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Draft Genome Sequence of *Serratia proteamaculans* MFPA44A14-05, a Model Organism for the Study of Meat and Seafood Spoilage

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ABSTRACT In this study, we present a draft genome sequence of *Serratia proteamaculans* MFPA44A14-05. This strain was isolated from a spoiled organic modified-atmosphere-packed beef carpaccio. The draft genome sequence will contribute to the understanding of the role of the *S. proteamaculans* species in meat and seafood spoilage.

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Members of the *Serratia* genus have a highly ubiquitous nature. Like most *Enterobacteriaceae*, they are commonly found in the digestive tracts of animals but also thrive very competitively in water and soil environments (1). Some species, like *Serratia proteamaculans*, are also well known for contaminating and spoiling protein-rich food, like raw meat and seafood (2–4), using a strong capacity to resist CO_2-enriched modified atmosphere (MA) (5) and to metabolize protein and amino acids for growth (6). Despite this key role in food waste, very little is known about the genomic background of *S. proteamaculans*, and the genomes of only two strains, those of the plant growth-promoting strain S4 (7) and the poplar tree root endophyte strain 568 (8), are currently available.

S. proteamaculans strain MFPA44A14-05 was isolated in 2009 from a highly spoiled slice of organic modified atmosphere-packed beef carpaccio (9). After 14 days of storage at 8°C, the strain was dominant and had reached a population level of 6.7 $\log_{10}$ CFU g^{-1}, turning the carpaccio slices into a brown/greenish color and diffusing a strong putrid smell. We thus undertook the genome sequence of this strain in order to use it as a model to understand the role of *S. proteamaculans* in meat and seafood spoilage.

The whole-genome sequencing of *S. proteamaculans* MFPA44A14-05 (CIP 110939) was carried out by Eurofins MWG Operon laboratories (Ebersberg, Germany) using Illumina MiSeq 2 × 150-bp paired-end libraries. The 2.94 million reads were assembled *de novo* using the Velvet software (10) after choosing the best k-mer value of 73. The draft assembly resulted in 80 contigs from 1,783 to 252,892 bp (N_{50}, 128,235 bp). The contigs were aligned against the *S. proteamaculans* strain 568 complete genome using progressiveMauve (11) to give one high-quality scaffold (5,368.81 bp; coverage, 46×), with an overall G+C content of 54.85%. Annotation performed with the MicroScope platform (12) detected 5,075 coding sequences (CDSs), 29 pseudogenes, 4 rRNAs, and 76 tRNAs. The MFPA44A14-05 strain has been deposited in the CIP Culture Collection under the reference CIP 110939.

The high proteolytic capacity of *S. proteamaculans* MFPA44A14-05 is confirmed by the detection of at least 5 extracellular proteases or proteinases, including a serralysin-like proteinase (13), a subtilisin-like protease, and an overall set of 18 peptidases. Similarly, the number of genes involved in peptide and amino acid metabolism (n =

594) largely exceeds the number of genes involved in carbohydrate metabolism (n = 473). This COG group is the biggest in proportion (11% of the whole genome). We also noticed that the *S. proteamaculans* MFPA44A14-05 genome contains biogenic amine production activity arising from amino acid catabolism, which involves two genes encoding a lysine decarboxylase to produce cadaverine (*cadA* and *ldcC* genes) and all genes of the polyamine superpathway II (*speA* to *speF*) to produce agmatine, putrescine, and spermidine from arginine, ornithine, and *S*-adenosylmethionine.

Accession number(s). This whole-genome shotgun project has been deposited in ENA BioProject number PRJEB20089 and assembly under the accession numbers FWWG01000001 to FWWG01000080. The version described in this paper is the first version.

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