

Supplementary Information for:

**Suspended sediment transport modulated by microbial activities in estuarine waters: Insights from
molecular and structural perspectives**

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Table S1. Information of key enzymes in the synthesis of EPS used in this study.

locus_tag	ftype	length_bp	gene	EC_number	COG	Description
gene 00102	CDS	996	<i>rpoS</i>			RNA polymerase sigma factor <i>RpoS</i>
gene 00599	CDS	1509	<i>rpoN</i>		COG1508	RNA polymerase sigma-54 factor
gene 02204	CDS	3720	<i>rscC</i>	2.7.13.3		Sensor histidine kinase <i>RcsC</i>
gene 03336	CDS	1398	<i>phoQ</i>	2.7.13.3	COG0642	Sensor protein <i>PhoQ</i>
gene 03337	CDS	678	<i>phoP</i>			Transcriptional regulatory protein <i>PhoP</i>
gene 03091	CDS	1428	<i>flgE</i>		COG1749	Flagellar hook protein <i>FlgE</i>
gene 03092	CDS	741	<i>flgF</i>		COG4787	Flagellar basal-body rod protein <i>FlgF</i>
gene 03093	CDS	786	<i>flgG</i>		COG4786	Flagellar basal-body rod protein <i>FlgG</i>
gene 03094	CDS	696	<i>flgH</i>			Flagellar L-ring protein
gene 03095	CDS	1101	<i>flgI</i>			Flagellar P-ring protein
gene 03098	CDS	909	<i>flgL</i>		COG1344	Flagellar hook-associated protein 3
gene 03064	CDS	777	<i>fliP</i>		COG1338	Flagellar biosynthetic protein <i>FliP</i>
gene 03069	CDS	1785	<i>fliF</i>		COG1766	Flagellar M-ring protein
gene 03070	CDS	1017	<i>fliG</i>		COG1536	Flagellar motor switch protein <i>FliG</i>
gene 03072	CDS	1359	<i>fliI</i>	7.1.2.2	COG1157	Flagellum-specific ATP synthase
gene 03076	CDS	1269	<i>fliD</i>		COG1345	Flagellar hook-associated protein 2
gene 01042	CDS	852	<i>motA</i>		COG1291	Motility protein A
gene 02110	CDS	843	<i>motB</i>		COG1360	Motility protein B
gene 03998	CDS	1239	<i>malE</i>		COG2182	Maltose/maltodextrin-binding periplasmic protein
gene 04006	CDS	1566	<i>malF</i>		COG1175	Maltose/maltodextrin transport system permease protein <i>MalF</i>
gene 04012	CDS	1629	<i>malL</i>	3.2.1.10	COG0366	Oligo-1,6-glucosidase 1
gene 03267	CDS	2451	<i>malP</i>	2.4.1.1	COG0058	Maltodextrin phosphorylase
gene 02529	CDS	2076	<i>malQ</i>	2.4.1.25	COG1640	4-alpha-glucanotransferase
gene 04004	CDS	2085	<i>malS</i>	3.2.1.1	COG0366	Periplasmic alpha-amylase
gene 03627	CDS	1065	<i>galE</i>	5.1.3.2	COG1087	UDP-glucose 4-epimerase
gene 02260	CDS	960	<i>glk</i>	2.7.1.2	COG0837	Glucokinase
gene 03806	CDS	915	<i>rmlD</i>	1.1.1.133		dTDP-4-dehydrorhamnose reductase
gene 03807	CDS	546	<i>rmlC</i>	5.1.3.13	COG1898	dTDP-4-dehydrorhamnose 3,5-epimerase
gene 01222	CDS	366	<i>pleD</i>			Response regulator <i>PleD</i>

locus_tag	ftype	length_bp	gene	EC_number	COG	Description
gene 02186	CDS	552	<i>epsL</i>	2.-.-.-	COG2148	putative sugar transferase <i>EpsL</i>
gene 02171	CDS	1131	<i>wecB</i>	5.1.3.14	COG0381	UDP-N-acetylglucosamine 2-epimerase
gene 04047	CDS	1338	<i>glmM</i>	5.4.2.10	COG1109	Phosphoglucosamine mutase
gene 03722	CDS	1362	<i>glmU</i>			Bifunctional protein <i>GlmU</i>
gene 03724	CDS	1851	<i>glmS</i>	2.6.1.16	COG0449	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]
gene 02562	CDS	840	<i>galU</i>	2.7.7.9		UTP--glucose-1-phosphate uridylyltransferase
gene 04065	CDS	1665	<i>pgi</i>	5.3.1.9	COG0166	Glucose-6-phosphate isomerase
gene 03659	CDS	1665	<i>pgm</i>	5.4.2.2	COG0033	Phosphoglucomutase
gene 02203	CDS	2217	<i>wzc</i>	2.7.10.-	COG0489	Tyrosine-protein kinase <i>wzc</i>
gene 02204	CDS	438	<i>wzb</i>	3.1.3.48	COG0394	Low molecular weight protein-tyrosine-phosphatase <i>Wzb</i>

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Table S2. Temporal expression dynamics of global regulatory genes.

Time (h)	12	15	18	21	24	30	36	42	48	Tendency
<i>rpoS</i>	7.82 ± 1.13 b	8.46 ± 1.01 ab	8.14 ± 0.13 ab	10.81 ± 0.59 ab	9.69 ± 0.76 a	9.82 ± 1.35 ab	10.61 ± 1.23 ab	10.77 ± 1.73 ab	10.87 ± 1.16 a	↑
<i>rpoN</i>	8 ± 0.22 ab	8.04 ± 0.11 a	7.81 ± 0.1 ab	7.6 ± 0.06 ab	7.68 ± 0.18 ab	7.37 ± 0.52 ab	7.5 ± 0.11 ab	7.23 ± 0.42 b	7.21 ± 0.36 b	↓
<i>rcsC</i>	7.54 ± 0.36 b	7.54 ± 0.39 b	8.16 ± 0.47 ab	8.67 ± 0.04 ab	8.41 ± 0.28 ab	8.61 ± 0.94 ab	9.09 ± 0.57 a	8.79 ± 0.11 ab	8.97 ± 0.2 a	↑
<i>phoQ</i>	8.21 ± 0.4 a	7.78 ± 0.14 a	8.04 ± 0.14 ab	6.59 ± 0.46 ab	6.92 ± 0.45 ab	6.24 ± 1.06 c	6.52 ± 0.59 ab	7.05 ± 0.79 ab	7.42 ± 0.92 ab	↓
<i>phoP</i>	9.62 ± 0.56 ab	8.99 ± 0.48 ab	9.43 ± 0.27 ab	8.06 ± 0.51 ab	8.53 ± 0.79 ab	7.9 ± 0.98 ab	8 ± 0.04 b	9.27 ± 0.76 ab	9.69 ± 0.76 a	↑

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rpoS: the general stress sigma factor; *rpoN*: the alternative sigma factor; *rcsC*: the capsule/envelope stress regulators; *phoP/Q*: the phosphate-sensing two-component system. (“↑” indicates a significant upward trend, while “↓” indicates a significant downward trend.)

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Table S3. Temporal expression dynamics of flagellar system.

Time (h)	12	15	18	21	24	30	36	42	48	Tendency
<i>flgE</i>	6.32 ± 0.42 ab	7.32 ± 1.02 a	4.7 ± 0.3 c	4.77 ± 0.26 bc	4.64 ± 0.51 c	4.17 ± 0.78 c	5.11 ± 0.4 bc	4.9 ± 0.64 c	4.44 ± 0.22 c	↓
<i>flgF</i>	5.9 ± 0.38 a	6.92 ± 0.78 a	3.98 ± 0.51 b	4.21 ± 0.35 b	4.02 ± 0.13 b	3.75 ± 0.13 b	4.61 ± 0.33 b	4.24 ± 0.26 b	4.02 ± 0.27 b	↓
<i>flgG</i>	5.8 ± 0.65 ab	6.74 ± 1.02 a	4.01 ± 0.55 c	3.74 ± 0.12 c	3.72 ± 0.4 c	3.86 ± 0.19 c	4.51 ± 0.42 bc	3.57 ± 0.24 c	3.86 ± 0.26 c	↓
<i>flgH</i>	4.71 ± 0.58 ab	5.73 ± 0.89 a	3.24 ± 0.61 bc	2.8 ± 0.46 c	2.32 ± 2.01 bc	2.87 ± 0.39 c	3.84 ± 0.47 bc	3.6 ± 0.24 bc	2.94 ± 0.75 bc	↓
<i>flgI</i>	5.59 ± 0.41 ab	6.64 ± 0.69 a	4.04 ± 0.53 cd	3.47 ± 0.37 cd	4.2 ± 0.18 cd	3.38 ± 0.25 d	4.55 ± 0.16 bc	4.28 ± 0.31 cd	3.87 ± 0.47 cd	↓

<i>flgL</i>	6.56 ± 0.45 b	8.14 ± 0.64 a	5.93 ± 0.31 bc	5.13 ± 0.42 c	4.9 ± 0.31 c	4.78 ± 0.36 c	5.13 ± 0.52 c	5.2 ± 0.22 c	5.33 ± 0.53 c	↓
<i>fliP</i>	4.23 ± 0.31 ab	4.9 ± 0.71 a	2.91 ± 0.23 ab	2.48 ± 0.91 b	2.44 ± 0.66 b	2.55 ± 0.76 b	3.75 ± 0.08 ab	3.01 ± 0.47 ab	2.27 ± 1.34 b	↓
<i>fliF</i>	6.11 ± 0.5 a	6.98 ± 0.89 a	3.73 ± 0.43 b	3.63 ± 0.7 b	3.51 ± 0.49 b	3.26 ± 0.43 b	3.72 ± 0.68 b	3.65 ± 0.14 b	3.41 ± 0.57 b	↓
<i>fliG</i>	6.82 ± 0.41 b	7.93 ± 0.7 a	4.9 ± 0.35 c	4.33 ± 0.08 c	4.76 ± 0.22 c	4.41 ± 0.22 c	5.28 ± 0.37 c	5.02 ± 0.08 c	4.67 ± 0.47 c	↓
<i>fliI</i>	5.68 ± 0.28 a	6.98 ± 0.73 a	3.52 ± 0.42 b	3.52 ± 0.21 b	3.81 ± 0.14 b	3.9 ± 0.94 b	4.23 ± 0.48 b	4.26 ± 0.27 b	4.13 ± 0.36 b	↓
<i>fliD</i>	7.29 ± 0.55 ab	9.02 ± 0.65 a	6.57 ± 0.67 bc	5.32 ± 0.1 cd	4.4 ± 0.03 d	4.2 ± 0.08 d	4.89 ± 1.05 cd	4.4 ± 1.16 d	4.49 ± 0.44 d	↓
<i>motA</i>	6.59 ± 0.02 ab	6.83 ± 0.23 a	6.72 ± 0.35 ab	6.7 ± 0.63 ab	6.79 ± 0.4 a	6.62 ± 0.61 a	6.79 ± 0.26 a	6.29 ± 0.2 ab	6.25 ± 0.32 b	↓
<i>motB</i>	5.66 ± 0.35 abc	6.16 ± 0.23 a	6.14 ± 0.14 a	5.54 ± 0.49 abc	6.33 ± 0.13 a	5.46 ± 1.34 abc	5.98 ± 0.75 ab	4.77 ± 0.39 bc	4.59 ± 0.42 c	↓

23 *fliP/F/G/I/D*: the export apparatus and filament cap proteins; *flgE/F/G/H/I/L*: the hook-basal body and rod proteins; *motA/B*: the motor torque generators. “↓” denotes a significant downward trend.

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25 **Table S4. Temporal expression dynamics of polysaccharide system.**

Time (h)	12	15	18	21	24	30	36	42	48	Tendency
<i>malE</i>	4.3 ± 0.28 c	4.53 ± 0.31 bc	4.15 ± 0.32 c	4.99 ± 0.19 abc	4.71 ± 0.5 abc	4.86 ± 0.23 abc	5.32 ± 0.03 ab	5.28 ± 0.42 ab	5.44 ± 0.2 a	↑
<i>malF</i>	4.67 ± 0.79 b	5.19 ± 0.66 ab	4.82 ± 0.37 ab	5.78 ± 0.51 ab	5.55 ± 0.35 ab	5.45 ± 0.7 ab	6.47 ± 0.63 ab	6.48 ± 0.96 ab	6.62 ± 0.74 a	↑
<i>malL</i>	4.32 ± 0.43 c	4.41 ± 0.62 bc	4.97 ± 0.24 abc	5.31 ± 0.24 abc	4.79 ± 0.34 abc	5.09 ± 1.41 abc	6.29 ± 0.69 ab	5.96 ± 1.18 abc	6.38 ± 0.95 a	↑
<i>malP</i>	7.33 ± 0.71 ab	6.72 ± 0.75 b	6.93 ± 0.42 b	7.76 ± 0.43 ab	7.63 ± 0.85 ab	7.69 ± 0.79 ab	8.43 ± 0.29 ab	8.67 ± 0.36 ab	8.73 ± 0.49 a	↑
<i>malQ</i>	6.91 ± 0.22 ab	4.87 ± 0.76 b	6.27 ± 0.17 ab	6.99 ± 0.52 ab	7.02 ± 0.92 ab	7.53 ± 1.55 a	7.7 ± 1.02 a	8.04 ± 0.13 a	7.83 ± 0.52 a	↑
<i>malS</i>	3.48 ± 0.3 b	3.41 ± 0.37 b	3.31 ± 0.63 b	4.08 ± 0.29 ab	4.03 ± 0.14 ab	4.18 ± 0.96 ab	5.03 ± 0.2 a	5.15 ± 0.61 a	5.14 ± 0.3 a	↑
<i>galE</i>	6.6 ± 1.05 ab	4.99 ± 0.69 b	5.69 ± 0.84 ab	7 ± 0.56 ab	6.66 ± 1.61 ab	6.5 ± 1.3 ab	7.31 ± 0.9 ab	7.65 ± 0.52 ab	7.82 ± 0.39 a	↑
<i>glk</i>	7.27 ± 0.44 c	7.38 ± 0.39 bc	7.39 ± 0.08 bc	7.79 ± 0.31 abc	7.65 ± 0.33 abc	7.63 ± 0.69 abc	7.97 ± 0.39 ab	8.26 ± 0.12 a	8.14 ± 0.24 a	↑
<i>rmlD</i>	7.33 ± 0.54 ab	7.18 ± 0.72 b	7.27 ± 0.15 ab	8.34 ± 0.34 a	7.63 ± 0.5 ab	7.54 ± 0.97 ab	8.09 ± 0.25 ab	7.67 ± 0.19 ab	7.7 ± 0.15 ab	↓
<i>rmlC</i>	8.31 ± 0.54 ab	8.14 ± 0.53 ab	8.04 ± 0.3 b	9.17 ± 0.17 a	8.17 ± 0.37 ab	8.02 ± 1.05 b	8.59 ± 0.32 ab	7.97 ± 0.43 b	7.84 ± 0.31 b	↓
<i>pleD</i>	6.94 ± 0.32 ab	7.3 ± 0.11 a	6.69 ± 0.3 abc	6.53 ± 0.57 abc	6.21 ± 0.41 abcd	5.29 ± 0.67 bcd	6.04 ± 0.16 bcd	5.9 ± 0.24 cd	5.54 ± 0.6 d	↓
<i>epsL</i>	6.12 ± 0.28 ab	6.47 ± 0.35 a	5.99 ± 0.2 abc	6.06 ± 0.43 abc	5.84 ± 0.07 abcd	5.5 ± 0.53 bcd	5.36 ± 0.31 bcd	5.13 ± 0.38 cd	5.03 ± 0.24 d	↓
<i>wecB</i>	7.94 ± 0.34 ab	8.71 ± 0.4 a	8.66 ± 0.28 abc	7.62 ± 0.58 ab	7.84 ± 0.56 bcd	7.27 ± 0.46 ab	7.15 ± 0.11 ab	7.25 ± 0.21 b	7.26 ± 0.25 b	↓
<i>glmM</i>	8.76 ± 0.17 a	9 ± 0.36 ab	8.72 ± 0.19 ab	8.5 ± 0.15 ab	8.39 ± 0.22 ab	8.23 ± 0.09 ab	8.46 ± 0.43 ab	8.14 ± 0.4 b	8.03 ± 0.09 b	↓
<i>glmU</i>	7.85 ± 0.09	7.84 ± 0.25	7.63 ± 0.09	7.3 ± 0.45	7.47 ± 0.44	7.13 ± 0.22	7.39 ± 0.42	7.29 ± 0.7	6.96 ± 0.66	-

<i>glmS</i>	7.62 ± 0.1	7.81 ± 0.3	7.29 ± 0.08	7.26 ± 0.48	7.56 ± 0.08	7.7 ± 0.36	7.44 ± 0.39	7.81 ± 1.01	7.99 ± 0.6	-
<i>galU</i>	9.92 ± 0.56	9.74 ± 0.54	10.17 ± 0.4	9.95 ± 0.63	9.86 ± 0.4	9.64 ± 0.62	9.95 ± 0.48	9.33 ± 0.64	9.74 ± 0.53	-
<i>pgi</i>	8.68 ± 0.61	9 ± 0.65	8.94 ± 0.16	9.67 ± 0.19	8.92 ± 0.35	8.96 ± 0.98	9.56 ± 0.41	8.89 ± 0.55	9.14 ± 0.57	-
<i>pgm</i>	7.87 ± 0.3	7.71 ± 0.48	8.04 ± 0.21	7.86 ± 0.79	7.66 ± 0.35	7.78 ± 0.91	8.06 ± 0.97	7.64 ± 1.08	7.81 ± 1.31	-
<i>wzc</i>	10.13 ± 0.48	10.26 ± 0.57	10.35 ± 0.19	11.22 ± 0.29	10.24 ± 0.46	10.29 ± 1.2	10.85 ± 0.26	10.31 ± 0.44	10.32 ± 0.46	-
<i>wzb</i>	6.95 ± 0.86	7.26 ± 0.41	6.78 ± 0.18	7.65 ± 0.69	7.03 ± 0.48	6.86 ± 1.12	7.64 ± 0.51	6.51 ± 0.67	6.65 ± 0.53	-

26 *malE/F/P/Q/L/S*: maltose transport; *glk*, *pgi*, *pgm*: central sugar metabolism; *galU* & *galE*: UDP-sugar synthesis; *glmS/M/U*: UDP-GlcNAc synthesis; *wecB*: UDP-ManNAc synthesis; *rmlC/D*: dTDP-rhamnose synthesis; *epsL*:
27 polysaccharide export; *pleD*: c-di-GMP synthesis; *wzc/wzb*: tyrosine kinase regulatory system. (“↑” indicates a significant upward trend, “↓” indicates a significant downward trend, “-” indicates no significant change trend.)

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The D_m , D_{50} , and D_{90} of the ISD showed no significant change throughout the experimental period (fig S1.a-c). However, the ISD bioflocculation process featured a triphasic pattern: rapid flocculation, flocculation equilibrium, and deflocculation (fig S1.d-f). During Stage 1 (12–18 h), the average D_m , D_{50} , and D_{90} values increased rapidly to 155.16 μm , 128.20 μm , and 209.82 μm , respectively, with corresponding slopes of 5.06, 6.12, and 4.30. Subsequently, an equilibrium phase was reached between 21 and 30 h, during which the D_m value slightly decreased to 152.98 μm . This stabilization was primarily attributed to the relative constancy of D_{50} (slope = 0.02) and D_{90} (slope = -0.63). Ultimately, when the slopes of D_m , D_{50} , and D_{90} for ISD all turned negative (-0.68, -1.43, and -1.77, respectively), it indicated that the system entered the deflocculation phase during Stage 3 (36–48 h).

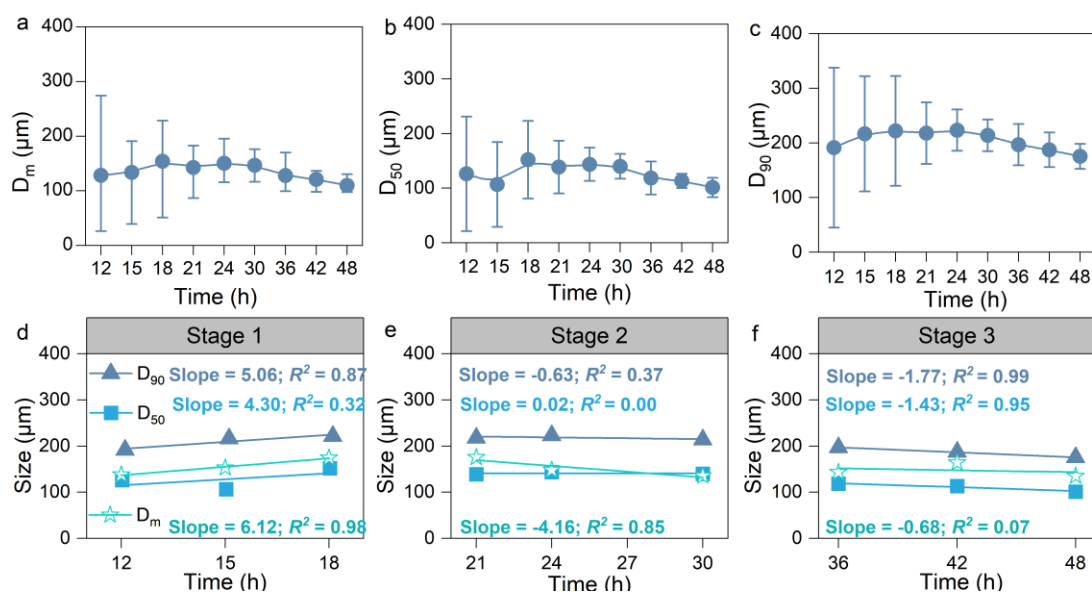


Figure S1. Temporal variations in (a) mean diameter (D_m), (b) D_{50} , (c) D_{90} , and stage-resolved floc size dynamics and slope transitions in ISD in (d) phase one (12–18 h), (e) phase two (21–30 h), and (f) phase three (36–48 h). (ISD: illite mineral and *S. decontaminans* mixed system.)

Under pure culture conditions, *S. decontaminans* entered the logarithmic growth phase at 9 hours post-inoculation and subsequently transitioned to the stationary phase between 42 and 72 hours. In the ISD, the *S. decontaminans* population was predominantly in the stationary phase, without significant changes in abundance during the 12–48 h period (fig S2).

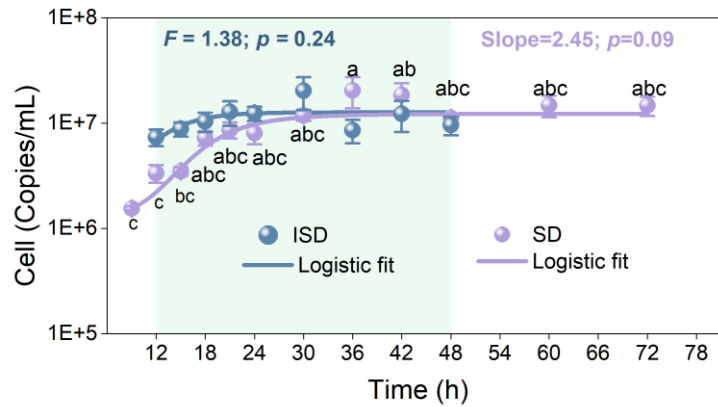


Figure S2. Temporal variations of bacteria abundance in ISD (blue) and SD (purple). (ISD: illite mineral and *S. decontaminans* mixed system. Different lowercase letters represented significant differences between treatments ($P < 0.05$) by HSD test.)

During this period, the total EPS content and polysaccharides decreased significantly in the ISD (fig S3a,b), but without significant changes in protein. The POC content in the ISD increased significantly from 16.63 ± 7.16 mg/L at 12 h to 48.59 ± 20.49 mg/L at 48 h, while the DOC decreased significantly from 262.88 ± 86.54 mg/L at 12 h to 115.81 ± 26.19 mg/L at 48 h (fig S3d-e). The turbidity level of ISD increased significantly from 93.26 ± 16.16 NTU at 12 h to 131.40 ± 18.56 NTU at 48 h (fig S3g). The zeta potential showed no significant variation during the experiment and remained at a low absolute level ($|14.78 \pm 1.87|$) (fig S3h). Besides, the accumulation of organic matter in the ISD led to a significant decrease in pH (fig S3i).

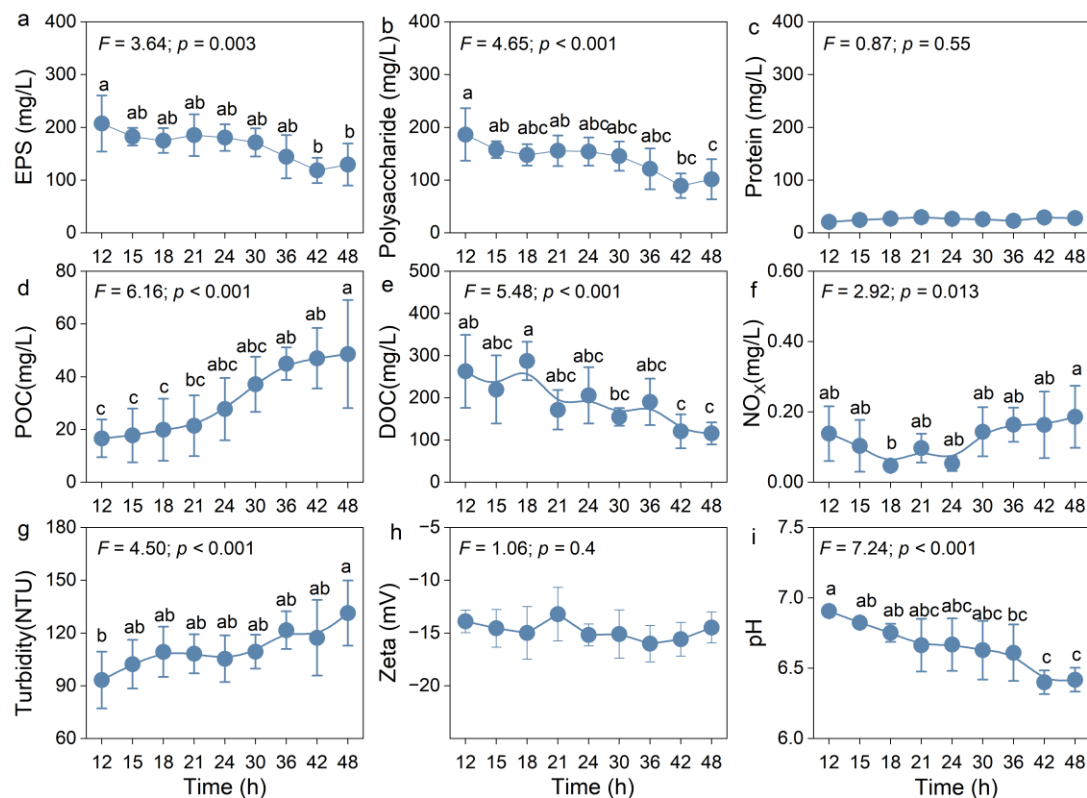


Figure S3. Temporal variations in (a) EPS, (b) polysaccharide, (c) protein, (d) particulate organic carbon (POC), (e) dissolved organic carbon (DOC), (f) $\text{NO}_x = \text{NO}_2^- + \text{NO}_3^- + \text{NH}_4^+$, (g) turbidity (NTU), (h) Zeta, (i) pH value in ISD. (ISD: illite mineral and *S. decontaminans* mixed system. Different lowercase letters represented significant differences between treatments ($P < 0.05$) by HSD test.)