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GENOME ANNOUNCEMENT

Draft Genome Sequence of the Biocontrol Strain *Serratia plymuthica* A30, Isolated from Rotting Potato Tuber Tissue

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***Serratia plymuthica* A30 is a Gram-negative bacterium expressing antagonistic activity toward blackleg- and soft rot-causing *Dickeya* sp. biovar 3 ("*Dickeya solani*"). Here, we present the draft genome sequence of strain A30, which has been isolated from rotten potato tuber tissue.**

Serratia plymuthica cells are Gram-negative, rod-shaped members of the genus *Serratia* in the family *Enterobacteriaceae*. *S. plymuthica* is widely found in nature and has a worldwide distribution (4). The bacterium is known for production of antimicrobial compounds (1, 6). Many isolates are successfully used for biological control of fungal and bacterial plant pathogens (3, 4, 9). *S. plymuthica* A30 (2) showed considerable activity toward "*Dickeya solani*," a blackleg- and soft rot-causing organism belonging to the family *Enterobacteriaceae* (10), both *in vitro* and on potato plants (2, 3). Strain A30 has been characterized for the features possibly involved in the antagonism and for promoting its survival in the environment (3).

The draft A30 genome sequence was determined using Roche 454 Titanium (8) (2.8×10^5 reads; median read length, 517 bp). The reads were assembled into 80 contigs with a total length of 5.55 Mbp (17.4× coverage) using NEWBLER v2.3 software (7). These 80 contigs were concatenated into two pseudomolecules with spacers between contigs that introduce starts and stops in all six frames. Structural and functional annotation was obtained from the IGS Annotation Service (PMID 21677861; Institute for Genome Sciences, University of Maryland School of Medicine) automated pipeline (http://ae.igs.umaryland.edu/cgi/index.cgi). The genome was mapped and annotated using the available genome sequence of *Serratia proteamaculans* 568 (http://www.ncbi.nlm.nih.gov/genome/1459), a species which is closely related to *S. plymuthica*. The draft genome sequence of strain A30 contains 5,557,279 nucleotides (pseudomolecule 1, 5,460,057 bp; pseudomolecule 2, 97,222 bp) and an average GC content of 52.3%. The draft genome comprises 5,381 predicted protein-encoding genes (PEGs) and 65 tRNA and 4 rRNA genes. The average gene length was estimated between 730 and 900 bp. Of the total 5,381 PEGs, 4,365 (81.1%) were assigned functions (some general, some specific) and 792 (14.7%) were genes for either hypothetical proteins or named proteins of unknown function. Of the 4,365 PEGs classified, 2,004 code for transport and binding proteins, 1,667 are involved in cellular processes, 324 take part in transcription, and 281 take part in energy metabolism. Of the PEGs, 188 are connected with cell envelope biosynthesis; 146 are involved in protein secretion, modification, folding, and degradation; 116 participate in protein synthesis; 94 participate in biosynthesis of cofactors and carriers; and 63 participate in amino acid biosynthesis. Of the PEGs, 51 participate in DNA metabolism and 46 in nucleotide biosynthesis and turnover; 45 PEGs contribute to signal transduction; 42 classified PEGs govern protein, DNA, and RNA interactions. Another 41 PEGs are responsible for central metabolism and 22 for fatty acid and phospholipid metabolism. Finally, 21 are connected with mobile and extrachromosomal elements. No homologs of genes coding for proteins involved in carbapenem, prodigiosin, tripyrrole, or serracin P biosynthesis, antimicrobials often produced by other members of the *Serratia* genus (4, 5), were found in the A30 genome. The information provided in the draft genome sequence of *S. plymuthica* A30 reported here will enable further studies on features involved in biological control of this strain and other *S. plymuthica* strains used as antagonists against fungal and bacterial plant pathogens.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AMSV00000000. The version described in this paper is the first version, AMSV01000000.

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