Harnessing *Serratia fonticola* (EBS19) as a Biocontrol Agent against *Botrytis cinerea*

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Abstract

Botrytis cinerea (*Bc*), a plant pathogenic fungus, causes gray mold disease and rapidly develops resistance to fungicides in cultivation areas. In this study, a gram-negative, soil-borne bacterial colony was isolated and exposed to phenol vaporization for 2 days. The colonies treated with phenol displayed restricted growth of *Bc*'s spores. The highest antibiosis effect was further confirmed using agar bioassays based on their ability to stably suppress pathogen growth. In vitro assays with the colonies showed an 84% inhibition of pathogen growth at 7 dpi using a one-layer agar diffusion test, and a 70% inhibition using a double-layer agar diffusion test, compared to the control plates. *In vivo* tests involving fruit inoculation, bacterial suspension, and filtrate showed a significant suppression of the pathogen's mycelium growth at 11 and 14 dpi, compared to the control group. The bacterial strain was identified as *Serratia fonticola* (EBS19) through whole genome sequence analysis. Comparative genomic analysis using the KEGG pathway database revealed genes encoding enzymes that play a role in inhibiting pathogen growth by *S. fonticola*. Additionally, BIOLOG analyses identified specific carbon sources utilized by the bacterial strain. This information could be advantageous for formulating an effective biopreparate composition, ensuring the stability of the bacterial strain's population. Computational studies were conducted to model the interaction between the stress regulator protein (BAG1) of the pathogen and the bacterial glycoside hydrolase enzyme. The predictive modeling results could complement the unclear property of bacterial glycoside hydrolase enzyme activity and its inhibitory effect on the pathogen's stress regulator protein.

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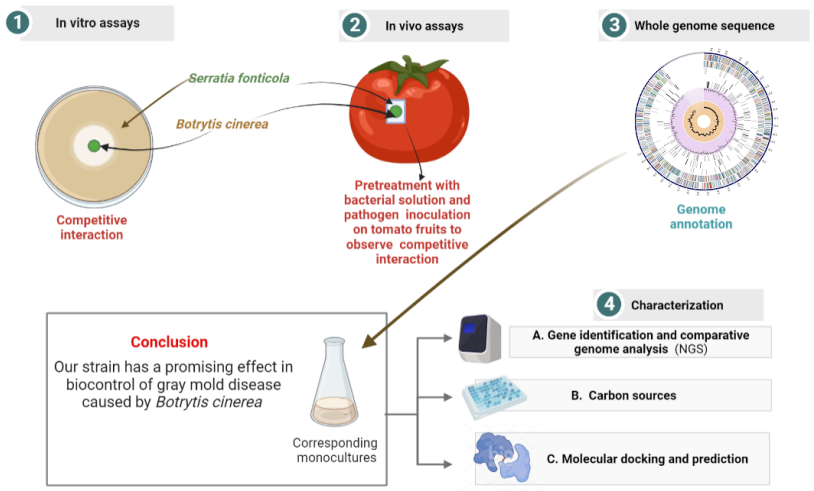

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