

FIGURE S1. Core-gene maximum likelihood phylogenetic tree showing the relationship of Haiti environmental *Vibrio cholerae* isolates (I) to several reference genomes and to the Haiti outbreak clone.<sup>30,31</sup>

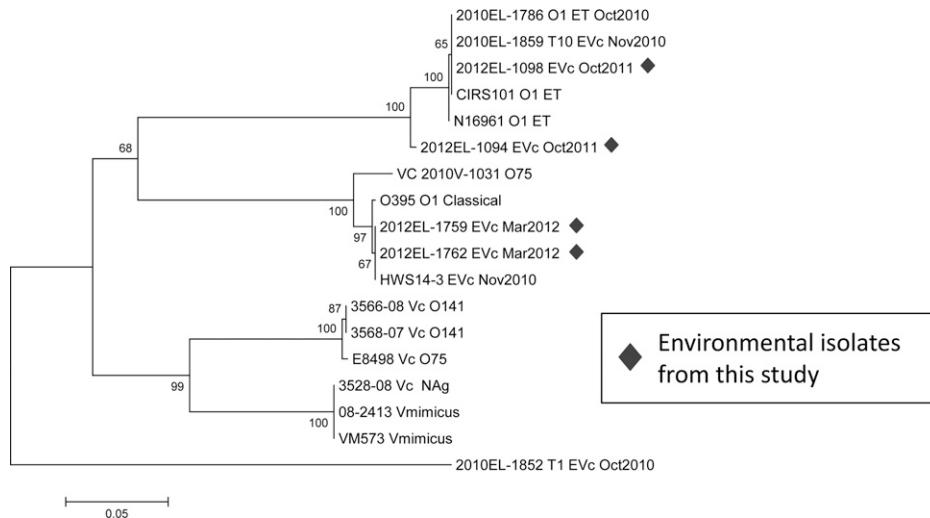


FIGURE S2. Environmental isolates from Haiti (I) in global *Vibrio cholerae-mimicus tcpA* phylogeny tree constructed using the Neighbor-Joining method with a statistical bootstrap test (500 replicates). The analysis involved 18 nucleotide sequences. There were a total of 675 positions in the final data set. Phylogeny constructed in MEGA5. ET = El Tor; EVc = environmental *Vibrio cholerae*; Nag = non-agglutinating in O1, O139, O75, and O141 antisera.

SUPPLEMENTAL TABLE S1  
Real-time PCR primers and probes used in this study

Name	Sequence
<i>ctxA</i> Fwd	5'-AGGGAAGAGCCGTGGAT-3'
<i>ctxA</i> Rvs	5'-ACTTTGGGTTTTTTCATCGCAAG-3'
<i>ctxA</i> Probe	5'-FAM-CATCATGCACCGCCGGTTGTG-BHQ1-3'
<i>ompW</i> Fwd	5'-CGCTTGGCTATATGTTTACTGACA-3'
<i>ompW</i> Rvs	5'-CACCACCAGAGGTAGAAATCTTAT-3'
<i>ompW</i> Probe	5'-Cy5-CATCAGTTTTGAAGTCCTCGCTGCTACGC-BHQ3-3'
<i>tcpA</i> <sub>EI Tor</sub> Fwd	5'- TTGGTCAGCCTTGGTAAGGTT 3'
<i>tcpA</i> <sub>EI Tor</sub> Rvs	5'- GCAGAGTTTCGTGGAAATGAGA -3'
<i>tcpA</i> <sub>EI Tor</sub> Probe	5'-Cy5- TCAGCTGATGAGGCAAAGAATCCTTTCA -BHQ3-3'
<i>tcpA</i> <sub>Classical</sub> Fwd	5'- CGCAGTAGCACTTGCAGATCTAG -3'
<i>tcpA</i> <sub>Classical</sub> Rvs	5'- AGCGGGAGCGATAGATTTGATC -3'
<i>tcpA</i> <sub>Classical</sub> Probe	5'-FAM- TTGAGAATTCTGCAGCAGCGGCT -BHQ1-3'