

Hydrocarbons removal from real marine sediments: analysis of degradation pathways and microbial community development during bioslurry treatment

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ABSTRACT

In this study, real marine sediments polluted by petroleum compounds were treated by means of a bioslurry pilot scale reactor. The treatment performance was evaluated by measuring the removal of total petroleum hydrocarbon (TPH), coupled to further analyses required to understand the mechanisms involved in the biodegradation process. The maximum TPH-removal efficiency reached 86% at the end of experiments. Moreover, high throughput 16S RNA gene sequencing was used to describe the microbiome composition in sediment prior to, and after, bioslurry treatment, in order to identify the taxa mostly entailed in the TPH removal process. The raw sediment was mostly colonized by members of *Sulfurimonas* genus; after bioslurry treatment, it was noticed a shift in the of the microbial community composition, with *Proteobacteria* phylum dominating the remediation environment (high increase in terms of growth for *Hydrogenophaga* and *Sphingorhabdus* genera) along with the *Phaeodactylibacter* genus (*Bacteroidetes*). Furthermore, the assessment of gaseous emissions from the system allowed to quantify the volatile hydrocarbon component and, consequently, to obtain a more accurate evaluation of TPH-removal pathway by the bioslurry system. Finally, phytotoxicity tests on sediment samples highlighted an increase of the treated sample quality status compared to the untreated one.

KEYWORDS: microbial community; hydrocarbon pollution; bioremediation; contaminated marine sediment; slurry reactor.

34 1. INTRODUCTION

35 Contaminated marine sediments poses a serious threat to ecosystems and human health, representing
36 a potential reservoir for the release of toxic compounds as they are often subject to anthropogenic
37 inputs, especially in industrial areas close to the coastline (**Rocchetti et al., 2012; Maletić et al.,**
38 **2018; Avona et al., 2022**). Sediment contamination is mainly due to the discharge of urban or
39 industrial waste streams entailing different environmental issues (**Labianca et al., 2022**). Petroleum
40 hydrocarbons (HCs) represent a class of contaminants of particular concern, since some of them are
41 mutagenic, carcinogenic, teratogenic and might also induce sterility in marine organisms (**Zhou et**
42 **al., 2014**). Moreover, HCs can move for long distances in water due to hydrophobicity and
43 persistency, and can accumulate within sediments for long time periods thus becoming a potential
44 release reservoir and representing an environmental threat for aquatic organisms and a public health
45 risk (**McGenity et al., 2012; Maletić et al., 2018**). In this light, the remediation of polluted sediments
46 has become an imperative need and several remediation techniques have been developed in the last
47 years, with the aim to remove HCs from sediments. They can be classified either by nature (thermal,
48 physicochemical, chemical or biological treatment) or by place (*in-situ* or *ex-situ*). Generally,
49 chemical and thermal treatments are more expensive compared to biological treatments as well as
50 less eco-friendly (**Pino-Herrera et al. 2017; Yan et al., 2021**).

51 As already mentioned, the remediation of polluted sediments can also be accomplished through
52 biological processes, which are based on pollutant degradation by microbial populations able to
53 exploit the organic pollutants as a source of carbon and energy (**Varjani, 2017; Varjani and**
54 **Upasani, 2017; Usman et al., 2018**). Several literature studies highlighted the advantages of
55 degradation pathways related to microbial activity, thus arousing the interest on biological processes
56 (**Huesemann et al., 2002; Perelo, 2010**). Bacteria revealed to be the prevailing class of
57 microorganisms responsible of hydrocarbon removal via aerobic oxidation (**Zhao and Wong, 2009;**
58 **Zhao et al., 2011**). In this context, the most abundant taxa found in marine sediments belongs to
59 *Proteobacteria* and *Bacteroidetes* phyla (**Iannelli et al., 2012; Chiellini et al., 2013**). Previous
60 studies highlighted an increase of *Alphaproteobacteria* and *Gammaproteobacteria* during
61 biodegradation of oily products (**Lamendella et al., 2014**).

62 Moreover, the autochthons bacteria associated to these classes showed a sort of adaptation during
63 bioremediation. Specifically, dynamics in indigenous microbial population during bioremediation
64 revealed a shift in the bacterial community composition (**Fuentes et al., 2014; Smith et al., 2015;**
65 **Fuentes et al., 2016**). This aspect relies on several factors, including the environmental compartment

66 (eg. soil or marine sediment, freshwater, or seawater), sediment properties (e.g. texture, pH, organic
67 matter, nutrients, temperature), the features of contamination (age and concentration), the indigenous
68 microbial community, and the bioremediation treatment selected (**Kaplan and Kitts, 2004;**
69 **Hamamura et al., 2013; Fuentes et al., 2014; Fuentes et al., 2016**). Particularly, the bioremediation
70 technology strongly affects the microbial population dynamics, especially for *Proteobacteria* phylum
71 (**Fuentes et al., 2014, Fuentes et al., 2016**).

72 Bioslurry reactors represent an interesting *ex-situ* technology for the remediation, under controlled
73 conditions, of soils and/or sediments polluted by hydrocarbons. In order to improve the mass transfer
74 rate as well as the contact between microorganisms, oxygen, nutrients and contaminants, the raw
75 matrix is mixed with water in the typical range of 10 to 60% w/v, to get a slurry suspension (**Gan et**
76 **al., 2009; Pino-Herrera et al., 2017; Lumia et al., 2020; Avona et al., 2022**). In this way, the
77 performance of biodegradation process might be enhanced.

78 Bioslurry reactors are commonly operated under batch conditions thus entailing higher process rates
79 (**Prasanna et al., 2008; Venkata Mohan et al., 2008**). The used reactors are generally characterized
80 by completely mixed conditions, in order to keep homogeneity of the suspension over time, and
81 equipped with aeration devices to ensure aerobic conditions (**Robles-González et al, 2008**).

82 Nevertheless, literature studies highlighted the need to consider volatilization among the possible
83 paths for contaminant removal; indeed, a proper mass balance of hydrocarbons, usually expressed as
84 total petroleum hydrocarbon (TPH), inside the system is required to exclude an overestimation of the
85 biodegradation pathway (**Pino-Herrera et al., 2017**). To evaluate the effectiveness of the treatment,
86 it is also useful to perform phytotoxicity tests on the sediment matrix (**Shen et al., 2016**); for matrices
87 contaminated by hydrocarbon compounds, *Lepidium sativum* seeds are considered effective
88 bioindicators, thanks also to the short germination period required (**Maila and Cloete, 2002;**
89 **Hosokawa et al., 2009**). However, to authors' best knowledge, very few studies on bioslurry
90 technology have been reported in literature so far and even fewer refer to the treatment of real
91 contaminated sediments. For the latter, the available studies usually report the results of laboratory-
92 scale experiences and rarely the results of experiments at pilot plant scale (with volumes greater than
93 1 litre) (**Pino-Herrera et al. 2017**). In general, there is still a lack of knowledge about the mechanisms
94 governing the process and basic aspects such as microbial diversity, role of bioaugmentation, removal
95 performance during the treatment of real sediment, potential and actual reuse of decontaminated
96 sediments. Basing on the above discussion, and after the preliminary results achieved by authors in a
97 forms study (**Avona et al., 2022**) the aim of the present paper is elucidate the mechanisms involved
98 in the treatment of real marine contaminated sediments through a bioslurry reactor, highlighting the

99 removal pathways as well as the behavior of the biological community involved in the process. In
100 detail, the paper shows the results achieved during an experimental study carried out on a lab scale
101 bioslurry reactor fed with real TPH-contaminated marine sediments sampled from the Augusta Bay
102 (Sicily, southern Italy). The systems performance has been assessed in terms of TPH removal. Given
103 the site-specific characteristics of the sediments used, a detailed characterization of the microbial
104 community was carried out using the high throughput 16S RNA gene sequencing. Furthermore, the
105 percentage of volatile solids in the sediment, an indicator of bacterial growth, was evaluated. Another
106 aspect examined was the potential toxic effect of sediments towards the biotic compartment, at the
107 beginning and at the end of treatment, by means of phytotoxicity tests. Finally, the contribution in
108 terms of TPH removal due to volatilization was assessed to evaluate the hydrocarbon mass balance
109 in the system. This work provides useful information in view of further research activity aimed at
110 assessing the potential feasibility of this treatment at full scale.

111

112 **2. MATERIALS AND METHODS**

113 **2.1 Sampling and Area of investigation**

114 The marine sediment samples used for the experiments were collected from the northern part of
115 Augusta Bay, near some petrochemical facilities (**Lumia et al., 2020a**). The industrial area of
116 Augusta-Priolo is one of the largest petrochemical areas in Italy and in Europe, characterized by the
117 presence of several industrial plants whose polluting impact pours into the Rada of Augusta (often
118 referred to as "Rada" only), causing considerable contamination of marine sediments. The Rada falls
119 on the eastern coast of Sicily, within the homonymous bay and it develops between Capo Santa Croce
120 and Punta Magnisi, for a length of about 8 km and a distance from the coastline of about 4 km,
121 reaching a surface extension of about 23.5 km² and a depth close to 15 m. In the past, part of the
122 natural inlet has been separated from the open sea by the construction of a breakwater, aimed at
123 forming a large port basin communicating with the sea through two narrow mouthpieces (east and
124 south), where the maximum depth is about 30 m b.s.l.

125 The sediment sampling involved three different locations within the Rada. All samples were mixed
126 to evaluate a statistically suitable matrix as well as to obtain a sufficient volume for the development
127 of the experimental analyses and the start-up of the pilot plant. In particular, basing on a previous
128 campaign (**Lumia et al., 2020a**), the sediment samples were characterized by a medium-high
129 hydrocarbons concentration; the TPH fractions revealed that C₂₀-C₃₀ was the fraction mainly
130 adsorbed on sediments (67%) followed by C₁₂-C₁₈ (25%), whereas the heaviest one (C₃₂-C₄₀)

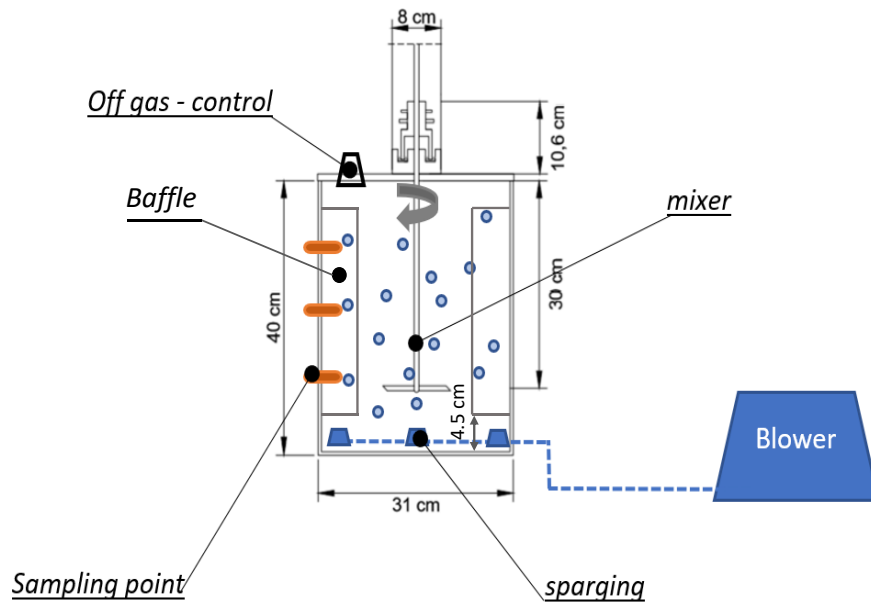
131 represented the 8% of the total. The chemical-physical characterization revealed a high organic
132 content (4.2%), moisture content (~44%), and sulphides (~61 mg kg⁻¹). The textural and
133 mineralogical analyses indicated the presence of silt and calcite (CaCO₃). The observed salinity was
134 also high (4.4% as pore water salinity concentration). The observed contamination mainly derived
135 from accidental leakage from tanker or pipes as well as from discharge of slop wastewater deriving
136 from washing of oil tankers with seawater.

137 In a previous experimental study, the sediment sample was subject to microcosm tests followed by a
138 preliminary bioslurry experiment. The main aim was to define the operational conditions of the
139 process and the pre-dimensioning of pilot plant (water-sediment ratio for slurry, potential
140 bioaugmentation and inoculum for start-up, biostimulation need, etc. The results of these preliminary
141 activities can be found in literature (**Avona et al., 2022**).

142

143 **2.1 Bioslurry reactor and operation**

144 The experimental set-up consisted of a closed cylindrical reactor realized in Polyvinyl chloride with
145 a glass reinforced plastic (GRP) bottom with an overall volume of 30 L (Ø: 31 cm; H: 40 cm),
146 according to what reported in Avona et al. (2022). The reactor was characterized by three baffles (H:
147 32 cm, W: 5.7 cm, S: 0.3 cm) disposed at 120° and fixed at 4.5 cm from the bottom, based on a former
148 hydrodynamic study, acting as vortex breaker (Supplementary Material). The mixing system was
149 realized with a mechanical stirrer, while the aeration system consisted of three porous cylindrical
150 diffusers placed on the bottom between the baffles and connected to a MEDO LA-45C membrane
151 blower, with a nominal power of 47 W and an airflow rate of 45 L min⁻¹ at a pressure of 0.11 bar.
152 The reactor was provided with slurry sampling sockets and closed at the top with a blind flange
153 equipped with a gas sampling section. A schematic layout of the pilot plant is shown in **Figure 1**. For
154 further details and the panoramic view of the experimental set-up, the reader is addressed to literature
155 (**Avona et al., 2022**).



156

157 **Figure 1** Schematic diagram of the Stirred Tank Reactor for bioslurry application

158

159 As above described, the study was conducted using a composite sample of real sediment collected
 160 from different points of the Augusta bay, previously characterized and subject to a preliminary
 161 evaluation (Falciglia et al., 2020; Lumia et al., 2020a-b). In detail, basing on the results observed
 162 in the previous experimental period (Avona et al., 2022), the sediment sample was achieved by
 163 mixing the highly polluted sediments used in the previous period with less polluted ones (even
 164 sampled from the “Rada”). The experiment duration was 102 days with a solid-liquid ratio of 10% as
 165 weight by volume (w/v) and a stirring speed of 675 ± 25 rpm. As inoculum, 2 L of slurry from the
 166 previous experimental campaign (Avona et al., 2022) were mixed with the initial sample to speed-
 167 up the start-up of the biological process, by shortening the acclimation period and avoiding
 168 bioaugmentation with allochthonous bacteria. The initial TPH concentration in the raw sediment
 169 sample was set at $1,001 \text{ mgTPH kgDW}^{-1}$. The main features of the experimental set-up are
 170 summarized in **Table 1**.

171

Table 1 Main features of the pilot scale configuration.

Slurry volume	V	26	L
Dry weight	M_{DW}	2.6	kg_{DW}
Moisture	θ_w	43.4	%
Solid-liquid ratio	w/w	10	%
TPH concentration	C_{TPH}	1001	$\text{mg}_{\text{TPH}} \text{kg}_{\text{DW}}^{-1}$
Duration	t	102	Days

172

173

174 2.2 Analytical methods

175 TPH concentration in the sediment and liquid phases was evaluated using the EPA 8010C and 3510C
176 methods by GC-FID (Agilent 6890), respectively. The solid to liquid hydrocarbons extraction was
177 carried out through EPA 3545A method “Pressurized Fluid Exaction (PFE)” and the “Speed Extractor
178 E-916”. Analysis of TPH was carried out in duplicate, and the standard error was computed according
179 to (Avona et al., 2022).

180 The composition of the bacterial community was defined by the high throughput analysis of the V1-
181 V3 region of the 16S rRNA gene. The methodology used for nucleic acid extraction, amplification,
182 genomic library preparation, sequencing on the Illumina MiSeq platform, and bioinformatic analysis,
183 are reported in Tonanzi et al. (2021). Untreated (NT) and after bioslurry (BS) sediment samples were
184 analyzed. Furthermore, the determination of Volatile Solids (VS) on the collected sediment samples
185 was performed according to Standard Methods (APHA, 1998) and then expressed as percentage of
186 total solids (TS).

187 The germination index (GI) of the liquid supernatant was assessed by using *Lepidium sativum* seeds,
188 after settling of slurry samples (Avona et al., 2022). The analyses were conducted on raw and treated
189 sediment samples. In detail, three different configurations have been considered for each sample:
190 undiluted sample, diluted with 50% and 75% distilled water. For each configuration, 1 ml of matrix
191 – water extract (1:10 w/v) was dosed to 10 seeds into a Petri dish that was subsequently incubated at
192 27°C for 72 h in the dark. Moreover, a control test was realized, with incubation of *Lepidium* seeds
193 with deionized water. Subsequently, for each test, the germinated seeds (G) and the root length (L)
194 were measured and compared with the control. Each test was carried out in triplicate.

195 The mass flow rate of volatilized hydrocarbons was estimated by multiplying the gaseous flow rate
196 leaving the reactor by the related hydrocarbon concentration. The gas flow rate was estimated by
197 measuring the flux velocity at the outlet by a hot wire anemometer, while the hydrocarbon
198 concentration was measured with a portable GAS-TEC® MK III flame ionization detector (FID). The
199 contaminant mass volatilized was determined as the time integral of the flow rate by weight. Finally,
200 pH and dissolved oxygen were monitored with a WTW type multimeter by means of dedicated
201 probes. These parameters remained almost constant throughout experiments, with average values of
202 8.5 and 9 mg_{OD} L⁻¹, respectively.

203

204 3. RESULTS AND DISCUSSIONS

205 3.1 Summary of the results achieved in the preliminary experimental campaign

206 Four different microcosm configurations were studied in the former study: in particular, Test 0 was
 207 the blank control to verify the bio-degradative potential of the autochthonous biomass in marine
 208 sediments. In Test 1 N and P were added in a 4:1 ratio, to assess the effect of a “biostimulation”
 209 process. Tests 2 and Test 3 were aimed at evaluating the effect of allochthonous biomass inoculum;
 210 bacteria acclimated to salt and hydrocarbons were added to Test 2 and Test 3, respectively (**Campo**
 211 **et al., 2018; Corsino et al., 2018a-b; Campo and Di Bella, 2019**). The initial TPH concentration in
 212 the microcosm tests was close to 450 mgTPH kg_{SS}⁻¹. The main results of the microcosm tests are
 213 summarized in Table 2.

214
 215 **Table 2** Main results achieved in the microcosm tests.

	Residual TPH [mg TPH kg _{SS} ⁻¹]		Removal efficiency [%]		Removal rate [mgTPH kg _{SS} ⁻¹ d ⁻¹]	
	Day 15	Day 24	Day 15	Day 24	Day 15	Day 24
Test 0	403	330	10	26	2.93	8.11
Test 1	354	315	21	30	6.20	4.33
Test 2	366	352	18	21	5.40	1.56
Test 3	298	223	33	50	9.93	8.33

216
 217 From the results reported in Table 2, it can be observed that the lowest concentrations at the end
 218 experiments were obtained in Test 3 thanks to the inoculation of halotolerant biomass, while similar
 219 but lower values are found in the other configurations (removal performance of about 26%, 30%, and
 220 21% respectively). Concerning the removal kinetics, for all tests the substrate removal rate slow down
 221 after the 15th day, excepting Test 0, which rate increased maybe for a slower adaptation of the
 222 autochthonous biomass, mainly emphasized by the lack of nutrients (**Avona et al., 2022**).

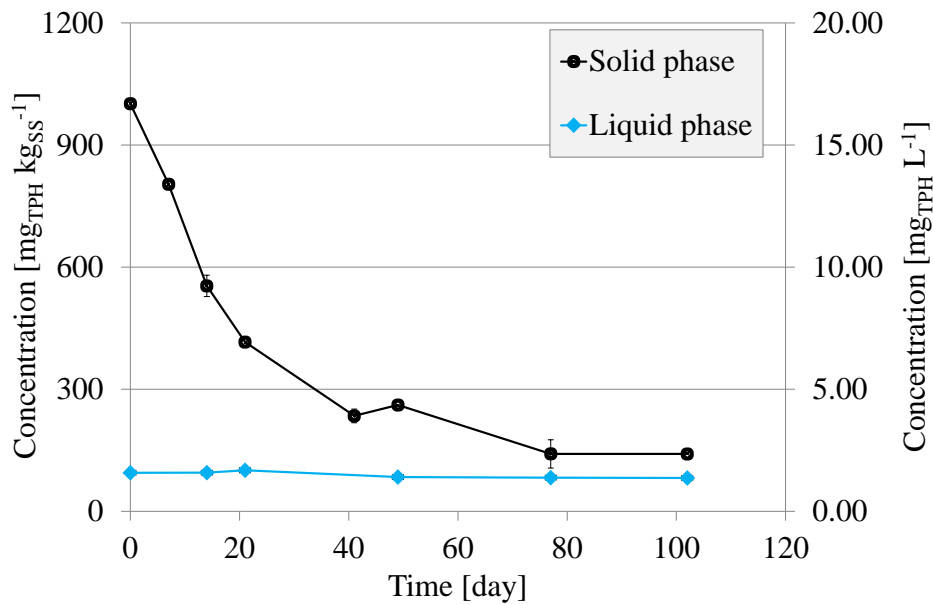
223 Concerning the bioslurry period, the achieved results highlighted a TPH decrease in the solid phase
 224 during the first experimental days, corresponding to a moderate TPH increase in the liquid phase,
 225 maybe due to a leaching effect. Subsequently, the TPH concentration in the liquid phase showed a
 226 constant value while it significantly decreased in the solid phase reaching an overall removal
 227 efficiency of 40% with a maximum removal rate of 220 mg TPH kg⁻¹ d⁻¹ at the end of experiments,
 228 thus suggesting the potential of sediment remediation through a bioslurry process. Despite promising,
 229 the residual TPH concentration was higher compared to regulation limits, therefore suggesting the
 230 opportunity to implement this treatment for lower contamination of the raw sediments. For further
 231 details, the reader is addressed to literature (**Avona et al., 2022**).

232

233 3.2 TPH removal from contaminated sediment

234 First, it is useful to underline that the TPH measurement allows evaluating the recalcitrant organic
235 pollution of contaminated marine sediments. Indeed, the global measurement enables to assess the
236 presence of different hydrocarbon groups as a whole. TPHs define a wide group of chemical
237 substances that includes aliphatic, aromatic and polyaromatic hydrocarbons, contained in petroleum
238 residues and other substances. **Figure 2** reports the TPH concentration on the sediment and liquid
239 phase during experiments, which enabled to evaluate the biodegradation ability of the system.

240 A rapid TPH removal in the solid phase was observed in the first 21 days of operation. The kinetics
241 were slower from day 40 until the end of the experiments. Data quality and reliability were proven
242 by the very low values of Standard Deviation ($15.98 \text{ mg}_{\text{TPH}} \text{ kg}_{\text{SS}}^{-1}$) and Standard Error (11.30)
243 respectively. The trend of TPH concentration in the liquid phase remained almost stationary for the
244 entire duration of experiments, with concentrations of $1.50 \pm 0.16 \text{ mg TPH L}^{-1}$; the data quality was
245 assured by the very low values of the Deviation Standard and Standard Error, equal to 0.16 mgL^{-1}
246 and 0.113, respectively. This trend is likely due to an equilibrium reached between pollutant release
247 from the solid matrix (desorption) and the contextual consumption by the bacterial population in the
248 liquid phase since the beginning of experiments. This result could be favored by the biomass
249 acclimation achieved in the previous experimental campaign with similar operating conditions
250 (**Avona et al., 2022**), from which the initial inoculum was taken. The system reached stationary
251 conditions from day 80 onward, as suggested by the constant trend of TPH concentration in the solid
252 phase. The overall removal efficiency achieved at the end of the experiment was 86%. The maximum
253 removal rate of $36 \text{ mg}_{\text{TPH}} \text{ kg}^{-1} \text{ d}^{-1}$ was achieved in the first 14 days of experiments. This is mainly
254 due to the metabolic consumption of the more easily biodegradable compounds by the bacterial
255 community.



256

257 **Figure 2** TPH residual concentrations in sediment and liquid phase.

258

259 The results obtained appeared very interesting; indeed, as previously pointed out, there are very few
 260 studies reported in the literature about the application of the bioslurry treatment for real contaminated
 261 marine sediments. Moreover, the degradation efficiencies obtained in previous experiments on
 262 contaminated sediments are quite lower than those obtained in the present work. In particular, **Table**
 263 **3** shows the contamination efficiencies and main operational features of recent studies, comparable
 264 with this work on the basis of: 1) treatment with aerobic bioslurry; 2) sediments contaminated by
 265 petroleum hydrocarbons, aromatic and non-aromatic hydrocarbons; 3) initial hydrocarbons
 266 concentration in sediments higher than the regulatory limit.

267

Table 3 Removal efficiency and main operational condition in bioslurry for sediment remediation

Percentage of sediment in the slurry (% w/v)	Maximum Hydrocarbon removal efficiency (%)	Remarks and Operational condition	References
3-5	55% at the end of incubation (measured in terms of TOC removal)	<ul style="list-style-type: none"> • Aeration (6.04×10^{-4} m/s) • Bioaugmentation enriched bacterial culture • Volume of flask < 1L • Biostimulated with lactose • 40-day operation (6 weeks) • No aeration control 	El-Gendy et al., 2009
10	70%	<ul style="list-style-type: none"> • Aeration (6.04×10^{-4} m/s) • No bioaugmentation • Volume of flask < 1L • Biostimulated with lactose • 4 different phase duration (from start-up to biostimulation) 	Giordano et al., 2005
10	38% (without bio-stimulation – Phase 1) 80% (with antibiotic-stimulation – Phase 2)	<ul style="list-style-type: none"> • Bioaugmentation with activated sludge • 4000-ml reactor. • Aeration 3 l/min. 	Lumia et al. 2020

		<ul style="list-style-type: none"> • 30-day operation for each phase. • Volatilization was considered and quantified. 	
5-15	5-20%	<ul style="list-style-type: none"> • Native microflora degradation • 300-ml flasks. • unmixed system • 7-day operation. 	Jee et al., 1998
5-15	29-41%	<ul style="list-style-type: none"> • Native microflora degradation • 300-ml flasks. • Aeration 0.015 l/min. • 7-day operation. • Volatilization was considered and quantified. 	Jee et al., 1998
20	40%	<ul style="list-style-type: none"> • Natural soil microflora. • Abiotic removal not considered. • 100-ml flask. • Open system (no aeration). • 35-d operation. 	Beolchini et al., 2010
10	86%	<ul style="list-style-type: none"> • Bioaugmentation with activated sludge • 30000-ml reactor. • Aeration 25 l/min. • 100-day operation. • Volatilization was considered and quantified. 	This work

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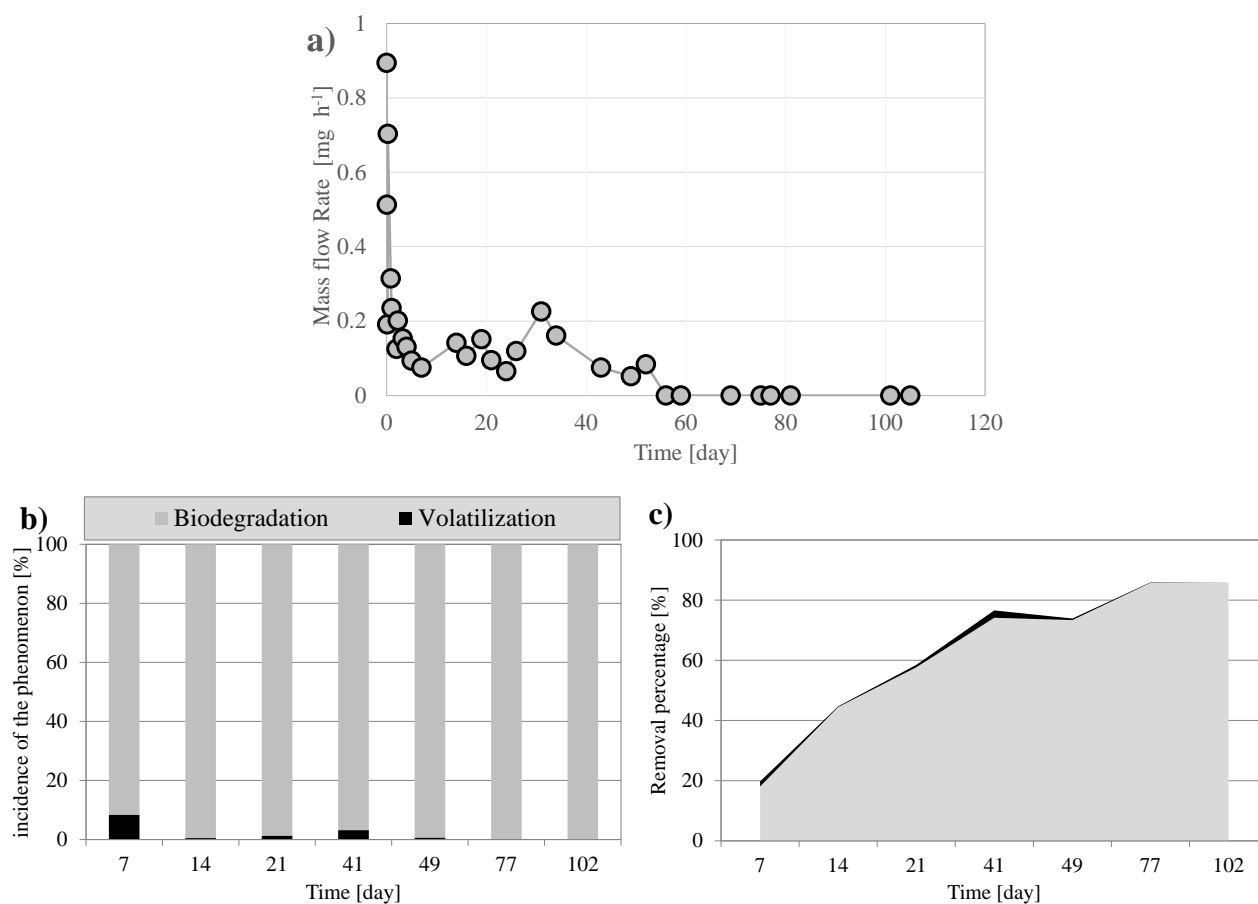
269 The few comparable literature references, mostly carried-out at batch scale (reactor volumes usually
270 less than 1 L) or with artificial contamination, usually did not exceed 40% removal, rarely reached
271 70%, only due to the aid of particular techniques of microbial biostimulation.

272 In contrast, the results of bioslurry treatment on soils showed removal efficiencies up to 90% but are
273 not comparable with the application on sediments. Few authors achieved efficiencies of 90% for the
274 hydrocarbon removal from sediments but only under optimized conditions for maximizing
275 performance. In particular, **Chikere et al. (2012)** and **Launen et al. (2014)**, achieved performance of
276 90% or higher only with artificially contaminated sediments and with initial concentrations of TPH
277 in the sediment of 100 mg L⁻¹, significantly lower than the regulation limits.

278 Obviously, data reported in **Table 3** do not allow a complete and equal comparison of the results. In
279 particular, the system performance achieved in the this work highlighted that after only 20 days of
280 experiment the residual TPH concentration in the sediments was lower than the regulatory limits (750
281 mg_{TPH} kg_{DW}⁻¹). The performances further improved after the following 20 days, On the other hand,
282 the significant removal efficiency at the end of the experimental campaign (over 85%), is significantly
283 higher than those reported in the literature: however, in other works similar performances have been
284 observed after almost 3 months of continuous treatment. This duration is however excessive for a
285 biological treatment, and the data is intended as a mere extension of the potential of the treatment.
286 Probably an "effective" duration of the biological pathway can be estimated between 30 and 40 days.

287 Finally, with the aim to define the real impact of bacterial degradation compared to the volatilization
288 of hydrocarbons potentially promoted by the air flow rate, the evaluation of the actual biodegradation

289 ability of the system must also evaluate the comparison between biodegradation and volatilization.
 290 In particular, the Mass Flow Rate (MFR) in the off gas was monitored by measuring the flow rate of
 291 gaseous emission and its TPH concentration in the specific sampling section (see **Figure 1**). As shown
 292 in **Figure 3a**, the MFR was quite high during the first two experimental days and subsequently
 293 decreased, reaching zero values from the 56th day until the end of the experimental observation. The
 294 volatilized mass of hydrocarbons was determined as the integral of the weight flow for each time
 295 interval considered, consisting of the time elapsed between two subsequent days of slurry sampling.
 296 The data obtained were processed with TPH measurements in liquid and solid phase to achieve a
 297 mass balance for the system. The change in the volume of slurry inside the reactor (batch operation)
 298 due to the sampling of 1 liter of slurry for each sampling was considered for this count. The mass of
 299 volatilized contaminant was equal to 158 mg at the end of the 102 days of experimentation, compared
 300 to 2,344 mg removed overall. The results of the mass balance were processed to determine the impact
 301 of the volatilization path on the hydrocarbons removal (**Figure 3b**) and its contribution to the overall
 302 removal efficiency (**Figure 3c**).



303
 304 **Figure 3** Weight flow (a), incidence of biodegradation and volatilisation (b), removal efficiency (c).
 305

306 The volatilization effect was greater during the start-up phase of the plant, equal to 8.4% of the mass
307 removed, and decreased to less than 1% from the forty-ninth day onwards (**Figure 3b**). In general,
308 the volatilization pathway contributed marginally to the overall removal of TPHs, which is mainly
309 attributable to biological degradation (**Figure 4c**). Nevertheless, it is worth noting that volatilization
310 of the lighter part of the contaminants likely occurred immediately after sediment contamination.

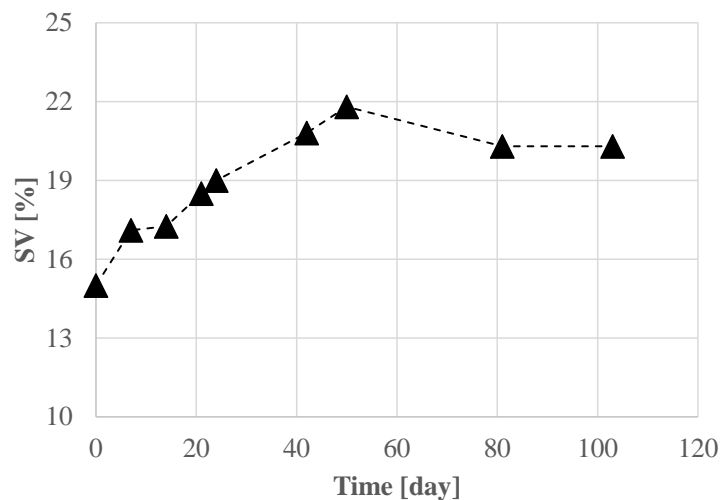
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312 **3.2 Biomass characterization**

313 The trend profile of Volatile Solids (VS) was monitored throughout the experimental campaign to
314 draw information about biomass growth tendency (**Figure 4**).

315 An increase in VS percentage was observed in sediment samples during the first days of experiments,
316 corresponding to a simultaneous sharp reduction of TPH concentration. The system reached
317 stationary conditions from day 49 onwards, in accordance with what observed for the TPH
318 concentration.

319



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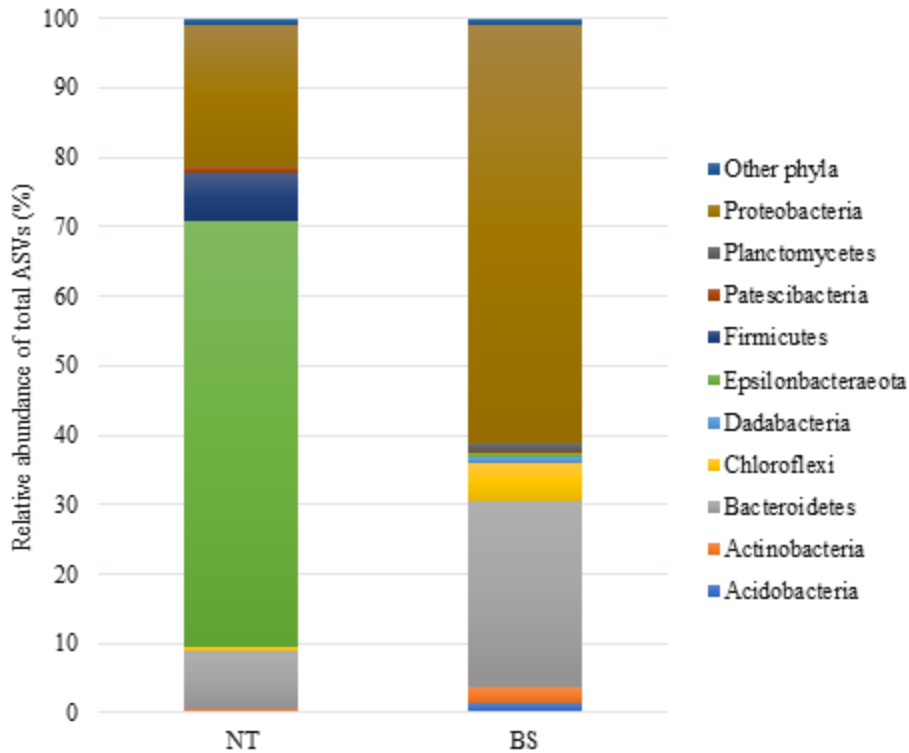
321 **Figure 4** Percentage of Volatile Solids.

322

323 High throughput analysis of the bacterial 16S rRNA gene was performed in order to describe the
324 microbial dynamics in the untreated sediment (NT) and after treatment in a bioslurry reactor (BS)
325 (**Figure 5 and 6**).

326 *Bacteroidetes*, *Epsilonbacteraeota*, *Firmicutes*, and *Proteobacteria* represented the major phyla in
327 the sediment at time zero (NT), covering up to 97% of the total ASVs retrieved in the sample (Figure

328 5). Conversely, ASVs affiliated with *Actinobacteria*, *Bacteroidetes*, *Chloroflexi* and *Proteobacteria*
 329 were predominant in the sample after treatment in a bioslurry reactor (BS) (up to 94.5% of the total
 330 AVSs; Figure 5).



331

332 **Figure 5** Bacterial microbial composition at phylum level estimated by high-throughput 16S rRNA gene sequencing
 333 in the sediment at time zero (NT) and after treatment in a bioslurry reactor

334

335 The major increase in ASVs at phylum level after the treatment was observed for *Actinobacteria*,
 336 *Bacteroidetes*, *Chloroflexi* and *Proteobacteria* (Figure 5).

337 A microbial shift was observed into the *Bacteroidetes* phylum. In particular, the *Phaeodactylibacter*
 338 genus (*Saprospiraceae* family) showed a significant increase over time zero and a relative abundance
 339 in the treated sample of 2.5% of the total ASVs (Figure 6). **Doyle et al. (2018)** found a parallel
 340 development of this taxa to the degradation of hydrocarbon compounds in the mesocosms of
 341 hydrocarbon-contaminated coastal seawater. Additionally, sequences affiliated with
 342 *Rhodothermaceae* family (*Bacteroidetes*) was present with an abundance of 8.2% in the treated
 343 sediment sample. This taxonomic group is also well related to the biodegradation of petroleum
 344 compounds. In particular, **Ribicic et al. (2018)** found a correspondence between the removal of PAHs
 345 and branched alkanes in seawater and the development of the *Rhodothermaceae* family.

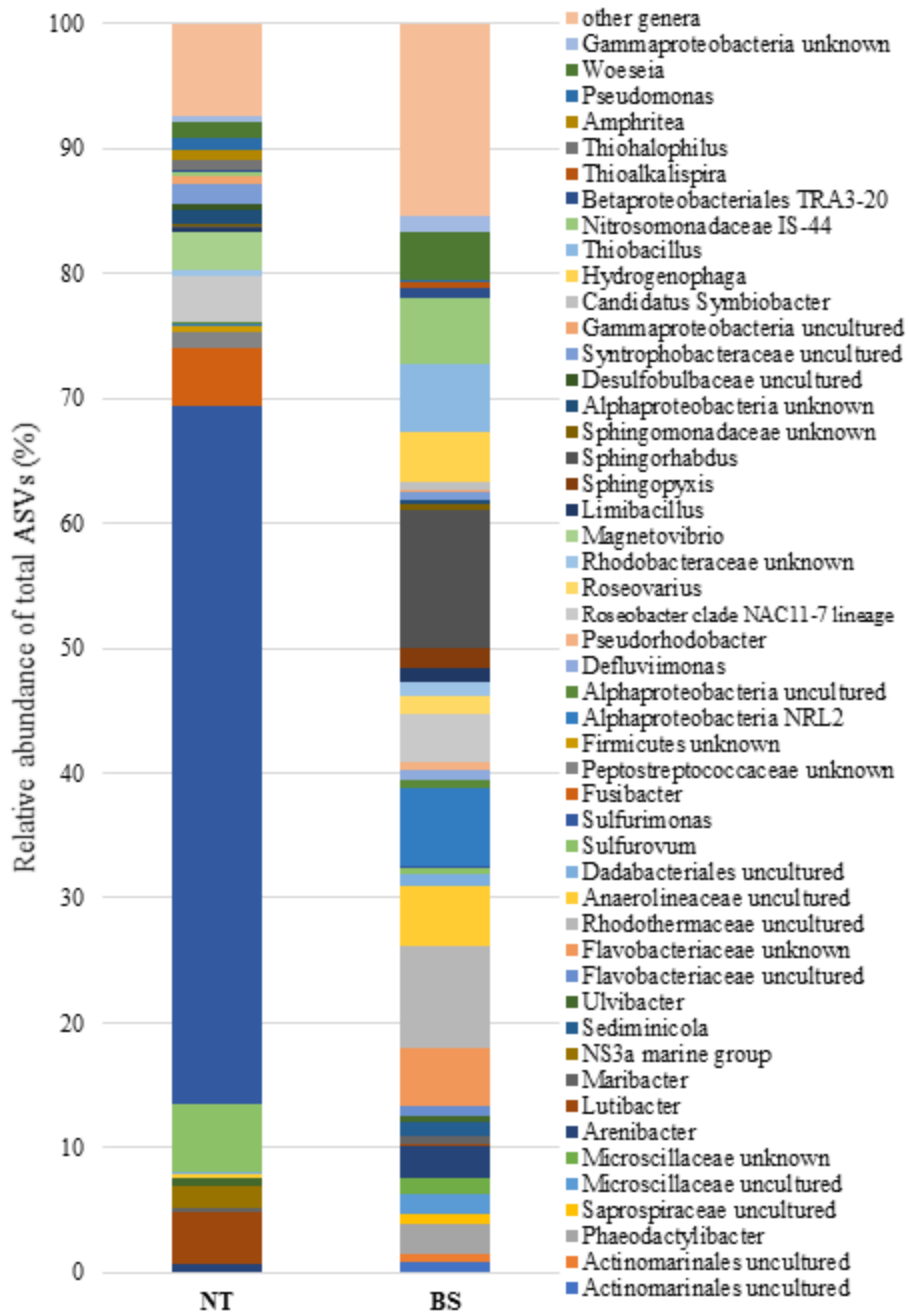
346 *Chloroflexi* phylum was dominated by ASVs affiliated to the *Anaerolineaceae* family. The latter
347 group represented 4.8% of the total ASVs and is commonly found in marine sediments. Studies
348 proved that some members of this family are heterotrophic microorganisms with anaerobic
349 metabolism and can play an important role in the degradation of hydrocarbons, such as long-chain n-
350 alkanes (Sherry et al., 2013; Sutton et al., 2013; Liang et al., 2016; Wang et al., 2019). Their
351 presence after treatment can be attributable to anaerobic niches in the stagnant areas of the reactor. In
352 fact, previous studies highlighted the co-presence of aerobic and anaerobic groups belonging to the
353 *Anaerolineaceae* family due to the formation of limited anaerobic zones even in the most superficial
354 layers of the soil (Liu et al., 2019).

355 A marked increase in BS sample with respect to NT was also observed for sequences associated with
356 *Alphaproteobacteria* and *Gammaproteobacteria* (*Proteobacteria* phylum), in particular for the
357 *Betaproteobacteriales* and *Sphingomonadales* orders respectively. Several studies proved that both
358 these groups contain microorganisms potentially active in hydrocarbon degradation (Martin et al.,
359 2012; McGenity et al., 2012a; Rojo, 2009). An important increase was observed in
360 *Burkholderiaceae* family (*Betaproteobacteriales*), as well as in the ASVs associated with
361 *Sphingomonadaceae* family (*Sphingomonadales*).

362 Analysing the microbial population at genus level into *Proteobacteria* phylum also highlighted an
363 increase in the total sequences especially for the genera *Hydrogenophaga*, *Sphingorhabdus*, and *IS-*
364 *44* (4.0%, 10.5% and 5.2% of the total ASVs, respectively. **Figure 6**). In particular, the genus
365 *Hydrogenophaga* has been identified as a potential degrader of petroleum compounds (Prince,
366 Gramain et al., 2010) and a wide range of hydrocarbon contaminants, including PAHs (Aburto and
367 Peimbert, 2011; McGenity et al., 2012b). Furthermore, Hou et al., 2015 found a positive correlation
368 between the genus *Hydrogenophaga* and the removal of hydrocarbon fractions of C₂₁-C₃₄ oil.
369 Members of the genus *Sphingorhabdus* have been isolated from coastal sediments which were
370 contaminated with crude oil and previous studies proved that several species belonging to this taxa
371 possess genes involved in the catalysing of aliphatic and aromatic hydrocarbons (Jeong et al., 2016).

372 Comparing the sediment at time zero (NT) and after bioslurry treatment (BS), a drastic decrease in
373 ASVs affiliated to the phylum *Epsilonbacteraeota* was observed (from 61.2% to 0.5% of the total
374 ASVs; Figure 5). The analysis showed that the typical ambient genera such as *Sulfurimonas* and
375 *Sulfurovum*, decrease in the treated sediment from about 55.8% to 0.17%, and from 5.4 to 0.36% of
376 the total sequences, respectively (**Figure 6**).

377 As expected, the treatment of the sediment promoted also the disappearance of anaerobic genera like
 378 *Magnetovibrio* (*Proteobacteria*) and *Fusibacter* (*Firmicutes*) which represented 3% and 4.6% of the
 379 total ASVs in the sediment at time zero (Ravot et al., 1995; Bazylinski et al., 2013).

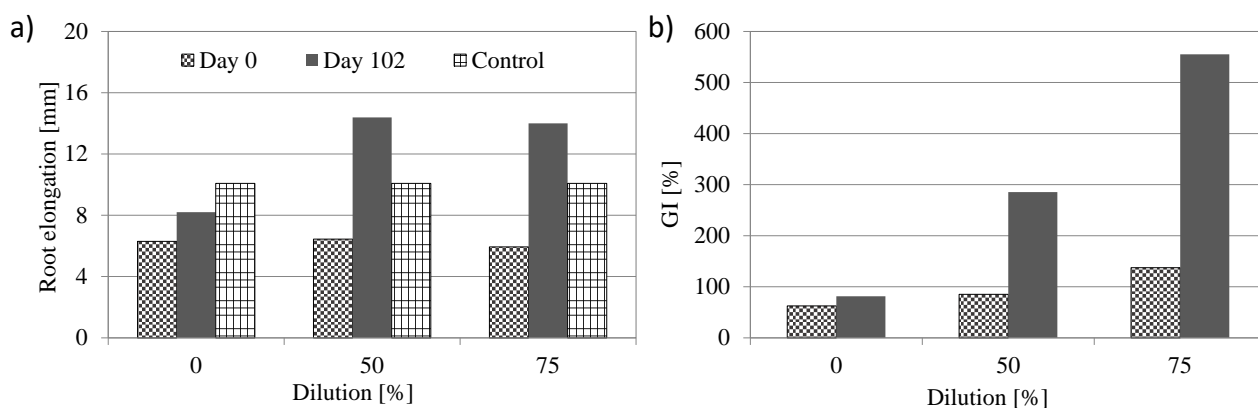


380
 381 **Figure 6** . Bacterial microbial composition at genus level estimated by high-throughput 16 S rRNA gene sequencing in
 382 the sediment at time zero (NT) and after treatment in a bioslurry reactor (BS).

383

384 3.3 Sediment phytotoxicity

385 **Figure 7** shows the results of phytotoxicity tests in terms of root system elongation (a) and
 386 germination index (b).



387

388 **Figure 7** Average root system length (a); germination index (b).

389

390 As expected, the configurations showing the best features in terms of phytotoxic qualities were those
 391 characterized by dilution ratios of 50% and 75%, both for the untreated sediment sample (day 0) and
 392 for the treated sediment (day 102). Additionally, the root length was approximately 14 mm for the
 393 treated sediment sample (day 102) at both 50% and 75% dilution ratios, compared to that of raw
 394 sediment sample equal to 6 mm at the same dilution (**Figure 7a**). All configurations showed a quality
 395 improvement after bioslurry treatment (102 days), and the germination index (GI) ranged between
 396 81% and 555%, compared to 62% and 137% for the untreated sediment (**Figure 7b**).

397

398 4. CONCLUSIONS

399 The treatment of contaminated marine sediments, from Augusta's Bay, by means of bioslurry reactors
 400 showed excellent performance for the removal of petroleum hydrocarbons. Volatilization contributed
 401 only marginally to the removal of the contaminant, despite the mixing and aeration conditions
 402 adopted. This result might be due to the age of the contamination and the resulting TPH composition.
 403 The main mechanism was biodegradation, as suggested by the increase in volatile solids and the shift
 404 in the dynamics of the microbial community after treatment. The taxonomic groups that best suited
 405 the process conditions were identified. Some groups originally present in the sediment with low
 406 relative abundance have developed predominantly. In particular, ASVs associated to the genera
 407 *Hydrogenophaga*, *Sphingorhabdus*, and *Phaeodactylibacter* had the largest increases. Scientific
 408 literature has confirmed their potential for degradation of hydrocarbons in particular matrices such as
 409 marine sediments. Finally, the phytotoxicity tests showed that after bioslurry treatment, the residual
 410 sediment improved its quality features compared to the original state. This is important for a possible
 411 reuse of the decontaminated matrix as an alternative to disposal.

412

413 **ACNOWLEDGEMENTS**

414 Authors warmly thank Mrs Rosa D'Addelfio and Eng. Gino Beringheli for the analytical and
415 technical support with pilot plant operations.

416

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