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*Original Research Article*



# **Pharmacokinetics and Molecular Docking Study of Siddha Polyherbal Preparation Shailam Against COVID-19 Mutated s Gene**

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# ARTICLE INFO ABSTRACT

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COVID-19 is a deadly disease; at the time of the first COVID-19 wave (January 2020 to November 2020), so many deaths were reported worldwide. There were no standard conventional treatments and vaccines, so the whole world turned to traditional medicine. Siddha system of medicine is one of the traditional medicines practiced in the southern part of India. *Shailam* is a polyherbal formulation (licence no. 1189/25D) which was analyzed by molecular docking, with AutoDockVina software, against SARS-CoV-2 Spike Protein (PDB ID 7DDD). Absorption, distribution, metabolism, and excretion (ADME) properties were also recorded for *Shailam's* phytocompounds using the online SwissADME tool. The results of the molecular docking study showed that the phytocompounds, like Caryophyllene, Aspidospermidin-17-ol, N,N'Dibenzylidene-3,3'-dichlorobenzidine, Beta-selinene, Curzerene, Germacrene B, Spathulenol, had the highest docking scores: -6.6 Kcal/mol, -8.8 Kcal/mol, -8.7 Kcal/mol, -6.2 Kcal/mol, -6.0 Kcal/mol, -6.6 Kcal/mol, -6.5 Kcal/mol, respectively, and the scores fall within the docking score range of the four standard conventional drugs; Azithromycin, Hydroxychloroquinone, Ivermectin, and Remdesivir which had binding energies of 7.7 Kcal/mol, -5.9 Kcal/mol, -9.2 Kcal/mol, and -7.5 Kcal/mol, respectively. ADME analysis predicted that all of *Shailam's* phytocompounds met four Lipinski's rule of five and have a higher bioavailability score (0.55) as compared to standard conventional drugs, Azithromycin, Hydroxychloroquinone, Ivermectin, and Remdesivir (0.17). Twelve of *Shailam's* phytochemical compounds have high GIT absorption and can cross the blood–brain barrier (BBB). In conclusion, Shailam's phytocompounds show a good docking score and ADME property against SARS-CoV-2 Spike Protein (PDB ID 7DDD**)** as compared to standard conventional drugs.

*Keywords*: Siddha medicine, COVID-19, Herbal medicine, Alternative medicine, Traditional medicine.

# **Introduction**

The human community has faced many pandemics in the past, in which COVID-19 is a deadly disease that originated in December 2019 in Wuhan, China. The World Health Organization (WHO) later declared COVID-19 as a pandemic in February 2020 and named it coronavirus disease-2019 (COVID-19).<sup>1</sup> The COVID-19 virus is the seventh coronavirus to infect humans; it is the third in recent years causing widespread infectious disease, leading to more severe respiratory infections and deaths worldwide. As of March 17, 2022, the outbreak of COVID-19 was in over 210 countries and territories and has infected about 450 million people, with six million people dying as a result. The most affected countries include the USA (17.95%), India (15.71%), and Brazil (9.91%).<sup>2</sup>

The world suffered drastic damage in terms of both human health and economy. Although vaccination started in January 2021, only 56.6% of the world population was completely vaccinated and 68.3% received the first vaccine dose.<sup>3</sup>

WHO Director-General Dr. Tedros Adhanom Ghebreyesus said that

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the pandemic could end in mid-2022 when vaccination is complete for 70% of the population, until traditional medicine could be the only hope for this pandemic. 4 The Siddha medicine is a type of traditional medicine used in the southern India. Siddhars are spiritual scientists who practiced this knowledge and passed it on to humanity.

Siddha medicine system has different forms of medicine; 32 internal and 32 external, Shailam is a Siddha polyherbal formulation having 20 ingredients. 5 (Table 1), which has already proven its efficacy in clinical trials, and most of the Siddha medicines have been used in practice for so many years. Usually, traditional medicines like Chinese traditional medicine, Ayurveda, and Unani were practiced widely among the people of a certain region and they have been tested pharmacologically. Therefore, this study was conducted to demonstrate *In silico* efficacy of Shailam, a Siddha polyherbal formulation against SARS-CoV-2 Spike Protein (PDB ID 7DDD) and to study SwissADME property of *Shailam's* phytocompounds.

#### **Materials and Methods**

# *Molecular docking*

The "key-and-lock" theory is used in molecular docking to discover the appropriate orientation of protein and ligand. **PDB ID 7DDD** target protein was docked with the selected phytochemical compounds using the AutoDock Vina software, and the binding energies were calculated. The ligands and target protein were synthesized, following routine ligand and protein preparation procedures, and the protein and ligand files were then uploaded to AutoDock Vina.<sup>28</sup>

Sl.no	<b>Compound name</b>	Formula	<b>Molecular Weight</b>	<b>Botanical name</b>	Pharmacological <b>Activity</b>
$\mathbf{1}$	Eugenol	$C_{10}H_{12}O_2$	164.2	Ocimum tenuiflorum	Antiaflatoxigenic,
					Genotoxicity,
					Antifungal <sup>6-8</sup>
2	Caryophyllene	$C_{15}H_{24}$	204.35	Ocimum tenuiflorum	Antibacterial,
					Anti-inflammatory,
					Anticonvulsant $9-11$
3	Amrinone	$C_{10}H_9N_3$	187.2	Justicia adhatoda	Muscle inhibition
					Cardiotonic <sup>12,13</sup>
4	Phytol	$C_{20}H_{40}O$	296.53	Justicia adhatoda	Hepatoprotective <sup>14,15</sup>
5	$2-(2,5-$	$C_{11}H_{14}O_2$	178.23	Glycyrrhiza glabra	
	Hexadiynyloxy)tetrahydro-				
	2H-pyran				
6	1,5-Hexadiyne	$C_6H_6$	78.11	Glycyrrhiza glabra	
7	Isopinocarveol	$C_{10}H_{16}O$	152.23	Tinospora cordifolia	
8	Di-n-Decylsulfone	$C_{20}H_{42}O_2$	346.61	Tinospora cordifolia	
9	1,8-cineole	$C_{10}H_{18}O$	154.25	Elettaria	Mucolytic, Anti-
				cardamomum	inflammatory,
					$Antitumor^{16,17}$
10	Aspidospermidin-17-ol	$C_{23}H_{30}N_2$	414.49	Solanum virginianum	
11	N,N'Dibenzylidene-3,3'-	$C_{26}H_{18}Cl$	429.34	Solanum virginianum	
	dichlorobenzidine				
12	Linolenic acid	$C_{18}H_{30}O_2$	278.43	Azadirachta indica	Anti-inflammatory,
					Antitumor,
					Antibacterial $18-20$
13	Hexadecanoic acid	$C_{16}H_{32}O_2$	256.42	Trigonella foenum-	Bactericidal <sup>21</sup>
				graecum	
14	Terpinen-4-ol	$C_{10}H_{18}O$	154.25	Myristica fragrans	Acaricidal,
					Anticonvulsant,
					Antibacterial <sup>22-24</sup>
15	Sabinene	$C_{10}H_{16}$	136.23	Myristica fragrans	
16	Beta-selinene	$C_{15}H_{24}$	204.35	Commiphora myrrh	
17	Curzerene	$C_{15}H_{20}O$	216.32	Commiphora myrrh	Antileishmanial
					activity <sup>25</sup>
18	Germacrene B	$C_{15}H_{24}$	204.35	Commiphora myrrh	
19	Myrcenol	$C_{10}H_{18}O$	154.25	Commiphora myrrh	
$20\,$	Spathulenol	$C_{15}H_{24}O$	220.35	Commiphora myrrh	Anti-mycobacterial,
					Immunomodulatory <sup>26,27</sup>

**Table 1: Siddha preparation,** *Shailam* **Ingredients, Phytocompounds and its Pharmacological activity**

For the current work, 20 phytochemical compounds or bioactive compounds identified from *Shailam* were used for the docking study. The chemical structures of all selected compounds were retrieved from the *National Center for Biotechnology Information* (NCBI's) PubChem compound database.<sup>29</sup>

#### *Swiss ADME*

To estimate individual absorption, distribution, metabolism, and excretion (ADME) characteristics of *Shailam's* phytocompounds, the SwissADME software of the Swiss Institute of Bioinformatics, a web server displaying the SwissADME Submission page, was accessed from Google.<sup>30</sup> The list is designed to contain one input molecule per row with multiple inputs, such as defined by the simplified molecularinput line-entry system (SMILES), with the results presented in graphs, tables, and an Excel spreadsheet for each molecule.

# **Results and Discussion**

*Molecular docking*

The biological activity of *Shailam* compounds against SARS-CoV-2 Spike Protein (PDB ID 7DDD) was evaluated using the 3D composition of the receptor retrieved from the protein data library site of SARS-CoV-2 Spike Protein (PDB ID 7DDD**).** Various compounds from *Shailam* were interacted with the SARS-CoV-2 Spike Protein (PDB ID 7DDD) as shown in Figure 1. The docking results of *Shailam* bioactive molecules and standard drugs are shown in Table 2. Docking studies show that the ligands bind to the active spot region of SARS-CoV-2 Spike Protein (PDB ID 7DDD**)** with good binding energy as compared to the standard control drugs, presented in the form of e-negative values. Higher negative e-values in docking scores indicate strong binding affinity between the receptor and ligand molecules, indicating that the bioactive substances are more efficient. Thus, it is clear that the bioactive compounds were able to effectively

interact with all available binding sites of the SARS-CoV-2 Spike Protein (PDB ID 7DDD**)**.

*Shailam's* compounds show docking score ranging from 3.8 to 8.8. The compounds like Caryophyllene, Aspidospermidin-17-ol, N,N'Dibenzylidene-3,3'-dichlorobenzidine, Beta-selinene, Curzerene, Germacrene B, Spathulenol showed the highest docking scores -6.6 Kcal/mol, -8.8 Kcal/mol, -8.7 Kcal/mol, -6.2 Kcal/mol, -6.0 Kcal/mol, -6.6 Kcal/mol, -6.5 Kcal/mol, respectively, among the 20 phytochemical compounds, and the scores fall within the docking score range of the four standard conventional drugs Azithromycin, Hydroxychloroquinone, Ivermectin, Remdesivir which have binding energies of 7.7 Kcal/mol, -5.9 Kcal/mol, -9.2 Kcal/mol, -7.5 Kcal/mol, respectively.



**Figure 1:**Molecular docking of target SARS-CoV-2 Spike Protein (PDB ID 7DDD) by phytocompounds of Shailam, Eugenol, Caryophyllene, Amrinone, Phytol, 2-(2,5 Hexadiynyloxy)tetrahydro-2H-pyran, 1,5-Hexadiyne, Isopinocarveol, Di-n-Decylsulfone, 1,8 cineole, Aspidospermidin-17-ol, N,N'Dibenzylidene-3,3'-dichlorobenzidine, Linolenic acid, Hexadecanoic acid, Terpinen-4-ol, Sabinene, Beta-selinene, Curzerene, Germacrene B, Myrcenol, Spathulenol, Azithromycin, Hydroxychloroquinone, Ivermectin, Remdesivir

#### *SwissADME*

The rationale for these *In silco* techniques came from the fact that they cost less and take less time than regular ADME profiling. For

example, in an *in silico* model, analyzing 20,000 compounds takes a fraction of a second, whereas in a "wet" laboratory, the same process takes 20 weeks. Many pharmaceutical companies are increasingly

adopting computer models to replace "wet" screens, owing to ADME data that was pooled in the late 1990s. Various theoretical models for estimating ADME parameters were created on the basis of this paradigm shift. Quantitative structure–activity relationships, QSAR, and knowledge-base approaches are frequently utilized in software tools intended to predict the ADME features of potential drug candidates.<sup>31</sup> The present study used SwissADME online software tool which is available free for the users to evaluate the ADME properties. The drug-likeness of active ingredients has been studied to determine if they have good ADME properties. The aqueous solubility of druglike molecules should be good as estimated by three techniques: ESOL, (ALI) logS, and (SILICOS-IT) logS. Orally bioavailable drugs must follow Lipinski's rule of five in Table 3, which require a molecular weight (MW) of not more than 500 g/mol, H-bond acceptors of not more than 10, H-bond donors of not more than 5, logP value of not more than 5, and number of rotatable bonds not less than 10, where a violation of two or more rules indicates that the molecule is orally inactive.

Drug-likeness analyses of phytocompounds are tabulated in Table 4. The phytocompounds, such as Eugenol, Amrinone, 2-(2,5- Hexadiynyloxy)tetrahydro-2H-pyran, 1,5-Hexadiyne, Isopinocarveol, 1,8-cineole, Aspidospermidin-17-ol, Terpinen-4-ol, Curzerene, Myrcenol, Spathulenol, followed all Lipinski's rule of five, and only some *Shailam's* compounds like Caryophyllene, Phytol, Di-n-Decylsulfone, N,N'Dibenzylidene-3,3'-dichlorobenzidine, Linolenic acid, Hexadecanoic acid, Sabinene, Beta-selinene, Germacrene B which violate one Lipinski's rule have rotatable bonds less than 10, while standard drugs Azithromycin, Ivermectin, Remdesivir violate 2 Lipinski's rules such as molecular weight, H-bond acceptor over 10, H-bond donor under 5.





Compounds with a logP higher above 1 and less below 4 are often more likely to get better physicochemical as well as ADME qualities for oral medications.<sup>32</sup> Among the four standard drugs, Remdesivir alone has good lipophilicity (Table 5). All phytocompounds, other than Phytol, Di-n-Decylsulfone,N,N'Dibenzylidene-3,3' dichlorobenzidine, Linolenic acid, have good [ADME](https://www.sciencedirect.com/topics/pharmacology-toxicology-and-pharmaceutical-science/adme) properties for oral drugs. Furthermore, for oral administration discovery studies, solubility is one of the most important factors determining absorption. A medicine intended for parenteral administration must also be highly water soluble so as to deliver a sufficient amount of active component in the small volume of such pharmaceutical dosage. SwissADME includes two topological approaches to predict water solubility. The first one is based on the ESOL model while the second is based on Ali *et al.*<sup>33</sup> Di-n-Decylsulfone1,8-cineole, N,N'Dibenzylidene-3,3'-

dichlorobenzidine, and only these two compounds of *Shailam* are slightly aqueous soluble, while all other eighteen compounds have good solubility (Table 6).

**Table 3:** Lipinski's rule of five (Ro5) violation

<b>Rules</b>	Values
Molecular weight	$< 500$ Daltons
Hydrogen bond acceptors No	>10
Number of rotatable bonds No	< 10
Hydrogen bond donors No	> 5
Octanol–water partition coefficient (logP)	$\leq 5$

# **Table 4:** General Characteristics of Phytoconstituents of *Shailam*



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**Table 5:** Lipophilicity of active compounds of *Shailam* formulation predicted from SwissADME



The importance of gastrointestinal (GI) absorption in maintaining appropriate therapeutic levels in the systemic circulation cannot be overemphasized. Drugs or potential compounds must be absorbed through the gastrointestinal tract and enter the systemic circulation in sufficient amounts or quantities to reach their target.<sup>34</sup> Drugs that are highly absorbed from the GI tract easily reach their target site and have a therapeutic effect. Out of four conventional drugs, Hydroxychloroquinone has high GIT absorption, and twelve *Shailam's* phytocompounds like Eugenol, Amrinone, 2-(2,5- Hexadiynyloxy)tetrahydro-2H-pyran, Isopinocarveol, 1,8-cineole, Aspidospermidin-17-ol, Linolenic acid, Hexadecanoic acid, Terpinen-4-ol, Curzerene, Myrcenol, Spathulenol have high GIT absorption (Table7).

Twelve *Shailam's* phytocompounds such as Eugenol, Caryophyllene, Amrinone, Phytol, Di-n-Decylsulfone, Aspidospermidin-17-ol, N,N'Dibenzylidene-3,3'-dichlorobenzidine, Hexadecanoic acid, Betaselinene, Curzerene, Germacrene B, Spathulenol are inhibitors of CYP1A2, CYP2C19 CYP2C9, CYP2D6 CYP3A4, enzyme (Table7). Inhibition of CYP3A4 has previously been found to reduce the probability of drug clearance from the systemic circulation and improve drug bioavailability.

The blood–brain barrier (BBB) is a protective system developed by the endothelial cells lining cerebral microvessels. The drugs or compounds that are not soluble in lipids with a molecular weight greater than 400 Dalton cannot penetrate the BBB, but smaller, lipophilic molecules can go across the BBB.<sup>35</sup> Accordingly, when formulating a medicine for neurodegenerative and associated disorders, the BBB permeability parameter is always taken into account. None of the four standard conventional drugs was predicted to permeate the BBB, and twelve phytocompounds from Shailam were predicted to go across the BBB, namely Eugenol, 2-(2,5- Hexadiynyloxy)tetrahydro-2H-pyran, Isopinocarveol, 1,8-cineole, Aspidospermidin-17-ol, Linolenic acid, Hexadecanoic acid, Terpinen-4-ol, Sabinene, Curzerene, Myrcenol, Spathulenol (Table7).

The degree of absorption and fraction of a given amount of unaltered medicine that enters the circulatory system are measured by drug bioavailability. When estimating pharmacological dosages, this is a crucial pharmacokinetic aspect of the medicine that should be thoroughly investigated. A higher level of bioavailability is required for a drug to reach a higher and optimal concentration in the circulatory system and exert a pharmacological effect. All of Shailam's phytochemical compounds have a higher bioavailability

score (0.55) as compared to standard conventional drugs, Azithromycin, Hydroxychloroquinone, Ivermectin, Remdesivir (0.17). *Shailam* compounds such as Linolenic acid and Hexadecanoic acid (0.85) also have a higher bioavailability as standard drug Hydroxychloroquinone (0.56) (Table8).

Synthetic accessibility (SA) is an important factor to consider in drug selection. Certainly, medicinal chemists are best at determining SA for a reasonable number of compounds. When there are too many molecular structures to evaluate manually, *in silico* estimation can be used as a pre-filter. Ertl and Schuffenhauer offered a fingerprint-based SA estimation solution, but it included closed-source fingerprintdefining information, which made it difficult to use in practice. The SA score ranges from 1 (very easy) to 10 (very difficult) (Table 9). Here, all phytocompounds have SA score below 5, which means they are easily converted into a synthetic form.

**Table 6:** Water solubility properties of all the active compounds of *Shailam* predicted from SwissADME



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**Table 7:** Pharmacokinetic Parameters of the Phytoconstituents of *Shailam* predicted from SwissADME



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**Table 8:** Drug likeliness of all the active compounds of *Shailam* predicted from SwissADME



# **Table 9:** Medicinal Chemistry Properties of Phytoconstituents of *Shailam* predicted from SwissADME





### **Conclusion**

The *In silico* molecular docking study of *Shailam's* phytoconstituents against the SARS-CoV-2 Spike Protein (PDB ID 7DDD**)** shows docking score ranging from 3.8 to 8.8**.** The compounds such as Aspidospermidin-17-ol, N,N'Dibenzylidene-3,3'-dichlorobenzidine bind effectively to the active spot region of SARS-CoV-2 Spike Protein (PDB ID 7DDD**).** ADME analysis predicts that all of *Shailam's* phytocompounds meet four Lipinski's rule of five and has a higher bioavailability score (0.55) as compared to standard conventional drugs, Twelve of *Shailam's* phytochemical compounds have high GIT absorption and can cross the blood–brain barrier (BBB). This information obtained can be used as a primary tool for the evaluation of interventional drug in pharmacodynamic studies, *in vitro, in vivo* studies, randomized clinical trials, etc.

### **Conflict of Interest**

The authors declare no conflict of interest.

# **Authors' Declaration**

The authors hereby declare that the work presented in this article is original and that any liability for claims relating to the content of this article will be borne by them.

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