

## Parallel evolution of *Vibrio mimicus* clones that carry *Vibrio cholerae* virulence genes

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*Vibrio mimicus* is an aquatic bacterium that shares genetic and phenotypic similarities with its close relative *V. cholerae*, including the capacity to cause disease in humans. Although much is known regarding the evolution and pathogenic mechanisms of *V. cholerae*, less is known about *V. mimicus*. We performed phylogenetic analysis of seven housekeeping genes from 65 *V. mimicus* strains to reconstruct their evolutionary relationships, and surveyed for virulence genes common among pathogenic variants of *V. cholerae*. Three lineages carry the cholera toxin genes (*ctxAB*): a cluster of *V. mimicus* strains isolated from illness cases in 2008, an older toxigenic *V. mimicus* cluster, and a single environmental isolate (ES10). Phylogenetic analysis of *ctxAB* showed the three lineages had different sequences; the 2008 strains had a *ctxAB* sequence that was identical to that of *V. cholerae* O141, and these sequences were similar to the classical variant of *ctxAB*. Multilocus sequence analysis (MLSA) showed the 2008 strains had a single sequence type (ST), while pulsed-field gel electrophoresis (PFGE) separated these strains into two groups. Interestingly, all but one isolate included in the *tcpA* phylogeny had identical *tcpA* sequences. The *nanH* gene was detected among nearly all *V. mimicus* strains suggesting VPI-2 is ancestral; however, the *nanH* of several lineages exhibited evidence of recent HGT with *V. cholerae*. Taken together these data support the notion that multiple acquisition events at different times have given rise to lineages of *V. mimicus* that share virulence mechanisms with *V. cholerae*.