



Complete Genome Sequence of Oxidase-Positive *Stenotrophomonas maltophilia* Strain SM7059

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ABSTRACT *Stenotrophomonas maltophilia* is an opportunistic pathogen which causes an increasing frequency of infections in hospitalized patients. Here, we present the complete genome sequence of *Stenotrophomonas maltophilia* SM7059, an oxidase-positive strain isolated from a female patient with hepatolithiasis in China.

Stenotrophomonas maltophilia is an aerobic Gram-negative bacillus typically found in soil and water, and it is also frequently isolated as an opportunistic pathogen in hospitalized patients (1). Standard microbiology references describe *S. maltophilia* as oxidase negative, while an analysis of a collection of 766 *S. maltophilia* isolates indicated that approximately 20% are oxidase positive, and this species should be reevaluated for other phenotypes (2). Here, we present the complete genome sequence of a clinical oxidase-positive *S. maltophilia* strain, SM7059, which is helpful in understanding the expression of oxidase.

S. maltophilia strain SM7059 was isolated from an ascites sample from a female patient admitted to the hospital for hepatolithiasis in 2017 in China. The isolate was identified as *S. maltophilia* using the Vitek 2 system (Sysmex-bioMérieux, Marcy-l'Étoile, France). Microbact oxidase strips impregnated with *N,N,N',N'*-tetramethyl-*p*-phenylenediamine dihydrochloride (Oxoid Ltd., UK) were used to detect cytochrome oxidase enzyme production in *S. maltophilia* strain SM7059. *Escherichia coli* (ATCC 25922) and *Pseudomonas aeruginosa* (ATCC 27853) were used as a negative control and a positive control, respectively.

Genomic DNA was extracted from a culture grown overnight in Luria-Bertani medium at 35°C under agitation (220 rpm) using the QIAamp DNA minikit (Qiagen, Hilden, Germany). Library preparations were constructed following the manufacturer's protocol (Illumina TruSeq DNA Nano library prep kit) and then sequenced using the Illumina HiSeq PE150 platform to generate 350-bp paired-end reads. The total number of reads after filtering and trimming for the SM7059 library was 11,249,876. For read trimming, raw data were processed, including removal of bases if the quality was below 20, removal of reads with a length below 50 bp, and removal of adapter contamination and duplicated reads, using Trimmomatic version 0.32 (3). Trimmed sequencing reads were then assembled *de novo* using the SPAdes pipeline version 3.9.0 (4), with default settings. The Prokka version 1.12 software was used to predict gene models (5). Then, all gene models were subjected to a BLAST search against the KEGG (<http://www.genome.jp/kegg/>) (6) and COG (<http://www.Ncbi.Nlm.Nih.gov/COG>) (7) databases to perform functional annotation. The assembled sequence contains 4,189 protein-coding genes, 6 ribosomal RNAs (rRNAs), and 75 transfer RNAs (tRNAs). The chromosome comprises 4,646,251 bp, with a G+C content of 66.41%. A total of 75 contigs were generated, and the N_{50} contig size was 204,159 bp. Multilocus sequence typing (MLST) was performed according to the reference method (8). Briefly, the seven housekeeping genes of *S. maltophilia* were PCR amplified and sequenced; the locus included *atpD*, *gapA*, *guaA*, *mutM*, *nuoD*, *ppsA*, and *recA*. The result showed that *S. maltophilia* SM7059

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belongs to sequence type 115 (ST115; MLST 2.0 [<http://www.genomicepidemiology.org>]). Notably, the genes *cc4* and *cccA*, encoding cytochrome c_4 and cytochrome c_{550r} , respectively, were annotated in the sequence of SM7059, which indicates the reason that strain SM7059 has a positive result in the oxidase test (9).

In conclusion, the genome sequence and the results of bioinformatics analysis of this *S. maltophilia* strain provide a basis for understanding the expression of oxidase in this strain. Complete genome sequencing may provide valuable information for the phenotypes of clinical species.

Data availability. This genome sequence has been deposited in GenBank under the accession number [QDID00000000](https://doi.org/10.1128/CMR.00019-11). Raw sequence reads have been deposited in the NCBI Sequence Read Archive under the accession number [SRR8776274](https://doi.org/10.1128/JCM.02204-10).

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REFERENCES

1. Brooke JS. 2012. *Stenotrophomonas maltophilia*: an emerging global opportunistic pathogen. *Clin Microbiol Rev* 25:2–41. <https://doi.org/10.1128/CMR.00019-11>.
2. Carmody LA, Spilker T, LiPuma JJ. 2011. Reassessment of *Stenotrophomonas maltophilia* phenotype. *J Clin Microbiol* 49:1101–1103. <https://doi.org/10.1128/JCM.02204-10>.
3. 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>.
4. 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>.
5. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.
6. Kanehisa M, Goto S. 2000. KEGG: Kyoto Encyclopedia of Genes and Genomes. *Nucleic Acids Res* 28:27–30. <https://doi.org/10.1093/nar/28.1.27>.
7. Tatusov RL, Fedorova ND, Jackson JD, Jacobs AR, Kiryutin B, Koonin EV, Krylov DM, Mazumder R, Mekhedov SL, Nikolskaya AN, Rao BS, Smirnov S, Sverdlov AV, Vasudevan S, Wolf YI, Yin JJ, Natale DA. 2003. The COG database: an updated version includes eukaryotes. *BMC Bioinformatics* 4:41. <https://doi.org/10.1186/1471-2105-4-41>.
8. Larsen MV, Cosentino S, Rasmussen S, Friis C, Hasman H, Marvig RL, Jelsbak L, Sicheritz-Pontén T, Ussery DW, Aarestrup FM, Lund O. 2012. Multilocus sequence typing of total-genome-sequenced bacteria. *J Clin Microbiol* 50:1355–1361. <https://doi.org/10.1128/JCM.06094-11>.
9. Sandri F, Musiani F, Selamoglu N, Daldal F, Zannoni D. 2018. *Pseudomonas pseudoalcaligenes* KF707 grown with biphenyl expresses a cytochrome caa_3 oxidase that uses cytochrome c_4 as electron donor. *FEBS Lett* 592:901–915. <https://doi.org/10.1002/1873-3468.13001>.