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GENOME SEQUENCES

Genome Sequence of *Morganella morganii* DG56-16, Isolated from *Shinisaurus crocodilurus*

Hai-Ying Jiang,[a] Li-Bo Lin,[b] Ming-Wei Huang,[b] Ying-An Zang,[b] Jin-Ping Chen[a]

[a]Guangdong Key Laboratory of Animal Conservation and Resource Utilization, Guangdong Public Laboratory of Wild Animal Conservation and Utilization, Guangdong Institute of Applied Biological Resources, Guangzhou, China

[b]Zhongkai University of Agriculture and Engineering, Guangzhou, China

ABSTRACT The complete genome sequence of *Morganella morganii* DG56-16 was sequenced. This strain was isolated from the liver of a dead crocodile lizard (*Shinisaurus crocodilurus*). The genome size was 3.9 Mb, with a G+C content of 50.9%.

Morganella morganii is a Gram-negative bacterium belonging to the *Enterobacteriaceae*. It can be found in vertebrate intestines as a normal commensal and is widely distributed in the environment. In humans, this bacterium is a nonnegligent opportunistic pathogen that causes sepsis, abscess, cellulitis, etc. (1). In addition, *M. morganii* is an important pathogen of iatrogenic infection, with a high mortality rate (2, 3). Domestic and wildlife animal diseases and deaths caused by *M. morganii* also have been widely reported (4–6). Recently, more and more concerns have been concentrated on *M. morganii* because of its increased levels of antibiotic resistance and virulence (1, 4, 6). To date, 44 draft or complete genome sequences have been reported in GenBank. Here, we report a complete genome sequence of *M. morganii* DG56-16, isolated from the liver of a juvenile crocodile lizard that died from disease. This would benefit the understanding of the pathogenicity of *M. morganii*.

The liver was resected from the dead crocodile lizard, homogenized, and spread on a Columbia blood agar base plate (Oxoid Ltd., UK). The plate was incubated at 30°C for 24 h. *Morganella morganii* DG56-16 was isolated and purified by the streak plate method. Total DNA was extracted using the TIANamp bacteria DNA kit DP302 (Tiangen Biotech [Beijing] Co., Ltd., China). A SMRTbell library was constructed by SMRTbell template prep kit 1.0 (Pacific Biosciences of California, Inc., USA). Sequencing was performed using a PacBio system. Quality control of raw sequences and genome assembly were conducted by SMRT Link version 5.0.1.

Paired-end (150-bp) Illumina sequencing was performed to correct the assembled sequence that resulted from the PacBio system. The Illumina sequencing library was constructed using the TruSeq DNA PCR-free sample preparation kit (Illumina, Inc., USA). Clean data resulting from Illumina sequencing was mapped onto the PacBio assembly genome sequence using the BWA software (http://bio-bwa.sourceforge.net/bwa.shtml). Alignment duplications were removed using Samtools (http://www.htslib.org/). Mapping quality was filtered by a personal Perl script. The correction was performed using the filtered result.

Gene prediction was performed using GeneMarkS 4.28 (7). Interspersed repetitive sequences were predicted by RepeatMasker 4.0.7 (http://www.repeatmasker.org/). Tandem repeats were searched by TRF 4.09 (http://tandem.bu.edu/trf/trf.download.html). The tRNA genes were predicted by tRNAscan-SE 2.0 (8), and the rRNA genes were analyzed using RNAmmer 1.2 (9). The small nuclear RNAs were predicted by BLAST against the Rfam database (10). Genomic islands (GIs) were predicted by IslandPath-DIMOB 1.0.0 (11). The prophage prediction was conducted by PHAST (12). Clustered

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Address correspondence to Jin-Ping Chen, chenjp@giabr.gd.cn.

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regularly interspaced short palindromic repeat (CRISPR) sequences were identified by CRISPRFinder. For gene function, DIAMOND version 0.9.16 (13), with an E value of ≤1e−5, was used for alignment against databases, and the item with highest score was selected. The databases included GO, KEGG, COG (14), NR, Pfam, TCDB (15), and Swiss-Prot. Default parameters were used in all softwares.

The total number of PacBio reads was 179,195, with an N_{50} read length of 9,194 bp. A total of 1,633 Mb was obtained by Illumina sequencing. Finally, the genome of *M. morganii* DG56-16 was assembled into a circular chromosome (3,902,034 bp), with 50.9% G+C content. The genome coverage of PacBio was ~368×. The annotation results showed that 3,817 coding genes and 124 noncoding RNAs were included. In addition, 11 GIs, 5 prophage sequences, 147 interspersed repeat sequences, and 125 tandem repeat sequences were found. However, no CRISPRs were found.

Data availability. The raw and assembled sequences of *M. morganii* DG56-16 have been deposited in GenBank under accession number CP032295, BioProject number PRJNA490253, and SRA number SRP162219.

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