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GENOMIC ANALYSIS OF A PATHOGENIC STRAIN OF *Clavibacter tessellarius* ISOLATED FROM WHEAT IN ARGENTINA

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The genus *Clavibacter* (family Microbacteriaceae) comprises gram-positive actinobacterial species that infect a variety of agricultural crops, including alfalfa, maize, pepper, potato, tomato, and wheat. *Clavibacter tessellarius*, which causes bacterial mosaic in wheat, was first reported in 1976 in Nebraska, USA. Since then, strains suspected to be *C. tessellarius* have been occasionally isolated from wheat samples worldwide. In Argentina, this species has been observed in wheat since 2016 in Entre Ríos, where it causes bacterial mosaic in certain cultivars, and it was recently reported in wheat in Córdoba. Unlike other bacterial infections and in the presence of high ambient humidity, bacterial exudate is not typically observed on the lesions. The primary means of disease transmission is through seeds. Our study aimed to investigate the genomic diversity of bacterial species associated with foliar lesions on wheat in Córdoba, Argentina. A total of 40 bacterial strains were isolated from foliar symptoms, of which 16 (40%) were gram-positive bacteria. Among these, 6 (38%) gram-positive, orange-pigmented strains were identified as *C. tessellarius*. One strain (ARGTR 8-1) was selected for genomic sequencing (MinION seq), and its species identity was confirmed through average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH) comparisons with type species (98% ANI, 97% dDDH, *C. tessellarius* ATCC 33566 type strain). Pathogenicity tests exhibited the ability of *C. tessellarius* ARGTR 8-1 to cause symptoms in two wheat varieties. Genomic analyses revealed the presence of numerous genes involved in virulence mechanisms described in a closely related, well-described strain of *C. michiganensis*, with high homology. Additionally, strain ARGTR 8-1 contained a plasmid, the analysis of which revealed high homology with pCM1 plasmid. This study provides a comprehensive phylogenetic analysis and whole-genome data of this bacterial pathogen, establishing a foundation for omics-based approaches to explore genetic diversity and virulence mechanisms. Effective crop disease management will require integrated strategies, and these findings contribute to the development of approaches aimed at improving wheat health and productivity in the face of bacterial diseases.

Palabras clave: Gram-positive bacterial phytopathogen – phylogenomic – effectors – wheat