Supporting Information

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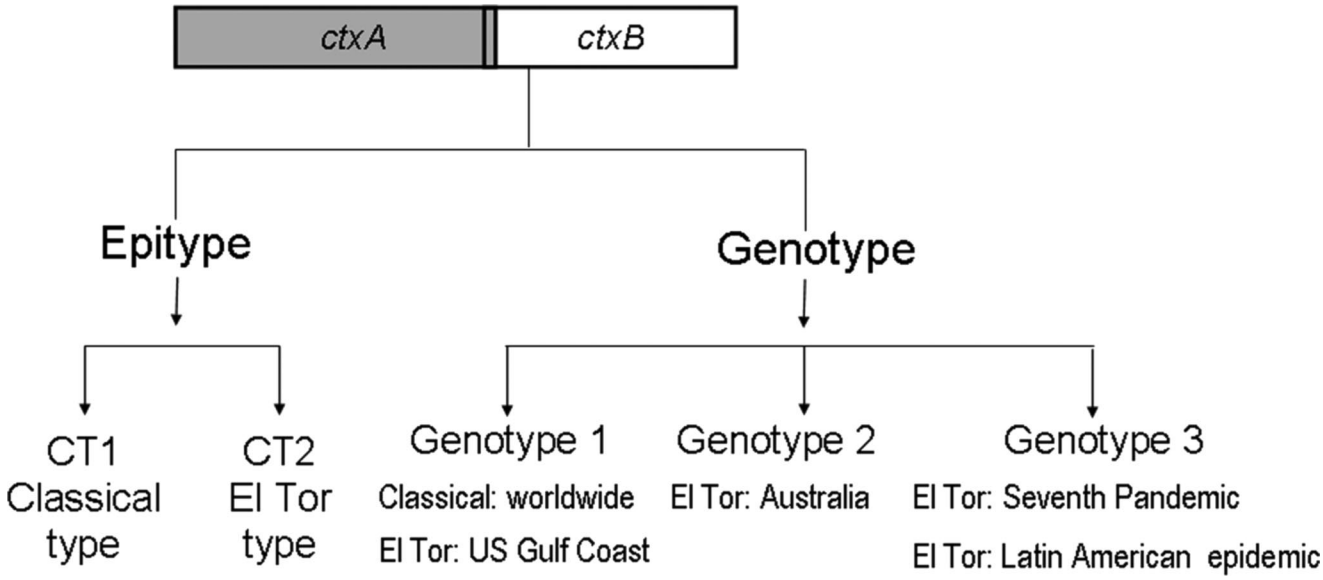

Fig. S1. Currently recognized epitypes (immunologic types) and genotypes of cholera toxin produced by *V. cholerae* O1.

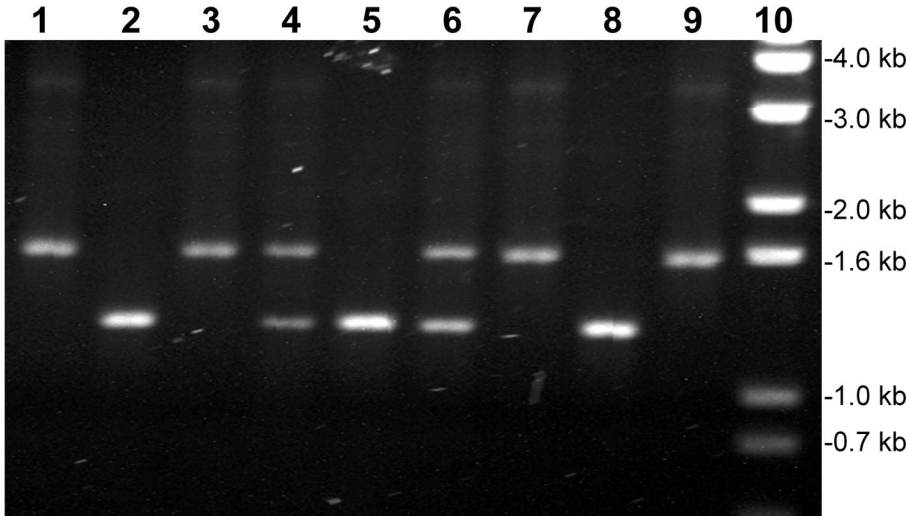

Fig. S2. Chitin-induced transformation resulting in replacement of the *ctxAB* operon in El Tor biotype strains by a genetically marked ≈1.6-kb PCR amplicon derived from strain O395NT, consisting of a K_m^R determinant flanked by remnants of the *ctxAB* operon. Lane 1 shows a PCR amplicon derived from O395NT; lane 2, strain 2344–17 (native); lane 5, strain 2434–44 (native); lane 8, strain 2749–129 (native); lane 9, a derivative of strain 2749–129 carrying the K_m^R marker; and lane 10, molecular size markers corresponding to the 1-kb DNA Ladder Plus (Invitrogen). Lanes 3 and 4 show derivatives of strain 2344–17 carrying the K_m^R marker, and lanes 6 and 7 show derivatives of strain 2434–44 carrying the K_m^R marker.

Table S1. Types of *rstR* gene of the CTX prophage and *tcpA* gene of the TCP pathogenicity island carried by environmental *V. cholerae* O1 and non-O1, non-O139 strains in Bangladesh

Serotype	Number of isolates	Presence of CTX	Type of *rstR* gene†				Type of *tcpA* gene†	
			rstR^{Class}	*rstR*^{ET}	*rstR*^{Cal}	*rstR*^{Env}	*tcpA*^{Class}	*tcpA*^{ET}
Unknown‡	3	+	—	—	—	+	+	—
Unknown‡	2	+	—	—	+		+	—
Unknown‡	5		—	—	—	—	+	—
O141	6	+	+	—	—	—	+	—
O141	9	—	—	—	—	—	—	—
O1	15	+	—	+	—	—	—	+
O1	3	—	—	—	—	—	—	+

These strains were identified as positive for CTX or TCP by screening a total of 254 *V. cholerae* non-O1, non-O139 strains and 18 *V. cholerae* O1 strains isolated from surface water.

†The types of *rstR* and *tcpA* genes were determined by DNA probes or PCR assays.

‡These are non-O1, non-O139 strains that did not react with the O141 antiserum.

Table S2. *V. cholerae* reference strains, plasmids, and phages used in the study

Strain	Relevant characteristic	Reference
O395	Classical Ogawa streptomycin-resistant strain	Laboratory collection
O395NT	Derivative of strain O395, in which the CTX element was marked with a kanamycin resistance determinant by marker exchange disrupting the *ctxAB* operon.	1
V47, V48, V49, V51	Toxigenic *V. cholerae* O141 clinical isolates carrying the CTX^{class} prophage	Laboratory collection
O141–2615, O141–2634	Toxigenic *V. cholerae* O141 environmental isolates	This study
O141–2615-Km, O141–2634-Km, V51-Km	Derivatives of strains O141–2615, O141 2634, and V51 respectively, in which the CTX^{class} prophage was marked by recombination of kanamycin marked PCR product derived from strain O395NT.	This study
JSF141Bϕ	Phage specific for *V. cholerae* O141 isolated from surface water in Bangladesh	This study
C6706, C6706 Δ*hapA*, H072260482, MG116926, MJ1485, MJ1236, 2749129, 2749720, 2756332, 2684756	Clinical isolates of toxigenic *V. cholerae* O1 El Tor strains	Laboratory collection
2344–11, 2344–16, 2344–17, 2434–44, 2434–47, 2434–49	Toxigenic *V. cholerae* O1 El Tor strains isolated from surface water in Bangladesh	This study

1. Mekalanos JJ, *et al.* (1983) Cholera toxin genes: Nucleotide sequence, deletion analysis and vaccine development. *Nature* 306:551–557.