

Supplementary information

Role of N-acyl-homoseine lactone (AHL) based quorum sensing on biofilm formation on packing media in wastewater treatment process

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Table

Table S1 Composition of synthetic wastewater

substance	concentration (mg/L)
CH ₃ COONa	400
NH ₄ Cl	107
MgSO ₄ · 7H ₂ O	90
CaCl ₂	10.55
K ₂ HPO ₄	64
KH ₂ PO ₄	28
yeast extract	1
elements solution	0.5 ml

Table S2 Composition of trace elements solution

substance	concentration (mg/L)
FeCl ₃ · 6H ₂ O	1.50
CuSO ₄ · 5H ₂ O	0.03
H ₃ BO ₃	0.15
KI	0.18
MnCl ₂ · 4H ₂ O	0.12
NaMoO ₄ · 2H ₂ O	0.06
ZnSO ₄ · 7H ₂ O	0.12
CoCl ₂ · 6H ₂ O	0.15
EDTA	10.00

Table S3 Composition of trace elements solution

AHL	Screening time (min)	Retention time (min)	Transitions ¹	Dwell	Cone	Collision
C4-HSL	/	/	172.2 → 102.1 172.2 → 71.1	0.015	22	12
3OC6-HSL	/	/	214.2 → 102.1 214.2 → 71.1	0.015	22	12
C6-HSL	1.81-2.18	2.12	200.2 → 99.1 200.2 → 102.1	0.015	20	10
3OC8-HSL	/	/	242.2 → 102.1 242.2 → 71.3	0.015	22	12
C7-HSL	/	/	214.2 → 113.1 214.2 → 102.1	0.015	22	12
C8-HSL	5.25-5.87	5.53	228.2 → 127.1 228.2 → 102.1	0.015	22	12
3OC10-HSL	/	/	270.3 → 102.1 270.3 → 169.1	0.015	22	12
C10-HSL	/	/	256.3 → 102.1 256.3 → 155.1	0.015	22	12
C12-HSL	/	/	283.3 → 102.1 284.3 → 183.2	0.015	22	12
3-oxo-C12-HSL	13.39-14.46	14.25	298.3 → 102.1 298.3 → 197.2	0.015	22	12
C14-HSL	18.85-19.16.	19.05	312.4 → 102.1 312.4 → 211.3	0.015	22	12

¹Two most prominent transition ions generated from each precursor ion based on the optimized MS/MS parameters were chosen. The first MRM transition was used for quantification while the second MRM transition was used for identity confirmation.

Table S4 The top 34 most abundant community members (relative abundance >1%) at genus level

Rank		Phase I				Phase II						Phase III			add-back	
		Blank	2W	4W	6W	8W	10W	12W	14W	16W	18W	20W	22W	24W	50 nM	1000 nM
<i>Brevundimonas</i>	0.34	0.53	0.35	0.68	0.67	0.87	1.09	1.55	1.44	1.21	0.98	1.03	1.07	1.14	0.97	
<i>Ilumatobacter</i>	0.34	0.23	0.56	0.78	1.78	2.32	2.34	3.55	3.09	2.12	1.89	1.67	1.63	1.51	1.57	
<i>Nitrospira</i>	0.45	0.32	0.43	0.45	0.67	0.78	0.85	0.94	0.84	0.90	5.78	6.35	5.71	5.82	4.93	▼
<i>Longilinea</i>	2.13	2.29	2.66	2.45	1.17	1.21	1.41	2.02	1.92	1.86	1.43	1.43	2.23	3.21	3.45	▲
<i>Pseudorhodoferax</i>	0.93	0.42	0.58	0.87	1.06	1.46	1.56	1.87	1.68	1.55	1.82	3.42	3.16	0.79	0.73	▼▼
<i>Pseudorhodoferax</i>	0.56	0.84	0.84	0.89	0.98	0.46	1.66	0.84	0.89	0.98	0.73	0.62	0.74	0.99	0.92	▲
<i>Rhodobacter</i>	0.29	0.38	0.32	0.54	1.13	1.87	1.43	1.97	2.07	2.10	0.92	0.48	0.84	1.01	1.14	▲
<i>Flavobacterium</i>	0.39	0.43	0.58	0.43	2.40	1.94	1.72	1.67	1.53	1.34	0.94	0.89	0.93	0.73	0.63	▼
<i>Cellulophaga</i>	0.69	0.78	0.95	0.84	1.44	1.01	1.10	1.32	1.12	1.08	0.69	0.72	0.54	0.62	0.67	▲
<i>Gemmimonas</i>	0.43	0.54	0.53	0.65	0.58	0.68	0.83	0.47	0.69	0.78	0.87	1.23	1.31	1.42	1.23	
<i>Dechloromonas</i>	4.52	5.30	5.65	5.58	7.68	8.05	9.46	10.43	8.34	7.96	7.41	6.92	7.00	8.32	8.12	▲
<i>Azospira</i>	0.32	0.12	0.32	0.23	0.21	1.09	0.48	0.85	0.67	1.68	2.87	3.30	2.98	3.02	3.11	

<i>TM7_genera</i>	0.19	0.18	0.21	0.23	0.65	0.87	1.24	2.49	1.56	1.04	1.17	1.22	1.49	1.78	1.95
<i>Ferruginibacter</i>	1.34	1.26	1.40	1.42	0.89	0.97	1.23	1.43	1.63	1.15	1.61	1.43	1.33	3.37	3.56
<i>Thermomonas</i>	0.58	0.43	0.54	0.43	1.34	1.42	1.48	2.52	1.43	1.10	0.54	0.67	0.58	0.47	0.42
<i>OD1_genera</i>	1.03	1.16	1.23	1.11	0.94	0.84	0.89	0.74	0.59	0.83	0.58	0.38	0.43	0.48	0.67
<i>Simplicispira</i>	0.38	0.43	0.43	0.73	1.14	0.98	2.44	0.78	1.43	0.84	0.43	0.66	0.75	0.42	0.34
<i>Caenimonas</i>	0.59	0.54	0.67	0.73	1.34	1.05	3.32	1.29	1.60	1.62	2.84	1.08	1.06	1.23	1.34
<i>Sphingopyxis</i>	0.55	0.45	0.78	0.89	1.54	1.43	1.38	1.82	1.62	1.32	0.93	0.84	0.87	1.11	0.93
<i>Hydrogenophaga</i>	3.12	3.34	4.77	4.60	1.25	1.56	2.68	3.17	2.17	1.36	0.92	0.98	0.94	0.99	0.67
<i>Arcobacter</i>	1.87	1.29	1.23	1.87	0.38	1.48	0.64	1.02	0.48	0.53	0.36	0.48	0.43	0.43	0.58
<i>Phycisphaera</i>	0.49	0.84	0.47	0.63	0.43	0.74	0.76	0.89	0.94	0.95	1.43	1.23	1.18	1.22	1.43
<i>Terrimonas</i>	0.47	0.54	0.74	0.87	0.85	1.12	1.67	3.91	4.20	1.23	2.20	2.37	2.34	0.75	0.94
<i>Leptothrix</i>	1.91	1.84	1.88	1.09	0.84	0.73	0.84	0.92	0.83	0.99	4.18	3.96	3.33	1.02	1.04
<i>Bdellovibrio</i>	1.29	1.27	1.19	1.11	0.75	0.78	0.84	0.63	0.62	0.68	0.59	0.63	0.52	0.42	0.57
<i>Perlucidibaca</i>	1.20	1.16	1.01	1.88	0.93	0.83	0.94	0.99	0.81	0.98	0.84	0.73	0.69	1.45	1.64
<i>Sulfuritalea</i>	2.15	1.78	1.81	2.30	2.20	1.90	1.59	1.03	0.84	2.65	5.27	5.57	6.97	3.29	4.39

<i>Gp4</i>	0.93	0.95	0.74	0.84	1.12	0.72	0.89	1.04	2.30	1.54	0.89	0.56	0.53	0.73	0.85
<i>Haliscomenobacter</i>	12.59	12.65	11.89	11.97	12.67	13.50	10.49	9.30	10.99	14.24	7.49	6.15	4.99	5.02	5.34
<i>Sediminibacterium</i>	1.53	1.52	1.53	1.45	2.20	1.10	1.68	1.12	1.87	1.54	0.95	0.69	0.79	0.83	0.97
<i>Aeromonas</i>	0.72	0.68	0.92	0.83	1.25	1.56	1.78	2.45	2.23	2.12	1.54	1.45	1.40	1.12	1.45
<i>Enterobacter sp.</i>	0.82	0.93	0.69	0.93	1.03	1.10	1.21	1.34	1.26	1.17	0.79	0.76	0.85	0.92	1.32
<i>Nitrosomonas</i>	0.17	0.52	0.66	0.79	1.12	1.35	1.76	1.87	1.42	1.32	1.16	1.14	1.05	2.29	3.45
<i>Stenotrophomonas sp.</i>	1.32	1.36	1.97	2.78	2.92	3.58	4.12	5.31	4.25	3.70	1.43	1.40	1.24	3.15	4.12

▼: decrease rate > 10%; ▼▼: decrease rate > 50%;

▲: increase rate > 10%; ▲▲: increase rate > 50%.

Figure



Figure S1 - Picture of polypropylene media used in the process