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Draft Genome Sequence of *Zobellella denitrificans* ZD1 (JCM 13380), a Salt-Tolerant Denitrifying Bacterium Capable of Producing Poly(3-Hydroxybutyrate)

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ABSTRACT *Zobellella denitrificans* ZD1, isolated from sediments of an estuarine mangrove ecosystem in Taiwan, exhibits growth-associated production of biopolymer poly(3-hydroxybutyrate) (PHB). This work reports the 4.05-Mbp draft genome sequence of *Z. denitrificans* ZD1, consisting of 217 contigs with a G+C content of 63.8% and 3,672 protein-coding sequences.

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Zobellella, a new genus, belongs to the gamma subgroup of *Proteobacteria*. *Zobellella denitrificans* ZD1 was isolated from sediment samples collected from the estuarine mangrove ecosystem of Chungkang, Miaoli County, Taiwan (1). Along with *Zobellella taiwanensis* ZT1, *Z. denitrificans* ZD1 was identified as one of the first two novel strains which are currently classified into the new *Zobellella* genus. *Z. denitrificans* ZD1 is characterized as a heterotrophic facultative anaerobic denitrifying bacterium. *Z. denitrificans* ZD1 is characterized as a Gram-negative straight rod, ranging from 1.6 to 2.6 mm long by 0.6 to 0.8 mm wide, with a single polar flagellum. The strain is also salt tolerant and capable of growth in the absence and presence of salt up to 12%, with optimal growth in 1 to 3% NaCl. The strain can also ferment different organics, including glucose, sucrose, and mannitol, and it can also use nitrate or nitrous oxide as an electron acceptor during denitrification. We recently observed a rapid growth of *Z. denitrificans* ZD1 with glycerol under aerobic conditions. The strain also exhibited growth-associated production of poly(3-hydroxybutyrate) (PHB), approximately 84% (wt/wt) of the dry cell weight (2), suggesting that this strain can be an ideal biocatalyst for PHB production.

The *Z. denitrificans* ZD1 strain was obtained from the Japan Collection of Microorganisms (JCM, Tsukuba, Japan). The genomic DNA was obtained from cells grown in R2A broth. The genomic DNA was processed into a sequencing library using a Nextera XT library preparation kit, according to the manufacturer guidelines. The sample was then barcoded using a Nextera XT index kit version 2. The draft genome of *Z. denitrificans* ZD1 was sequenced by 250-bp paired-end sequencing on an Illumina MiSeq sequencing system. After trimming adaptors and low-quality regions using bbduk (http://jgi.doe.gov/data-and-tools/bbtools/), the sequencing reads (two million pairs) were assembled *de novo* using SPAdes 3.10.1 (with the -careful option) (3). The final assembly of the genome produced 4,051,699 bp in 217 contigs, with an N_{50} value of 33,403 bp and a G+C content of 63.8%. The genome coverage is 101×. The assembled contigs were functionally annotated using the NCBI prokaryotic genome annotation pipeline (PGAP) annotation system (4). In total, 3,672 protein-coding genes along with 114 RNA genes were annotated. One clustered regularly interspaced short palindromic

repeat (CRISPR) array spanning 7.1 kbp along with upstream CRISPR-associated (Cas) genes was also identified from the genome.

Accession number(s). The draft genome sequence of *Z. denitrificans* ZD1 has been deposited in DDBJ/EMBL/GenBank with the accession number NMUO00000000.

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REFERENCES

1. Lin YT, Shieh WY. 2006. *Zobellella denitrificans* gen. nov., sp. nov. and *Zobellella taiwanensis* sp. nov., denitrifying bacteria capable of fermentative metabolism. Int J Syst Evol Microbiol 56:1209–1215. https://doi.org/10.1099/ijs.0.64121-0.
2. Asiri F. 2015. Production of valued biopolymer, polyhydroxybutyrate (PHB), from glycerol: effects of impurities on selected salt-tolerant microbial strains. Texas A&M University, College Station, TX.
3. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
4. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.