Complete Genome Sequence of *Vibrio parahaemolyticus*

Environmental Strain UCM-V493

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*Vibrio parahaemolyticus* is the leading bacterial cause of seafood-related gastroenteritis in the world. Here, we report the complete genome sequence and annotation of an environmental strain of *V. parahaemolyticus*, UCM-V493, with the aim of understanding the differences between the clinical and environmental isolates of the bacteria. We also make some preliminary sequence comparisons with the clinical strain RIMD2210633.

Received 7 February 2014  Accepted 21 February 2014  Published 13 March 2014


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Acknowledgments

We thank Brewster Kingham and Olga Shevchenko at the Sequencing and Genotyping Center at the Delaware Biotechnology Institute (DBI) for assistance with the genome sequencing. Computational infrastructure and other support provided by the University of Delaware Center for Bioinformatics and Computational Biology Core Facility and DBI was made possible through Delaware INBRE (NIH NIGMS 8 P20 GM103446-12) and Delaware EPSCoR (NSF EPS-081425).

This research was supported by a National Science Foundation CA-REER award DEB-0844409 to E.F.B.
REFERENCES


