

Comparative genomic and phenotypic analyses of the core group pathogens *Vibrio campbellii* and *Vibrio harveyi*

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Two central members of the *Vibrio* core group, *Vibrio campbellii* and *Vibrio harveyi*, are known to thrive in similar environments and share a high degree of genetic and phenotypic similarity; so much so that traditional identification methods are often unable to confidently differentiate these sister species. Most recently, this has been evidenced by the fact that the purported *V. harveyi* genome sequenced strains BAA-1116 and HY01 actually belong to the species *campbellii*. In this study, we used microarray-based comparative genomic hybridization, pulsed field gel electrophoresis, whole genome sequencing and phenotypic microarray analyses in order to provide a better genetic and phenotypic definition of these species to enable the development of tools to prevent the misidentification of core group members. The sequencing and comparative analyses of *V. campbellii* strain BAA-1116, the *V. campbellii* type strain (ATCC 25920 / CAIM 519T), the *V. harveyi* type strain (ATCC 14126) and *V. harveyi* strain CAIM 1792 provide important insights into the metabolic capability, pathogenicity and genetic plasticity of each and aid in adjusting the attribution of certain characteristics (e.g. bioluminescence, obligate organoheterotrophy) that have previously been used to define *V. harveyi* and *V. campbellii*. Overall, the results (i) provide a genetic definition for *V. campbellii* and *V. harveyi* and highlight loci involved in membrane transport, metabolism and virulence that appear to be unique to each, (ii) suggest that *V. campbellii* is evolving faster and is more genetically heterogeneous than *V. harveyi*, and (iii) provide foundational knowledge for the development of new tools to aid in the accurate identification of these two species.