

TITLE: SECONDARY METABOLITE BIOSYNTHETIC GENE CLUSTER OF THE BANANA ANTHRACNOSE PATHOGEN *Colletotrichum musae*

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ABSTRACT:

Bananas (*Musa* spp.) are an important food crop and a staple food for more than 400 million people. Bananas are highly susceptible to infections, and anthracnose disease caused by fungus from *Colletotrichum* genus (especially *Colletotrichum musae* described as banana-specialist pathogen) is a major post-harvest problem. The unavailability of genomic sequences from *C. musae* is a hindrance for characterization of fungal virulence determinants. Here we present the genome sequence and annotation of *C. musae* isolate GM20. We focused in secondary metabolites (SMs) as we recently provided evidences of their participation in fungal infection. The genes involved in SM synthesis are underexploited as virulence determinants and despite progress in the study of pathogen-host relationships, SM production in *Colletotrichum* spp. is uncharacterized. To better understand the metabolic potential of *C. musae*, a deep survey and description of SM biosynthetic gene clusters (BGCs) was conducted. BGCs survey and description was also conducted in the close relative generalist pathogen *Colletotrichum gloeosporioides*, in order to compare the metabolic potential of specialist and generalist species. Among 74 BGCs identified in *C. musae*, a total of 15% have already characterized orthologs in other fungal species, allowing insights on their final products. From this work, apicidin- and alternapyrone-like compounds gene clusters were identified in *C. musae* with presumably virulence-related roles. Moreover, 97% of the identified BGCs of *C. musae* were conserved in *C. gloeosporioides*, while only 75 % of the identified BGCs of *C. gloeosporioides* were conserved in *C. musae*. Notably, fragments of one of the absent gene clusters were found in *C. musae* genome, indicating BGC loss/pseudogenization. These results reinforce the importance of SMs in phytopathogens infection and suggest that SM acquisition/retention could be crucial for host range in *Colletotrichum* species. Moreover, the detailed analyses conducted paves the way for future in-depth research.

KEYWORDS: *Colletotrichum musae*, anthracnose, secondary metabolite biosynthetic gene clusters, phytopathogens.

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