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PHYLOGENOMICS AND INCONSISTENCES IN THE TAXONOMY OF *Serratia marcescens*: DATA FROM WHOLE GENOMES[1] / Análise filogenômica e inconsistências na taxonomia de *Serratia marcescens*: dados de genomas completos.

L. C. Ferreira[2], M. V. C. Viana[3], D. Roberts[4], J. Maul[4], V. A. C. Azevedo[3], J. T. de Souza[2]. [2]Department of Plant Pathology, Federal University of Lavras, Lavras, Brazil / [3]Laboratory of Cellular and Molecular Biology, Federal University of Minas Gerais, Belo Horizonte, Brazil / [4]Agricultural Research Service, United States Department of Agriculture. E-mail: larissacarvalhoferreiraa@gmail.com

Serratia marcescens is a Gram-negative bacteria with multiple ecological functions, including pathogenicity to plants, insects and humans, symbiosis with fungi, plant growth promotion and biocontrol of plant pathogens. The aim of this study was to perform a comparative genome analysis of the following *Serratia marcescens* strains deposited in public databases: strain RSC-14, a plant growth promoter; B3R3, a phytopatogen; U36365, a clinical strain; FGI94, a fungal symbiont; and the newly sequenced strain N4-5, a biocontrol agent. Whole genomes of these isolates were analyzed in PATRIC (Pathosystems Resource Integration Center, www.patricbrc.org). Average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH) was calculated among all the strains using JespeciesWS and ggdc 2.1, respectively. The results showed that the genome sizes varied from 4858216 bp in strain FGI94 to 5594610 bp in B3R3, the GC% content oscillated between 58.7% in U36365 and 59.7% in N4-5 and the number of CDS varied from 4425 in strain FGI94 up to 5223 in strain B3R3. All strains had one chromosome and only B3R3 and N4-5 harbored plasmids. The analysis of specialty genes showed that the phytopathogenic strain B3R3 has 221 genes related to virulence factors (VF) and 71 antibiotic resistence (AR) genes while the average of the other strains was 208 genes for VF and 56 for AR. The results for the measures of genomic relatedness presented values above 95% (ANI) and 70% (dDDH) for *S. marcescens* N4-5, RSC-14, B3R3 and U36365, which indicates that they are from the same species. On the other hand, the data obtained for strain FGI94 were below the cutoff values for both ANI (average between strains=81.6%) and dDDH (average between strains=37.9%). Phylogenetic analyses done with sequences of the 16S of the rDNA and with whole genome sequences performed with the PEPR (Phylogenomic Estimation with Progressive Refinement) are in agreement and evidentiate the proximity of strain FGI94 with *S. rubidaea* 1122. The ANI and dDDH for FGI94 and 1122 were 97.36% and 85.2%, respectively. Therefore, all three criteria to define bacterial species, namely ANI, dDDH and 16S sequences corroborate the reclassification of strain FGI94 as *S. rubidaea*. The precise taxonomical identification of strains is essential in the determinations of Pan and Coregenomes of bacterial species.

Key words: Bacterial species; Comparative genomics; *Serratia rubidaea*

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