

An efficient and rapid method for the enumeration of heterotrophic prokaryotes in coastal sediments by flow cytometry

Lavergne Céline, Beugeard Laureen, Dupuy Christine, Courties Claude, Agogué Hélène

► **To cite this version:**

Lavergne Céline, Beugeard Laureen, Dupuy Christine, Courties Claude, Agogué Hélène. An efficient and rapid method for the enumeration of heterotrophic prokaryotes in coastal sediments by flow cytometry. *Journal of Microbiological Methods*, Elsevier, 2014, 105, <http://www.journals.elsevier.com/journal-of-microbiological-methods/>. <10.1016/j.mimet.2014.07.002>. <hal-01086641>

HAL Id: hal-01086641

<https://hal.archives-ouvertes.fr/hal-01086641>

Submitted on 24 Nov 2014

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

1 **An efficient and rapid method for the enumeration of**
2 **heterotrophic prokaryotes in coastal sediments by flow**
3 **cytometry**

4

5 Lavergne Céline¹, Beaugéard Laureen¹, Dupuy Christine¹, Courties Claude², Agogué Hélène¹

6

7 ¹ LIENSs, UMR 7266 Université de La Rochelle – CNRS, 2 rue Olympe de Gouges, 17000

8 La Rochelle, France

9 ² Sorbonne Universités, UPMC Univ Paris 06, UMS 2348, Laboratoire d’Océanographie

10 Microbienne, Observatoire Océanologique, F-66650 Banyuls/Mer, France

11

12 Corresponding author: Lavergne Céline LIENSs, UMR 7266 Université de La Rochelle –

13 CNRS, 2 rue Olympe de Gouges, 17000 La Rochelle, France.

14 Tel : +33 (0)5 46 50 76 44

15 Fax : +33 (0)5 46 50 76 63

16 E-Mail : celine.lavergne@univ-lr.fr

17

18 Running title: FCM for counting benthic prokaryotes

19

Abstract

Flow cytometry offers an easy and powerful way to assess multi-parametric data in different domains, notably in the environmental sciences. Because evaluating heterotrophic prokaryotic abundance is crucial to understand an ecosystem's functioning, we propose a quick and efficient protocol for 1) cell's detachment in muddy coastal sediments followed by 2) enumeration of prokaryotes by flow cytometry compared to epifluorescence microscopy and 3) a type of storage adapted for benthic samples. First, samples preparation by incubation in a detergent mix containing sodium pyrophosphate (0.01 M final concentration) and Tween 80 (0.1% final concentration) drastically increased cell detachment from sediment particles (+130.40 %) compared to extraction with sodium pyrophosphate only. Cell sorting allowed to control the efficiency of the extraction as few cells were found attached to sediment particles in epifluorescence microscopy after sorting. Flow cytometry gave consistent results with strong reliability by counting 1.81 times more cells compared to epifluorescence microscopy. Thirdly, results revealed that sediment samples fixed with formaldehyde and then liquid-N₂ frozen and directly stored at -80°C can be analysed within 3 months. In routine, our method of extraction and counting allowed to evaluate 83.67% of the real abundance in a sediment sample. Finally, this optimized technique was applied on sandy and muddy coastal and freshwater sediments and allowed us to prove the high efficiency of this new method. Flow cytometry is a fast, replicable and low-cost method for counting heterotrophic prokaryotes, even for sediment samples. The two-step method that we developed enables high frequency analyses (30 samples in less than 4 hours).

Keywords : prokaryotes; cell enumeration; flow cytometry; coastal sediments

42 **1 Introduction**

43 Microorganisms dominate marine ecosystems (DeLong et al., 2006) and were often
44 considered as a “Black Box” by scientists (Fuhrman et al., 2002). To investigate this “Black
45 Box”, many studies have focused on new technologies and advances in molecular biology
46 methods, allowing researchers to acquire a huge quantity of phylogenetic and potential
47 physiologic information from oceans and marine coastal ecosystems. But these revolutionary
48 “omics” data need to be completed by single-cell analysis, metabolic studies, and basic
49 determination of prokaryotic abundances. Prokaryotes (Bacteria and Archaea) are key
50 organisms in biogeochemical cycles in all marine environments (Azam and Malfatti, 2007,
51 DeLong, 2009) and the first step to study these communities is to estimate their abundance
52 within the microbial assemblage. Estimations of abundance showed that prokaryotes are as
53 abundant as 10^6 cells.mL⁻¹ in ocean water (Whitman et al., 1998) and more than 10^8 cells.mL⁻¹
54 ¹ in marine surface sediments (Jorgensen and Boetius, 2007). In sediments, prokaryotes play a
55 crucial role in the food web as they remineralize organic matter and lead major cycles such as
56 nitrogen and carbon cycles. Most specifically, heterotrophic prokaryotes are a majority
57 throughout the whole sediment depth and can be present until almost 2 km below the surface
58 (Ciobanu et al., 2014).

59 The first advances in heterotrophic prokaryotic enumeration were made using
60 epifluorescence microscopy (EFM) (Porter and Feig, 1980). Fluorochromes combined with
61 EFM have been used to develop standardized methods to successfully count bacteria in
62 freshwater and marine water columns (Daley, 1979). The most widespread way of staining
63 cells is to target DNA with a fluorescent dye such as DAPI (4', 6-diamidino-2-phenylindole),
64 currently used in microscopy (Porter and Feig, 1980). Montagna (1982) showed under
65 Acridine Orange (AO)-EFM observation that bacteria in muddy sediments occur at levels two
66 orders of magnitude greater than in sandy sediments. Nowadays, EFM is still the most

67 widespread technique for estimating the abundance of prokaryotes (see Supplementary
68 Information Table 1 for references). Nevertheless, Robertson and Button (1989) were the first
69 to use flow cytometry (FCM) to enumerate heterotrophic prokaryotic cells by DAPI-staining
70 in marine and freshwater samples. Even if FCM seemed to be an accurate and rapid method
71 for determining heterotrophic prokaryotic cells, advances were needed in storage conditions
72 or fixative effects on benthic samples. These fixatives were known to permeate cells
73 (Troussellier et al., 1995); consequently, the interactions between dyes and fixatives needed to
74 be taken into account when choosing dyes. During the exponential phase of FCM utilization
75 for environmental marine samples, many dyes have been reported in the literature such as
76 DAPI, Hoechst 33342, TO-PRO-1, SYBRGreen (I or II), SYTO13 etc... (details are
77 reviewed in Gasol and Del Giorgio (2000)). With technological advances, FCM became more
78 and more useful in marine microbiology and offered new challenges to scientists, such as the
79 prokaryotic enumeration in soils and sediments and the use of specific probes (Fluorescence
80 in situ hybridization - FISH) (Llobet-Brossa et al., 1998). For sediment and soil analysis, the
81 dye mostly used to stain DNA is SYBRGreen I (Kallmeyer et al., 2008), and many authors
82 fixed cells with formaldehyde (Epstein and Rossel, 1995) preferentially, but the best
83 temperature for long time storage is still unclear.

84 FCM is now widely used for water column samples, but sediment samples carry the
85 difficulties of a solid matrix rich in detritus, minerals and exopolymeric substances (EPS).
86 Indeed, sediments are particularly hard to study because dyes (e.g. AO or DAPI) can produce
87 a high fluorescence background with clay and silt-rich sediments containing a high quantity of
88 detritus and EPS (Kuwae and Hosokawa, 1999). Additionally, in such environments,
89 prokaryotic cells are often attached to sediment particles by EPS (Decho, 2000), creating a
90 complex with organic and mineral particles (Epstein and Rossel, 1995, Kallmeyer, et al.,
91 2008). The point of divergence between microbiologists remains the separation method to

92 detach cells from the solid matrix. In order to improve counting yield in sediment, chemical
93 dispersion and physical detachment should be applied. Physical detachment can be achieved
94 by isoelectric method (Jaspers and Overmann, 1997), capillary electrophoresis
95 (Schneiderheinze et al., 2000), sonication bath (Duhamel and Jacquet, 2006, Ellery and
96 Schleyer, 1984, Gasol, 1993), or probes (Albright et al., 1986, Epstein and Rossel, 1995,
97 Kallmeyer, et al., 2008), vortexing (Frischer et al., 2000, Whiteley et al., 2003), or by blender
98 homogenization (Lindahl and Bakken, 1995, Maron et al., 2006, Yamamoto and Lopez,
99 1985). The sonication probes appear to be the best way to mechanically detach prokaryotic
100 cells from sediment particles, and applying it with an intensity of 60W for 30 seconds has
101 been shown to be a good compromise between high counting yield and avoiding lysing cells
102 (Garet, 1996, Lei et al., 2010). Concerning the chemical dispersion solution, the most cited is
103 the sodium pyrophosphate (NaPp), which is often found in detergent solutions in combination
104 with Tween 20 (Amalfitano and Puddu, 2009) or Tween 80 (Duhamel and Jacquet, 2006,
105 Epstein and Rossel, 1995), the phosphate buffer saline (PBS) solution (Barra Caracciolo et al.,
106 2005), the sodium chloride (Fazi et al., 2005), or methanol (Kallmeyer, et al., 2008, Lunau et
107 al., 2005). Moreover, it is possible to apply a density gradient (Kallmeyer, et al., 2008,
108 Morono et al., 2013) after the chemical separation in order to improve the time and reliability
109 of the counting (Fazi, et al., 2005). However, in the literature, it remains unclear which best
110 dilution and detergent mix need to be applied to sediment samples in order to detach the
111 maximum of aggregates and cells adsorbed on particles.

112 Nowadays, no simple and standardize method existed to study microorganisms in
113 different type of sediments. On that basis, this study aims at optimizing sediments fixation
114 and storage, cells separation and comparing two analysis methods (EFM and FCM) to count
115 benthic heterotrophic prokaryotes.

116 **2 Materials and Procedures**

117 *2.1 Sample collection, fixation and storage*

118 Muddy sediments from the French Atlantic coast were sampled in the Moëze Bay and
119 the Aiguillon Bay from the surface to 10 cm-deep. The sediment samples were collected in
120 2012 and 2013 at low tide using cores (15 cm diameter). Back in the laboratory (less than one
121 hour), the sediments were homogenized, and sub-samples were put in containers using sterile
122 50 mL syringes with cutoff tips. Finally, subsamples were fixed with 0.2 µm-filtered
123 formaldehyde solution (vol/vol, 2% final concentration) and kept according two conditions: at
124 +4°C in the dark or frozen in liquid-N₂ directly followed by storage at -80°C. Different storage
125 times were tested on five different muddy samples in duplicates: 1 week, 1 month, 3 months,
126 and 6 months after sampling.

127 *2.2 Protocol development*

128 Here, we described the proceedings of the protocol development. Different steps of the
129 procedure were investigated in order to improve the enumeration of prokaryotes in sediment:
130 1) sample preparation before mechanical extraction; 2) utility of centrifugation to remove
131 sediment particles; 3) repetitive steps of extraction to improve cell counting yield.

132 2.2.1 Sample preparation before mechanical extraction

133 First tests were achieved by preparing sediment slurries with a solution of NaPp 0.01M
134 (Pascal et al., 2009, Tso and Taghon, 1997). Then, in order to disaggregate the attached cells,
135 Tween 80 (0.1% final concentration) was added to the NaPp solution (0.01 M). Indeed,
136 Tween 80 is a non-ionic surfactant known to decrease particle aggregates and to enhance
137 detachment of cells from particles in sediment samples (Velji and Albright, 1986, Yoon and
138 Rosson, 1990). The influence of Tween 80 addition on the cell recovery efficiency was

139 evaluated on 55 samples. According to preliminary tests, using NaPp solution or
140 NaPp+Tween 80 mixture, slurries were prepared by processing to successive dilutions until
141 1:2,000 (1:10; 1:100; 1:500; 1:1,000 and 1:2,000) to reduce sediment background (dos Santos
142 Furtado and Casper, 2000, Duhamel and Jacquet, 2006). A vortexing step of 5 sec was applied
143 before and after each successive dilution.

144 According to Epstein and Rossel (1995) and Velji and Albright (1986)
145 recommendations, 30 minutes of incubation at +4°C was used to detach cells from sediment
146 particles. Then, mechanical extraction consisted of sonicating samples 30 s at 60W in ice with
147 a sonicator probe (Branson, SLPE-150, 1/8" or 3 mm microtip, 40KHz) (Lei, et al., 2010).

148 2.2.2 Utility of centrifugation to remove sediment particles

149 The impact of a centrifugation step was tested by applying or not a low speed centrifugation.
150 A first part of extracted samples was centrifuged at 1 000 g at +4°C during 1 min, after which
151 supernatant was transferred and then stained for EFM and FCM analysis (see below for
152 staining settings). On the second part of extracted samples, a proportion was mixed,
153 transferred and then stained for EFM and FCM analysis and centrifugation was applied on the
154 remaining proportion to collect sediment and attached cells for a second extraction step.

155 In any case, after centrifugation step, the remaining supernatant was discarded and the
156 pellet was re-suspended in the detergent mix [0.01 M NaPp and Tween 80 (0.1% final conc.)]
157 with the same volume of supernatant. By this way, the cells remaining attached to the
158 sediment particles in the pellet can be detached and counted in a second step.

159 2.2.3 Repetitive steps of extraction to improve cell counting

160 Because cells can be still attached to sediment particles even after the first extraction, we
161 evaluated the number of repetitive extraction steps needed to improve cell counting yield. The
162 second step was processed as the first one, by incubating the samples in the detergent mix

163 [0.01 M NaPp and Tween 80 (0.1% final conc.)] for 30 min at +4°C. Then, sonication was
164 repeated (same settings as above) before the analysis.

165 Aiming at evaluating how many steps were needed, extraction process was repeated
166 until cells recovery reaches a plateau on 15 different samples. Thus, the total prokaryotic cell
167 abundance corresponded to the sum of all the counting values obtained in each extraction
168 step.

169 2.3 *Microscopic count*

170 Extracted samples were stained with 4',6-diamidino-2-phenylindole (DAPI, 250
171 $\mu\text{g}\cdot\text{ml}^{-1}$, 15 min, +4°C) and filtered through black polycarbonate membrane (0.2 μm pore size,
172 25 mm, Nucleopore) (Porter and Feig, 1980). Next, filters were mounted on slides using anti-
173 fading oil type F (Olympus, Japan), and conserved at -20°C until counting. Finally, counts
174 were made with an epifluorescence microscope (Axioskop2, Carl Zeiss Microscopy, LLC,
175 United-States) at 1,000 x magnification under UV excitation (Filter set 01, 397 nm – Zeiss).
176 For each sample, a minimum of 20 fields (> 600 cells) were counted and averaged (Lebaron
177 et al., 1994).

178 2.4 *Flow cytometric and cell sorting analysis*

179 For each extraction step, the flow cytometric analysis consisted of SYBRGreen I-
180 stained (1:10,000 final concentration) extracted sample during 15 min in the dark at room
181 temperature. Fluorescent beads (Fluoresbrite Multi fluorescent microsphere 1.0 μm ,
182 Polysciences, Germany) were added simultaneously to each sample in order to analyze cell
183 fluorescence and scatter properties of samples. Each sample was analyzed for 30 s at low flow
184 speed with FacsCanto II cytometer (3-laser, 8-color (4-2-2), BD Biosciences) equipped with a
185 20-mW 488-nm coherent sapphire solid state blue laser. Data were acquired using DIVA
186 software provided by BD-Biosciences.

187 A cell sorter (FACSAria BF-Biosciences) was used to control extraction yield on
188 prokaryotic population. Then, sorted fraction were observed using EFM (BX300, Olympus)
189 to take pictures.

190 Stained cells were discriminated according to green fluorescence (FL1) from
191 SYBRGreen staining and side scatter properties (SSC). Picophytoplanktonic cells are also
192 discriminated based on their red fluorescence (FL3) and SSC properties and excluded from
193 final prokaryotic counts measured on a gate SSC-FL1 (Marie et al., 2001).

194 Accurate cell concentrations were performed using TruCount beads from BD-
195 Biosciences (excitation: red laser 633 nm; emission: FL5 660/20 nm).

196 2.5 *Statistical analysis*

197 All statistical analysis was performed using R software (R core Team, 2013). The
198 effect of the addition of Tween 80 was tested with a Paired t-test. The influence of the
199 parameters tested or percentage of sand in samples was evaluated by applying a Kruskal-
200 Wallis rank sum test for one sample and Wilcoxon test for two paired samples on cell
201 abundance values. The relationship between FCM and EFM was shown by fitting a
202 significant linear regression. Effects of storage conditions were tested with a 2-way analysis
203 of variance (ANOVA), residuals were tested for application validation and a TukeyHSD post-
204 hoc test was used.

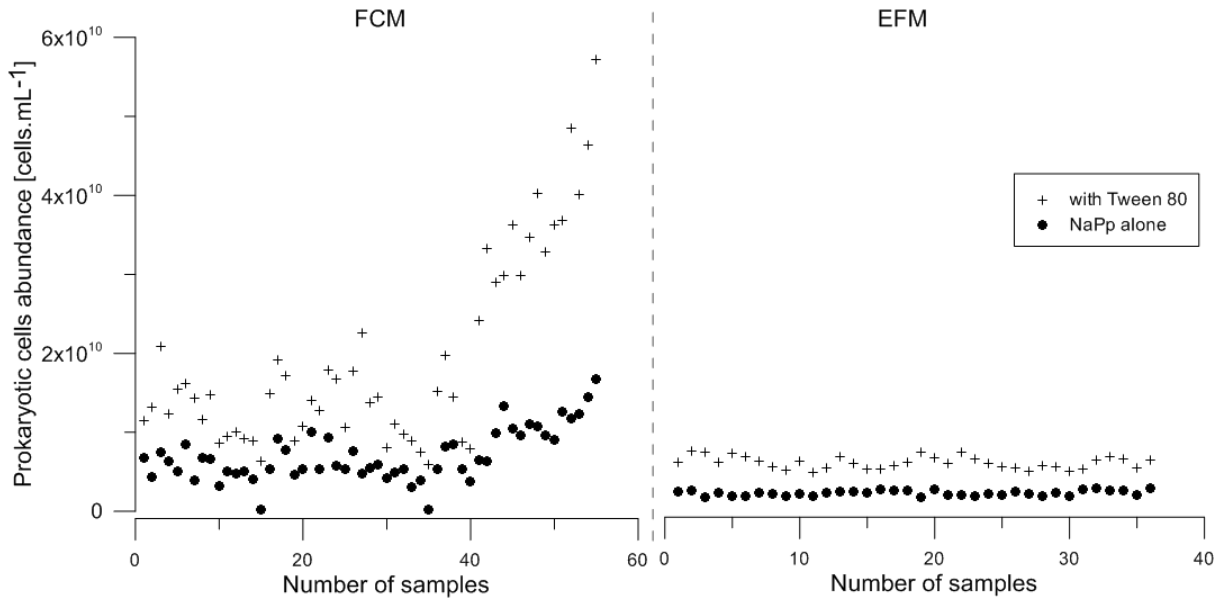
205 3 Results

206 Hereby, we described the results of the protocol development proceedings and then the final
207 protocol that we succeed to establish.

208 3.1 Sample preparation

209 First, slurries were prepared with NaPp 0.01M alone and cell sorting flow cytometry
210 followed by EFM observations were used to visualize the extracted populations. Two
211 populations were observed: free prokaryotic cells population and attached-prokaryotic cells
212 population. The NaPp alone at 0.01 M was apparently not efficient enough to separate cells
213 from sediment particles, because attached prokaryotic cells were still present in the samples
214 and represented 27.7% of the total abundance. On this basis, the effect of adding Tween 80
215 was evaluated to minimize cell aggregation (Yoon and Rosson, 1990). Both FCM and EFM
216 counting revealed a higher cell counting yield (Fig. 1), with an increase of $130.40 \% \pm 12.49$
217 SE and $176.79 \% \pm 14.25$ SE respectively, compared to the treatment without Tween 80.
218 Adding Tween 80 to NaPp in the mixture significantly improve the number of cells counted in
219 FCM (Paired t-test: $t = -9.6127$, $df = 54$, p -value <0.001) and EFM (Paired t-test: $t = -$
220 27.1056 , $df = 35$, p -value <0.001). After two repetitive steps, cell recovery efficiency rose
221 from $43.3 \% \pm 2.0$ SE without Tween to $92.5\% \pm 2.0$ SE with addition of Tween 80.
222 Moreover, microscopic analysis on sorted populations confirmed that the counted cells were
223 free cells, clearly separated from sediment particles when Tween 80 was added to the mixture.
224 Consequently, it appears that Tween 80 disaggregated efficiently benthic cells and therefore
225 improved the cell counting results (Fig. 1). The recommended protocol is thus to use sodium
226 pyrophosphate (NaPp) and Tween 80 treatment to prepare sediment samples for heterotrophic
227 prokaryotes enumeration by FCM (Fig. 5).

228



229

230 **Fig. 1.** Effects of the addition of Tween 80 to sodium pyrophosphate (NaPp) on prokaryotic
 231 cell abundance in sediment samples (FCM counts from SYBRGreen: n = 55; EFM counts
 232 from DAPI: n= 36). Values for all the samples tested are presented. Crosses represented
 233 samples extracted with Tween 80 and NaPp, and circles represented samples extracted with
 234 NaPp alone.

235

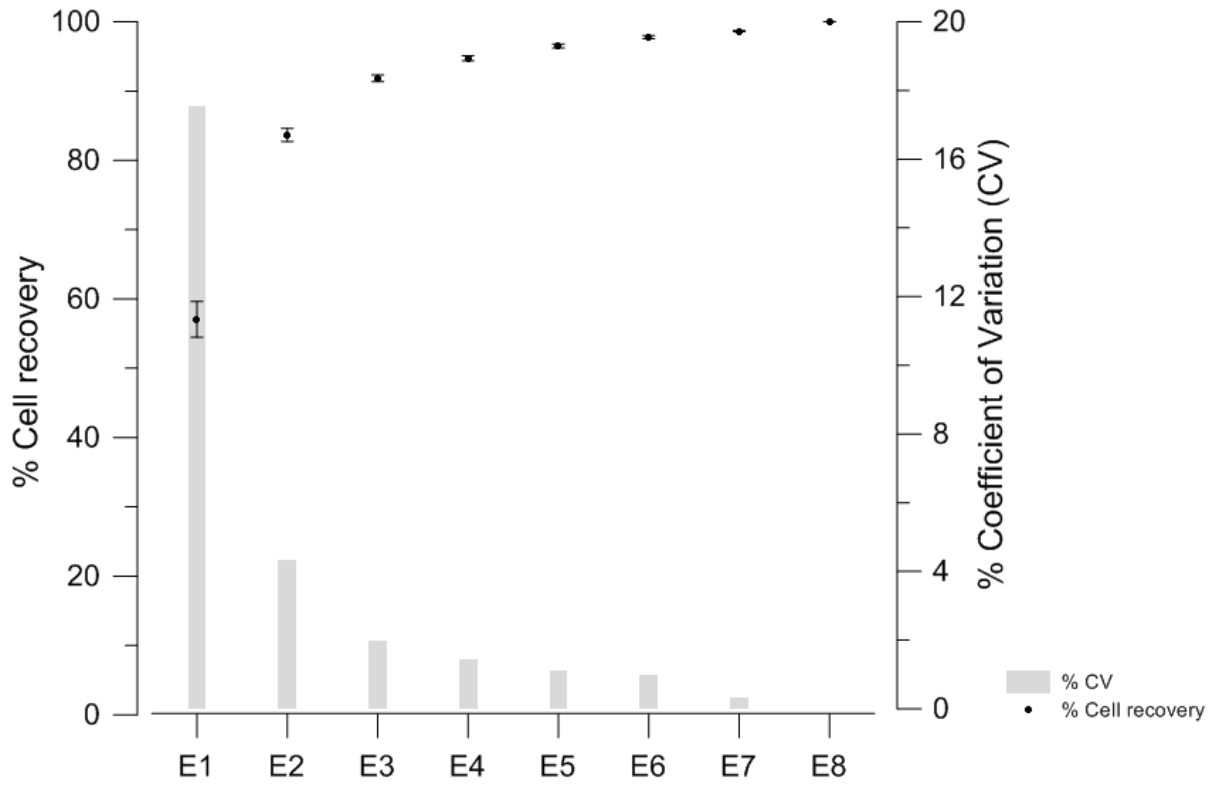
2-column	fitting
----------	---------

236 3.2 *Utility of centrifugation*

237 The utility of a centrifugation step before counting analysis was tested by performing
238 an experiment with and without low speed centrifugation (1,000 g, 1 min, +4°C). Experiments
239 showed that centrifugation moderately decreased cell counts (-1.71%) in FCM and EFM
240 because cells that remained attached to the particles were removed (data not shown). Settling
241 velocities of sands have been calculated according to Soulsby (1997), and we evaluated that
242 the settling time of particles is inferior to the standing step applying on cytometer to acquire
243 data before recording. Indeed, particles of 62 µm will take 4.8 seconds to settle in the tube and
244 the cytometer takes 5 seconds to acquire and 10 seconds to record. The particles cannot
245 collapse the flow cell chamber. Thus, we proposed to analyse samples without the
246 centrifugation step and then to centrifuge samples afterward to proceed to a second cells
247 extraction on the pellet.

248 3.3 *Repetitive steps of extraction*

249 After the first extraction, $57.04 \% \pm 2.58 \text{ SE}$ of cells were extracted and counted. The
250 cumulative cell recovery increased strongly and reached a plateau after the fourth extraction
251 (Fig. 3), showing that in routine analysis it will not be necessary to do more than four
252 extractions. The coefficient of variation of the first extraction was the highest, reaching 17.52
253 %. The strongest decrease in CV was observed between the first and the second extraction
254 (Fig. 2) showing that the second extraction allowed counting a higher number of cells
255 ($83.67\% \pm 0.94 \text{ SE}$) with a lower imprecision ($\text{CV} < 5\%$). After that, the CV continued to
256 decrease with lower range values. Doing eight extractions can be time consuming and
257 expensive. In our case, with sediment samples, eight extractions were not necessary. Thus, for
258 routine analysis of benthic samples by FCM, we propose a 2-step extraction as a good
259 compromise among 1) cell recovery efficiency ($83.67\% \pm 0.94 \text{ SE}$) and accuracy ($\text{CV} = 4.34$);
260 and 2) analysis time (4 hours for 30 samples) and cost.



261

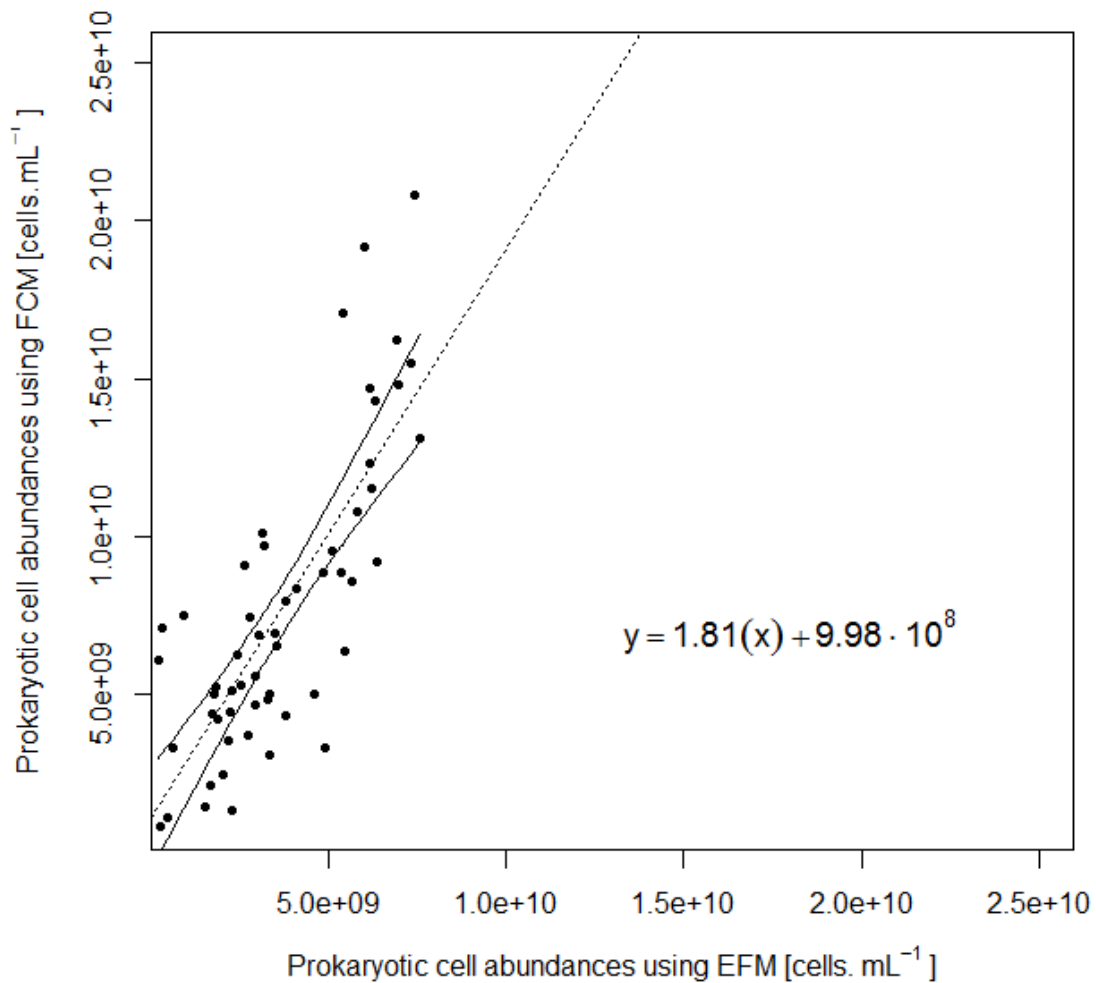
262 **Fig. 2.** Cumulative percentage of cell recovery using the final extraction protocol (extended to
 263 eight extractions), counting by flow cytometry (FCM) and percentage coefficient of variation
 264 (% CV) (n=15). Black dots represent cell recovery efficiency with standard errors and grey
 265 bars represent % CV, E = extraction number.

266

single column fitting image

267 3.4 *Microscopy versus flow cytometry*

268 Fifty five muddy samples were tested and highly significant correlations were found
269 between EFM and FCM counts (Fig. 3; t-test: $R^2= 0.615$, $df =53$, $p\text{-value} <0.001$). Moreover,
270 cell abundance estimated by FCM was always higher than cell abundance counted by EFM,
271 by a factor of 1.81. Thus, EFM and FCM results followed the same trends but FCM always
272 allowed detecting more cells than EFM. We prove by this way that the traditional method by
273 EFM need to be re-evaluated and that FCM can be a better method to assess the heterotrophic
274 prokaryotic abundance.



275

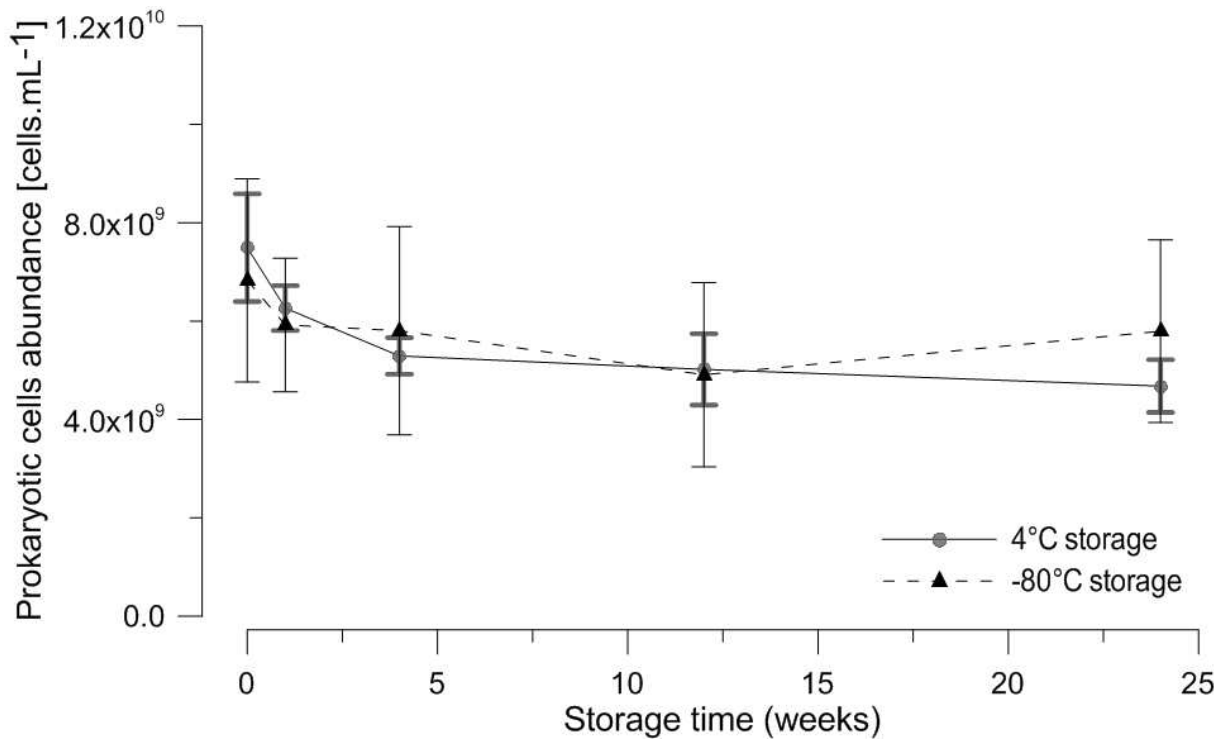
276 **Fig. 3.** Linear regression between prokaryotic cell abundance determined by flow cytometry
 277 (FCM) and observed by epifluorescence microscopy (EFM). Samples come from the Moëze
 278 mudflat at different depths and sampling seasons (n=55), dot line corresponding to the
 279 regression line and envelopes represent 95% confidence intervals. Significant adjusted R-
 280 squared: 0.615 (t-test: F-stat : 87.3, df =53, p-value <0.001).

281

single column fitting image

282 3.5 *Which type of storage?*

283 The influence of storage conditions on prokaryotic cells was studied. After the first
284 month of storage, a loss of $24.46 \% \pm 4.5 \text{ SE}$ of cells was observed under the two storage
285 conditions (-80°C and $+4^{\circ}\text{C}$). After that, prokaryotic abundances remained stable until 6
286 months (-4% ; Fig. 4). High standard error bars on Fig. 4 were due to the differences in
287 prokaryotic abundances between sample depths, but the results brought out that prokaryotic
288 abundances in samples stored at -80°C tend to be higher than in those conserved at $+4^{\circ}\text{C}$. A
289 significant difference was detected between T0 and 12 weeks after sampling (Tukey HSD; p -
290 value <0.05), nevertheless, neither the temperature of storage nor the interaction with time
291 influenced the abundance of prokaryotes counted (2-way ANOVA, p -value > 0.05). After 3
292 months, the abundances measured with the final protocol were more variable. The
293 recommended protocol is to store fixed sediment samples at -80°C (as for water samples,
294 (Marie et al., 1997)) and to analyse samples within 3 months after sampling.



295

296 **Fig. 4.** Effects of storage temperature and time on heterotrophic prokaryotic cell abundance
297 obtained by flow cytometry (FCM) with the two-step protocol (mean values +/- standard
298 errors from five samples in duplicate are shown).

1.5-column fitting image

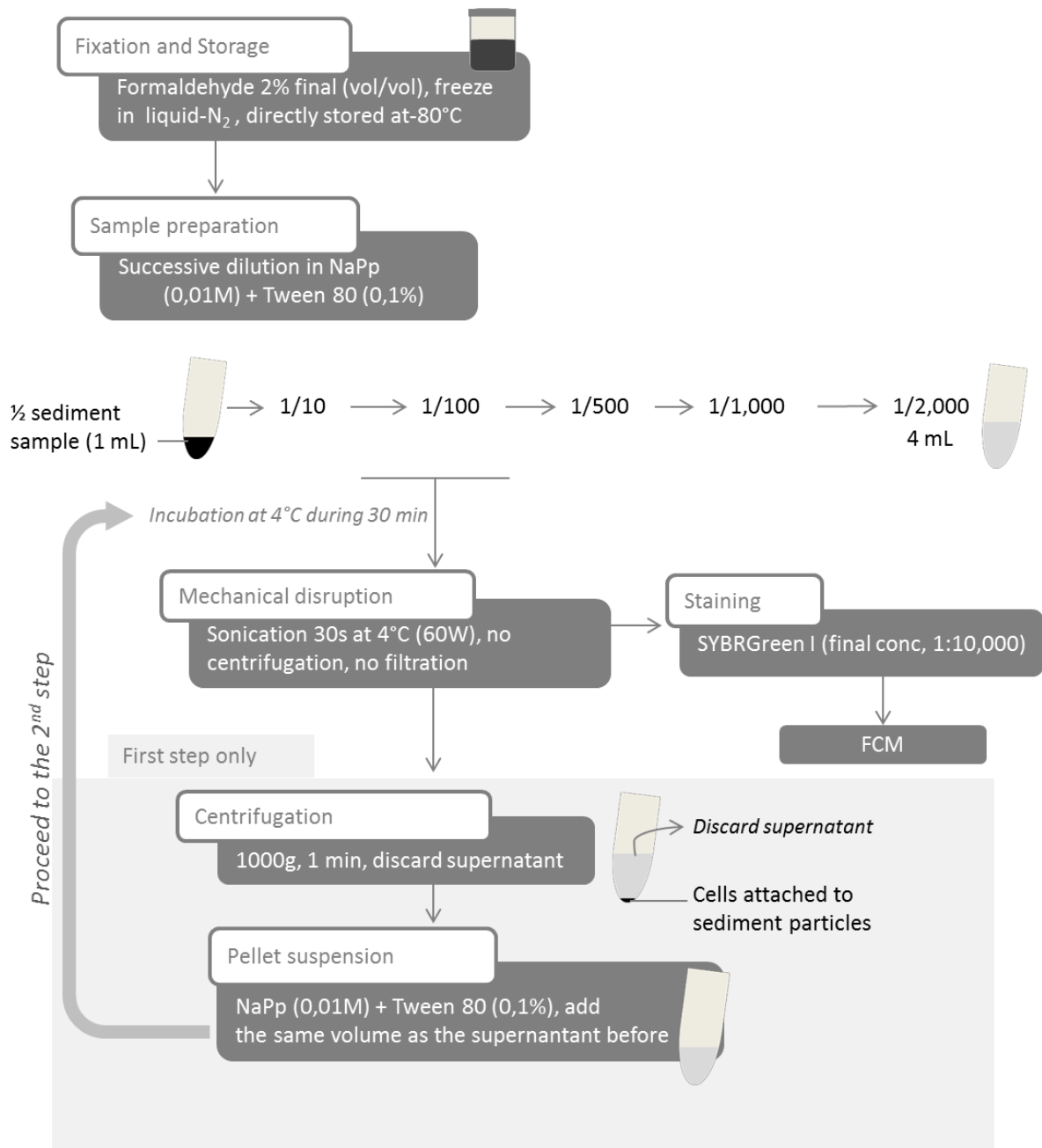
299 3.6 *Final protocol*

300 All the assessments above resulted in a final protocol. This final protocol (Fig. 6)
301 detached and homogenized cells in sediment samples thanks to 2 successive extractions (§
302 3.3) and allowed to count the prokaryotic cells using FCM.

303 1) Samples were prepared and extracted using: a dilution (1:1,000 to 1:2,000) in a
304 detergent mix (§ 3.1) [sodium pyrophosphate (0.01 M) + Tween 80 (0.1%)] and a vortexing
305 step and 30 min of incubation at +4°C. After the vortexing step, a sonication separation for 30
306 sec (60W) in ice with a sonication probe (3 mm) was applied. Without any centrifugation step
307 (§ 3.2), an aliquot of the sample was stained with SYBRGreen I (1:10,000) 15 min in the dark
308 and analyzed by flow cytometry (FCM).

309 2) the remaining part of the sample was centrifuged at low speed (1 min at 1,000 g at
310 +4°C); the pellet was then resuspended in the detergent mix and step 1 was repeated once
311 more.

312 Using this two-step protocol, $83.67\% \pm 3.63$ SD (§ 3.3) of total cells can be extracted from a
313 solid matrix and counted by SYBRGreenI-stained FCM.



314

315 **Fig. 5.** Final protocol of the improved two-step separation method. FCM = Flow Cytometry ;

316 NaPp = sodium pyrophosphate.

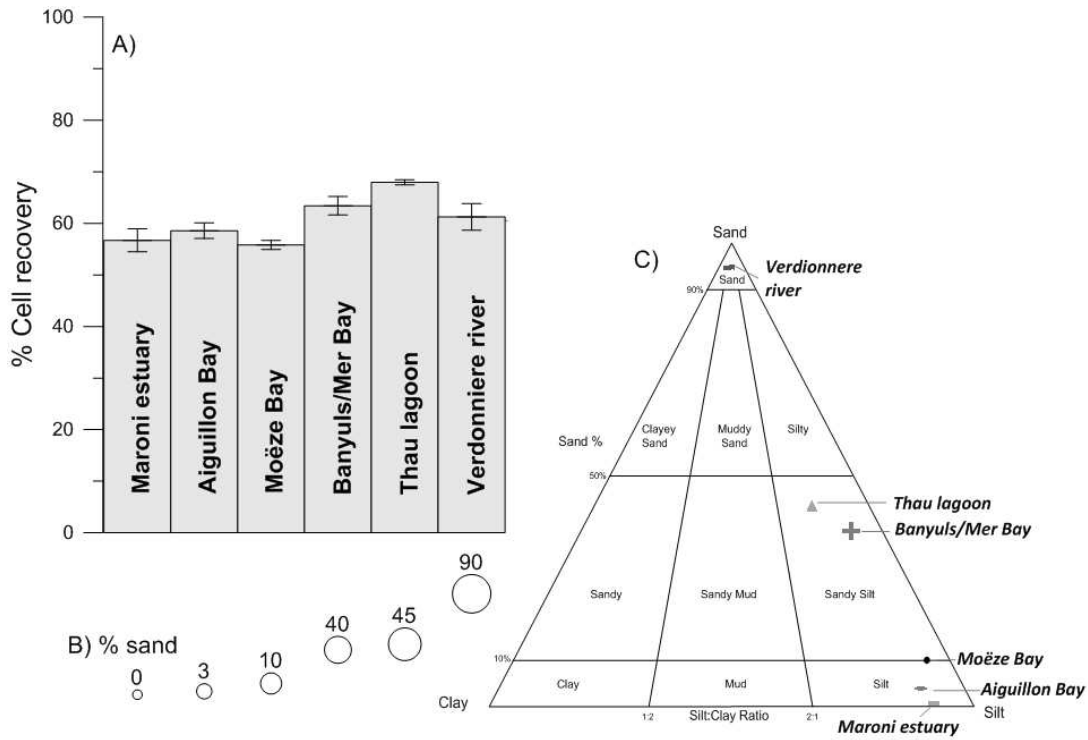
317

2-column fitting image

318 *3.7 Application on different types of sample*

319 To validate the protocol, the method for FCM analysis was applied to sandy, sandy-
320 mud and muddy sediments from different locations with different values of sand contents
321 (from 0 to 90%) following a range of silt/sand content. For each sample, the cell recovery
322 percentages of the first step extraction were high, by mean 61% ranging from 55% to 68%
323 (Fig. 6; Supplementary Information Table 2.). The cell recovery efficiencies of these samples
324 were in the same range and there were no significant effects of the sand content on the cell
325 recovery of the first extraction (Kruskal-Wallis test; $\chi^2 = 5$; $df = 5$; p -value = 0.4159). These
326 results showed that our developed method is efficient for sandy, sandy-mud and muddy
327 sediments tested whatever the location and sand content or composition.

328



329

330 **Fig. 6.** A) Percentage of cells extracted after the first step by applying our two-step extraction
 331 method followed by FCM heterotrophic prokaryotic enumeration on sandy and muddy
 332 sediment samples from diverse locations with a range of sand percentages. B) Sand
 333 percentages for each sample. C) Sand/Silt/Clay diagram for each sample.

334

2-column fitting image

335 4 Discussion and Conclusions

336 Flow cytometry (FCM) is now widely used for water column analysis in order to
337 estimate autotrophic diversity and abundance, and to enumerate heterotrophic prokaryotes
338 (Legendre et al., 2001). For sediment analysis, technical advances have been made but not
339 well optimized to get an efficient and rapid method for FCM. The main difficulty remains the
340 necessary step of cell preparation and separation from sediment which need to be adapted for
341 each sediment type (Duhamel and Jacquet, 2006). Many authors have tried to find the best
342 protocol for separating prokaryotic cells from a solid matrix. One particularly powerful way
343 seems to be the density gradient application on various sediments (Aakra et al., 2000,
344 Amalfitano and Fazi, 2008, Kallmeyer, et al., 2008, Lunau, et al., 2005, Morono, et al., 2013,
345 Whiteley, et al., 2003), but these techniques are relatively time-consuming and expensive. The
346 present study demonstrates a quick and efficient protocol for the enumeration of heterotrophic
347 prokaryotes in coastal sediments.

348 Since EFM is the classic method of counting heterotrophic prokaryotic cells in
349 sediment, our protocol of extraction followed by FCM analysis needs to be validated by EFM.
350 We compared the cell abundance obtained by EFM (DAPI-stained cells) and FCM
351 (SYBRGreenI-stained cells). The staining protocol used was different with the two methods
352 (i.e. DAPI preferentially bind on A and T bases). The choice was to compare the traditional
353 protocol (DAPI-stained cells) and the most used protocol in FCM (SYBRGreenI-stained
354 cells). It is known that the two dyes may differ in terms of binding and affinity on DNA and
355 RNA (simple and double-stranded) (Marie, et al., 1997, Troussellier et al., 1999) and thus can
356 produce different results. Nevertheless, DAPI-stained samples (sorted and non-sorted
357 sediment samples) were counted using FCM equipped with a violet laser (407 nm).
358 Cytograms were weakly exploitable because DAPI fluorescence yield was not optimal at 407
359 nm (optimal wave length = 375 nm) resulting in a low signal resolution and thus high

360 fluorescence background of DAPI (data not shown). Moreover, observations of SYBRGreenI-
361 stained cells under EFM were not satisfactory.

362 Finally, FCM appeared to be a consistent method to count benthic prokaryotes as it
363 allows the detection of 1.81 times more cells than EFM with a significant correlation. The
364 explanation could be that EFM is human-dependent and biased by the cell location of the
365 filter (can be hidden by sediment particles). FCM allows assessment of particle count as well
366 as multi-parameters analysis for each cell (Bouvier et al., 2001, Porter et al., 1997). The use of
367 FCM increases counting efficiency as compared to the classic EFM method, and the
368 estimation of prokaryotic abundance is consistent.

369 Liquid N₂ storage is the most widely used method of conserving prokaryotic cells in
370 water samples for FCM analysis (Vaulot et al., 1989), but in the case of benthic prokaryotic
371 cells, samples are usually directly counted or stored at +4°C before EFM counting (Ellery and
372 Schleyer, 1984, Epstein and Rossel, 1995). We then propose to fix the sediment samples with
373 2% formaldehyde solution and after liquid-N₂ fixation, store them immediately at -80°C and
374 then count within 3 months after sampling.

375 Many authors had proposed protocols for FCM analysis including a centrifugation step
376 and/or a filtration through 5 µm because it can limit detritus clogging in the cytometer nozzle
377 (Duhamel and Jacquet, 2006). The present study brings out that without centrifugation, the
378 sediment particles can settle in the tube and did not accumulate in the flow cytometer nozzle,
379 and FCM analysis was possible. To develop a rapid and easy protocol, we proposed to analyse
380 samples without the centrifugation step and then to centrifuge samples afterward to proceed to
381 the second extraction (on the pellet).

382 Taking into considerations all these features, the development of the protocol focused
383 on a method of cell separation to define a simple, inexpensive, and rapid method to enumerate
384 prokaryotes in sediment.

385 Kallmeyer, et al. (2008) extracted between 65 and 100% of prokaryotic cells in deep
386 subsurface sediments by applying a bilayer density gradient. In soil, Barra Caracciolo, et al.
387 (2005) also used a bilayer gradient density as well, and were able to extract up to 77% of total
388 prokaryotic cells. More recently, Morono, et al. (2013) applied a multilayer density gradient
389 on samples from marine subsurface and obtained from 50 to 80% cell recovery. Lunau, et al.
390 (2005) worked on muddy and sandy sediments and opted for a low-speed centrifugation
391 method combined with a methanol purification step; by an EFM analysis, they achieved 54 to
392 114% cell recovery. Even if the cell recovery had been found to be variable among the
393 physico-chemical parameters of a solid matrix (Maron, et al., 2006), we confirmed that our
394 method is consistent and quicker, and can be applied to different kind of benthic samples. It
395 allows the extraction of a large quantity of prokaryotic cells (between 10^8 and 10^{10} cells.mL⁻¹)
396 and the possibility of determining prokaryotic abundances (83.67% mean cell recovery).

397 Nevertheless, it is clear that some optimization details must be done for each type of
398 samples. We suggest staining cells with more concentrated SYBRGreen I (1:5,000 final
399 concentration) if the prokaryotic population is not easily distinguishable from background
400 noise due to organic and mineral matter. Obviously, during the FCM analysis, threshold and
401 fluorescent parameters must be adapted to population characteristics as well as the dilution of
402 the sample.

403 Our two-step extraction method is simple to apply, as it allows the estimation of
404 heterotrophic prokaryotic abundance of 30 sediment samples within 4 hours. This method was
405 applied successfully on different types of sediments (muddy and sandy, coastal marine
406 sediments and freshwater sediment) and among the different types of sediments, our method

407 was reproducible. Moreover, these applications showed that our method was suitable not only
408 for coastal sediments but also for freshwater sediment (from the Verdonniere river streambed,
409 France). Aiming at finding a method suitable for a large range of sediments samples, this
410 study prove that our optimized method offers a better efficiency for different marine sediment
411 types even for freshwater sediments. In soils, Williamson et al. (2013), showed a strong
412 influence of clay content and recommended testing the influence of the extraction mixture
413 prior to analyse the samples. Further analyses remain possible to establish whether our two-
414 step protocol is efficient on clay-containing sediments.

415 This fast protocol using FCM is a methodological issue but is also crucial for
416 ecological studies by allowing in the end a better understanding of marine benthic
417 ecosystems. Finally, we can confirm that our protocol worked well for turbid water with high
418 organic matter content in a study on prokaryotic community distribution among a salinity
419 gradient in the Charente River (France). For this study, the dilution was adapted because
420 prokaryotic abundance was between two and three orders of magnitude less than in the
421 sediment samples.

422 In the future, we are convinced that our study can be useful for assessing activity,
423 productivity or diversity analysis in sediments. Although, the abundance of prokaryotes is a
424 central parameter to measure in all ecosystems, the next step to understand the functioning is
425 evaluating the unknown genetic diversity (DeLong, 2009, Karl, 2007). And activity and
426 productivity are powerful indices to characterize the community and are needed to show the
427 key role of prokaryotic community in biogeochemical cycles. The combinations of our
428 protocol and cell sorting (Wang et al., 2010) can be a great progress for sediment analysis.
429 With cell sorting, it will be possible to sort cells according to their average side-angle-
430 scattered (SSC) light (Bernard et al., 2000) (proxy of size-class) for example and then do
431 diverse analysis on different population of the prokaryotic community.

432 **Acknowledgments**

433 This research was supported by a PhD grant from the Charente Maritime Department,
434 by the CPER 2006-2013 (Contrat Projet Etat Région) of Charente Maritime and by EC2CO
435 project (CAPABIOC, CNRS and INSU, 2013-2014). We are grateful to the cytometry and
436 imaging platform that provided organization and service in our lab. We also appreciate the
437 cytometry platform of Banyuls/Mer, which allows us to use cell-sorting cytometry. Authors
438 are grateful to E. Pante (LIENSs, La Rochelle) for his help. In our study, we analysed various
439 sediments and the authors would like to thank all those who provided the environmental
440 samples: P. Bocher (LIENSs, La Rochelle) in collaboration with D.S. Mizrahi (project
441 supporting by the US Fish and Wildlife Service and the Western Hemisphere Shorebird
442 Reserve Network, New Jersey Audubon Society), K. Guizien and S. Lucas (DynDiagHyd
443 project, EC2CO - LECOB, Banyuls/Mer), H. Montanie (Biofilms Project, FREDD - LIENSs,
444 La Rochelle) and F. Rossi (CHARM project, EC2CO - ECOSYM, Montpellier). Authors are
445 grateful to the anonymous reviewers for their thorough evaluations which help us to improve
446 the quality of manuscript.

447

448 **References**

- 449 Aakra, A., Hesselsoe, M., Bakken, L.R., 2000. Surface Attachment of Ammonia-Oxidizing Bacteria in
450 Soil. *Microb Ecol.* 39, 222-235.
- 451 Albright, L.J., McCrae, S.K., May, B.E., 1986. Attached and Free-Floating Bacterioplankton in Howe
452 Sound, British Columbia, a Coastal Marine Fjord-Embayment. *Appl Environ Microbiol.* 51, 614-621.
- 453 Amalfitano, S., Fazi, S., 2008. Recovery and quantification of bacterial cells associated with
454 streambed sediments. *J Microbiol Methods.* 75, 237-243.
- 455 Amalfitano, S., Puddu, S.F., 2009. Flow cytometric analysis of benthic prokaryotes attached to
456 sediment particles. *J Microbiol Methods.* 79, 246-249.
- 457 Azam, F., Malfatti, F., 2007. Microbial structuring of marine ecosystems. *Nat Rev Micro.* 5, 782-791.
- 458 Barra Caracciolo, A., Grenni, P., Cupo, C., Rossetti, S., 2005. In situ analysis of native microbial
459 communities in complex samples with high particulate loads. *FEMS Microbiol Lett.* 253, 55-58.
- 460 Bernard, L., Courties, C., Servais, P., Troussellier, M., Petit, M., Lebaron, P., 2000. Relationships
461 among Bacterial Cell Size, Productivity, and Genetic Diversity in Aquatic Environments using Cell
462 Sorting and Flow Cytometry. *Microb Ecol.* 40, 148-158.
- 463 Bocher, P., Piersma, T., Dekinga, A., Kraan, C., Yates, M., Guyot, T., Folmer, E., Radenac, G., 2007.
464 Site- and species-specific distribution patterns of molluscs at five intertidal soft-sediment areas in
465 northwest Europe during a single winter. *Mar Biol.* 151, 577-594.
- 466 Bouvier, T., Troussellier, M., Anzil, A., Courties, C., Servais, P., 2001. Using light scatter signal to
467 estimate bacterial biovolume by flow cytometry. *Cytometry.* 44, 188-194.
- 468 Ciobanu, M.-C., Burgaud, G., Dufresne, A., Breuker, A., Redou, V., Ben Maamar, S., Gaboyer, F.,
469 Vandenebeele-Trambouze, O., Lipp, J.S., Schippers, A., Vandenkoornhuyse, P., Barbier, G., Jebbar,
470 M., Godfroy, A., Alain, K., 2014. Microorganisms persist at record depths in the subseafloor of the
471 Canterbury Basin. *ISME J.*
- 472 Compton, T., Troost, T., van der Meer, J., Kraan, C., Honkoop, P., Rogers, D., Pearson, G., de Goeij,
473 P., Bocher, P., Lavaleye, M., Leyrer, J., Yates, M., Dekinga, A., Piersma, T., 2008. Distributional
474 overlap rather than habitat differentiation characterizes co-occurrence of bivalves in intertidal soft
475 sediment systems. *Mar Ecol Prog Ser.* 373, 25-35.
- 476 Daley, R., 1979. Direct epifluorescence enumeration of native aquatic bacteria: uses, limitations, and
477 comparative accuracy. In: J. W. Costerton, R. R. Colwell (Eds.), *Native aquatic bacteria: enumeration,*
478 *activity and ecology*, Vol. 605, American Society for Testing Materials, pp. 29-45.
- 479 Danovaro, R., Dell'Anno, A., Trucco, A., Serresi, M., Vanucci, S., 2001. Determination of virus
480 abundance in marine sediments. *Appl Environ Microbiol.* 67, 1384-1387.
- 481 Decho, A.W., 2000. Microbial biofilms in intertidal systems: an overview. *Cont Shelf Res.* 20, 1257-
482 1273.
- 483 DeLeo, P.C., Baveye, P., 1996. Enumeration and biomass estimation of bacteria in aquifer microcosm
484 studies by flow cytometry. *Appl Environ Microbiol.* 62, 4580-4586.
- 485 DeLong, E.F., 2009. The microbial ocean from genomes to biomes. *Nature.* 459, 200-206.
- 486 DeLong, E.F., Preston, C.M., Mincer, T., Rich, V., Hallam, S.J., Frigaard, N.U., Martinez, A.,
487 Sullivan, M.B., Edwards, R., Brito, B.R., Chisholm, S.W., Karl, D.M., 2006. Community genomics
488 among stratified microbial assemblages in the ocean's interior. *Science.* 311, 496-503.
- 489 dos Santos Furtado, A.L., Casper, P., 2000. Different methods for extracting bacteria from freshwater
490 sediment and a simple method to measure bacterial production in sediment samples. *J Microbiol*
491 *Methods.* 41, 249-257.
- 492 Duhamel, S., Jacquet, S., 2006. Flow cytometric analysis of bacteria- and virus-like particles in lake
493 sediments. *J Microbiol Methods.* 64, 316-332.
- 494 Ellery, W., Schleyer, M., 1984. Comparison of homogenization and ultrasonication as techniques in
495 extracting attached sedimentary bacteria. *Mar Ecol Prog Ser.* 15, 247-250.
- 496 Epstein, S.S., Rossel, J., 1995. Enumeration of sandy sediment bacteria: search for optimal protocol.
497 *Mar Ecol Prog Ser.* 117, 289-298.
- 498 Fazi, S., Amalfitano, S., Pernthaler, J., Puddu, A., 2005. Bacterial communities associated with
499 benthic organic matter in headwater stream microhabitats. *Environ Microbiol.* 7, 1633-1640.

- 500 Frischer, M.E., Danforth, J.M., Healy, M.A.N., Saunders, F.M., 2000. Whole-Cell versus Total RNA
 501 Extraction for Analysis of Microbial Community Structure with 16S rRNA-Targeted Oligonucleotide
 502 Probes in Salt Marsh Sediments. *Appl Environ Microbiol.* 66, 3037-3043.
- 503 Fuhrman, J.A., Griffith, J.F., Schwalbach, M.S., 2002. Prokaryotic and viral diversity patterns in
 504 marine plankton. *Ecol Res.* 17, 183-194.
- 505 Garet, M.-J., 1996. Transformation bactérienne de la matière organique dans les sédiments côtiers:
 506 relation entre les métabolismes respiratoires et les activités exoprotéolytiques bactériennes Ph. D.
 507 thesis Univ. of La Rochelle.
- 508 Gasol, J.M., 1993. Benthic flagellates and ciliates in fine freshwater sediments: calibration of a live
 509 counting procedure and estimation of their abundances. *Microb Ecol.* 25, 247-262.
- 510 Gasol, J.M., Del Giorgio, P.A., 2000. Using flow cytometry for counting natural planktonic bacteria
 511 and understanding the structure of planktonic bacterial communities. *Sci Mar.* 64, 197-224.
- 512 Gough, H.L., Stahl, D.A., 2003. Optimization of direct cell counting in sediment. *J Microbiol*
 513 *Methods.* 52, 39-46.
- 514 Ifremer, 2008. Réseau de suivi Lagunaire du Languedoc-Roussillon : Bilan des résultats 2008 Rapport
 515 RSL 08-9 pp. 50.
- 516 Ishii, K., Musmann, M., MacGregor, B.J., Amann, R., 2004. An improved fluorescence *in situ*
 517 hybridization protocol for the identification of bacteria and archaea in marine sediments. *FEMS*
 518 *Microbiol Ecol.* 50, 203-213.
- 519 Jaspers, E., Overmann, J., 1997. Separation of bacterial cells by isoelectric focusing, a new method for
 520 analysis of complex microbial communities. *Appl Environ Microbiol.* 63, 3176-3181.
- 521 Jorgensen, B.B., Boetius, A., 2007. Feast and famine - microbial life in the deep-sea bed. *Nat Rev*
 522 *Micro.* 5, 770-781.
- 523 Kallmeyer, J., Smith, D.C., Spivack, A.J., D'Hondt, S., 2008. New cell extraction procedure applied to
 524 deep subsurface sediments. *Limnol Oceanogr Methods.* 6, 236-245.
- 525 Karl, D.M., 2007. Microbial oceanography: paradigms, processes and promise. *Nat Rev Micro.* 5, 759-
 526 769.
- 527 Kuwae, T., Hosokawa, Y., 1999. Determination of Abundance and Biovolume of Bacteria in
 528 Sediments by Dual Staining with 4',6-Diamidino-2-Phenylindole and Acridine Orange: Relationship
 529 to Dispersion Treatment and Sediment Characteristics. *Appl Environ Microbiol.* 65, 3407-3412.
- 530 Lebaron, P., Troussellier, M., Got, P., 1994. Accuracy of epifluorescence microscopy counts for direct
 531 estimates of bacterial numbers. *J Microbiol Methods.* 19, 89-94.
- 532 Legendre, L., Courties, C., Troussellier, M., 2001. Flow cytometry in oceanography 1989-1999:
 533 Environmental challenges and research trends. *Cytometry.* 44, 164-172.
- 534 Lei, Y., Stumm, K., Volkenborn, N., Wickham, S., Berninger, U.-G., 2010. Impact of *Arenicola*
 535 *marina* (Polychaeta) on the microbial assemblages and meiobenthos in a marine intertidal flat. *Mar*
 536 *Biol.* 157, 1271-1282.
- 537 Lindahl, V., Bakken, L.R., 1995. Evaluation of methods for extraction of bacteria from soil. *FEMS*
 538 *Microbiol Ecol.* 16, 135-142.
- 539 Llobet-Brossa, E., Rosselló-Mora, R., Amann, R., 1998. Microbial Community Composition of
 540 Wadden Sea Sediments as Revealed by Fluorescence In Situ Hybridization. *Appl Environ Microbiol.*
 541 64, 2691-2696.
- 542 Lunau, M., Lemke, A., Walther, K., Martens-Habbena, W., Simon, M., 2005. An improved method for
 543 counting bacteria from sediments and turbid environments by epifluorescence microscopy. *Environ*
 544 *Microbiol.* 7, 961-968.
- 545 Marie, D., Partensky, F., Jacquet, S., Vaulot, D., 1997. Enumeration and cell cycle analysis of natural
 546 populations of marine picoplankton by flow cytometry using the nucleic acid stain SYBR Green I.
 547 *Appl Environ Microbiol.* 63, 186-193.
- 548 Marie, D., Partensky, F., Vaulot, D., Brussaard, C., 2001. Enumeration of Phytoplankton, Bacteria,
 549 and Viruses in Marine Samples, *Curr Protoc Cytometry*, John Wiley & Sons, Inc.
- 550 Maron, P.-A., Schimann, H., Ranjard, L., Brothier, E., Domenach, A.-M., Lensi, R., Nazaret, S., 2006.
 551 Evaluation of quantitative and qualitative recovery of bacterial communities from different soil types
 552 by density gradient centrifugation. *Eur J Soil Biol.* 42, 65-73.
- 553 Montagna, P.A., 1982. Sampling Design and Enumeration Statistics for Bacteria Extracted from
 554 Marine Sediments. *Appl Environ Microbiol.* 43, 1366-1372.

- 555 Morono, Y., Terada, T., Kallmeyer, J., Inagaki, F., 2013. An improved cell separation technique for
 556 marine subsurface sediments: Applications for high-throughput analysis using flow cytometry and cell
 557 sorting. *Environ Microbiol.* 15, 2841-2849.
- 558 Pascal, P.Y., Dupuy, C., Richard, P., Mallet, C., Arminot du Châtelet, E., Niquil, N., 2009. Seasonal
 559 variation in consumption of benthic bacteria by meio- and macrofauna in an intertidal mudflat. *Limnol*
 560 *Oceanogr.* 54, 1048-1059.
- 561 Porter, J., Deere, D., Hardman, M., Edwards, C., Pickup, R., 1997. Go with the flow – use of flow
 562 cytometry in environmental microbiology. *FEMS Microbiol Ecol.* 24, 93-101.
- 563 Porter, K., Feig, Y., 1980. The use of DAPI for identification and enumeration of bacteria and blue-
 564 green algae. *Limnol Oceanogr.* 25, 943-948.
- 565 Riis, V., Lorbeer, H., Babel, W., 1998. Extraction of microorganisms from soil: evaluation of the
 566 efficiency by counting methods and activity measurements. *Soil Biol Biochem.* 30, 1573-1581.
- 567 Robertson, B.R., Button, D.K., 1989. Characterizing aquatic bacteria according to population, cell
 568 size, and apparent DNA content by flow cytometry. *Cytometry.* 10, 70-76.
- 569 Schneiderheinze, J., Armstrong, D., Schulte, G., Westenberg, D., 2000. High efficiency separation of
 570 microbial aggregates using capillary electrophoresis. *FEMS Microbiol Lett.* 189, 39-44.
- 571 Troussellier, M., Courties, C., Lebaron, P., Servais, P., 1999. Flow cytometric discrimination of
 572 bacterial populations in seawater based on SYTO 13 staining of nucleic acids. *FEMS Microbiol Ecol.*
 573 29, 319-330.
- 574 Troussellier, M., Courties, C., Zettelmaier, S., 1995. Flow cytometric analysis of coastal lagoon
 575 bacterioplankton and picophytoplankton: fixation and storage effects. *Estuar Coast Shelf Sci.* 40, 621-
 576 633.
- 577 Tso, S.F., Taghon, G.L., 1997. Enumeration of Protozoa and Bacteria in Muddy Sediment. *Microb*
 578 *Ecol.* 33, 144-148.
- 579 Vaultot, D., Courties, C., Partensky, F., 1989. A simple method to preserve oceanic phytoplankton for
 580 flow cytometric analyses. *Cytometry.* 10, 629-635.
- 581 Velji, M., Albright, L., 1986. Microscopic enumeration of attached marine bacteria of seawater,
 582 marine sediment, fecal matter, and kelp blade samples following pyrophosphate and ultrasound
 583 treatments. *Can J Microbiol.* 32, 121-126.
- 584 Wang, Y., Hammes, F., De Roy, K., Verstraete, W., Boon, N., 2010. Past, present and future
 585 applications of flow cytometry in aquatic microbiology. *Trends in Biotechnology.* 28, 416-424.
- 586 Whiteley, A.S., Griffiths, R.I., Bailey, M.J., 2003. Analysis of the microbial functional diversity
 587 within water-stressed soil communities by flow cytometric analysis and CTC+ cell sorting. *J*
 588 *Microbiol Methods.* 54, 257-267.
- 589 Whitman, W.B., Coleman, D.C., Wiebe, W.J., 1998. Prokaryotes: The unseen majority. *Proc Natl*
 590 *Acad Sci USA.* 95, 6578-6583.
- 591 Williamson, K., Corzo, K., Drissi, C., Buckingham, J., Thompson, C., Helton, R., 2013. Estimates of
 592 viral abundance in soils are strongly influenced by extraction and enumeration methods. *Biol Fertil*
 593 *Soils,* 1-13.
- 594 Yamamoto, N., Lopez, G., 1985. Bacterial abundance in relation to surface area and organic content of
 595 marine sediments. *J Exp Mar Biol Ecol.* 90, 209-220.
- 596 Yoon, W.B., Rosson, R.A., 1990. Improved Method of Enumeration of Attached Bacteria for Study of
 597 Fluctuation in the Abundance of Attached and Free-Living Bacteria in Response to Diel Variation in
 598 Seawater Turbidity. *Appl Environ Microbiol.* 56, 595-600.

599

600

601 **5 Figures**

602 **Fig. 1.** Effects of the addition of Tween 80 to sodium pyrophosphate (NaPp) on prokaryotic
 603 cell abundance in sediment samples (FCM counts from SYBRGreen: n = 55; EFM counts
 604 from DAPI: n= 36). Values for all the samples tested are presented. Crosses represented
 605 samples extracted with Tween 80 and NaPp, and circles represented samples extracted with
 606 NaPp alone.

607 **Fig. 2.** Cumulative percentage of cell recovery using the final extraction protocol (extended to
 608 eight extractions), counting by flow cytometry (FCM) and percentage coefficient of variation
 609 (% CV) (n=15). Black dots represent cell recovery efficiency with standard errors and grey
 610 bars represent % CV, E = extraction number.

611 **Fig. 3.** Linear regression between prokaryotic cell abundance determined by flow cytometry
 612 (FCM) and observed by epifluorescence microscopy (EFM). Samples come from the Moëze
 613 mudflat at different depths and sampling seasons (n=55), dot line corresponding to the
 614 regression line and envelopes represent 95% confidence intervals. Significant adjusted R-
 615 squared: 0.615 (t-test: F-stat : 87.3, df =53, p-value <0.001).

616 **Fig. 4.** Effects of storage temperature and time on heterotrophic prokaryotic cell abundance
 617 obtained by flow cytometry (FCM) with the two-step protocol (mean values +/- standard
 618 errors from five samples in duplicate are shown).

619 **Fig. 5.** Final protocol of the improved two-step separation method. FCM = Flow Cytometry ;
 620 NaPp = sodium pyrophosphate.

621 **Fig. 6.** A) Percentage of cells extracted after the first step by applying our two-step extraction
 622 method followed by FCM heterotrophic prokaryotic enumeration on sandy and muddy
 623 sediment samples from diverse locations with a range of sand percentages. B) Sand
 624 percentages for each sample. C) Sand/Silt/Clay diagram for each sample.

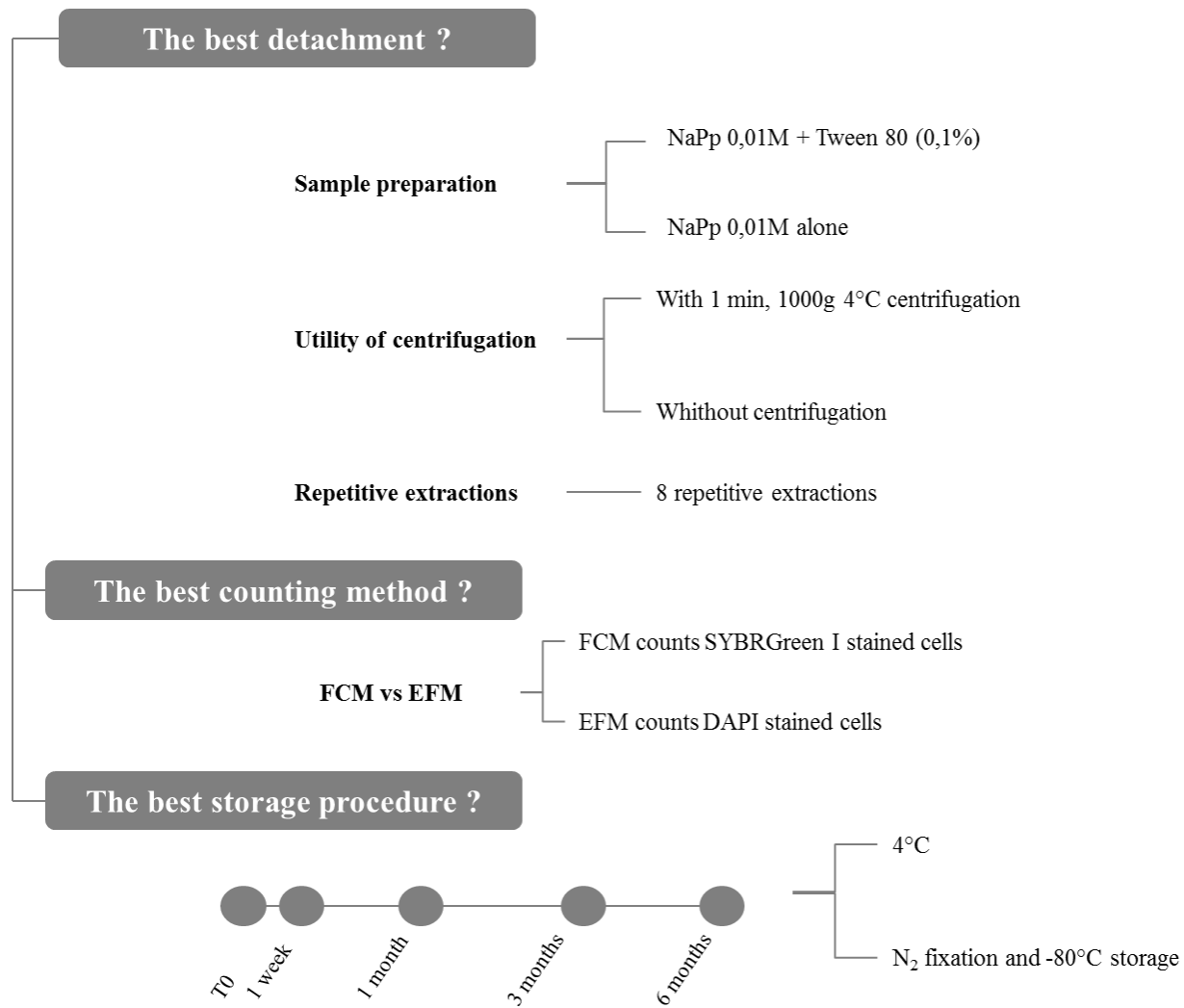
625 **6 Supplementary information**

626 **Figure 1.** Searching for the best protocol for enumeration of heterotrophic prokaryotes in
627 sediments

628

629 **Table 1.** Extraction, fixation and staining methods in literature

630 **Table 2.** Heterotrophic prokaryotes abundance (mean \pm SD) in different sediments and cell
631 recovery (% with mean \pm SD, min and max) of the first extraction using the two-step
632 extraction protocol analysed by flow cytometry (FCM).



633

634 **Figure 1.** Searching for the best protocol for enumeration of heterotrophic prokaryotes in sediments

635 **Table 1.** Extraction, fixation and staining methods in literature

Sample type	Fixation (final concentration)	Chemical separation	physical disruption	Centrifugation	Additional step	% recovery efficiency	Organisms	Staining (method)	References
<i>Turbid seawater</i>	Glutaraldehyde (2%)	Sterile seawater + 0.001% Tween 80	Sonication probe 10W 30s + blending 5 min at 22000 rpm	-	-	-	Prokaryotes	DAPI (EFM)	Yoon and Rosson (1990)
<i>Lake sediments</i>	Formaldehyde (2%)	10 mM NaPp + 10% Tween 80 + MilliQ Water	Sonication 3 min stopped for 30s every minute+ shaking	800g 1 min RT	Filtration through 5-µm filter	-	Prokaryotes, Viruses	SYBRGreen II (EFM + FCM)	Duhamel and Jacquet (2006)
	Formalin (3%) 4°C	-	-	750g 10 min 4°C	-	-	Prokaryotes	DAPI (EFM)	dos Santos Furtado and Casper (2000)
	Paraformaldehyde (4%) 4°C	10 mM NaPp + 120 mM NaCl + 10 mM NaPO4	Sonication bath 15 min	-	-	-	Prokaryotes	DAPI (EFM)	Gough and Stahl (2003)
<i>Streambed sand</i>	Formaldehyde (2%)	0.1 % NaPp + 0,5% Tween 20	Shaking 30 min, 720 rpm + sonication 1 min 20W	14000 g 90 min 4°C	NGD ^b	93%	Prokaryotes	DAPI (EFM) SYTO13 (FCM)	Amalfitano and Fazi (2008)
<i>Marine Sediments</i>									
- <i>Sands and muddy sediments</i>	Glutaraldehyde (2%)	10 mM P2O7	3 min sonication	800g 1 min RT	-	60%	Virus	SYBRGreen I	Danovaro et al. (2001)
- <i>Sandy sediments</i>	Formaldehyde (4%)	1:1 PBS/Ethanol	Sonication min power 20s	-	3 washes before storage	-	Prokaryotes	DAPI (CARD-FISH)	Ishii et al. (2004)
	Formaldehyde	Sterile seawater + 0.0001 % Tween80	Sonication bath 200W 2.5 min	-	-	-	Prokaryotes	AO (EFM)	Ellery and Schleyer (1984)
	Formaldehyde (4%) 4°C	0.1 mM NaPp + 0.0001% Tween80	Sonication probe 3x60s 109µm	500g 5min RT	8 washes	-	Prokaryotes	DAPI (EFM)	Epstein and Rossel (1995)
- <i>Deep subsurface sediments</i>	Formaldehyde (2%) 6h 4°C + washing steps	DT ^c	Shaking 60 min 500 rpm + sonication probe 20 W 1 min	4500g 15 min and 15000 300 min	MIGD ^c	-	Prokaryotes	SYBRGreen I (FCM)	Morono, et al. (2013)
	Formaldehyde (2%) 4°C	DT ^c	Vortexing 60 min + sonication probe 5x10 s	3000g 10 min RT	Carbohydrates dissolution + 2 NGD ^b steps	65 to 100%	Prokaryotes	SYBRGreen I + 0.1% <i>p</i> -phenylenediamine (EFM)	Kallmeyer, et al. (2008)
- <i>Muddy sediments</i>	-	10% methanol	Sonication bath 320W 15 min 35°C	190g 1min	-	54-114%	Prokaryotes	SYBRGreen I (EFM)	Lunau, et al. (2005)
<i>Soil</i>	no fixation	0.2% NaP2O7	0.5h intensive shaking	600g 5 min RT	-	45%	Bacteria, fungi	DAPI (EFM)	Riis et al. (1998)
	Formaldehyde (2%)	PBS+Tween20 + NaPp	Shaking 15 min at 400 rpm (orbital shaker)	14000g 90 min 4°C	NGD ^b + filtration through 0,2-µm filter	77%	Prokaryotes	DAPI (FISH)	Barra Caracciolo, et al. (2005)
<i>Aquifere</i>	Formaldehyde (0,5 %)	0.1% NaP2O7	Shaking 60 min at 155 rpm at 25°C	-	-	-	-	Propidium iodide (EFM)	DeLeo and Baveye (1996)
	Formaldehyde (2%)	PBS+ 0,5% Tween20	Shaking 15 min at 400 rpm (orbital shaker)	14000g 90 min 4°C	NGD ^b + filtration through 0,2-µm filter	78%	Prokaryotes	DAPI +(FISH)	Barra Caracciolo, et al. (2005)

^aDI-H2O + 100mM EDTA + 100mM NaPp+ 1% Tween80 + NaCl + MeOH^bNicodenz gradient density^cMultilayer Gradient density

636

637 **Table 2.** Heterotrophic prokaryotic abundance (mean \pm SE) in different sediments tested and
 638 cell recovery (% with mean \pm SE, min and max) of the first extraction using the two-step
 639 extraction protocol analysed by flow cytometry (FCM).

	Prokaryotes abundance [cells.mL ⁻¹]			% sand	Cell recovery [%]			
	mean	+/- SE			Mean (+/- SE)	Min	Max	
<i>Salt Lagoon sediment</i>								
Thau lagoon (n=48), France	1.53.10 ⁹	+/-	4.46.10 ⁷	45 ^a	67.98	+/- 0.49	60.72	75.06
<i>Intertidal Mudflat sediment</i>								
Moëze Bay (n=45), France	7.31.10 ⁹	+/-	2.92.10 ⁸	10	55.81	+/- 0.87	40.77	65.96
Aiguillon Bay (n=42), France	1.40.10 ¹⁰	+/-	4.34.10 ⁸	3 ^b	58.57	+/- 1.51	32.31	69.35
Maroni estuary (n=9), Surinam	3.99.10 ⁹	+/-	3.37.10 ⁸	0	56.70	+/- 2.23	38.16	68.72
<i>Sandy muddy coastal sediment</i>								
Banyuls s/ mer Bay, France Proteic enrichment (n=32)	2.81.10 ¹⁰	+/-	5.52.10 ⁸	40	62.81	+/- 1.29	38.14	72.90
Banyuls s/ mer Bay, France Glucidic enrichment (n=60)	1.46.10 ¹⁰	+/-	3.47.10 ⁸	40	64.03	+/- 0.88	41.56	72.75
<i>Sandy streambed sediment</i>								
Verdonniere River (n=11)	6.75.10 ⁹	+/-	1.41.10 ⁹	90	61.25	+/- 2.57	48.86	81.59
TOT					61.02	+/-	1.40	

^a Ifremer (2008)

^b Bocher et al. (2007), Compton et al. (2008)

640