

Isolation and Characterization of Lytic Bacteriophages from *Ralstonia solanacearum* Phylotype II in Ecuador

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Abstract

Ralstonia solanacearum is the causative agent of a wilting disease in different plant species. In banana, *R. solanacearum* causes the so-called Moko disease, which severely impairs fruit production. Since Ecuador is a top producer and exporter of bananas, the impact of Moko is extremely worrying. Chemical and biological control of Moko have limitations, making it necessary to find other approaches. The purpose of this study was to explore an alternative strategy for disease management using bacteriophages. *R. solanacearum* strains were isolated from banana fields naturally infested with Moko in Ecuador, and they served as the bacterial hosts for the exploration of phages. A total of 10 different bacteriophages were isolated from banana fields and displayed clear, circular plaques measuring 1–3 mm. We tested the host range of the bacteriophages using the spot test method on 65 different *R. solanacearum* strains representing all phylotypes of the species complex and 35 different sequevars. Results show that bacteriophages have high specificity, producing lysis plaques in strains belonging to phylotype IIB, sequevar 4. Based on plaque lysis and genomic sequence analyses, the bacteriophages belong to different viral families, grouped into the Podoviridae or the Myoviridae. We are conducting additional analyses to improve bacteriophage growth conditions, stability, and multiplication rates. In parallel, we are testing bacteriophages to determine their effectiveness in suppressing wilting symptoms in banana plants under greenhouse conditions. In conclusion, these bacteriophages are promising agents for the development of virus-based biocontrol for banana Moko disease, an alternative highly sought by Ecuadorian farmers.

Keywords

Bacteriophage, Moko disease, *Musa* spp., Banana and Plantain, Biocontrol.