poorly known [*Boudot et al., 1989; White*
77 *and Knowles, 2000; Nancharaiah et al., 2006*].

78 Fe can indirectly alter the biodegradation of OM by influencing the speciation and
79 availability of P. In soils and sediments, Fe reduces the availability of P by binding it to insoluble
80 non-available forms [*Heiberg et al., 2012; Baken et al., 2015*]. Fe can associate with DOM and
81 absorb phosphate also in water column [*Francko and Heath, 1982; Steinberg and Baltes, 1984;*
82 *Cotner and Heath, 1990; De Haan et al., 1990; Sundman et al. 2016*]. A tight association
83 between Fe and P reduces the bioavailability of P and can potentially limit the activity of
84 decomposers e.g., in lakes where the concentration of P is low [*Karlsson et al., 2001; Vidal et*
85 *al., 2011*].

86 The proton donating functional groups (carboxyl, hydroxyl, sulfhydryl, and phosphoryl) on
87 the bacterial cell surface can bind Fe [*Fein et al., 1997; Pokrovsky et al., 2008; Yee et al., 2004*].
88 Such binding can transfer and immobilize microbes on solid surfaces when Fe forms insoluble
89 precipitates [*Liu et al., 2015*], e.g., during the oxidation of dissolved Fe(II) to
90 Fe(III)(oxy)hydroxides along with an increasing redox potential [*Hatamie et al., 2016*]. An
91 extensive accumulation of Fe on the cell surfaces (Fe coating; [*Franzblau et al., 2016*]) or

92 embedding under a layer of Fe(III)(oxy)hydroxides can be expected to reduce the metabolic
93 activity of decomposers and the biodegradation of OM.

94 Besides the possible negative effects of Fe on the biodegradation of OM, Fe can also
95 stimulate the decomposition of OM. Fe associated with quinone moieties of DOM can cause
96 abiotic oxidation-reduction reactions, which, for instance, convert the reduced hydroquinones
97 through semiquinone radicals to oxidized quinones [Yuan *et al.*, 2016]. Such reactions can be
98 sources of reactive oxygen (O₂) species and lead to the breakage of aromatic rings [Miller *et al.*,
99 2013; Comba *et al.*, 2015; Yuan *et al.*, 2016]. This ring cleavage can produce volatile
100 hydrocarbons, CO₂, and organic acids such as oxalic acid [Pracht *et al.*, 2001; Studenroth *et al.*,
101 2013; Comba *et al.*, 2015]. These reactions can take place abiotically between the reduced and
102 oxidized forms of natural organic matter and those of Fe (FeII/III). Thus, the abiotic reactions of
103 Fe can facilitate decomposition of OM and produce substrates for microbes.

104 Fe also facilitates the decomposition of OM through the active metabolism of microbes.
105 Brown rot fungi and an ectomycorrhizal fungus, *Paxillus involutus*, use Fe in a biochemical
106 Fenton reaction to break down particulate organic matter in wood and soil, respectively [Arantes
107 *et al.*, 2012; Rineau *et al.*, 2012]. These fungi secrete reducing components that convert Fe(III) to
108 Fe(II) and dioxygen through superoxide to hydroxyl peroxide to yield the two reactants of the
109 Fenton reaction [Arantes *et al.*, 2012]. The Fenton reaction produces hydroxyl radicals that can
110 break down organic matter non-selectively.

111 Heterotrophic bacteria can use extracellular enzymes to break down molecules that are too
112 large (>600 g mol⁻¹) for direct uptake [Arnosti, 2004]. This enzymatic catalysis is selective and
113 primarily limited to the hydrolysis of predictable biopolymers [Arnosti, 2004]. In many
114 freshwaters, the bulk DOM is dominated by high molecular mass (>600 g mol⁻¹) heterogeneous

115 humic substances that also include non-hydrolysable bonds [Tranvik, 1988; Arnosti, 2004].
116 Although much of freshwater DOM is too large for direct uptake or non-hydrolysable by
117 extracellular enzymes of bacterioplankton, typically a half of the bulk DOC is lost in <2.5 years
118 in Swedish lakes [Algesten *et al.*, 2003]. Flocculation may direct DOM into sediments and solar
119 radiation can break down a part of the DOM, but these processes cannot alone explain the loss of
120 DOM that is apparently refractory to biodegradation in lakes or in long laboratory incubations
121 [Vähätalo and Wetzel, 2008; Vähätalo *et al.*, 2010; Koehler *et al.*, 2012]. Therefore, it is possible
122 that the decomposition of DOM in freshwaters may also include other dark reactions, e.g.,
123 catalyzed by Fe abiotically or through active metabolism by bacteria.

124 The communities of bacteria in bacterioplankton contain hundreds of species with their
125 specific metabolic functions [Taipale *et al.*, 2011]. If bacteria are able to utilize Fe to break down
126 DOM extracellularly, it is likely that this functional trait is limited to certain species or groups of
127 species. Such species may possibly mediate extracellular redox reactions of Fe through organic
128 or inorganic (e.g., superoxide) redox shuttles [Melton *et al.*, 2014] and/or have extracellular
129 oxidoreductases [Diaz *et al.*, 2013]. Although bacteria may have potential mechanisms for
130 extracellular decomposition of DOM with the help of Fe [Diaz *et al.*, 2013; Melton *et al.*, 2014],
131 such Fe-stimulated decomposition of DOM and the species of bacteria involved has not been
132 reported.

133 The laboratory experiments of this study assessed the role of Fe on the biodegradation of
134 natural DOM extracted from a humic lake using a community of bacterioplankton from the same
135 lake. In the experiments, Fe was introduced in several different ways and had a possibility to
136 associate with DOM, P, and the cell surface of bacteria to form insoluble Fe(oxy)hydroxides. We

137 examined the growth and respiration of a bacterial community on DOM up to 28 days and
138 identified genus-level changes in the composition of bacterial community along the experiments.

139 **2 Materials and Methods**

140 2.1 Sampling and DOM extraction

141 Surface water samples were collected from humic Lake Valkea-Kotinen (61°14'N,
142 25°04'E), a pristine headwater lake in southern Finland mainly surrounded by coniferous forest
143 [Vähätalo *et al.*, 1999; Arvola *et al.*, 2010]. In the acidic (pH 5.4) surface water of Lake Valkea-
144 Kotinen, the concentrations are 945 $\mu\text{mol L}^{-1}$ for DOC, 5 $\mu\text{mol L}^{-1}$ for total Fe, and 0.16 μmol
145 L^{-1} for dissolved P [Keskitalo *et al.*, 1998; Vähätalo *et al.*, 2003; Einola *et al.*, 2011]. The
146 majority of DOM (75%) consists of humic substances and has a high molecular mass [Vogt *et*
147 *al.*, 2004]. The weighted average molecular mass of DOM is 1130 g mol^{-1} according to mass
148 spectrometry and ca. 4000 g mol^{-1} according to size exclusion chromatography [Vogt *et al.*,
149 2004].

150 A water sample collected on 26 October 2012 was immediately filtered through a 0.45- μm
151 filter (AcroPakTM 1000 capsule, Pall). On the following day, the water sample was further
152 filtered through a 0.2- μm filter (Sartobran 300 sterile capsule, Sartorius Stedim) and acidified to
153 pH ~2 with 37% HCl (Titrisol®, Merck). The acidified water sample was stored in the dark at 11
154 °C, and NaF was added to the final concentration of 0.01 mol L^{-1} before solid-phase extraction
155 (SPE) of DOM according to Dittmar *et al.* [2008]. Fluoride ions were expected to exchange Fe
156 from their DOM ligands and reduce the Fe content of the extracted DOM [Gao and Zepp, 1998].
157 In order to examine the extraction efficiency of DOC and the removal efficiency of Fe, a small
158 aliquot of extracted DOM was re-dissolved in Milli-Q water. The extraction efficiency of DOC

159 was 76% and the removal efficiency of Fe was 97% according to analytical measurements
160 described in 2.3.1.

161 2.2 Experimental design and procedures

162 The experiments briefly described in Tables 1–2 and Fig. 1 were designed to address the
163 following study questions:

- 164 1) “Fe” – Can Fe influence the biodegradation of DOM?
- 165 2) “DOM-Fe” – Is DOM-Fe bioavailable?
- 166 3) “DOM-Fe low/high P” – Does the bacterial growth on DOM-Fe depend on the concentration
167 of P?
- 168 4) “Fe coating” – Can precipitation of Fe on the bacterial cell surface affect the biodegradation of
169 DOM?

170 In this section, we first describe the features common to all experiments and then present the
171 details of each experiment. Iron(III) sulfate hydrate ($\text{Fe}_2(\text{SO}_4)_3 \cdot n\text{H}_2\text{O}$, 399.88 g mol⁻¹, AnalaR)
172 and iron(II) sulfate hydrate ($\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 278.01 g mol⁻¹, Sigma-Aldrich) were used as Fe
173 sources. The β -glycerophosphate disodium salt hydrate (GlyP, $\text{C}_3\text{H}_{17}\text{Na}_2\text{O}_6\text{P} \cdot 5\text{--}6\text{H}_2\text{O}$, 216.04 g
174 mol⁻¹, VWR International) was used as a source of P for bacteria. All chemicals used in the
175 experiment were >98% pure, and all solutions were prepared in deionized water (Milli-Q,
176 Millipore).

177 An indigenous grazer-free bacterial community was isolated and used as an identical
178 inoculum of the bacterial community in the consecutive experiments. Bacteria present in the
179 collected lake water sample were first passed through a 0.8- μm polycarbonate filter
180 (CycloporeTM track etched membrane, Whatman) and then diluted 100 times with <0.2 μm
181 filtered lake water. This diluted bacterial community was cultured in the dark at room

182 temperature for 4 days, after which the bacterial suspension was divided into 50-mL aliquots and
183 stored at $-20\text{ }^{\circ}\text{C}$. Before each experiment, an aliquot of frozen bacterial suspension was thawed
184 at $30\text{ }^{\circ}\text{C}$ in a water bath for 15 min and was introduced as a bacterial inoculum (10% vol/vol in
185 “Fe” and 5% vol/vol in the other experiments).

186 For the experimental bioassays, DOM, Fe, nutrients, artificial lake water (ALW), and
187 bacteria were introduced in different concentrations, combinations and ways (Fig. 1; Tables
188 1–2). DOM was introduced as a stock solution (50 mg L^{-1}), which was prepared by dissolving
189 the extracted DOM in Milli-Q water and filtering the solution through a $0.2\text{-}\mu\text{m}$ filter (Supor[®]-
190 200, Pall). The concentration of introduced DOM was adjusted to 20 mg L^{-1} ($= 948\text{ }\mu\text{mol C L}^{-1}$),
191 matching the concentration in the study lake [Vähätalo *et al.*, 2003; Einola *et al.*, 2011] or in
192 Finnish boreal lakes in general [Kortelainen, 1993]. An acidic (pH 1) stock solution (0.5 mmol
193 $\text{L}^{-1}\text{ Fe}_2(\text{SO}_4)_3\cdot n\text{H}_2\text{O}$ in $0.1\text{ mol L}^{-1}\text{ HCl}$ (Titrisol[®], Merck) was used as a source of Fe(III) in all
194 experiments with introduced Fe(III). The stock solution of ALW was prepared according to
195 Kester *et al.* [1967] and was added to form the final inorganic ion concentrations presented in
196 Table 1 and an ionic strength of 0.87 (calculated as mmol L^{-1}), which is close to the average
197 ionic strength of Finnish river waters (0.8 , [Xiao *et al.*, 2015]). The nutrients N and P were
198 introduced as separate solutions of NH_4Cl and GlyP, respectively (Table 1). GlyP was selected as
199 a source of P instead of inorganic phosphate, which can effectively complex with Fe(III) into
200 insoluble precipitates [Francis and Dodge, 1993]. GlyP is one of the few organophosphates that
201 can be transported across the cell membrane, forming a source of P but not serving a carbon
202 substrate [Schweizer *et al.*, 1982]. An isolated identical bacterial community indigenous to Lake
203 Valkea-Kotinen was used as a bacterial inoculum. Finally, the volume of bioassays was adjusted
204 to 100 mL with Milli-Q water. Biodegradation of DOM was assessed as bacterial growth

205 determined as the bacterial density and the consumption of dissolved O₂ in bioassays extending
206 up to 25 days in the dark at 22 °C.

207 The “Fe” experiment (Fig. 1) assessed the growth of bacteria on DOM in the presence and
208 absence of introduced Fe(III). DOM, Fe(III), ALW, nutrients, and bacteria were mixed together
209 at pH ~2 and titrated to pH 7 with 1 mol L⁻¹ NaOH using a Titrette® bottle-top burette (Brand
210 GMBH, Germany). During the titration, Fe(III) had the possibility to associate with DOM, GlyP,
211 the salts of ALW, and/or bacteria. The “Fe” experiment included two concentrations of Fe: no
212 introduced Fe (DOM alone treatment) and 130 μmol L⁻¹ Fe(III) (DOM+130Fe treatment; Fig. 1
213 and Table 2). The treatment containing DOM alone was calculated to contain a low (<0.43 μmol
214 L⁻¹) concentration of Fe that originated from the bacterial inoculum (0.25 μmol L⁻¹) and
215 extracted DOM (0.17 μmol L⁻¹; Table 2).

216 The “DOM-Fe” experiment addressed the bioavailability of DOM-Fe. DOM-Fe was created
217 before the introduction of bacteria, ALW, and nutrients (Fig. 1). The concentration of Gly-P was
218 adjusted to 21 μmol L⁻¹ (high P, Table 2), which is two orders of magnitude higher than the
219 concentration of dissolved P in the study lake. To create DOM-Fe, a stock solution of Fe(III) was
220 introduced to an acidic (pH ~2) stock solution of DOM and then slowly titrated to pH ~7 (Fig.
221 1). During the titration, the proton donating sites of DOM became available to bind Fe(III), and
222 DOM-Fe(III) was formed. Three concentrations of Fe(III) were used: no introduced Fe (DOM
223 alone), 20 μmol L⁻¹ Fe (DOM-20Fe), and 80 μmol L⁻¹ Fe (DOM-80Fe; Table 2). The loadings
224 of Fe(III) on DOM ranged from 1 μmol Fe [mg]⁻¹ to 4 μmol Fe [mg]⁻¹ when calculated as the
225 ratio of the introduced μmol Fe to the mass of DOM (20 mg L⁻¹) used in the experiments (Table
226 2). The corresponding loading in the collected water was 0.22 μmol Fe [mg]⁻¹ based on our
227 analytical measurements for Fe (4.98 μmol L⁻¹) and DOC (945 μmol L⁻¹) explained in 2.3.1, and

228 assuming a 50% carbon content in the mass of DOM. The content of potential binding sites for
229 Fe was estimated at $3.7 \mu\text{mol} [\text{mg}]^{-1}$ as the content of proton-donating carboxyl and hydroxyl
230 groups in the reverse-osmosis-extracted DOM from our study lake [Vogt *et al.*, 2004;
231 unpublished data]. The introduced concentrations of Fe(III) resulted in a partial (DOM-20Fe) or
232 a full (DOM-80Fe) occupancy of potential binding sites on DOM. The actual complexation of
233 Fe(III) to DOM was not evaluated, but no visible precipitates were observed. The DOM-Fe(III)
234 created for the experiments may include oligomers of Fe(III) stabilized by DOM in addition to
235 true complexes between Fe(III) and DOM molecules.

236 The “DOM-Fe high/low P” experiment addressed the role of P in the biodegradation of
237 DOM-Fe using two concentrations of P (21 and $0.16 \mu\text{mol L}^{-1}$). The low concentration of P
238 matched the concentration of dissolved P in the study lake [Vähätalo *et al.*, 2003] or in oligo-
239 mesotrophic lakes in general [Wetzel, 2001]. In “DOM-Fe high/low P”, DOM-Fe was created as
240 in “DOM-Fe” experiments, but only one concentration of Fe ($60 \mu\text{mol L}^{-1}$) was used (Fig. 1,
241 Table 2).

242 The “Fe coating” experiment aimed to associate Fe on the surface structures of bacterial
243 cells and immobilize some of the cells into insoluble precipitates (Fig. 1, Table 2). This
244 experiment used a 0.5 mmol L^{-1} stock solution of Fe(II) prepared by dissolving $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$ in
245 0.1 mol L^{-1} HCl. The acidic (pH 2) solution of Fe(II) was slowly titrated to $\text{pH } 5.0 \pm 0.1$ and
246 incubated for 1 h to oxidize part of Fe(II) to Fe(III) [Ferris *et al.*, 1987]. The bacterial inoculum
247 was introduced as a ligand for Fe, and the pH of the mixture was titrated to 7. Finally, the rest of
248 ingredients (DOM, ALW, and nutrients) were introduced as in the other experiments, except that
249 two different concentrations of P were used ($0.16 \mu\text{mol L}^{-1}$ in #5, $21 \mu\text{mol L}^{-1}$ in #7, Table 2).

250 The “No Fe” experiment consisted of control treatments without introduced Fe. The growth
251 of bacteria on the introduced inorganic salts was tested in treatment #1. In #1, acidified MQ
252 water was titrated to pH 7, after which it received ALW, bacteria, and nutrients, including a low
253 concentration of GlyP, but no DOM. Treatment #2 evaluated whether bacteria can use GlyP as a
254 source of carbon. Treatment #2 was prepared similarly to #1, except that a high concentration of
255 GlyP ($21 \mu\text{mol L}^{-1}$) was used. Treatments #3 and #4 evaluated the growth of bacteria on DOM
256 without introduced Fe at a low and high concentration of GlyP, respectively. For #3 and #4, an
257 acidic solution of DOM was first titrated to pH 7 and then received ALW, nutrients, and bacteria,
258 as in the “DOM-Fe” and “DOM-Fe low/high P” experiments.

259 2.3 Analytical methods

260 2.3.1 Fe and DOC measurements

261 Fe samples were preserved by adding 50 μL super-purity nitric acid (Romil) to 10 mL of
262 samples. Fe concentrations were determined using inductively coupled plasma mass
263 spectroscopy (Elan Dynamic Reaction Cell II, Perkin-Elmer Sciex). DOC samples were acidified
264 to pH~2 with 1 mol L^{-1} HCl and measured with a total organic carbon analyzer (TOC-V_{CPN},
265 Shimadzu). The inorganic carbon was purged (by acidifying and bubbling) following a high
266 temperature ($670 \text{ }^\circ\text{C}$) catalytic combustion oxidation of organic carbon into CO_2 , which was
267 detected a by an infrared analyzer. The standard solutions for DOC measurement were prepared
268 from potassium hydrogen phthalate (VWR chemicals) dissolving in Milli-Q water. Milli-Q water
269 was used as blank [Benner and Strom, 1993].

270 2.3.2 Bacterial counting

271 Bacterial samples were collected after shaking the culture flasks, except in the “Fe coating”
272 experiment. These treatments included obvious precipitates, and only supernatant was collected

273 from the flasks without shaking. Collected bacterial samples (1 mL) were fixed with
274 paraformaldehyde (1% final concentration) and glutaraldehyde (0.05% final concentration),
275 incubated for 10 min in the dark and stored at $-86\text{ }^{\circ}\text{C}$ in an ultra-low temperature freezer
276 (Thermo Scientific Forma) [Marie *et al.*, 1996].

277 Bacterial densities were measured by flow cytometry (LSR II, BD Biosciences, USA)
278 [Gasol and Del Giorgio, 2000]. Bacterial samples were thawed at room temperature for 1 h, and
279 stained with SYBR Green I (Sigma-Aldrich) for 10 min in the dark before measurement. A
280 volume of 10 μL reference beads with a known density (CountbrightTM absolute counting beads,
281 Life TechnologiesTM, Invitrogen) was added to each 1 mL sample to relate the number of
282 detected bacterial cells to the volume. Bacterial densities (cells L^{-1}) were converted to bacterial
283 biomass ($\mu\text{mol C L}^{-1}$) using a carbon content of 30 fg C cell⁻¹ [Fukuda *et al.*, 1998].

284 2.3.3 Bacterial respiration

285 Bacterial respiration (BR) was estimated as the consumption of dissolved O_2 measured with
286 needle-type O_2 microsensor optodes (PreSens GmbH, Regensburg) [Warkentin *et al.*, 2007] at 15-
287 min intervals. The aliquots were closed in biological O_2 demand bottles incubated in dark
288 conditions in a water bath maintained at $20\text{ }^{\circ}\text{C}$ with a thermostat (Lauda Ecoline Staredition
289 RE112, Germany). An optode was inserted into the sample via a hole drilled through the ground-
290 glass stopper and sealed with parafilm. The drift of the instrument defining the detection limit for
291 BR was measured in three blank experiments in which Milli-Q water was incubated for 300
292 hours under conditions identical to the respiration measurements. During the blank experiments,
293 the apparent decline in O_2 was $1.5 \pm 0.5\ \mu\text{mol L}^{-1} (300\ \text{h})^{-1}$ (mean \pm sd, $n = 3$). The decline in
294 the concentration of O_2 was converted into an increase in the concentration of CO_2 , assuming a
295 1:1 molar ratio between the consumed O_2 and the produced CO_2 in BR. This respiratory quotient

296 is similar to earlier studies, which have used values ranging from 0.82 to 1.2 [*Søndergaard and*
297 *Middelboe, 1995; Del Giorgio and Cole, 1998; Cory et al., 2014*]. The temporal trend in
298 accumulated CO₂ (μmol C L⁻¹) was determined by a polynomial fitting to the measurements
299 using R-language and the smooth spline function from the R package “stats” [*R Core Team,*
300 2014].

301 2.3.4 Bacterial growth efficiency

302 The bacterial growth efficiency (BGE) was calculated by dividing the increase in bacterial
303 biomass (BP) by the sum of the increase in bacterial biomass and bacterial respiration (BR):
304 $BGE = (BP)/(BP+BR)$ [*Del Giorgio and Cole, 1998*]. The BGE in #5 may be an underestimate,
305 because bacteria immobilized with precipitates were not included in BP although they possibly
306 contributed to BR.

307 2.3.5 16S rRNA sequencing

308 Bacterial samples (1.5 mL) were collected on day 28 of the simultaneous “No Fe”, “Fe
309 coating”, and “DOM-Fe high/low P” experiments. The samples were centrifuged at 14000 rpm
310 for 30 min and the bacterial cell pellets were frozen at -20 °C for later extraction. Bacterial DNA
311 was extracted using Quick Extract DNA Extraction Solution (Epicentre) according to the
312 manufacturer’s instructions. From the extracts, the V1–V2 region of the 16S rRNA gene was
313 amplified using the universal bacterial primer pair 27F (5’-
314 AGAGAGTTTGATCMTGGCTCAG-3’) and 338r (TGCTGCCTCCCGTAGGAGT). A 30 μL
315 PCR reaction contained 15 μL 1×Dream Taq Master mix (Fermentas), 0.3 μmol L⁻¹ of each
316 primer, and 2 μL of the DNA sample. PCR amplification was carried out on a CFX96
317 thermocycler (Biorad) with 98 °C for 30 s, followed by 35 cycles of 98 °C for 10 s; 52 °C for 30
318 s; and 72 °C for 180 s, and a final elongation step of 5 min at 72 °C. Successful PCR products

319 were re-amplified for 9 cycles with the same primer pair, but including adaptor A (5'–
320 CCATCTCATCCCTGCGTGTCTCCGAC–3') and unique 10–12-bp-long barcodes at the
321 beginning of the forward primer and P1_338r (5'–CCTCTCTATGGGCAGTCGGTGAT
322 TGCTGCCTCCCGTAGGAGT–3') as the reverse primer to allow Ion Torrent sequencing and
323 assignment to specific samples. PCR products were cleaned using the Agencourt AMPure XP
324 magnetic beads purification system (Beckman Coulter) and quantified using the Qubit dsDNA
325 HS Assay Kit (Invitrogen). Amplicons were subsequently combined in equimolar concentrations
326 for sequencing. The product was then seeded into an Ion PGM Template OT2 reaction following
327 the manufacturer's instructions (Life Technologies). Templated beads were enriched using the
328 Ion OneTouch ES system and sequencing libraries were loaded on an Ion 314 Chip and
329 sequenced using the Ion PGM Sequencing 400 Kit. Sequences were analyzed using Mothur
330 software packages [*Boyle and Edmond, 1977*]. Sequences shorter than 200 bp or which
331 contained >2 ambiguities and a maximum of 8 homopolymers were removed. Unique sequences
332 were identified and aligned using the Silva bacteria database. Loosely aligned and chimeric
333 sequences were removed before taxonomic classification. After quality filtering, 174700 reads
334 were obtained, with an average of 8735 reads per sample (min = 3804, max = 11201).
335 Taxonomic assignment of the OTUs was carried out using the ribosomal database project (RDP)
336 reference database (trainset 9_032012) with a confidence threshold of 80%. The sequences were
337 added to the European Nucleotide Archive (ENA) under submission number PRJEB8364.
338 Similarities of the microbial communities were analyzed by cluster analysis using the Sorensen
339 similarity index and the PC-ORD 6.0 software package (MjM Software Design).

340 2.4 Statistical analyses

341 The design of “DOM-Fe” experiment included three replicated incubations for each
342 treatment, which allows to test differences between replicates. The differences were estimated
343 using standard deviation (SD) and shown as standard error bars in Fig. 2b. The designs of other
344 four experiments only included single incubation for each treatment, and therefore we were not
345 able to test differences between true replicates. However, we calculated the coefficient of
346 variation (CV) for each treatment of “DOM-Fe” experiment, which was used for estimating the
347 SD of bacterial production determinations in “No Fe”, “Fe coating”, and “DOM-Fe low/high P”
348 experiments.

349 The statistical differences between treatments were tested with paired t-test using two-tailed
350 distributions, which was performed using Microsoft Excel 2013. The level of significance was
351 set at $p = 0.05$.

352 **3 Results**

353 3.1 Effects of Fe on bacterial density

354 In the “Fe” experiment (Fig. 1, Tables 1–2), the introduction of Fe(III) (DOM+130Fe)
355 significantly reduced the density of bacteria growing on DOM compared with the corresponding
356 treatment without Fe (DOM alone; paired t-test, $t = 4.47$, $df = 9$, $p = 0.0016$; Fig. 2a). In this
357 experiment, Fe was potentially able to associate with DOM to form DOM-Fe, with GlyP to form
358 P-Fe, and/or with bacteria to form bacteria-Fe (Fig. 1, Table 2), and any of these complexes
359 could potentially have been responsible for the reduction in bacterial density (Fig. 2a).

360 3.1.1 Effects of DOM-Fe on bacterial density

361 The “DOM-Fe” experiment was designed to generate DOM-Fe (Fig. 1, Table 1–2), which
362 had no consistent negative effect on bacterial density (Fig. 2b). From day 4 to day 12, the

363 bacterial densities of the DOM-80Fe treatment were significantly higher than in the DOM alone
364 treatment (paired t-test, $t = -6.98$, $df = 7$, $p = 0.0002$). This experiment revealed that when Fe
365 was associated with DOM, it did not reduce the bacterial density, but to some extent even
366 stimulated bacterial growth.

367 The potential stimulatory role of DOM-Fe was further tested in the “DOM-Fe high/low P”
368 experiment (Fig. 1, Tables 1–2), in which the growth of bacteria was consistently highest with a
369 maximum density of $13 \pm 0.7 \times 10^9$ cells L^{-1} in treatment #9 with DOM-Fe and $21 \mu\text{mol } L^{-1}$
370 GlyP (Fig. 3a). In the corresponding treatment #4 without Fe, the maximum density of bacteria
371 was an order of magnitude lower ($2.4 \pm 0.4 \times 10^9$ cells L^{-1}) than in treatment #9 with DOM-Fe.
372 These results indicate that DOM-Fe was able to stimulate bacterial growth when the
373 concentration of GlyP was high (Figs 2 and 3a).

374 When the experiments were carried out with a low concentration of GlyP representative of
375 dissolved P in Lake Valkea-Kotinen ($0.16 \mu\text{mol } L^{-1}$ in #3 and #8), DOM-Fe reduced bacterial
376 densities (max $0.4 \pm 0.02 \times 10^9$ cells L^{-1} ; #8) to lower than one-third of those in the
377 corresponding treatment without Fe (max $1.5 \pm 0.3 \times 10^9$ cells L^{-1} ; #3, Fig. 3a). The bacterial
378 growth was consistently higher in the high ($21 \mu\text{mol } L^{-1}$, #4 and #9) than in the low ($0.16 \mu\text{mol}$
379 L^{-1} , #3 and #8) concentration of GlyP (Fig. 3a), indicating that a high concentration of GlyP
380 stimulated the growth of bacteria.

381 Because bacterial densities were elevated in the high concentration of GlyP (treatments #9
382 and #4; Fig. 3a), we tested whether bacteria can use GlyP as a carbon source (treatments #1 and
383 #2, Fig. 1). Bacteria reached a density that was less than two orders of magnitude lower in ALW
384 with $0.16 \mu\text{mol } L^{-1}$ GlyP ($0.06 \pm 0.01 \times 10^9$ cells L^{-1} in #1) or with $21 \mu\text{mol } L^{-1}$ GlyP ($0.02 \pm$
385 0.004×10^9 cells L^{-1} in #2) than in the corresponding treatments with DOM (#3 or #4,

386 respectively; Fig. 3b). These results indicate that GlyP or other salts in ALW (Table 1) were
387 negligible sources of organic carbon for bacteria, and GlyP acted as a source of P.

388 3.1.2 Effect of Fe coating on bacterial density

389 When bacteria were coated with Fe (“Fe coating”, #5–#7; Fig. 1, Table 2), obvious
390 precipitates were observed after a few hours of incubation. The planktonic bacterial density
391 measured above the precipitates reached $0.04 \pm 0.002 \times 10^9$ cells L^{-1} in treatment #5 with low P
392 and $0.19 \pm 0.009 \times 10^9$ cells L^{-1} in #7 with high P (Fig. 3b). No obvious increase in planktonic
393 bacterial numbers was found in treatment #6 without DOM (Fig. 3). The results of the “Fe
394 coating” experiments support the earlier findings: GlyP was not a source of carbon (#2, #6), but a
395 source of P and stimulated the growth of bacteria on DOM (Figs 3a and 3b). When Fe associated
396 with bacteria (#5 and #7), the bacterial densities were orders of magnitude lower than in the
397 DOM-Fe treatments (#8 and #9, Fig. 3a and 3b).

398 These results demonstrate that the growth of bacteria was dependent on the type of Fe
399 association. Fe associated with bacterial cells (Fe coating) or with P reduced bacterial densities,
400 but DOM-Fe in the presence of high P even increased the bacterial densities (Figs 1–3).

401 3.2 Effects of Fe on bacterial respiration

402 We selected four treatments, namely #3 (DOM alone), #5 (Fe coating with DOM), #8
403 (DOM-Fe with low P), and #9 (DOM-Fe with high P), to follow the cumulative bacterial
404 respiration ($\mu\text{mol C L}^{-1}$) during the incubations (Fig. 4). After a lag phase of several days, the
405 cumulative bacterial respiration was eventually highest and lowest in treatments #9 and #5,
406 respectively (Fig. 4), in agreement with the bacterial densities among the selected treatments
407 (Fig. 3). In contrast to the bacterial densities (Fig. 3), the cumulative bacterial respiration was

408 higher on DOM with Fe (#8) than without Fe (#3; paired t-test, $t = -52.6$, $df = 1538$, $p = 0$; Fig.
409 4), indicating that Fe also changed the metabolic performance of bacteria.

410 3.3 Effects of Fe on BGE

411 The metabolic performance was estimated as the BGE (Table 3) by dividing the
412 accumulated planktonic bacterial biomass (mol C; Fig. 3) by the estimated bacterial carbon
413 demand. The latter was calculated as the sum of the planktonic bacterial biomass (mol C; Fig. 3)
414 and bacterial respiration (mol C; Fig. 4), which also includes the potential respiration of bacteria
415 in the precipitated Fe-oxyhydroxides and the potential oxidation of Fe(II) by O₂ in treatment #5
416 (Fig. 4). The BGEs were highest in treatment #9 (DOM-Fe and 21 $\mu\text{mol L}^{-1}$ GlyP) followed by
417 treatment #3 (DOM alone, Table 3). The BGE was very low in treatment #8, DOM-Fe with a
418 low concentration of P, as well in treatment #5, in which bacteria were coated with Fe (Table 3).

419 3.4 Effects of Fe on the bacterial community composition

420 The bacterial inoculum primarily consisted of *Betaproteobacteria* (mean \pm SE, 67.0% \pm
421 1.4%) mostly affiliated to the genera *Duganella*, *Polynucleobacter*, and *Undibacterium*, and of
422 *Alphaproteobacteria* (12.9% \pm 0.3%), including the genus *Novosphingobium* (Figs 5 and 6,
423 Table S1). In the treatments without DOM and no significant growth (treatments #1 and #2), or
424 when Fe was coated on the bacterial surface (treatments #5–#7), these remained the major
425 classes together with *Actinobacteria* (Table S1). If DOM was added without Fe (treatments #3
426 and #4) or as DOM-Fe with high P (treatment #9), the community became dominated by
427 *Alphaproteobacteria*, and especially by the genus *Caulobacter* (Figs 5 and 6, Table S1). In these
428 treatments, the frequency of *Caulobacter*-associated sequences increased from 1% to 95% (Fig.
429 6). In the “No Fe” experiment with DOM and high P (#4), *Caulobacter*-associated sequences
430 (34% of sequences) were also accompanied by other *Alphaproteobacteria* (*Sphingomonas* and

431 *Bradyrhizobium*) and *Betaproteobacteria* (*Burkholderia* and *Sediminibacterium*) (Fig. 6 and
432 Table S1). Altogether, the experimental treatments changed the initial composition of the
433 bacterial community towards the dominance of *Caulobacter*, which was also primarily
434 responsible for highest bacterial biomass in the DOM-Fe treatment with high P.

435 **4 Discussion**

436 Our experimental results demonstrate that Fe has multiple and contrasting effects on
437 bacterial growth, respiration, growth efficiency, and the composition of the bacterial community.
438 Table 4 summarizes our main findings and outlines the division of the discussion into four
439 sections.

440 4.1 Fe coating and the formation of particulate Fe(oxy)hydroxide reduces bacterial growth and
441 the consumption of DOM

442 Many functional groups on the surface of bacteria, e.g., carboxylic, hydroxyl, and
443 phosphoryl, can bind Fe [Beveridge and Murray, 1980; Ferris *et al.*, 1987; González *et al.*,
444 2014]. At the beginning of our “Fe coating” experiments, the concentration of these binding sites
445 was 6.0×10^{-7} mmol L⁻¹ when calculated from the initial bacterial biomass of 0.08 $\mu\text{mol C L}^{-1}$
446 and 3.1×10^{-4} moles of proton-donating surface sites per gram of cells reported by *Ha et al.*
447 [2010]. The concentration of Fe used in the “Fe coating” experiment was eight orders of
448 magnitude higher than the available binding sites on the surface of bacteria, and must have
449 resulted in an extensive coating of the bacterial surface structures with Fe. The extensive
450 occupation of the surface binding sites by Fe can be expected to impair the normal functioning of
451 cell surfaces (e.g., the transport of solutes across cell membranes), which may partly explain the
452 low growth and respiration in the experiments with Fe-coated bacteria.

453 In the Fe coating experiments of the present study, red-brown precipitates were observed
454 after a few hours of incubation. These precipitates adsorbed and immobilized bacteria, because
455 the initial densities of planktonic bacteria in the Fe coating treatments were only a fraction of
456 those observed in the other treatments (Fig. 3). The growth of immobilized bacteria is expected
457 to be limited, for example, because Fe(oxy)hydroxides effectively adsorb negatively charged
458 ions such as DOM [Riedel *et al.*, 2012; Riedel *et al.*, 2013] and limit the substrate availability for
459 bacteria trapped in Fe(oxy)hydroxides. In the environment, the regrowth of bacteria or an
460 inflow/import of new bacteria likely compensates the immobilization of bacterioplankton into
461 Fe(oxy)hydroxides. Therefore, in most environments, the immobilization of bacteria into
462 Fe(III)(oxy)hydroxides has likely only low impact on the biodegradation of DOM.

463 The results of the Fe coating experiments additionally demonstrated that despite the
464 extensive coating and immobilization of the bacterial inoculum at the beginning of experiments,
465 some bacteria were able to grow as planktonic forms (treatments #7 in Fig. 3b). However, their
466 densities did not reach the levels found in the other DOM treatments (treatments #3, #4, #8, and
467 #9 in Fig. 3a), suggesting that Fe precipitates also reduced the availability of substrates for the
468 planktonic bacteria. The precipitated Fe(oxy)hydroxides can adsorb DOM from the water
469 column and convert it into a particulate form [Boyle and Edmond, 1977; Riedel *et al.*, 2012;
470 Riedel *et al.*, 2013; Swenson *et al.*, 2015]. Such adsorption of OM by particulate
471 Fe(oxy)hydroxides may lead to the long-term preservation of OM in marine [Lalonde *et al.*,
472 2012] and freshwater sediments [Kortelainen *et al.*, 2004; Einola *et al.*, 2011].

473 It is also possible that in our “Fe coating” experiments, the Fe(oxy)hydroxides adsorbed a
474 part of GlyP and reduced the availability of P to planktonic bacteria. The adsorption of P by
475 Fe(oxy)hydroxides in oxic sediments is the primary mechanism limiting the bioavailability of P,

476 which regulates the overall productivity of lakes [Wetzel, 2001], because osmotrophic organisms
477 such as bacteria or phytoplankton poorly utilize P bound to particulate Fe(oxy)hydroxides. Thus,
478 the immobilization of P into solid Fe(oxy)hydroxides may reduce the bioavailability of P,
479 bacterial growth, and the biodegradation of DOM.

480 4.2 Fe associated with DOM binds P and reduces bacterial growth

481 In the present study, bacterial growth on DOM was significantly higher in the high
482 concentration of P compared to the low P concentration, as earlier observed in our study lake
483 [Vähätalo *et al.*, 2003]. Bacteria from Lake Valkea-Kotinen reached a higher biomass in
484 hypolimnetic water with an elevated concentration of P than in epilimnetic water depleted in P
485 [Vähätalo *et al.*, 2003]. The availability of P has also been observed to limit the growth of
486 bacterioplankton in other lakes with a high concentration of DOM [Karlsson *et al.*, 2001; Vidal
487 *et al.*, 2011]. Bacterioplankton requires high amounts of P in its biomass, with a typical C-to-P
488 ratio of 45 [Goldman *et al.*, 1987]. According to this ratio, the low concentration of P ($0.16 \mu\text{mol}$
489 L^{-1}) can support $7.2 \mu\text{mol C L}^{-1}$ of bacterial biomass, which is close to the observed biomass of
490 bacteria ($3.6 \mu\text{mol C L}^{-1}$) grown on DOM in the low P treatment (treatment #3 in Fig. 3), but
491 lower than $33 \mu\text{mol C L}^{-1}$ found in the high P treatment #9 (Fig. 3). The results from the present
492 study and earlier investigations, as well as the stoichiometric calculations, indicate that the
493 maximum bacterial biomass in this study was limited by the availability of P in the treatments in
494 which an environmentally relevant low concentration of P was used.

495 In our study, DOM-Fe reduced the growth of bacteria when the concentration of P was low.
496 Fe(III) associated with DOM can bind phosphate to form DOM-Fe(III)-P associations [Francko
497 and Heath, 1982; De Haan *et al.*, 1990; Sundman *et al.*, 2016]. The photochemical release of P
498 from the DOM of our study lake indicates that DOM-Fe(III)-P are present in Lake Valkea-

499 Kotinen and can bind ca. 0.03–0.05 $\mu\text{mol P L}^{-1}$ [Vähätalo *et al.*, 2003]. In the present study, we
500 selected organic phosphate (GlyP) as a source of P to avoid the strong complexation between
501 Fe(III) and inorganic phosphate. In GlyP, one oxygen atom of phosphate forms an ester bond
502 with glycerol, but three other oxygen atoms of phosphate can potentially form a coordination
503 bond with Fe(III). Thus, it is likely that 60 $\mu\text{mol L}^{-1}$ DOM-Fe(III) bound a part of 0.16 $\mu\text{mol L}^{-1}$
504 GlyP into DOM-Fe(III)-P-Gly associations, where P and Gly refer to phosphate and glycerol
505 moieties of GlyP, respectively. The formation of DOM-Fe(III)-P-Gly can be expected to reduce
506 the availability of P, which was probably the primary reason for the reduced bacterial growth in
507 the treatments, in which the availability of P already limited the growth of bacteria without
508 introduced Fe(III). Fe has been shown to play a key role in regulating the availability of P in both
509 sediment and soils [Ekholm and Lehtoranta, 2011; Heiberg *et al.*, 2012; Baken *et al.*, 2015], but
510 our results indicate that DOM associated species of Fe can also regulate the availability of P to
511 bacteria and reduce the biodegradation of DOM in the water column.

512 Despite the suspected reduced bioavailability of P due to DOM-Fe(III)-P-Gly, bacteria did
513 grow on DOM, but their growth was delayed and associated with a marked consumption of O_2
514 (treatment #8 versus #3 in Figs 3 and 4). These results indicate that bacteria were able to
515 assimilate P (and DOM) from DOM-Fe(III)-P-Gly, but at an additional metabolic cost. The
516 photochemical and microbial reduction of Fe(III) in DOM-Fe(III)-P can break apart DOM, Fe(II)
517 and P [Francko and Heath, 1982; Cotner and Heath, 1990; Schröder *et al.*, 2003]). Therefore, it
518 is possible that microbes in our study retrieved P by reducing the Fe(III) in DOM-Fe(III)-P-Gly.

519 4.3 DOM-Fe(III) is bioavailable

520 According to our study, the association of Fe(III) with DOM does not reduce microbial
521 growth on DOM compared to DOM without Fe when P is not limiting microbial growth. In

522 agreement with our results, aerobic microbes such as *Pseudomonas*, a community of microbes
523 from soil or activated sludge, can degrade bidentate (or non-specified) complexes between citrate
524 and Fe(III) with similar or reduced rates compared to uncomplexed citric acid [Boudot *et al.*,
525 1989; Francis and Dodge, 1993; Nancharaiah *et al.*, 2006]. These findings also apply to fulvic
526 acid associated with Fe(III) [Boudot *et al.*, 1989]. The biodegradation rates of citrate or fulvic
527 acids markedly decrease when Fe(III) is introduced at amounts exceeding the binding capacity of
528 organic ligands and the substrates for microbes are adsorbed or immobilized into solid
529 Fe(oxy)hydroxides ([Boudot *et al.*, 1989]; treatments #5, #6, and #7 of the present study). Our
530 study, together with others [Boudot *et al.*, 1989; Francis and Dodge, 1993; Nancharaiah *et al.*,
531 2006], indicates that the association of Fe with DOM does not reduce the bioavailability of DOM
532 as long as DOM is not precipitated and adsorbed into insoluble metal (oxy)hydroxides.

533 Although some bacteria can take up a few specific organic Fe complexes (siderophore-Fe
534 and heme-Fe [Ma *et al.*, 2009]), little is known about the mechanism for the uptake of organic
535 moiety from DOM-Fe(III). When Fe is bound on a microbial substrate, the uptake of substrate
536 with Fe is expected to be blocked or reduced, because the Fe atom is nearly two times larger than
537 those of carbon, oxygen, and nitrogen, the common atoms in bacterial substrates [Pyykkö, 2015].
538 Therefore, Fe is likely extracellularly removed from a DOM-Fe(III) prior to the transport of the
539 DOM substrate into the cytoplasm. Extracellular reduction of DOM-associated Fe(III) followed
540 by the release of Fe(II) is a mechanism for Fe acquisition in cyanobacteria (e.g., *Synechocystis*
541 *sp.*) [Kranzler *et al.*, 2011; Lis *et al.*, 2015]. This mechanism can be also used for the uptake of
542 DOM substrate from DOM-Fe(III). Outer-membrane *c*-type cytochromes and pilin (in bacteria
543 that lack *c*-cytochromes) are crucial for transferring electrons to extracellular electron acceptors,
544 such as Fe(III) oxides, in soils and sediments [Richardson, 2000; Reguera *et al.*, 2005]. In

545 cyanobacteria, pilin (e.g., PilA1) facilitates the donation of electrons to external electron
546 acceptors, such as DOM-Fe(III) and Fe oxides [*Lamb et al.*, 2014]. Pili may also have
547 contributed to the bacterial consumption of DOM-Fe in our experiments, because *Caulobacter*
548 can have pili [*Skerker and Shapiro*, 2000].

549 4.4 DOM-Fe(III) stimulates the growth of bacteria

550 In some treatments of our study with a high concentration of Fe, the association of Fe(III)
551 with DOM increased microbial growth, respiration, and growth efficiency on DOM. This
552 increase may result from purely abiotic Fe-catalyzed reactions [*Pracht et al.*, 2001; *Studenroth et*
553 *al.*, 2013; *Comba et al.*, 2015] and/or involve the active metabolism of microbes, as described
554 earlier for fungi [*Arantes et al.*, 2012; *Rineau et al.*, 2012]. Abiotic reactions may already have
555 broken quinone-type parts of our DOM into small organic acids [*Studenroth et al.*, 2013; *Comba*
556 *et al.*, 2015] during the preparation of DOM-Fe under acidic starting conditions. This was
557 possibly seen as elevated O₂ consumption during the first four days of incubation in the Fe(III)
558 supplied treatments compared to the DOM alone treatment (Fig. 4). Therefore, it is possible that
559 the abiotic formation of oxalic, maleic, fumaric, and malonic acids found earlier in soils
560 [*Studenroth et al.*, 2013] may also take place in an aquatic environment rich in iron and the
561 humic type of DOM.

562 A steep increase in O₂ consumption by bacteria growing on DOM-Fe with a high
563 concentration of P after 12 days of incubation (Fig. 4) was not likely supported by the abiotic
564 formation of bioavailable carbon during the formation of DOM-Fe, but rather indicates the active
565 metabolism of bacteria to obtain carbon from DOM-Fe. In brown rot fungi, the utilization of Fe
566 in the biochemical Fenton reaction requires large investments in the form of organic compounds
567 or/and enzymes secreted in wood [*Arantes et al.*, 2012]. Brown rot fungi first secrete small

568 molecular mass organic acids (e.g., oxalic acid) to acidify the external milieu next to hyphae and
569 solubilize Fe(III), and then also reduced quinones such as 2,3-dimethoxyhydroquinone to reduce
570 Fe(III) to Fe(II) for the biochemical Fenton reaction [Arantes *et al.*, 2012]. The biochemical
571 Fenton reaction is profitable, as it facilitates access to cellulose, the primary carbon source of
572 fungi in wood. It is notable that the organic carbon content per unit volume is four orders of
573 magnitude higher than in a typical solution of DOM in freshwater. The active metabolism of
574 bacterioplankton for the utilization of DOM-Fe is probably different, simpler, and less costly
575 than the biochemical Fenton used by brown rot fungi.

576 Bacteria may produce superoxide to utilize DOM-Fe. Numerous bacterial phyla, such as
577 *Alphaproteobacteria*, including *Caulobacter*, can mediate single-electron transfer from their
578 intracellular metabolites such as NAD(P)H to dioxygen at their cell surface and thus generate
579 superoxide [Rose, 2012; Diaz *et al.*, 2013]. In circumneutral waters, the half-life of superoxide
580 ranges from tens of seconds to hours [Rose, 2012], which allows it to diffuse away from the cells
581 into the external milieu to reach DOM-Fe within the 50 μm to 500 μm range [Fenchel, 2002].
582 Superoxide can reduce DOM-associated Fe(III) to Fe(II), which can be oxidized back to Fe(III)
583 primarily by O_2 [Fujii *et al.*, 2008]. The oxidation of Fe(II) converts O_2 to superoxide, which can
584 be further converted to H_2O_2 [Fujii *et al.*, 2008]. H_2O_2 can react with Fe(II) and produce highly
585 reactive hydroxyl radicals (Fenton reaction, [Rose, 2012]). These hydroxyl radicals can
586 transform DOM into bioavailable substrates [Goldstone *et al.*, 2002]. As the generation of H_2O_2
587 requires the acidic form of superoxide, HOO^\bullet ($\text{pK}_a = 4.8$, [Rose, 2012]), the formation of H_2O_2
588 was presumably not as effective in our experiments (pH 7) as it can be in acidic conditions.

589 It is possible that oxidation-reduction reactions of Fe associated with DOM and initiated by
590 microbial superoxide lead to the breakdown of organic matter through mechanisms different

591 from the Fenton chemistry. For example, Fe catalyzes the breakage of the aromatic ring of
592 catechol or related derivatives in dioxygenase enzymes, which are also found in *Caulobacter*
593 [Orville *et al.*, 1997; Bugg and Winfield, 1998]. However, dioxygenase enzymes are located in
594 the cytoplasm [Arras *et al.*, 1998], which is an unlikely site for the enzymatic cleavage of DOM-
595 Fe(III). The same cleavage reaction can also take place without enzymes through a Fe(III)-
596 semiquinone-superoxide complex [Bugg and Winfield, 1998]. Fe(III) forms complexes
597 preferentially with aromatic moieties of DOM [Fujii *et al.*, 2014], indicating the close
598 association of Fe(III) with the quinonoid structures in DOM. When such complexes react with
599 superoxide, the oxidation of DOM and breakage of the quinonoid ring catalyzed by Fe(III) may
600 take place [Bugg and Winfield, 1998].

601 The electron donating (or accepting) capacity linked to quinonoid structures is about 0.6
602 $\mu\text{mol} [\text{mg}]^{-1}$ in Nordic Lake DOM [Aeschbacher *et al.*, 2012]. Assuming the same capacity for
603 our DOM, the concentration of electron donating (or accepting) group was $12 \mu\text{mol L}^{-1}$ in our
604 experiments. The related concentration of quinonoid structures can be estimated as $6 \mu\text{mol L}^{-1}$
605 assuming two electron donating (or accepting) sites for each quinonoid structure. A complete
606 breakage of quinonoid structures into bioavailable low molecular weight aliphatic (carbonyl)
607 compounds can release $36 \mu\text{mol L}^{-1}$ carbon, accounting for 6 carbons per quinonoid structure.
608 This could explain the enhanced microbial metabolism of *Caulobacter* in treatment #9. It is
609 notable that quinonoid structures constitute only a small part of the total aromatic content of
610 humic substances, which is, however, a potential source of new quinonoids through many types
611 of oxidative reactions [Aeschbacher *et al.*, 2012].

612 4.5 Environmental relevance and conclusions

613 The processes examined in this study, the associations of Fe with DOM, P, or cell surfaces
614 and the precipitation of Fe into insoluble forms, are common processes in numerous
615 environments (see *Xiao et al.* [2013]). The gradients of pH, redox potential and ionic strength in
616 soils and sediments as well as aquatic systems in their vicinity are the hotspots for the formation
617 of DOM-Fe [*Boyle and Edmond*, 1977; *Riedel et al.*, 2012 and 2013; *Neubauer et al.*, 2013b;
618 *Xiao et al.*, 2013]. If in these instances the loading of Fe exceeds the binding capacity of DOM,
619 insoluble precipitates of Fe(III)(oxy)hydroxides will form [*Nierop et al.*, 2002]. When the
620 precipitates of Fe(III)(oxy)hydroxides are associated with DOM and/or P [*Blomqvist et al.*, 2004;
621 *Helms et al.*, 2013; *Angelico et al.*, 2014], they direct the bioavailable forms of OM and P into
622 poorly bioavailable particulate forms and decrease the overall biodegradation of OM ([*Boudot et*
623 *al.*, 1989], this study). Earlier studies indicate that this decrease in biodegradation can be so
624 extensive, that it leads into a long term preservation of OM [*Kortelainen et al.*, 2004; *Einola et*
625 *al.*, 2011; *Lalonde et al.*, 2012]. Thus, Fe has a clear negative impact on biodegradation of DOM
626 when it converts dissolved and bioavailable forms of DOM and P into poorly bioavailable
627 particulate forms associated to Fe(III)(oxy)hydroxides.

628 Although Fe associated to DOM can be expected to reduce the availability of organic
629 component in DOM-Fe, this seems not to be the case [*Boudot et al.*, 1989; *Francis and Dodge*,
630 1993; *Nancharaiah et al.*, 2006; this study]. Even the microbial mechanisms for removing Fe
631 from DOM-Fe are poorly known, it is good to remember that DOM-Fe has existed in the Earth
632 as long as there has been organic matter and posed a challenge to microbial evolution since the
633 origin of life. Our study suggests that the association of Fe with DOM can increase the
634 biodegradation of DOM by bacterioplankton. The mechanism for this increase is likely different

635 than described earlier for fungi growing on solid substrates [Arantes *et al.*, 2012; Rineau *et al.*,
636 2012], and may involve abiotic and/or biochemical redox reactions of Fe [Pracht *et al.*, 2001;
637 Studenroth *et al.*, 2013; Comba *et al.*, 2015]. In our study, a single genus *Caulobacter* dominated
638 the bacterial communities when the biodegradation of DOM was stimulated by Fe. It is possible
639 that the active metabolisms of *Caulobacter* (e.g., superoxide produced by extracellular
640 oxidoreductases [Diaz *et al.*, 2013] can promote extracellular non-selective degradation of
641 humic-like DOM. Such mechanism would have a high environmental relevance, since humic-
642 like DOM dominates the pool of DOM in many soils, sediments, fresh and coastal waters. Due to
643 its heterogenous composition, the extracellular enzymatic hydrolysis of humic-like DOM is poor
644 [Arnosti, 2004] but its intense absorption of solar radiation makes it sensitive for photochemical
645 degradation [Vähätalo *et al.*, 2000]. Photodegradation takes place only on sunlit solid surfaces
646 [Vähätalo *et al.*, 1998] or in a shallow stratum of surface waters [Salonen and Vähätalo, 1994;
647 Vähätalo *et al.*, 2000]. Fe-stimulated biodegradation of DOM can target also such humic-like
648 DOM that remains below the sunlit surfaces in the dark. In aquatic environments, Fe-stimulated
649 biodegradation of DOM is expected to be most intensive at sites with high concentration of
650 DOM.-Fe. Such sites include low-order humic-rich streams and lakes with low concentrations of
651 Ca^{2+} and Mg^{2+} hydrologically closely connected to soils and sediments that act as sources of Fe.

652 The selective removal of Fe from water column with increasing residence time of water
653 [Köhler *et al.*, 2013; Weyhenmeyer *et al.*, 2014] decreases the contribution of Fe to the
654 biodegradation of DOM. The additional selective removal of Fe in marine waters [Sholkovitz,
655 1976] reduces the concentration of Fe to very low (nM) level [Boyd and Ellwood, 2010], which
656 contrasts to the orders of magnitude higher concentrations in freshwaters (e.g., a mean of 29 μM
657 in Finnish rivers, [Xiao *et al.*, 2015]). In the deep dark ocean, the turnover time of chromophoric

658 DOM (a tracer of Fe-poor humic-like DOM) is 634 years [Catalá *et al.*, 2015], while the
659 turnover time for bulk organic carbon (dominated by humic-like and Fe-rich DOM) in Swedish
660 lakes is 2.5 years [Algesten *et al.*, 2003; Weyhenmeyer *et al.*, 2014]. These turnover times are not
661 directly comparable, because the turnover time of OC in Swedish lakes includes sedimentation
662 and photodegradation although the latter explains <10% of OC loss [Koehler *et al.*, 2014]. The
663 comparison nevertheless indicates that the biodegradation rates of humic-like DOM are
664 considerably faster in Fe-rich freshwaters than in Fe-poor marine waters [Algesten *et al.*, 2003;
665 Catalá *et al.*, 2015]. Our study suggests that Fe associated with DOM can stimulate the
666 biodegradation of humic-like DOM in Fe-rich freshwaters.

667

668 **Acknowledgments**

669 This work was funded by the Finnish Cultural Foundation (103757-47394) and Kone
670 Foundation (35-3243), Finland, and by Academy of Finland grant 260797 and European
671 Research Council (ERC) Consolidator grant 615146 for M. Tiirola. We thank Timo Sara-Aho for
672 the measurement of water Fe concentrations and Sukithar Kochappi Rajan for the help in
673 bioinformatics. We also thank Prof. Rolf D. Vogt (University of Oslo) and Prof. Schmitt-Kopplin
674 Philippe (German Research Center for Environmental Health) for providing the carboxyl and
675 hydroxyl group data from Lake Valkea-Kotinen. The data used are presented in the figures,
676 tables, and supporting information which are available from the corresponding author upon
677 request (yihuaxiao2010@gmail.com). The sequences have been added to the European
678 Nucleotide Archive (ENA) under submission number PRJEB8364.

679 **Tables**

680 Table 1. Composition of inorganic ions in the bioassays.

Chemical	Final concentration ($\mu\text{mol L}^{-1}$)
<i>Artificial lake water (ALW)</i>	
NaCl	699
Na ₂ SO ₄	48.2
KCl	15.5
NaHCO ₃	3.99
KBr	1.41
H ₃ BO ₃	0.72
NaF	0.12
MgCl ₂ ·6H ₂ O	4.17
CaCl ₂ ·2H ₂ O	4.17
<i>Nutrient</i>	
NH ₄ Cl	208

681

682 Table 2. The concentrations of DOM, Fe, and GlyP in each treatment of the experiments. All
 683 treatments included ALW (Table 1) and bacterial inoculum introduced in the sequence shown in
 684 Fig. 1.

“Experiment” with treatments	DOM ($\mu\text{mol C L}^{-1}$)	Fe ($\mu\text{mol L}^{-1}$)	GlyP ($\mu\text{mol L}^{-1}$)
“Fe”			
DOM alone	948	(0.42)*	21
DOM+130Fe	948	130	21
“DOM-Fe”			
DOM alone	948	(0.42)*	21
DOM-20Fe	948	20	21
DOM-80Fe	948	80	21
“No Fe”			
#1 No DOM+low P	–	(0.25)*	0.16
#2 No DOM+high P	–	(0.25)*	21
#3 DOM+low P	948	(0.42)*	0.16
#4 DOM+high P	948	(0.42)*	21
“Fe coating”			
#5 (Fe coating)+DOM+low P	948	60	0.16
#6 (Fe coating)+No DOM+high P	–	60	21
#7 (Fe coating)+DOM+high P	948	60	21
“DOM-Fe high/low P”			
#8 (DOM-Fe)+low P	948	60	0.16
#9 (DOM-Fe)+high P	948	60	21

685 –, no addition of extracted DOM.

686 * Fe concentrations in parentheses indicate no addition of Fe, and the Fe is from the introduced original bacterial
 687 inoculum ($0.25 \mu\text{mol L}^{-1}$) and extracted DOM ($0.17 \mu\text{mol L}^{-1}$). “Fe” and “DOM-Fe” experiments were carried out
 688 consecutively, but “No Fe”, “Fe coating” and “DOM-Fe high/low P” experiments were conducted simultaneously.

689 Table 3. Bacterial growth efficiencies (BGE) determined for days 7 and 11 of treatments #3, #5,
 690 #8, and #9. Determinations used the bacterial biomass (Fig. 3) and accumulated cumulative
 691 bacterial respiration (Fig. 4).

Time	Treatments			
	#3 DOM+low P	#5† (Fe coating)+DOM+low P	#8 (DOM-Fe)+low P	#9 (DOM-Fe)+high P
7 d	21.1%	0.05%	-0.02%*	63.4%
11 d	17.5%	0.38%	0.26%	36.8%

692 * A negative BGE refers to a decline in the bacterial biomass during the bioassay.

693 † The biomass of bacteria associated with precipitates is not included in BP and thus BGE calculated as
 694 BP/(BP+BR) is possibly underestimated.

695 Table 4. The conclusions based on our results and references supporting them.

	Conclusions	Supporting references
1	Fe coating and the formation of particulate Fe(oxy)hydroxide reduce bacterial growth and the consumption of DOM (section 4.1).	[Boyle and Edmond, 1977; Riedel et al., 2012; Riedel et al., 2013; González et al., 2014]
2	Fe associated with DOM binds P and limits bacterial growth (section 4.2).	[Francko and Heath, 1982; De Haan et al., 1990; Karlsson et al., 2001; Vähätalo et al., 2003; Vidal et al., 2011; Sundman et al., 2016]
3	DOM-Fe is bioavailable (section 4.3).	[Boudot et al., 1989; Francis and Dodge, 1993; Nancharaiah et al., 2006]
4	Fe associated with DOM can stimulate bacterial growth and the biodegradation of DOM (section 4.4).	Abiotic [Pracht et al., 2001; Studenroth et al., 2013; Comba et al., 2015]; biochemical Fenton [Arantes et al., 2012; Rineau et al., 2012]; superoxide mediated [Rose, 2012; Diaz et al., 2013]; enzyme-like reactions [Bugg and Winfield, 1998]

696

697 **Figures captions**

698 Figure 1. The preparation of experiments to address the study questions. The preparation of
699 experiments shows the sequence of introduction of solutes and bacteria to acidified (pH 2) Milli-
700 Q water during the titration (with NaOH). Blue and orange colors indicate that “Fe” and “DOM-
701 Fe” experiments were carried out consecutively. The green color indicates that “No Fe”, “Fe
702 coating” and “DOM-Fe high/low P” were carried out simultaneously. Nutrients refer to the
703 solutions of NH₄Cl and glycerophosphate (GlyP; Tables 1–2). ALW is the solution of inorganic
704 ions (Table 1). In the experiments marked with *, some treatments did not receive Fe(III) or
705 DOM (Table 2).

706 Figure 2. Bacterial density and biomass in the “Fe” (a) and “DOM-Fe” (b) experiments. (a) The
707 “Fe” experiment included two treatments: DOM alone and DOM with 130 μmol L⁻¹ Fe. (b) The
708 “DOM-Fe” experiment included three treatments: DOM alone, DOM-20Fe (DOM with 20 μmol
709 L⁻¹ Fe), and DOM-80Fe (DOM with 80 μmol L⁻¹ Fe). Standard error bars in panel b were
710 calculated from three replicated incubations. The experimental design is presented in Fig. 1 and
711 Tables 1–2.

712 Figure 3. Bacterial density and biomass in (a) the “DOM-Fe low/high P” and (b) “Fe coating”
713 experiments with their corresponding “No Fe” controls. Panel (a) shows the experiments (#3–4,
714 8–9) that addressed the impact of P and the association of Fe with DOM on the bacterial growth.
715 Panel (b) shows the experiments that addressed bacterial growth when coated with Fe (#5–7) or
716 when grown in artificial lake water without DOM and Fe (#1–2). For clarity, the panels have
717 different scales. Standard error bars represent the typical variability of three replicated
718 incubations in the “DOM-Fe” experiment (Fig. 2). The experimental design for the treatments is
719 presented in Fig. 1 and Tables 1–2.

720 Figure 4. Cumulative bacterial respiration during treatments #3, #5, #8, and #9 explained in
721 Table 2 and Fig. 1. Milli-Q represents the blank and shows apparent respiration in ion-exchanged
722 water without introduced bacteria.

723 Figure 5. Dendrogram of Sorensen cluster analysis and the log-transformed percentage of
724 sequences (range 0–98%) assigned at the subclass level in the original inoculum (triplicates) and
725 on day 28 of treatments #1–#9 (in duplicate, except #9). The average standard error for duplicate
726 (or triplicate) samples was 1.2% when calculated for the class *Alphaproteobacteria*. The
727 percentage of the sequences in main bacterial phyla and genus-level assignments are shown in
728 supplementary data Table S1. Treatments #1–#9 are explained in Fig. 1 and Table 2.

729 Figure 6. Taxonomic classification of the 16S rRNA gene sequences in the original inoculum
730 and treatments #3, #4, #8, and #9 on day 28. Genus-level percentage assignments of sequences
731 (Table S1) are shown in each pie. *Caulobacter* (red slice) represented <1% of bacterial
732 community in both original inoculum and #8, but dominated in treatments #3, #4, and #9 after
733 incubation. The pie area of treatments #3, #4, #8, and #9 was plotted according to the cube root
734 of the bacterial biomass (BP). The treatments are explained in Fig. 1 and Table 2. Results are
735 shown in genus level in Table S1.

736

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