AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Draft Genome Sequence of *Serratia* sp. 1D1416

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ABSTRACT This work reports the draft genome of *Serratia* sp. 1D1416. The assembled genome contains a 5,552,016-bp circular chromosome. The strain was discovered in a mixed culture from a gall isolated from *Euonymus japonicas*.

Although strains of *Serratia* are often associated with human infections, such as *Serratia marcescens* and the *Serratia liquefaciens* complex, other *Serratia* spp. ("unusual" *serratiae*) are isolated from the environment (1, 2). Published unusual *Serratia* spp. include *Serratia ficaria*, *Serratia fonticola*, *Serratia odorifera*, *Serratia plymuthica*, and *Serratia rubidaea* (3). *Serratia ficaria* was the first nonpathogen microbe associated with plant growth and was characterized in 1979 as an important part of the fig tree ecosystem (4). *Serratia plymuthica*, *S. liquefaciens*, and *S. rubidaea* have been observed as part of the rhizosphere microbiome (5, 6) and may have antibacterial or antifungal properties or both (7). The recently isolated strain *Serratia* sp. 1D1416 appears to have low-level resistance to tetracycline but is susceptible to chloramphenicol, kanamycin, and gentamicin. This is a typical feature of *Serratia* spp. and may include the entire genus *Serratia* (3). Here we present the novel genome from *Serratia* sp. 1D1416, isolated from a mixed culture along with an *Agrobacterium tumefaciens* isolated from a *Euonymus japonicus* (Japanese spindle) gall within the UC Davis microbe collection of Dr. Kobe. The strain was grown in Luria broth at 30°C with shaking at 200 rpm.

Genomic DNA was isolated from our strains (8) using the Qiagen blood and cell culture DNA Maxi kit (number 13362) and genomic DNA buffer set (number 19060) (9). DNA samples were evaluated with gel electrophoresis and quantified with a 2100 Nanodrop spectrophotometer (Thermo Fisher Scientific) and a Qubit fluorimeter (Invitrogen) with the Qubit dsDNA HS assay kit (Invitrogen). The genomic DNA was sheared with g-TUBE (Covaris). A 20-kb DNA library was constructed according to the manufacturer's instructions and the BluePippin size selection system, and it was sequenced using single-molecule real-time (SMRT) sequencing technology on a PacBio RS system. SMRT sequencing data were generated at an average coverage of 88.53×, with a mean read length of 16,608 bp. *De novo* genome assembly was conducted with the sequence reads using the Hierarchical Genome Assembly Process (HGAP) workflow (SMRT Portal; Pacific Biosciences), protocol RS_HGAP_Assembly.3 (10), and SMRTAnalysis_2.3.0 software (https://www.pacb.com/wp-content/uploads/2015/09/SMRT-Analysis-Software-Installation-v2.3.0.pdf). This allowed the generation of a single contig with an N_{50} contig length of 5,577,755 bp. The linear DNA was manually circularized with a 25,739-bp chimeric overlap. The circular chromosome is composed of 5,552,016 bp, with a GC content of 59.6%. Assembled and raw read sequences were entered into the National Center for Biotechnology Information (NCBI), and BLAST was used for identification (http://blast.ncbi.nlm.nih.gov/). During genome comparison with other published *Serratia*, a unique cluster of opine genes were detected. We used this gene cluster to develop primers as a marker to identify specifically the *Serratia* sp. 1D1416 genome. Primers STNop 5304 F61 5′ ggtgctgaaaagataatgaatccgcacagg and STNop 5304 R61 5′ cctggttggaaatgaagaaattcaggtaagcactg were used to produce a unique 1,560-bp am-

Citation Alabed D, Huo N, Gu Y, McCue KF, Thomson JG. 2019. Draft genome sequence of *Serratia* sp. 1D1416. Microbiol Resour Announc 8:e01354-18. https://doi.org/10.1128/MRA.01354-18.

Editor Julie C. Dunning Hotopp, University of Maryland School of Medicine

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Received 22 October 2018
Accepted 14 December 2018
Published 17 January 2019

plicon from a unique ABC transporter substrate-binding protein gene. Automated annotation was performed with the Rapid Annotation Using Subsystem Technology (RAST) Pipeline for annotation of the genome (11). *Serratia* sp. 1D1416 contains 5,234 predicted coding sequences, 570 subsystems, and 118 predicted RNA-coding genes.

Data availability. The whole-genome assembly for *Serratia* sp. 1D1416 has been deposited in DDBJ/ENA/GenBank under the accession number CP032738, BioProject accession number PRJNA493633, and SRA accession number SRX5036357.

ACKNOWLEDGMENTS

This work was supported by the USDA Agricultural Research Service CRIS project 2030-21000-020. Mention of trade names or commercial products is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture. The USDA is an equal opportunity provider and employer.

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