

Title: Emergence of multidrug resistant, *ctx* negative seventh pandemic *Vibrio cholerae* O1 El Tor sequence type (ST) 69 in coastal water of Kerala, India

Ahthors:

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Supplementary Table 1: Sequence information of the isolate VC6

S. No	Sequence Information	VC6
Genome Statistics		
1.	Contigs	75
2.	Genome Length	4018937
3.	GC Content	47.4938
4.	Contig L50	6
5.	Contig N50	204396
Annotation Statistics		
1.	tRNA	75
2.	rRNA	4
3.	CDS	3724
4.	CDS Ratio	0.92661315
5.	Hypothetical CDS	633
6.	Hypothetical CDS Ratio	0.2714823
7.	PLFAM CDS	3640
8.	PLFAM CDS Ratio	0.97744364
Genome Quality		
1.	Coarse Consistency	99.8
2.	Fine Consistency	99.4
3.	CheckM Completeness	100
4.	Genome Quality	Good

Supplementary Table 2: List of genes found in *Vibrio cholerae* isolate genome (VC6) with gene description

Genes found	
Relevance	Gene(s)
Specie specific gene	<i>ompW</i>
Serogroup specific	<i>rfbV_O1</i>
Biotypespecific	<i>tcpA_et3</i>
7th Pandemic	VC2346
Virulence	<i>als, VgrG, makA, rtxA, ompT, ompU, hlyA, toxR, VasX, mshA</i>
Mobile Genetic Elements	None
Phage susceptibility	None
Pathogenicity Islands	VPI1_VC0827, VSP1_VC0183, VPI2_VC1783, VPI2_VC1776, VPI2_VC1758, VPI2_VC1790, VSP1_VC0175, VSP1_VC0180, VPI2_VC1765, VSP2_VC0493, VSP2_VC0514, VSP1_VC0178, VPI1_VC0847, VPI1_VC0819, VSP2_VC0490, VSP2_VC0504, VPI2_VC1809, VPI2_VC1760, VSP2_VC0512, VSP2_VC0502, VSP2_VC0498, VSP2_VC0516, VSP1_VC0185, VPI1_VC0840
Antibiotic Resistance	<i>sul2, parE, dfrA1, strA, catB9, strB, parC, gyrA, VC1786ICE9_floR</i>

Genes description						
Gene for 7th Pandemic						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
VC2346	100	687 / 687	VC_6_contig_15	46064..46750	7 th pandemic <i>V. cholerae</i> strain specific gene (vc2346)	AE003852

Pathogenicity Islands						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
VPI1_VC0819	100	1626 /1626	VC_6_contig_10	58957..60582	Aldehyde dehydrogenase (<i>Vibrio cholerae</i> pathogenicity island 1, VPI-1)	AE003852
VPI1_VC0827	100	411 / 411	VC_6_contig_10	45948..46358	Toxin co-regulated pilus biosynthesis protein H (<i>Vibrio cholerae</i> pathogenicity island 1, VPI-1)	AE003852
VPI1_VC0840	100	1881 /1881	VC_6_contig_10	32479..34359	Accessory colonization factor <i>AcfB</i> (<i>Vibrio cholerae</i> pathogenicity island 1, VPI-1)	AE003852
VPI1_VC0847	100	1269 /1269	VC_6_contig_10	21729..22997	Integrase, phage family (<i>Vibrio cholerae</i> pathogenicity island 1, VPI-1)	AE003852
VPI2_VC1758	100	1236 /1236	VC_6_contig_8	39399..40634	Integrase, phage family (<i>Vibrio cholerae</i> pathogenicity island 2, VPI-2)	AE003852
VPI2_VC1760	100	2823 /2823	VC_6_contig_8	35895..38717	Helicase, putative (<i>Vibrio cholerae</i> pathogenicity island 2, VPI-2)	AE003852
VPI2_VC1765	100	3069 /3069	VC_6_contig_8	27869..30937	Type I restriction enzyme <i>HsdR</i> , putative (<i>Vibrio cholerae</i> pathogenicity island 2, VPI-2)	AE003852
VPI2_VC1776	100	897 /897	VC_6_contig_8	9635..10531	N-acetylneuraminate lyase, putative (<i>Vibrio cholerae</i> pathogenicity island 2, VPI-2)	AE003852

VPI2_VC1783	100	1137 /1137	VC_6_contig_8	3841..4977	N-acetylglucosamine-6-phosphate deacetylase (<i>Vibrio cholerae</i> pathogenicity island 2, VPI-2)	AE003852
VPI2_VC1790	100	306 /345	VC_6_contig_46	878..1183	Transposase <i>OrfAB</i> , subunit A (<i>Vibrio cholerae</i> pathogenicity island 2, VPI-2)	AE003852
VPI2_VC1809	100	231 /231	VC_6_contig_2	487797..488027	Transcriptional regulator, putative (<i>Vibrio cholerae</i> pathogenicity island 2, VPI-2)	AE003852
VSP1_VC0175	100	1599 /1599	VC_6_contig_14	101070..102668	Deoxycytidylate deaminase-related protein (<i>Vibrio cholerae</i> seventh pandemic island 1, VSP-1)	AE003852
VSP1_VC0178	100	1068 /1068	VC_6_contig_14	97606..98673	Patatin-related protein (<i>Vibrio cholerae</i> seventh pandemic island1, VSP-1)	AE003852
VSP1_VC0180	99.94	1755 /1755	VC_6_contig_14	94525..96279	ThiF domain-containing protein (<i>Vibrio cholerae</i> seventh pandemic island 1, VSP-1)	AE003852
VSP1_VC0183	100	2112 /2112	VC_6_contig_14	91540..93651	Uncharacterized protein (<i>Vibrio cholerae</i> seventh pandemic island1, VSP-1)	AE003852
VSP1_VC0185	100	1215 /1215	VC_6_contig_14	88631..89845	Transposase, putative (<i>Vibrio cholerae</i> seventh pandemic island1, VSP-1)	AE003852
VSP2_VC0490	100	1962 /1962	VC_6_contig_13	116029..117990	Uncharacterized protein (<i>Vibrio cholerae</i> seventh pandemic island2, VSP-2)	AE003852
VSP2_VC0493	100	876 /876	VC_6_contig_13	119918..120793	Uncharacterized protein (<i>Vibrio cholerae</i> seventh pandemic island2, VSP-2)	AE003852
VSP2_VC0498	100	441 /441	VC_6_contig_27	1559..1999	Ribonuclease HI, putative (<i>Vibrio cholerae</i> seventh	AE003852

					pandemic island2, VSP-2)	
VSP2_VC0502	100	525 /525	VC_6_contig_27	5080..5604	Type IV pilin, putative (<i>Vibrio cholerae</i> seventh pandemic island2, VSP-2)	AE003852
VSP2_VC0504	100	228 /228	VC_6_contig_9	839..1066	Uncharacterized protein (<i>Vibrio cholerae</i> seventh pandemic island2, VSP-2)	AE003852
VSP2_VC0512	100	1590 /1590	VC_6_contig_9	5281..6870	Methyl-accepting chemotaxis protein (<i>Vibrio cholerae</i> seventh pandemic island 2, VSP-2)	AE003852
VSP2_VC0514	100	1881 /1881	VC_6_contig_9	9136..11016	Methyl-accepting chemotaxis protein (<i>Vibrio cholerae</i> seventh pandemic island 2, VSP-2)	AE003852
VSP2_VC0516	100	1242 /1242	VC_6_contig_9	12742..13983	Phage integrase (<i>Vibrio cholerae</i> seventh pandemic island 2, VSP-2)	AE003852

Other ICE genes						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
VC1786ICE1	100	1854 /1854	VC_6_contig_9	168872..170725	Conserved hypothetical protein	JN648379
VC1786ICE10	100	540 /540	VC_6_contig_24	2817..3356	Putative transposase	JN648379
VC1786ICE14	100	1309 /1353	VC_6_contig_43	142..1450	Transposase	JN648379
VC1786ICE15	100	1212 /1212	VC_6_contig_44	36..1247	Transposase Mutator family	JN648379
VC1786ICE16_mutL	100	503 /504	VC_6_contig_11	1..503	MutL protein	JN648379
VC1786ICE17	100	270 /270	VC_6_contig_11	656..925	Error-prone repair proteinUmuC	JN648379
VC1786ICE18	100	450 /450	VC_6_contig_11	933..1382	DNA polymerase V	JN648379

VC1786ICE19	100	906 /906	VC_6_contig_11	2022..2927	DNA polymerase III subunit epsilon	JN648379
VC1786ICE2	100	1242 /1242	VC_6_contig_9	170855..172096	Phage integrase family protein	JN648379
VC1786ICE20	100	300 /300	VC_6_contig_11	3015..3314	Conserved hypothetical plasmid-related protein	JN648379
VC1786ICE21	100	921 /921	VC_6_contig_11	3632..4552	Conserved hypothetical protein	JN648379
VC1786ICE22	100	801 /801	VC_6_contig_11	4570..5370	Conserved hypothetical protein	JN648379
VC1786ICE23	100	3690 /3690	VC_6_contig_11	5915..9604	Conserved hypothetical protein	JN648379
VC1786ICE24	100	3741 /3741	VC_6_contig_11	9609..13349	Conserved hypothetical protein	JN648379
VC1786ICE25_ <i>pglZ</i>	100	2304 /2304	VC_6_contig_11	13362..15665	<i>PglZ</i> domain protein	JN648379
VC1786ICE26	100	2052 /2052	VC_6_contig_11	15704..17755	ATP-dependent protease	JN648379
VC1786ICE27	100	771 /771	VC_6_contig_11	17782..18552	Conserved hypothetical protein	JN648379
VC1786ICE28	100	816 /816	VC_6_contig_11	18587..19402	Conserved hypothetical protein	JN648379
VC1786ICE29_ <i>traI</i>	100	2151 /2151	VC_6_contig_11	19524..21674	Conjugal transfer pilus assembly protein <i>TraI</i>	JN648379
VC1786ICE3	100	975 /975	VC_6_contig_9	172370..173344	Putative PRTRC system protein D	JN648379
VC1786ICE30_ <i>traD</i>	100	1821 /1821	VC_6_contig_11	21723..23543	Conjugal transfer pilus assembly protein <i>TraD</i>	JN648379
VC1786ICE31	100	561 /561	VC_6_contig_11	23553..24113	Conserved hypothetical protein	JN648379
VC1786ICE32	100	636 /636	VC_6_contig_11	24100..24735	integrating conjugative element membrane protein	JN648379
VC1786ICE33	100	588 /588	VC_6_contig_11	24762..25349	Conserved hypothetical protein	JN648379
VC1786ICE34_ <i>traL</i>	100	282 /282	VC_6_contig_11	25638..25919	Type IV conjugative transfer system protein <i>TraL</i>	JN648379

VC1786ICE35_ <i>traE</i>	100	627 /627	VC_6_contig_11	25916..26542	Type IV conjugative transfer system protein <i>TraE</i>	JN648379
VC1786ICE36_ <i>traK</i>	100	900 /900	VC_6_contig_11	26523..27422	Conjugal transfer pilus assembly protein <i>TraK</i>	JN648379
VC1786ICE37_ <i>traB</i>	100	1290 /1290	VC_6_contig_11	27425..28714	<i>TraB</i> pilus assembly family protein	JN648379
VC1786ICE38_ <i>traV</i>	100	651 /651	VC_6_contig_11	28711..29361	Type IV conjugative transfer system protein <i>TraV</i>	JN648379
VC1786ICE39_ <i>traA</i>	100	387 /387	VC_6_contig_11	29358..29744	Conjugal transfer pilus assembly protein <i>TraA</i>	JN648379
VC1786ICE4	100	444 /444	VC_6_contig_9	173809..174252	Conserved hypothetical protein	JN648379
VC1786ICE40	100	834 /834	VC_6_contig_11	29923..30756	Conserved hypothetical protein	JN648379
VC1786ICE41	100	939 /939	VC_6_contig_11	30749..31687	Conserved hypothetical protein	JN648379
VC1786ICE42	100	693 /693	VC_6_contig_11	31819..32511	Putative thiol	JN648379
VC1786ICE43_ <i>traC</i>	100	2400 /2400	VC_6_contig_11	32511..34910	Type-IV secretion system protein <i>TraC</i>	JN648379
VC1786ICE44	100	348 /348	VC_6_contig_11	34903..35250	Conserved hypothetical protein	JN648379
VC1786ICE45_ <i>trbI</i>	100	513 /513	VC_6_contig_11	35234..35746	K12062 conjugal transfer pilin signal peptidase <i>TrbI</i>	
VC1786ICE46_ <i>traW</i>	100	1125 /1125	VC_6_contig_11	35757..36881	Type-F conjugative transfer system protein <i>TraW</i>	JN648379
VC1786ICE47_ <i>traU</i>	100	1029 /1029	VC_6_contig_11	36865..37893	Conjugative transfer pilus assembly protein <i>TraU</i>	JN648379
VC1786ICE48_ <i>traN</i>	100	3693 /3693	VC_6_contig_11	37896..41588	type-F conjugative transfer system mating-pair stabilization protein <i>TraN</i>	JN648379
VC1786ICE49	100	1617 /1617	VC_6_contig_11	41679..43295	Putative SMC protein	JN648379

VC1786ICE5	100	1173 /1173	VC_6_contig_9	174263..175435	UV repair DNA polymerase	JN648379
VC1786ICE50	100	756 /756	VC_6_contig_11	43375..44130	<i>IstB</i> ATP binding domain-containing protein	JN648379
VC1786ICE51	100	1509 /1509	VC_6_contig_11	44120..45628	Integrase catalytic subunit <i>IstA</i>	JN648379
VC1786ICE52	100	1080 /1080	VC_6_contig_11	45727..46806	Putative SMC domain protein	JN648379
VC1786ICE53	100	684 /684	VC_6_contig_11	46974..47657	Endonuclease I	JN648379
VC1786ICE54	100	603 /603	VC_6_contig_11	47766..48368	Conserved hypothetical protein	JN648379
VC1786ICE55_ssb	100	420 /420	VC_6_contig_11	49078..49497	Single-strand binding protein <i>ssb</i>	JN648379
VC1786ICE56_bet	100	819 /819	VC_6_contig_11	49577..50395	Phage recombination protein <i>Bet</i>	JN648379
VC1786ICE57	100	1017 /1017	VC_6_contig_11	50681..51697	Putative phage-type endonuclease	JN648379
VC1786ICE58_cobs	100	960 /960	VC_6_contig_11	51907..52866	Cobaltochelatase, <i>CobS</i> subunit	JN648379
VC1786ICE59	100	768 /768	VC_6_contig_11	52866..53633	Conserved hypothetical protein	JN648379
VC1786ICE6	100	1309 /2979	VC_6_contig_43	142..1450	Transposase Tn3 family protein	JN648379
VC1786ICE60	100	954 /954	VC_6_contig_11	53732..54685	Conserved hypothetical plasmid-related protein	JN648379
VC1786ICE61	100	441 /441	VC_6_contig_11	54747..55187	Conserved hypothetical protein	JN648379
VC1786ICE62	100	1656 /1656	VC_6_contig_11	55257..56912	Conserved hypothetical protein	JN648379
VC1786ICE63	100	498 /498	VC_6_contig_11	56997..57494	DNA repair protein <i>RadC</i>	JN648379
VC1786ICE64	100	342 /342	VC_6_contig_11	57494..57835	Conserved hypothetical protein	JN648379
VC1786ICE65	100	1074 /1074	VC_6_contig_11	57926..58999	Putative zinc-binding domain of primase-helicase family	JN648379

VC1786ICE66	100	708 /708	VC_6_contig_11	59089..59796	Conserved hypothetical protein	JN648379
VC1786ICE67	100	702 /702	VC_6_contig_11	60469..61170	Conserved hypothetical protein	JN648379
VC1786ICE68	100	960 /960	VC_6_contig_11	63602..64561	Integron integrase	JN648379
VC1786ICE69_traF	100	945 /945	VC_6_contig_11	64818..65762	Type-F conjugative transfer system pilin assembly protein <i>TraF</i>	JN648379
VC1786ICE7	100	1494 /1494	VC_6_contig_24	6147..7640	Transposase <i>InsA</i>	JN648379
VC1786ICE70_traH	100	1389 /1389	VC_6_contig_11	65765..67153	Conjugative transfer pilus assembly protein <i>TraH</i>	JN648379
VC1786ICE71_traG	100	3570 /3570	VC_6_contig_11	67157..70726	Conjugal transfer mating pair stabilization protein <i>TraG</i>	JN648379
VC1786ICE72_flhC	100	534 /534	VC_6_contig_11	71248..71781	Flagellar transcriptional activator <i>FlhC</i>	JN648379
VC1786ICE73_flhD	100	300 /300	VC_6_contig_11	71778..72077	Flagellar transcriptional activator <i>FlhD</i>	JN648379
VC1786ICE74	100	549 /549	VC_6_contig_11	72074..72622	Lytic transglycosylase	JN648379
VC1786ICE75	100	663 /663	VC_6_contig_11	72609..73271	Conserved hypothetical protein	JN648379
VC1786ICE76	100	870 /870	VC_6_contig_11	73258..74127	Conserved hypothetical protein	JN648379
VC1786ICE77	100	648 /648	VC_6_contig_11	74552..75199	Putative phage regulatory protein	JN648379
VC1786ICE78	100	195 /195	VC_6_contig_9	168367..168561	Putative DNA-binding protein	JN648379
VC1786ICE79	100	276 /276	VC_6_contig_9	172098..172373	Conserved hypothetical protein	JN648379
VC1786ICE8	100	822 /822	VC_6_contig_24	5232..6053	Conserved hypothetical protein	JN648379
VC1786ICE80	100	566 /594	VC_6_contig_9	175719..176284	Transposase Tn3	JN648379
VC1786ICE81	100	192 /192	VC_6_contig_24	7752..7943	Replication-associated proteinA, <i>RepA</i>	JN648379
VC1786ICE83	100	306 /306	VC_6_contig_24	3468..3773	Helix-turn-helix multiple antibiotic resistance	JN648379

					protein, Transcriptional regulator <i>LysR</i> family	
VC1786ICE84	100	183 /183	VC_6_contig_24	139..321	Conserved hypothetical protein	JN648379
VC1786ICE85	100	549 /549	VC_6_contig_11	5354..5902	Conserved hypothetical protein	JN648379
VC1786ICE86	100	240 /240	VC_6_contig_11	25363..25602	Conserved hypothetical protein	JN648379
VC1786ICE87	100	327 /327	VC_6_contig_11	48736..49062	Conserved hypothetical protein	JN648379
VC1786ICE88	100	201 /201	VC_6_contig_11	50420..50620	Hypothetical protein	JN648379
VC1786ICE89	100	405 /405	VC_6_contig_11	60068..60472	Glyoxalase/bleomycin resistance protein/ Dioxygenase	JN648379
VC1786ICE90	100	369 /369	VC_6_contig_11	61270..61638	Conserved hypothetical protein	JN648379
VC1786ICE91	100	411 /411	VC_6_contig_11	61703..62113	DNA-binding HTH domain-protein	JN648379
VC1786ICE92	100	546 /546	VC_6_contig_11	62311..62856	Hypothetical protein	JN648379
VC1786ICE93_ <i>dfrA1</i>	100	474 /474	VC_6_contig_11	62841..63314	Dihydrofolate reductase, resistance to Trimethoprim	JN648379
VC1786ICE94	100	456 /456	VC_6_contig_11	70759..71214	Putative phage membrane protein	JN648379
VC1786ICE95	100	252 /252	VC_6_contig_11	74183..74434	Putative phage regulatory protein	JN648379

Antibiotic resistance genes						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
VC1786ICE9_ <i>floR</i>	100	1215 /1215	VC_6_contig_24	3801..5015	Warning	
<i>catB9</i>	100	630 /630	VC_6_contig_36	1574..2203	Chloramphenicol resistance Chloramphenicol acetyl transferase	AF462019

<i>dfrA1</i>	100	474 /474	VC_6_contig_11	62841..63314	Trimethoprim resistance, dihydrofolate reductase, from the ICE VchHai1 (VC1786ICE93)	AF221901
<i>gyrA</i>	99.78	453 /453	VC_6_contig_1	356745..357197	Mutated DNA gyrase subunit A. Resistance to Fluoroquinolone	GQ502315
<i>parC</i>	100	210 /210	VC_6_contig_12	70835..71044	Mutated Topoisomerase IV subunit A, resistance to Quinolone	KJ596550
<i>parE</i>	99.72	354 /354	VC_6_contig_12	69869..70222	Mutated Topoisomerase subunit B, resistance to Quinolone	GQ502316
<i>strA</i>	100	804 /804	VC_6_contig_24	1206..2009	Streptomycin resistance protein <i>StrA</i> , from the ICE VchHai1(VC1786ICE12)	AF321551
<i>strB</i>	100	831 /831	VC_6_contig_24	2015..2845	Streptomycin resistance protein <i>StrB</i> , from the ICE VchHai1(VC1786ICE11)	M28829
<i>sul2</i>	100	816 /816	VC_6_contig_24	330..1145	Sulphonamid resistance dihydropteroate synthase 2, from the ICE VchHai1(VC1786ICE13)	AY034138

Serogroup specific genes						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
<i>rfbV_O1</i>	100	1233 / 1233	VC_6_contig_14	13785..15017	O-antigen synthesis, O1serogroup	AE003852
Specie specific gene (<i>ompW</i>)						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
<i>ompW</i>	100	416 / 416	VC_6_contig_3	271857..272272	Outer Membrane Protein specific of <i>Vibrio</i>	FJ462451

					<i>cholerae</i>	
Virulence genes						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
<i>VasX</i>	99.74	8853 /10411	VC_6_contig_7	2..8854	Type VI secretion system effector module used by VC against competing eucaryotic and procaryotic cells	KF228943.1
<i>VgrG</i>	98.31	2368 /8442	VC_6_contig_6	625..2989	Type VI secretion system effector module used by VC against competing eucaryotic and procaryotic cells	KC955251.1
<i>als</i>	100	1704 /1704	VC_6_contig_6	168711..170414	Als operon involved in glucose metabolism	vc1590
<i>hlyA</i>	100	217 / 217	VC_6_contig_19	53689..53905	<i>Vibrio cholerae</i> hemolysin, causes cytolysis by forming heptameric pores	HQ452880
<i>makA</i>	100	1110 /1110	VC_6_contig_3	256267..257376	Flagella-associated cytotoxin	VCA0883
<i>mshA</i>	100	537 / 537	VC_6_contig_13	28325..28861	Mannose-sensitive hemagglutinin, adhesins/adherence factor	X77217
<i>ompT</i>	99.23	1041 /1035	VC_6_contig_2	446890..447930	pore-forming proteins of the outer membrane, adhesins/adherence factor	AF079766
<i>ompU</i>	99.9	1026 /1026	VC_6_contig_9	138794..139819	Pore-forming proteins of the outer membrane, adhesins/adherence factor	KF434513
<i>rtxA</i>	100	203 / 203	VC_6_contig_6	52431..52633	Multi-functional repeats-in-toxin	AY101181

<i>toxR</i>	98.2	721 / 720	VC_6_contig_1	73544..74264	Transcriptional regulator of <i>ctx</i>	HM042639
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Biotype specific genes						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
<i>tcpA_et3</i>	100	675 / 675	VC_6_contig_10	44730..45404	Toxin-coregulated pilus specific for El Tor and El Tor Variant biotypes	AF325734

Mobile genetic elements (ICEVchHai1 not included)						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						
Phage susceptibility elements						
<i>Vibrio cholerae</i> Gene	Identity	Query /Template length	Contig	Position in contig	Predicted phenotype	Accession number
No hit found						

Supplementary Table 3: Mobile genetic elements (MGEs) detected in the isolate

contig	MGEs	Resistance
VC 6 contig 24	ISVsa3	<i>sul2</i> , <i>floR</i> , aph (3')-Ib, aph (6)-Id
VC 6 contig36	0	<i>catB9</i>
VC 6 contig11	0	<i>dfrA1</i>
VC 6 contig 10	ISVch1	-
VC 6 contig 27	ISVch8	-
VC 6 contig 45	ISVch5	-

Gene name	Phenotype	Accession	Position in contig	Coverage	Identity
<i>sul2</i>	sulfamethoxazole	AY034138	1145-330	100%	100%
<i>floR</i>	florfenicol, chloramphenicol	AF118107	3802-5015	99.92%	98.35%
aph(3")-Ib	streptomycin	AF321551	1206-2009	100%	99.87%
aph(6)-Id	streptomycin	M28829	2009-2845	100%	100%
<i>catB9</i>	chloramphenicol	AF462019	1574-2203	100%	100%
<i>dfrA1</i>	trimethoprim	X00926	62841-63314	100%	100%