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Draft Genome Sequence of *Stenotrophomonas maltophilia* Strain PE591, a Polyethylene-Degrading Bacterium Isolated from Savanna Soil

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ABSTRACT We report the genome sequence of a polyethylene-degrading bacterial strain identified as *Stenotrophomonas maltophilia* strain PE591, which was isolated from plastic debris found in savanna soil. The genome was assembled in 16 scaffolds with a length of 4,751,236 bp, a GC content of 66.5%, and 4,432 predicted genes.

Stenotrophomonas maltophilia strain PE591 was isolated from plastic debris found in the soil of the Brazilian Cerrado biome (1). The strain showed both metabolic activity and cellular viability after incubation with unpretreated polyethylene (PE) (molecular weight, 191,000) films as the sole carbon source for periods of up to 90 days (1). Moreover, *S. maltophilia* PE591 was capable of inducing significant physicochemical changes in PE after a 90-day incubation, revealing its great potential for plastic biodegradation processes (1). The *Stenotrophomonas* genus currently comprises 20 species, and its first species, *S. maltophilia*, was described in 1993 (2–4). *S. maltophilia* is a Gram-negative, obligate aerobic, rod-shaped, and motile bacterium that is considered to be an important human pathogen (5). *Stenotrophomonas* species are ubiquitous microorganisms that colonize multiple natural (e.g., soils and plants) and clinical environments (6, 7). In addition, *Stenotrophomonas* spp. may have resistance to different metals and antibiotics; therefore, they qualify as promising microorganisms for bioremediation applications (6).

S. maltophilia strain PE591 was grown in 5 ml of nutrient broth medium (Difco, Holland) and incubated for 24 h at 28°C with agitation (150 × *g*). Subsequently, cells were harvested by centrifugation at 5,500 × *g* for 5 min at 4°C. Bacterial DNA was purified using the GenElute bacterial genomic DNA kit (Sigma-Aldrich, USA). A sequencing library was created using the MiSeq reagent kit (Illumina, San Diego, CA) according to the manufacturer's instructions, the MiSeq system user guide, revision L (part number 15027617; Illumina), was used in the sequencing protocol, and genome sequencing was performed with the Illumina MiSeq system (2 × 300-bp paired-end reads) (Macrogen, Seoul, South Korea). The resultant reads were subjected to quality analysis using FastQC software v. 0.11.3 (8). Sequence reads were *de novo* assembled following the A5-miseq pipeline, which includes Trimmomatic v. 0.35 to trim low-quality sequences (Phred scores of <20) and IDBA-UD v. 1.1.1 to assemble contigs (9–11). The package Stats from BBmap v. 38.76 was used to generate assembly statistics (12). The genome was annotated with Prokka v. 1.14.6 using the UniProt database (13). The completeness and contamination of genomic data were estimated by CheckM v. 1.0.13 (14). Coverage was assessed with SAMtools v. 1.9, Bowtie2 v. 2.3.4.1, and the package Pileup from BBmap v. 38.76 (12, 15, 16). Default parameters were used for all software unless otherwise noted. Finally, the

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taxonomic classification was assessed following the analysis of (i) the average nucleotide identity (ANI) obtained through the web server JSpeciesWS (<http://jspecies.ribohost.com/jspeciesws/#analyse>), which generates the ANIb (ANI algorithm using BLAST), and (ii) digital DNA-DNA hybridization (dDDH) obtained through the Type (Strain) Genome Server (TYGS) (<https://tygs.dsmz.de>) (17, 18).

The genome sequencing generated a total of 13,411,628 reads, with a total of 4,019,163,037 bp. The genome of *S. maltophilia* PE591 was assembled in 16 contigs, with a total length of 4.75 Mb and a GC content of 66.5%. Genome coverage, completeness, and contamination were $\sim 800\times$, 100%, and 0%, respectively. N_{50} and L_{50} values for the assembly were 473,413 bp and 3 contigs, respectively. Genomic functional features include a total of 4,432 genes, 4,350 protein-coding genes, 7 rRNAs, 74 tRNAs, and 1 transfer-messenger RNA.

The genomic ANI of *S. maltophilia* PE591 in relation to *Stenotrophomonas maltophilia* strain NCTC10258 (GenBank accession number [NZ_LS483377.1](#)) was 97.75% (ANIb). The dDDH (d4) value provided by the TYGS against *Stenotrophomonas maltophilia* NBRC 14161 (RefSeq assembly accession number [GCF_001591205.1](#)) was 80.2%. According to these results and the minimum parameters for taxonomic classification of prokaryotes using genomic data (19), strain PE591 is classified as a novel strain of *Stenotrophomonas maltophilia*. Unraveling the genomes of PE degraders contributes to efforts to find strategies to address the worldwide accumulation of persistent plastics. The potential of *S. maltophilia* PE591 to break and to oxidize the most recalcitrant plastic qualifies it as a promising biological tool for tackling this urgent global issue.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number [JAAOKO000000000.1](#), with BioProject accession number [PRJNA609181](#) (sample, *Stenotrophomonas* sp. strain PE591 [BioSample accession number [SAMN14238446](#)]; experiment, PE591 [SAR accession number [SRX10931469](#)]; run, PE_591_1.fastq.gz [SRA accession number [SRR14584137](#)]).

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We declare no conflicts of interest regarding this article.

REFERENCES

- Peixoto J, Silva LP, Krüger RH. 2017. Brazilian Cerrado soil reveals an untapped microbial potential for unpretreated polyethylene biodegradation. *J Hazard Mater* 324:634–644. <https://doi.org/10.1016/j.jhazmat.2016.11.037>.
- Palleroni N, Bradbury J. 1993. *Stenotrophomonas*, a new bacterial genus for *Xanthomonas maltophilia* (Hugh 1980) Swings et al. 1983. *Int J Syst Bacteriol* 43:606–609. <https://doi.org/10.1099/00207713-43-3-606>.
- Parte AC. 2014. LPSN: List of Prokaryotic Names with Standing in Nomenclature. *Nucleic Acids Res* 42:D613–D616. <https://doi.org/10.1093/nar/gkt1111>.
- Bian D, Xue H, Piao C, Li Y. 2020. *Stenotrophomonas cyclobalanopsis* sp. nov., isolated from the leaf spot disease of *Cyclobalanopsis patelliformis*. *Antonie Van Leeuwenhoek* 113:1447–1454. <https://doi.org/10.1007/s10482-020-01453-y>.
- Brooke JS. 2012. *Stenotrophomonas maltophilia*: an emerging global opportunistic pathogen. *Clin Microbiol Rev* 25:2–41. <https://doi.org/10.1128/CMR.00019-11>.
- Ryan RP, Monchy S, Cardinale M, Taghavi S, Crossman L, Avison MB, Berg G, van der Lelie D, Dow JM. 2009. The versatility and adaptation of bacteria from the genus *Stenotrophomonas*. *Nat Rev Microbiol* 7:514–525. <https://doi.org/10.1038/nrmicro2163>.
- Weber M, Schünemann W, Fuß J, Kämpfer P, Lipski A. 2018. *Stenotrophomonas lactitubi* sp. nov. and *Stenotrophomonas indicatrix* sp. nov., isolated from surfaces with food contact. *Int J Syst Evol Microbiol* 68:1830–1838. <https://doi.org/10.1099/ijsem.0.002732>.
- Wingett SW, Andrews S. 2018. FastQ Screen: a tool for multi-genome mapping and quality control. *F1000Res* 7:1338. <https://doi.org/10.12688/f1000research.15931.1>.
- Coil D, Jospin G, Darling AE. 2015. A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. *Bioinformatics* 31:587–589. <https://doi.org/10.1093/bioinformatics/btu661>.
- Peng Y, Leung HCM, Yiu SM, Chin FYL. 2012. IDBA-UD: a de novo assembler for single-cell and metagenomic sequencing data with highly uneven depth. *Bioinformatics* 28:1420–1428. <https://doi.org/10.1093/bioinformatics/bts174>.
- 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>.
- Bushnell B, Rood J, Singer E. 2017. BBMerge: accurate paired shotgun read merging via overlap. *PLoS One* 12:e0185056. <https://doi.org/10.1371/journal.pone.0185056>.
- Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.
- Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from

- isolates, single cells, and metagenomes. *Genome Res* 25:1043–1055. <https://doi.org/10.1101/gr.186072.114>.
15. Langmead B, Salzberg SL. 2012. Fast gapped-read alignment with Bowtie 2. *Nat Methods* 9:357–359. <https://doi.org/10.1038/nmeth.1923>.
 16. Danecek P, Bonfield JK, Liddle J, Marshall J, Ohan V, Pollard MO, Whitwham A, Keane T, McCarthy SA, Davies RM, Li H. 2021. Twelve years of SAMtools and BCFtools. *Gigascience* 10:giab008. <https://doi.org/10.1093/gigascience/giab008>.
 17. Richter M, Rosselló-Móra R, Oliver Glöckner F, Peplies J. 2016. JSpeciesWS: a web server for prokaryotic species circumscription based on pairwise genome comparison. *Bioinformatics* 32:929–931. <https://doi.org/10.1093/bioinformatics/btv681>.
 18. Meier-Kolthoff JP, Göker M. 2019. TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. *Nat Commun* 10:2182. <https://doi.org/10.1038/s41467-019-10210-3>.
 19. Chun J, Oren A, Ventosa A, Christensen H, Arahal DR, da Costa MS, Rooney AP, Yi H, Xu X-W, De Meyer S, Trujillo ME. 2018. Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. *Int J Syst Evol Microbiol* 68:461–466. <https://doi.org/10.1099/ijsem.0.002516>.