World Journal of Pharmaceutical Technology

IDAAM Publications

World J Pharm Technol 2023; 1(1): 8-12

RESEARCH ARTICLE

Molecular docking study of *Barleria Prionitis* L. as antiviral to coronavirus COVID-19

AKSHAY R YADAV*

Department of Pharmaceutical Chemistry, Rajarambapu College of Pharmacy, Kasegaon, Maharashtra, India-415404

***Author for Correspondence:** *Email:* akshayyadav24197@gmail.com

ARTICLE DETAILS

Article history:
Received on 18 February 2023
Modified on 21 March 2023
Accepted on 28 March 2023

Keywords:
Barleria prionitis L.,
Molecular Docking,
Coronavirus Disease,
Antiviral.

ABSTRACT

A pandemic of international concern is Coronavirus disease (Covid-19). It poses significant health risks all over the world and there is no successful cure for it. Usage in studies of silico docking. In this respect the docking evaluation was for active plant constituent ligands. In-silico docking studies have taken the place of the new version of *GLIDE Software v5.5,* built by Schrödinger. These findings showed that the binding energy in all active components ranged from -3.1 to -8.3 kcal/mol. If compared to the standard (-8.5 kcal/mol). It was found that, as opposed to the standard drugs, the investigated phytoconstituents showed potent inhibiting activity as the MolDock score directly represents possible binding to the enzyme.

INTRODUCTION

COVID-19 is a deadly disease in which SARS-CoV-2 is responsible for the infection. The coronavirus particles are spherical in shape with surrounding spike proteins [1]. In human host cells, these proteins are responsible for virus replication. Spike proteins undergo structural changes after attachment to human cells, resulting in a fusion of the viral particulate membrane with the human host cell membrane [2]. Thus, the viral RNA enters the host cell and, after copying its genome, releases more viruses [3].

In contrast to modern pharmaceutical medicines, herbal medicines play an important role in treating various chronic diseases. Because of its limited side effects they are very healthy. Proper understanding of the crude medicinal product is very important for developing the herbal formulation, protection and effectiveness of the herbal product. Pharmacognosy, a discipline devoted to the full knowledge gathered on the crude drug. B. prionitis is also known as the flower of porcupine that is part of the Acanthaceae Family, the Barleria genus. It is native to India and is widely spread throughout Asia, including Malaysia, Pakistan, the Philippines, Sri Lanka, Bangladesh, Yemen and tropical Africa. The tubes, typically single-groove, grow to about 1.5 meters above a single taproot in height, are erect, permanent, snug, and perennial. The branching lateral roots all over the place. Because of its normal usage for various forms of pharmacological activities B. prionitis has been studied. Several studies have been recorded in vitro and in vivo in various cell lines and animals. Now for a few days herb means any part of the plant such as fruit, seed, stem, bark, flower, leaf, stigma, or root and a non-woody plant. In the past, only non-woody plants, including those derived from trees and shrub, used to use the word "herb." These herbs are also being used in many spiritual practices as food, flavonoids, medicines or perfume. Plants were used even before ancient times for medicinal purposes.

Old Unani manuscripts the use of herbs was described by Egyptian papyrus and Chinese texts. There is evidence that for over 4000 years, herbs have been used as medicines in Unani Hakims, Indian Vaids and in European and mediterranean cultures [4, 5]. In their healing

rituals indigenous cultures like Rome, Egypt, Iran, Africa, and America have used herbal herbs while other traditional medical system systems have been developed, such as unani, ayurvedic and Chinese medicines. On various sources, traditional medical methods are still commonly practised. Increased population, insufficient supply of medicines, prohibitive treatment costs, side-effects of various synthetic medicine and the growth of resistance against currently-used drugs for contagious diseases have resulted in greater emphasis on the use as a source of medicines for a wide range of human ailments of plant material. India is recognized as a rich repository of medicinal plants among ancient civilizations [5]. The Indian forest is the main depot of many medicinal and aromatic plants that are collected primarily as raw ingredients in the production of drugs and perfumery products. In the INDIA system of AYUSH approximately 8,000 herbal remedies were codified. The key systems of indigenous medicines are Ayurveda, Unani, Siddha and Folk (tribal) medicines. Among these systems are most developed and widely practiced Ayurveda and Unani Medicine in India. Recently, the WHO reports that 80% of the worldwide population relies on herbal medicines for some part of their primary health needs.

According to the World Health Organization (WHO), about 21,000 plants have potential for medicinal use. More than three quarters of the world's population, according to available data, relies primarily on plants and plant extracts for their medical needs [6, 7]. More than 30% of the whole plant species is used for medicinal purposes at one time or for another. The estimate is that plant medicinal products make up as much as 25% of the total drugs in developed countries like the United States, whereas the contribution is as high as 80% in the rapidly developing countries like India and China. Thus for countries such as India than the world, the economic value of medicinal plants is much greater. Two thirds of the plants used in the modern medicine system are developed in these countries and the rural health care system relies upon indigenous medicine systems. Many herbs in different parts of the world honor their Kings as a sign of happiness. Now, when many consumers had found the role of herbs in medicine, tulsi and other medicinal plants started plantation in their home gardens. The rich ingredients of medicinal plants that can either be used as pharmacopeia, non-pharmacopoya or synthetic drugs in drug production are regarded. These plants play a crucial role in the growth of human societies all over the world. In addition, certain plants are recognized as essential nutrient sources and are recommended for their therapeutic values which includes ginger, green tea, aloe, pepper, and turmeric [7].

Certain plants and their derivatives are seen as an essential source of actives used in aspirin, toothpaste etc. In addition, in natural dye, pest prevention, food, perfume and tea weeds are also used in the treatment of medicinal goods. Various medicinal plants/herbs are used in many countries to keep the ounces, the flies, the mouse and escape from home and office. Medicinal herbs have been essential sources for pharmaceutical development for many days now [6].

Molecular docking is an appealing scaffold for understanding medicinal biomolecular interactions in rational drug design as well as in the mechanical analysis in order, primarily noncovalently, to insert the molecule (ligand) into the favorite binders of the particular target area of the DNA/protein (receptor) . The information gathered from the docking method can be used to demonstrate the binding energy, free energy and complex stability. The docking are currently used to forecast the preliminary ligand-receptor complex binding parameters [8-13].

MATERIALS AND METHODS

Molecular Modeling Studies

The GLIDE software v5.5 built by Schrödinger on the Red Hat Enterprise Linux5 workstation has also been used for molecular modeling studies. For all steps involved in ligand preparation, protein preparation, HTVS, Maestro v9.5 Graphical User Interface (GUI) workspace was used (High Throughput Virtual Screening) [14].

Ligand Preparation

The ligands used in this study have been developed with the Schrödinger Suite 2013 LigPrep module v2.3. LigPrep follows the energy minimization force fields in OPLS-AA (Optimized Potential Liquid Simulations for All Atoms) [15].

Protein Preparation

Structure of COVID-19 virus spike receptor-binding domain complexed with a neutralizing antibody (PDB code- 7BZ5), only high atoms,

water, cofactors and metal ions can be used in a standard PDB structure, and multimerical structures can be used. These entities are not familiar with bond instructions, topologies, or formal atomic costs. The raw PDB structure should therefore be prepared for docking in a suitable way. GLIDE software protein preparation Wizard for the processing and preparation of protein was used. This is also in line with the optimized power potentials in the energy reduction fields for liquid simulations-all atoms (OPLS-AA) [16].

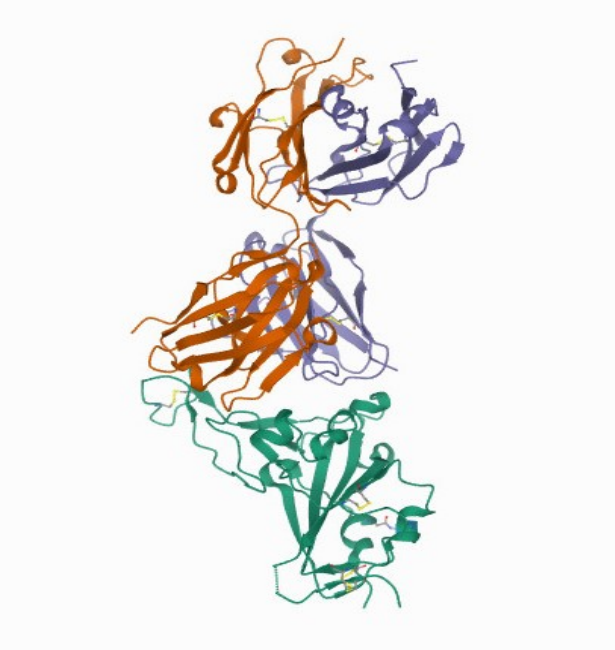

Figure 1: 3D View of Structure of COVID-19 virus spike receptor-binding domain complexed with a neutralizing antibody (PDB code- 7BZ5)

Docking Protocol

The GLIDE Extra Precision (XP) mode was used for all docking calculations. The position of the bond for the different energy networks is defined in two concentration-cubed terms: the bounding box with the center of every appropriate ligand pose and the enclosing box with a Root Mean Square Diversion (RMSD) of less than 0.5 Å and a maximum atomic displacement of less than 1,3 Å The binding site for which various energy grids have been determined and stored. For those atoms with absolute partial loads below 0, 15 (scale factor of 0.8) and 1,0 electrons of the ligand and proteins, respectively, the scale factor for van der Waals radii was added. In the initial calculation process, the maximum number of poses produced by the max keep variable was set at five thousand and the best hold variable was set at one thousand, which determines the number of poses per ligand in the energy minimum. Energy minimization protocol includes dielectric constant of 4.0 and 1000 cycle of conjugate gradient. At most 100 poses per ligand were produced when each docking calculation was completed. A GLIDE (Gscore) function was used to choose the best docked structure. The E-model, which comes from a combination of gscore, coulombic, van der Waals and the ligand strain energy, is another scoring feature used by GLIDE [17, 18].

RESULTS AND DISCUSSION

To assess the size of the active site, the GLIDE receptor grid has been created. The ligands are most likely to orientate in the binding pocket and a score function is employed to calculate the frequency of the interaction that a molecule may conduct with a specific orientation. The GLIDE XP precision was preferred over the standard mode to provide a stronger connection between good poses and good score. The study of the docking was performed using GLIDE docking software for ligands such as the target protein and the pictures are shown. GLIDE docking structures are usually graded as per GLIDE scoring feature (more negative). The GLIDE docking software scoring feature is viewed as a G-score. The easiest way to test the accuracy of the docking method is to decide how near, with the object score feature, the lowest energy (binding conformation) is expected. Extra Precision GLIDE docking procedure was assessed by removing the α-amylase protein compound from G-score (GLIDE), GLIDE energy (GLIDE) and H-bonds. In this study both ligands are docked into the active site to explore the molecular basis for the interaction and affinity between ligand analogs and protein. Table 1 shows the docking result of the ligands. For each of the minimized complexes, the interaction energy involves the energy of van der Waal, electrostatic energy, and intermolecular hydrogen bonding. GLIDE attraction ranged from to -3.1 to -8.3. The standard α-amylase chloroquine score for GLIDE was found to be -8.5. This shows that the plant's chemical component may be potential drugs for the development of anti-diabetic activity drug. The GLIDE score may be used to describe ligands to bind to a certain conformation of a protein receptor as a semi-quantitative descriptor. In general, a strong ligand affinity to the receptor can be expected for a low GLIDE score. Especially, compounds Lupulinoside and shanzhiside methyl ester were found to be potent with a docking score of -8.1 and -7.9

respectively. The position of the inhibitor at the docking and the crystal structures of the protein were very well agreed. We have found Compliance studies of different docking complexes also show that residues of α-amylase protein (ILE 435, LYS 400, ASP 241, ALA 764, HIS 101, GLU 433, HIS 405 and ALA 207) play an important role. GLIDE-led docking studies have verified that the above-mentioned inhibators fit into the α-amylase protein binding pocket. The findings show that intermolecular hydrogen and liphophilic interactions between the ligand and the receptor are very necessary for effective docking. The key explanation why the GLIDE score has improved is because of intra-ligand penalties.

Table 1: Glide score of Phytoconstituents of *Barleria prionitis L.*

S. No	Compounds	Glide score
1	Balarenone	-5.2
2	Pipataline	-3.8
3	Lupeol	-5.6
4	Prioniside A	-6.1
5	Prioniside B	-4.9
6	Prioniside C	-5.5
7	Verbascoside	-3.6
8	Shanzhiside methyl ester	-7.9
9	6-O-trans-p-coumaroyl-8-O-acetylshanzhiside methyl ester	-6.8
10	Barlerin	-5.4
11	Acetylbarlerin	-3.2
12	7-methoxydiderroside	-4.4
13	Lupulinoside	-8.3
14	1,8-dihydroxy-2,7-dimethyl 3, 6-dimethoxy anthraquinone	-3.8
15	1,3,6,8-tetramethoxy-2,7-dimethyl anthraquinone	-4.4
16	Scutellarein	-5.6
17	Melilotic acid	-3.1
18	Syringic acid	-6.7
19	Glucoside	-5.2
20	β-sitosterol	-4.9
21	Scutellarein 7-neohesperidoside	-6.1
22	Apigenin 7-O-glucoside	-5.9
23	13,14-seco-stigmasta-5, 14-diene-3-a-ol	-4.8
24	Standard (chloroquine)	-8.5

CONCLUSION

The attraction of the ligand's binding affinity towards protein is determined by the force between the protein fragment and Lupulinoside. Protein-ligand binding strength is known as binding affinity. This affinity specifies whether a ligand can eventually bind or separate from the surface of the protein and return to its unbound state. Docking servers calculate the binding affinity of various docking structures in the absence and presence of spike protein for non-competitive modulators.

ACKNOWLEDGMENTS

I express my sincere thanks to Vice-principal Prof. Dr. S. K. Mohite and Principal Prof. Dr. C. S. Magdum for providing me all necessary facilities.

REFERENCES

[1] Yadav A, Mohite S. A Review on severe acute respiratory infection (SARI) and its clinical management in suspect/confirmed novel coronavirus (nCoV) cases Res. J. Pharma. Dosage Forms and Tech. 2020; 12(3): 178-180.

[2] Yadav A, Mohite S. A Review on Novel Coronavirus (COVID-19). International Journal of Pharma Sciences and Research. 2020; 11(5): 74-76.

[3] Yadav A, Mohite S. A Novel approach for treatment of COVID-19 with Convalescent Plasma. Res. J. Pharma. Dosage Forms and Tech. 2020; 12(3): 227-230.

[4] Yadav A, Mohite S. A Review on Zika Virus Infection. Res. J. Pharma. Dosage Forms and Tech. 2020; 12(4): 245-249.

[5] Yadav A, Mohite S. An Overview on Ebola Virus Disease. Res. J. Pharma. Dosage Forms and Tech.2020; 12(4): 230-235.

[6] Yadav A, Rajput M, Gavali K, Mohite S. In-vitro Hypoglycemic Activity of Barleria prionitis L. Int J Sci Res Chemi. 5(5): 63-70.

[7] Chitruk A, Yadav A Rode P, Mohite S, Magdum C. Microwave assisted synthesis, antimicrobial and anti-inflammatory potential of some novel 1,2,4-triazole derivatives. Int. j. sci. res. sci. technol. 2020; 7(4): 360-367.

[8] Amoo, S.O., J.F. Finnie, and J. van Staden. *In vitro* pharmacological evaluation of three *Barleria* species. J. Ethanopharmacol. 2009; 121: 274-277.

[9] Amoo, S. O., A. R. Ndhlala, J. F. Finnie and J. Van Staden. Antifungal, acetylcholinesterase inhibition, antioxidant, and phytochemical properties of three *Barleria* species. S. Afr. J. Bot. 2011; 77: 435-445.

[10] Aneja, K.R., R. Joshi, and C. Sharma, 2010. Potency of *Barleria prionitis* L. bark extracts against oral diseases causing strains of bacteria and fungi of clinical origin. New York Sci. J., 3: 5-12.

[11] Ata, A., K.S. Kalhari and R. Samarasekera. Chemical constituents of *Barleria prionitis* and their enzyme inhibitory and free radical scavenging activities. Phytochem. Lett., 2009; 2: 37-40.

[12] Rode P, Yadav A, Chitruk A, Mohite S, Magdum C. Synthesis, Anticancer and Molecular Docking Studies of N-(1H-benzimidazol-2-yl-carbamothioyl)benzamide Analogues. Int. j. sci. res. sci. technol. 2020; 5(6): 204-212.

[13] Bhosale M, Yadav A, Magdum C, Mohite S. Molecular Docking Studies, Synthesis, Toxicological Evaluation using Brine Shrimp (Artemia salina L.) Model and Anti-inflammatory Activity of Some N-(substituted)-5-phenyl-1,3,4-thiadiazol-2-amine Derivatives. Int J Sci Res Sci & Technol. 2020; 7(5): 51-62.

[14] Jagtap N, Yadav A, Mohite S. Synthesis, Molecular Docking Studies and Anticancer Activity of 1,3,4-Oxadiazole-3(2H)-thione Derivatives. Journal of University of Shanghai for Science and Technology. 2020; 22(11):535-550.

[15] Bhosale M, Yadav A, Magdum C, Mohite S. Microwave Assisted Synthesis, Molecular Docking Studies and Anticancer Screening of Some 1,3,4-thiadiazole Derivatives. Journal of University of Shanghai for Science and Technology.2020; 22(11):520-534.

[16] Birajdar R, Yadav A, Patil S, Chitruk A, Kane S, Mohite S, Magdum C. Pharmacognostic and Phytochemical Investigation, Molecular Docking Studies of Phytoconstituents and Anticancer Potential of Capparis Decidua (Forsk) Edgew. Journal of University of Shanghai for Science and Technology. 2020; 22(11): 500-519.

[17] Pathade K, Mohite S, Yadav A. Synthesis, Molecular Docking Studies of Novel 4-(Substituted Ph Phenyl Amino)-6-(Substituted Aniline)-N'-Aryl-1,3,5-Triazine-2-Carbahydrazide Derivatives As Potent Antitubercular Agents. Journal of University of Shanghai for Science and Technology. 2020; 22(11): 1891-1909.

[18] Bhosale M, Yadav A, Magdum C, Mohite S. Synthesis, molecular docking studies and biological evaluation of 1,3,4-thiadiazole derivatives as antimicrobial agents. Int. J. Curr. Adv. Res. 2020; 09(08)(A): 22894-22899.