

## **Si–C interactions during degradation of the diatom Skeletonema marinoi**

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► **To cite this version:**

Brivaëla Moriceau, Madeleine Goutx, Catherine Guigue, Cindy Lee, Robert Armstrong, et al.. Si–C interactions during degradation of the diatom *Skeletonema marinoi*. Deep Sea Research Part II: Topical Studies in Oceanography, Elsevier, 2008, pp.1381-1395. <http://www.sciencedirect.com/science/article/pii/S0967064508004141> . 10.1016/j.dsr2.2008.11.026 . hal-00381507

**HAL Id: hal-00381507**

**<https://hal.univ-brest.fr/hal-00381507>**

Submitted on 23 Jun 2009

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

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*Deep Sea Research II special volume*

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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 (bSiO<sub>2</sub>), and the  
33 associated degradation of organic matter. Three different models were applied to our results to  
34 help elucidate the mechanisms driving bSiO<sub>2</sub> dissolution and organic compound degradation.  
35 Results of this modelling exercise suggest that the diatom frustule is made up of two bSiO<sub>2</sub>  
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 bSiO<sub>2</sub>. In this phase, bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase effectively protected much of  
41 the organic matter from degradation: POC degradation rate constants increased from  $0.025 \text{ d}^{-1}$   
42 to  $0.082 \text{ d}^{-1}$  after the total dissolution of this phase, and PON degradation rate constants  
43 increased from  $0.030 \text{ d}^{-1}$  to  $0.094 \text{ d}^{-1}$ . Similar to POC and PON, the THAA degradation rate  
44 constant increased from  $0.054 \text{ d}^{-1}$  to  $0.139 \text{ d}^{-1}$  after dissolution of the first bSiO<sub>2</sub> 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 bSiO<sub>2</sub>. In contrast, most lipid degradation was not prevented by  
49 association with the more soluble bSiO<sub>2</sub> phase as the average lipid degradation rate constant  
50 decreased from  $0.048 \text{ d}^{-1}$  to  $0.010 \text{ d}^{-1}$  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 bSiO<sub>2</sub> 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 ( $\text{CaCO}_3$ ,  $\text{SiO}_2$  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 ( $\text{CaCO}_3$  of coccolithophorids;  $\text{SiO}_2$  of diatoms; aluminosilicates in dust) provide  
62 excess density needed for organic matter to sink;  $\text{SiO}_2$  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  $\text{SiO}_2$  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<sub>3</sub> 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<sub>2</sub> 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<sub>2</sub>  
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<sub>2</sub> 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 ( $6.5 \times 10^6$  cells ml<sup>-1</sup>), 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- $\mu$ 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  $\mu$ 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- $\mu$ 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 (bSiO<sub>2</sub>), 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<sup>-1</sup> HgCl<sub>2</sub>  
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 (bSiO<sub>2</sub>)* 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- $\mu$ m polycarbonate filters. Filters were analyzed for bSiO<sub>2</sub> and the filtrate for  
135 dSi. For bSiO<sub>2</sub>, filters were digested in 20 ml of 0.2N NaOH for three hours at 95°C to ensure  
136 the dissolution of all bSiO<sub>2</sub>; dSi concentrations in the solution remained far below the solubility  
137 equilibrium of bSiO<sub>2</sub> 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 bSiO<sub>2</sub> was < 5%.

140 *Silicic acid (dSi)* concentrations were determined on 10-ml filtered samples and on  
141 digested bSiO<sub>2</sub> 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- $\mu$ 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- $\mu$ m GFF filters; 10 ml of each sample was  
151 transferred into glass ampoules and sealed after addition of H<sub>3</sub>PO<sub>4</sub> 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 CO<sub>2</sub>-free air to purge them of inorganic carbon. Three or four 100



157  $\mu\text{l}$  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- $\mu\text{m}$  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;  $\text{H}_2$  flow 160  $\text{ml min}^{-1}$ ; air flow 2 l  $\text{min}^{-1}$ ) 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- $\mu\text{m}$  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  $\beta$ -alanine and  $\gamma$ -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- $\mu\text{m}$  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 ( $\mu\text{M}$ ) estimated at time  $t$  (d),  $C_0$  is the initial concentration, and  
192  $k$  is the dissolution/degradation rate constant ( $\text{d}^{-1}$ ).

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 ( $\mu\text{M}$ ) of phase or pool 1  
197 and 2, and  $k_1$  and  $k_2$  ( $\text{d}^{-1}$ ) 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 **3. Results**

228  
229

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

### 231 *3.1.1 General trends*

232 Changes in bSiO<sub>2</sub>, POC, TLip and THAA concentrations over time are shown in  
233 logarithmic scale in Fig. 1. While bSiO<sub>2</sub> 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<sup>-1</sup> and peaked at day 14 with  
238 a concentration of  $30 \pm 2.7 \times 10^6$  cell ml<sup>-1</sup> (Fig. 2). The bacterial population increased between  
239 days 0 and 14 with a rate equal to  $0.015 \text{ d}^{-1}$  (calculated between days 2 and 14) and then  
240 generally stabilized reaching a final concentration of  $20 \pm 4 \times 10^6$  cell ml<sup>-1</sup> 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 ( $62 \pm 3$   
245  $\text{mg C L}^{-1}$ ). The bacterial carbon ( $C_{\text{bact}}$ ) 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  $0.09 \pm 0.01$ , 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  $\alpha$  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  $0.09 \pm 0.01$  mol of Si/mol of C to  $0.06 \pm 0.01$  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  $0.11 \pm 0.01$  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  $0.13 \pm 0.02$  mol of C/mol of  
285 C and  $0.23 \pm 0.03$  mol of C/mol of C during the first 50 days. Then the ratio decreased to a final  
286 value of  $0.06 \pm 0.01$  mol of C/mol of C at day 102. THAA/POC decreased regularly during the  
287 whole experiment from  $0.36 \pm 0.09$  mol of C/mol of C initially to  $0.10 \pm 0.02$  mol of C/mol of C  
288 after 102 days, except for a sudden increase between day 11 and 15 from  $0.28 \pm 0.7$  mol of  
289 C/mol of C to  $0.38 \pm 0.10$  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  $\text{L}^{-1}$ , bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> dissolution showed that Model 2 is  $4.3 \times 10^{16}$  times better than Model 1  
316 ( $\Delta \log(L) = 38.3$ ) and almost  $4.5 \times 10^5$  times better than Model 3 ( $\Delta \log(L) = 13$ ). bSiO<sub>2</sub> 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 bSiO<sub>2</sub> constituted 31% of the total bSiO<sub>2</sub> and was more  
320 soluble, with a dissolution rate constant of  $0.27 \text{ d}^{-1}$ . The second phase was more refractory with  
321 a dissolution rate constant of  $0.016 \text{ d}^{-1}$  (Table 4). For direct comparison with POC and PON,  
322 the initial loss rate constant of the total bSiO<sub>2</sub> was calculated using Model 1 over 10 days as  
323  $0.049 \text{ d}^{-1}$ . The three dissolution constants are within the range ( $0.005 \text{ d}^{-1}$  to  $1.3 \text{ d}^{-1}$ ) 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<sup>-1</sup> (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<sup>-1</sup> (Table 4). The first POC degradation rate constants are similar to rate  
336 constants measured in previous studies (0.036 d<sup>-1</sup> for POC, Lee and Fisher, 1992; 0.035 d<sup>-1</sup> for  
337 POC and 0.047 d<sup>-1</sup> for PON, Harvey *et al.*, 1995). For comparison with bSiO<sub>2</sub>, we also applied  
338 Model 1 over 10 days to calculate the initial loss rate of POC and PON: 0.025 d<sup>-1</sup> for POC and  
339 0.029 d<sup>-1</sup> 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<sup>-1</sup>.

343

### 344 3.2.3 Lipid kinetics

345 From an initial TLip concentration of 1400 ± 70 μmol C L<sup>-1</sup>, 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<sup>-1</sup> during the first 17 days of the experiment and then decreased to 0.01 d<sup>-1</sup>.  
352 The initial degradation rate constant was 0.046 d<sup>-1</sup>, slightly higher than the 0.023 d<sup>-1</sup> 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  $0.011 \text{ d}^{-1}$  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 ( $0.078 \text{ d}^{-1}$ ) during the first 2 days, but then much more  
358 quickly ( $0.52 \text{ d}^{-1}$ ; 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  $0.045 \text{ d}^{-1}$ , 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 bSiO<sub>2</sub> 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  $0.054 \text{ d}^{-1}$ . After 13 d THAA turned over with a faster degradation rate constant  
371 of  $0.139 \text{ d}^{-1}$  (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* ( $0.058 \text{ d}^{-1}$ ) by Harvey *et al.* (1995).  
375 Initially, the degradation rate constant of the 14 individual amino acids ranged between 0.015  
376 and  $0.070 \text{ d}^{-1}$ , except for ASP and SER, which turned over more slowly with constants of 0.001  
377 and  $0.007 \text{ d}^{-1}$ , 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  $39 \pm 13$  %,  $58 \pm 10$  % and  $46 \pm 12$  %, 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  $0.012 \text{ d}^{-1}$  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  $0.182 \text{ d}^{-1}$ . The degradation rate  
385 constant of SER increased even more than the other amino acids reaching  $0.897 \text{ d}^{-1}$  (Table 4).

### 386 **3.3 Relation between bSiO<sub>2</sub> dissolution and degradation of individual** 387 **organic compounds or compound classes**

#### 388 *3.3.1 Lipid degradation versus bSiO<sub>2</sub> dissolution*

389 There was a strong linear relationship between total bSiO<sub>2</sub> and TLip over the whole range  
390 of bSiO<sub>2</sub> concentrations ( $r^2 = 0.85$ ,  $n = 26$ ) measured. There was no correlation between bSiO<sub>2</sub>  
391 and PIG, so that the relationship between bSiO<sub>2</sub> 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 bSiO<sub>2</sub> concentrations ( $r^2 = 0.95$ ,  $n = 26$ ); they were completely degraded during the dissolution  
394 of the second bSiO<sub>2</sub> phase, when bSiO<sub>2</sub> concentrations eventually reached  $260 \mu\text{mol L}^{-1}$ .

395 Relationships among individual lipid classes and bSiO<sub>2</sub> phases showed three distinct  
396 periods (Fig. 7a and b), which were related to bSiO<sub>2</sub> dissolution using the bSiO<sub>2</sub> model (Figure  
397 5a). Period 1 (P1) is the time corresponding to dissolution of 85% of the first bSiO<sub>2</sub> phase and  
398 10% of the second bSiO<sub>2</sub> phase; Period 2 (P2) is the time corresponding to dissolution of most of  
399 the remaining bSiO<sub>2</sub> from the first phase and another 10% of the second bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase, and most TLip except PIG degraded during P3 with the second bSiO<sub>2</sub> 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 ( $0.016 \text{ d}^{-1}$  and  $0.001 \text{ d}^{-1}$ , 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 bSiO<sub>2</sub>; generally there was a 36%-degradation  
421 during P1, then a fast release of DPG+PG in P2 (40-50%), possibly when the first bSiO<sub>2</sub> 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 bSiO<sub>2</sub> dissolution

426 The relationship of THAA with the two bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase (Table 2).

433 At the end of period 2, a pool of THAA was released when 95 % of the first bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 ( $23 \pm 8 \%$ ) and LYS ( $23 \pm 8 \%$ ; 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 HgCl<sub>2</sub>, 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 HgCl<sub>2</sub>, organic matter turned over with a low rate constant ( $0.02 \text{ d}^{-1}$ ,  $r^2 = 0.86$ ,  $n$   
451  $= 8$ ), which appeared to decrease even more after day 5 ( $0.007 \text{ d}^{-1}$ ,  $n = 4$ ; 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 HgCl<sub>2</sub>-poisoned  
 457 batches. Degradation of particulate matter in the presence of HgCl<sub>2</sub> 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 O<sub>2</sub> could have been a limiting factor. We did not measure O<sub>2</sub> 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 O<sub>2</sub> consumption rate ( $R_{loss}$ ) and O<sub>2</sub> 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  $\delta$  is the thickness of the diffusion layer, and is strongly dependent on stirring;  $D$  is the O<sub>2</sub>  
 468 diffusion coefficient (1.83 cm<sup>2</sup> d<sup>-1</sup>, Ploug, 2001);  $S$  is the surface of contact between air and  
 469 water (415.5 cm<sup>2</sup>);  $V$  is the volume of the solution, which changed progressively during  
 470 sampling; and  $C_{sO_2}$  is the saturation concentration of the O<sub>2</sub> in seawater (229.9 μM). Using these  
 471 equations and parameters, we estimated the maximum  $\delta$  above which the solution will be anoxic.  
 472 Considering that the risk of consuming all O<sub>2</sub> 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 cm<sup>3</sup>).

475 We seek a value of  $\delta_{max}$ , 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 cm<sup>3</sup> 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 O<sub>2</sub> 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).

492

#### 493 **4.2 Importance of Si-C interactions to bSiO<sub>2</sub> dissolution**

494 Previous dissolution studies have assumed that the diatom frustule is composed of a  
495 single bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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) bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase could be due to protection by the  
520 organic matrix. We suggest (1) that only a part of the bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase lasted so  
523 long, while in previous studies the protection was only temporary. The linear correlation between  
524 FFA and the total bSiO<sub>2</sub> indicates that these compounds are associated with both phases of  
525 bSiO<sub>2</sub>, even though all FFA were completely degraded while 31% of the bSiO<sub>2</sub> 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 bSiO<sub>2</sub>  
530 phases, and the fact that FFA were completely degraded before the total dissolution of the bSiO<sub>2</sub>,  
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 bSiO<sub>2</sub> concentration (Figs. 7 and 8). The modelling experiment showed that  
534 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> dissolution rate constants stem mainly from the  
546 compositions of the pools. Some membrane lipids mainly MGDG were mostly associated with  
547 the first bSiO<sub>2</sub> phase. DPG+PG still had high concentrations at the end of P2 when most  
548 degradation occurred. The second bSiO<sub>2</sub> 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 bSiO<sub>2</sub>  
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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> and organic carbon in each of the two bSiO<sub>2</sub> phases explains the differences  
555 between bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phases.

566           The different dissolution rates of the two bSiO<sub>2</sub> phases might also be due to different  
567 physico-chemical properties in the silica structure itself. In the presence of some sillafins, 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub>. 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 bSiO<sub>2</sub> to carbon degradation.

588

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

590 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase was almost complete, from which we conclude that the first bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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  $2.4 \pm 0.3$  % 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  $\text{bSiO}_2$ ) obtained after complete dissolution of the  $\text{bSiO}_2$  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  $\text{bSiO}_2$  phase; Si(2)-THAA is the  
613 pool of THAA that are enclosed between the two  $\text{bSiO}_2$  phases. Both of these pools were  
614 protected by the first  $\text{bSiO}_2$  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  $\text{bSiO}_2$  phase, which suggests that this pool of THAA  
627 is not directly bound to  $\text{bSiO}_2$ . 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase is consistent with the increase in Si-THAA/THAA with depth in their  
641 study.

642 The bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase. It is hardly a coincidence that the end of dissolution of the first bSiO<sub>2</sub>  
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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase of the diatom frustule also protects most of

657 the intracellular carbon; at the end of the dissolution of the first bSiO<sub>2</sub> phase 69% of the POC  
658 was still not degraded. Due to the very low dissolution rate of the second bSiO<sub>2</sub> 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 bSiO<sub>2</sub>.

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 bSiO<sub>2</sub>  
666 sedimentation.

667

668 Acknowledgements

669 We are grateful to Annick Masson for her technical assistance with POC analyses. Thanks to  
670 everyone in the LMGEM for their kindness and help during the experimental work. This work  
671 was funded by the EU, partly through the ORFOIS (EVK2-CT2001-00100) project and partly  
672 through the program Marie Curie, project CARBALIS (MOIF- CT-2006-022278). This is  
673 contribution # 1081 of the IUEM and xxx of Stony Brook University. Support was also provided  
674 by the MedFlux program of the U.S. NSF Chemical Oceanography division, and this is MedFlux  
675 contribution No. XXX.

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860 Figure legends

861 Fig. 1. Changes in the relative concentrations of POC (closed black diamonds), bSiO<sub>2</sub>  
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 bSiO<sub>2</sub>. In this experiment, bSiO<sub>2</sub> 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 bSiO<sub>2</sub>  
877 phase and 10% of the second bSiO<sub>2</sub> phase. During period 2, the last 15% of the first bSiO<sub>2</sub>  
878 dissolved and 10% more of the second bSiO<sub>2</sub> phase dissolved. In Period 3 only the second  
879 bSiO<sub>2</sub> phase dissolved as less than 1.5% of the first bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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 bSiO<sub>2</sub> phase and 10% of the second bSiO<sub>2</sub> phase. During period 2, the last 15% of the first  
899 bSiO<sub>2</sub> dissolved, and 10% more of the second bSiO<sub>2</sub> phase dissolved. In Period 3 only the  
900 second bSiO<sub>2</sub> phase dissolved as less than 1.5% of the first bSiO<sub>2</sub> phase remained.

901 Fig. 8. Si-THAA interactions during the degradation of *S. marinoi*. (a) Correlation  
902 between the concentration of the dissolved bSiO<sub>2</sub> 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 bSiO<sub>2</sub> 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.

<b>Biogenic Silica</b>	bSiO <sub>2</sub>	<b>Total Organic Carbon</b>	TOC
<b>Silicic acid</b>	dSi	<b>Particulate organic carbon</b>	POC
<b>Particulate organic nitrogen</b>	PON	<b>Dissolved Organic carbon</b>	DOC
<b>Total Lipid classes</b>	TLip	<b>Total Hydrolyzed Amino Acids</b>	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
		$\gamma$ -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 bSiO<sub>2</sub> phase, Si(2)-THAA is the pool of THAA enclosed between the bSiO<sub>2</sub> phases and  
 916 Si(3)-THAA is the pool associated with the second bSiO<sub>2</sub> 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 <sub>tot</sub>	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 <sub>tot</sub>	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 <sub>tot</sub>	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 <sub>tot</sub>	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 bSiO<sub>2</sub> phase, Si(2)-Lip is the pool of THAA associated with the second bSiO<sub>2</sub> 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

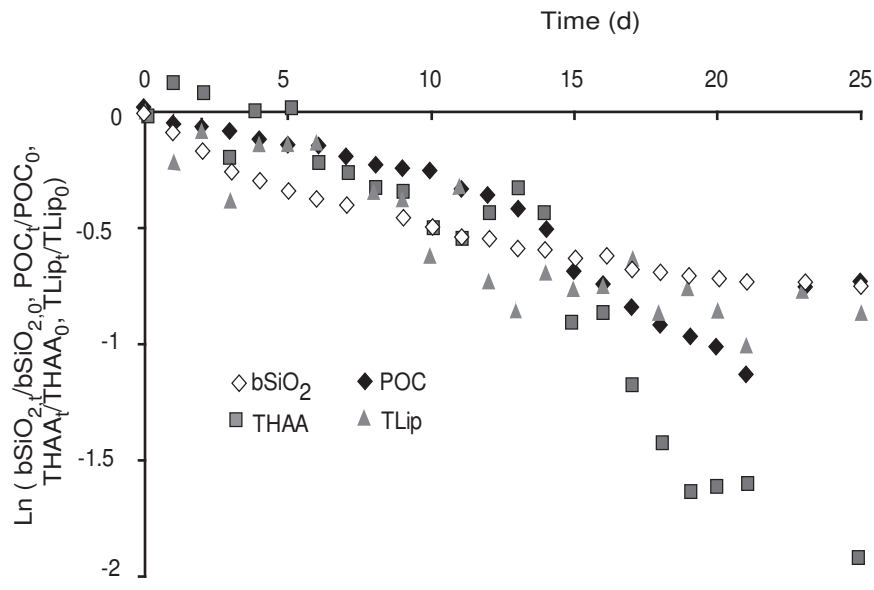
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924 Table 4: Kinetic parameters and likelihood ( $\log(L)$ ) calculated by the 3 models.  $C_0$  is the initial  
 925 concentration of the compound.  $C_1$  and  $C_2$  are the initial concentrations of the two phases (for  
 926  $\text{bSiO}_2$ ) or the two pools (organic compounds).  $k$  is the degradation/dissolution rate constant  
 927 calculated with Model 1.  $k_1$  and  $k_2$  are degradation/dissolution rate constants of  $C_1$  and  $C_2$  in  
 928 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	
	$C_0$	$k$	$\log(L)$	$C_1$	$C_2$	$k_1$	$k_2$	$\log(L)$	$C_0$	$ts$	$k_1$	$k_2$		$\log(L)$
<b>PON</b>	1499	0.050	98.5	26	1473	0.051	0.051	98.5	1364	12	0.030	0.094	135.6	III
<b>POC</b>	8297	0.047	98.7	6884	1412	0.047	0.047	98.7	7614	10	0.025	0.082	174.7	III
<b>bSiO<sub>2</sub></b>	591	0.030	70.7	209	462	0.268	0.016	109.0	658	6	0.063	0.019	97.7	II
<b>TLip</b>	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
<b>THAA</b>	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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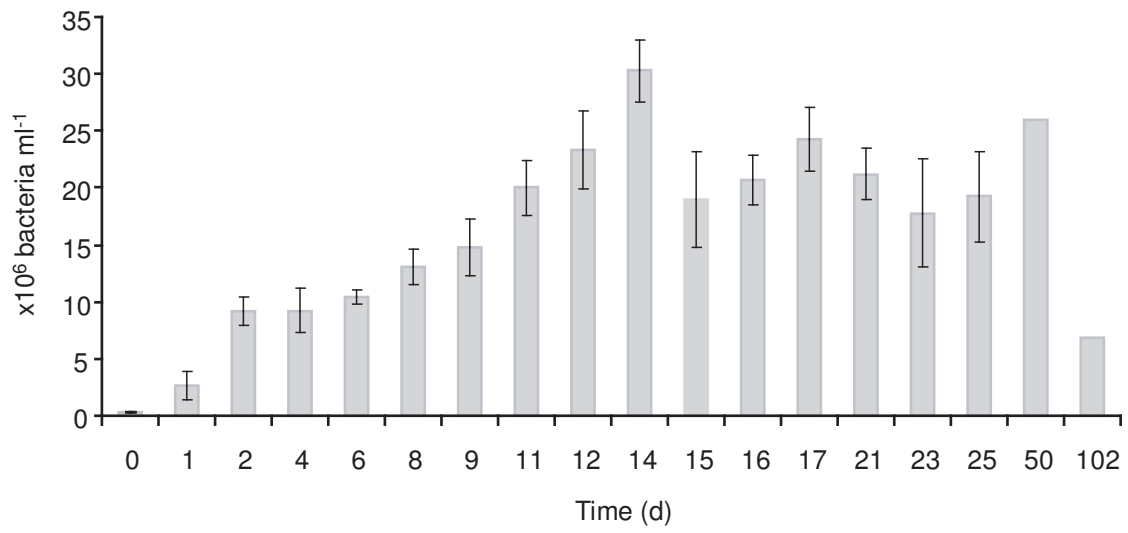
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937 Fig. 2

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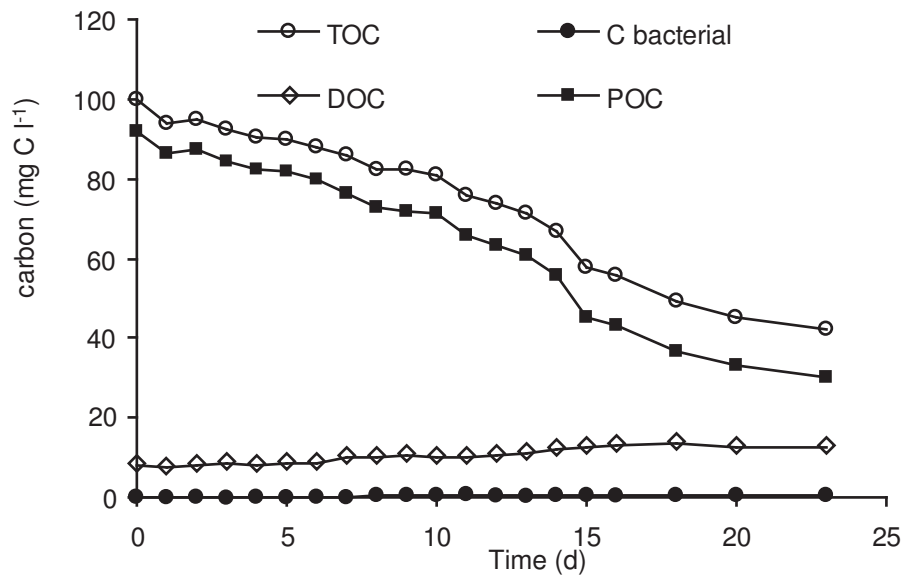
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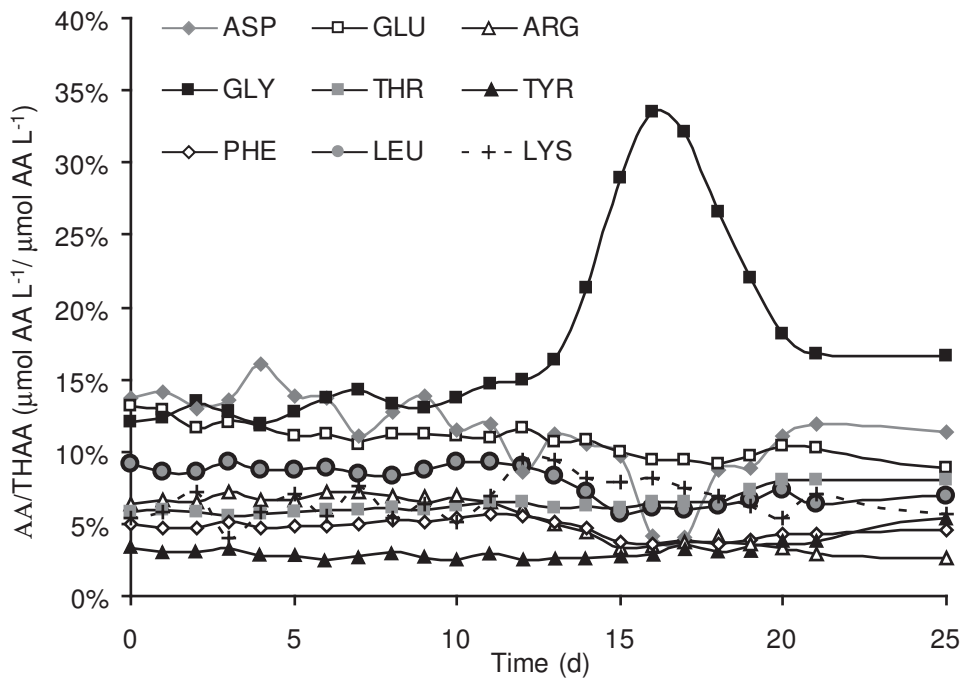
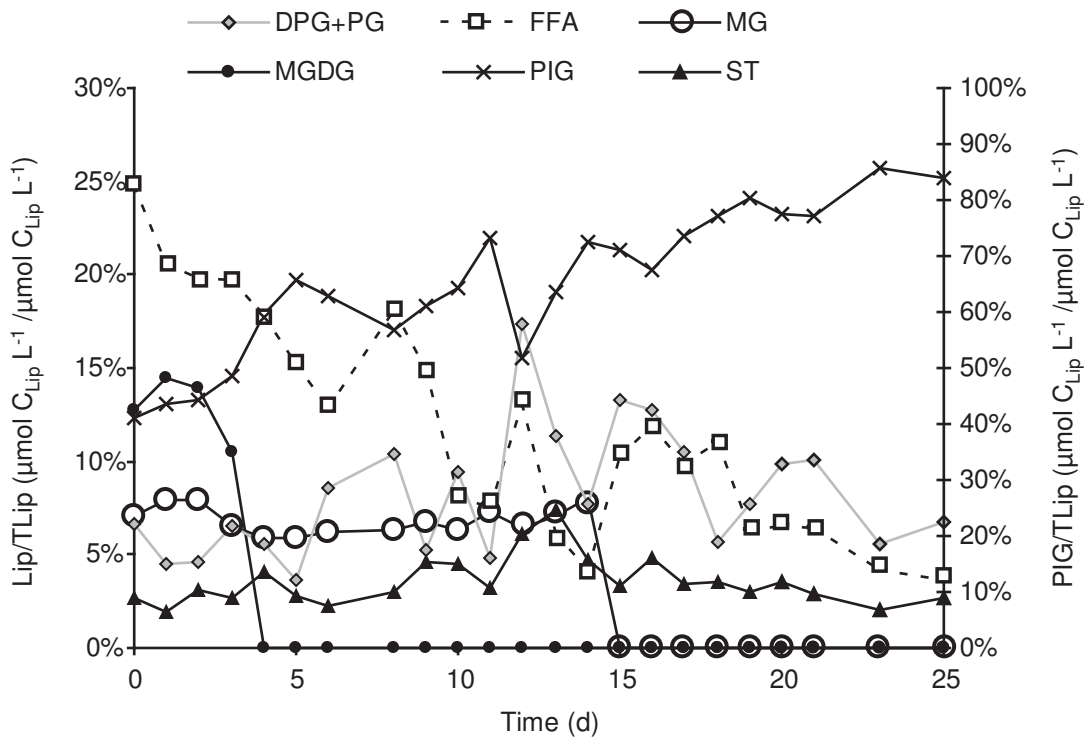
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945 Fig. 3



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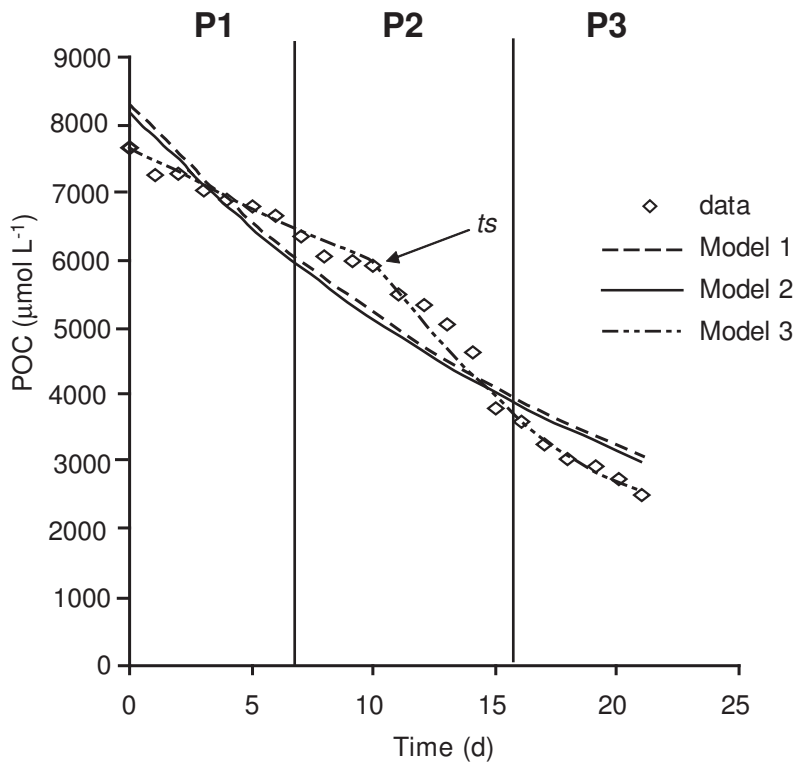
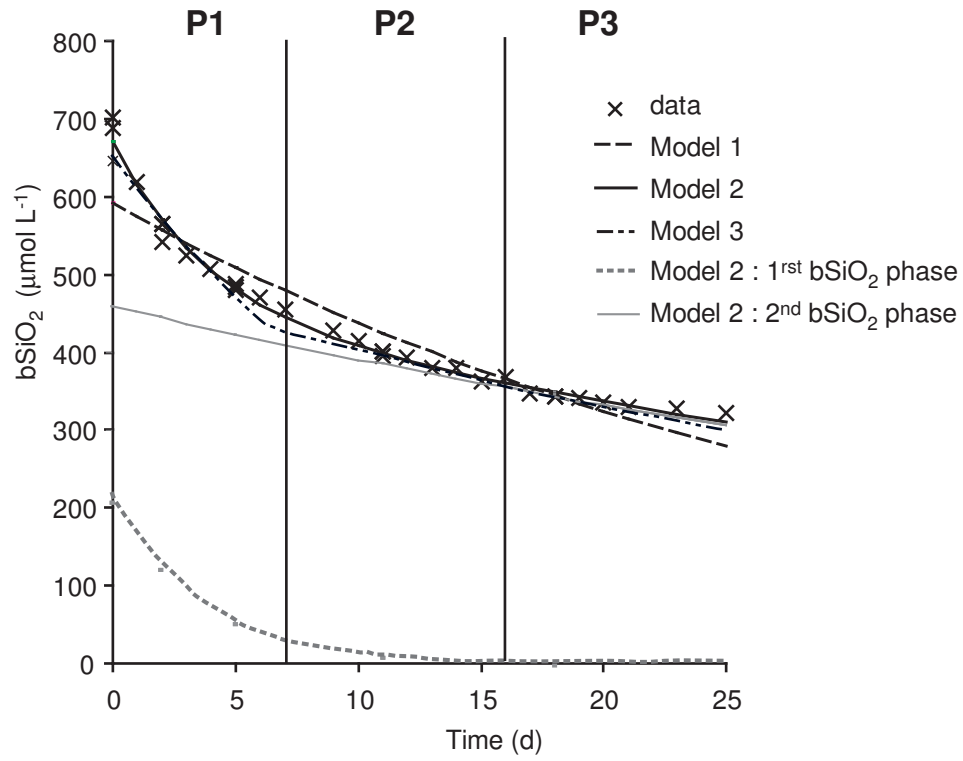
947 Fig. 4



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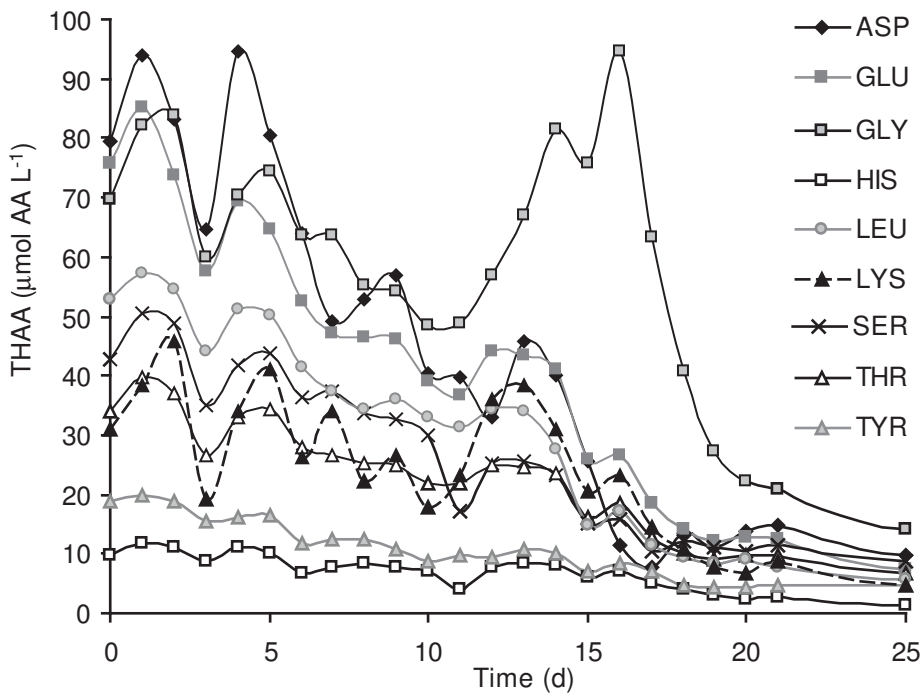
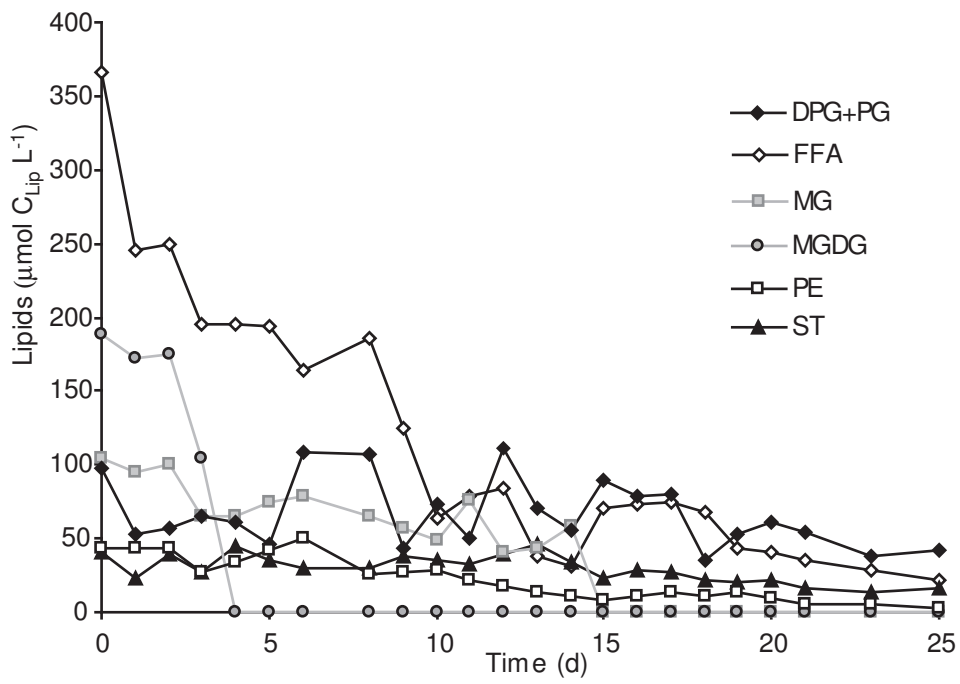
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950 Figure 5:



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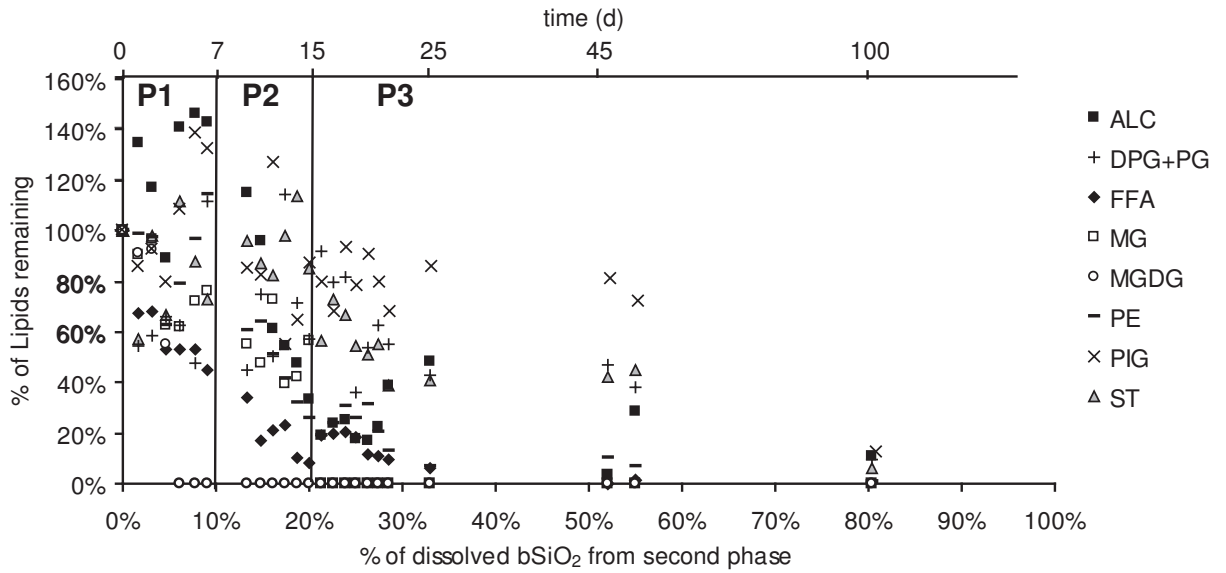
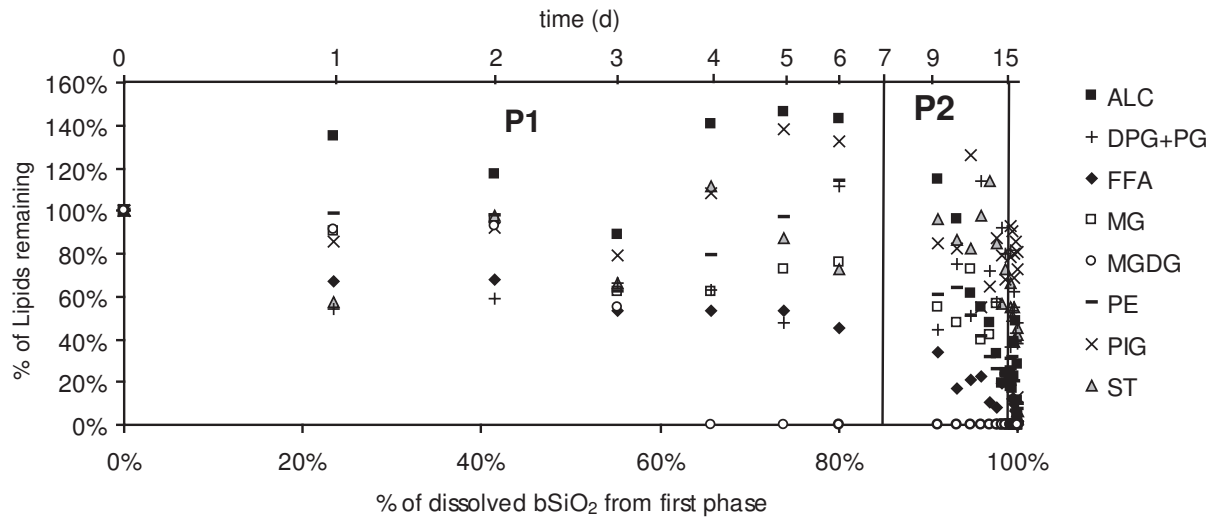
952 Fig. 6:



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955 Fig. 7:



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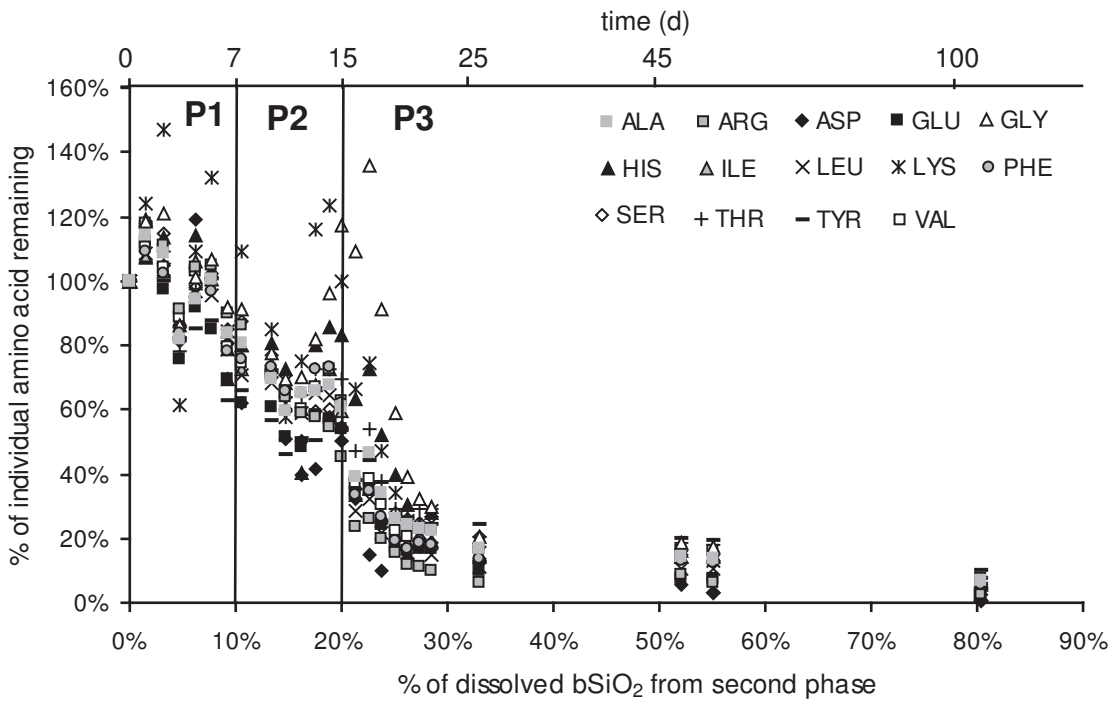
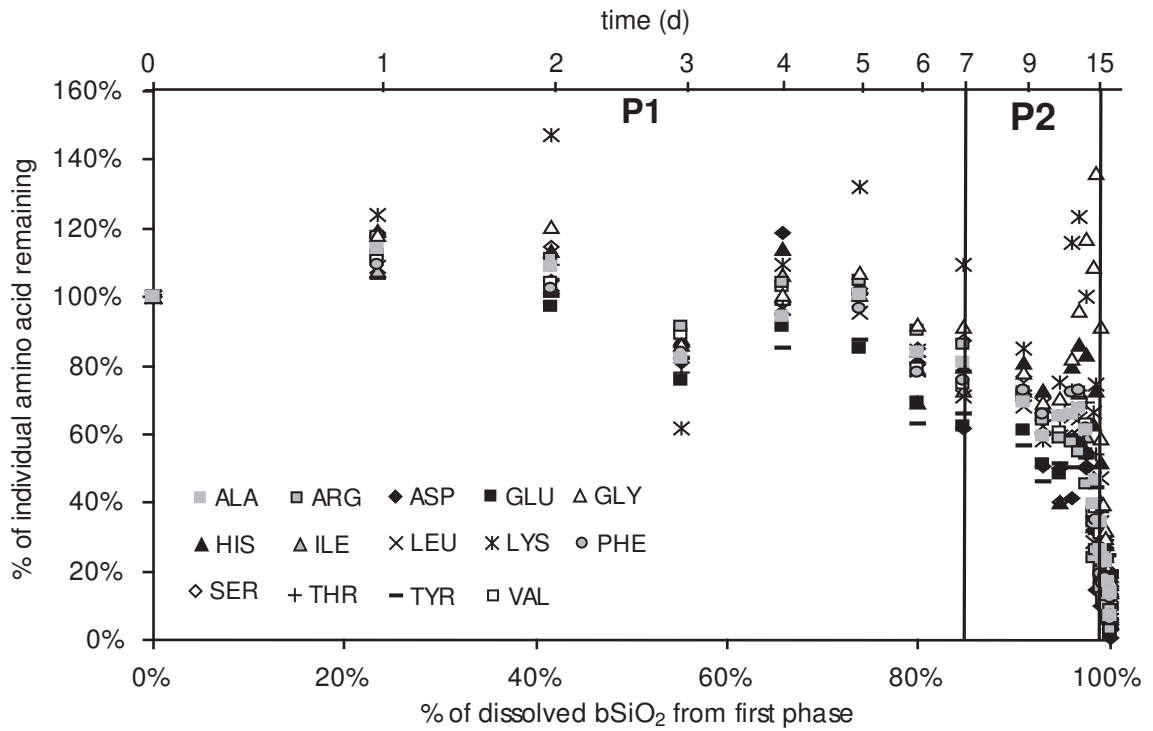
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962 Fig. 8:



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