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1 **Evaluation of contact time and fiber morphology on bacterial**
2 **immobilization for development of novel surfactant degrading nanofibrous**
3 **webs**

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Abstract

26 **Abstract**

27 Novel electrospun fibrous biocomposites were developed by immobilizing two different
28 sodium dodecyl sulfate (SDS) biodegrading bacterial strains, *Serratia proteamaculans* STB3
29 and *Achromobacter xylosoxidans* STB4 on electrospun non-porous cellulose acetate (nCA)
30 and porous cellulose acetate (pCA) webs. The required contact time for bacterial
31 immobilization was determined by SEM imaging and viable cell counting of the immobilized
32 bacteria, and bacterial attachment was ended at day 25 upon these results. SDS biodegradation
33 capabilities of bacteria immobilized webs were evaluated at different concentrations of SDS,
34 and found as highly efficient at concentrations up to 100 mg/L. It was observed that, SDS
35 remediation capabilities of bacteria immobilized webs were primarily based on the bacterial
36 existence and very similar to the free-bacterial cells. Reusability test was applied on the two
37 most efficient webs (STB3/pCA and STB4/pCA) at 100 mg/L SDS, and the results suggest
38 that, the webs are potentially reusable and improvable for SDS remediation in water. SEM
39 images of bacteria immobilized webs after the reusability test demonstrate strong bacterial
40 adhesion onto fibrous surfaces, which was also supported by the viable cell counting results.
41 Our results are highly promising and suggesting that bacteria immobilized electrospun fibrous
42 webs have a potential to be used effectively and continually for remediation of SDS from
43 aqueous environments.

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49 **Keywords:** Electrospinning, cellulose acetate, sodium dodecyl sulfate (SDS), bioremediation

50 **1. Introduction**

51 Surface active agents (surfactants) are the major components of detergents and commonly
52 used in various industrial and domestic applications, leading a significant contribution to
53 water pollution.¹ According to the United States Environmental Protection Agency (USEPA),
54 surfactants may negatively influence the endocrine system of both animals and humans, so
55 constituting a considerable health hazard.² Therefore, decontamination of water sources from
56 surfactants is of substantial importance.

57 There are different methods to treat surfactant contaminated environments and
58 bioremediation is becoming an emerging technology for decontamination of these pollutants,
59 since it is cost-effective, eco-friendly and effective for a wide variety of pollutants such as
60 petroleum hydrocarbons, heavy metals and surfactants.³ Although there are numerous reports
61 in the literature about isolation and discovery of novel surfactant degrading microorganisms,
62 their *in situ* application is not so simple, since the environmental parameters are highly
63 variable and the rate of surfactant degradation is very low under natural conditions.⁴
64 Therefore, alternative application procedures should be studied and the degradation conditions
65 should be optimized for specific microorganisms to obtain better remediation performances
66 under variable physical and environmental conditions.

67 The genus *Achromobacter* comprises Gram-negative, aerobic, non-fermentative and
68 rod-shaped bacteria.⁵ It has been reported that *Achromobacter xylosoxidans* has petroleum
69 hydrocarbon degrading capability and resistant to grow in crude oil contaminated
70 environments,⁶ which may indicate the potential surfactant degrading capability of this
71 species, since high amounts of industrial surfactants are derived from petroleum. The genus
72 *Serratia* is a member of the Enterobacteriaceae, and comprises Gram-negative, non-spore
73 forming, glucose fermenting, facultatively anaerobic and rod-shaped bacteria.^{7,8} *Serratia*

74 *odorifera*, a member of the genus *Serratia*, has shown efficient surfactant degrading
75 capability in consortia against two different common surfactants, LAS and SLES,^{9,10}
76 highlighting the potential of this family for applications of surfactant bioremediation.

77 Bioremediation techniques can be applied with either free microorganisms or
78 immobilized microorganisms which are adhered on a carrier matrix. Application of
79 immobilized microorganisms is more advantageous than the freely floating cells in terms of
80 lower space and growth medium requirements and potential reusability of the system.¹¹
81 Furthermore, it is also advantageous for the resistance of cells to harsh environmental
82 extremes.¹² As a carrier material, electrospun fibrous webs have become a promising
83 candidate since electrospinning is a simple, versatile and cost-effective technique and
84 electrospun fibrous webs can have unique properties such as large surface-to-volume ratio and
85 high porosity, hence these materials have a potential to be used in membrane/filter
86 applications.¹³⁻¹⁸ Among different immobilization procedures, natural adhesion is the most
87 advantageous one since it provides the formation of biofilms, maximizes the cell viability and
88 biochemical activity.¹⁹ In recent years, few studies regarding environmental applications of
89 microorganism immobilized electrospun fibrous webs have been published.^{11,20-24}

90 In the current study, *Serratia proteamaculans* STB3 and *Achromobacter xylosoxidans*
91 STB4 cells, which have biodegradation capabilities on a known anionic surfactant: sodium
92 dodecyl sulfate (SDS), were immobilized onto cellulose acetate nanofibers that have either
93 non-porous or porous morphology to obtain reusable materials for surfactant remediation in
94 aqueous systems. We describe here the development procedure of bacteria immobilized
95 biocomposites and their potential reusability. Our reusability test results indicate that the
96 biocomposites have a potential to be reused for continuous remediation of surfactants in
97 water.

98 **2. Experimental**

99 **2.1. Materials**

100 The dichloromethane (DCM, $\geq 99\%$ (GC), Sigma-Aldrich), acetone ($\geq 99\%$ (GC), Sigma-
101 Aldrich), methanol (99.7%, Riedel), cellulose acetate, (CA, Mw: 30000 g/mol, 39.8wt. %
102 acetyl, Sigma-Aldrich), sodium dodecyl sulfate (SDS, $\geq 98.5\%$ (GC), Sigma-Aldrich),
103 methylene blue ($\geq 82\%$, Sigma-Aldrich), Nutrient broth (Sigma-Aldrich), LB broth (Sigma-
104 Aldrich) and Agar (Sigma-Aldrich) were purchased and used without any purification.

105 **2.2. Electrospinning of non-porous and porous cellulose acetate webs**

106 Porous cellulose acetate (pCA) and non-porous cellulose acetate (nCA) nanofibers
107 were produced by using different binary solvent systems. For pCA nanofibers, the
108 procedure was determined from our previous study.²⁵ The homogenous electrospinning
109 solutions were prepared by dissolving CA in DCM/methanol (4/1 (v/v)) and
110 DCM/acetone (1/1 (v/v)) solvent mixture at 12% (w/v) and 10% (w/v) polymer
111 concentrations for nCA and pCA nanofibers, respectively. Afterwards, these clear
112 solutions were loaded in 3 mL syringe fitted with a metallic needle of 0.4 mm inner
113 diameter and they were located horizontally on a syringe pump (model KDS-101, KD
114 Scientific, USA). One of the electrodes of high-voltage power supply (Spellman, SL30,
115 USA) was clamped to the metallic needle and the plate aluminum collector was
116 grounded. Electrospinning parameters were arranged as follows: feed rate of solutions
117 = 0.5 mL/h, applied voltage = 10-15 kV, tip-to-collector distance = 10-12 cm. The
118 grounded stationary metal collector covered with an aluminum foil was used to deposit
119 the electrospun nCA and pCA nanofibers. The electrospinning apparatus was enclosed
120 in a Plexiglas box and electrospinning was carried out at about 23 °C at 20% relative

121 humidity. The collected nanofibers/nanowebs were dried overnight at room
122 temperature in a fume hood.

123 **2.3. Isolation, preliminary characterization and 16S rRNA gene sequence analysis of** 124 **STB3 and STB4 strains**

125 It was aimed to find and isolate specific and efficient bacterial strains for surfactant
126 remediation and therefore, different water samples were collected from the area nearby the
127 wastewater effluent (which contain low amounts of anionic surfactants) of a glassware
128 producing factory (Trakya Glass Bulgaria EAD). The bacterial isolates were then enriched in
129 LB medium (Luria-Bertani: 10 g/L tryptone, 5 g/L yeast extract, 10 g/L NaCl in 1 L of
130 distilled water) and plated on LB-agar plates to obtain pure cultures. All reagents utilized in
131 this study were purchased from Sigma-Aldrich (USA). The pure cultures were collected from
132 the plates, enriched in LB medium, named with the designation “STB” and their preliminary
133 characterization for surfactant remediation were performed with lower amounts of (5-10
134 mg/L) SDS containing LB growth media. The remaining concentrations of SDS in the culture
135 media were measured by MBAS (methylene blue active substances) assay in each
136 biodegradation experiment, in which methylene blue binds with anionic surfactants in an
137 aqueous medium and the mixture gives an absorbance peak at 652 nm.²⁶ The most efficient
138 bacterial isolates for SDS remediation were selected as STB3 and STB4 strains.

139 The species identity of STB3 and STB4 were determined via 16S rRNA gene
140 sequencing analysis. Bacterial DNA isolation was carried out via DNeasy Blood & Tissue Kit
141 (QIAGEN, Germany). A modified protocol for PCR amplification and further sequencing was
142 utilized with the concentrations of: 1.25 U Platinum Taq polymerase, 0.2 mM dNTP, 0.4 pmol
143 T3 (ATTAACCCTCACTAAAGGGA) and T7 (TAATACGACTCACTATAGGG) primers
144 which encompass the entire 16S gene, 1.5 mM MgCl and 1X Taq buffer.²⁷ The PCR steps

145 were adjusted as: initial denaturation at 96 °C for 5 min and further 30 cycles of denaturation
146 at 96 °C for 30 s, annealing at 55 °C for 30 s, elongation at 72 °C for 30 s and a final
147 elongation at 72 °C for 5 min. The sequencing was done via a 3130xl Genetic Analyzer by
148 using BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, USA), and the
149 analysis was performed with ABI 3130xl Genetic Analyzer. The 16S rRNA gene sequences
150 of the isolates were analyzed by NCBI's Bacterial Blast Tool (<http://www.ncbi.nlm.nih.gov>)
151 and an online phylogenetic tree printer (PhyloHendron,
152 <http://iubio.bio.indiana.edu/treeapp/treeprint-form.html>) was utilized to construct and
153 visualize the phylogenetic trees.

154 **2.4. Growth and immobilization of STB3 and STB4 cells**

155 Immobilization of STB3 and STB4 cells was provided by the inclusion of cellulose acetate
156 nanofibrous webs (which have either porous (pCA) or non-porous (nCA) morphology) into
157 the growth media of newly inoculated bacteria. The procedure including electrospinning and
158 bacterial immobilization is represented in Fig. 1 schematically. Nutrient broth (1 g/L meat
159 extract, 2 g/L yeast extract, 5 g/L peptone, 5 g/L NaCl in 1 L of distilled water) was utilized as
160 the bacterial growth medium. Bacterial growth was maintained in 100 mL culture flasks for
161 about 25 days at 25 °C and 180 rpm, and the growth media were refreshed for every 7 days.
162 For the evaluation of bacterial attachment, equivalent samples with equal weights (w/v ratio
163 of 0.5 mg/mL) were taken at day 7, 21 and at the end of the reusability test; and the bacterial
164 quantity was determined via a modified protocol in which the immobilized bacterial cells
165 were detached via sonication and viable cell counting was applied on the detached cells.²⁸
166 Briefly, the bacteria immobilized web samples were first collected and gently washed via PBS
167 (Phosphate-Buffered Saline) to remove unattached cells. The web samples were then
168 transferred to 1 mL buffer containing sterile microcentrifuge tubes and vortexed for 30 s
169 before sonication. Sonication was conducted at 40 kHz and 4 °C (the sonication bath was pre-

170 cooled and the temperature was kept constant to prevent excess heat generation and
171 subsequent cell viability loss) by using an ultrasonic cleaner (B2510, Branson Ultrasonics,
172 USA). The cycles were adjusted at 1 min sonication and 30 s rest for each run, till 10 min of
173 sonication was completed. At the end of sonication, the web samples were vortexed for 30 s
174 and the detached bacteria containing buffer samples were transferred to new sterile
175 microcentrifuge tubes. The sonication was repeated once again with fresh buffers and the
176 detached cells for each sample were combined in single tubes. Viable cell counting (VCC)
177 assay was applied for detached cells by spreading them on Nutrient-Agar plates. After
178 overnight incubation, *cfu* (colony forming unit) values for each sample were determined.
179 Bacterial immobilization was also checked with SEM microscopy, which is detailed in further
180 sections. After deciding 25 days of incubation is enough for both STB3 and STB4 cells'
181 attachment, equivalent bacteria immobilized nCA and pCA web samples (with equal w/v
182 ratios) were prepared for SDS biodegradation experiments.

183 **2.5. SDS biodegradation experiments**

184 Nutrient broth was utilized as the bacterial growth medium for SDS biodegradation
185 experiments. Samples were collected periodically to analyze remaining SDS concentrations
186 by MBAS assay. In the first experiment, free STB3 and STB4 cells were tested for SDS
187 biodegradation capability at variable pH levels (6.0-8.0). The initial SDS concentration was
188 10 mg/L and the bacterial samples were incubated for 72 h at 180 rpm and 30 °C. For further
189 experiments, the pH level was adjusted at 7.0, since it was the optimum level for STB4 strain
190 which exhibited the highest degradation capacity. In the second and third experiment, pristine
191 nCA and pCA webs, STB3 immobilized nCA and pCA webs, and STB4 immobilized nCA
192 and pCA webs were tested for their SDS remediation capability at 10 and 100 mg/L of initial
193 SDS, with the same conditions of the first experiment. In the fourth experiment, STB3
194 immobilized pCA webs and STB4 immobilized pCA webs were tested for SDS

195 biodegradation capability at a high concentration (1 g/L) and the samples were incubated for
196 168 h at 180 rpm and 30 °C. Only STB3 immobilized pCA webs and STB4 immobilized pCA
197 webs were selected for this experiment since they have shown the highest biodegradation
198 capability among STB3 and STB4 immobilized web samples in the previous experiment. In
199 each experiment, the utilized web samples were washed gently with PBS before the initiation
200 of the experiment. The w/v ratios were equal for each web sample (0.5 mg/mL). All tests were
201 done in triplicate.

202 The removal capacities (Q_{eq}) of free STB3 and STB4 cells, and bacteria immobilized
203 web samples were calculated by Eq. 1 (1)

$$204 \quad Q_{eq} \text{ (mg/g)} = (C_0 - C_f) \cdot V / M \quad (1)$$

205 where C_0 is the initial SDS concentration (mg/L), C_f is the final SDS concentration (mg/L), V
206 is the solution volume (L) and M is the total bacterial cell biomass (g) at equilibrium.²⁹

207 **2.6. Adsorption isotherms and kinetics studies**

208 Adsorption coefficients of STB3/pCA and STB4/pCA webs were estimated for three isotherm
209 models (Freundlich, Langmuir and Toth) by using the calculated Q_{eq} and C_f values, that are
210 required for the isotherm parameter fitting software IsoFit³⁰ to generate adsorption isotherms,
211 from three different experiments (Fig. 4b, 4c and 4d). The order of reactions for SDS removal
212 were evaluated by plotting zero, first, second and third order plots of STB3/pCA and
213 STB4/pCA webs, and comparing their R^2 values afterwards.

214 **2.7. LC-MS (Liquid Chromatography - Mass Spectroscopy)**

215 LC-MS analysis was performed without column separation for the samples; SDS only,
216 nutrient broth only, STB3 post-incubation and STB4 post-incubation by using a TOF LC/MS
217 system (6224, Agilent Technologies, USA). SDS only sample was containing 100 mg/L of

218 SDS, while STB3 and STB4 samples were containing 100 mg/L of SDS before starting
219 bacterial growth at 72 h and 30 °C. STB3 and STB4 post-incubation samples were prepared
220 by first collecting the bacterial cultures after incubation period in sterile centrifuge tubes,
221 centrifuging them at 6000 rpm for 5 min, and then transferring the supernatant portions to
222 HPLC vials to be analyzed with LC-MS. The experimental parameters were; ion polarity:
223 negative, LC stream: MS, mass range: 50-3000 m/z, acquisition rate: 1.03 spectra/s,
224 acquisition time: 966.5 ms/spectrum, flow: 0.5 ml/min, pressure limit: 0-400 bar.

225 **2.8. Scanning Electron Microscopy (SEM)**

226 Millimeter-length nCA and pCA webs were prepared for SEM analysis to evaluate bacterial
227 attachment. The sample fixation was done by using a modified protocol, similar to the Greif
228 and colleagues'.³¹ Briefly, web samples were washed twice with PBS and then incubated
229 overnight in 2.5% glutaraldehyde (prepared in PBS) for sample fixation. After overnight
230 incubation, the web samples were washed twice with PBS and a dehydration protocol was
231 applied on those samples by immersion in a series of EtOH solutions (30% - 96%). At the end
232 of dehydration, samples were coated with 5 nm Au-Pd for SEM imaging (Quanta 200 FEG
233 SEM, FEI Instruments, USA).

234 **2.9. Reusability test**

235 Reusability of STB3/pCA and STB4/pCA biocomposites was tested for remediation of SDS.
236 Prior to each cycle, the web samples were washed gently with PBS to remove unattached
237 bacteria. The experiments were performed at an initial SDS concentration of 100 mg/L with
238 the parameters of: incubation at 180 rpm and 30 °C for 72 h. SDS concentrations in the media
239 were measured at the beginning and at the end for each run, and the percentile removal of

240 SDS was calculated upon these results. The washing step was repeated for each web sample
241 before starting the next one. All tests were done in triplicate.

242 **3. Results and discussion**

243 **3.1. Identification and preliminary characterization of the bacterial isolates**

244 STB3 and STB4 isolates were collected nearby an industrial effluent which contains low
245 amounts of anionic surfactants, and therefore thought as potential candidates for
246 bioremediation of anionic surfactants. According to the preliminary characterization studies,
247 both strains have shown biodegradation capability against SDS at the concentrations of 5-10
248 mg/L. 16S rRNA gene sequencing analysis was applied on these two strains and the neighbor-
249 joining phylogenetic tree of STB3 and STB4 strains are shown in Fig. S1 in the supporting
250 information. As seen in Fig. S1, STB3 strain shows closest identity (95%) with *Serratia*
251 *proteamaculans* and STB4 strain shows closest identity (97%) with *Achromobacter*
252 *xylooxidans*, hence the isolates were designated as *Serratia proteamaculans* STB3 and
253 *Achromobacter xylooxidans* STB4. The strains STB3 and STB4 were deposited in GenBank
254 with the accession numbers of KR094855 and KR094856, and the gene sequences are
255 accessible with those accession numbers.

256 **3.2. Immobilization of bacterial cells on nCA and pCA webs and evaluation of contact** 257 **time on bacterial integration**

258 Depending on the solvent type for the electrospinning solution, CA nanofibers can be
259 obtained in non-porous (nCA) or porous (pCA) morphology. It is known that electrospun CA
260 nanofibers are suitable matrices for biological use, and the high porosity along with the higher
261 surface area of pCA nanofibers may have a greater potential to be utilized in biological
262 applications.²⁰ The morphologies of nCA and pCA nanofibers are shown in Fig. 2,
263 demonstrating nanoscale pores are present on pCA nanofibers. The fiber diameters of nCA

264 and pCA nanofibers were ranging between 0.5 to 3 μm . A modified protocol²⁷ was applied for
265 web samples to quantify the approximate amount of the attached bacteria at different time
266 periods, and SEM imaging was performed to support these results. Fig. S2a and S2b show
267 *Serratia proteamaculans* STB3 cells on nCA and pCA nanofibers after 7 days of incubation,
268 wherein the bacterial attachment was not sufficient. Fig. S2c and Fig. S2d show
269 *Achromobacter xylosoxidans* STB4 cells on nCA and pCA nanofibers, which revealed
270 bacterial cells attached more strongly on nCA nanofibers. Fig. 3a and Fig. 3b show *Serratia*
271 *proteamaculans* STB3 cells on nCA and pCA nanofibers, while Fig. 3c and Fig. 3d show
272 *Achromobacter xylosoxidans* STB4 cells on nCA and pCA nanofibers after 21 days of
273 incubation, which all revealed bacterial attachment became adequate for each sample to
274 initiate biodegradation studies, this was also supported by the viable cell counting results
275 (Table 1). Therefore, at least 21 days was found to be required for both STB3 and STB4
276 strains, and the web samples were collected after 25 days of incubation. From the viable cell
277 counting results, it was inferred that, bacterial cells have difficulty to adhere on nanoporous
278 surfaces since lower number of bacterial immobilization was achieved for pCA samples at
279 days 7 and 21. A similar behavior was also observed for different kinds of Gram-negative
280 bacteria (*Pseudomonas fluorescens* and two different strains of *Escherichia coli*), which
281 showed that bacterial cells attach preferably on nanosmooth silica surfaces rather than
282 patterned, nanoporous surfaces at mature biofilm stage, and it has been elucidated by the
283 tendency of bacterial cells to maximize their contact area with the substrate surface during
284 immobilization.³² Since bacterial attachment came into saturation in STB4/nCA sample after
285 7 days, no significant increase in bacterial number could be observed after 21 days for this
286 sample; nevertheless, the bacterial attachment on STB4/pCA sample was not saturated after 7
287 days, hence the bacterial number highly increased and became closer to the STB4/nCA
288 sample's, barely after adequate time of incubation (21 days). This result implies that, while

289 the nanoporous morphology of pCA webs complicates bacterial cells' initial colonization, it
290 might not lead to a significant effect on the maximal bacterial attachment capacity, since
291 higher numbers of bacterial attachment was obtained on pCA samples latterly.

292 To summarize, morphological difference in CA webs was found to be effective on bacterial
293 adhesion and the required contact time. After finishing the bacterial immobilization process at
294 day 25, the web samples were collected and SDS biodegradation experiments were started
295 with those samples.

296 **3.2. SDS biodegradation capability of STB3/nCA, STB3/pCA, STB4/nCA and** 297 **STB4/pCA webs**

298 *Serratia proteamaculans* STB3 and *Achromobacter xylosoxidans* STB4 cells have shown
299 slight differences in SDS biodegradation profiles at different pH levels (6.0-8.0) for an initial
300 SDS concentration of 10 mg/L (Fig. 4a), suggesting both strains can be utilized efficiently
301 within this pH range. For further studies, the pH was adjusted at 7.0, since the best SDS
302 biodegradation profile was obtained by *Achromobacter xylosoxidans* STB4 cells at this pH
303 level. In the second experiment (Fig. 4b), STB4/nCA and STB4/pCA biocomposite webs have
304 shown better SDS biodegradation profiles than free STB4 cells and the other webs,
305 STB3/nCA and STB3/pCA biocomposite webs have shown similar SDS biodegradation
306 profiles with free STB3 cells, and pristine nCA and pCA webs have shown only slight
307 decreases in the initial SDS concentration (10 mg/L) with a relatively more decrease for
308 pristine pCA webs. This result suggests the biocomposite webs can provide the same
309 remediation performance without adding any additional bacterial inocula to the aqueous
310 system. In the third experiment (Fig. 4c), the same samples were tested at a higher
311 concentration of SDS (100 mg/L) with the same conditions of the previous experiment.
312 Interestingly, it was observed that, STB3/pCA web has shown the best SDS biodegradation

313 profile among different samples for degradation of 100 mg/L of SDS. STB4/pCA and
314 STB3/nCA samples have shown very similar SDS biodegradation profiles, while STB4/nCA
315 web has shown the lowest SDS biodegradation among four different biocomposite webs.
316 Similar to the previous experiment, pristine nCA and pCA webs have shown slight decreases
317 in the initial SDS concentration, which occurred possibly due to adsorption. In this case,
318 decreases in SDS concentrations for pristine nCA and pCA webs were observed as very
319 similar, which contradicted our previous thought that pCA webs may have a higher adsorption
320 capability for SDS due to their higher porosity. In the final SDS biodegradation experiment
321 (Fig. 4d), we increased both the initial SDS concentration and incubation time to test the SDS
322 biodegradation capability of our best biocomposite webs (including both bacterial strains) at
323 considerably high concentrations of SDS (1 g/L). Similar to the third experiment, STB3/pCA
324 web has shown a better SDS biodegradation profile (85%) than STB4/pCA web (63%) within
325 168 h, which suggests STB3 cells may have a higher SDS biodegradation capability than
326 STB4 cells at higher concentrations of SDS. Degradation capacities (Q_{eq}) of free cells and
327 biocomposite webs were calculated at pH 7.0 for the concentrations of 10 and 100 mg/L
328 wherein nearly complete degradation of SDS was observed, and they are presented in Table 2.
329 The Q_{eq} value of free STB3 cells was higher than free STB4 cells at both 10 and 100 mg/L
330 SDS, which was also observed in STB3 immobilized web samples. Furthermore, it was
331 observed that, Q_{eq} values of both STB3 and STB4 immobilized webs increased with an
332 increase in the initial SDS concentration, but more notable increases in Q_{eq} values occurred in
333 STB3 immobilized webs and the percentile degradation of these webs were highly increased
334 (96.5% for STB3/nCA and 98.8% for STB3/pCA) and reached or surpassed the percentile
335 degradation levels of STB4 immobilized webs at 100 mg/L of initial SDS. This result may
336 support our previous statement that, STB3 cells have a higher SDS biodegradation capability
337 than STB4 cells at higher concentrations.

338 3.3. Adsorption isotherms and order of reactions

339 The estimated values of adsorption coefficients for three isotherm models (Langmuir,
340 Freundlich and Toth) are listed in Table S1. All of the tested models in two different samples
341 have shown good fitting properties. For STB3/pCA sample, Langmuir and Toth isotherms
342 have shown slightly better correlation with the R_y^2 value of 0.992, while this value is 1.000
343 for STB4/pCA sample in all three models. Since Langmuir model is not a single best fitting
344 model in both samples, the SDS removal process is not likely to be monolayeric, rather it is
345 heterogenous and multilayeric by bacteria immobilized web samples.³³ The maximum
346 removal capacities (Q_{\max}) of web samples were estimated to be 3367 mg/g for STB3/pCA and
347 1464 mg/g for STB4/pCA under the Langmuir model, while they were 3023 mg/g for
348 STB3/pCA and 1350 mg/g for STB4/pCA under the Toth model, implying STB3/pCA has a
349 much higher removal capacity for SDS.

350 The R^2 values of different order plots for STB3/pCA and STB4/pCA are listed in Table S2.
351 STB3/pCA and STB4/pCA samples have shown the highest correlation for the zero order
352 model with the R^2 values of 0.9319 and 0.8531, respectively; suggesting the SDS removal
353 process by both web samples is an enzyme-catalyzed degradation, as enzyme-catalyzed
354 reactions often fall under the zero order model.³⁴ Since the total surface area has an essential
355 role in the zero order model, the higher SDS removal capacities of bacteria/pCA samples can
356 also be attributed to the higher surface area of the immobilized bacteria, in contrast to the
357 bacteria/nCA samples where higher bacterial immobilization might lead to aggregation and
358 decrease in the total surface area.

359 3.4. LC-MS analysis

360 LC-MS analysis was performed to monitor the remaining SDS and its byproducts in bacterial
361 growth media after the incubation process. Biodegradation of SDS has been studied

362 previously and the known byproducts of SDS before proceeding to the fatty acid metabolism
363 are 1-dodecanol, dodecanal and laurate.³⁵ According to the LC-MS analysis results, SDS
364 (molar mass: ~288 g/mol) was observed at around 265 m/z by releasing sodium ions (Fig.
365 S3), and nutrient broth gave various peaks in the range of 100-180 m/z. For post-incubation
366 samples, no explicit peaks at around 184, 186 and 199 m/z were observed, corresponding to
367 the molar masses of dodecanal, 1-dodecanol and laurate, respectively. It was concluded that,
368 while the remaining SDS in media can be monitored by LC-MS analysis, the byproducts
369 cannot be seen since these metabolites have very short lifetime and they are quickly processed
370 for further fatty acid metabolism. The counts (%) ratio for the remaining SDS at around 265
371 m/z was higher for the STB4 sample, revealing lower SDS degradation was occurred for this
372 sample, which was also observed in the SDS biodegradation experiments of free STB4 cells
373 (Table 2).

374 **3.5. Reusability and applicability of STB3/pCA and STB4/pCA biocomposites**

375 After the end of biodegradation experiments, the same web samples were tested for
376 reusability in five consecutive cycles. Although significant portions of SDS were degraded by
377 STB3/pCA and STB4/pCA webs at 1 g/L, 100 mg/L was selected as the initial concentration
378 for the reusability test rather than 1 g/L, since complete degradation could not be achieved
379 and the degradation time highly increased at 1 g/L of SDS. As seen in Fig. 5, while the SDS
380 biodegradation capabilities of STB3/pCA and STB4/pCA webs were considerably low for the
381 initial cycles, they recovered in the following cycles, especially for the STB3/pCA web. This
382 result might be related with losses of viable bacterial cells and metabolic activity for the
383 biocomposite webs, after exposure to a very high concentration of SDS (1 g/L) in the previous
384 experiment. On the other hand, the degradation performances and viable cell counts started to
385 recover at convenient conditions, during the test period at an initial SDS concentration of 100
386 mg/L where bacterial cells can rapidly grow and immobilize on the fibrous surfaces with a

387 high metabolic activity, leading higher bacterial attachment and higher degradation
388 efficiencies, and indeed at the end of the reusability test, higher numbers of viable cells were
389 counted for both STB3/pCA and STB4/pCA web samples (Table 1). The test results indicated
390 that, STB3/pCA has a more efficient SDS biodegradation profile than STB4/pCA during the
391 reusability test, and has a higher recovery capability for long term use at the tested
392 concentration. Since the viable cell numbers increased for both samples (especially for
393 STB3/pCA) during the reusability test, their removal capacities have altered and differed from
394 the pre-reusability test conditions. It was inferred that, while 1 g/L of initial SDS might be
395 toxic and constrain the metabolic activities of bacterial cells, 100 mg/L of initial SDS is
396 appropriate for seeing the maximal biodegradation performances of the bacteria immobilized
397 webs and for their repeated use. SEM imaging was applied on STB3/pCA and STB4/pCA
398 webs to monitor the presence of immobilized bacteria at the end of the reusability test. As
399 seen in Fig. S4, robust attachment of bacterial cells and biofilm-like structures on both web
400 samples were observed, supporting the viable cell counting results of STB3/pCA and
401 STB4/pCA after the reusability test (Table 1).

402 Remediation of anionic surfactants from water systems is a critical issue and greener
403 approaches have been received more attention.^{4,9,10,36,37} In addition, use of biointegrated
404 functional electrospun fibrous webs for remediation of contaminated water systems has been
405 explored in recent years and there are few examples in the literature for the applications of
406 these kind of materials. For remediation of nitrate in aqueous systems, Eroglu *et al.* produced
407 a novel biocomposite by immobilization of microalgal cells on electrospun chitosan nanofiber
408 mats.¹¹ In recent studies performed by our group, specific bacterial or algal strains have been
409 attached on electrospun fibrous webs for ammonium bioremoval,²⁰ methylene blue dye
410 biodegradation,²¹ reactive dye biodegradation²² and simultaneous removal of hexavalent
411 chromium and a reactive dye.²³ In the present study, we focused on anionic surfactant

412 bioremediation and therefore produced novel biocomposite webs by immobilization of two
413 different SDS degrading bacterial strains on electrospun nCA and pCA webs. It was observed
414 that, bacterial cells strongly immobilized on nCA and pCA fibrous surfaces, the bacteria
415 immobilized webs exhibited similar biodegradation performances with free STB3 and STB4
416 cells and can be reused for several cycles of SDS biodegradation with recovery capabilities. 1
417 g/L of SDS was found as potentially toxic for STB3 and STB4 cells since the degradation
418 profiles of STB3/pCA and STB4/pCA highly decreased right after this experiment as seen in
419 Fig. 5, still STB3/pCA and STB4/pCA webs were able to degrade significant portions of SDS
420 at this concentration. The bacterial strains have shown efficient biodegradation profiles at
421 differential pH levels for the initial SDS concentration of 10 mg/L, indicating the
422 biodegradation performances of both strains were not significantly affected by pH differences
423 within 6.0-8.0. Although highly efficient results could be achieved at different concentrations
424 for SDS biodegradation, the bacteria immobilized webs are still improvable by increasing the
425 number of attached bacteria or optimizing the bacterial growth conditions. Overall, these
426 results are highly promising and with successful optimizations, STB3/pCA and STB4/pCA
427 webs may be utilized continually for SDS biodegradation in aqueous environments.

428 **4. Conclusions**

429 Here, we present novel biocomposite webs that were obtained by immobilization of SDS
430 degrading bacterial strains on electrospun cellulose acetate (CA) webs (non-porous (nCA) and
431 porous (pCA) webs). The bacterial attachment has been evaluated regularly by bacterial cell
432 counting (VCC assay) and SEM imaging, and the bacterial attachment was ended after 25
433 days upon these results. The results of biodegradation experiments revealed that, SDS
434 remediation capabilities of bacteria immobilized webs were mainly based on the bacterial
435 existence and highly similar to the unimmobilized bacterial cells. Since bacteria immobilized

436 web samples were highly efficient for SDS remediation up to 100 mg/L of initial SDS, two
437 most effective webs (STB3/pCA and STB4/pCA) were therefore selected for testing their
438 SDS remediation capability at a considerably high concentration (1 g/L). Although significant
439 portions of SDS were degraded by STB3/pCA and STB4/pCA in this experiment, 1 g/L of
440 SDS was found as stringent for the metabolic activity and viability of bacterial cells, therefore
441 the test concentration of the reusability test was adjusted at 100 mg/L. While the initial SDS
442 biodegradation performances of STB3/pCA and STB4/pCA were considerably low in the
443 reusability test (due to the harmful effects of the previous experiment on bacterial cells), they
444 recovered in the next cycles and reached adequate levels especially for the STB3/pCA sample.
445 It was concluded that, the bacteria immobilized webs are potentially reusable and improvable,
446 suggesting they may be used repeatedly for SDS remediation in water systems.

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Figure Captions

530

531 **Fig. 1** (a) Schematic representation of electrospinning process for nCA and pCA webs, and
532 photographs of nCA and pCA webs, (b) representative images for bacteria immobilized webs
533 including a SEM micrograph and schematic representation of bacterial cells on fibrous surfaces.

534 **Fig. 2** SEM micrographs of (a) pristine nCA and (b) pristine pCA webs. Pores can be seen on a
535 pCA nanofiber in the inset figure.

536 **Fig. 3** SEM micrographs of (a-c) nCA and (b-d) pCA nanofibers showing immobilization of
537 STB3 cells onto (a) nCA nanofibers and (b) pCA nanofibers; and immobilization of STB4 cells
538 onto (c) nCA nanofibers and (d) pCA nanofibers after 21 days of incubation.

539 **Fig. 4** SDS biodegradation profiles of (a) STB3 and STB4 strains for differential pH levels at 10
540 mg/L SDS, (b) pristine nCA, pristine pCA, STB3/nCA, STB3/pCA, STB4/nCA and STB4/pCA
541 webs at 10 mg/L SDS, (c) pristine nCA, pristine pCA, STB3/nCA, STB3/pCA, STB4/nCA and
542 STB4/pCA webs at 100 mg/L SDS and (d) STB3/pCA and STB4/pCA webs at 1 g/L SDS. Error
543 bars represent mean of three independent replicates.

544 **Fig. 5** Reusability test results of STB3/pCA and STB4/pCA webs for 5 cycles of SDS
545 biodegradation at an initial concentration of 100 mg/L. Error bars represent mean of three
546 independent replicates.

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551 **Table 1.** Viable cell counting (VCC) results of STB3/nCA, STB3/pCA, STB4/nCA and
552 STB4/pCA webs at different time periods. The results are presented in *cfu*/mL. The w/v ratio
553 of each web that was utilized for the detachment process was equal (0.5 mg/mL).

554 Attachment time	STB3/nCA	STB3/pCA	STB4/nCA	STB4/pCA
555 7 days	$0.3 \times 10^9 \pm 0.04$	$0.25 \times 10^9 \pm 0.04$	$3.1 \times 10^9 \pm 1.2$	$1.4 \times 10^9 \pm 0.17$
556 21 days	$1.15 \times 10^9 \pm 0.4$	$0.6 \times 10^9 \pm 0.11$	$3.15 \times 10^9 \pm 0.85$	$2.65 \times 10^9 \pm 0.54$
557 After reusability test	–	$2.97 \times 10^9 \pm 0.42$	–	$2.8 \times 10^9 \pm 0.33$

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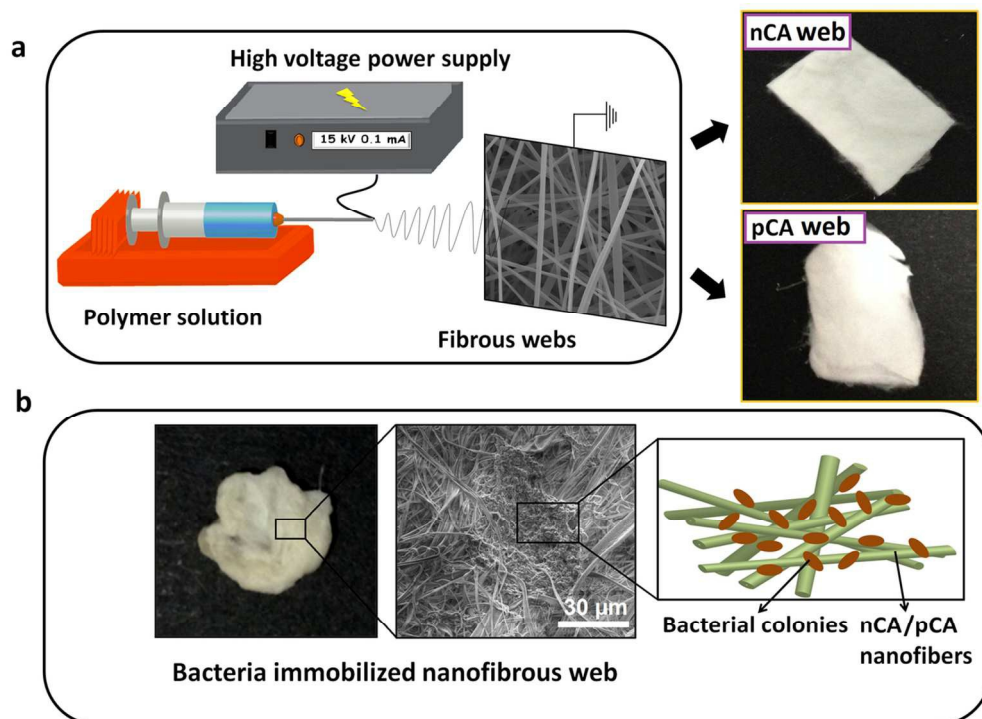
571 **Table 2.** Degradation capacities of free STB3 and STB4 cells, and STB3/nCA, STB3/pCA,
 572 STB4/nCA, STB4/pCA webs at equilibrium at the end of the degradation period. T = 30 °C, agitation
 573 rate: 180 rpm.

574	Sample name	Initial concentration (C ₀)	Removed SDS amount	Q _{eq} (mg/g)	Removal (%)
575	STB3 only	10 mg/L	8.3 mg/L	29.66 ± 0.54	83%
576	STB4 only	10 mg/L	9.37 mg/L	20.06 ± 0.23	93.7%
577	STB3/nCA	10 mg/L	8.03 mg/L	28.68 ± 1.15	80.3%
578	STB3/pCA	10 mg/L	8.96 mg/L	32.02 ± 1.24	89.6%
579	STB4/nCA	10 mg/L	9.52 mg/L	20.38 ± 0.29	95.2%
580	STB4/pCA	10 mg/L	9.7 mg/L	20.76 ± 0.02	97%
581	STB3 only	100 mg/L	95 mg/L	339.46 ± 1.53	95%
582	STB4 only	100 mg/L	66.8 mg/L	142.97 ± 27.7	66.8%
583	STB3/nCA	100 mg/L	96.5 mg/L	344.63 ± 6.3	96.5%
584	STB3/pCA	100 mg/L	98.8 mg/L	352.88 ± 1.7	98.8%
585	STB4/nCA	100 mg/L	72.4 mg/L	155.55 ± 27.8	72.4%
586	STB4/pCA	100 mg/L	96.28 mg/L	206.16 ± 3.98	96.28%
587	STB3/pCA	1 g/L	846.47 mg/L	3023.01 ± 413.5	84.66%
588	STB4/pCA	1 g/L	630.61 mg/L	1350.34 ± 345.9	63.01%

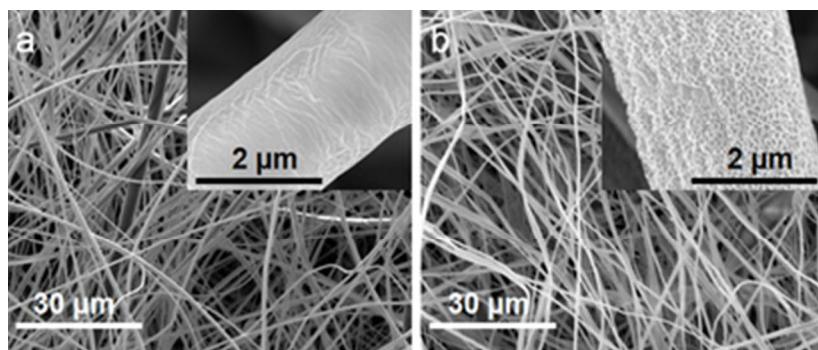
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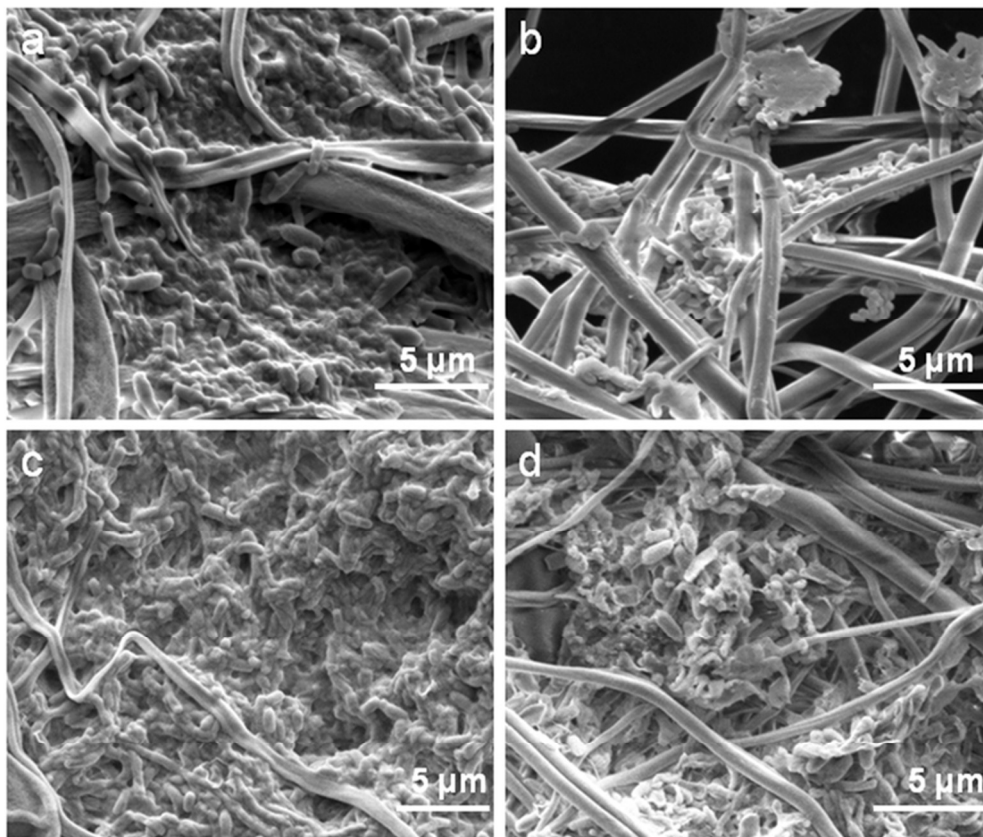
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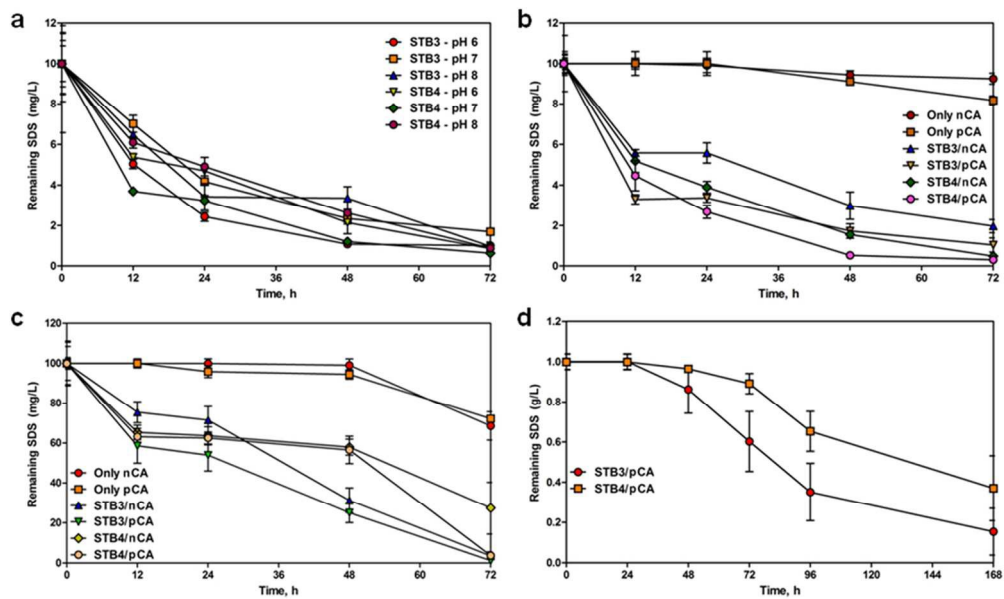
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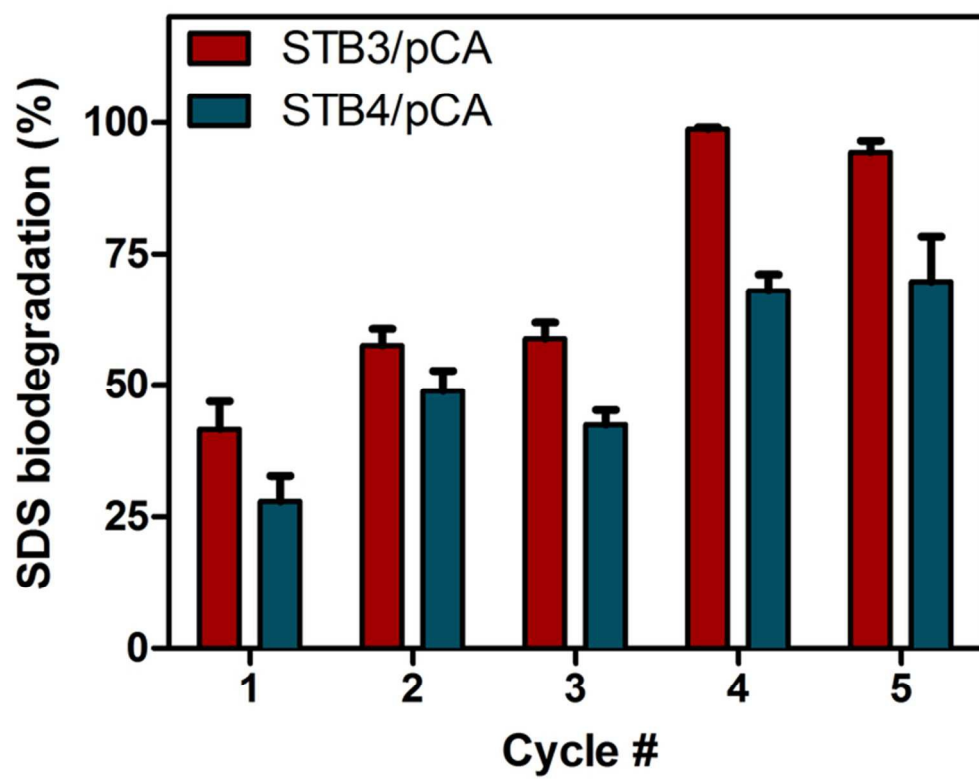
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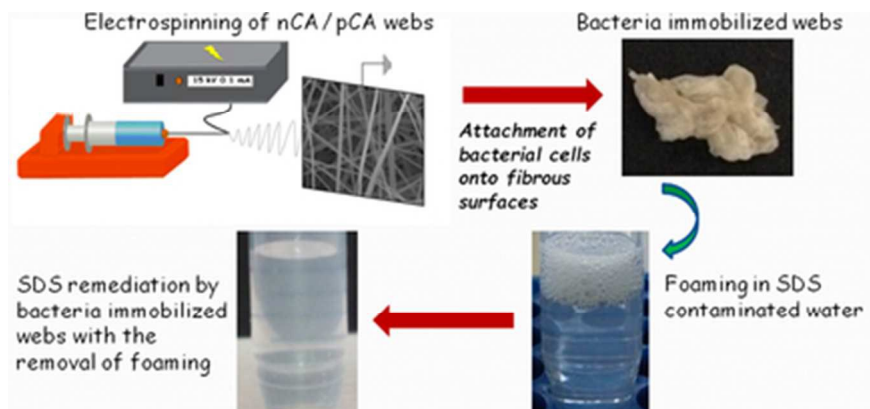
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