

Puerto Real, 20th May 2024

Dear Reviewer,

We deeply appreciate your detailed analysis and constructive comments on our manuscript titled "Identification of Novel Genes in the Secondary Metabolism of *Botrytis cinerea* Using Bioinformatic Methods". Your observations have been invaluable in enhancing the quality of our work. Below, we provide responses to each of your comments and explain the modifications made to the manuscript.

<i>Comments</i>	<i>Responses</i>
1. The significance of the biosynthesis of secondary metabolites needs to be emphasized in the introduction section, particularly the potential applications in practice.	We have revised the introduction to further emphasize the significance of secondary metabolite biosynthesis and their practical applications in agriculture and fungicide development. Specifically, we have elaborated on how these compounds serve as potential targets for new antifungal agents and how understanding their pathways can lead to advancements in agricultural biotechnology. These changes are reflected in lines 86 to 105 of the revised manuscript.
2. For each protein target, it is better to include further interpretation or analysis for the identified genes. For example, for the genes located in domains that code for PKS, the authors analyzed the potential mechanisms of how these genes are involved in the pathogenic advantages. But for other targets, like STC and DTC, the corresponding information is missing.	We have revised sections 2.2, 2.3, 2.4, and 2.5 to provide more detailed analysis and context for the genes within the NRPS, STC, DTC, and DMATS domains in <i>Botrytis cinerea</i> . Specifically, we have expanded the discussion on the functional roles of these genes and their contributions to the pathogenicity and adaptability of the fungus. Section 2.2: We added detailed insights into the roles of NRPS genes in synthesizing non-ribosomal peptides, which directly impact host plant immune responses and facilitate fungal colonization. We also highlighted the evolutionary advantages provided by the diversity of these

	genes. Section 2.3: The discussion on STC genes was enhanced to emphasize their role in producing sesquiterpenes, which affect plant physiology and immune responses. We discussed the evolutionary significance of these genes and their contribution to the fungus's adaptability. Section 2.4: We provided a more comprehensive analysis of DTC genes, the discovery of a new gene within this domain. Section 2.5: We expanded the analysis of DMATS genes, focusing on the discovery of a new gene and its implications for the metabolic pathways in <i>B. cinerea</i> . We discussed the potential roles of these genes in the fungus's adaptability and pathogenicity.
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We hope that these modifications meet your expectations and are in line with your suggestions. Thank you again for your valuable feedback, and we trust that the revised version of our manuscript meets your standards of quality.

Yours sincerely,



Dr. Carlos Garrido Crespo
Laboratorio de Microbiología.
Facultad de Ciencias del Mar y Ambientales (CASEM)