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Rikesh Jain, Bianca Habermann, Tâm Mignot. Complete Genome Assembly of Myxococcus xanthus Strain DZ2 Using Long High-Fidelity (HiFi) Reads Generated with PacBio Technology. Microbiology Resource Announcements, 2021, 10 (28), 10.1128/MRA.00530-21. hal-03451605

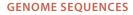
HAL Id: hal-03451605 https://amu.hal.science/hal-03451605

Submitted on 26 Nov 2021

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Complete Genome Assembly of *Myxococcus xanthus* Strain DZ2 Using Long High-Fidelity (HiFi) Reads Generated with PacBio Technology

Microbiology[®]

Resource Announcements

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ABSTRACT *Myxococcus xanthus* is a Gram-negative social bacterium belonging to the order *Myxococcales* of the class *Deltaproteobacteria*. It is a facultative social predator found in soils across the globe and is thought to be crucial for the microbial ecosystem. Here, we report a complete high-quality reference genome of the *M. xanthus* strain DZ2.

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DZ2 cells were grown at 32°C in CYE (Casitone yeast extract) medium, and genomic DNA was extracted using a MasterPure DNA purification kit (catalog [cat.] number 85200) (Epicentre/Lucigen, Middleton, WI) following the manufacturer's protocol. The high-fidelity (HiFi) sequencing library was prepared using the SMRTbell express template prep kit (PacBio, CA), and genome sequencing was performed using single-molecule real-time (SMRT) sequencing on the PacBio Sequel II system at the DRESDEN-concept Genome Center, Germany. A total of 98,235 subreads were generated with a mean subread length of 6,019 bp, totaling 591 Mb, which represents approximately 60fold coverage. Circular consensus reads were called using Code Composer Studio (CCS) version 5 (PacBio) on the raw PacBio subreads, and the resulting consensus reads with a quality value (QV) of >20 or >99% accuracy were used to assemble the genome with HiCanu version 2.1 (6). This resulted in a single circular contig of 9,359,382 bp (approximately 220 kb larger than the DK1622 genome) with a GC content of 68.86%. Genome annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 5.1 (7), which predicted a total of 7,408 protein-coding sequences (CDSs), 12 rRNA genes, 66 tRNA genes, 4 noncoding RNA (ncRNA) genes, 86 pseudogenes, and 4 CRISPR arrays in the DZ2 genome. Default parameters were used for all software unless otherwise noted.

A previous version of the DZ2 genome sequence (8) existed as a draft assembly with 87 contigs. It is around 88 kb shorter than our PacBio complete assembly, suggesting large coverage gaps and possibly missing important loci. It was sequenced with 454 GS-FLX Titanium technology, a second-generation sequencing technology,

Citation Jain R, Habermann BH, Mignot T. 2021. Complete genome assembly of *Myxococcus xanthus* strain DZ2 using long high-fidelity (HiFi) reads generated with PacBio technology. Microbiol Resour Announc 10:e00530-21. https:// doi.org/10.1128/MRA.00530-21.

Editor Frank J. Stewart, Montana State University

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Received 27 May 2021 Accepted 18 June 2021 Published 15 July 2021

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which generates much shorter reads (average read length, 450 bp) than the third-generation sequencing platform PacBio Sequel II (average read length, 10,000 bp). Highly accurate (99.8%) long high-fidelity PacBio reads enabled the resolving of large repetitive and low-complexity genomic regions, thus closing all the gaps, a task which remains challenging with short-read sequencing (9).

Uninterrupted and accurate genome sequence information is crucial for many downstream genomic analyses, such as biosynthetic gene cluster mining and gene synteny comparison, as well as for understanding genome plasticity, the patterns of transposon distribution, and gene expression regulation.

Data availability. The raw sequencing data can be found at the NCBI SRA database under the accession number PRJNA701418. The complete genome sequence has been deposited in GenBank under accession number CP070500.

ACKNOWLEDGMENTS

We thank Sylke Winkler and Thomas Brown for the useful suggestions and data analysis.

This work was supported by a research grant from the European Research Council (ERC JAWS 885145) to T.M. and a postdoctoral fellowship from the Turing Center for Living Systems (CENTURI) to R.J.

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