Fine-scale bacterioplankton turnover across a narrow low-salinity estuarine gradient in northern Vietnam

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Supplementary Material

Table S1. Sequencing depth, read retention, and quality-filtering statistics across successive DADA2 processing stages for the four sequencing libraries. Read counts are reported from the original sequencing-processing summary.

Sample_ID	Associated Station	Raw Reads	Quality Filtered	Merged Reads	Non-Chimeric Reads	Retention Rate (%)
748_T_02	E1	48,915	43,210	40,512	37,218	76.1%
748_T_03	E2	42,110	36,912	34,215	31,984	76.0%
748_T_04	E3	51,045	45,118	42,109	38,912	76.2%
748_T_05	E4	62,318	55,219	52,114	47,515	76.2%
Total	-	204,388	180,459	168,950	155,629	76.1% (Mean)

Table S2. Genus-level taxonomic assignments and abundances of the 25 most abundant ASVs within the study-specific four-station core. Core ASVs were operationally defined as ASVs detected in all four sequencing libraries (100% prevalence; n = 216) without an additional abundance threshold. ASVs are ranked by total read abundance across the four rarefied libraries.

Rank	Total reads	E1	E2	E3	E4	Genus
1	1352	348	363	341	300	hgcI clade
2	874	189	192	234	259	hgcI clade
3	684	270	242	131	41	Unassigned
4	667	243	221	154	49	C39

Rank	Total reads	E1	E2	E3	E4	Genus
5	666	102	140	225	199	hgcI clade
6	552	138	185	139	90	*Polynucleobacter*
7	540	72	86	148	234	hgcI clade
8	511	95	117	169	130	hgcI clade
9	438	67	90	193	88	CL500-29 marine group
10	391	94	140	107	50	*Polynucleobacter*
11	384	106	121	92	65	hgcI clade
12	372	130	100	128	14	C39
13	362	98	70	102	92	hgcI clade
14	359	146	128	77	8	C39
15	356	171	126	46	13	*Ottowia*
16	327	73	86	94	74	hgcI clade
17	327	110	86	80	51	Unassigned
18	326	70	64	126	66	CL500-29 marine group
19	316	71	45	113	87	CL500-29 marine group
20	283	133	114	30	6	*Limnohabitans*
21	278	121	105	37	15	*Ramlibacter*
22	272	80	92	87	13	*Ramlibacter*
23	264	81	41	18	124	*Ottowia*
24	258	40	69	96	53	hgcI clade
25	254	39	35	98	82	*Candidatus Methylopumilus*

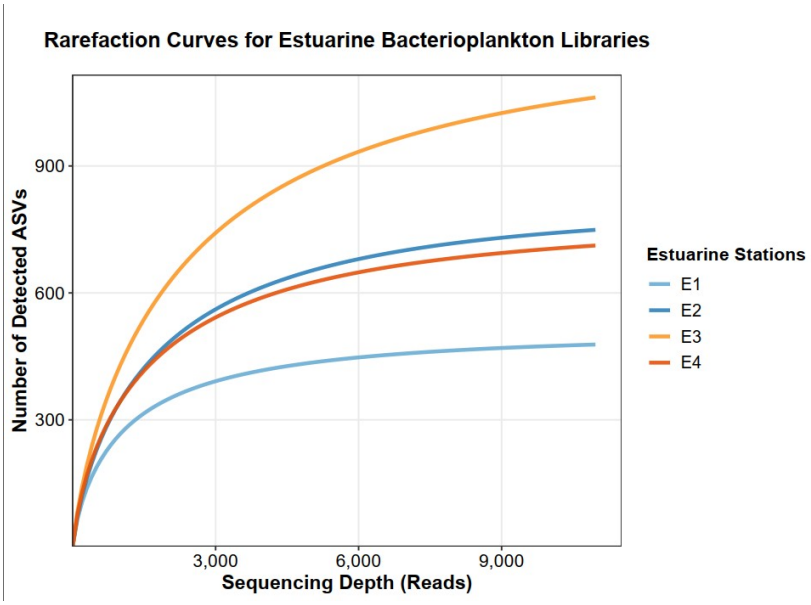


Figure S1. Rarefaction curves for the four bacterioplankton libraries (E1–E4). The standardized depth used for diversity analyses (10,968 reads per library) is indicated.

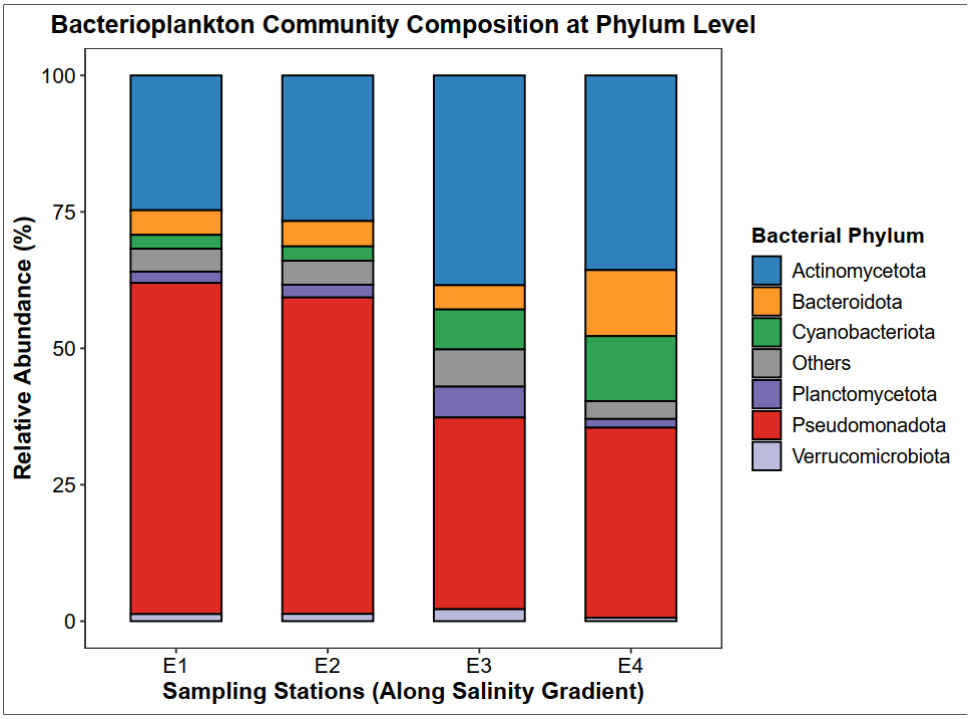


Figure S2. Relative abundance of major bacterial phyla across the four sampling stations (E1–E4).

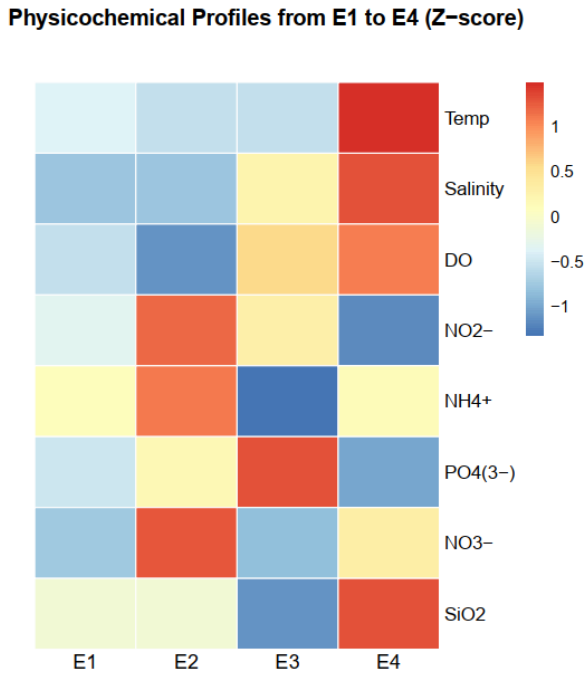


Figure S3. Physicochemical profiles across the four sampling stations (E1–E4), represented as row-standardized Z-scores for visualization of among-station variation.

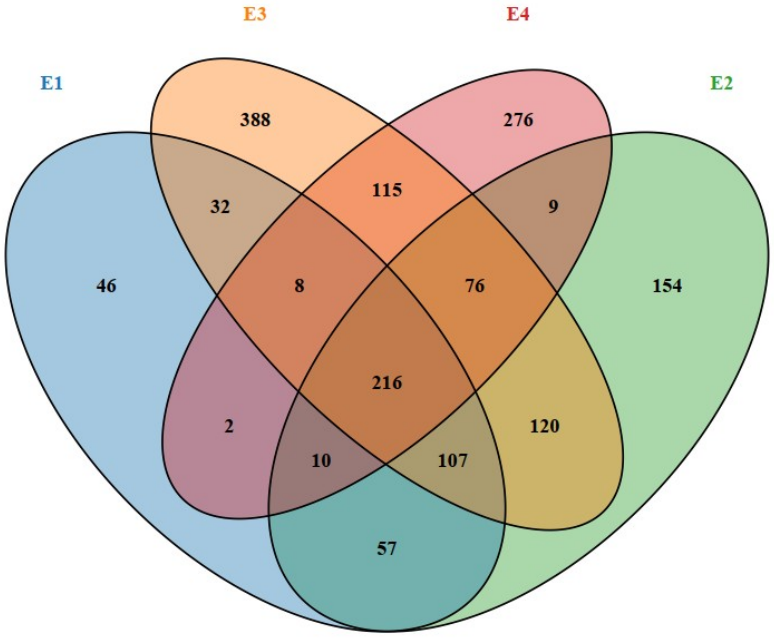


Figure S4. Four-way Venn diagram showing ASV occurrence across the four bacterioplankton libraries. A total of 216 ASVs were detected in all four libraries (100% prevalence) and were operationally defined as the study-specific core.

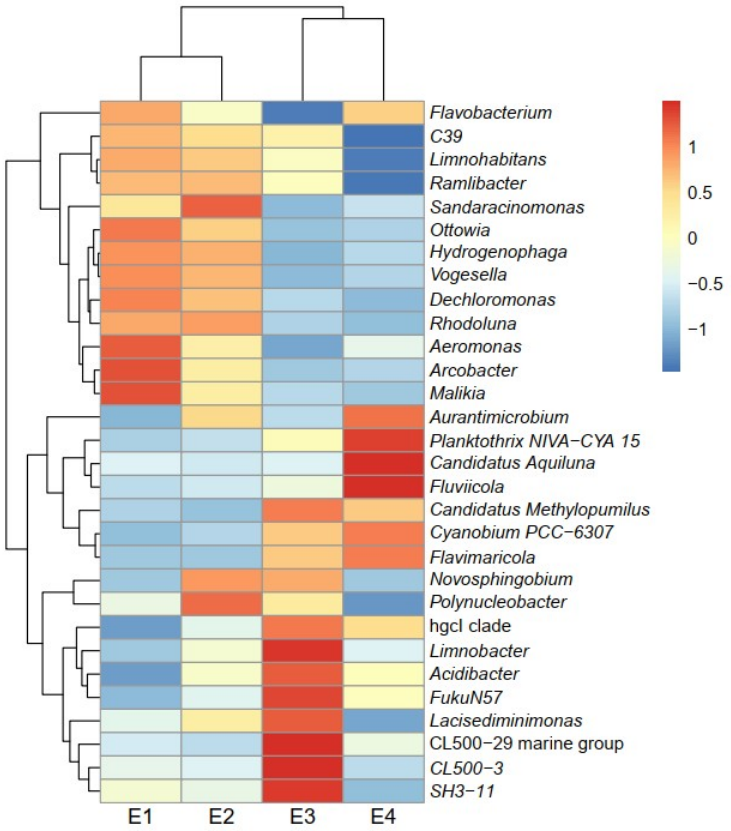


Figure S5. Hierarchical clustering heatmap of the 30 most abundant bacterial taxa across the four sampling stations. Relative abundances were log1p-transformed and standardized as row-wise Z-scores; clustering was based on Euclidean distance with average linkage.