Draft Genome Sequence of the Antagonistic Rhizosphere Bacterium *Serratia plymuthica* Strain PRI-2C.

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***Serratia plymuthica* strain PRI-2C is a rhizosphere bacterial strain with antagonistic activity against different plant pathogens. Here, we present the 5.39-Mb (G+C content 55.67%) draft genome sequence of *S. plymuthica* strain PRI-2C with the aim of providing insight into the genomic basis of its antagonistic activity.**

Serratia plymuthica strain PRI-2C is a Gram-negative rod-shaped member of the Enterobacteriaceae, which was isolated from the maize (*Zea mays* L.) rhizosphere (5). The maize plants were grown on a long-term ecological site at the Wildekamp field, located in Bennekom , The Netherlands (8)

Serratia spp. are known as ubiquitous inhabitants of the rhizospheres of different plant species and include strains that are antagonistic to soil-borne pathogens (1-3, 7). *S. plymuthica* strain PRI-2C exhibits very strong antimicrobial activity against a range of phytopathogens such as *Rhizoctonia solani* anastomosis groups AG3 and AG2; *Verticillium dahliae*, *Fusarium oxysporum*, *Fusarium moniliforme* and *Pythium spp* (4, 5). The biological activity of this strain is linked to the production of a secondary metabolite (pyrrolnitrin), to chitinase activity and to the emission of broad-spectrum volatile organic compounds (5, 6).

Based on the 16S rRNA gene sequence, *Serratia plymuthica* strain PRI-2C shared high similarity (97%) with *Serratia plymuthica* RVH1.

The genome sequence of *Serratia plymuthica* strain PRI-2C was determined based on paired-end sequencing using the Illumina GAIIx platform (21,182,518 reads). The pair-end reads were *de novo* assembled using the CLC Genomic Workbench version 4.7.2 (CLC bio). The resulting assembly consists of 195 contigs with an average length of 27,646bp. The draft genome, of about 5.39Mb, has a G+C content of 55.67%.

Annotation was performed on the assembled contig sequences using the IOGMA system of Genostar. The annotation provided genomic data constructed from the annotations imported from the Genostar MicroB database. MicroB integrates and updates data from several databases like

Genome Reviews: http://www.ebi.ac.uk/GenomeReviews/; UniProtKB: http://www.uniprot.org; ENZYME: http://www.expasy.org/enzyme/; Gene Ontology: http://www.geneontology.org/ and KEGG: http://www.genome.ad.jp/kegg.

The annotation procedure predicted 4,435 protein-encoding sequences (CDS). The total size of the CDS regions, including overlapping ones is 4,448,445 bp.

In the draft sequence, we were able to identify several predicted genes or operons that are related to antagonistic activity, such as chitinases (3 genes); cation-binding chitinase activity (3 genes); antibiotic

biosynthesis monooxygenase (7 genes); an aerobactin siderophore biosynthesis protein and proteases (12 genes). Moreover, using the antiSMASH and NaPDos software for rapid identification, annotation and analysis of secondary metabolite biosynthesis genes, five PKS/NRPS gene clusters were identified. These gene clusters are presumably involved in the production of antimicrobial nonribosomal peptides such as (predicted) pyochelin, bacitracin, microcystin, bacillibactin and cyclomarin.

Furthermore, several genes for the biosynthesis of amylases and cellulases were detected, which may be involved in the utilization of plant-derived polysaccharides in the rhizosphere or even in the endoplant.

A more detailed analysis of this genome and comparative analysis with other *Serratia* spp. genomes and rhizobacterial genomes remain to be done in future studies.

Nucleotide sequence accession number.

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession AJTB00000000. The version described in this paper is the first version, AJTB01000000.

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