

Supplementary materials

Table S1. Oligonucleotide primers used in this study.

Target gene	Primer	Sequence (5' to 3')	Predicted size (bp)	Reference
16S rDNA	27-F	AGAGTTTGATCCTGGCTCAG	1,500	[13]
	1492-R	TACGGCTACCTTGTACGAC		
<i>tdh</i>	<i>tdh</i> -F	GTAAAGGTCTCTGACTTTTGGAC	269	[13]
	<i>tdh</i> -R	GGAATAGAACCTTCATCTTCACC		
<i>trh</i>	<i>trh</i> -F	TTGGCTTCGATATTTTCAGTATCT	500	[13]
	<i>trh</i> -R	CATAACAAACATATGCCCATTTC		

Table S2. The identified GIs in the six *V. parahaemolyticus* genomes.

<i>V. parahaemolyticus</i> isolate	GI ID	Location	Scaffold size (bp)	Start (bp)	End (bp)	CDS gene	COG gene
L7_7	GI 1	Scaffold 2	537,433	520,198	533,845	14	10
	GI 2	Scaffold 11	165,828	82,015	105,291	15	9
	GI 3	Scaffold 12	163,666	3,027	13,476	11	5
	GI 4	Scaffold 15	117,372	9,480	25,462	20	8
	GI 5	Scaffold 18	87,591	38,174	65,569	24	23
	GI 6	Scaffold 20	67,327	18,229	35,367	20	14
N1-22	GI 1	Scaffold 1	1,138,216	332,673	418,529	79	16
	GI 2	Scaffold 2	851,121	215,670	240,066	26	18
	GI 3	Scaffold 2	851,121	332,299	345,198	10	5
	GI 4	Scaffold 2	851,121	86,080	95,320	7	5
	GI 5	Scaffold 4	558,996	368,668	406,329	29	13
	GI 6	Scaffold 6	348,360	182,705	213,595	24	12
	GI 7	Scaffold 7	249,645	149,195	180,176	29	19
	GI 8	Scaffold 9	133,586	913	13,741	13	6
	GI 9	Scaffold 10	124,863	21,112	35,850	18	12
N3-33	GI 1	Scaffold 1	815,932	679,258	690,241	11	4
	GI 2	Scaffold 1	815,932	793,795	810,371	12	9
	GI 3	Scaffold 5	329,323	274,185	297,314	33	7
	GI 4	Scaffold 7	237,962	149,488	168,293	16	12
	GI 5	Scaffold 9	184,635	2,319	9,214	7	4
	GI 6	Scaffold 10	161,468	1,073	7,750	8	5
N4_46	GI 1	Scaffold 1	816,784	1,601	15,956	15	9
	GI 2	Scaffold 1	816,784	687,093	713,968	21	15
	GI 3	Scaffold 8	202,489	101,075	105,707	7	1
	GI 4	Scaffold 8	202,489	127,554	144,961	16	12
	GI 5	Scaffold 14	99,227	51,180	63,901	13	6
	GI 6	Scaffold 15	60,986	489	9,030	12	2
N8_42	GI 1	Scaffold 1	1,070,881	782,122	802,295	26	9
	GI 2	Scaffold 3	552,513	151,970	183,907	28	13
	GI 3	Scaffold 4	508,421	499,417	503,439	3	3
	GI 4	Scaffold 5	436,482	292,305	308,974	15	12
	GI 5	Scaffold 7	185,860	69,424	87,114	16	11
	GI 6	Scaffold 9	160,850	4,534	22,139	13	7
	GI 7	Scaffold 12	122,913	19,798	32,666	17	11
Q8-15	GI 1	Scaffold 1	1,750,007	798,843	822,531	23	9

GI 2	Scaffold 2	1,320,740	1,232,265	1,249,025	16	11
GI 3	Scaffold 2	1,320,740	1,355	13,342	17	8
GI 4	Scaffold 4	538,126	176,674	198,941	19	10
GI 5	Scaffold 6	109,343	88,831	102,356	9	8

Table S3. The identified prophages in the *V. parahaemolyticus* genomes.

<i>V. parahaemolyticus</i> isolate	Prophage ID	Location	Scaffold size (bp)	Start (bp)	End (bp)	Possible phage	NCBI accession No.
N1-22	Ph01	Scaffold 2	851,121	232,499	264,407	<i>Vibrio</i> _phage_K139	NC_003313
N4-46	Ph01	Scaffold 20	47,985	160	22,773	<i>Pseudomonas</i> _phage_D3	NC_002484
N8-42	Ph01	Scaffold 5	436,482	267,809	300,776	<i>Vibrio</i> _phage_K139	NC_003313
	Ph02	Scaffold 1	1,070,881	785,045	795,581	<i>Vibrio</i> _phage_fs2	NC_001956
Q8-15	Ph01	Scaffold 2	1,320,740	467,112	489,931	<i>Pseudomonas</i> _phage_D3	NC_002484

Table S4. The identified ISs in the *V. parahaemolyticus* genomes.

<i>V. parahaemolyticus</i> isolate	IS ID	Location	Scaffold size (bp)	Start (bp)	End (bp)	IS Family
L7-7	IS001	Scaffold 30	17,420	14,615	15,847	IS3
	IS002	Scaffold 42	1,055	2	1,055	IS5
	IS003	Scaffold 5	317,607	259,342	260,304	IS5
N3-33	IS001	Scaffold 10	161,468	2,682	3,711	IS3
N8-42	IS001	Scaffold 5	436,482	299,512	300,931	IS91
Q8-15	IS001	Scaffold 1	1,750,007	257,621	258,583	IS5

Table S5. The identified repeats at the end of scaffolds of the *V. parahaemolyticus* genomes

<i>V. parahaemolyticus</i> isolate	Repeat ID	Location	Scaffold size (bp)	Repeat		
				Start	End	Length (bp)
L7-7	Scaffold 1_TR01	Scaffold 1	640,149	1	788	788
	Scaffold 1_TR02	Scaffold 1	640,149	1	922	922
	Scaffold 6_TR22	Scaffold 6	314,969	314,270	314,969	700
	Scaffold 11_TR29	Scaffold 11	165,828	1	542	542
	Scaffold 16_TR38	Scaffold 16	93,035	1	284	284
	Scaffold 19_TR39	Scaffold 19	72,724	1	492	492
N8-42	Scaffold 4_TR14	Scaffold 4	508,421	2	887	886
	Scaffold 15_TR47	Scaffold 15	52,447	51,920	52,447	528
	Scaffold 25_TR56	Scaffold 25	9,075	7,847	9,072	1,226
	Scaffold 35_TR63	Scaffold 35	1,131	507	1,131	625
N3-33	Scaffold 18_TR41	Scaffold 18	61,769	1	554	554
	Scaffold 42_TR57	Scaffold 42	887	1	887	887
N4-46	Scaffold 6_TR12	Scaffold 6	315,367	1	400	400
	Scaffold 15_TR34	Scaffold 15	60,986	59,989	60,986	998
	Scaffold 16_TR35	Scaffold 16	60,880	60,576	60,880	305
	Scaffold 18_TR39	Scaffold 18	52,044	51,287	52,044	758
	Scaffold 28_TR46	Scaffold 28	9,441	8,222	9,441	1,220
Q8-15	Scaffold 7_TR38	Scaffold 7	89,261	88,746	89,261	516
	Scaffold 32_TE45	Scaffold 32	379	272	379	108