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GENOME SEQUENCES

Complete Genome Sequence of *Vibrio harveyi* Strain ATCC 33866

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ABSTRACT Here, we report the complete genome sequence of *Vibrio harveyi* strain ATCC 33866, generated from Illumina and Oxford Nanopore sequencing. The assembled genome sequence comprises two circular chromosomes with lengths of 3,504,760 bp and 2,218,060 bp, respectively.

Vibrio harveyi is a notorious zoonotic pathogen infecting marine organisms but also humans (1). Due to the high social and economic burden caused by vibriosis (2), together with the emergence of multidrug-resistant and highly virulent strains (3, 4), it is imperative to gain more knowledge on the biology and genomics of *Vibrio* species in order to develop strategies to combat the pathogen. To date, only six complete genomes of *V. harveyi* strains are available (ATCC 33843, FDAARGOS_107, WXL538, 345, QT520, and 2011V-1164), and due to this sparsity of genomic data, species identification, comparative genomic analyses, or pathogenesis studies are challenging (5, 6). Here, we report the complete genome sequence of *V. harveyi* strain ATCC 33866, which will contribute to the genetic data available of the *Vibrio* genus to facilitate further research.

Vibrio harveyi ATCC 33866, isolated from seawater, was purchased from China General Microbiological Culture Collection Center (CGMCCC). It was cultured on a Columbia blood agar plate for 24 h. A single colony was selected and grown in tryptone soya broth at 28°C overnight. Genomic DNA was extracted using the QIAamp DNA Mini kit (Qiagen, Germany) and then analyzed on 1% agarose gel. The same genomic DNA preparation was used for both Illumina and Oxford Nanopore Technologies (ONT) sequencing. Illumina sequencing libraries were prepared by Nextflex rapid DNA sequencing (DNA-Seq) kit. For Nanopore sequencing, libraries were generated using the native barcoding expansion set (EXP-NBD104) and SQK-LSK109 ligation sequencing kit without size selection or shearing. Pooled libraries were qualified and quantified by Qubit 3.0 (Invitrogen, USA) prior to sequencing.

Whole-genome sequencing was performed on the HiSeq X Ten platform (Illumina Inc., USA) as well as on the Nanopore MinION platform (Oxford Nanopore Technologies, UK). Reads were base called using Guppy v5.1.2 (Oxford Nanopore Technologies) with parameters "–flowcell FLO-MIN106 –kit SQK-LSK109 –barcode_kits 'EXP-NBD104 EXP-NBD114' and "high-accuracy" was the default mode. Trimmomatic v0.30 was used to trim the Illumina reads (7). Hybrid assembly using the filtered MinION and Illumina reads were assembled with Raven v1.1.10 (8) with error correction (Pilon v1.24 [9]). Default parameters were used for all software unless otherwise specified. The resulting complete genome sequence was annotated by the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/).

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TABLE 1 Genome features of *V. harveyi* ATCC 33866

Genome feature	Data for[a]: Chr I	Chr II
Size (bp)	3,504,760	2,218,060
GC content (%)	45.0	44.9
No. of rRNAs	31	3
No. of tRNAs	114	16
No. of ncRNAs	4	0
No. of coding sequences	3,175	1,922
Accession no.	CP090179.1	CP090178.1

[a] Chr, chromosome.

For Illumina, a total of 4,447,844 150-bp paired-end reads were obtained. For Nanopore, a total of 74,917 reads were obtained, with an average length of 9,527 bp and an N_{50} value of 17,008 bp. The depth of Illumina sequencing was on average 126.6 times, while for Nanopore it was 290 times. The assembled genome sequence contains two circular chromosomes (3,504,760 bp and 2,218,060 bp) with a slight difference in GC content (45.0% and 44.9%). The final coverage of the genome is 122.0 x. Annotation showed the genome sequence contains 5,097 protein-coding genes, 34 rRNA (5S-16S-23S rRNA) genes, 130 tRNA genes, 4 noncoding RNA (ncRNA) genes, and 55 pseudogenes (Table 1). Genome data of ATCC 33866 provided here can help to increase our understanding of *V. harveyi* and *Vibrio* species in general.

Data availability. The whole genome sequence of *V. harveyi* ATCC 33866 is available in GenBank under the accession numbers CP090179.1 and CP090178.1. The BioSample and BioProject accession numbers are SAMN24371565 and PRJNA791971, respectively. The raw sequence data have been deposited in the Sequence Read Archive (SRA) under accession number SRR18249428 (Nanopore) and SRR17729643 (Illumina).

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REFERENCES

1. Yu G, Yu H, Yang Q, Wang J, Fan H, Liu G, Wang L, Bello BK, Zhao P, Zhang H, Dong J. 2022. Vibrio harveyi infections induce production of proinflammatory cytokines in murine peritoneal macrophages via activation of p38 MAPK and NF-κB pathways, but reversed by PI3K/AKT pathways. Dev Comp Immunol 127:104292. https://doi.org/10.1016/j.dci.2021.104292.
2. Bondad-Reantaso MG, Subasinghe RP, Arthur JR, Ogawa K, Chinabut S, Adlard R, Tan Z, Shariff M. 2005. Disease and health management in Asian aquaculture. Vet Parasitol 132:249–272. https://doi.org/10.1016/j.vetpar.2005.07.005.
3. Deng Y, Xu H, Su Y, Liu S, Xu L, Guo Z, Wu J, Cheng C, Feng J. 2019. Horizontal gene transfer contributes to virulence and antibiotic resistance of Vibrio harveyi 345 based on complete genome sequence analysis. BMC Genomics 20:761. https://doi.org/10.1186/s12864-019-6137-8.
4. Tu Z, Li H, Zhang X, Sun Y, Zhou Y. 2017. Complete genome sequence and comparative genomics of the golden pompano (Trachinotus ovatus) pathogen, Vibrio harveyi strain QT520. PeerJ 5:e4127. https://doi.org/10.7717/peerj.4127.
5. Culot A, Grosset N, Bruey Q, Auzou M, Giard JC, Favard B, Wakatsuki A, Baron S, Frouel S, Techer C, Gautier M. 2021. Isolation of Harveyi clade Vibrio spp. collected in aquaculture farms: how can the identification issue be addressed? J Microbiol Methods 180:106106. https://doi.org/10.1016/j.mimet.2020.106106.
6. Morot A, El Fekih S, Bidault A, Le Ferrand A, Jouault A, Kavousi J, Bazire A, Pichereau V, Dufour A, Paillard C, Delavat F. 2021. Virulence of Vibrio harveyi ORM4 towards the European abalone Haliotis tuberculata involves both quorum sensing and a type III secretion system. Environ Microbiol 23:5273–5288. https://doi.org/10.1111/1462-2920.15592.
7. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/bioinformatics/btu170.
8. Vaser R, Šikić M. 2021. Time- and memory-efficient genome assembly with Raven. Nat Comput Sci 1:332–336. https://doi.org/10.1038/s43588-021-00073-4.
9. Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, Earl AM. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS One 9:e112963. https://doi.org/10.1371/journal.pone.0112963.