

## PAN-GENOME AND BIOSYNTHETIC GENE CLUSTERS IN *Bacillus velezensis* RHIZOBACTERIA, AND PROTECTION OF CHILI PEPPER AGAINST ROOT ROT PATHOGENS.

Saúl Fraire-Velázquez, Hilda Mabel Sosa-Esquivel, Yumiko De la Cruz-Rodríguez, Alejandro Alvarado-Gutiérrez.

Biología Integrativa de Plantas y Microorganismos, Unidad de Ciencias Biológicas, Universidad Autónoma de Zacatecas. Av. Preparatoria s/n Col. Agronómica, Zacatecas Zac. CP.- 98067.

E-mail: [sfraire@uaz.edu.mx](mailto:sfraire@uaz.edu.mx)

Biocontrol of phytopathogens is a sustainable strategy to reduce reliance on broad-spectrum pesticides that negatively affect the environment. Root rot in chili (*Capsicum annuum*), primarily caused by *Phytophthora capsici*, *Fusarium solani*, *Rhizoctonia solani* and *Fusarium oxysporum*, is a major production constraint in Mexico, the world's second-largest producer of green chili<sup>1</sup>. The bacterium *Bacillus velezensis* has emerged as a promising biocontrol agent. Previous isolation of rhizobacteria from cultivated and wild plants in Zacatecas, Mexico, identified four *B. velezensis* strains (2A-2B, 3A-6A, 2A-10A and 3A-25B) with high *in vitro* inhibition rates against root rot pathogens; their genomes have been sequenced<sup>2</sup>. This study evaluated their ability to induce systemic resistance (ISR) in chili plants against a pathogen consortium causing root rot, using a split-root inoculation system. Genomic analyses explored correlations between phenotype and biosynthetic gene clusters (BGCs) for antibiotics, and to characterize the pan-genome and core genome of the four strains, in comparison with global *B. velezensis* strains available in the NCBI database. Results demonstrated that pre-inoculation with individual bacteria strains reduced disease incidence by 49-65%, with 2A-2B being the most effective and 3A-25B the least. The four strain consortium achieved an 87.9% reduction. All strains contained 21-26 BGCs; notably, 2A-2B possessed two additional clusters for the biosynthesis of thermoactinoamide A and butirosin A-B, both bactericides. The pan-genome comprised 4,163 genes, of which 3,391 constitute the core genome. Strain 3A-25B contained the largest number of singletons (259) compared to 23-26 found in the other strains; most of these singletons encode proteins of currently unknown function. Phylogenetic analysis grouped strains 2A-2B, 3A-6A and 2A-10A into the same clade, while 3A-25B consistently clustered separately at continental and global scales. In conclusion, the tested *B. velezensis* strains applied individually or in consortium, effectively induced ISR in chili plants and substantially reduced root rot incidence, achieving nearly 88% reduction. Strain 2A-2B stood out for its high biocontrol performance. 3A-25B phylogenetically distant from the others. Differences in singletons could explain in part the differential phenotype in these *B. velezensis* strains. These results underscore the potential of specific bacteria, particularly 2A-2B, as valuable biocontrol agents contributing to reduced pesticide use in agriculture.

### References

1. Aguirre Hernández E. y Muñoz Ocotero V. (2015). *Ciencia*, 16-23.
2. Martínez-Raudales, I., De la Cruz-Rodríguez, Y., *et al.* (2017). *Stand in Genomic Sci* 12, 73.