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GRADUATE RESEARCH ARTICLE

Evaluation of Fungal Activity Through *In Silico* Analysis of Medicinal Plants Against *Exophiala Jeanselmei*

V. Sankara Vel and A. Arunprasath*

Department of Botany, PSG College of Arts & Science, Coimbatore, Tamil Nadu, India

* Corresponding Author email:

arunprasath@psgcas.ac.in

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Student(s)

- V. Sankara Vel

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Mentor(s)

- Dr. A. Arunprasath

ABSTRACT

Phaeohyphomycosis is a fungal infectious disease commonly called as dermal problem which is caused by dematiaceous fungi, *Exophiala jeanselmei*. Chitin was the main component of fungal cell and no effective inhibitor was identified still in chitin synthase I. The protein chitin synthase I play a major role in drug metabolism as well as signal processing molecule and therefore have been targeted in the present study. The medicinal plants being a solution for several human ailments, also act as a reservoir for secondary metabolites, has taken its credit as a cure from our ancient times. The biological activity of the Myricetin was analysed using the pass online tool. The value of Probability to be active (Pa) = 0.241 Probability to be inactive (Pi) = 0.021. The several compounds retrieved from the plants *Acalypha indica, Achyranthus aspera, Brassica niger, Cassia auriculata, Cleome gynandra, Clitoria ternatea, Ipomoea hederaceae, Leucas aspera, Mimosa pudica, Phyllanthus niruri, Ocimum basilicum, Ocimum sanctum, Tridax procumbens, Vitex negundo and Waltheria indica* were analyzed for its possible significant interaction with the target protein using molecular docking studies. The compound Myricetin had Binding energy of -7.32 Kcal/mol and formed hydrogen bonds with the residue HIS 29 showing the bond length of 1.8 Å and residue THR 3 showing the bond length of 1.9 Å. The future perspective of the study is to determine the stability of the protein-compound interaction through docking studies.

Keywords: Phaeohyphomycosis, Medicinal plants and Molecular docking.

1 Introduction

Bioinformatics is computational biology in terms of molecules and applying informatics techniques from various disciplines to understand and organize the information associated with these molecules, on a large scale [1]. Modern bioinformatics research does not necessarily require more resources than any other field of Computer Science; almost all processes can be efficiently designed and modeled on a personal computer or workstation [2]. For more than a century, vast progress has been made in hereditary qualities and molecular biology. New high-throughput exploratory methods continued to develop rapidly. The mechanization of DNA sequencing set up for the Human Genome Project in 1990 [3], which has prompted genomics and a scope of related disciplines, for example, transcriptomics (the investigation of the total

quality articulation state), proteomics (the investigation of the full arrangement of proteins encoded by a genome), and metabolomics (the investigation of extensive metabolite profiles), here and there every one of these areas are all things considered alluded to as genomics. Numerous institutes use PC bunches to expand handling time, increment information base stockpiling and actualize quicker information putting away and recovering techniques [4]. The significant favorable circumstances of utilizing PC bunches are clear when an association requires enormous scope processing like in bioinformatics educating and research. At the point when utilized along these lines, PC groups offer: Cost productivity: the bunch method is practical for the measure of intensity and preparing speed being delivered. At present, progressed bioinformatics is amassed in a couple of exploration bases and privately owned businesses on the world that have the ability to utilize staff with profoundly particular preparing. Notwithstanding the way that bioinformatics techniques are openly available, there is obviously a hole between the creating and the industrialized world, which must be intentionally limited.

Following the development of the first algorithms in the 1980s, molecular docking became an essential tool in drug discovery [5]. In molecular docking, in light of the protein structures, a great many potential stances of association are attempted and assessed; the posture with the least energy score is anticipated as the "best match", i.e., the coupling mode. Since Kuntz and associates spearheading work [6], critical advancement has been made in mooring exploration to improve the computational speed and precision. Among them, protein-ligand docking is an especially energetic exploration region in view of its significance to structure-based medication design [7] and will be the subject of the current survey [8].

Bioinformatics was characterized as the assortment, order, stockpiling, and investigation of biochemical and biological data utilizing through *in silico* analysis of molecular genetics and genomics. Phaeohyphomycosis is a rare mycotic infection caused by various heterogeneous groups of black colored fungi (dematiaceous) involving the skin and subcutaneous tissue. Phaeohyphomycosis is due to an irresistible pigment called melanin which is regularly known for dermal issues brought about by dematiaceous growths, *Exophiala jeanselmei*. It is a crafty microorganism skilled to most regularly display phaeomycotic cyst/subcutaneous phaeohyphomycosis. Chitin a basic segment of parasitic cell divider is one of a kind to contagious realm and interim, no practical inhibitor was so far distinguished for chitin synthase, however the melanin shade present in the cell mass of *Exophiala jeanselmei* causes the destructiveness reason for the microorganism. In later phases of this illness goes to the mind and causes the demise [9]. The most widely recognized etiological operators of subcutaneous Phaeohyphomycosis are *E. jeanselmi* followed by *E. dermatitidis* [10]. The genus *Exophiala* is generally right in the earth and may cause contaminations in both immune compromised and once in a while, in immunocompetent people. *E. jeanselmi* ordinarily causes gentle cutaneous and subcutaneous diseases which are often limited and singular (phaeohypomycotic blister) [11]. Indeed, even in seriously immune suppressed patients *Exophiala* contamination regularly will in general remain restricted [12]. Ajello recorded 71 types of dematiaceous organisms from 39 genera which have been found to cause phaeohyphomycosis in people and in lower creatures [13]. There have been two distributed reports of Phaeohyphomycosis brought about by *Exophiala jeanselmei* in a household feline [14] and in Australia Phaeohyphomycosis brought about by *Exophiala spinifera* in two felines [15]. There are various cases in the writing in which the analysis was founded exclusively on histopathology, which, albeit trademark, gives in sign with regards to the character of the organism included [16]. Phaeohyphomycosis is a less frequent, progressively disfiguring and sometimes fatal infection. Although the diseases will be quite opposite, their drug therapy has become a common feature for both infections [17]. *Exophiala jeanselmei* is clinically deflected as an uncommon operator of subcutaneous. Our results will be discussed about its extraordinary clinical introduction and etiological operator, *Exophiala jeanselmei*. The patient recouped totally after treatment with Ketoconazole [18].

Therapeutic plants were made use of customary medication rehearses since ancient occasions. Plants incorporate many compounds for size comprises guard against parasites, infections, and herbivorous warm-blooded creatures. Various photochemical with potential or set up organic action had been recognized.

Restorative plants are the "spine" of customary medication, which implies more than 3.3 billion people in the less evolved nations use therapeutic plants all the time [19]. There are about 2000 ethnic gatherings on the planet, and pretty much every gathering their own conventional clinical information and encounters [20]. Recent screenings of most of the medicinal plant extracts with antibacterial, anticandidal and antidermatophytic efficacy shown better because of those active compounds which could be isolated and has been able to identify promising compounds that might represent future solutions in critical areas of human health [21, 22]. Therapeutic plant compounds have just been utilized to effectively treat various viral illnesses. Thus, we screened a therapeutic plant information base containing 32,297 potential enemies of viral phytochemicals and chosen the main nine hits that may repress SARS-CoV-2 3CLpro action also, thus infection replication [23].

As indicated by WHO, the vast majority of the developing and developed nations accept on home grown items for its therapeutic accessibility, in light of this philosophy the accompanying medicinal plants are utilized for the treatment of Phaeohyphomycosis. The aim of this study is to cure this dermal disease by knockout the Melanin pigment which is the main virulent factor by Molecular docking studies (*Acalypha indica, Achyranthus aspera, Brassica niger, Cassia auriculata, Cleome gynandra, Clitoria ternatea, Ipomoea hederaceae, Leucas aspera, Mimosa pudica, Phyllanthus niruri, Ocimum basilicum, Ocimum sanctum, Tridax procumbens, Vitex negundo and Waltheria indica*)

2 Materials and Methods

2.1 Pdb, Pubchem & Pass Online

The 3D protein structure for Chitin syntheses (Chs) of *Exophiala jeanselmei* is recovered from the Protein Data Bank database (PDB ID: 2MPK). Dynamic web page region was anticipated utilizing LigSite online apparatus. The concoction mixes from the referenced plants are recovered from the PubChem database. The PASS ONLINE predicts 4130 types of biological activities, for which the difference between probabilities will be active (Pa) and probabilities will be inactive (Pi) was calculated. The Pa-Pi values for activities randomly selected from the total list of predicted biological activities will be used as independent regression variables are perused.

2.2 Drugability

Lipinski rule of 5 helps in distinguishing between drug like and non-drug like molecules. It predicts high probability of success or failure due to drug likeness for molecules complying with 2 or more of the following rules [22 & 24]. Molecular mass less than 500 Dalton

- High lipophilicity (expressed as LogP less than 5)
- Less than 5 hydrogen bond donors
- Less than 10 hydrogen bond acceptors
- Molar refractivity must between 40-130

2.3 Molecular Docking Study

MGL tools with AutoGrid4 and AutoDock4 [25] will be used to set up and to perform blind docking calculations between the Ligands and Protein. Crystallized 3-dimensional structure was obtained from the Protein Data Bank (PDB). Receptor (protein) and ligand (complex) files were prepared using Auto Dock Tools. The protein was enclosed in a box with grid points in x, y and z directions and a grid spacing of 0.375 Å. The center of the grid set to -6.516, 30.278 and -1.951 Å. Lamarckian genetic algorithms, as implemented in Auto Dock, were employed to perform docking calculations. All other guidelines are default settings. For every individual the docking cases, the lowest energy docked conformation, according to the Auto Dock scoring function and number hydrogen bonds was selected as the binding mode. The output from Auto Dock was rendered with PyMol [26].

2.4 PyMOL

PyMOL is one of a few open source visualization tools which are used in a structural biology. A part of the software's name refers to the fact that it extends, and is extensible by the python programming language. All the bindings are visualized by using the Structure Visualing tool Pymol viewer, the interaction between the chemical compounds and target protein.

3 Results and discussion

3.1 PDB, PUBCHEM & Pass Online

In a progression of novel InhA inhibitors was recognized through a virtual screening technique. The creators utilized a multistage approach, incorporating pharmacophore demonstrating and atomic docking [27]. Most of the plants tried are a significant wellspring of hostile to parasitic aggravates that may give sustainable wellsprings of helpful antifungal medications against dermatophytic diseases in people [28]. Plants produce a combination of restorative portions as helper metabolites, for instance, phenolic blends, principal oils, tannins, terpenes, etc that can stifle microorganism advancement and are for the most part surveyed for its sensibility and reasonableness [29] various components add to anti-toxin opposition remembering abuse and abuse of anti-microbials for people, creatures and horticulture; patient's interest for and receipt of anti-infection agents when they needn't bother with them; and inability to complete an anti-microbial solution. Accordingly, the utilization of Ayurveda drugs has expanded now days [30]. The aeronautical pieces of *C. auriculata* L. shows higher antibacterial and antifungal action against bacterial and contagious microbes, for example, *Bacillus subtilis*, *Staphylococcus aureus, Pseudomonas aeruginosa, Escherichia coli, Candida albicans and Aspergillus niger* [31].

Table 1: *Structure of Protein*

ORGANISM NAME	PROTEIN NAME & ID	STRUCTURE	RESIDUES COUNT
Exophiala jeanselmei	Chitin Synthase I & 2MPK		74

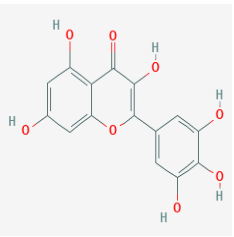
The 3D structure of a protein (Chitin synthase I) was recovered from the Protein Data Bank (PDB) and the information was mentioned (Table 1). It was visualized by utilizing the visualizing tool pymol. The three dimensional structure of the protein was distinguished utilizing Ligsite online device. The 3D structures of the phytochemical compounds of the plants chosen in the current investigation were retrieved from Pubchem Chemical database. The compounds which are segregated and revealed from earlier mentioned restorative plants were organized (Table 2) along with their molecular weight, molecular formula and pubchem ID, where pubchem is the database for getting small molecules. The biological activity of the Myricetin was broke down utilizing the pass online device which predicts the pharmacological and biochemical properties. The estimation of Probability to be dynamic (Pa) = 0.241 Probability to be idle (Pi) = 0.021. The properties anticipated for each plant compounds were recorded (Table 3).

Table 2: *List of compounds isolated from medicinal plants*

S.No	Compound Name	Pubchem ID	Molecular formula	Molecular Weight
1.	Myricetin	5281672	$C_{15}H_{10}O_8$	318.237 g/mol
2.	Quercetin	5280343	$C_{15}H_{10}O_7$	302.238 g/mol
3.	Daucosterol	5742590	$C_{35}H_{60}O_6$	576.859 g/mol
4.	Baicalein	5281605	$C_{15}H_{10}O_5$	270.24 g/mol
5.	Cosmosin	5280704	$C_{21}H_{20}O_{10}$	432.381 g/mol
6.	Kaempferol	5280863	$C_{15}H_{10}O_6$	286.239 g/mol
7.	Robinetin	5281692	$C_{15}H_{10}O_7$	302.238 g/mol
8.	Luteolin	5280445	$C_{15}H_{10}O_6$	286.239 g/mol
9.	Acacetin	5280442	$C_{16}H_{12}O_5$	284.267 g/mol
10.	Catechin	9064	$C_{15}H_{14}O_6$	290.271 g/mol
11.	Epicatechin	72276	$C_{15}H_{10}O_6$	290.271 g/mol
12.	Isovitexin	162350	$C_{21}H_{20}O_{10}$	432.381 g/mol
13.	+)- Gallacatechin	65084	$C_{15}H_{14}O_7$	306.27 g/mol
14.	3-o-Methyl-D-Glucose	8973	$C_7H_{14}O_6$	194.183 g/mol
15.	Chanoclavine	5281381	$C_{15}H_{20}N_2O$	256.349 g/mol
16.	Adenosine	60961	$C_{10}H_{13}N_5O_4$	267.245 g/mol
17.	Naringenin	932	$C_{15}H_{15}O_2$	272.256 g/mol
18.	Daidzein	5281708	$C_{15}H_{10}O_4$	254.241 g/mol
19.	Penninclavine	115247	$C_{16}H_{18}N_2O_2$	270.332 g/mol
20.	Isopenniclavine	12311156	$C_{16}H_{18}N_2O_2$	270.332 g/mol
21.	Esculetin	5281416	$C_9H_6O_4$	178.143 g/mol
22.	Ciprofloxacin	2764	$C_{17}H_{18}N_3O_3$	331.347 g/mol
23.	Lyserol	14987	$C_{16}H_{18}N_2O$	254.333 g/mol
24.	Pueranin	5281807	$C_{21}H_{20}O_9$	416.382 g/mol
25.	6-Hydroxy lavone	72279	$C_{15}H_{10}O_3$	238.242 g/mol
26.	Teucladiol	1604618	$C_{15}H_{26}O_2$	238.371 g/mol
27.	Ethyl caffetate	5317238	$C_{11}H_{12}O_6$	208.213 g/mol
28.	Buetin	5281222	$C_{15}H_{12}O_5$	272.256 g/mol
29.	20-hydroxyecdysone	5459840	$C_{22}H_{44}O_7$	480.642 g/mol
30.	Rubiadin	5124062	$C_{15}H_{10}O_6$	473.943 g/mol

31.	Mimosic acid	190359	$C_7 H_2 NO_4$	169.136 g/mol
32.	Octadecatrienoic acid	5739740	$C_{28} H_{34} O_4$	434.576 g/mol
33.	Tetracaine	5411	$C_{15} H_{24} N_2 O_2$	264.369 g/mol
34.	Chicanine	5336043	$C_{20} H_{22} O_5$	342.391 g/mol
35.	Saupirin	181128	$C_{19} H_{22} O_6$	346.379 g/mol
36.	Elymoclavine	440904	$C_{16} H_{18} N_2 O$	254.333 g/mol
37.	Tyrosine	6057	$C_9 H_{11} NO_3$	181.191 g/mol
38.	p-coumaric acid	637542	$C_9 H_8 O_3$	164.16 g/mol
39.	Nectandrin-b	156517	$C_{20} H_{24} O_5$	344.407 g/mol
40.	Caffeic acid	689043	$C_9 H_8 O_4$	180.159 g/mol
41.	Linoleic acid	5280450	$C_{18} H_{32} O_2$	280.452 g/mol
42.	Negundin A	10043572	$C_{20} H_{16} O_6$	352.342 g/mol
43.	Buchariol	101009028	$C_{15} H_{26} O_2$	238.371 g/mol
44.	Phyllnirurin	179963	$C_{20} H_{22} O_5$	342.391 g/mol
45.	Waltherine A	100978900	$C_{31} H_{42} N_4 O_4$	534.701 g/mol
46.	Steroid O sulfate	439761	$C_{18} H_{24} O_4 S$	336.446 g/mol
47.	9,12-octadecadiynoic acid	1931	$C_{18} H_{28} O_2$	276.42 g/mol
48.	Silymarin	5213	$C_{25} H_{22} O_{10}$	482.441 g/mol
49.	Oleic acid	445639	$C_{18} H_{34} O_2$	282.468 g/mol
50.	Waltherine C	100994181	$C_{30} H_{37} N_5 O_4$	531.657 g/mol
51.	Phyllanthin	358901	$C_{24} H_{34} O_8$	418.53 g/mol
52.	9-Octadecenoic acid	965	$C_{18} H_{34} O_2$	282.468 g/mol
53.	Viteagnuside A	38362716	$C_{26} H_{42} O_9$	498.613 g/mol
54.	Niranthin	13989915	$C_{24} H_{32} O_7$	432.513 g/mol
55.	Bufadienolide	46173848	$C_{24} H_{34} O_2$	354.534 g/mol
56.	Palmitic acid	985	$C_{16} H_{32} O_2$	256.43 g/mol
57.	Adouetine X	5281577	$C_{28} H_{44} N_4 O_4$	500.684 g/mol
58.	Lignans	443013	$C_{22} H_{22} O_8$	414.41 g/mol
59.	Oleanolic acid	10494	$C_{30} H_{48} O_3$	456.711 g/mol
60.	Gledigenin 1	45483610	$C_{30} H_{48} O_3$	456.711g/mol

Table 3: *Prediction of pharmacological activity for plant compounds*

Compound Name & Id	Compound structure	Compound Activity
Myricetin 5281672		0,269 0,043 Chemopreventive 0,242 0,018 Protein kinase stimulant 0,282 0,059 CYP2E1 substrate 0,280 0,060 CYP2E substrate 0,241 0,021 Melanin inhibitor★ 0,311 0,097 CYP2E1 inducer 0,244 0,032 UGT1A5 substrate

★ The Symbol indicates the main activity of the compound for the disease.

3.2 Drugability

The compounds were first oppressed for dissecting Absorption, Distribution, Metabolism and Excretion properties. Earlier ADME profiling of little atoms are noteworthy committed to the field of medication revelation by having sway on cost, work request and length [32]. Computational estimation of the docked phytochemical's medication likeliness was found based on limits set by "Lipinski's Rule of Five" through Drug examine apparatus at Molinspiration server. The subjective appraisals of ingestion, statement, digestion, discharge and poisonousness profile of these hits were anticipated basically by utilizing ADMET sar worker [33].

In the current investigation, Lipinski's standard of five in any case called Pfizer's standard of five or general guideline to assess tranquilize similarity shows the accompanying properties like atomic weight, octanol/water parcel coefficient, hydrogen bond giver and acceptor. After the filtration involving through Lipinski rule totally 39 out of 60 bioactive compounds from medicinal plants. Since the standard has a cutoff point in products of five, the name has been given as rule of five. Aside from the above properties, extra boundaries, such as, surface territory in square Armstrong (polar surface region, PSA); cerebrum/blood hindrance and level of human oral assimilation were additionally anticipated (Table 4).

Table 4: *ADME toxicity for plant molecules*

Molecular ID	Molecular weight	Donor Hydrogen Bonds	Acceptor Hydrogen Bonds	High lipophilicity (Log P)	Molar refractivity
Normal range	**500**	**5**	**10**	**<5**	**40-130**
8973	194	4	6	-2.72	41.96
5411	264	1	2	2.89	80.43
5280704	432	5	10	-0.10	103.54
5280863	286	4	6	0.64	62.82
5281672	318	5	8	1.71	75.715
5280343	302	5	7	0.52	64.36
637542	164	2	3	0.15	40.19
124062	254	2	4	1.66	61.13
181128	346	2	6	2.65	87.76

6057	181	3	3	0.56	44.23
932	272	3	5	1.17	64.16
2764	331	2	3	1.49	81.89
9064	290	5	6	1.09	68.13
14987	254	2	1	2.35	74.53
60961	267	5	5	-2.45	55.22
65084	306	6	7	0.79	69.01
72276	290	5	6	1.09	68.34
72279	238	1	3	1.8	58.81
94477	154	3	2	0.55	40.135
115247	270	3	2	2.06	75.35
190359	169	2	4	-0.9	44.862
440904	254	2	1	2.35	74.53
162350	432	6	10	1.63	97.03
5280442	284	2	5	1.65	67.17
5280445	286	4	6	0.83	63.34
5281222	272	4	5	1.19	64.86
5281381	256	3	1	2.67	76.63
5281416	178	2	4	0.45	46.6
5281605	270	3	5	1.42	61.24
5281692	302	5	7	0.52	64.36
5281708	254	2	4	1.24	61.06
5281807	416	6	9	1.74	96.34
5317238	208	2	4	1.31	51.03
5459840	480	4	7	5.6	141.7
5742590	312	5	6	-0.05	77.62
57397401	434	0	4	5.77	130.09
16046185	238	1	2	3.778	78.84
12311156	270	3	2	2.06	75.6
53360432	342	1	5	3.468	91.73

3.3 Molecular Docking Study

Molecular docking and pharmacology studies are beneficially involved to screen the anti-inflammatory constituents of *Cinnamomum cassia* twigs, with a total of 69 bioactive compounds found to have potential drug-like properties. These findings will facilitate the development of bioactive compounds from *C. cassia* twigs for the treatment of inflammatory disorders [34]. *Senna alata* leaves are generally antifungal specialists they were exposed to *in silico* Molecular docking studies to locate their antifungal activities. As per Glide docking score selective compounds were exposed for drug-likeliness (ADME/T) investigation to foresee their conceivable potential to be used as a normally determined antifungal agent. As finalizing the results, the anthraquinones are promising applicants as an antifungal agent [35]. The results of docking studies 29 compounds were recorded (Table 5). The compound Myricetin had Binding energy of -7.32 Kcal/mol and formed hydrogen bonds with the residue HIS 29 showing the bond length of 1.8 Å and residue THR 3 showing the bond length of 1.9 Å. The compound Quercetin had Binding energy of -6.82 Kcal/mol and formed hydrogen bonds with the residue ALA 26 (H-O), ASP 6 (H-O), HIS 29 (O-H) showing the bond length of 2.2, 1.7, 1.8 Å. The compound Daucosterol had Binding energy of -6.64 Kcal/mol and formed hydrogen bonds with the residue HIS-66 showing the bond length of 1.6 Å. The compound Baicalein had Binding energy of -6.62 Kcal/mol and formed hydrogen bonds with the residue HIS 29 and THR 3 showing the bond length of 2.2 and 2.5 Å. The compound Cosmosin with binding energy of -6.58 Kcal/mol and formed hydrogen bonds with the residue ASP 32 and ASP 6 showing the bond length of 1.9 and 1.7Å. Further, the interactions of plant compounds with the target would compare to the presently available drug molecule, to study its potency. As well as the simulation studies would provide an insight about the stability of protein-compound complex. The plant compounds indicating collaboration with the protein are arranged with the Binding energy. The plant compounds and the information of their hydrogen bond, collaborating deposits and individual bond lengths were organized independently (Table 6). Utilizing Pymol tool, the cooperation between the synthetic mixes and target protein are visualized and the communication of the Compound Myricetin was appeared in the figure 1.

Table 5: *Docking result for plant molecules*

S.No	Plant name	Compounds	Binding energy
1.	*Achyranthus aspera*	20-hydroxyecdysone (5459840)	-4.74
2.	*Brassica niger*	Tetracaine (5411)	-4.25
3.	*Cassia auriculata*	Myricetin (5281672) Naringenin (932) Quercetin (5280343) Rubiadin (124062)	-7.32 -5.17 -6.82 -4.67
4.	*Cleome gynandra*	Daucosterol(5742590) Teucladiol(16046185)	-6.64 -4.81
5.	*Clitoria ternatea*	Adenosine (60961) p-coumaric acid (637542)	-5.53 -4.13
6.	*Ipomoea hederaceae*	Chanoclavine (5281381) Penniclavine (115247) Isopenniclavine (12311156) Lysergol (14987) Ethyl Caffeate (5317238) Elymoclavine (440904)	-5.65 -4.93 -4.93 -4.87 -4.78 -4.18
7.	*Leucas aspera*	Catechin (9064) Acacetin (5280442) Chicanine (53360432)	-5.76 -5.91 -4.22
8.	*Mimosa pudica*	6-hydroxy flavones (72279)	-4.86

		Isovitexin (162350) Mimosinamine (94477) Mimosinic acid (190359) Tyrosine (6057)	-5.73 -5.00 -4.66 -4.18
9.	*Ocimum basilicum*	3-o—methyl-d-glucose (8973) Cosmosin (5280704) Kaempferol (5280863)	-5.67 -6.58 -6.43
10.	*Tridax procumbens*	(+)- Gallacatechin (65084) Daidzein (5281708) Butein (5281222) Robinetin (5281692) Luteolin (5280445) Baicalein (5281605) Ciprofloxacin (2764) Esculetin (5281416) Puerarin (5281807)	-5.67 -5.1 -4.74 -6.4 -6.29 -6.62 -4.89 -4.93 -4.86
11.	*Vitex negundo*	Octadecatrienoic acid (57397401) Saupirin (181128)	-4.46 -4.21
12.	*Waltheria indica*	Epicatechin (72276)	-5.76

Table 6: *Interaction of plant compounds with 2MPK*

S.No	Name of the ligand / PubChem ID	Residues Interaction	Bond length	No of Bonds	Binding energy
1.	Myricetin/5281672	HIS - 29 (H-O)	1.7	2	-7.32
		THR - 3 (H-O)	2.1		
2.	Quercetin/5280343	ALA - 26 (H-O)	2.2	3	-6.82
		HIS - 29 (O-H)	1.8		
		ASP - 6 (H-O)	1.7		
3.	Daucosterol/5742590	HIS - 66 (H-O)	1.6	1	-6.64
4.	Baicalein/5281605	THR - 3 (O-H)	2.5	2	-6.62
		HIS - 29 (O-H)	2.2		
5.	Cosmosin/5280704	ASP – 32 (H-O)	1.9	2	-6.58
		ASP - 6 (H-O)	1.7		
6.	Kaempferol/5280863	HIS - 29 (O-H)	1.8	3	-6.43
		ALA - 26 (H-O)	2.1		
		ASP - 6 (H-O)	1.7		
7.	Robinetin/5281692	HIS - 29 (H-O)	1.7	3	-6.4
		HIS - 29 (O-H)	2.6		
		ASP - 6 (O-H)	2.1		
8.	Luteolin/5280445	HIS - 29 (H-O)	2.2	3	-6.29

		ALA - 26 (H-O)	1.9		
		THR - 3 (O-H)	2.4		
9.	Acacetin/5280442	HIS – 29 (O-H)	2.2	2	-5.91
		GLY - 2 (O-H)	2.6		
10.	Catechin/9064	THR - 3 (H-O)	1.8	2	-5.76
		ASP - (H-O)	1.7		
11.	Epicatechin/72276	ASP - 6 (H-O)	1.7	2	-5.76
		THR - 3 (H-O)	1.8		
12.	Isovitexin/162350	ASP - 6 (H-O)	2.1	4	-5.73
		ASP - 6 (H-O)	2.3		
		ASP - 6 (H-O)	1.6		
		MET - 1 (O-H)	2.2		
13.	(+)- Gallacatechin/65084	ASP - 6 (H-O)	2.1	2	-5.67
		THR - 3 (H-O)	1.9		
14.	3-o-Methyl-D-glucose/8973	ALA - 7 (H-O)	2.0	2	-5.67
		ALA - 26 (H-O)	1.8		
15.	Chanoclavine/5281381	ASP - 6 (H-O)	1.7	2	-5..65
		ASP - 6 (H-O)	1.3		
16.	Adenosine/60961	THR - 3 (H-O)	2.0	3	-5.53
		ASP - 6 (H-O)	1.7		
		ASP - 6 (H-O)	2.1		
17.	Naringenin/932	HIS - 29 (O-H)	2.3	4	-5.17
18.	Daidzein/5281708	HIS - 29 (O-H)	2.0	1	-5.1
19.	Penninclavine/115247	ASP - 6 (H-O)	1.6	2	-4.93
		HIS - 29 (H-N)	1.9		
20.	Isopenniclavine/12311156	ASP - 6 (H-O)	1.6	2	-4.93
		HIS – 29 (H-N)	1.9		
21.	Esculetin/5281416	HIS - 29 (O-H)	2.2	1	-4.93
22.	Ciprofloxacin/2764	GLU - 59 (H-O)	1.9	1	-4.89
23.	Lysergol/14987	ASP - 6 (H-O)	1.7	2	-4.87
		THR - 3 (H-O)	1.9		
24.	Pueranin/5281807	ASP - 6 (H-O) ASP - 6 (H-O)	2.3 1.8	2	-4.86

25.	6-Hydroxy flavone/ 72279	HIS - 29(O-H)	2.1	2	-4.81
		THR - 3 (O-H)	2.5		
26.	Teucladiol/16046185	ALA - 26 (H-O)	2.0	1	-4.8
27.	Ethyl caffetate/ 5317238	HIS - 29 (O-H)	2.4	2	-4.78
		ASP - 6 (H-O)	1.8		
28.	Buetin/5281222	ASP - 5 (H-O)	2.0	3	-4.74
		ASP - 5 (H-O)	1.9		
		ARG - 9 (O-H)	2.1		
29.	20-hydroxyecdysone/5459840	PHE - 8 (H-O)	2.0	2	-4.74
		PHE - 8 (H-O)	2.3		
30.	Rubiadin/ 5124062	ASP - 6 (H-O)	1.8	1	-4.67
31.	Mimosic acid/190359	THR – 3 (H-O)	1.9	3	-4.66
		THR – 3 (O-H)	1.6		
		GLY – 2 (O-H)	2.3		
32.	Octadecatrienoic acid/57397401	LYS – 56 (O-H)	2.4	1	-4.46
33.	Tetracaine/5411	ALA – 26 (H-O)	2.0	1	-4.25
34.	Chicanine/53360432	ARG – 9 (O-H)	2.1	2	-4.22
		ASP – 5 (O-H)	1.8		
35.	Saupirin/181128	ASP – 6 (H-O)	1.7	2	-4.21
		ALA – 26 (H-O)	1.8		
36.	Elymoclavine/440904	ASP – 6 (H-O)	1.6	1	-4.18
37.	Tyrosine/6057	THR – 3 (O-H)	2.3	3	-4.18
		ASP – 6 (H-O)	1.8		
		ALA – 26 (H-O)	1.9		
38.	p-coumaric acid/637542	ALA – 26 (H-O)	2.1	3	-4.13
		THR – 3 (O-H)	2.2		
		GLY – 2 (O-H)	2.3		

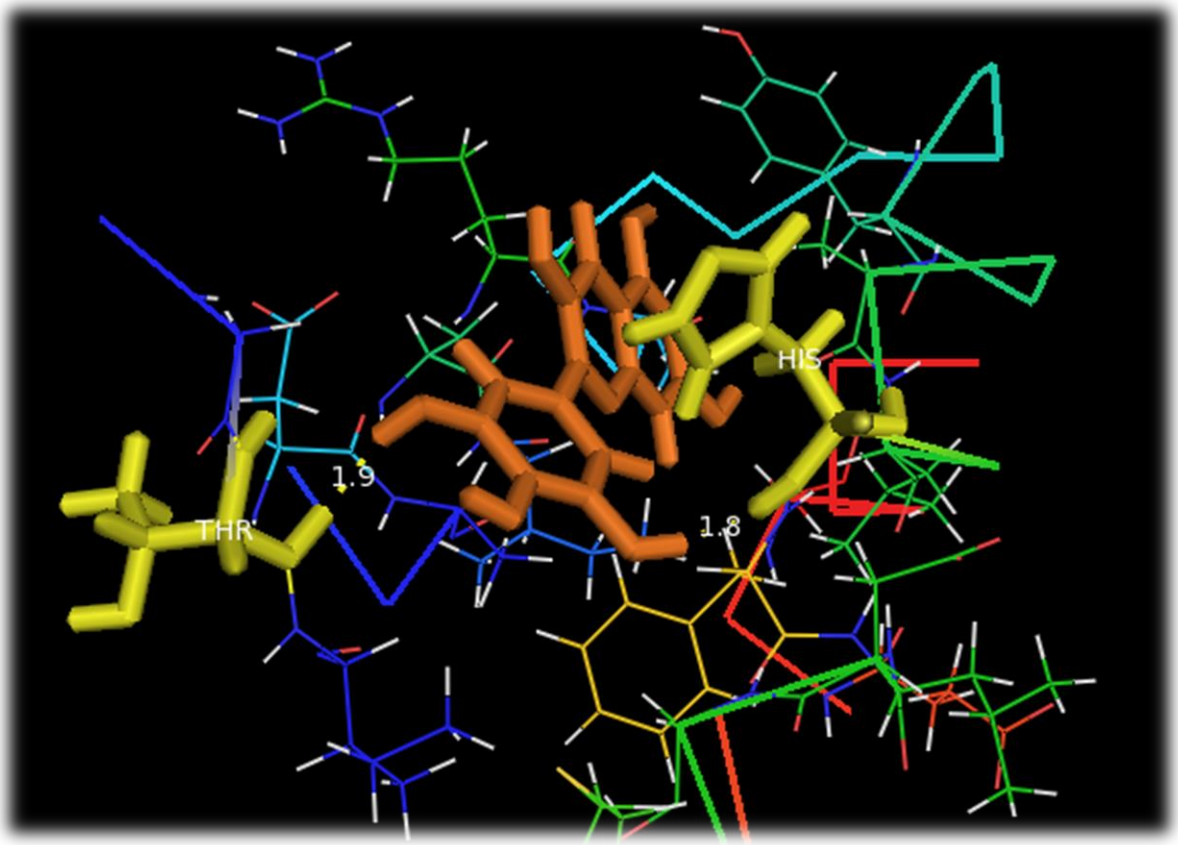


Figure 1: *Interaction between 2mpk and Myricetin*

The ligand was exposed in TV orange color and interacting residues in yellow color. The dotted lines indicating the hydrogen bond formation. The compound Myricetin had Binding energy of -7.32 Kcal/mol and formed hydrogen bonds with the residue HIS 29 showing the bond length of 1.9 Å.

4 Conclusions

The development of computational methods for protein flexibility is still in its infancy and thereby remains one of the major future directions in protein ligand docking. Rising new contagious species and the occurrence of raised medication obstruction for fungal infections keeps on rising and the height of contagious contaminations is disturbing. Medicinal plants are an important part of our natural health. They serve as important therapeutic agents as well as valuable raw materials for manufacturing numerous traditional and modern medicines. *Cassia auriculata* leaves have been traditionally used worldwide for its versatile therapeutic properties. A study of molecular docking stimulation undertaken to identify and accesses the binding capacity of ligands. The chemical compounds are used to cure disease and those compounds are found in aerial parts of the plant. The purpose of this study is to analyze the inhibitory potential Chitin synthase I through *in silico* molecular docking studies on active compounds of plant extract. The protein and ligand docking studies are done by using 3D structure of protein. Most of the molecular docking studies successfully predict the binding modes of small-molecule ligands within receptor binding sites. The phytochemical compounds of Myricetin were isolated from *C. auriculata* exhibit a good binding efficiency with the target showing high binding energy of -7.32 Kcal/mol is used to cure the Phaeohyphomycosis. The biological activity of plant compounds is predicted using pass prediction and the results are proved the chemical compounds have a dermatological property. This indicates that the Myricetin compound has the highest Melanin (main virulent factor) inhibiting activity and also other plant compounds. Those bioactive compounds should be explored more in order to identify an efficient and

potential drug molecule. As shown in the highlighted case studies, molecular docking has been able to identify promising compounds that might represent future solutions in critical areas of human health.

5 Declarations

5.1 Acknowledgements

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5.2 Competing Interests

The authors declared that they do not have any conflict of interest.

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