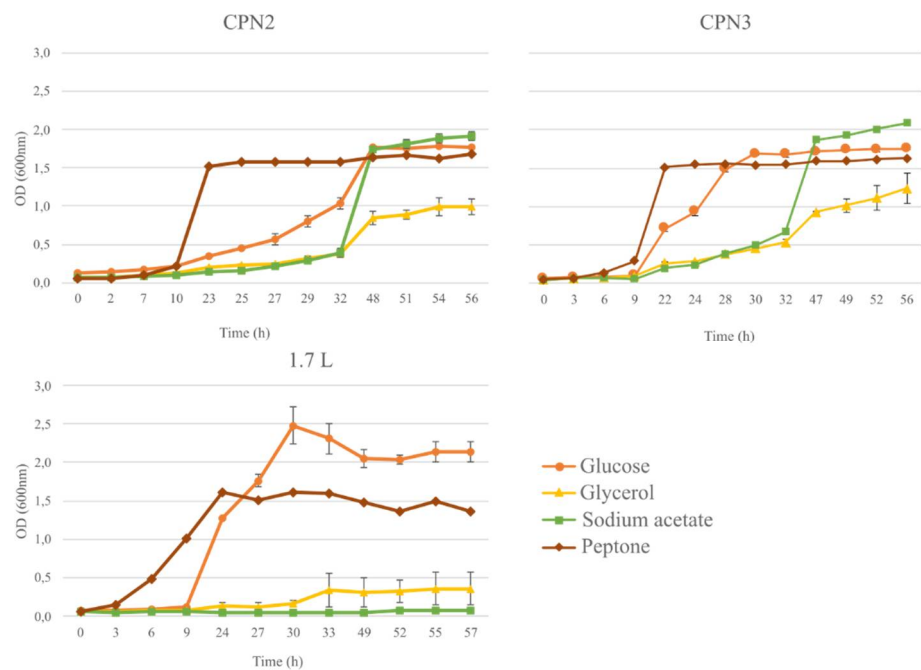
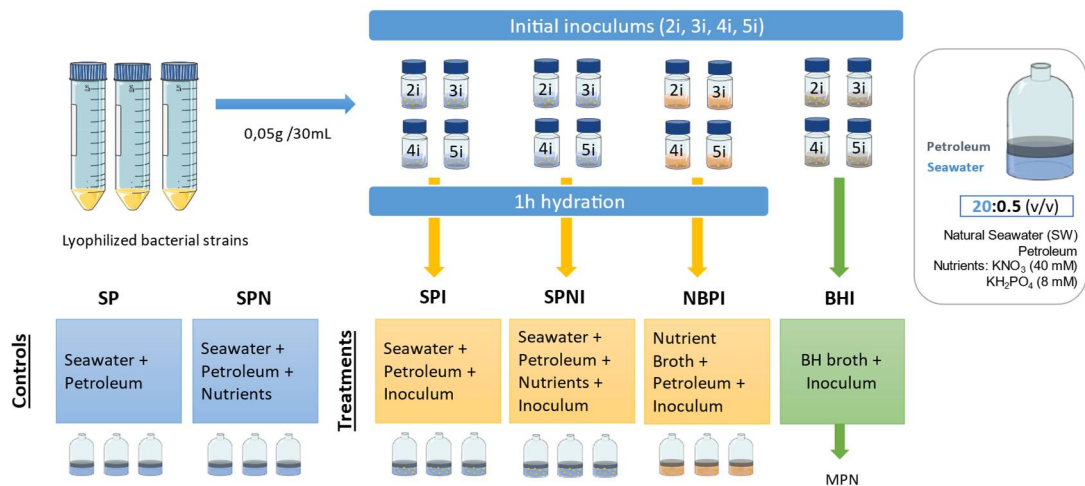


Supplementary Materials

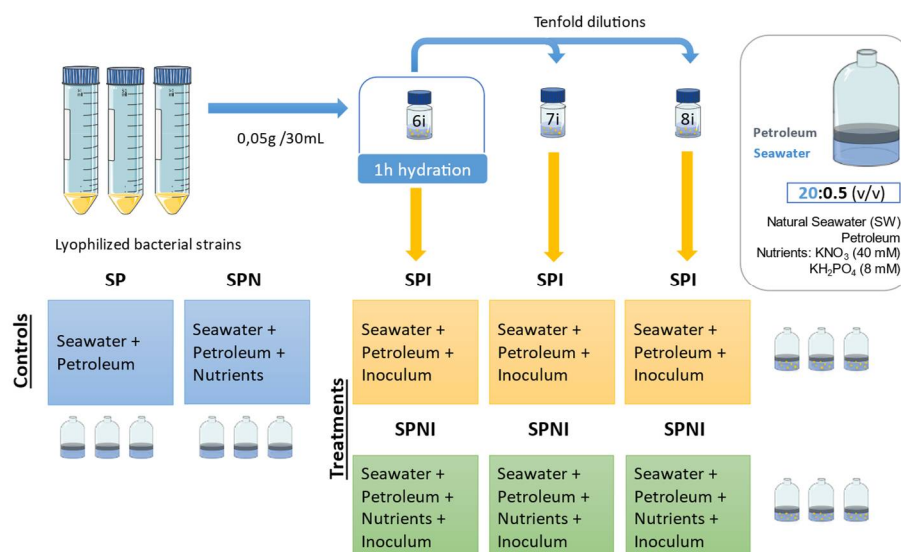
Manuscript Perdigão et al.



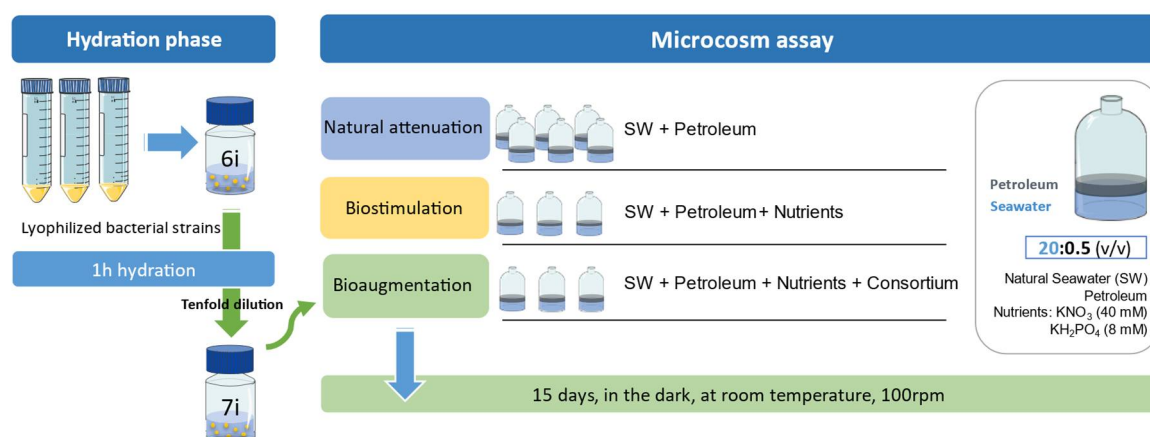
**Figure S1.** Biomass growth (mean value, standard deviation, n=3) of the bacterial isolates CPN2, CPN3 and 1.7 L with different carbon sources (10 g.L<sup>-1</sup>).



**Figure S2.** Representative scheme of the experiment with the lyophilized strains CPN2 (2i), CPN3 (3i), 1.7 L (4i) and a consortium (5i), in the controls SP (sterile seawater + petroleum), SPN (sterile seawater + petroleum + nutrients) and the treatments SPI (sterile seawater + petroleum + inoculum), SPNI (sterile seawater + petroleum + nutrients + inoculum), NBPI (nutrient broth + petroleum + inoculum) and BHI (bushnell-haas + inoculum).



**Figure S3.** Representative scheme of the experiment with the controls SP (natural seawater + petroleum), SPN (natural seawater + petroleum + nutrients) and with different concentrations of the consortium of the lyophilized strain: 6i ( $1.7 \text{ g L}^{-1}$ ), 7i ( $1.7 \cdot 10^{-1} \text{ g L}^{-1}$ ) and 8i ( $1.7 \cdot 10^{-2} \text{ g L}^{-1}$ ), applied to the treatments SPI (natural seawater + petroleum + inoculum) and SPNI (natural seawater + petroleum + nutrients + inoculum).



**Figure S4.** Representative scheme of the microcosms experiments with natural seawater (SW), petroleum and the optimum concentration of the consortium of lyophilized strains 7i ( $1.7 \cdot 10^{-1} \text{ g L}^{-1}$ ), with the treatments natural attenuation, bioaugmentation and bioaugmentation.

**Table S1.** Phylogenetic identification of bacterial strains isolated in the microcosms bioremediation experiment for the natural seawater at T0 (0SW) and for the different treatments: natural attenuation (NA) and biostimulation (BS) at T15, and bioaugmentation (BA) at T0, T7 and T15.

Isolates	Closest Identification	Sequence length	% similarity*	Class	Accession number
1.7 L	<i>Pseudomonas</i> sp.	1407	99.86	Gammaproteobacteria	OK482776
0SW_A	<i>Enterovibrio</i> sp.	1392	99.64	Gammaproteobacteria	MW486132
0SW_B	Rhodobacteraceae**	1333	99.63	Alphaproteobacteria	MW486149
0SW_C	<i>Winogradskyella multivorans</i>	1365	99.71	Flavobacteriia	MW486161
0BA_A <sup>a</sup>	<i>Rhodococcus erythropolis</i>	1386	99.93	Actinobacteria	MW486151
0BA_B <sup>a</sup>	<i>Pseudomonas</i> sp.	1408	99.86	Gammaproteobacteria	MW486147
7BA_A	<i>Pseudomonas oleovorans</i>	1409	99.79	Gammaproteobacteria	MW486144
7BA_B	Rhodobacteraceae**	1335	99.10	Alphaproteobacteria	MW486150
7BA_C	<i>Pseudomonas pachastrellae</i>	1412	99.86	Gammaproteobacteria	MW486146
7BA_D	<i>Maribacter thermophilus</i>	1401	99.29	Flavobacteriia	MW486135
7BA_F	<i>Vibrio alginolyticus</i>	1426	99.86	Gammaproteobacteria	MW486158
7BA_G	<i>Maribacter thermophilus</i>	1404	99.07	Flavobacteriia	MW486136
7BA_H	<i>Vibrio tritonius</i>	1374	99.71	Gammaproteobacteria	MW486160
7BA_I	<i>Pseudoalteromonas</i> sp.	1404	99.93	Gammaproteobacteria	MW486141
7BA_J	<i>Shewanella</i> sp.	1415	99.72	Gammaproteobacteria	MW486156
15NA_A	<i>Sediminicola luteus</i>	1389	98.78	Flavobacteriia	MW486153
15NA_B	<i>Sulfitobacter pontiacus</i>	1335	99.78	Alphaproteobacteria	MW486157
15NA_C	<i>Alteromonas</i> sp.	1408	99.57	Gammaproteobacteria	MW486130
15NA_D	<i>Alteromonas</i> sp.	1404	99.64	Gammaproteobacteria	MW486131
15NA_E	<i>Paraglaciicola mesophila</i> .	1401	99.57	Gammaproteobacteria	MW486140
15NA_F	<i>Idiomarina</i> sp.	1416	99.79	Gammaproteobacteria	MW486133
15BS_A	<i>Neptunomonas phycophila</i>	1410	99.72	Gammaproteobacteria	MW486138
15BS_B	<i>Pseudomonas marincola</i>	1399	99.86	Gammaproteobacteria	MW486142
15BS_C	<i>Pseudomonas pachastrellae</i>	1410	99.79	Gammaproteobacteria	MW486145
15BS_D	<i>Shewanella</i> sp.	1417	99.58	Gammaproteobacteria	MW486155
15BS_F	<i>Pseudomonas marincola</i>	1413	99.79	Gammaproteobacteria	MW486143
15BA_A <sup>a</sup>	<i>Rhodococcus erythropolis</i>	1391	99,86	Actinobacteria	MW486152
15BA_B	<i>Shewanella</i> sp.	1418	99,58	Gammaproteobacteria	MW486154
15BA_C	<i>Maribacter thermophilus</i>	1405	98,93	Flavobacteriia	MW486134
15BA_D <sup>a</sup>	<i>Pseudomonas oleovorans</i>	1406	99,79	Gammaproteobacteria	MW486144
15BA_E	<i>Microbacterium paraoxydans</i>	1391	99,93	Actinobacteria	MW486137
15BA_F	<i>Paracoccus seriniphilus</i>	1337	99,63	Alphaproteobacteria	MW486139
15BA_G	<i>Vibrio</i> sp.	1402	99,86	Gammaproteobacteria	MW486159

\* similarity percentages according to the nucleotide collection database of the NCBI; \*\* the identification of the isolates was made only until the family level; <sup>a</sup> isolate similar to the introduced lyophilized bacterial strains (CPN2, CPN3 and 1.7L) used as inocula for the bioaugmentation treatments.