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SARS-COV-2 AND MUCORMYCOSIS: IN SILICO EXPLORATION OF MARINE NATURAL PRODUCTS AS POTENT PROTEIN TARGET INHIBITORS

Omkar Pokharkar,[1] Hariharan Lakshmanan,[2] Grigory Zyryanov, [1, 3] Mikhail Tsurkan,[4]

[1]Department of Organic & Bio-Molecular Chemistry, Chemical Engineering Institute, Ural Federal University, 19 Mira St., 620002 Yekaterinburg, Russia

[2]La Trobe Institute of Molecular Science, Plenty Rd & Kingsbury Dr., Bundoora, Melbourne, VIC 3086, Australia

[3]Postovsky Institute of Organic Synthesis of RAS (Ural Division), 22/20 S. Kovalevskoy/Akademicheskaya St., 620990 Yekaterinburg, Russia

[4]Leibniz Institute of Polymer Research, 01005 Dresden, Germany

E-mail: Omkarpokharkar93@gmail.com

Abstract. The world is now desperately looking for a relief from the SARS-CoV-2 pandemic and mucormycosis epidemic. The purpose of this work aims at In-silico identification of ligands from a wide range of Marine organisms that potentially inhibit SARS-Cov-2 and mucormycosis target proteins. For mucormycosis study, information about proven drug targets and natural products from marine sponges, were obtained through literature search. Thirty-five compounds were chosen using the PASS online program and seven protein targets were selected. Available 3D structures of protein targets for were obtained from RCSB PDB. In case of unavailability of structures, FASTA sequences were obtained from NCBI database for homology modelling. Active site prediction was predicted using CASTp 3.0 webserver. Autodock Vina in PyRx 0.8 was used for blind docking. Further, MD simulations were performed using the IMODS server for top-ranked docked complexes. Moreover, the drug-like properties and toxicity analyses were performed using Lipinski parameters in Swiss-ADME, OSIRIS, ProTox-II, pkCSM, and StopTox servers. The results indicated that naamine D, latrunculin A and S, (+)-curcudiol, (+)-curcuphenol, aurantoside I, and hyrtimomine A had the highest binding affinity values of −8.8, −8.6, −9.8, −11.4, −8.0, −11.4, and −9.0 kcal/mol, respectively. In sum, all MNPs included in this study are good candidates against mucormycosis. (+)-curcudiol and (+)-curcuphenol are promising compounds due to their broad-spectrum target inhibition potential. For SARS-Cov-2 study, targets such as 3CLpro, PLpro, RdRp, NSP15 and spike protein were obtained from RCSB PDB. They were subjected to site specific docking for binding affinity studies with several ligands from marine bacteria, marine algae and corals using Autodock Vina software. 2D interaction maps were analyzed to determine hydrophobic, hydrogen and electrostatic bonds formed with the catalytic amino acids of aforementioned targets.

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