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GENOME SEQUENCES

Complete Genome Sequence of *Serratia quinivorans* Strain 124R, a Facultative Anaerobe Isolated on Organosolv Lignin as a Sole Carbon Source

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ABSTRACT The complete genome sequence of the gammaproteobacterial isolate *Serratia quinivorans* 124R consists of 5 Mb over 2 scaffolds and a G+C content of 52.85%. Genes relating to aromatic metabolism reflect its isolation on organosolv lignin as a sole carbon source under anoxic conditions as well as the potential for lignin biorefinery applications.

Lignin is an abundant, natural resource for aromatic chemical production; yet, only 1% to 2% of lignin produced annually in the paper and pulp industry is processed (1). Bacterial anoxic depolymerization techniques need further development to valorize lignin, but exact mechanisms remain largely undefined (2–4). Known enzymes include glutathione *S*-transferases (GSTs) in the β-etherase system (5–8); however, isolation and characterization of anaerobic lignin-degrading bacteria will help advance understanding of and discover new mechanisms.

In this study, temperate forest soil was used to inoculate minimal medium (9) containing organosolv lignin as the sole carbon source under anoxic conditions and was transferred onto fresh medium every 4 to 9 weeks for 465 days. Consortia were diluted to 1 to 5 cells/ml onto a 0.001% five-carbon mixture (10) incubated anaerobically in the dark at 25°C for 6 weeks and then were streaked onto R2A agar for colony isolation. To screen for lignin depolymerization capabilities, isolates were grown anoxically on R2A plates containing lignin-mimicking dyes, malachite green and Congo red (11). Isolate 124R was selected for genome sequencing due to the formation of clearing zones for both dyes.

Genomic DNA was extracted using the Qiagen Genomic-tip protocol for bacteria. A >10-kbp PacBio SMRTbell library was constructed and sequenced on the PacBio RS II platform (12). This generated 296,135 filtered subreads, totaling 591,980,396 bp. Raw reads were assembled using Hierarchical Genome Assembly Process 3 (HGAP3; SMRT Analysis v2.3.0.p5) (13). The final draft assembly contained 2 contigs in 2 scaffolds, covering a total of 5,025,603 bp, with an N/L_{50} value of 1/4,986,851, a G+C content of 52.85%, and an average sequence coverage of 86.8×. Gene prediction and functional annotation were performed using the Department of Energy Joint Genome Institute (DOE JGI) annotation pipeline (14), available through the Integrated Microbial Genomes data management system (15, 16). 124R contains 4,636 predicted protein-coding sequences, of which 86.06% were assigned a function, as well as 85 tRNAs and 7 rRNA operons. Putative aromatic metabolic pathways were analyzed using the MetaCyc and KEGG databases via the Integrated Microbial Genomes and Microbiomes (IMG/M) database

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(16). Seventy-six enzymes were identified (encompassing 41 functions under KEGG map 01220), including complete metabolism of benzoate and 4-hydroxyphenylacetate. Genes for anaerobic degradation of gallate, phenylacetate, and 4-coumarate were found within MetaCyc. Additionally, two homologues to the *Nu*-class GSTs were identified via IMG/M NCBI BLAST (16).

The 16S rRNA gene of 124R was queried using NCBI BLASTn (17) and shared 99% sequence identity with *Serratia quinivorans* strain 4364 and *Serratia proteamaculans* DSM 4543, which are in the class *Gammaproteobacteria* and family *Yersiniaceae*. However, 124R shared <89% average nucleotide identity (18) and <95% two-way average amino acid identity (19) with *Serratia quinivorans* (strains NCTC13194, NCTC13189, and NCTC11544) and *Serratia proteamaculans* (strains 568, MFPA44A14, and NCTC10861). DNA-DNA hybridization (DDH) calculations (20) resulted with a <34% DDH estimate across comparisons, further supporting this species demarcation (21). These findings suggest that 124R is a distinct *Serratia* species with both lignin depolymerization and catabolic potential for lignin biorefinery applications.

Data availability. This whole-genome shotgun project has been deposited in GenBank under accession no. NZ_SHMO00000000 (SRA accession no. SRX5216996). The version described in this paper is the first version, NZ_SHMO01000000.

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