

## Deep Sea Bacteria Related to Human Pathogenic *Vibrio* Species

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### ABSTRACT

Because *Vibrio* species are both ubiquitous and abundant in marine coastal waters, estuaries, ocean sediment, and aquaculture settings worldwide, it was of interest to pursue the potential origin and evolution of vibrios from the deep sea environment. When samples collected from deep sea hydrothermal vents revealed the presence of vibrios phenotypically similar to *Vibrio* species pathogenic for humans, the genomes of deep sea isolates were sequenced. Draft sequences were obtained from a blend of Sanger and 454 sequences. Complete genome of the deep sea *Vibrio* EX25 was sequenced and extensive genomic comparisons was carried out which demonstrated high genomic similarity with its phylogenetic near-neighbors *V. alginolyticus*, *V. parahaemolyticus*, and *V. cholerae* but genome-wide nucleotide sequence divergence indicated characteristics of a unique species, therefore, concluded to be a new *Vibrio* species, *Vibrio antiquarius*. The *V. antiquarius* genome encodes many genes that can be interpreted as contributing to its being native to the deep sea but at the same time, a relative of coastal, estuarine, and riverine *Vibrio* species. Virulence genes homologous to those of *V. parahaemolyticus* and *V. cholerae* are known to be widely distributed among *Vibrio* species, including *V. parahaemolyticus*, *V. cholerae*, serotype non-O1, *V. mimicus*, *V. hollisae*, *V. fluvialis* and *V. alginolyticus*. Presence of these virulence genes in a deep sea *Vibrio* sp. raises important questions about these genes serving much more basic purposes in the environment, rather than its pathogenicity for humans. Our results show that the genome of *V. antiquarius* possesses homologues of *V. parahaemolyticus* and *V. cholerae* virulence genes, such as *toxR*, *tlh*, the Pre-CTX prophage, and VPI, which suggests that *V. antiquarius* may represent a component of evolutionary history of *Vibrio* spp. in the aquatic environment. The deep sea has been postulated as an origin of evolution among microorganisms and genomic evolution enables *Vibrio* species to adapt to changing conditions in their aquatic environment. The commensal relationship of *V. cholerae* with zooplankton, notably copepods, is well known and the current observation provides a further explanation for functions of the virulence genes encoding attachment, signaling, and interactions with copepods present around hydrothermal vents. Thus deep sea *Vibrio* species carry out ecological functions in the ocean ecosystem where chitin, metals, nitrogen metabolism, etc. are critical. In summary, a new perspective is offered for understanding the intersecting roles of *Vibrios* in the environment, rather than only as a pathogen of humans and marine animals.