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METABOLOMIC PROFILE AND ANTIMICROBIAL POTENTIAL OF THE ENDOPHYTE *COLLETOTRICHUM KARSTI*, FROM *DUGUETIA LANCEOLATA*: A MULTI-OMICS APPROACH INTEGRATING *IN SILICO* SCREENING

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The escalating crisis of antimicrobial resistance (AMR) necessitates innovative strategies to accelerate the discovery of novel antibiotic scaffolds from underexplored sources such as endophytic fungi. To address this, we implemented a modern dereplication workflow integrating multi-omics data with predictive *in silico* tools to rapidly prioritize bioactive candidates from *Colletotrichum karsti*, an endophyte isolated from *Duguetia lanceolata*. The fungus was cultivated under four distinct conditions (solid-state fermentation on rice and wheat bran; liquid culture in Potato Dextrose and Czapek broths), and its metabolic profiles were acquired using LC-MS/MS. The resulting data was processed into molecular networks on the GNPS2 platform, where key metabolites were annotated by integrating spectral library matches and molecular family information. This chemical data was then correlated with the fungus's biosynthetic potential, mapped through genome mining with FungiSmash, which revealed a rich repertoire of 65 Biosynthetic Gene Clusters (BGCs). This multi-omics evaluation allowed the high-confidence annotation of several expressed metabolites, including a putative Betaenone analog, a Botrydial derivative, and the diketopiperazine Maculosin, directly linked to their corresponding BGCs. Crucially, an *in silico* pipeline was employed prior to any in vitro assays, predicting potent antibacterial activity against clinically relevant genera such as *Staphylococcus* sp., *Pseudomonas* sp., and *Klebsiella* sp., including resistant phenotypes. A subsequent selectivity screen (KinScreen) distinguished candidates with ideal safety profiles, such as the Betaenone analog, from others predicted to be potent but non-selective inhibitors of human kinases. Therefore, *in vitro* antimicrobial assays are currently in progress to confirm the predicted bioactivity of the crude extracts from all culture conditions. These experiments, targeting a panel of the selected bacterial genera including clinically relevant resistant strains like MRSA, will serve to bridge the gap between computational prediction and experimental validation in the search for novel antibiotics.

Keywords: *Colletotrichum karsti; Endophytic Fungus; Multi-omics; In silico Screening; Antibacterial Activity.*