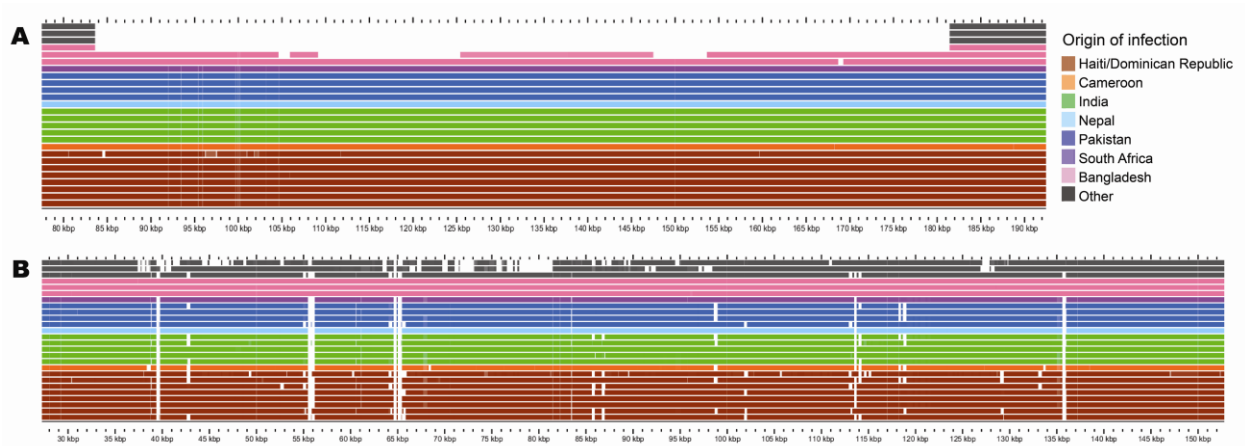
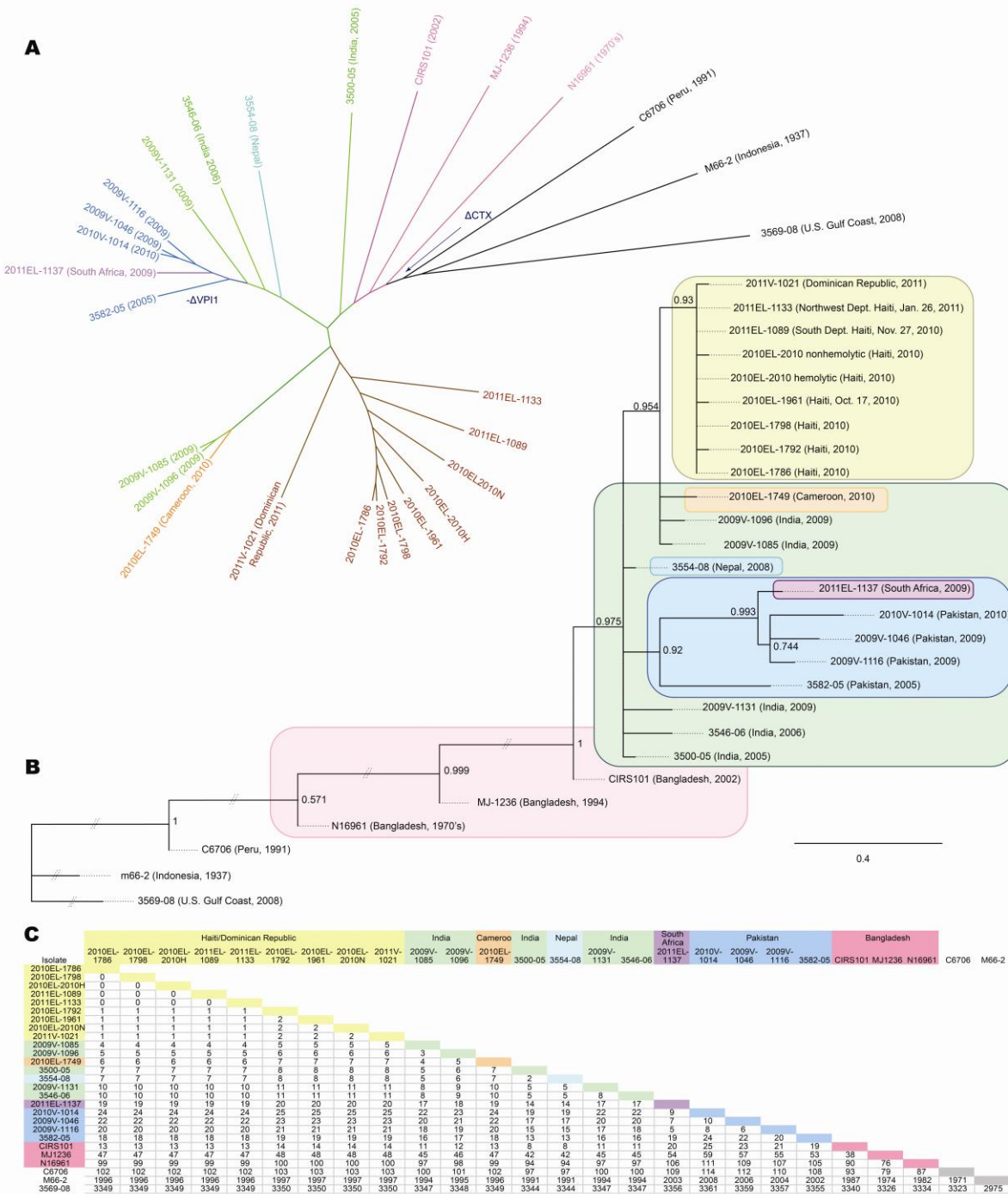


# Comparative Genomics of *Vibrio cholerae* from Haiti, Asia, and Africa

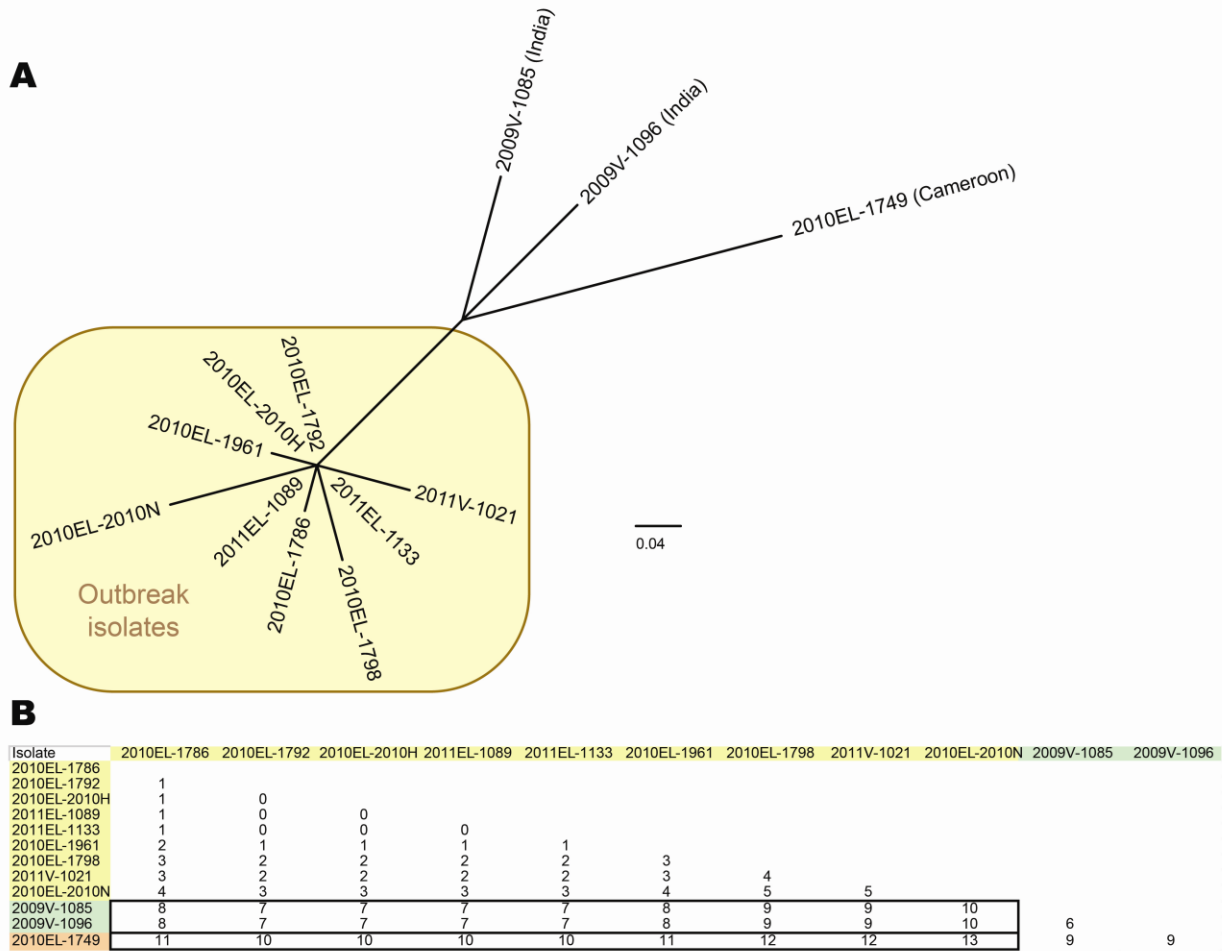
## Technical Appendix 2



Technical Appendix 2 Figure 1. Contig data (>500 bp) mapped to A) integrative conjugative element belonging to the SXT/R391 family and B) superintegron regions of Haiti outbreak *Vibrio cholerae* isolate 2010EL-1786, fall 2010.



Technical Appendix 2 Figure 2. Reconstructed core genome phylogeny of *Vibrio cholerae* based on 4,376 high-quality, single-nucleotide polymorphisms among 632 fully sequenced orthologous genes with >97% homology between alleles. A) Proportional cladogram. Dept., department. B) Maximum-likelihood phylogenetic tree with node confidences expressed as approximate likelihood ratios. C) Pair-wise single-nucleotide polymorphism matrix used to calculate phylogenetic distances and generate trees in A and B. Scale bar indicates nucleotide substitutions per site.



Technical Appendix 2 Figure 3. Reconstructed core genome phylogeny of *Vibrio cholerae* based on 25 high-quality, single-nucleotide polymorphisms among 24 fully sequenced orthologous genes with >97% homology between alleles. A) Proportional cladogram. Scale bar indicates nucleotide substitutions per site. B) Pair-wise single-nucleotide polymorphism matrix used to calculate phylogenetic distances and generate tree in panel A.