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Article

Antigen specific antibody production by the Breadfruit (*Artocarpus altilis)* contains some promising inhibitors of the M^{pro} enzyme of SARS-CoV-2: an *in silico* molecular docking and pharmacological analysis

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Abstract

The world experienced a sudden outbreak of an abruptly emerging virus, SARS-CoV-2, in late December 2019 in the city of Wuhan, China. Within a few months, the resulting disease, COVID-19, had taken over a major portion of the world. Researchers have since been working with the viral targets, aiming to unwrap an absolute cure. Because of the severity and concerns about the virus, we conducted a computational assessment of compounds derived from breadfruit (*Artocarpus altilis*) to study. The assessment aims to unveil some promising compounds as inhibitors of SARS-CoV-2. We selected the main protease (M^{pro}) enzyme of SARS-CoV-2, since this enzyme is responsible for the replication process of the virus. Initially we had gone for a drug-likeness analysis to screen the most suitable compounds. Afterwards, molecular dockings were performed with the selected compounds from *A. altilis*. Nirmatrelvir was taken as a standard inhibitor in this study, as it is an FDA approved drug in combination with ritonavir. In molecular docking, the test compounds, cycloartomunin, dihydrocycloartomunin, cycloartobiloxanthone, artomunoxanthentrione, and cycloartomunoxanthone exhibited binding affinities of −7.6, −7.7, −7.7, −8.3, and −8.1 kcal/mol, respectively. Nirmatrelvir showed an affinity of −8.1 kcal/mol while docking on the same server. Consequently, a pharmacological analysis was conducted with the top five test compounds compared with the standard inhibitor. A computational toxicity analysis was also involved in this assessment. Finally, the test compounds were found to have promising docking outputs, and moderate pharmacological profiles. After all, this study scrutinized the test compounds and suggests further validations to confirm the potentiality of the compounds inhibiting the SARS-CoV-2 M^{pro} enzyme.

Keywords: COVID-19, SARS-CoV-2, mpro, breadfruit, *Artocarpus altilis*, molecular docking.

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INTRODUCTION

The SARS-CoV-2 outbreak in late 2019 and its global propagation have had substantial global consequences on public health, economics, and social aspects (Miyah et al., 2022). SARS-CoV-2, also known as COVID-19, is a highly pathogenic virus that was discovered in Wuhan, China, near the end of 2019. Since then, it has swiftly spread over the world, and the World Health Organization (WHO) designated it a global pandemic in March 2020 (Patnaik, 2021). As a result of the pandemic, many countries throughout the world imposed tight measures such as lockdowns and travel restrictions to prevent the spread of COVID-19 (Inoue & Todo, 2020; Zhong et al., 2021). Until April 15, 2023, the World Health Organization (WHO) had recorded over 762 million COVID-19 cases globally (https://covid19.who.int/). Regrettably, the aforementioned has led to a total of more than 6.84 million fatalities, which is a substantial figure in comparison to other diseases (WHO, 2023).

The causative agent of COVID-19, SARS-CoV-2, is a positive-sense, single-stranded RNA virus belonging to the family of Coronaviridae (Hu et al., 2020). The virus has a unique spike protein on its surface that binds to the human angiotensin-converting enzyme 2 (ACE2) receptor, facilitating its entry into host cells and subsequent replication (Deng et al., 2021). The SARS-CoV-2 virus has undergone significant mutations, leading to the emergence of several new variants (WHO, 2022).

Among the proteins of SARS-CoV-2, the main protease (M^{pro}) enzyme plays a critical role in viral replication and is considered a promising drug target for therapeutic intervention against COVID-19 (Huynh et al., 2021). M^{pro}, also known as 3CL pro, is responsible for the proteolytic cleavage of the viral polypeptide during replication, which is essential for the production of functional viral proteins (Dharmashekara et al., 2021). The inhibition of M^{pro} can potentially prevent viral replication and transmission, making it a valuable target for drug development against COVID-19. The structural and functional characteristics of M^{pro} have been extensively studied in recent times, leading to the development of several inhibitors targeting this protease. These inhibitors have shown effective inhibition of M^{pro} in vitro and in vivo, demonstrating their potential as a therapeutic option for treating COVID-19 (Li et al., 2021).

Artocarpus altilis, commonly referred to as breadfruit, belongs to the family Moraceae. It is a notable plant with a substantial therapeutic profile (Sikarwar et al., 2014). Many ongoing studies are looking at the pharmacological effects of Artocarpus altilis. Anti-inflammatory activity, antifungal potential, sexual behavior study, immunomodulatory potential, anti-diabetic activity, antibacterial activity, anti-cholinergic effect, chelating activity, nutritional assessment, as a cosmetic agent, ACE inhibitors, and other studies are being conducted on these plants. Surprisingly, the activity of this plant against SARS-CoV-2 was previously undocumented in the literature. As a result, it was chosen for this investigation to investigate its action against the targets of Omicron variant SARS-CoV-2.

Nirmatrelvir–ritonavir (Paxlovid™), which has received Emergency Use Authorization by the Food and Drug

Administration (FDA) for the outpatient treatment of COVID-19 infection in adults (Gui et al., 2023). Nirmatrelvir is a SARS-CoV-2 M^{pro} inhibitor, which actively inhibits the viral replication process by blocking the virus from cleaving viral polyproteins into their functional parts, thus limiting the infection's spread in the body (Park et al., 2022). Multiple studies have shown that nirmatrelvir–ritonavir has potent inhibitory activity against SARS-CoV-2 proteases, making it a promising candidate for COVID-19 treatment (Rodrigues et al., 2022). A clinical trial by Pfizer, the developer of nirmatrelvir/ritonavir, reported that nirmatrelvir/ritonavir treatment reduced the risk of hospitalization or death by 89% in patients with mild to moderate COVID-19 symptoms (Huang et al., 2022). Thus, we have considered nirmatrelvir as a standard inhibitor in our assessment.

Computer-aided drug design (CADD) is a computational method that uses various software tools and algorithms to create, optimize, and test new drugs before they can be synthesized and tested in the lab (Yu & MacKerell, 2017). In this computational assessment, we implemented molecular docking, pharmacokinetic and pharmacodynamic property studies to discover the best possible drug candidate. Molecular docking provided us with information on each ligand's binding affinity, direction, and kind of interaction with the appropriate target proteins. The pharmacokinetic profiles were obtained in order to analyze data on the absorption, distribution, metabolism, and excretion (ADME) of chemicals that occur inside the body following medication delivery. To determine the LD50 values and toxicity classes of the various ligands, a toxicology scrutiny was conducted.

In the current work, we used a screening method to filter out 10 phytochemical compounds from *A. altilis* based on drug-likeness criteria. Through preliminary computational analysis, the compounds were examined across a wide spectrum of studies. As a result, this framework evaluates and offers potential promising *A. altilis* medication candidates against the SARSCoV-2 Omicron B.1.1.529 strain.

MATERIALS AND METHODS

Selection and Preparation of Ligands

A total of ten phytochemicals derived from *Artocarpus altilis* were chosen for this investigation based on their drug-likeness. The molecules were chosen using Lipinski's rule of five and Ghose filter (Ghose et al., 1999; Lipinski et al., 1997). Only molecules that followed both rules were chosen for this investigation. The chosen ligands' 3D conformers were obtained in SDF format from the online databases PubChem (https://pubchem.ncbi.nlm.nih.gov/) and IMPPAT 2.0 (Indian Medicinal Plants, Phytochemistry, and Therapeutics; https://cb.imsc.res.in/imppat/) (Kim et al., 2016; Vivek-Ananth et al., 2023).

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Retrieval and Preparation of Target Protein

The crystal structure of the M^{pro} enzyme (PDB ID: 8D4L) of SARS-CoV-2 was retrieved in PDB format from the RCSB

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A diagrammatic scheme of the types of 3D conformations (obtained from CB-Dock2 server) and 2D interactions (obtained from BIOVIA Discovery Studio software) have been shown in Figure 2.

Protein Data Bank database (https://www.rcsb.org/) (Dejnirattisai et al., 2022; Rose et al., 2016). The resolution of the downloaded spike protein was 1.70°A. The protein structures were cleaned by eliminating unwanted atoms and molecules (including ligands) with PyMOL version 2.5.2 software (Schrodinger, LLC) (Lill et al., 2011). The receptor-binding domain (RBD) of the spike protein was extracted from the crystal structure, and the superfluous chains of proteins were eliminated using PyMOL. The proteins' chains were stored in PDB formats for molecular docking.

Molecular Docking

The CB-Dock2 server (https://cadd.labshare.cn/cb-dock2/php) was used to execute molecular dockings on the chosen ligands against the target proteins (Liu et al., 2022). The binding affinity (kcal/mol) for each protein-ligand combination, as well as noncovalent interactions and docking orientations, were examined using the Dassault Systmes BIOVIA Discovery Studio 2021 Client version 21.1.0 software. The 2D and 3D schematic drawings of the protein-ligand docking complexes were obtained from BIOVIA Discovery Studio.

ADME and Toxicity Prediction

The top-docking ligands' canonical SMILES were taken from the PubChem and IMPPAT 2.0 databases and entered into the SwissADME website (https://www.swissadme.ch/) (Daina et al., 2017). SwissADME provided the ADME (absorption, distribution, metabolism, and excretion) statistics for each ligand. Following that, the ProTox-II service (https://tox-new.charite.de/protox_II/) was used to estimate the toxicity profile of each ligand (Banerjee et al., 2018). These two sources were used to record the physicochemical, pharmacokinetic, and pharmacodynamic aspects of each ligand. During the ADME and toxicity prediction, each ligand's topological polar surface area (TPSA), lipophilicity (MLogP), water solubility (LogS), bioavailability score, blood-brain barrier (BBB) permeability, interaction with P-glycoprotein (P-gp), LD50 value, and toxicity class were explored.

RESULTS AND DISCUSSION

The docking score or binding affinity of a ligand denotes the level of attraction at which the ligand is supposed to bind to the target. The docking conformations shows at which orientation the ligands bind to the respective targets. A complete docking operation includes the bond types, bond lengths, and a complete overview on the ligands static interactions with the target. Artomunoxanthentrione displayed the highest binding affinity, that is −8.3 kcal/mol. It was found to exhibit almost 20 interactions with the amino acid residues of M^{pro}. The interactions obtained from the CB-Dock2 server for each molecule has been mentioned in table 1. the binding affinities of cycloartomunin, cihydrocycloartomunin, cycloartobiloxanthone, artomunoxanthentrione, cycloartomunoxanthone, and nirmatrelvir (standard) in complex were −7.6, −7.7 , −7.7, −8.1, and −8.1 kcal/mol, respectively. Figure 1 depicts a graphically comparative overview of the docking scores (binding affinities) of all test compounds and the standard inhibitor.

A diagrammatic scheme of the types of 3D conformations (obtained from CB-Dock2 server) and 2D interactions (obtained from BIOVIA Discovery Studio software) have been shown in Figure 2.

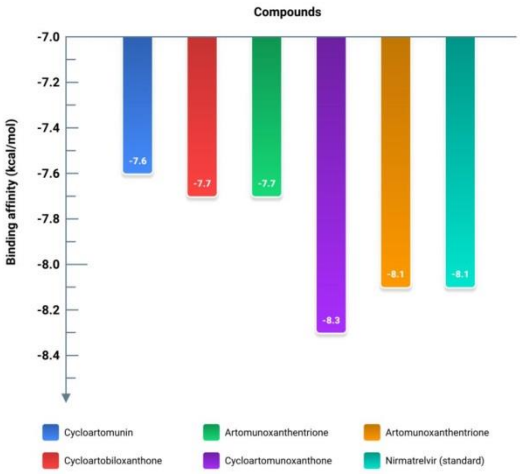

Figure 1: Binding affinity chart of each compound in complex with M^{pro} enzyme of SARS-CoV-2.

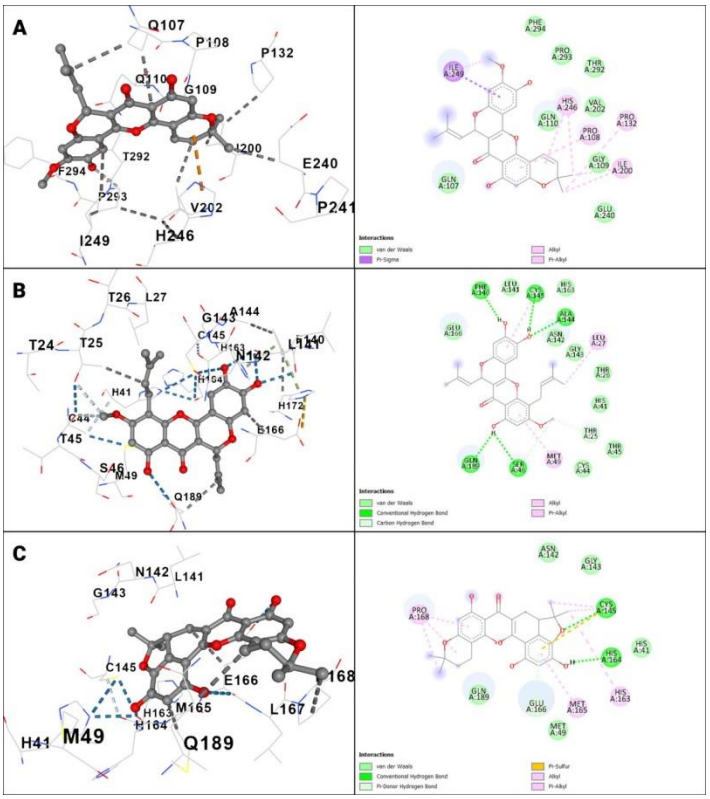

Figure 2: 3D conformations (left) and 2D view of the docking outputs of (A) cycloartomunin, (B) dihydrocycloartomunin, (C) cycloartobiloxanthone, (D) artomunoxanthentrione, (E) cycloartomunoxanthone, and (F) nirmatrelvir in complex with M^{pro}.