Entophytic Fungi as Potential Source for Anti-COVID-19 Metabolites

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Abstract

COVID-19 is a severe pandemic viral disease caused by SARS-CoV 2, In this study, we reported the isolation of *Aspergillus terreus*, the endophytic fungus associated with healthy soybean roots. Analytical analysis of the fermented extract using liquid chromatography coupled with high-resolution mass spectrometry was carried out. Molecular docking studies were carried out for the dereplicated metabolites against COVID-19 main protease (M^{pro}). Metabolomic profiling revealed the presence of eighteen compounds belonging to the chemical classes, quinones, polyketides, isocoumarins, alkaloids, anthraquinones, butyrolactones and lactones, where quinones, polyketides and isocoumarins were the most abundant classes.. Molecular docking studies declared that the metabolites Aspergillide B1 and 3a-Hydroxy-3, 5-dihydromonacolin L showed the highest binding energy scores towards COVID-19 main protease (M^{pro}) (-9.473) and (-9.386), respectively,

Introduction

COVID-19 is a severe pandemic viral disease caused by SARS-CoV 2, it launched in Wuhan, China at the end of 2019 and tremendously invaded the world causing severe acute respirtory symptoms and high mortality rate. Soybean (*Glycine max* L., family: Leguminoseae) is an ancient edible legume. Endophytic fungi inhabiting medicinal plants are considered as an important and novel resource of natural bioactive compounds, they have the ability to produce the same or similar bioactive compounds as those originated from their host plants also they may produce secondary metabolites completely different from those isolated from the plant itself. Metabolomics is a technique concerned with providing a chemical fingerprint or an entire chemical profile for a specific organism at a specific conditions. It plays a vital role in the search for novel bioactive metabolites and natural drug dicovery, Molecular docking or computer aided drug design (CADD) is one of the *in-silico* techniques that provides a simulation of a candidate ligand binding to a receptor so can be used in finding out potent drugs through virtual screening of metabolites databases.

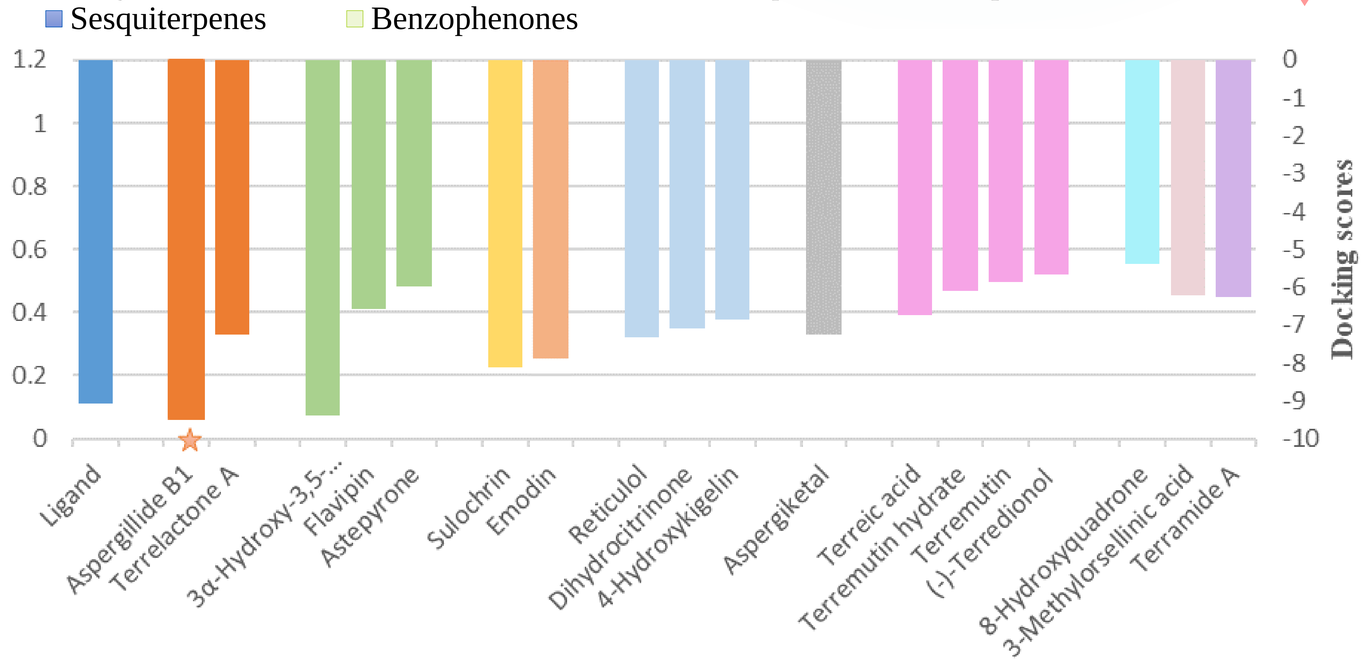
Materials & Methods

Healthy fresh roots, stems and leaves of *Glycine Max* L. were collected from the botanical garden of Department of Botany and Microbiology, Faculty of Science, Minia University. Taxonomic identification of the isolated fungal strain recovered from the G. Max L. root (A1), was achieved by DNA amplification and sequencing of the fungal internal transcribed spacer (ITS) region using the universal primers ITS1 and ITS4. 3D chemical structure files in mol2 format were obtained using Open Babel v.2.3.1.

Results

Chemical classes of the metabolites dereplicated from *Aspergillus terreus* culture extracts.

The binding energy scores of Aspergillus terreus dereplicated metabolites



Conclusion & future aspects

In conclusion, Aspergillide B1 and 3a-Hydroxy-3, 5-dihydromonacolin L were found to be potent anti-COVID-19 drug candidates in the molecular docking study. *Aspergillus terreus* can be considered as a potential source of natural, bioactive products. Further *in-vivo* and *in-vitro* studies are required to investigate the potential of Aspergillide B1 and 3a-Hydroxy-3, 5-dihydromonacolin L to be developed as phytopharmaceuticals for the management of COVID 19.

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