

### **Research Article**

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# In-silico screening of active molecules from medicinal plant resources for controlling SARS-CoV-2 infection

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## ABSTRACT

The entire human population is under treat of SARS-Cov-2 virus causing life threatening complicacies. Three proteins namely papain-like protease (PLpro), 3C-like protease (3CLpro) and spike protein isolated from the virus have been targeted for formulating the antiviral medicament. Ayurvedic medicinal plants with established antiviral efficacy are great choice to design immediate treatment strategies in this trying time. Here, 9 active molecules from ayurvedic medicinal plant resources were selected, out of which only 6 have screened through ADME analysis and molecular docking was performed with the three viral proteins to understand their antiviral performances in in silico model. Outcome of this study will surely open up a floodgate of thousand new possibilities in exploiting the existing natural herbs in COVID 19 treatments.

Keywords: ADME analysis, Antiviral activity, Medicinal Plants, Molecular Docking, SARS-CoV-2, Viral proteins

#### INTRODUCTION

At the beginning of 2020, a new novel SARS-CoV-2 viral disease with flu or influenza like symptoms has introduced a global pandemic causing a mammoth human loss. The epicenter of the disease is believed to be Wuhan province of China <sup>[1]</sup>. The zoonotic transmission of the contagious disease quickly transformed its course into human to human transmission, resulting in rapid spread of the disease in a very short time span. On 30<sup>th</sup> January, 2020, declaration of a public health emergency and temporary recommendations by the Director-General of the World Health Organization (WHO)emerged a global concern on the pandemic issue <sup>[2]</sup>. Thespecific vaccines and antiviral agents needed to overcome the emergency, demands adequate research and time to serve the population. A number of medicines has been surfaced in the meanwhile as an effective mean of disease control, but failed to sustain for long due to the quick alteration of the virus nature and character <sup>[3-5]</sup>.

Among the SARS-CoV-2 encoded proteins reported till date, three proteins namely papain-like protease (PLpro), 3C-like protease (3CLpro) and spike protein play pivotal role in invasion, infection establishment and replication of the virus inside the host body. Being mandatory tool for the virus in disease causing and continuing the life cycle, these proteins draw special attention to the scientific community in preventing and treating the viral infection. For example, Successful inactivation or structural alteration of viral 3C-like protease (3CLpro) or spike (S) protein hold promises in arresting the viral life cycle progression and entry into the host body respectively. Thus, working on drug designing, these proteins are considered as target molecules to fight against the notorious virus SARS-Cov-2 <sup>[6-11]</sup>.

In search of a suitable and sustainable alternative to cope up with the newly emerged scenario, the traditional medical systems are of special attention. Ayurveda is considered by many scholars to be the oldest healing science. In Sanskrit, Ayurveda means "The Science of Life." The knowledge originated in India more than 3000 years ago and is often called the "Mother of All Healing." The knowledge of plant sciences resides in several Nighantus which may be termed as Ayurvedic Lexicons. Several plants in Ayurveda exhibits potent antibacterial, antifungal and antiviral activities through several stages of research by means of modern scientific community. In day to day practice or home remedies we used these plants from generations after generation for the management of several viral diseases, such as for the management of viral fever or common cold, specially for juvenile patients we usually administers basil leaves juice as a normal house hold remedy. We also use ginger and black piper infusion for the treatment. Modern science supports the antiviral activities of several ayurvedic plants through several published papers. Till date in

\*Corresponding author: Dr. Debasish Ghosh Vishwanath Ayurved Mahavidhyalaya And Hospital, 94, Grey Street, Kolkata, India Email: drdghosh71@gmail.com Asian and African continent, herbal medicines are effectively practiced and serving the mankind in disease control <sup>[12]</sup>. Literature say, > 250,000 higher plant species reserve the unexplored active molecules of enormous medicinal importance <sup>[13]</sup>. The plant based natural products not only exhibit potential antimicrobial efficacy that limits the chances of microbial infections onto the host body, but also imparts an immunemodulatory role which strengthen the host immune system to fight against the pathogen. The multifaced approach of the plant based medicines provide better protection to the host in terms of disease control. For instance, in 2003, SARS outbreak in China was successfully controlled by the traditional herbal treatments <sup>[14-20]</sup>.

However, the impressive medicinal properties of thousands of plants, impose critical challenge in deciding the appropriate ones effective against SARS-Cov-2. Based on the established evidences available in scientific literature, 9 medicinal plants with significant antiviral efficacy were selected for this study. Traditional utility, availability and disease curing ability were the primary criteria followed for this selection. To determine their possible exploitation in combating

SARS-Cov-2, a two-step screening protocol has been followed. Initially, the active components of the selected herbs, playing pivotal role in pathogen control have been screened through network pharmacology analysis that ensures their medicinal application for treating illness. Further, the most suitable compounds were docked with the important viral protein molecules, ensuring the antiviral potency of these compounds at molecular level. The entire study has been performed in *in silico* model to achieve conclusion in short time span.

## METHODOLOGY

**Plant selection:** The medicinal plants selection was based on the established efficacy in treating viral infections with cough and cold, flu or influenza like symptoms. Ayurvedic plants in table 1 have been selected by us through the support of the data as available in the articles, published in the English language from Web of Science, Cochrane Library, AMED, CISCOM, EMBASE, MEDLINE, Scopus, and PubMed by using relevant keywords including plants possessing antiviral activity, the antiviral effects of plants, and plants used in viral disorders.

Table 1: Selected Medicinal plants with antiviral potency and the related active compounds.

		1	r	
Traditional name	Botanical name	Active component	References	
Neem	Azadirachta indica	Azadirachtin	[21]	
Pipul	Piper longum	Piperine	[22]	
bhuiamlaki	Phyllanthus niruri	Phyllanthin	[23]	
Tulsi	Ocimumsanctum	Ursolic acid	[24]	
Haldi	Curcuma longa	Curcumin	[25]	
Durva	Cynodondactylon	Hexadecanoic acid	[26]	
Ginger	Zingiber officinale	α, β zingiberene	[27]	
Anantamool	Hemidismus indicus	Hexatriacontane	[28]	
Parijat	Nyctanthes arbor-tristis	Nicotiflorin	[29]	

**Network pharmacology analysis:** Considering the oral intake as most preferable route of drug administration, ADME (absorption, distribution, metabolism and excretion) screening was performed using SwissADME online tool. The parameters used for this screening study includes drug likeness, solubility, bioavailability, GI absorptionof the active components of the medicinal herbs. The screening of the herbs wasbased on their fitness in Veber, Egan and Lipinski's rule of five <sup>[30]</sup>.

**Molecular docking:** Molecular docking is a bioinformatic modelling that involves the interaction of two or more molecules to give the stable adduct. Depending upon binding properties of ligand and target, it predicts the three-dimensional structure of any complex.

The 3D structure of the 6M0J.pdb (spike protein), 6W9C.pdb (papainlike protease) and 7BQY.pdb (3C-like protease) were downloaded from the protein data bank. The molecular docking and visualization using discovery studio are performed as followed by Sribalan *et al.*, 2016 and Banuppriya *et al.*, 2018 [31, 32]. Molecular docking was performed using the Autodock 4.2 software. The 3D structures of molecules were optimized using Chemdraw 13.0 using MMFF 94 (Maximum number of interactions: 5000, minimum RMS gradient: 0.100). All avoidable water and ligand were removed from the protein and the default docking parameters were fixed and performed.

#### **RESULTS AND DISCUSSIONS**

#### Network pharmacology analysis:

The selected ayurvedic herbs presented in Table 1 were subjected to ADME screening and results are presented in Table 2. Analyzing the data presented in Table 2, the low bioavailability and GI absorption of azadirachtin, hexatriacontane and nicotiflorin restricts the oral administration of Neem, Anantamool and Parijat in SARS-Cov-2 treatment. In contrast, the higher bioavailability of piperin, phyllanthin, ursolic acid, curcumin, hexadecanoic acid and zingiberene signifies their possible utilization in the mentioned purpose. Furthermore, better fitting into Lipinski, Egan and Veber filter of these molecules strengthen their medicinal applicability compared to the other molecules. Among these 6 molecules, piperine and curcumin is of greater importance due to their high solubility in aqueous medium that facilitates better GI absorption (Table 2). Table 2: Pharmacology Network analysis through ADME screening of the active molecules in selected ayurvedic herbs.

Plant resource	Name of the Active	GI	Bioavailability	Solubility (in	Drug likeness		
	Molecules	Absorption		water)	Lipinski filter	Egan filter	Veber filter
Azadirachtaindica (Neem)	Azadirachtin	Low	17%	Moderately soluble	No	No	No
Piper longum(Pipul)	Piperine	High	55%	Soluble	Yes	Yes	Yes
Phyllanthus niruri (bhuiamlaki)	Phyllanthin	High	55%	Moderately soluble	Yes	Yes	No
Oscimumsanctum(Tulsi)	Ursolic acid	Low	56%	Poorly soluble	Yes	No	Yes
Curcuma longa(Haldi)	Curcumin	High	55%	Soluble	Yes	Yes	Yes
Cynodondactylon (Durva)	Hexadecanoic acid	High	56%	Moderately soluble	Yes	Yes	No
Zingiber officinale (Ginger)	Zingiberene	Low	55%	Moderately soluble	Yes	Yes	Yes
Hemidismus indicus (Anantamool)	Hexatriacontane	Low	17%	Insoluble	No	No	No
Nyctanthes arbor- tristis(Parijat)	Nicotiflorin	Low	17%	Soluble	No	No	No

**Molecular docking:** The six active molecules with higher possibility of oral administration were then docked with three target protein molecules isolated from SARS-CoV-2. Inhibition of these target proteins directly restricts the viral activity like defending host immunity,

replication and infection establishment into the host body (Zhang *et al.*, 2020).The binding energy and inhibition constantbetween the targetligand molecules determine the stability of the 3Dcomplex (Table 3).

Table 3: Interaction of active molecules with target proteins

Plant resource	binding energy (Kcal/mol)			Inhibition constant (µM)		Interacted amino acids				
		PLpro	3CLpro	spike	PLpro	3CLpro	spike	PLpro	3CLpro	spike
Piper longum(Pipul)	piperine	-5.93	-7.8	-6.17	45.19	1.92	6.65	TYR273,	TYR54,	TRP48,
								GLY163	GLN189,	GLN340,
									GLN192	THR334
Phyllanthus niruri	Phyllanthin	-4.2	-5.37	-4.1	827.56	111.41	985.88	LEU162,	HIS164,	VAL343,
(bhuiamlaki)								GLY16,	GLY143	HIS345,
								TYR264,		THR347,
								ASN267		ASN51,
										TRP349,
										TRP349
Oscimumsanctum(Tulsi)	Ursolic acid	-5.82	-6.72	-5.76	54.25	11.89	59.8	TYR264,	GLU166,	SER47,
								TYR273,	HIS164,	ALA348,
								GLY163,	ARG188,	TRP349,
								THR301	THR190	TRP349,
										HIS378
Curcuma longa(Haldi)	Curcumin	-6.99	-7.31	-5.64	7.48	4.4	73.49	GLN250,	HIS41,	GLU406,
								ASN267	GLN189,	GLU402,
									GLN192,	SER47,
									THR190,	HIS378,
									PRO168,	HIS378
									GLU166	
Cynodondactylon	Hexadecanoic	-2.62	-4.45	-1.68	11.98 mM	546.72	58.44 mM	TYR273,	GLN192,	ASN51,
(Durva)	acid							THR301	MET49,	TRP349
Zingiber officinale	zingiberene	-5.4	-6.65	-4.99	109.21	13.38	218.33	TYR264,	GLN192,	SER44, SER44,
(Ginger)								GLY163	THR190,	ASP350,
									GLN189,	ASP382,
									HIS41,	ASP382,
									ARG188,	TYR395,
									ASP187, TYR54	HIS401

In Table 3, the binding energy and the inhibition constant between active molecule and protein interactions denotes promising activities of

piperine, ursolic acid, curcumin and zingiberene in combating the SARS-CoV2 virus. Piperine (from Pipul) blocks the 3CLpro and spike protein of the virus, thus capable of restricting the virus entry and multiplication inside the host body. Similarly, ursolic acid (from Tulsi) and zingiberene (from Zinger) show promising interactionswith 3CLpro protein and expected to be active in inhibiting viral replication inside the host cell. Again, curcumin (from Haldi) actively binds with PLpro and 3CLpro proteins, thus arrests the viral efficacy against host immunity and multiplication inside the host cell (Fig 1). comparing the antiviral efficacy, piperine and curcumin are most preferable followed by ursolic acid and zingiberene. It is noteworthy to mention, the *in-silico* performances of phyllanthin and hexadecanoic acid found against SARS-CoV 2 are not promising and thus not recommended for COVID 19 treatment.



Figure 1: Pictorial presentation of molecular docking between Piperineand (a) 3CLpro (b) Spike protein; Ursolic acid and (c) 3CLpro; Curcumin and (d) PLpro (e) 3CLpro; Zingiberene and (f) 3CLpro protein.

## CONCLUSION

The antiviral efficacy of the active molecules from natural resources has been studied here in *in silico* model. The interactions between the active molecules and the target protein of SARS-Cov 2 virus, ensures the higher probability of their successful utilization in overcoming the pandemic situation.

The important finding of this work can be summarized as:

- Piperine (from Pipul) interacts with the 3CLpro and spike protein of the virus, that ensures inhibition of the virus entry and multiplication inside the host body.
- Ursolic acid (from Tulsi) and zingiberene (from Ginger) are expected tosuccessfully arrest viral replication by interacting with 3CLpro protein, that is mandatory for viral replication.
- Curcumin (from Haldi) blocks PLpro and 3CLpro proteins, thus capable of restricting the viral efficacy against host immunity and multiplication inside the host cell.

The *in-silico* study outcomes can be taken further for *in vivo* study and clinical trials for dose determination, immunomodulation efficacy and many more prior to recommendation for SARS-CoV 2 treatment by the scientific community. The results show enormous scope and promise as effective medication for SARS-CoV2 infection. Further, we suggest, along with independent application of these active molecules, their synergistic

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application is also recommended in *invivo* study and clinical trials, which may show greater efficacy in controlling the viral infection.

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