



1 **Si-C interactions during degradation of the diatom *Skeletonema***
2 ***marinoi***
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27 Abstract

28 While a relationship between ballast and carbon in sedimenting particles has been well-
29 documented, the mechanistic basis of this interaction is still under debate. One hypothesis is that
30 mineral ballast protects sinking organic matter from degradation. To test this idea, we undertook
31 a laboratory experiment using the diatom *Skeletonema marinoi* to study in parallel the
32 dissolution of one of the most common mineral ballasts, biogenic silica (bSiO₂), and the
33 associated degradation of organic matter. Three different models were applied to our results to
34 help elucidate the mechanisms driving bSiO₂ dissolution and organic compound degradation.
35 Results of this modelling exercise suggest that the diatom frustule is made up of two bSiO₂
36 phases that dissolve simultaneously, but at different rates. In our experiments, the first phase was
37 more soluble ($k_{bSiO_2} = 0.27 \text{ d}^{-1}$) and made up 31% of the total bSiO₂. In this phase, bSiO₂ was
38 mainly associated with membrane lipids and the amino acids glutamic acid, tyrosine, and
39 leucine. The second phase was more refractory ($k_{bSiO_2} = 0.016 \text{ d}^{-1}$), and contained more neutral
40 lipid alcohols and glycine. Until it dissolved, the first bSiO₂ phase effectively protected much of
41 the organic matter from degradation: POC degradation rate constants increased from 0.025 d^{-1}
42 to 0.082 d^{-1} after the total dissolution of this phase, and PON degradation rate constants
43 increased from 0.030 d^{-1} to 0.094 d^{-1} . Similar to POC and PON, the THAA degradation rate
44 constant increased from 0.054 d^{-1} to 0.139 d^{-1} after dissolution of the first bSiO₂ phase. The
45 higher THAA degradation rate constant is attributed to a pool of amino acids that was produced
46 during silicification and enclosed between the two silica phases. This pool of amino acids might
47 come from the incorporation of silica deposition vesicles into the diatom wall and might not be
48 directly associated with bSiO₂. In contrast, most lipid degradation was not prevented by
49 association with the more soluble bSiO₂ phase as the average lipid degradation rate constant
50 decreased from 0.048 d^{-1} to 0.010 d^{-1} after 17 days of degradation; This suggests that most
51 lipids were associated to rather than protected by silica, except pigments that appeared resistant

52 to degradation, independantly from silica dissolution. When the only organic compounds
53 remaining were associated with the second bSiO₂ phase, degradation rate constants decreased
54 greatly; concentrations changed only slightly after day 25.

55

Key Words: Biogenic silica, dissolution, carbon, amino acids, lipids, degradation, diatom

56 1. Introduction

57 Organic carbon produced in the ocean's surface layer by phytoplankton is conveyed to depth
58 by particle sedimentation, and fluxes of carbon and minerals (CaCO_3 , SiO_2 and aluminosilicates)
59 are highly correlated in the deep water column. Based on these observations, Armstrong *et al.*
60 (2002) highlighted the importance of modeling both carbon and mineral fluxes at the same time.
61 Mineral ballast (CaCO_3 of coccolithophorids; SiO_2 of diatoms; aluminosilicates in dust) provide
62 excess density needed for organic matter to sink; SiO_2 and carbonate sedimentation are also
63 linked through the ability of phytoplankton to aggregate and through grazing by zooplankton.
64 The combination of these processes strongly increases the sedimentation rate of phytoplankton
65 (e.g., Gehlen *et al.*, 2006; Moriceau *et al.*, 2007).

66 The role of mineral ballast in carbon transport is more complex than a simple impact on
67 excess density (Lee *et al.*, 2008), but we are far from fully understanding the processes involved.
68 Lee *et al.* (2000) and Hedges *et al.* (2001) hypothesized that mineral ballast could protect organic
69 carbon from degradation; their hypothesis is consistent with the observation of Ingalls *et al.*
70 (2006) that organic matter was more degraded in areas where diatoms were not the dominant
71 bloom species when compared to sites where diatoms were the main phytoplankton group. Engel
72 *et al.* (2008) also showed that the presence of the calcite test in coccolithophorids lowers the
73 POC degradation rate during the recycling of these cells. Continuously increasing pressure
74 reduced rates of SiO_2 dissolution of diatom detritus relative to rates measured under
75 atmospheric pressure conditions (Tamburini *et al.* 2006). In parallel, naturally collected sinking
76 particles, were also less degraded by prokaryotes when pressure was continuously increased to
77 simulate descent from 200 to 1500 (Tamburini *et al.* 2008). Despite all these findings, few
78 studies (e.g., Ingalls *et al.*, 2003; 2006) have investigated both organic matter degradation and
79 biogenic mineral dissolution in natural settings. The work of Engel *et al.* (2008) investigated the

80 role of CaCO_3 in carbon degradation, while the present study aims to better understand the role
81 of Si-C interactions during diatom degradation.

82 Diatoms are the dominant species in many ecosystems; they are responsible for up to 35% of
83 the total primary production in oligotrophic oceans and up to 75% in coastal waters and the
84 Southern Ocean (Nelson *et al.*, 1995; Tréguer *et al.*, 1995). Jin *et al.* (2006) estimated their
85 global contribution to net primary production and to carbon export to be 15% and 40%,
86 respectively. The high diatom contributions to primary production and carbon export, could
87 potentially explain the empiric relation established by Ragueneau *et al.* (2002). This relation
88 shows that Si/C ratios decrease with depth and follow the same pattern everywhere in the world
89 ocean. Is there a link between bSiO_2 dissolution and POC degradation such as the one
90 hypothesized in the work cited above?

91 The objective of the present study was to understand how biogenic silica influences the
92 degradation of diatom organic carbon, and conversely the role of organic compounds in bSiO_2
93 dissolution. With this aim, a monospecific culture of the diatom *Skeletonema marinoi* was
94 incubated in the presence of a natural coastal bacterial community and allowed to degrade over a
95 102-day period. bSiO_2 dissolution and the quantity and composition of organic compounds,
96 including amino acids and lipids, were assessed throughout the incubation period and used to
97 investigate Si-C interactions during decomposition. Three dissolution/degradation models were
98 applied to the experimental data to elucidate the dissolution/degradation pattern of the
99 components of *S. marinoi*. This modeling experiment yields a better understanding of the
100 structure of the diatom frustule in *S. marinoi* and of the role of Si-C interactions during diatom
101 recycling.

102

103 **2. Material and methods**

104 **2.1 Biodegradation experiment**

105 *Skeletonema marinoi* (CCAP 1077/3) obtained from IFREMER (Argenton station, France) was
106 grown in f/2 medium (Guillard and Ryther, 1962; Guillard, 1975) under 12/12 dark/light
107 illumination. When cells reached stationary growth phase (6.5×10^6 cells ml⁻¹), they were
108 transferred into a 4°C chamber and kept in the dark for 5 days. During this period, cells sank to
109 the bottom of the flask, and previous tests showed that diatom viability (number of living cells
110 versus total cells) decreased (unpublished data, method described in Garvey *et al.* 2007). The
111 supernatant was poured off, and the overlying medium was replaced with natural seawater that
112 had been passed through a 0.7- μ m GFF filter to preserve the natural bacteria assemblage. The
113 seawater was collected from a small inlet (Endoume) near Marseille, France, at the end of fall,
114 when the water is naturally poor in silicic acid (dSi~2.5 μ M). The mixture of *S. marinoi* and
115 filtered sea water was then transferred to an incubation flask equipped with a magnetic stirrer
116 and a stopper through which gas exchange could occur via a 0.2- μ m Swinnex® filter. The
117 diatoms were incubated for 102 days in the dark at 20°C. Using a peristaltic pump, samples were
118 taken daily for the first 21 days and then at 23, 25, 46, 50, and 102 days; triplicate samples were
119 taken at 0, 5, 11, 46, 50, and 102 days. The sampled solution was well-mixed, allowing the ratio
120 of solid matter to solution to remain constant (Dixit *et al.*, 2001). Ten percent of the liquid
121 volume remained at the end of the experiment. Chemical parameters measured were biogenic
122 silica (bSiO₂), silicic acid (dSi), particulate organic carbon and nitrogen (POC, PON), dissolved
123 organic carbon (DOC), total particulate lipids (TLip), and total hydrolyzable amino acids
124 (THAA). In addition total bacterial abundances (diamidinophenylindole: DAPI counts) were
125 counted. Si contamination by dissolution of glassware was measured by analyzing dSi in an
126 incubation bottle with no cells added. We also sampled controls poisoned with 20 mg l⁻¹ HgCl₂
127 at 4 times (0, 2, 5, and 11 days) to verify that degradation was due to bacteria and not abiotic
128 factors.

129

130 **2.2 Analytical Methods**

131 *Biogenic Silica (bSiO₂)* was determined at the beginning and end of the experiment using
132 a variation of the method of Ragueneau and Tréguer (1994). As no lithogenic silica was present
133 in the algal culture, the second digestion step using HF was not necessary. Ten-ml samples were
134 filtered onto 0.2- μ m polycarbonate filters. Filters were analyzed for bSiO₂ and the filtrate for
135 dSi. For bSiO₂, filters were digested in 20 ml of 0.2N NaOH for three hours at 95°C to ensure
136 the dissolution of all bSiO₂; dSi concentrations in the solution remained far below the solubility
137 equilibrium of bSiO₂ at all times. After cooling, the solution was acidified with 5 ml of 1N HCl,
138 centrifuged to remove remaining solids, and analyzed for dSi. The precision for triplicate
139 measurements of bSiO₂ was < 5%.

140 *Silicic acid (dSi)* concentrations were determined on 10-ml filtered samples and on
141 digested bSiO₂ samples using the molybdate blue spectrophotometric method of Mullin and
142 Riley (1965), as adapted by Tréguer and Le Corre (1975) and modified by Gordon *et al.* (1993)
143 for use in segmented flow colorimetry. We used a Bran and Luebbe Technicon Autoanalyzer
144 (<1% precision).

145 *POC* and *PON* concentrations were measured using a Carlo Erba NA 2100 CN analyzer
146 coupled to a Finnigan Delta S mass spectrometer. Five-ml samples were filtered through 0.7- μ m
147 GFF filters. The filters were desiccated overnight in an oven at 50°C and then placed in tin
148 capsules to be introduced into the oven of the analyzer. The precision for triplicate N analyses
149 was \pm 1-6%, and for C analysis \pm 1-5%.

150 *DOC* was analyzed after filtration through 0.7- μ m GFF filters; 10 ml of each sample was
151 transferred into glass ampoules and sealed after addition of H₃PO₄ as preservative. All glassware
152 was pre-rinsed with 1N HCl and Milli-Q water before being combusted at 465°C; care was taken
153 to minimize contamination during sampling and handling. DOC was measured by high-
154 temperature catalytic oxidation using a Shimadzu TOC 5000 Analyzer (Sempéré *et al.*, 2003;
155 Sohrin and Sempéré, 2005). Samples were acidified to pH 1 with 85% phosphoric acid and
156 bubbled for 10 minutes with CO₂-free air to purge them of inorganic carbon. Three or four 100

157 μl replicates of each sample were injected into the 680 °C column. The precision of these
158 replicates was $\leq 6\%$.

159 *Total particulate lipids* were analyzed after filtering 10 ml samples onto 0.7- μm GFF
160 glass fiber filters. Filters were extracted according to Bligh and Dyer (1959). Lipid extracts
161 were separated into classes of compounds and quantified on an Iatroscan model MK-6s (Iatron,
162 Tokyo; H_2 flow 160 ml min^{-1} ; air flow 2 l min^{-1}) as described by Goutx *et al.* (2007). The
163 elution scheme allows reliable separation and quantification of degradation metabolites from
164 acyl-lipid classes (Striby *et al.*, 1999). Total particulate lipids (TLip) are the sum of the
165 separated lipid classes (Table 1). In the present work, the variability within triplicates was <
166 13%.

167 *Amino acids* were analyzed on 0.7- μm GFF filters after filtration of 10-ml samples.
168 Thawed filters were treated as described in the study of Ingalls *et al.* (2003). Individual
169 compounds were separated by HPLC using pre-column OPA derivatization after acid hydrolysis
170 as described in Lee and Cronin (1982) and Lee *et al.* (2000). Amino acids were detected by
171 fluorescence and identified by comparison to retention times of standards made from an amino
172 acid mixture (Pierce, Standard H). The non-protein amino acids β -alanine and γ -aminobutyric
173 acid (BALA and GABA) were added individually to the standard mixture. Aspartic acid (ASP)
174 and glutamic acid (GLU) measurements include the hydrolysis products of asparagine and
175 glutamine. THAA is the sum of the 16 characterized amino acids (Table 1). Variation among
176 replicates was generally 15-30%. LYS replicates, however, varied more greatly at times, e.g.,
177 50% at day 11.

178 *Total bacterial abundances (DAPI counts)*: Subsamples for bacterial cell counts were
179 fixed immediately with buffered formalin (final volume 2%). Cells were collected onto a 25-mm
180 0.2- μm polycarbonate Nuclepore® membrane and stained with diamidinophenylindole (DAPI;
181 Porter and Feig, 1980). Slides were stored frozen until counting by epifluorescence microscopy
182 (Olympus, BH2).

183

184 2.3 Kinetics

185 Kinetic parameters were calculated over the first 25 days where experimental data are
186 available every 1-2 days. For each compound of interest we tested three degradation/dissolution
187 models. Model 1 is a simple first-order rate equation as described in Greenwood *et al.* (2001)
188 and used in many dissolution studies (e.g. Kamatani and Riley, 1979; Kamatani *et al.*, 1980;
189 Kamatani, 1982):

$$190 \quad \hat{C}(t) = C_0 \exp(-k t), \quad (1)$$

191 where $\hat{C}(t)$ is the concentration (μM) estimated at time t (d), C_0 is the initial concentration, and
192 k is the dissolution/degradation rate constant (d^{-1}).

193 Model 2 assumes simultaneous dissolution/degradation of two phases. The equation used
194 is similar to that used for carbon degradation in the study of Westrich and Berner (1984):

$$195 \quad \hat{C}(t) = C_1 \exp(-k_1 t) + C_2 \exp(-k_2 t) \quad (2)$$

196 In Model 2, four parameters are estimated: C_1 and C_2 are concentrations (μM) of phase or pool 1
197 and 2, and k_1 and k_2 (d^{-1}) are their respective dissolution or degradation rate constants.

198 As it uses 2 more parameters, Model 2 always gives a better fit than Model 1 except
199 when the initial degradation rate is slower than later rates. In this specific case Model 2
200 performs no better than Model 1. We therefore developed Model 3, which employs one first-
201 order equation initially, and a second first-order equation after that. The time at which the
202 dissolution/degradation rate constant changes is called the substitution time (t_s), and is allowed
203 to take on any value >0 .

$$204 \quad \hat{C}(t) = C_0 \exp(-k_1 t), \quad 0 < t < t_s; \quad (3a)$$

$$205 \quad \hat{C}(t) = C(t_s) \exp(-k_2 t), \quad t > t_s. \quad (3b)$$

206 Model 3 also contains 4 parameters.

207 If dissolution/degradation for a given compound is best reconstructed using Model 2, this
 208 compound is constituted by at least two phases or pools; on the other hand if Model 3 gives a
 209 better description of the dissolution/degradation pattern, either the compound studied is present
 210 in 2 phases/pools remineralizing one after the other, or a change in environmental parameters
 211 provoked a change in the dissolution/degradation rate constant at time t_s .

212 In addition, to allow direct comparison of the degradation/dissolution pattern among all
 213 compounds, and between this study and previous studies, an initial disappearance rate constant
 214 was calculated for each compound over the first 10 days using Model 1.

215 **2.4 Statistics**

216 Each fit was optimized by maximizing the likelihood statistic $\log(L)$ as described in
 217 equation 4 (Armstrong *et al.*, 2002, and references therein). Eq. (4) is based on a Gaussian
 218 distribution with a constant variance on a logarithmic scale:

$$219 \quad \log(L) = -\frac{N}{2} \times \log \left(\frac{\sum (\log(\hat{C}_j) - \log(C_j))^2}{N} \right), \quad (4)$$

220 where N is the number of data points, C_j is a measured concentration for data point j , and the \hat{C}_j
 221 is the corresponding model prediction. The difference in $\log(L)$ ($\Delta \log(L)$) between fits of two
 222 different models to the same data gives the goodness of fit of one model compared to the other.
 223 If one model gives a value for $\log(L)$ that is at least 2 points higher per added parameter than
 224 another model, it is considered to fit the data better (Hilborn and Mangel, 1997). In the present
 225 work, the simplest model (Model 1) was considered to be the best fit unless Model 2 or Model 3
 226 yielded a $\log(L)$ more than 4 points better than that of Model 1.

227

228 **3. Results**

229

230 **3.1 Change in biochemical composition of the diatom *Skeletonema marinoi* over time**

231 *3.1.1 General trends*

232 Changes in bSiO₂, POC, TLip and THAA concentrations over time are shown in
 233 logarithmic scale in Fig. 1. While bSiO₂ concentrations decreased smoothly over the first 25 d,
 234 POC, PON and THAA concentrations decreased until about day 14, when the loss rate increased,
 235 especially for THAA. In contrast, TLip concentration decreased rapidly at the beginning of the
 236 experiment and reached a plateau after day 13.

237 Bacterial concentrations started at $0.33 \pm 0.03 \times 10^6$ cell ml⁻¹ and peaked at day 14 with
 238 a concentration of $30 \pm 2.7 \times 10^6$ cell ml⁻¹ (Fig. 2). The bacterial population increased between
 239 days 0 and 14 with a rate equal to 0.015 d^{-1} (calculated between days 2 and 14) and then
 240 generally stabilized reaching a final concentration of $20 \pm 4 \times 10^6$ cell ml⁻¹ until the end of the
 241 experiment. The bacterial growth efficiency (bacterial carbon increase divided by POC decrease)
 242 between days 0 and 14 was 2%. Bacterial carbon made up a maximum of $2.4 \pm 0.6\%$ of the POC.

243 TOC concentrations over time showed a pattern similar to those of POC (Fig. 3). DOC
 244 concentrations increased slightly ($5.6 \pm 0.2 \text{ mg C L}^{-1}$) but much less than POC decreased (62 ± 3
 245 mg C L^{-1}). The bacterial carbon (C_{bact}) is so low compared to the algal organic carbon that the
 246 mineralization rate for POC algal ($\text{POC} + \text{DOC} - C_{\text{bact}}$) is the same as for the total organic carbon
 247 ($C_{\text{org}} = \text{POC} + \text{DOC}$). This rate calculated as the slope of TOC change over time (Fig. 3) was
 248 $2.68 \text{ mg C L}^{-1} \text{ d}^{-1}$ during the first 20 days of the experiment and was equivalent to 91% of the
 249 POC loss.

250

251 *3.1.2 Initial biochemical composition*

252 At the beginning of the experiment, the Si/POC ratio was 0.09 ± 0.01 , which is slightly
 253 lower than the value of 0.13 measured in fresh diatoms by Brzezinski (1985) but in the range of
 254 coastal diatoms measured by Rousseau *et al.* (2002). TLip made up $19 \pm 2\%$ of *S. marinoi*

255 organic carbon which is a little bit higher than Lip/POC ratios measured previously for the same
256 specie (Lavens and Sorgeloos, 1996). TLip mainly included FFA and other degradation
257 metabolites (ALC and MG; see Table 1 for abbreviations) (Fig. 4a). Cellular membrane
258 phospholipids (PE, DPG+PG) and chloroplast membrane glycolipids (MGDG) accounted for 10
259 $\pm 1\%$ and $13 \pm 1\%$ of TLip, respectively. FFA were the most abundant lipid degradation
260 metabolites ($24.8 \pm 0.5\%$) among those present. PIG included both chlorophyll α and its
261 degradation products (Striby *et al.*, 1999); PIG was the largest lipid class (initially $41 \pm 5\%$; Fig.
262 4a). ST are involved in membrane rigidity (Parrish, 1988); they were initially minor components
263 of *S. marinoi*.

264 THAA constituted a larger portion ($36 \pm 9\%$) of total organic carbon than the lipids,
265 similar to the 45% found in *Thalassiosira weissflogii* by Cowie and Hedges (1996) and the 25%
266 observed in diatom-rich sediments by Ingalls *et al.* (2006). THAA include the monomer
267 constituents of protein as well as adsorbed amino acids and peptides. Sixteen amino acids were
268 quantified. GLU, ASP and LEU (see Table 1 for abbreviations) together made up one third of
269 the THAA, each more than $11 \pm 3\%$ (Table 2). Other amino acids were between $2.1 \pm 0.6\%$ and
270 $9.3 \pm 2.8\%$ of the THAA except for MET and GABA, which were less than 0.8%. As GABA
271 and MET concentrations were very low throughout the incubation, they are not described in the
272 following paragraphs. The initial mole% amino acid compositions we found for *S. marinoi*
273 (Table 2) were very similar in pattern to those of cultured diatoms reported by Ingalls *et al.*
274 (2003) and Cowie and Hedges (1996), with highest mole% values for ASP, GLU, and GLY. *S.*
275 *marinoi* was higher in mole% LEU than in reports of other diatoms. THAA do not include the
276 amino acids incorporated inside the silica frustule, unless part of the frustule is dissolved during
277 acid hydrolysis (see later discussion). We define Si-bound amino acids as Si-THAA as in Ingalls
278 *et al.* (2003).

279

280 *3.1.3 Change in biochemical composition during degradation*

281 Si/POC decreased from 0.09 ± 0.01 mol of Si/mol of C to 0.06 ± 0.01 mol of Si/mol of C
282 during the first 2 days of incubation and then stabilized until day 15 of the experiment. After
283 increasing to 0.11 ± 0.01 mol of Si/mol of C between days 15 and 21, the Si/POC ratio remained
284 constant until the end of the experiment. TLip/POC varied between 0.13 ± 0.02 mol of C/mol of
285 C and 0.23 ± 0.03 mol of C/mol of C during the first 50 days. Then the ratio decreased to a final
286 value of 0.06 ± 0.01 mol of C/mol of C at day 102. THAA/POC decreased regularly during the
287 whole experiment from 0.36 ± 0.09 mol of C/mol of C initially to 0.10 ± 0.02 mol of C/mol of C
288 after 102 days, except for a sudden increase between day 11 and 15 from 0.28 ± 0.7 mol of
289 C/mol of C to 0.38 ± 0.10 mol of C/mol of C.

290 Most of the change in TLip composition (Fig. 4a) occurred between days 0 and 25. Most
291 compounds decreased or remained the same relative to TLip (mol of C/mol of C) except for PIG,
292 which increased from $41 \pm 5\%$ to $80 \pm 7\%$ of the TLip over the course of the experiment.
293 Relative concentrations (mol of C/mol of C) of FFA, the second most abundant lipid class in the
294 algae, decreased regularly from $24.8 \pm 0.5\%$ to $4.0 \pm 0.4\%$. MGDG initially made up $13 \pm 1\%$ of
295 TLip, but totally disappeared by day 4. The MG contribution was constant ($7.0 \pm 0.3\%$) until day
296 14, when it was completely degraded. The contribution of membrane lipids, the glycolipid
297 MGDG and the phospholipids (PE and DPG+PG) to TLip was low compared to results from
298 Berge *et al.* (1995) and d'Ippolito *et al.* (2004). However, lipid composition is highly dependent
299 on culture conditions (d'Ippolito *et al.*, 2004), and in our case the high FFA content probably
300 masked the relative contribution from membrane lipids.

301 The THAA composition was relatively constant throughout the degradation experiment
302 except between days 15 and 20 where we observed a strong peak of GLY, which increased from
303 $13 \pm 2\%$ to $33 \pm 8\%$ (Fig. 4b). The relative concentrations of HIS (data not shown) and LYS also
304 peaked slightly between days 15 and 20. Relative proportions of other amino acids especially
305 ASP decreased at this time in response to the increases in HIS, GLY and LYS.

306

307 3.2 Dissolution and degradation kinetics of *S. marinoi* constituents

308 3.2.1 Silica kinetics

309 The experiment was conducted in glass bottles to eliminate carbon contamination.

310 Controls showed that after 102 days, dSi due to leaching from the glass was a maximum of 5%

311 of the dSi due to dissolution of diatom frustules. From an initial concentration of $680 \pm 30 \mu\text{mol}$

312 L^{-1} , bSiO₂ decreased rapidly during the first 3 to 5 days of the experiment and then more slowly

313 (Fig. 1). After 25 days, 52% of the initial bSiO₂ was dissolved and 76% of the initial was

314 dissolved at the end of the experiment (102 d). The comparison between the $\log(L)$ of the three

315 models describing bSiO₂ dissolution showed that Model 2 is 4.3×10^{16} times better than Model 1

316 ($\Delta \log(L) = 38.3$) and almost 4.5×10^5 times better than Model 3 ($\Delta \log(L) = 13$). bSiO₂ was the

317 only constituent of the diatom with a dissolution pattern that was best described by Model 2

318 (Fig. 5a, Table 4) meaning that the frustule is most likely composed of two phases dissolving

319 simultaneously. The first phase of bSiO₂ constituted 31% of the total bSiO₂ and was more

320 soluble, with a dissolution rate constant of 0.27 d^{-1} . The second phase was more refractory with

321 a dissolution rate constant of 0.016 d^{-1} (Table 4). For direct comparison with POC and PON,

322 the initial loss rate constant of the total bSiO₂ was calculated using Model 1 over 10 days as

323 0.049 d^{-1} . The three dissolution constants are within the range (0.005 d^{-1} to 1.3 d^{-1}) given in

324 the review by Van Cappellen *et al.* (2002b).

325

326 3.2.2 POC and PON kinetics

327 POC concentration decreased in two steps from the initial value of $7660 \pm 150 \mu\text{mol L}^{-1}$

328 (Fig. 1). Even with more parameters Model 2 did not improve the fit to the data obtained by

329 Model 1 (Fig. 5b); $\log(L)$ calculations for POC loss showed that Model 3 gave the best fit

330 ($\Delta \log(L) = 76.5$). This suggests that either two pools of POC exist and are degraded

331 successively, or a change in some parameter not directly linked to POC chemistry provoked an

332 increase of the degradation rate at day 10 from 0.025 to 0.082 d⁻¹ (Table 4). PON followed the
333 same pattern; Model 3 reproduced the data with more accuracy as shown by the $\Delta \log(L)$ of 37.3
334 compare to Models 1 and 2. Model 3 estimated an increase in PON degradation rate at day 12
335 from 0.03 to 0.094 d⁻¹ (Table 4). The first POC degradation rate constants are similar to rate
336 constants measured in previous studies (0.036 d⁻¹ for POC, Lee and Fisher, 1992; 0.035 d⁻¹ for
337 POC and 0.047 d⁻¹ for PON, Harvey *et al.*, 1995). For comparison with bSiO₂, we also applied
338 Model 1 over 10 days to calculate the initial loss rate of POC and PON: 0.025 d⁻¹ for POC and
339 0.029 d⁻¹ for PON.

340 The POC degradation pattern in the Hg-poisoned controls was similar to that in
341 unpoisoned flasks during the first 5 days but was lower between days 5 and 11. The degradation
342 rate constant measured over the first 11 days using Model 1 was 0.021 d⁻¹.

343

344 3.2.3 Lipid kinetics

345 From an initial TLip concentration of 1400 ± 70 μmol C L⁻¹, almost half (42 ± 4%)
346 degraded in 25 days; 7.0 ± 0.3 % of TLip remained after 102 days. The degradation of 7 of the 8
347 lipid classes is shown in Fig. 6a. TLip degradation is better described by Model 2 and 3 than by
348 Model 1 ($\Delta \log(L)$ = 15.6 and 17 respectively). With only 1.5 point of $\log(L)$ difference between
349 Model 2 and 3 but the same degree of complexity (4 parameters each) we chose the best fit from
350 the best likelihood which was given by Model 3 (Table 4). The degradation rate constant for
351 TLip was 0.048 d⁻¹ during the first 17 days of the experiment and then decreased to 0.01 d⁻¹.
352 The initial degradation rate constant was 0.046 d⁻¹, slightly higher than the 0.023 d⁻¹ measured
353 in the study of Harvey *et al.* (1995).

354 Using Model 1 we calculated that FFA, PIG, MG and PG+DPG had degradation rate
 355 constants of 0.104, 0.012, 0.045 and 0.011 d^{-1} over 25 days respectively. For MGDG, ST, PE,
 356 and ALC, Model 3 gives the best fit to the data (Table 4).

357 MGDG turned over slowly (0.078 d^{-1}) during the first 2 days, but then much more
 358 quickly (0.52 d^{-1} ; Table 4) and were completely gone after only 4 days. MG were also
 359 completely lost very quickly; the initial degradation rate constant of MG was 0.045 d^{-1} , but the
 360 remaining MG was gone after 14 days. This pattern does not fit any of the models used, and
 361 suggests an association of these lipids only with the first bSiO₂ phase, or no association at all.

362 MGDG, ST, and PE degradation rate constants increased by a factor of 8 to 10 during the
 363 experiment. They followed the same pattern as POC and PON. ALC degradation rate constant
 364 decreased after 19 days.

365 3.2.4 Amino acid kinetics

366 From the initial THAA concentration of $3020 \pm 200 \mu\text{mol C L}^{-1}$, $86 \pm 17 \%$ of the THAA
 367 were degraded after 25 days; $5.0 \pm 0.5 \%$ of the THAA still remained after 102 d. As for POC
 368 and PON, Model 3 was the best fit for THAA degradation ($\Delta \log(L) = 9.9$ with both Model 1 and
 369 Model 2). Concentrations of THAA decreased from day 1 to day 13 with an average degradation
 370 rate constant of 0.054 d^{-1} . After 13 d THAA turned over with a faster degradation rate constant
 371 of 0.139 d^{-1} (Table 4), before reaching a period of very low rate constants after day 25; THAA
 372 concentrations were almost constant until day 102. This last rate was not calculated by models
 373 as the modelling exercise was applied only over the first 25 days. The first degradation phase of
 374 THAA was similar to that measured on *T. weissflogii* (0.058 d^{-1}) by Harvey *et al.* (1995).
 375 Initially, the degradation rate constant of the 14 individual amino acids ranged between 0.015
 376 and 0.070 d^{-1} , except for ASP and SER, which turned over more slowly with constants of 0.001
 377 and 0.007 d^{-1} , respectively (Table 4). At day 11 when on average $49 \pm 10 \%$ of the THAA had

378 degraded, all concentrations except ARG and SER suddenly increased by 6 to 58 % in 1 to 2
 379 days (Fig. 6b). The largest releases were observed for HIS, GLY and LYS, which increased by
 380 39 ± 13 %, 58 ± 10 % and 46 ± 12 %, respectively. For every amino acid except TYR,
 381 degradation rate constants increased after this peak. For ASP and SER the increase occurred
 382 earlier at day 5, and for TYR the degradation rate constant decreased from 0.070 to 0.012 d^{-1} at
 383 day 21. Except for TYR, amino acids turned over faster during the second degradation phase,
 384 and degradation rate constants ranged between 0.110 and 0.182 d^{-1} . The degradation rate
 385 constant of SER increased even more than the other amino acids reaching 0.897 d^{-1} (Table 4).

386 **3.3 Relation between bSiO₂ dissolution and degradation of individual** 387 **organic compounds or compound classes**

388 *3.3.1 Lipid degradation versus bSiO₂ dissolution*

389 There was a strong linear relationship between total bSiO₂ and TLip over the whole range
 390 of bSiO₂ concentrations ($r^2 = 0.85$, $n = 26$) measured. There was no correlation between bSiO₂
 391 and PIG, so that the relationship between bSiO₂ and TLip became even better when pigments
 392 were excluded from the other lipids ($r^2 = 0.94$, $n = 26$). FFA were well correlated with total
 393 bSiO₂ concentrations ($r^2 = 0.95$, $n = 26$); they were completely degraded during the dissolution
 394 of the second bSiO₂ phase, when bSiO₂ concentrations eventually reached $260 \mu\text{mol L}^{-1}$.

395 Relationships among individual lipid classes and bSiO₂ phases showed three distinct
 396 periods (Fig. 7a and b), which were related to bSiO₂ dissolution using the bSiO₂ model (Figure
 397 5a). Period 1 (P1) is the time corresponding to dissolution of 85% of the first bSiO₂ phase and
 398 10% of the second bSiO₂ phase; Period 2 (P2) is the time corresponding to dissolution of most of
 399 the remaining bSiO₂ from the first phase and another 10% of the second bSiO₂ phase; and Period
 400 3 (P3) is the time when less than 1.5% of the first phase remained and 60% of the second phase
 401 dissolved. At the end of P3 20% of the bSiO₂ from the second phase remained. On average, 26-
 402 34% of the TLip degraded during Period 1; only 14-19% of TLip remained at the beginning of

403 Period 3. The slow decrease of concentrations observed for each lipid class except PIG, during
 404 P1 and P3 compared to P2 despite the fact that the three periods lasted the same time (~7 days,
 405 Fig. 5a), might show that most TLip except PIG degraded during P1 were associated with the
 406 first bSiO₂ phase, and most TLip except PIG degraded during P3 with the second bSiO₂ phase.
 407 These specific lipids are denoted as Si(1)-Lip and Si(2)-Lip; their composition is shown Table 3.

408 Of the individual classes, PE, ALC concentrations remained almost constant during P1.
 409 In contrast, MGDG was completely degraded within the first 4 days, in P1. Despite the high
 410 variability in PE and ST concentration measurements, we determined that ST and MG
 411 concentrations decreased only slightly in P1 (>27%). This trend is illustrated by their low
 412 degradation constants (0.016 d^{-1} and 0.001 d^{-1} , respectively).

413 Degradation of MG, ALC, PE and ST mainly occurred in P2. PE and ST concentrations
 414 dropped in P2 and ALC degradation was even faster; Model 3 gave a higher k_1 and a longer t_s
 415 for ALC than for PE and ST. After the precipitous drop, which corresponded to the beginning of
 416 P3, 80% of ALC, FFA and PE and 40% of ST were degraded. MG were completely degraded so
 417 quickly at the beginning of P2 that the loss is more likely due to sudden release of MG adsorbed
 418 onto particles or dissolution (i.e. involving chemical mechanisms) rather than degradation (i.e.
 419 biological mechanisms).

420 DPG+PG were not well correlated with bSiO₂; generally there was a 36%-degradation
 421 during P1, then a fast release of DPG+PG in P2 (40-50%), possibly when the first bSiO₂ phase is
 422 completely dissolved. Due to the release in P2, 80% of the initial DPG+PG remained at the
 423 beginning of P3.

424

425 3.3.2 Amino acid degradation versus bSiO₂ dissolution

426 The relationship of THAA with the two bSiO₂ phases showed changes at the same times
 427 as many of the lipid classes, so we used the same three periods. During Period 1, when the first
 428 bSiO₂ phase was dissolving, only 3-22 % of the THAA degraded. For the reason described in the

429 previous section for lipids (3.3.1), this portion of the THAA is referred to as Si(1)-THAA. GLY
430 and LYS lost less than 10 % of their initial concentrations; ASP and GLU lost 40 % of their
431 initial concentrations. GLU, ASP, and LEU constituted most of the pool degrading during P1;
432 LYS is not correlated to the first bSiO₂ phase (Table 2).

433 At the end of period 2, a pool of THAA was released when 95 % of the first bSiO₂ phase
434 was dissolved (Fig. 8a and b). THAA concentrations decreased by 32 % compared to initial
435 values. Measurement of THAA does not release Si-bound amino acids so that they would not be
436 observed until the bSiO₂ dissolved; the THAA released (Si(2)-THAA) may have been trapped
437 between the 2 phases. The amount of Si(2)-THAA can be calculated from the difference between
438 the concentrations of amino acids at and before the peak maximum (Table 2). In total, THAA
439 concentration increased by 11-16 % (in $\mu\text{mol C L}^{-1}$); the Si(2)-THAA were composed mainly of
440 GLY (23 ± 8 %) and LYS (23 ± 8 %; see Table 2).

441 During P3, relative THAA concentrations declined from 34 % to 5 % of the original
442 THAA. The THAA lost during P3 are called Si(3)-THAA, they had a composition similar to that
443 of total THAA, except that the contribution of GLY was higher (Table 2).

444

445 **4. Discussion**

446 **4.1 Importance of bacteria in *S. marinoi* degradation**

447 The very high concentration of algae, when compared to the bacterial concentrations, and
448 the continued degradation in the presence of HgCl₂, suggest that the loss of organic matter was
449 due not only to biological degradation, but also to physical and chemical factors (dissolution). In
450 the presence of HgCl₂, organic matter turned over with a low rate constant (0.02 d^{-1} , $r^2 = 0.86$, n
451 $= 8$), which appeared to decrease even more after day 5 (0.007 d^{-1} , $n = 4$; 2 replicates). This
452 could be due to initial dissolution of organic matter as the cell begins to fall apart; smaller rate
453 constants after some time would then be due to the absence of bacterial degradation. However,

454 the lack of appropriate samples makes this observation tentative. The slower increase of DOC
 455 concentrations compared to the decrease in POC (Fig. 3) suggests that most of the POC loss may
 456 be due to bacterial degradation despite the similar degradation rate measured in HgCl₂-poisoned
 457 batches. Degradation of particulate matter in the presence of HgCl₂ has been noted before (Liu
 458 *et al.*, 2006).

459 It was not clear why bacteria grew so slowly after day 14 in the unpoisoned experiment.
 460 Three factors could have contributed to the decrease and stabilization of bacterial growth. First,
 461 O₂ could have been a limiting factor. We did not measure O₂ during the experiment but we
 462 calculated average TOC loss, $R_{loss} = 221.6 \mu\text{mol L}^{-1}$. Change in oxygen concentrations (C_{O_2})
 463 with time (t) can be reconstructed from O₂ consumption rate (R_{loss}) and O₂ diffusion rate (R_{diff})
 464 (eq. 5). The latter is given by the Whitman film model (Gladyshev 2002; eq. 6).

$$465 \quad \frac{dC_{O_2}}{dt} = R_{diff} - R_{loss} \quad (5)$$

$$466 \quad R_{diff} = \frac{D}{\delta} \times \frac{S}{V} \times (C_{sO_2} - C_{O_2}) \quad (6)$$

467 where δ is the thickness of the diffusion layer, and is strongly dependent on stirring; D is the O₂
 468 diffusion coefficient (1.83 cm² d⁻¹, Ploug, 2001); S is the surface of contact between air and
 469 water (415.5 cm²); V is the volume of the solution, which changed progressively during
 470 sampling; and C_{sO_2} is the saturation concentration of the O₂ in seawater (229.9 μM). Using these
 471 equations and parameters, we estimated the maximum δ above which the solution will be anoxic.
 472 Considering that the risk of consuming all O₂ is greater for a larger volume of solution (with the
 473 same surface area), we conservatively used the volume of solution at the beginning of the
 474 experiment $V=V_0$ (8100 cm³).

475 We seek a value of δ_{max} , at which $\frac{dC_{O_2}}{dt}$ will always be positive when C_{O_2} approaches 0 so that
 476 the system can never go anoxic. This condition is met when

477
$$R_{loss} \leq R_{diff} = \frac{D}{\delta} \times \frac{S}{V} \times C_{SO_2} \quad (7)$$

478 or whenever

479
$$\delta_{max} = \frac{D}{R_{loss}} \times \frac{S}{V_0} \times C_{SO_2} \quad (8)$$

480 We calculated that when the volume is at its maximum in the flask (8100 cm³ at the beginning
481 of the experiment), the depth of the diffusive layer must be less than 0.1 cm for the solution to
482 remain oxic. The thickness of the diffusion layer is 0.27 cm with no stirring and can be as small
483 as 0.0015 cm when the stirring is intense (Gladyshev, 2002). Since our flasks were well mixed, it
484 is very unlikely that O₂ was a limiting factor.

485 A second explanation is that degradation products built up in the flask and poisoned the
486 bacteria (Westrich and Berner, 1984; Aller and Aller, 1998). We cannot exclude this possibility,
487 but calculating kinetic parameters over only 25 days should alleviate some of this problem. This
488 period of time is a reasonable compromise between the need to follow the degradation of *S.*
489 *marinoi* as long as possible so as to better understand reactions in the water column and the risk
490 of accumulating inhibiting metabolites. Finally, the bacteria might have stopped growing due to
491 viral lysis, grazing or a lack of labile substrate fuelling their growth (Fig. 2).

493 **4.2 Importance of Si-C interactions to bSiO₂ dissolution**

494 Previous dissolution studies have assumed that the diatom frustule is composed of a
495 single bSiO₂ phase (see review in Van Cappellen *et al.*, 2002b). Results from our modelling
496 exercise suggest instead that the frustule of *S. marinoi* is composed of two phases of bSiO₂ with
497 different dissolution characteristics. This idea, previously hypothesized by Kamatani and Riley
498 (1979) from dissolution rate measurements and by Gallinari *et al.* (2002) from solubility
499 equilibrium measurements, is consistent with the complexity of the frustule structure. During
500 silicification, polyamines and silaffin proteins catalyze precipitation of organo-silicon particles

501 of different shape and structure that determine the morphology of different diatom species
502 (Kröger *et al.*, 2000; Hildebrand, 2003). As a result of these interactions, diatom frustules have a
503 complex 3-D structure and are shaped like an elliptic or cylindrical box. Each half is composed
504 of a valve and girdle bands that are built at different times in the cell cycle (Hildebrand and
505 Wetherbee, 2003). In our study we distinguish two bSiO₂ phases and calculate their dissolution
506 rate constants. Even though we didn't determine a direct relation between these dissolution
507 characteristics and the structure of the frustule, we were able to determine the impact of two-
508 phase dissolution on the organic matrix of the cells as discussed below (see section 4.3).

509 Diatom frustules include organic layers that consist mainly of sugars and amino acids
510 (Hildebrand *et al.*, 2006). The major amino acids in this coating are GLY, THR, and SER,
511 suggesting that bonding with silica occurs through SER and THR, using their OH groups (Hecky
512 *et al.*, 1973). GLY enrichment observed during our study in the refractory (second) bSiO₂ phase
513 might suggest a more important role of GLY. Si-C or Si-O-C interactions are thought to protect
514 silica from dissolution until the organic matrix is removed by bacteria (Hecky *et al.*, 1973;
515 Patrick and Holding, 1985; Bidle and Azam, 2001). The different dissolution parameters of the
516 bSiO₂ phases may be due to different associations between silica and organic compounds in
517 different sections of the frustule. Indeed, Abramson *et al.* (2008) observed changes in the
518 distribution of organic compounds inside the frustule that would support this argument. The very
519 slow dissolution rate constant for the second bSiO₂ phase could be due to protection by the
520 organic matrix. We suggest (1) that only a part of the bSiO₂ is protected by the organic coating,
521 and (2) that this protection lasts for a longer time than was previously thought. Low bacterial
522 concentration could also partially explain why the protection of the second bSiO₂ phase lasted so
523 long, while in previous studies the protection was only temporary. The linear correlation between
524 FFA and the total bSiO₂ indicates that these compounds are associated with both phases of
525 bSiO₂, even though all FFA were completely degraded while 31% of the bSiO₂ still remained.
526 Few FFA were associated with the intracellular pool of lipids. Because of their amphipathic

527 properties due to the carboxyl group bonded to the long carbon chain, FFA probably play a role
528 in the organization of the organic matrix involved in building the frustule (Chevallard and
529 Guenoun, 2006). The relationship between FFA degradation and dissolution of the two bSiO₂
530 phases, and the fact that FFA were completely degraded before the total dissolution of the bSiO₂,
531 might also indicate another type of interaction, possibly adsorption of FFA on the silica surface.

532 In the present study, lipid classes and individual amino acids showed a general
533 correlation with bSiO₂ concentration (Figs. 7 and 8). The modelling experiment showed that
534 bSiO₂ and carbon pool degradation followed different patterns; they are represented in our model
535 by different sets of equations. Moreover, in our in vitro experiment, external parameters like
536 temperature were constant and can not be responsible for the relation observed in Figures 7 and
537 8. Thus we can safely suppose that a causal correlation exists between bSiO₂ dissolution and the
538 amino acids or lipids degradation. The turnover of the portion of these organic compounds that is
539 correlated with dissolution of either the first or second bSiO₂ phase (P1 and P3) was very slow
540 compared to the degradation of the remaining pool of these compounds. For example, for the
541 amino acids, the turnover of Si(1)-THAA and Si(3)-THAA was slow compared to the loss of
542 THAA in general. This correlation suggests that there may exist a direct association between
543 each bSiO₂ phase and the corresponding organic compounds (Si(1)-THAA, Si(3)-THAA, Si(1)-
544 Lip and Si(2)-Lip). Since the amounts of Si-THAA and Si-Lip related to each phase were
545 similar (~10-30 %), differences between bSiO₂ dissolution rate constants stem mainly from the
546 compositions of the pools. Some membrane lipids mainly MGDG were mostly associated with
547 the first bSiO₂ phase. DPG+PG still had high concentrations at the end of P2 when most
548 degradation occurred. The second bSiO₂ phase was more strongly correlated with neutral lipid
549 alcohols (ST and ALC) but also with membrane lipids DPG+PG and PE. In the first bSiO₂
550 phase, GLU, ASP, and LEU constituted most of the Si(1)-THAA pool and this phase contains no
551 LYS at all. In contrast in the second bSiO₂ phase, Si(3)-THAA had a composition similar to the
552 diatom's intracellular THAA, except for an increase of the GLY composition.

553 It is not clear whether differences in organic carbon content and/or different associations
554 between bSiO₂ and organic carbon in each of the two bSiO₂ phases explains the differences
555 between bSiO₂ dissolution rates and also between solubility equilibria. The organic matter that
556 makes up part of the diatom frustule helps strengthen the structure, thus increasing its resistance
557 to mechanical forces like those from grazers (Hamm *et al.*, 2003). The role of organic
558 compounds in silica dissolution is, however, more difficult to determine. In addition to the
559 bonds between silica and the OH moiety of SER or THR (Hecky *et al.*, 1973), silica particles are
560 linked to organic compounds by nitrogen bonds (Sumper and Kröger, 2004). Indeed, Gendron-
561 Badou *et al.* (2003) noted that Si-C and Si-N bonds are present in fresh diatoms while only Si-O-
562 Si and Si-O-R bonds are visible in fossilized diatoms. Different associations between silica and
563 organic compounds resist degradation and dissolution differently and may explain the
564 differences we observed between dissolution rate constants and solubility equilibria of the two
565 bSiO₂ phases.

566 The different dissolution rates of the two bSiO₂ phases might also be due to different
567 physico-chemical properties in the silica structure itself. In the presence of some sialafins, silica
568 precipitation of porous blocks has been observed *in vitro*; in contrast, when silica precipitation is
569 catalyzed by polyamines, spherical silica particles are formed (Sumper and Kröger, 2004). If the
570 first silica phase is more porous due to the presence of organic matter or due to the compounds
571 that catalyzed silica formation, the dissolution rate constant of this bSiO₂ will be higher (Van
572 Cappellen *et al.*, 2002a). Also, when the silica structure is chemically more organized (in mineral
573 form, as opposed to amorphous, like opal), dissolution rate and solubility are lower. Gendron-
574 Badou *et al.* (2003) determined that the structure of bSiO₂ from fossilized diatoms from
575 sediments is more organized than that of fresh diatom frustules due to condensation processes
576 that continue after they are deposited. It is also possible that fresh diatoms already have a more
577 organized phase, as suggested by the low dissolution rate (in the present study) and the low
578 solubility equilibrium (Gallinari *et al.*, 2002) of the second bSiO₂ phase. During dissolution, the

579 two different rate constants will cause an increase of the ratio of the more organized phase to the
580 amorphous phase.

581 The difference between dissolution rate constants and between solubility equilibria could
582 be due to chemical bonds between silica and organic matter or to structural characteristics of the
583 bSiO₂. In any case it may be closely linked to the presence of organic compounds either inside
584 the frustule itself or during the silicification process. This conclusion emphasizes the need to link
585 studies of carbon and silica production and recycling if we are to better understand both C and Si
586 cycles. The following section will accentuate this conclusion by showing the reverse: the
587 importance of bSiO₂ to carbon degradation.

588

589 **4.3 Si-C interactions and their role on carbon degradation**

590 bSiO₂ dissolution was best described by Model 2, while the turnover of each organic
591 compound investigated here was best fit by Model 1 or 3 (Fig. 5). The use of Model 3 to
592 describe compound turnover means that either (1) most organic compounds were present as two
593 pools of matter degrading one after the other or (2) degradation rate constants increased at some
594 point due to a change in environmental factors. In most cases the loss rate constant increased
595 (POC, PON, THAA, PE, and MGDG) or decreased (other lipid classes) when the dissolution of
596 the first bSiO₂ phase was almost complete, from which we conclude that the first bSiO₂ phase
597 must have influenced loss of organic matter.

598 Most of the ALC, PE and ST present in the intracellular pool of organic compounds
599 seems to have been protected by the first bSiO₂ phase, but due to the high variability of lipid
600 class behaviour the pattern for TLip is less clear than the one for THAA. THAA degradation is
601 consistent with the idea that Si(2)-THAA is encased within diatom frustules, and is released as
602 soon as the first bSiO₂ phase is completely removed. While several amino acids increased in
603 concentration between day 11 and day 20 (Fig. 6b), bacterial numbers peaked at day 13, which
604 corresponds to the THAA maximum (Fig. 1 and Fig. 2). However, bacterial carbon accounted

605 for only 0.2 to 2.4 ± 0.3 % of total carbon (Fig. 3). Bacterial biomass cannot account for the
606 increase of THAA, but the increase of bacterial number could be explained by this input of labile
607 organic carbon. Ingalls *et al.* (2003, 2006) measured Si-THAA (THAA bound and/or within
608 bSiO_2) obtained after complete dissolution of the bSiO_2 using successive treatments with 6N HCl
609 and HF. They found that Si-THAA made up 0.7-7 % of the total THAA in diatoms from
610 plankton tows and sediment trap samples. In our study, Si-THAA was a larger portion of total
611 THAA than in the studies of Ingalls *et al.* (2003, 2006). We define three pools of THAA: Si(1)-
612 THAA degradation is correlated to the dissolution of the first bSiO_2 phase; Si(2)-THAA is the
613 pool of THAA that are enclosed between the two bSiO_2 phases. Both of these pools were
614 protected by the first bSiO_2 phase. The third pool, Si(3)-THAA, is attached to the second phase
615 of the frustule; due to the low dissolution rate constant of this phase, it was protected for longer
616 time.

617 The composition of Si(2)-THAA is dominated by GLY and LYS, which are major
618 components of silaffins (Table 2). As part of the silicification process (Hildebrand, 2003;
619 Sumper and Kröger, 2004), these proteins are present in the silica deposition vesicles (SDV) that
620 become part of the diatom wall at the end of frustule formation (Martin-Jézéquel *et al.*, 2000).
621 Thus the Si(2)-THAA pool may be assembled during the silicification process, and may result
622 from the integration of the SDV's into the frustule. Similarity between most of the substitution
623 times t_s listed in Table 4 and the release time of Si(2)-THAA suggests that k_2 represents the
624 degradation rate constant of this portion of THAA. After being released, Si(2)-THAA turned
625 over very fast (k_2 in Table 4). Most of these amino acids were completely dissolved or degraded
626 shortly after the total dissolution of the first bSiO_2 phase, which suggests that this pool of THAA
627 is not directly bound to bSiO_2 . The high loss rate constant of Si(2)-THAA may suggest that this
628 pool of THAA was dissolved (chemical mechanism) rather than degraded (biological
629 mechanism) as soon as it was exposed. Another possible explanation to this fast turn over rate is
630 a change in degradation mechanism. During degradation, amino acids are released from protein

631 by enzymatic cleavage at the end of the proteins (exopeptidase) or in the middle of the
632 polypeptide chain (endopeptidase). If the proteins are opened up during the silicification process,
633 exopeptidases could act at both ends of the protein and degradation would be faster.

634 Due to their high turnover rate Si(2)-THAA may have been dissolved during the strong
635 HCl treatment or degraded before analysis in the study of Ingalls *et al.* (2003; 2006).
636 Accordingly, the quantification of Si-THAA made by Ingalls *et al.* (2003) might have only
637 targeted THAA bound to the second bSiO₂ phase of the frustule (Si(3)-THAA). The
638 composition of Si-THAA in Ingalls *et al.* (2003) is similar to our Si(3)-THAA except that LYS is
639 more abundant in Si(3)-THAA and GLY slightly less abundant (Table 2). The low solubility of
640 the second bSiO₂ phase is consistent with the increase in Si-THAA/THAA with depth in their
641 study.

642 The bSiO₂ protected from degradation the organic matter that was directly associated
643 with the frustule (Si(1)-THAA, Si(3)-THAA and Si-Lip). The first bSiO₂ phase also protected
644 the lipids (some DPG+PG) and amino acids (Si(2)-THAA) trapped inside the frustule possibly
645 between the 2 phases, as shown by the correlation curve (Figs. 7 and 8). Moreover, the sudden
646 increase in POC degradation rate (Fig. 1) after release of the trapped material is not associated
647 with an increase in bacterial concentration (Figs. 2 and 3) but with the end of the dissolution of
648 the first bSiO₂ phase. It is hardly a coincidence that the end of dissolution of the first bSiO₂
649 phase occurred exactly when the degradation of the POC, PON and THAA increased. The
650 mechanisms behind this observation are not clear yet; the dissolution of this phase probably gave
651 bacteria better access to the internal carbon of the cell, possibly because the integrity of the
652 frustule can not be maintained without the presence of the first bSiO₂ phase. This could happen
653 through increasing pores size as sometimes shown by pictures of diatom frustules during
654 dissolution, or because the box-shaped frustule opens at the end of the first bSiO₂ phase
655 dissolution as observed after sexual phases (Crawford 1995), both triggering cell lysis. In any
656 case we can safely conclude that the first bSiO₂ phase of the diatom frustule also protects most of

657 the intracellular carbon; at the end of the dissolution of the first bSiO₂ phase 69% of the POC
658 was still not degraded. Due to the very low dissolution rate of the second bSiO₂ phase, the
659 associated organic compounds (Si(3)-THAA and Si(2)-Lip) might be protected for a long period
660 of time; they would even be preserved in the sediment with the bSiO₂.

661 The presence of organic compounds inside the frustule and/or during silicification
662 determines the solubility of the different parts of the frustule. Moreover, intracellular carbon and
663 Si-bound organic compounds may be protected by at least some part of the frustule. These
664 reverse interactions prove that carbon and silica production and recycling must be studied in
665 parallel if we want to improve our understanding of mechanisms driving both POC and bSiO₂
666 sedimentation.

667

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860 Figure legends

861 Fig. 1. Changes in the relative concentrations of POC (closed black diamonds), bSiO₂
862 (open diamonds), THAA (closed grey squares) and TLip (closed grey triangles) during the
863 degradation of *S. marinoi* in the dark at 20°C during the first 25 days of the experiment. The
864 concentrations relative to initial values are on a logarithmic scale.

865 Fig. 2. Change in total bacterial concentration over time during the 102-day degradation
866 experiment.

867 Fig. 3. Change in algal TOC (open circles), DOC (open diamonds), POC (closed squares)
868 and bacterial carbon (closed circles) with time during the degradation experiment.

869 Fig. 4. Change in the concentration of (a) 6 of the 8 lipid classes in $\mu\text{mol C L}^{-1}$ relative to
870 TLip concentrations in $\mu\text{mol C L}^{-1}$ (b) 9 of the 14 individual amino acids in $\mu\text{mol AA L}^{-1}$
871 relative to THAA in units of $\mu\text{mol AA L}^{-1}$, over time during the first 25 days of the 102-days
872 degradation experiment. Note that due to the low number of C atoms in GLY, the GLY peak in
873 $\mu\text{mol AA L}^{-1}$ is more visible than if using $\mu\text{mol C L}^{-1}$.

874 Fig. 5. Model comparisons (a) Dissolution of bSiO₂. In this experiment, bSiO₂ is the only
875 compound whose loss is best represented by Model 2. $\Delta \log(L)$ between Model 2 and Model 3
876 is 13. Period 1 is the period of time corresponding to the dissolution of 85% of the first bSiO₂
877 phase and 10% of the second bSiO₂ phase. During period 2, the last 15% of the first bSiO₂
878 dissolved and 10% more of the second bSiO₂ phase dissolved. In Period 3 only the second
879 bSiO₂ phase dissolved as less than 1.5% of the first bSiO₂ phase remained. (b) The curve depicts
880 the loss of POC (or any organic compound) with a dissolution or degradation rate constant that
881 increases with the *ts*. Model 1 fits the curve using $C_0 = 8297 \mu\text{mol C L}^{-1}$ and $k = 0.047 \text{ d}^{-1}$ with a
882 likelihood $\log(L) = 98.7$. Model 2 fits the model with the same likelihood using the same
883 parameters, i.e. $C_1 + C_2 = 8297 \mu\text{mol C L}^{-1}$, $k_1 = k_2 = 0.047 \text{ d}^{-1}$. Model 3 give the best fit

884 (log(L) = 174.7) using $C_0 = 7614 \mu\text{mol C L}^{-1}$, $t_s = 10 \text{ d}$, $k_1 = 0.025 \text{ d}^{-1}$ and $k_2 = 0.082 \text{ d}^{-1}$. This
885 example clearly shows that only Model 3 can depict accurately the loss when the rate constant
886 increases at some point in the experiment. Moreover, Model 2 never gives a better likelihood
887 than Model 1 under these conditions.

888 Fig. 6. Change in organic compound concentrations with time during the degradation of *S.*
889 *marinoi*. For clarity, 7 of the 8 lipid class concentrations in $\mu\text{mol Clip L}^{-1}$ over time are shown
890 (5a) and only 10 of the 14 amino acids in $\mu\text{mol AA L}^{-1}$ over time (5b). Results depicted are only
891 for the first 25 days. Note that THAA concentrations are in $\mu\text{mol AA L}^{-1}$.

892 Fig. 7. Si-TLip interactions during the degradation of the *S. marinoi*. (a) Correlation
893 between the concentrations of the dissolved bSiO₂ from the first phase relative to its initial
894 concentration (estimated by the model) and each lipid class relative to its initial concentration.
895 (b) Correlation between concentration of the dissolved bSiO₂ from the second phase relative to
896 its initial concentration (estimated by the model) and each lipid class relative to its initial
897 concentration. Period 1 is the period of time corresponding to the dissolution of 85% of the first
898 bSiO₂ phase and 10% of the second bSiO₂ phase. During period 2, the last 15% of the first
899 bSiO₂ dissolved, and 10% more of the second bSiO₂ phase dissolved. In Period 3 only the
900 second bSiO₂ phase dissolved as less than 1.5% of the first bSiO₂ phase remained.

901 Fig. 8. Si-THAA interactions during the degradation of *S. marinoi*. (a) Correlation
902 between the concentration of the dissolved bSiO₂ from the first phase relative to its initial
903 concentration (estimated by the model) and individual THAA concentrations relative to their
904 initial concentrations. (b) Correlation between concentration of the dissolved bSiO₂ from the
905 second phase relative to its initial concentration (estimated by the model) and individual THAA
906 concentrations relative to their initial concentrations. The periods shown are the same as in Fig.
907 7.

908

909 Table 1: List of abbreviations used in the text to refer to organic and inorganic compounds

910 measured during the degradation experiment.

Biogenic Silica	bSiO ₂	Total Organic Carbon	TOC
Silicic acid	dSi	Particulate organic carbon	POC
Particulate organic nitrogen	PON	Dissolved Organic carbon	DOC
Total Lipid classes	TLip	Total Hydrolyzed Amino Acids	THAA
Alcohols	ALC	Alanine	ALA
Di- and monophosphatidyl glycerides	DPG+PG	Arginine	ARG
Free fatty acids	FFA	Aspartic acid	ASP
Monogalactosyldiglycerides	MGDG	Glutamic acid	GLU
Monoglycerides	MG	Glycine	GLY
Phosphatidylethanolamines	PE	Histidine	HIS
Pigments	PIG	Isoleucine	ILE
Sterols	ST	Leucine	LEU
		Lysine	LYS
		Methionine	MET
		Phenylalanine	PHE
		Serine	SER
		Threonine	THR
		Tyrosine	TYR
		Valine	VAL
		γ -Aminobutyric acid	GABA

911

912 Table 2: Concentration in $\mu\text{mol C L}^{-1}$ and composition in mole% of the different pools of THAA
 913 in *S. marinoi*. The THAA row shows the initial concentration and composition of THAA before
 914 dissolution began and does not include Si-THAA. Si(1)-THAA is the pool associated with the
 915 first bSiO₂ phase, Si(2)-THAA is the pool of THAA enclosed between the bSiO₂ phases and
 916 Si(3)-THAA is the pool associated with the second bSiO₂ phase.

THAA	ALA	ARG	ASP	GLU	GLY	HIS	ILE	LEU	LYS	PHE	SER	THR	TYR	VAL	TOT
THAA	105	223	318	379	139	59	174	317	187	260	128	136	170	174	2769
% THAA / THAA _{tot}	4%	8%	11%	14%	5%	2%	6%	11%	7%	9%	5%	5%	6%	6%	
Si(1)-THAA	20	31	122	143	12	12	48	92	0	63	16	29	58	45	691
% Si(1)-THAA / Si(1)-THAA _{tot}	3%	5%	19%	22%	2%	2%	7%	14%	0%	10%	2%	5%	9%	7%	
Si(2)-THAA	9	0	52	37	92	17	21	19	96	21	0	12	18	21	332
% Si(2)-THAA / Si(2)-THAA _{tot}	2%	0%	13%	9%	23%	4%	5%	5%	24%	5%	0%	3%	5%	5%	
Si(3)-THAA	20	28	51	64	72	20	26	43	53	35	29	30	26	26	523
% Si(3)-THAA / Si(3)-THAA _{tot}	4%	5%	10%	12%	14%	4%	5%	8%	10%	7%	5%	6%	5%	5%	

917

918 Table 3: Concentration in $\mu\text{mol C L}^{-1}$ and composition in mole% of the different lipid class in *S.*
 919 *marinoi*. The lipid row shows the initial concentration and composition of lipid before
 920 dissolution began and does not include Si-lipid. Si(1)-Lip is the pool associated with the first
 921 bSiO₂ phase, Si(2)-Lip is the pool of THAA associated with the second bSiO₂ phase.

Lipid class	ALC	DPG+PG	FFA	MG	MGDG	PE	PIG	ST	total
Lipids	30	98	366	104	189	44	604	40	1475
lipid class/ total lipid	2%	7%	25%	7%	13%	3%	41%	3%	
Si(1)-Lip	0	0-36	180-201	15-25	0	1-19	NC	1-11	386-469
Si(1)-Lip/ tot Si(1)-Lip	0%	0-8%	43-47%	4-5%	41-49%	0-4%		0-2%	
Si(2)-Lip	0-4	40-69	3	0	0	7-13	NC	9-20	125-175
Si(2)-Lip/ tot Si(2)-Lip	0-2%	32-39%	39-55%	0%	0%	6-7%		7-11%	

922 NC: No correlation

923

924 Table 4: Kinetic parameters and likelihood ($\log(L)$) calculated by the 3 models. C_0 is the initial925 concentration of the compound. C_1 and C_2 are the initial concentrations of the two phases (for926 bSiO₂) or the two pools (organic compounds). k is the degradation/dissolution rate constant927 calculated with Model 1. k_1 and k_2 are degradation/dissolution rate constants of C_1 and C_2 in928 Model 2, respectively, or used before and after the substitution time ts in Model 3, respectively.

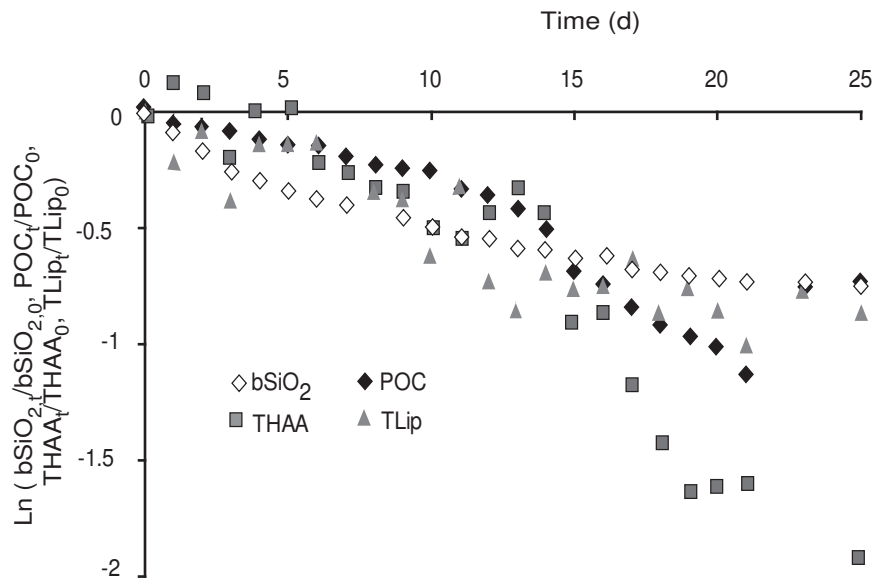
929 The last column indicates which model has been chosen in this study to determine the

930 degradation/dissolution rate constant and the initial concentration of each compound. For

931 compounds, see abbreviations table (Table 1).

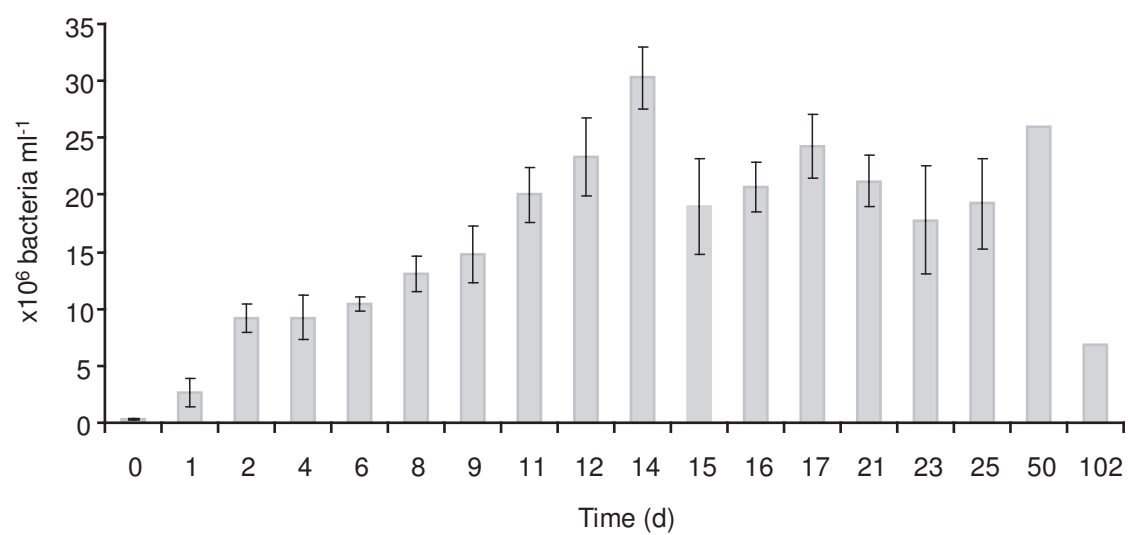
	Model 1			Model 2				Model 3					Best Model fit	
	C_0	k	$\log(L)$	C_1	C_2	k_1	k_2	$\log(L)$	C_0	ts	k_1	k_2		$\log(L)$
PON	1499	0.050	98.5	26	1473	0.051	0.051	98.5	1364	12	0.030	0.094	135.6	III
POC	8297	0.047	98.7	6884	1412	0.047	0.047	98.7	7614	10	0.025	0.082	174.7	III
bSiO₂	591	0.030	70.7	209	462	0.268	0.016	109.0	658	6	0.063	0.019	97.7	II
TLip	1232	0.033	27.9	704	724	0.014	0.100	43.5	1420	17	0.048	0.010	44.9	III
ALC	44	0.080	9.2	46	5	0.122	0.001	10.1	52	19	0.099	0.001	13.5	III
FFA	297	0.104	21.8	139	207	0.068	0.214	23.1	330	15	0.125	0.077	25.0	I
MG	97	0.045	24.5	21	85	0.497	0.033	25.0	107	5	0.094	0.036	25.5	I
MGDG	199	0.145	9.0	93	107	0.145	0.145	9.0	189	2	0.078	0.520	19.6	III
PE	54	0.097	22.3	51	3	0.097	0.097	22.3	42	6	0.016	0.119	26.6	III
PG+DPG	69	0.011	17.9	55	13	0.011	0.011	17.9	65	16	0.001	0.054	19.0	I
PIG	641	0.012	29.7	32	610	0.012	0.012	29.7	627	5	0.000	0.016	30.4	I
ST	41	0.031	30.0	11	30	0.031	0.031	30.0	35	13	0.001	0.080	38.3	III
THAA	3599	0.080	32.9	1903	1696	0.080	0.080	32.9	3137	13	0.054	0.139	42.8	III
ALA	132	0.070	42.3	31	102	0.073	0.073	42.3	117	12	0.048	0.120	54.1	III
ARG	339	0.113	26.6	39	300	0.113	0.113	26.6	243	9	0.024	0.175	54.3	III
ASP	419	0.100	24.5	312	107	0.100	0.100	24.5	324	5	0.001	0.121	29.1	III
GLU	454	0.080	39.2	23	431	0.080	0.080	39.2	405	13	0.065	0.147	50.5	III
GLY	172	0.045	24.9	67	105	0.045	0.045	24.9	147	16	0.015	0.182	39.3	III
HIS	73	0.063	28.9	44	29	0.063	0.063	28.9	65	16	0.039	0.167	38.6	III
ILE	223	0.082	34.4	210	13	0.082	0.082	34.4	192	12	0.050	0.137	44.8	III
LEU	413	0.090	34.0	117	299	0.091	0.091	34.0	348	12	0.050	0.150	48.2	III
LYS	268	0.068	18.1	181	88	0.068	0.068	18.1	223	14	0.031	0.170	26.1	III
PHE	336	0.083	31.6	332	4	0.083	0.083	31.6	280	12	0.040	0.148	45.8	III
SER	162	0.075	42.6	21	140	0.075	0.075	42.6	135	5	0.007	0.090	49.7	III
THR	165	0.064	43.1	17	149	0.064	0.064	43.1	151	13	0.045	0.110	51.1	III
TYR	185	0.068	48.3	157	28	0.068	0.068	48.3	187	21	0.070	0.012	49.3	I
VAL	219	0.076	37.9	179	39	0.076	0.076	37.9	194	12	0.050	0.124	46.5	III

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Fig. 2

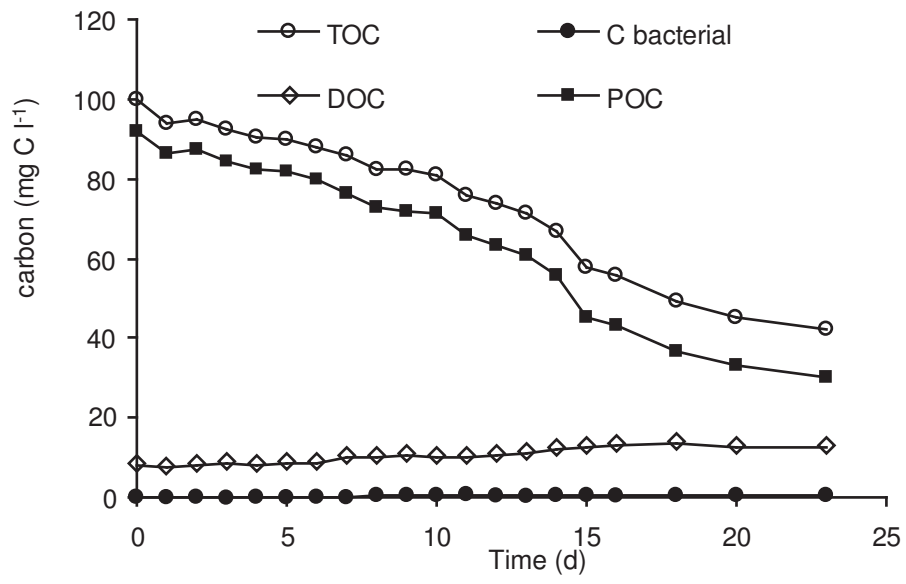


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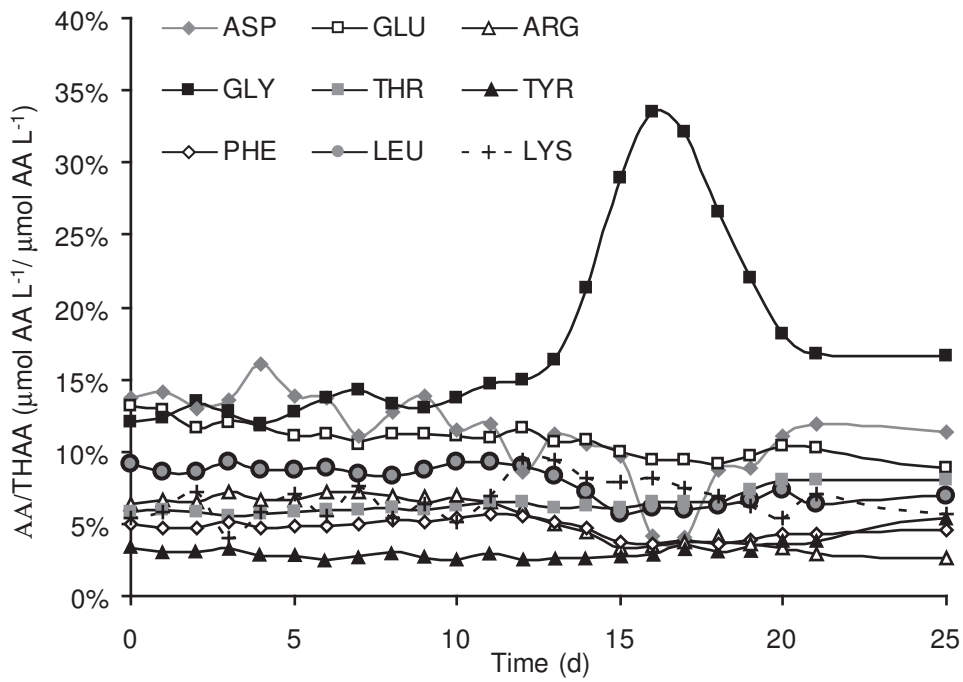
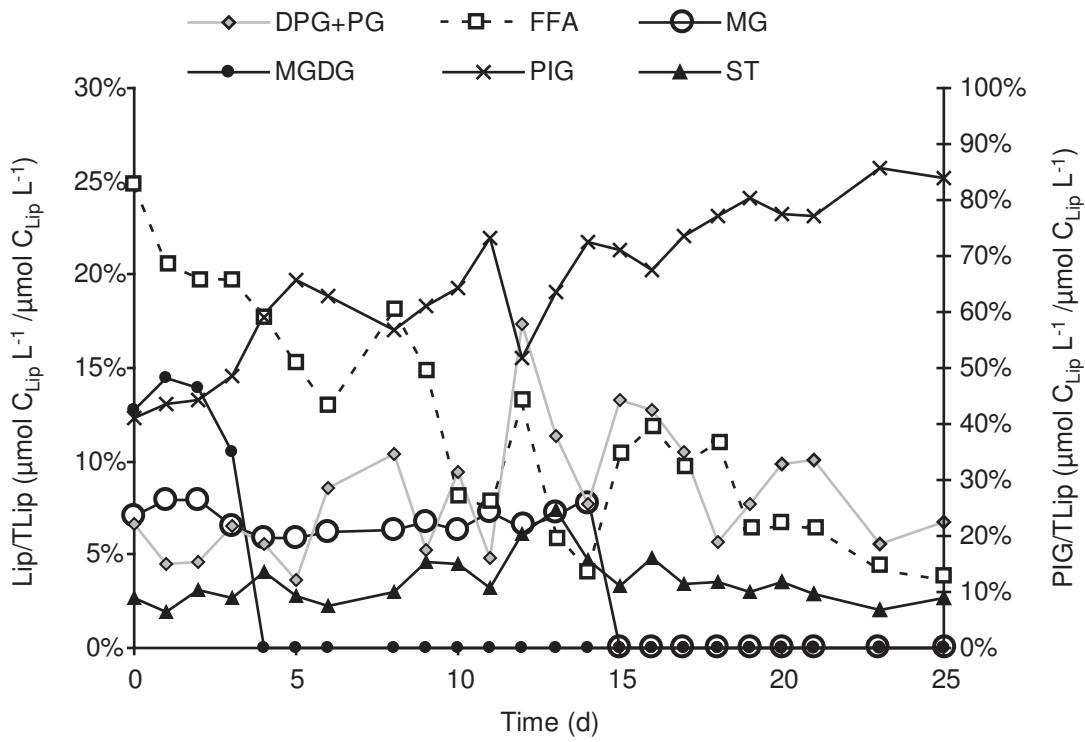
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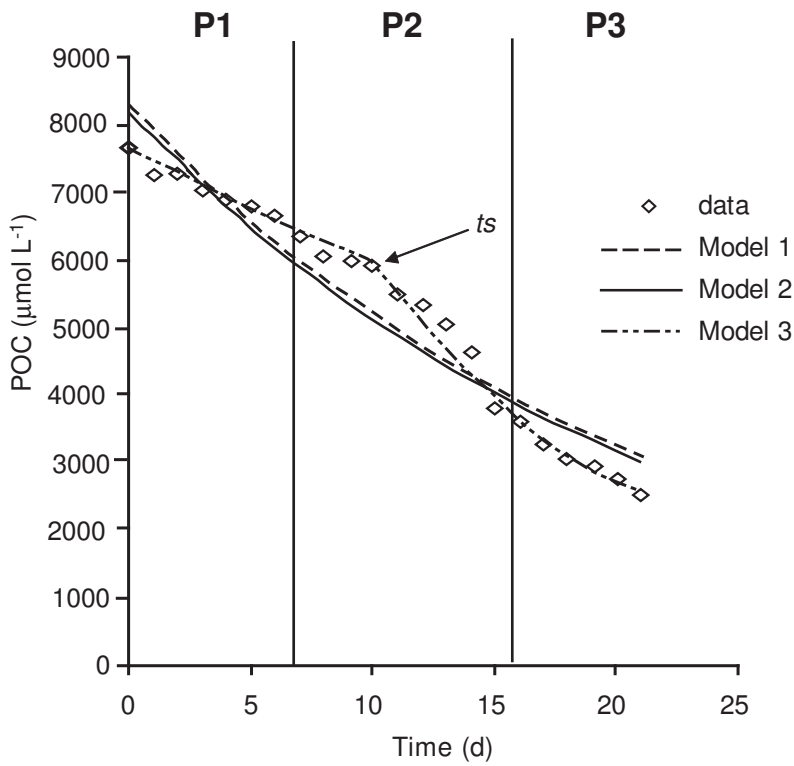
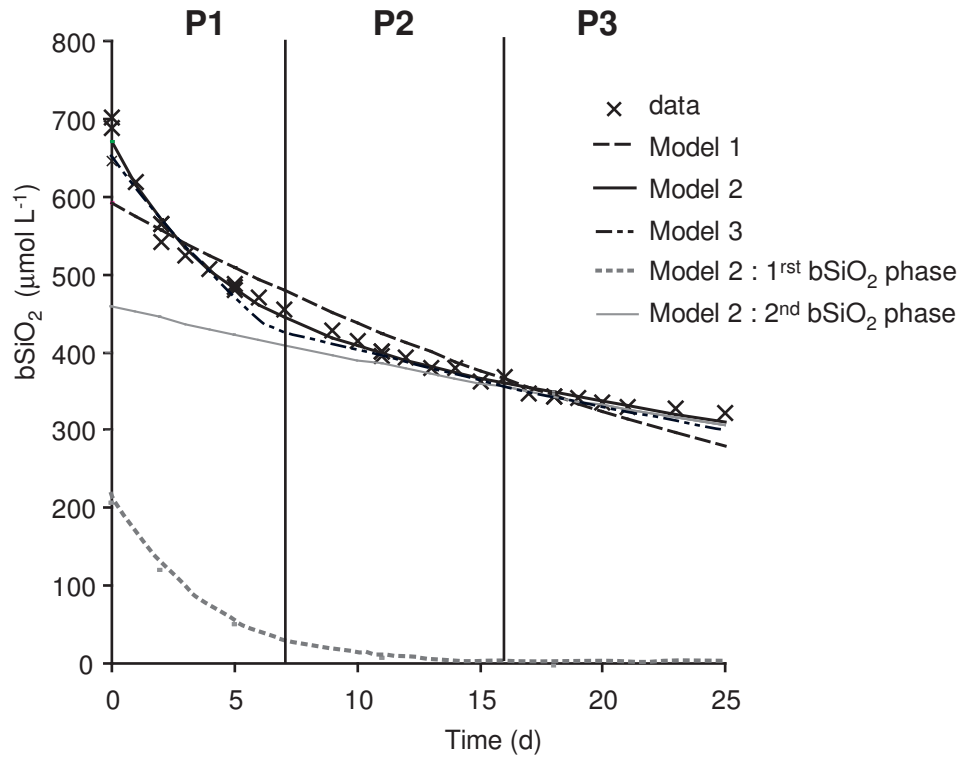
945 Fig. 3



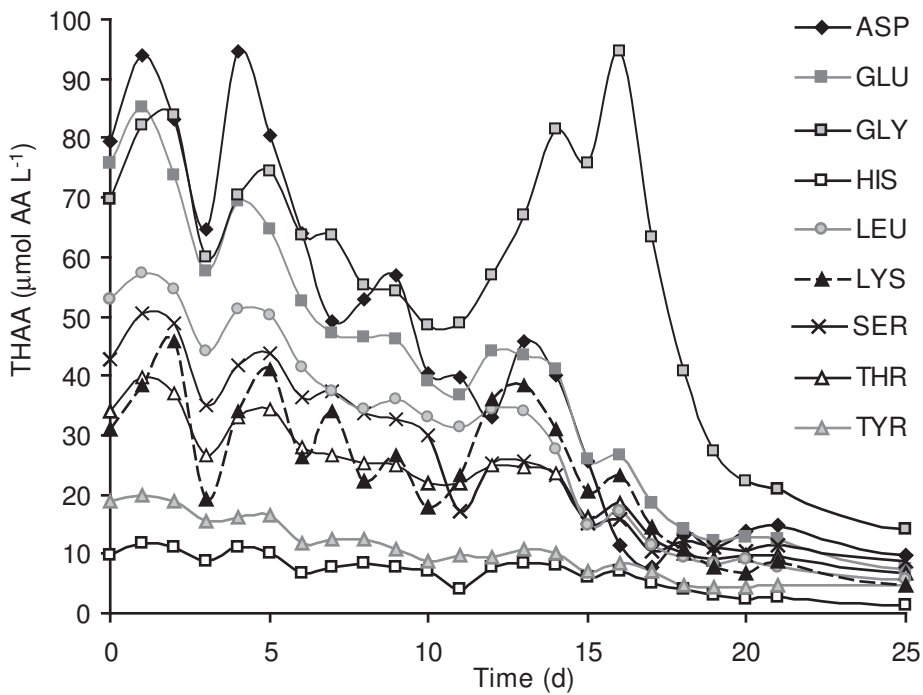
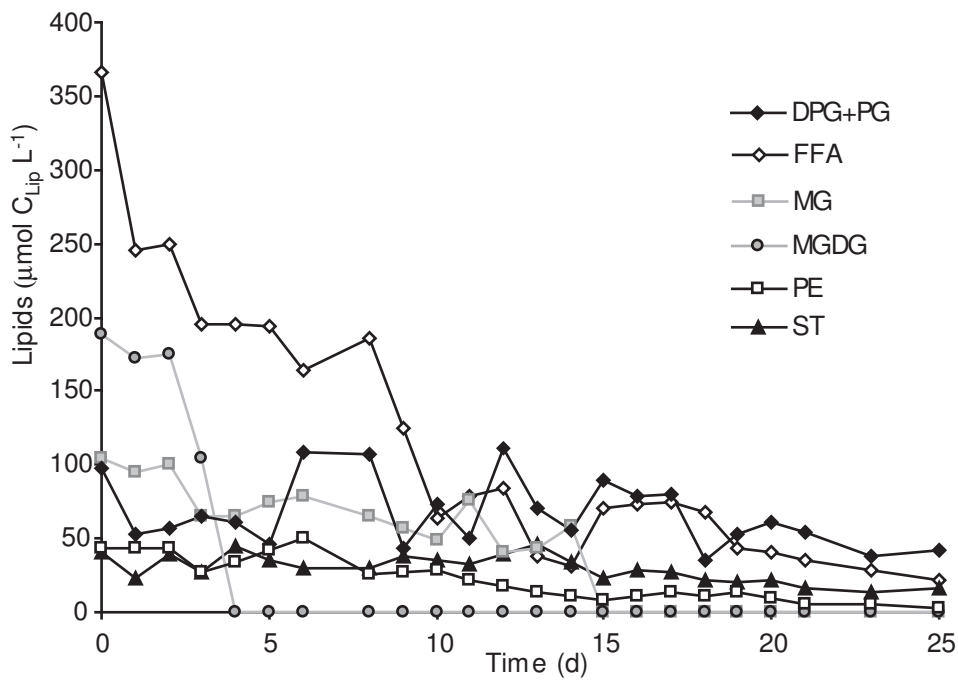
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950 Figure 5:



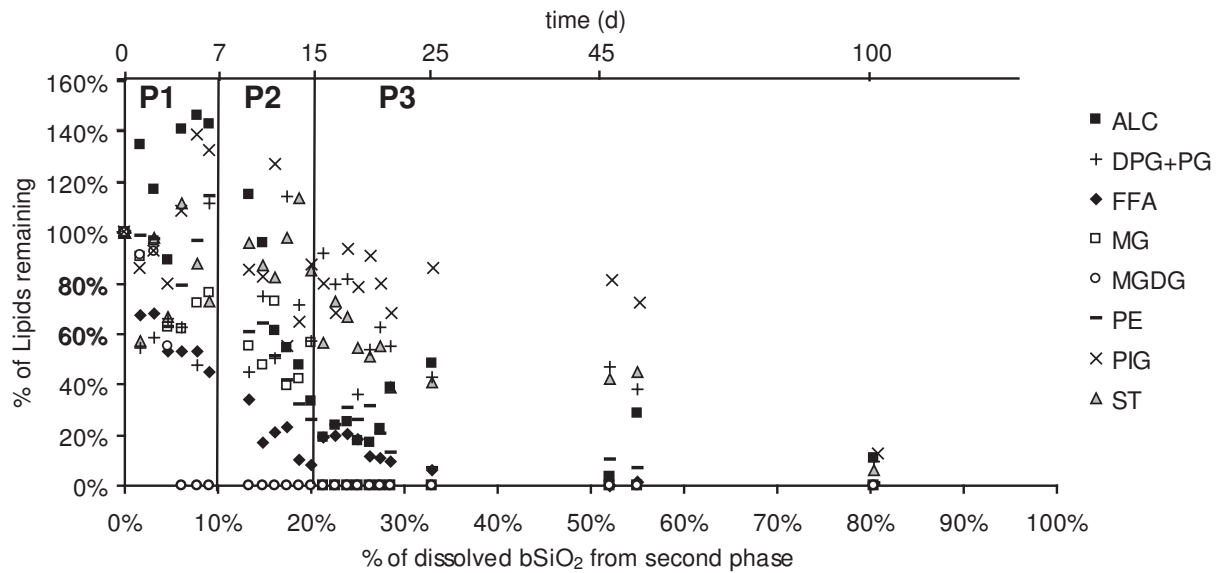
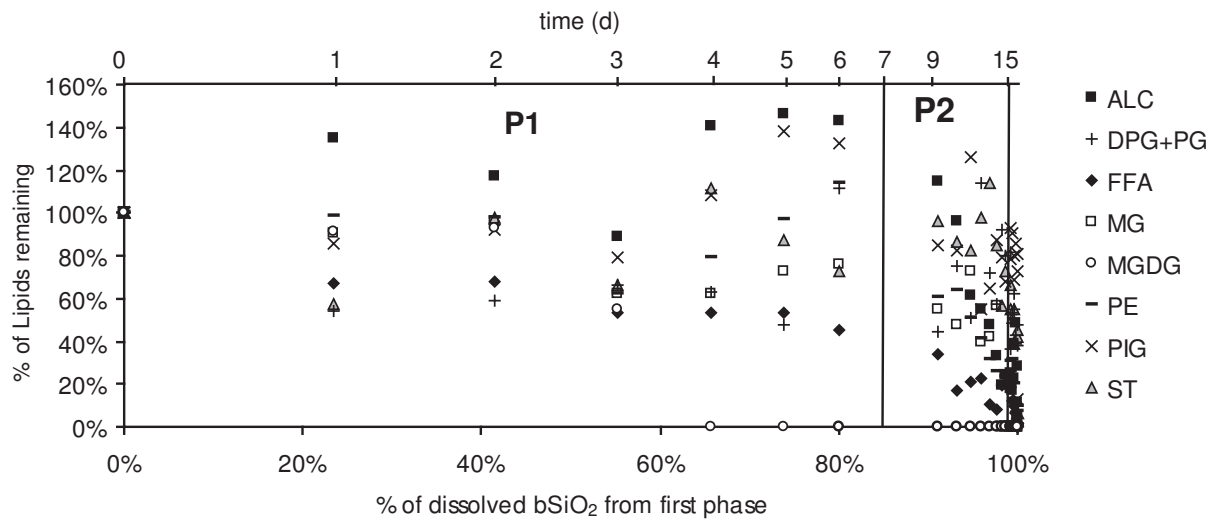
952 Fig. 6:



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955 Fig. 7:



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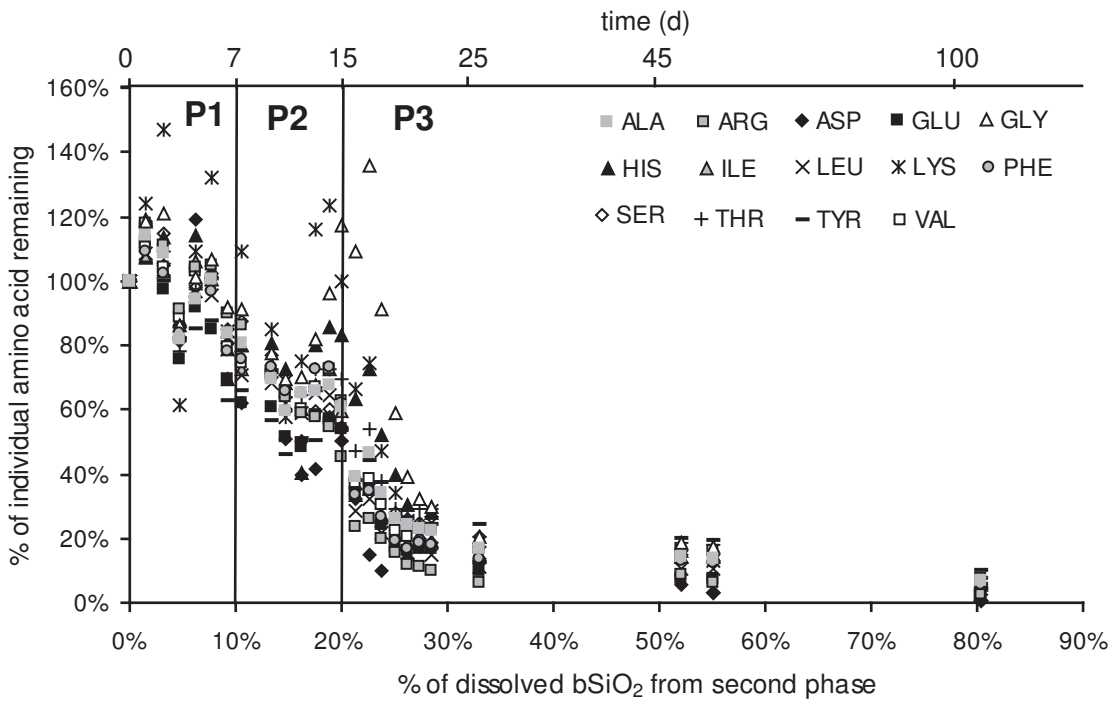
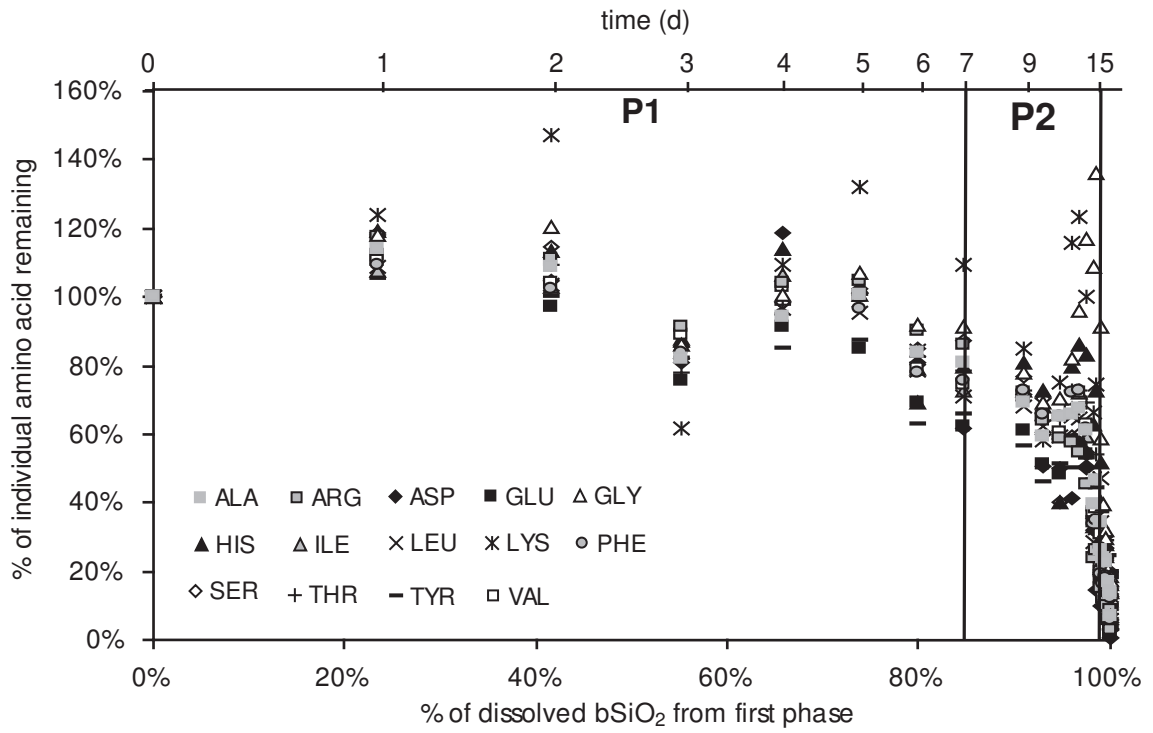
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962 Fig. 8:



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