ABSTRACT - APPLICATIONS OF BIOTECHNOLOGY IN ENVIRONMENTAL AND AGRICULTURAL AREAS;

A NOVEL AMAZONIAN TRICHODERMA SPECIES ACHIEVES COMPLETE IN VITRO INHIBITION OF MONILIOPHTHORA RORERI

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Frosty pod rot, caused by Moniliophthora roreri, remains one of the most destructive diseases of cacao in the Americas, demanding biological control options that can be integrated into sustainable management programs. Since 2021, the pathogen has been detected in northern Brazil and currently poses a threat to cacao and cupuaçu cultivation. In this work, we selected biocontrol agents from the Amazon biome, focusing on Trichoderma spp., ubiquitous filamentous fungi widely deployed in agriculture as biological control agents. Their efficacy derives from multiple, complementary modes of action, including mycoparasitism, antibiosis through secondary metabolites, competition for space and nutrients, rhizosphere competence, and induction of systemic resistance in plants. These attributes, coupled with biosafety and formulation versatility, have enabled successful applications across diverse crops and environments. To identify promising antagonists, ninety-six Trichoderma isolates originating from Amazonian habitats were screened in vitro against M. roreri using dual culture assays. The isolate CPAA-TM58, obtained from sediments of the Juruá River, was prioritized based on superior performance. Molecular identification was conducted to resolve its taxonomic placement, and whole-genome analyses were used to investigate biosynthetic potential. Genome mining of biosynthetic gene clusters (BGCs) was carried out to assess the diversity of putative secondary metabolite pathways. Results demonstrated that Trichoderma sp. CPAA-TM58 completely suppressed M. roreri growth in dual culture, achieving 100% inhibition and displaying pronounced mycoparasitic behavior at the interaction zone. Molecular and phylogenetic evidence based on partial sequences of tef1a and rpb2 genes supported that CPAA-TM58 represents a novel Trichoderma species, with Trichoderma stilbohypoxyli as its sister group. Genome mining revealed 44 BGCs spanning multiple secondary metabolite classes consistent with antifungal potential, including nonribosomal peptide synthetases, polyketide synthases, terpene pathways, hybrids, and RiPP-like loci. This genomic repertoire aligns with the observed phenotype and indicates a rich arsenal of mechanisms for pathogen inhibition. Taken together, the in vitro antagonism, mycoparasitic activity, and expanded BGC content position CPAA-TM58 as a strong candidate for biocontrol development against M. roreri, offering promising prospects for sustainable management of frosty pod rot in Brazilian and regional cacao production systems.

Palavras-chave: trichoderma; moniliophthora roreri; biocontrol; biosynthetic gene clusters.