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An integrated *in silico* approach to identify bioactive Phytochemicals in Bauhinia Variegata plant as potential lead candidates against SARS-CoV-2 transmission targets

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Abstract
Bauhinia variegata, a medicinal plant commonly known as Kachnar, belongs to the Leguminosae family. It is primarily found in tropical and warm regions around the world. It is known for its high pharmacological and commercial significance due to the presence of terpenoids, flavanoids, tannins, steroids, reducing sugars and cardiac glycosides, which aid in the cure of number of diseases. This study carried out profiling of Phytochemicals of this medicinal plant by using several in silico computational methodologies against SARS-CoV-2 virus. The 3D structure of Phytochemicals and the three target sites of the SARS-CoV-2 were constructed using Swiss-Model server and pre-processed in BIOVIA Discovery Studio followed by molecular docking carried on with Autodock tools-1.5.6. The pharmacokinetic and toxicological properties of these compounds were assessed using the Swiss ADME and admetSAR web servers, respectively. The potential toxicities generated by these compounds, as well as the energies of molecule-target interactions, hydrogen bonding, and hydrophobic interactions, were determined and analyzed. According to the findings, Phytochemicals such as Beta-sitosterol, Lupeol, Ombuin, and Quercetin exhibited higher binding affinity than the two reference drugs Ivermectin and Lopinavir, taken as comparison in the study. According to the preliminary results, these bioactive compounds exhibit the most promising docking scores with the three target sites of Corona virus. Hence, they could be regarded as prospective Phytochemicals found in Bauhinia variegata, potentially making this plant an active source of Phytochemicals required for the treatment of corona virus infections. Further experimental validation may necessitate the application of bioethics principles, laws, and regulations.

Keywords*: Bauhinia variegata; In silico; SARS-CoV-2; Molecular docking; Phytochemicals*

INTRODUCTION

The COVID-19 pandemic has sparked an unprecedented wave of research. Novel corona virus, 2019-nCoV, has been identified as the cause of a respiratory ailment outbreak that began in Wuhan, China and has now spread to numerous other nations[1]. This could infect humans and a multitude of animal species, producing a wide range of diseases. In the search for efficacious therapeutics, three promising targets for anti-CoV drug design are considered. They are Furin, a type of proprotein convertase, and the receptor binding domain of SARS-CoV-2 spike protein, which work together to prevent entry of virus, and the corona virus main protease (M^{pro}), which has a key function in expression of viral gene as well as replication by proteolytically processing replicase polyproteins[2-3].These are critical targets for developing effective COVID-19 antiviral medicines.For thousands of years, plants have an important role in the cure of human diseases. The Leguminosae family includes *Bauhinia variegata*, often known as Kachnar. It is well-known

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for its ornamental value and is spread all over India, growing to a height of 1300 meters in the Himalayas[4-5]. According to studies, *B. variegata* contains a diverse spectrum of secondary metabolites, including terpenoids, flavanoids, steroids, saponins, tannins, reducing sugars, and cardiac glycosides [6]. Its metabolites make it effective in the treatment of a multitude of health diseases, including cancer[7], ulcers[8], inflammation [9], bacterial infections, and much more[10]. Gallic acid, quercetin, kaempferol, Beta-sitosterol, lupeol, kaempferol-3-glucoside, rutin, and ombuin are some of the bioactive components of *B. variegata* that have been studied for their medicinal potential [11]. These Phytochemicals were chosen based on earlier studies [11], which showed interaction of these bioactive compounds with protein targets of SARS-CoV-2. Since millennia, plants have actively assisted in the treatment and cure of numerous diseases. According to research studies, Catechin, beta-sitosterol, Quercetin, Lupeol, Kaempferol, Gallic Acid, Piperitone, Limonene, plus Rutin were identified from Djiboutian therapeutic plants (Acacia seyal, Indigofera caerulea, and Cymbopogon commutatus). These compounds were evaluated against the SARS-CoV-2 target sites, together with two other reference drugs namely, hydroxychloroquine and remdesivir. According to the findings, phenolic compounds such rutin, kaempferol, and catechin had a higher binding affinity than two reference drugs[11]. These compounds had the best early results with the three target sites, with the minimized docking scores [11]. Based on this research, we speculate that *B. variegata* could be a source of bioactive compounds including kaempferol, rutin, quercetin, gallic acid, lupeol, and beta-sitosterol, which have been shown to be effective against coronavirus infection. As a result, they might be regarded possible Phytochemicals that are also found in *B. variegata*, potentially making this plant an active source of Phytochemicals vital to treat coronavirus infections. To determine, whether *B. variegata* is a potential source of Phytochemicals in development of treatment against SAR-CoV-2, research studies applied a molecular docking technique to look for bioactive compounds in *B. variegata* extracts that have pharmacological effects on SAR-CoV-2 target sites [12]. Post docking analysis was performed to examine the interaction between these compounds and specific corona virus targets, and ADME (adsorption, distribution, metabolism, and excretion) parameters were acquired using the Protein- Ligand Interaction Profiler. For docking studies, available medications like ivermectin and lopinavir against SARS CoV-2 (2019-nCoV) could be used as a reference [13]. Ivermectin, which is widely used to treat and cure a variety of tropical ailments, has shown to be extremely safe, with more than 2.5 billion doses reaching the public in the last 30 years. Ivermectin is a competent inhibitor of SARS-CoV-2 replication, according to *Caly et al.*, and has therefore been frequently mentioned in the global press [14]. It has shown strong binding affinity for a variety of viral proteins, according to *Eweas et al.* As a result, they might be effective inhibitors of SARS-CoV-2. Furthermore, Lopinavir, an inhibitor of HIV-1 protease, is used in conjunction with rotanavirin to extend the plasma half-life of the drug. It also has antiviral inhibitory efficacy in opposition to SARS-CoV-2 strains, in vitro [15].

Since this plant is loaded with Phytochemicals of medicinal significance, we conducted *in silico* research to find prospective Phytochemicals which could actively interact with the corona virus proteins and aid to inhibit its mechanism of action. In this study, we evaluated the potential anti-Covid biomolecules of *B. variegata* through molecular docking on the target sites SARSCoV-2 receptor binding domain, main protease, and human furin protease. Energies of molecule-target viral interaction, ADME (absorption, distribution, metabolism, and excretion), and potential toxicities created by these chemicals were determined.

MATERIALS AND METHODS

A. Biological Sequence Retrieval

All Three proteins were chosen as target sites of the corona virus. The entire amino acid sequence of SARS

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CoV-2 main protease (PDB ID- 5R84), human Furin protease (PDB ID - 5MIM) and receptor binding domain (PDB ID - 6VW1) was retrieved from online database Protein Data Bank (https://www.rcsb.org) [16] ,and kept in PDB format, intended for protein modelling in SWISS-MODEL server (http://swissmodel.expasy.org/) . Nine ligands were also retrieved; 1. Beta-Sitosterol (PubChem CID 222284), 2. Quercetin (PubChem CID 5280343), 3. Lupeol (PubChem CID 259846), 4. Rutin (PubChem CID 5280805), 5. Kaempferol (PubChem CID 5280863), 6. Gallic acid (PubChem CID 370), 7. kaempferol-3-glucoside (PubChem CID 5282102). The structures of two reference drugs, ivermectin (DrugBank Accession Number :DB00602) and lopinavir(DrugBank Accession Number: DB01601) were retrieved from drug bank (https://go.drugbank.com/) .

B. Protein preparation and validation

The 3-D protein structures were Pre-processed in BIOVIA Discovery Studio (https://www.3ds.com/products-services/biovia/products/molecular-modeling simulation/biovia-discovery-studio/) to eliminate multiple target sites. Furthermore, optimization by adding H-atoms and Gasteiger charges and energy minimization at 1000 steepest descent and conjugate gradient steps was done by using the Protein Preparation program, UCSF Chimera (https://www.cgl.ucsf.edu/chimera/) for the preparation of proteins[17]. The PROCHECK web interface evaluated the stability of protein structures (http://www.ebi.ac.uk/thornton-srv/). As specified by Ramachandran plot analysis, for all modelled protein structures, the major part of the protein residues is in favourable regions (Figure 1).

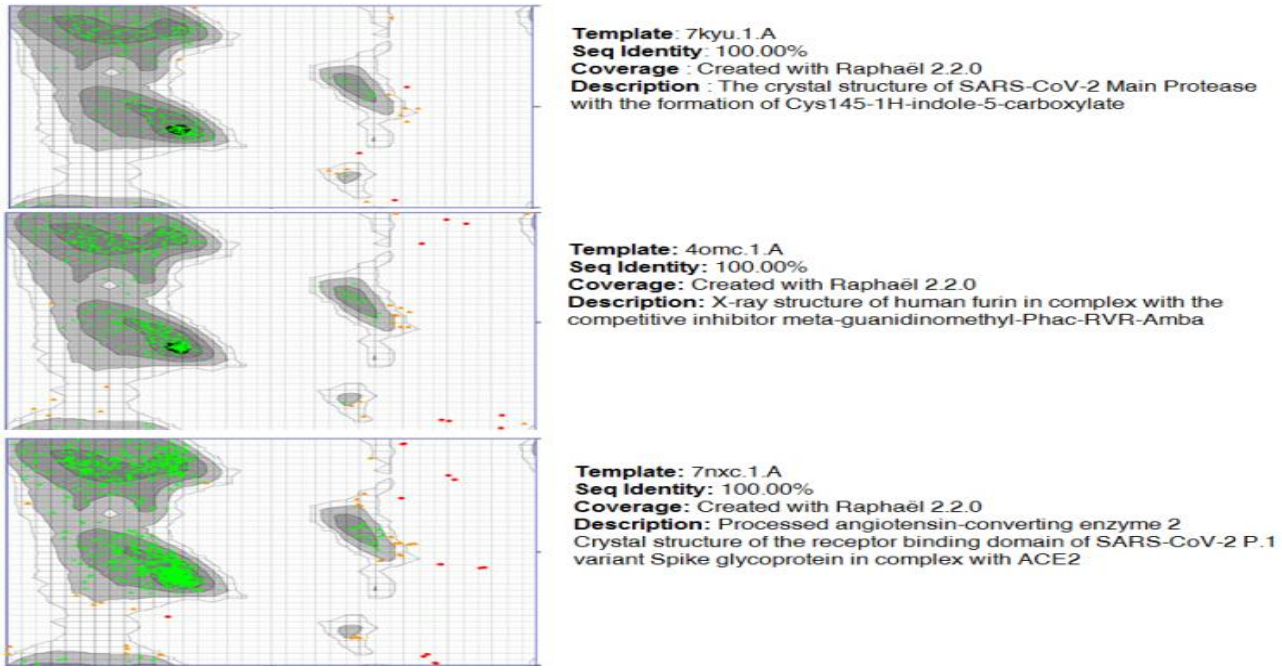

Figure 1: Protein structural assessment by Ramachandran Plot analysis

C. Ligand preparation

The chemical structures of seven selected biomolecules were procured from PubChem, (https://pubchem.ncbi.nlm.nih.gov/) and the structures of two reference drugs were obtained from drug

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bank (https://go.drugbank.com). These 3-D structures were obtained in the form of smiles string format and further, these were prepared and minimized in the UCSF Chimera (https://www.cgl.ucsf.edu/chimera/) and Lipinski's law of five (http://www.scfbi o-iitd.res.in/) was authenticated (Table 1). All input ligand files were kept in mol2 format.

Table 1: Molecular properties of ligands outlined by Lipinski's rule of five.

S. no	Compound	Molecular weight (g\mol) <500	H-bond donar <5	H-bond acceptor <10	Log P <5	Pubchem Cid
1	Gallic acid	170.12	4	5	0.7	370
2	Beta-sitosterol	414.7	1	1	9.34	222284
3	Kaempferol	286.24	4	6	2	5280863
4	Lupeol	426.7	1	1	9.23	259846
5	Kaempferol-3-glucoside	448.4	7	11	0.16	5282102
6	Quercetin	302.23	5	7	1.48	5280343
7	Rutin	610.5	10	16	-0.33	5280805
8	Lopinavir	628.8	4	5	5.94	92727
9	Ivermectin	875.1	3	14	4.37	6321424

D. Molecular Docking

The molecular docking approach was used to recognize the selective inhibition mechanism of the chosen compounds compared to the two reference drugs against the viral receptors of COVID-19. Docking was performed with Autodock 4.2.6 (http://autodock.scripps.edu/) [18]. Using Autodock software, water molecules were removed from the protein domains before hydrogens, Kollman charges, and Gasteiger charges were added to the proteins. To generate and save AD4 atoms, the PDBQT format was adopted. The UCSF chimera-prepared ligands were uploaded and saved in PDBQT format. Autogrid tool was used to build grid affinity maps with 1.0 spacing and 126 x 126 xyz grid points to cover whole protein molecules. Docking parameter was set on 50 runs and information was obtained from the topmost run for further analysis. Electrostatic energy, free binding energy, constant and final intermolecular energy for inhibition, as well as H-bond, Van der Waals, and desolvation energy, were resulted [19]. Autodock 4.2.6 tool was used for enhanced comprehension via 3d visualisation (Figure 2).

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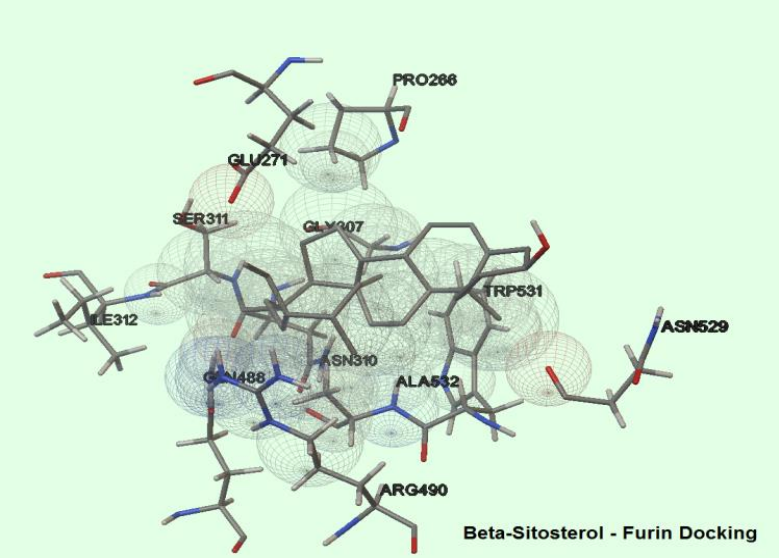

Figure 2: Docking Interactions between Beta-sitosterol and human furin protease

E. Post Docking Analysis

Protein-Ligand Interaction Profiler (https://plip-tool.biotec.tu-dresden.de/plip-web/plip/index) was applied to study the H-bond and hydrophobic interactions connecting the ligands with the docked complex receptor [20]. PLIP (Protein Ligand Interaction Profiler) allowed to quickly detect non-covalent interactions between biological macromolecules and their ligands. Further, 3-D visualization was done using PyMOL.

F. Pharmacokinetic and Toxicological properties prediction

Absorption, distribution, metabolism, and excretion (ADME) are all crucial pharmacokinetic aspects to consider while developing a drug [20]. SwissADME (http://www.swissadme.ch/) , an online tool for determining several biochemical parameters, examines these attributes[21]. On the basis of Lipinski and Veber's rules [22], several factors were established for assessing the substances from the SwissADME database. The molecular weight, hydrogen bond acceptor, hydrogen bond donor, logP value, Lipinski's Violations value, number of rotatable bonds (NRB), as well as topological polar surface area were the parameters evaluated. Toxicological testing is one of the most important factors to consider while designing new drugs. The toxicological qualities of desire compounds were assessed using Admet SAR(http://lmmd.ecust.edu.cn/admetsar2/), an online bioinformatics tool [23]. This study looked into acute oral toxicity, ames toxicity, rat acute toxicity plus carcinogenic tendencies.

RESULTS AND DISCUSSION

This study aimed at identifying possible bioactive compounds from *Bauhinia variegata* based on their molecular docking results and their interactions with SARS-CoV-2 target proteins. As a result, focusing on these proteins to find antiviral drugs for corona viruses proved to be an effective approach. Hence, antiviral drugs could target SARS-CoV-2 primary sites that are, main protease, receptor binding domain, and human furin protease.Molecular interactions of potential *B. variegata* phytochemicals with selected corona virus target proteins were investigated using Autodock software, and the docking results are summarized in Table

2 [24]. For the three targeted covid proteins, the prominence-derived dock scores for free binding energy, intermolecular energy and electrostatic energy values were compared. The hydrogen bonding with the active site residues is most important of many interactions between bioactive chemicals and target protein sites, and the affinity of this bond was measured in terms of binding energy (Kcal/mol), as lower is the binding energy (more negative), better is the affinity of the bond between the two bonding molecules [19].

In this study, SARS-CoV-2 human furin protease and SARS-CoV-2 Main protease proved to be the best target site, with more than five compounds having binding energies (BE) less than -7 kcal/mol (Table 2). Following additionally includes the ranking of ligands as per the least BE among ligands:

SARS-CoV-2 main protease: lupeol> β-sitosterol> ivermectin> ombuin> quercetin> kaempferol> lopinavir>kaempferol-3-glucoside> gallic acid> rutin

SARS-CoV-2 receptor binding domain: lupeol> ivermectin> β-sitosterol> kaempferol> quercetin> ombuin> kaempferol-3-glucoside> gallic acid> lopinavir> rutin

ARS-CoV-2 human furin protease: lupeol> β-sitosterol> kaempferol> ombuin> quercetin> ivermectin> kaempferol-3-glucoside> gallic acid> lopinavir> rutin

Lupeol was found to have the most promising results among all three target sites. In addition, when compared to the reference drug lopinavir, beta-sitosterol, kaempferol, ombuin, and quercetin have demonstrated efficacious results with all three of the covid target sites.

Lupeol, beta-sitosterol, ombuin, quercetin, and kaempferol have showed better binding to active site of the SARS-CoV-2 main protease than lopinavir. In addition, lupeol and beta-sitosterol have demonstrated to be more effective at binding than ivermectin. And, as for the human furin protease target, lupeol, beta-sitosterol, kaempferol, ombuin, quercetin, kaempferol-3-glucoside, and gallic acid have higher binding energies as compared to lopinavir. Moreover, lupeol, beta-sitosterol, kaempferol, ombuin, and quercetin have exhibited to bind better than ivermectin. On the other hand ,lupeol, beta-sitosterol, kempferol, quercetin, ombuin, kaempferol-3-glucoside, and gallic acid , have showed better affinity than lopinavir in the SARS-CoV receptor binding domain. And, only lupeol outperforms ivermectin in terms of binding energy.

Table 2: Molecular Docking Results

	SARS-CoV main protease			SARS-CoV receptor binding domain			SARS-CoV human furin protease		
Compound	BE (kcal/mol)	EE (kcal/mol)	IE (kcal/mol)	BE (kcal/mol)	EE (kcal/mol)	IE (kcal/mol)	BE (kcal/mol)	EE (kcal/mol)	IE (kcal/mol)
Gallic acid	-4.77	-0.48	-6.26	-4.86	-0.13	-6.35	-4.68	-0.29	-6.17
Quercetin	-5.73	-0.18	-7.52	**-5.79**	-0.14	-7.58	**-6.53**	-0.16	-8.32
Kaempferol	-5.72	-0.20	-7.21	-7.04	-0.13	-8.53	-7.13	-0.36	-8.62
Beta-sitoster	**-7.88**	-0.11	-9.97	**-7.07**	-0.04	-9.16	**-7.39**	-0.13	-9.48

ol									
Lupeol	**-8.00**	-0.04	-8.60	**-8.30**	0.01	-8.90	**-8.75**	+0.02	-9.35
Kaempferol-3-glucoside	-4.37	-0.30	-7.66	-5.20	-0.31	-8.48	-5.54	-0.44	-8.83
Rutin	-1.36	-0.20	-6.13	-1.10	-0.26	-5.87	-2.66	-0.52	-7.43
Ombuin	**-6.01**	-0.14	-7.80	**-5.56**	-0.15	-7.35	**-6.71**	-0.10	-8.50
*Ivermectin	-6.39	-0.04	-9.68	-7.54	-0.22	-10.82	-5.77	-0.22	-9.05
*Lopinavir	-5.05	-0.08	-9.82	-4.39	-0.21	-9.16	-3.77	-0.02	-8.54[1]

Studies show as per in vivo experiments, quercetin demonstrated potential anticovid effects, with an IC50 of 73 M for SARS-Cov 3CL (pro) [25] and 8.6 M for SARS-Cov PL (pro) [26]. Numerous polyphenols compounds have been described to provide effective inhibition against SARS-Cov on 3CL protease due to presence of their hydrophobic aromatic rings along with hydrophilic hydroxyl groups [27]-[28]. In current study, we showed that there are a multitude of additional potential targets that can be targeted to combat Covid.

Among the eight bioactive components of Bauhinia variegata, Beta-sitosterol, lupeol, ombuin, and Quercetin showed the highest binding affinity. Therefore, protein ligand profiler [29] was used to analyze their interactions with three target proteins. Therefore, protein ligand interaction profiler was used to analyze the hydrogen bonding and hydrophobic active sites of these compounds with three target proteins. Protein-Ligand interaction profiler showed that Quercetin forms 9 H-bonds with SARS-CoV-2 Main protease amino acids HIS41A,GLY143A,SER144A, SER144A, SER144A, SER144A, CYS145A, GLU166A, ARG188A; 5 H-bonds with SARS-CoV-2 RBD amino acids GLU527A, GLU527A, GLN531A,GLU536A,ASN586A, and 7 H-bonds with human furin protease amino acids GLN399A, GLN399A, ASN440A, THR442A,ALA445A,ARG483A,SER575A (Figure 3A/B/C). Ombuin forms 4 H-bonds with SARS-CoV-2 Main protease amino acids ARG4A, ARG4A,GLY127A, LEU282A; 7 H- bonds with SARS-CoV-2 RBD amino acids TRP48A, THR52A, GLN305A, TRP328A, GLU329A, LEU333A, GLN340A and 7 H-bonds with human furin protease amino GLN399A, GLN399A, ALA445A, ARG483A, ARG483A, SER575A, GLY576A (Figure 3A/B/C).Beta-sitosterol forms 2 H-bonds with SARS-CoV-2 Main protease amino GLY192A,GLY192A; 1 H-bond with SARS-CoV-2 RBD amino acid ALA348A, and 3 H-bonds with human furin protease amino acids ASN310A,ILE312A,GLN488A (Figure 3A/B/C). Lupeol forms 1 H-bond with SARS-CoV-2 main protease amino acid HIS164A and 1 H-bond with human furin protease amino acid GLU271A (Figure 3A/B/C).

[1] BE= Binding Energy, EE= Electrostatic Energy, IE= Intermolecular Energy, *Ivermectin and lopinavir taken as reference drugs

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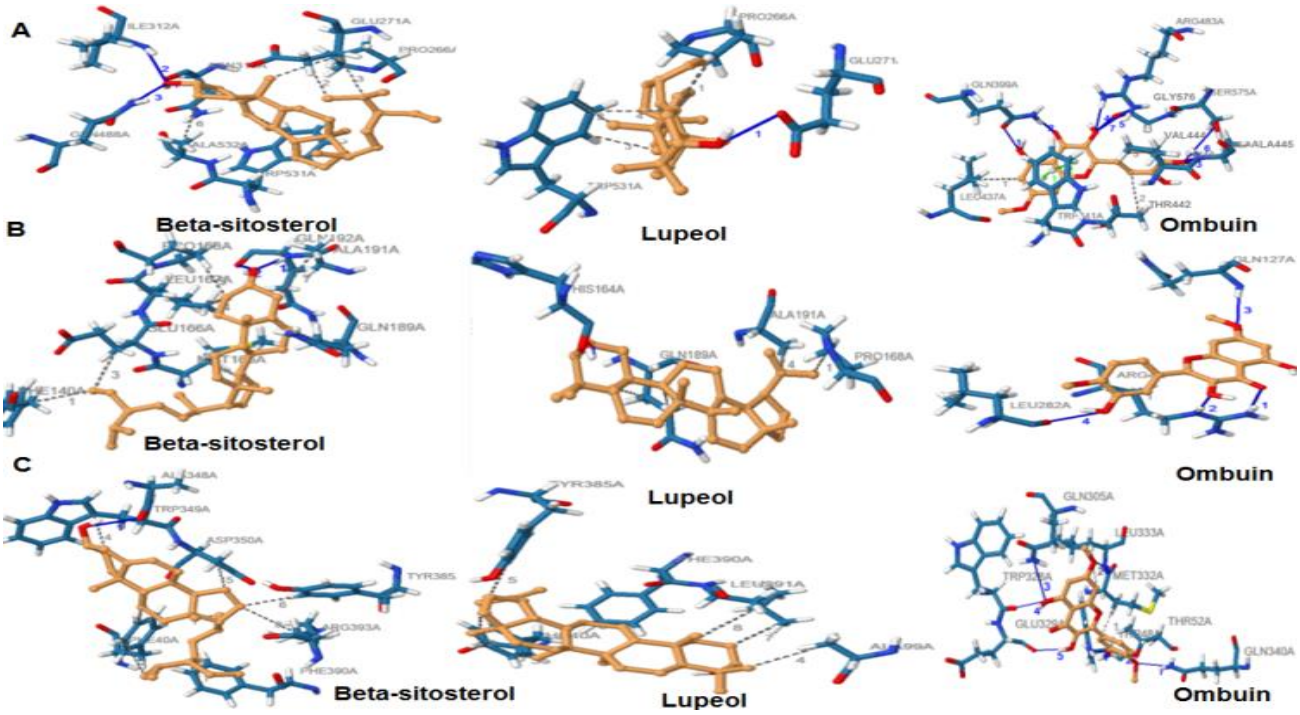

Figure 3: 3-D visualisation of SARS-CoV-2 main protease (A), SARS-CoV-2 receptor binding domain (B), and human furin protease (C) molecular interactions with biomolecules that have greater BE than atleast one reference drug (Lopinavir/ Ivermectin)

Quercetin formed the largest number of hydrogen bonds with 21 H-bonds on all three targets followed by Ombuin (18 H-bonds), Beta-sitosterol (6 H-bonds) and lupeol(2 H-bonds). As these compounds exhibit the highest binding potential (largest number of hydrogen bonding) with protein targets, they can inhibit by effectively binding to Covid-19 proteins. The comparative analysis is shown in Table 3.

Table 3: Protein-Ligand Interactions (Hydrogen and Hydrophobic Bonding)

Proteins	Ligands	Parameters			
		No. of H-bonds	Hydrogen bonding	No. of Hydrophobic Interactions	Hydrophobic bonding
SARS-CoV receptor binding	Beta-sitosterol	1	ALA348A	9	PHE40A,PHE40A,PHE40A,TRP349A,ASP350A,TYR385A,PHE390A,PHE390A,ARG393A

domain	Lupeol	0	-	8	PHE40A,PHE40A,PHE40A,ALA99A,TYR385A,PHE390A,LEU391A,LEU391A
	Ombuin	7	TRP48A,THR52A,GLN305A,TRP328A,GLU329A,LEU333A,GLN340A	2	MET332A,LEU333A
	Quercetin	5	GLU527A,GLU527A,GLN531A,GLU536A,ASN586A	2	LEU339A,LEU339A
SARS-CoV main protease	Beta-sitosterol	2	GLY192A,GLY192A	7	PHE140A,MET165A,GLU166A,LEU167A,PRO168A,GLN189A,ALA191A
	Lupeol	1	HIS164A	4	PRO168,GLY189A,GLY189A,ALA191A
	Ombuin	4	ARG4A, ARG4A,GLY127A, LEU282A	1	ARG4A
	Quercetin	9	HIS41A,GLY143A,SER144A, SER144A, SER144A, SER144A,CYS145A, GLU166A,ARG188A	0	-
SARS-CoV human furin protease	Beta-sitosterol	3	ASN310A,ILE312A,GLN488A	6	PRO266A,GLU271A,GLU271A,TRP531A,TRP531A,ALA532A
	Lupeol	1	GLU271A	4	PRO266A,TRP531A, TRP531A, TRP531A
	Ombuin	7	GLN399A, GLN399A, ALA445A, ARG483A, ARG483A, SER575A, GLY576A	3	LEU437A, THR442A, VAL444A

	Quercetin	7	GLN399A,GLN399A, ASN440A,THR442A, ALA445A,ARG483A, SER575A	2	LEU437A, VAL444A

Furthermore, understanding the pharmacokinetic characteristics and degree of toxicity of potential chemicals for therapeutic development is essential. Early on, computer simulation allows scientists to eliminate out compounds that would not respond to the above parameters. To commence, for calculating ADME (absorption, distribution, metabolism, and excoriation) with Lipinski and Veber's Rules, we used Swiss ADME. Only rutin, Ombuin and ivermectin have shown values beyond the standard limits by Lipinski's and Veber's Rules (Table 4).

Table 4: SwisADME's physicochemical properties of the compounds identified for ideal oral bioavailability

Compounds	Lipinski Rules				Lipinski's Violations ≤1	VEBER RULES	
	MW (g/mol) <500	HBA <10	HBD <5	Log P ≤5		NRB ≤10	TPSA ≤140
Gallic acid	170.12	5	4	0.70	0	1	97.99
Quercetin	302.24	7	1	1.54	0	1	131.36
Kaempferol	286.24	6	4	1.90	0	1	111.13
Beta-sitosterol	414.711	1	1	9.34	1	6	20.23
Lupeol	426.72	1	1	9.87	1	1	20.23
Kaempferol-3-glucoside	448.38	11	7	0.53	2	1	190.28
Rutin	610.52	16	10	-0.33	3	6	269.43
Ombuin	330.29	7	3	2.83	0	0	109.36
*Ivermectin	875.09	14	3	5.93	2	1	170.06
*Lopinavir	628.80	5	4	3.57	1	1	120.00[2]

[2] MW: molecular weight, HBA: hydrogen bond acceptor, HBD: hydrogen bond donor, Log P: lipophilicity, AMR: molar refractivity; Ro5V-Rule of five violation.

However, Ivermectin was found to reduce COVID-19 mortality by a considerable percentage, according to evidence of moderate certainty[30].Early use of ivermectin has been suggested as a way to reduce the number of people who acquire severe illness. Ivermectin had considerable effect on the SARS-CoV-2

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pandemic worldwide due to its apparent safety and low cost [30].
Then again, for the determination of toxological characteristics, we used admetSAR server. The considered compounds were found to be non-carcinogenic (Table 5).In acute oral toxicity, β-Sitosterol is in category I (with LD50 ≤ 50 mg/kg), quercetin in category II (50 mg/kg > LD50 < 500 mg/kg) and, Lupeol, rutin, gallic acid, ombuin, Kaempferol, Kaempferol-3-glucoside in category III (500 mg/kg > LD50 < 5000 mg/kg). All of these compounds demonstrated no possibility of ames toxicity, carcinogenicity, acute oral toxicity, and rat acute toxicity (Table 5).

Table 5: Toxicological properties evaluated by AdmetSAR

Compound	Parameters			
	Ames Toxicity	Carcinogens	Acute Oral Toxicity	Rat Acute Toxicity
Gallic acid	NAT	NC	III	1.8670
Quercetin	NAT	NC	II	3.0200
Kaempferol	NAT	NC	III	3.0825
Beta-sitosterol	NAT	NC	I	2.6561
Lupeol	NAT	NC	III	3.3838
Kaempferol-3-glucoside	NAT	NC	III	2.3869
Rutin	NAT	NC	III	2.4984
Ombuin	NAT	NC	III	3.0584
*Ivermectin	NAT	NC	III	3.5130
*Lopinavir	NAT	NC	III	2.2503[3]

[3] NAT: Non-Ames toxic; NC: Non-carcinogenic. (Category-I compound with LD50 50 mg/kg ;Compounds in category II with LD50 values between 50 and 500 mg/kg; Compounds in category III with LD50 values between 500 and 5000 mg/kg; Compounds in category IV with LD50 values less than 5000 mg/kg).

CONCLUSION

Bauhinia variegata yields phytochemicals such as terpenoids, flavonoids, tannins, steroids, reducing sugars, and cardiac glycosides, which have pharmacological effects such as anticancer, anti-inflammatory, antibacterial, wound healing, antiulcer, and antiobesity. However, when compared to two reference drugs, ivermectin and lopinavir, bioactive *B. variegata* compounds lupeol and beta-sitosterol have shown highest binding affinity. In addition, ombuin, kaempferol, and quercetin have also demonstrated significant docking outcomes.Therefore, our study states that these phytochemicals are potential inhibitors of corona virus target proteins (main protease, receptor binding domain and human furin protease) and could be effective in the treatment of infections caused by these viruses.

AUTHOR CONTRIBUTION

HS, SA and CT conceived and designed the research articles. SA and CT carried the work. HS contributed materials or analytical tools and supervised the work. CT and SA wrote the manuscript. All authors read and approved the manuscript.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

ETHICAL APPROVAL

This article does not contain any studies with human participants or animals performed by any of the authors.

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