PHYTOCHEMICALS FROM *MUCUNA PRURIENS* AS POTENTIAL INHIBITORS OFALPHA-SYNUCLEINTO COMBAT PARKINSON'S DISEASE: A COMPUTATIONAL STUDY

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ABSTRACT

Objectives: Parkinson's disease is a progressively debilitating condition, and its prevalence is increasing globally due to aging populations. Alpha-synuclein can be studied as a potential therapeutic target as it plays a role in the progression of the condition. This study investigates the efficacy of phytochemicals of *Mucuna pruriens*in inhibiting alpha-synuclein protein.

Methods: In the current study, the inhibitory properties of thirty-one phyto-compounds of M. pruriens were examined against the target protein, alpha-synuclein. The pharmacological and physiological analysis of the ligands along with the Lipinski filter criteria, were performed using Swiss ADME. The virtual screening tool PyRx and Biovia Discovery tool were used to perform molecular docking and observe the protein-ligand interaction.

Results: Luteolin was found to be the most effective blocker for alpha-synucle in with the binding affinity of –9, using molecular docking analysis. So, this molecule can be a good fit for developing medications that aid in the prevention of Parkinson's disease.

Conclusion: Luteolin was predicted to be the potential treatment for Parkinson's disease. This study can be used as a foundation for further experimental validation and potential drug development.

Keywords: Parkinson's disease; *Mucuna pruriens;* Alpha-synuclein; Swiss ADME; PyRx; Luteolin; Molecular docking.

ABBREVATIONS

amino acid	aa
alpha-synuclein	α-syn
Absorption, Distribution, Metabolism, Elimination	ADME
Dassault Systems	DS
Hydrogen Bond	H-Bond
Gastro-Intestinal	GI
Indian Medicinal Plants, Phytochemistry and Therapeutics	IMPPAT
Molecular Weight	MW
Parkinson's Disease	PD
Topological Polar Surface Area	TPSA

INTRODUCTION

Millions of people worldwide suffer with Parkinson's disease (PD). It is a crippling neurological condition marked by gradual movement dysfunction, cognitive decline, and emotional difficulties[1].Among the most common signs of Parkinson's disease are bradykinesia, postural instability or facial dyskinesia, rigidity, tremor and muscle stiffness. Other than these, non-motor problems include sleep difficulties, mood swings, dementia, depression, and cognitive impairment. Because there are two types of neurodegenerative disorders acute and chronic the central nervous system can be protected against neuronal harm by neuroprotection. In people 80 years of age and older, Parkinson's disease is present at a prevalence rate of 0.5-0.1% [20].

The biological hallmark of PD is the misfolding and aggregation of alpha-synuclein (α-syn) protein, a presynaptic neuronal protein typically implicated in neurotransmitter release and synaptic plasticity. The aggregation of α-syn leads to the formation of insoluble fibrils, which accumulate in Lewy bodies and neuritis, causing neurodegeneration and neuronal death [13, 18].

The α-syn protein is a natively unfolded structure that can adopt various conformations. Its misfolding and

aggregation are thought to be triggered by genetic mutations, environmental toxins, or aging-related factors, leading to a toxic gain-of-function [7].The α-syn (presynaptic neuronal protein) is associated with PD, both neuropathologically and genetically. It belongs to the family of proteins called synuclein, which also comprises β- and γ-synuclein. The NAC region is what structurally differentiates α-syn from the other components. All three of the family's members are primarily neuronal proteins that preferentially localize to presynaptic terminals in a physiological context [32].

The α-syn may be involved in the pathogenesis of Parkinson's disease (PD) in a number of ways, but it is widely acknowledged that its toxic protofibrils in aberrant soluble oligomeric conformations are what disrupt cellular homeostasis and ultimately lead to neuronal death by impacting a range of intracellular targets, including synaptic function. Moreover, the discharge of α-syn could potentially cause adverse reactions in adjacent cells, such as initiating aggregation, which would hasten the disease's progression [32]. Many current therapy approaches concentrate on managing symptoms, and α-syn aggregation-targeting disease-modifying therapies are desperately needed[15].

Researchers have encountered many difficulties in their quest for a potential therapy for PD. The current therapeutics applied for this disorder has only helped individuals with symptoms; in addition, it may have serious adverse effectslater in their life. Ayurveda offers a minimally invasive, efficient, and alternative method of treating this illness [23].

*Mucuna pruriens*belongs to the family Leguminosaeand is also known as velvet bean or cowhage [30].It is an annual twining herb that grows over India's plains in bushes and hedges near moist areas, ravines, and scrub jungles. It is grown for young leaves that are used as fodder and for its vegetable pods[2].*M. pruriens* is used as a traditional medicine in Ayurveda and Unani to treat PD, infertility, snake bites, arthritis, sexual dysfunction and treat various ailments, including fever, rheumatism, and skin conditions[3].

The phytochemicals of *M. pruriens*have been implicated in various biological activities. There is L-DOPA (levodopa), a precursor to neurotransmitters like dopamine, norepinephrine and epinephrine, alkaloids, glycosides and phenolic compounds.It has been discovered that eating its seeds can have antidepressant

effects in patients with depressive neurosis, and powdered seed formulations have demonstrated potential in the management and treatment of Parkinson's disease[30].The generalized therapeutic activities of *M. pruriens*areanabolic, analgesic, anti, anti-inflammatory, anti-spasmodic, anti-venom, aphrodisiac, cholesterol lowering, anti-oxidant, neuroprotective, immune modulator, anti-diabetic, anti-bacterial, anti-parasitic, cough suppressant, blood purifier, anti-neoplastic and hypotensive[20, 30].

This study aims to explore the potential of phytochemicals from *M. pruriens* as inhibitors of α-syn aggregation, a key event in PD pathogenesis. Using computational molecular docking, thirty-one phytochemicals of *M. pruriens* were screened to identify the promising candidates that may prevent or reduce α-syn aggregation. This research provides a foundation for further experimental validation and potential drug development, offering a novel approach to PD therapy.

MATERIALS & METHODS:

Target Retrieval

The most suitable α-synprotein structure was downloaded from RCSB Protein Data Bank (https://www.rcsb.org/) in protein data bank (PDB)format. Prior to docking, proteins are purified since heteroatoms and water molecules might affect docking scores. Additionally, the prebound ligands are also removed from the crystal structures so as to accelerate the binding with the targeted ligands. Extra chains were removed from the protein structures, leaving only chain A for examination. The conformer model was present at some of the aa in the protein which showed error at the time of molecular docking. This was removed by selecting each aa in the protein structure. The Dassault Systems BIOVIA Discovery Studio was used to perform the protein purification.

Phytocompound Retrieval

The phytocompounds present in the*M. pruriens* were obtained from the IMPPAT database (https://cb.imsc.res.in/imppat/). All of the compounds were chosen, and their canonical SMILES and three-dimensional (3D) models were obtained in standard data format using PubChem (https://pubchem.ncbi.nlm.nih.gov/).

Target Validation

The secondary structure of the protein α-syn was analyzed using PDB sum database (http://www.ebi.ac.uk/pdbsum/). The Ramachandran plot of α-syn was obtained using PROCHECK. A Ramachandran plot analysis of the protein structure provide

valuable insights into its stereo-chemical quality and overall structure.

ADME Analysis

The ADME characteristics of a chemical are the main predictors of whether it is an appropriate choice for medicinal development. The physicochemical properties of a compound include lipophilicity, molecular weight, and topological polar surface area (TPSA). These qualities were investigated using Swiss ADME (http://www.swissadme.ch/). This webserver was also used to analyze the Lipinski rule of 5.

Molecular Docking

The prepared protein and the plant's phytocompounds were loaded into PyRx. The protein was auto docked to make it as a macromolecule. Theenergy of ligands was minimized and were converted from Sdf format topdbqt format using the OPENBABEL Grid dimensions of centerX=-9.8970, center Y=5.5904, and center Z=-12.8077 were chosen for the active site. The ligands were docked against 3Q27 using the PyRx web server. The most effective compounds were chosen for further research based on theirbinding affinity with the target protein and were saved in pdb format. Using DS BIOVIA Discovery Studio, theinteraction of the ligand with the highest binding score and the proteinwas observed and the 2D and 3D models were produced.

RESULT

Target Retrieval

The crystal structure of α-syn protein with PDB ID 3Q27 was successfully downloaded from the RCSB PDB as shown in figure 1(a). The resolution of the protein downloaded is 1.30 Å and the method of retrieval of the protein is X-ray diffraction. The crystal structure of protein was then purified using BIOVIA as shown in the figure 1(b). The process of purification involved the elimination of water molecules and ligand groups. The purpose of doing this is to accelerate the computing process because these molecules are not critical to the ongoing research.

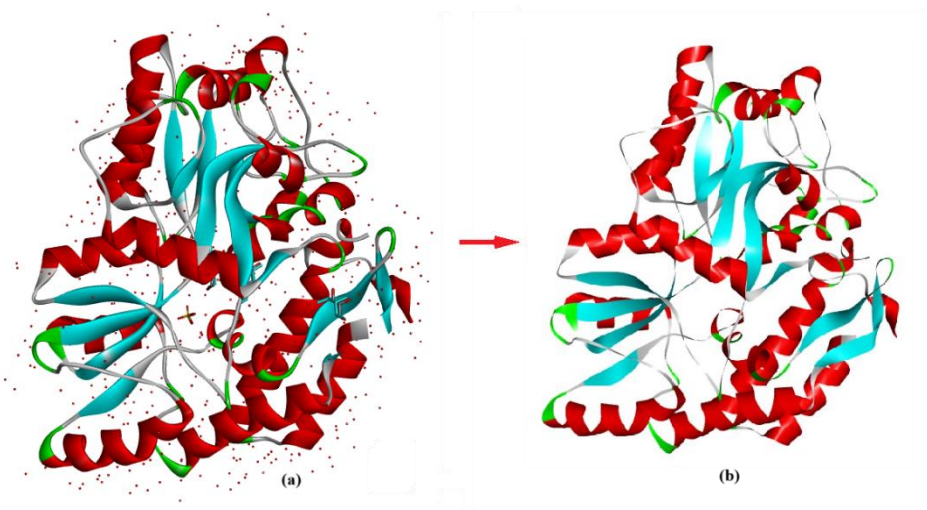

Figure 1: 3D models of α-syn obtained using BIOVIA. (a) 3D structure of 3Q27 and (b) 3D structure of purified 3Q27

Phytocompound Retrieval

There is total 31 phytocompounds present in the leaves, roots, stem, fruit and seed of *M. pruriens*, as given in the IMPPAT database. The names are as follows: bufotenine, N, N-dimethyl-5-methoxytryptamine, choline, serotonin, dimethyltryptamine, 9-pyrido [3,4-] indole, levodopa, dopamine, alpha-amyrenyl, acetate, acacetin, luteolin, 6-methoxyharman, oleic acid, ursolic acid, betulinic acid, beta-sitosterol, stigmasterol, myristic acid, tryptamine, coumarin, stearic acid, nicotine, palmitic acid, arachidic acid, vernolic acid, gallic acid, sterol, glutathione, linoleic acid, genistein, ascorbic acid. The structural details of all the phytocompounds were recorded with their respective PubChem CID as shown in table 1.

Table 1: Structural details of the Phytocompounds (Source: IMPPAT database)

S.No.	Phytocompounds	PubChem CID	Formula	Plant Part
1	Bufotenine	10257	C12H16N2O	Fruit, Leaf, Stem, Root, Seed
2	N, N-Dimethyl-5-methoxytryptamine	1832	C13H18N2O	Fruit, Leaf, Stem, Root, Seed
3	Choline	305	C5H14NO+	Fruit, Leaf, Stem, Root, Seed

4	Serotonin	5202	C10H12N2O	Fruit, Seed
5	Dimethyltryptamine	6089	C12H16N2	Fruit, Leaf, Stem, Root, Seed
6	9H-Pyrido[3,4B] indole	64961	C11H8N2	Fruit, Leaf, Stem, Root, Seed
7	Levodopa	6047	C9H11NO4	Fruit, Seed
8	Dopamine	681	C8H11NO2	Leaf
9	alpha-Amyrenyl acetate	92842	C32H52O2	Root
10	Acacetin	5280442	C16H12O5	Root
11	Luteolin	5280445	C15H10O6	Root
12	6-Methoxyharman	5376026	C13H12N2O	Leaf, Stem
13	Oleic Acid	445639	C18H34O2	Seed
14	Ursolic Acid	64945	C30H48O3	Root
15	Betulinic Acid	64971	C30H48O3	Root
16	Beta-Sitosterol	222284	C29H50O	Root, Seed
17	Stigmasterol	5280794	C29H48O	Root
18	Myristic Acid	11005	C14H28O2	Seed
19	Tryptamine	1150	C10H12N2	Seed
20	Coumarin	323	C9H6O2	Seed
21	Stearic Acid	5281	C18H36O2	Seed
22	Nicotine	89594	C10H14N2	Seed
23	Palmitic Acid	985	C16H32O2	Seed
24	Arachidic Acid	10467	C20H40O2	Seed
25	Vernolic acid	6449780	C18H32O3	Seed
26	Gallic Acid	370	C7H6O5	Seed
27	Sterol	1107	C17H28O	Seed
28	Glutathione	124886	C10H17N3O6S	Seed

29	Linoleic Acid	5280450	C18H32O2	Seed
30	Genistein	5280961	C15H10O5	-
31	Ascorbic Acid	54670067	C6H8O6	-

Target Validation

The secondary structure of 3Q27 consists of 4 sheets, 1 beta alpha beta unit, 2 beta hairpins, 1 psi loop, 3 beta bulges, 15 strands, 21 helices, 16 helix-helix interacts, 26 beta turns and 2 gamma turns as shown in Figure 2.The Ramachandran plot shows a good distribution of residues in the allowed regions, indicating a well-structured protein as shown in Figure 3.314 aa residues or 94.3% fall within the most favored regions (A, B, and L), indicating a good stereochemical quality.19 residues or 5.7% are in the additionally allowed regions (a, b, l and p), which is acceptable. No residues arein the 'Generously allowed regions'and 'Disallowed regions', indicating absence of outliers. Out of the 390 residues, 333 are non-glycine and non-proline residues, 32 are glycine residues, 21 are proline residues, and 4 is an end residue.

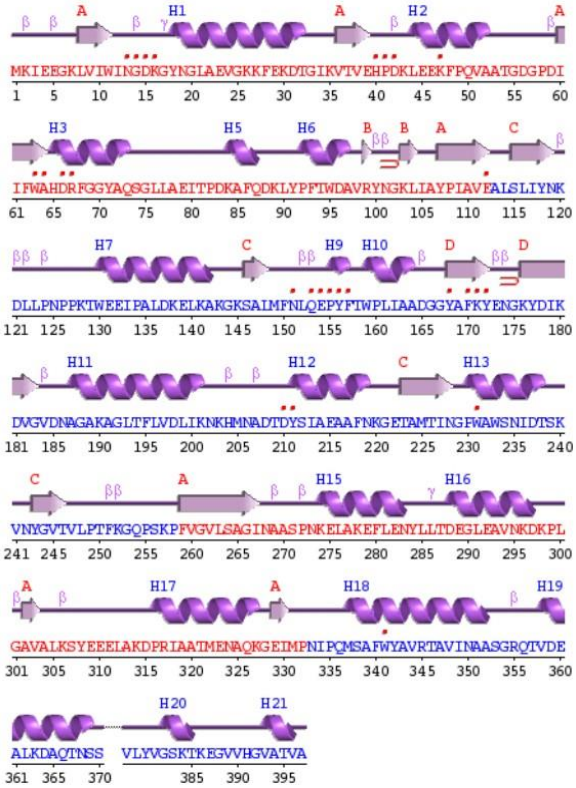

Figure 2: Secondary structure of α-syn protein

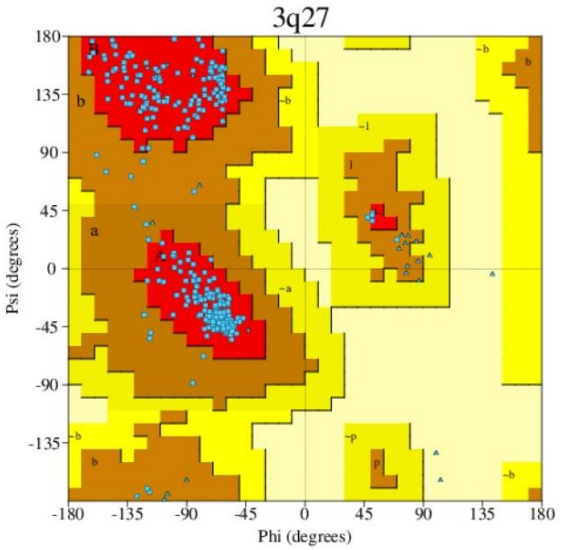

Figure 3: Ramachandran plot of α-syn protein

ADME Analysis

For a compound to be employed in drug products, the prediction of physicochemical and pharmacological properties, and Lipinski filter is crucial. Therefore, the phytocompounds retrieved from *M. pruriens*were subjected to ADME analysis. The amount of gastrointestinal (GI) adsorption should be substantial to maximize the drug's efficacy. The TPSA value less than 140 are usually believed to be good at permeating cell membranes and has good oral bioavailability. In addition, the material must be easily soluble. The ADME analysis of all the ligands are listed in Table 2. The Lipinski rule has five parameters(MWT ≤ 500, log P ≤ 5, H-bond donor's ≤ 5, and H-bond acceptors ≤ 10) [25] and a compound is chosen with zero violation. Table 3 clearly shows the compounds which are passing the Lipinski rules with zero violation. As per the results, it is evident that the top eighteen ligands fulfill the Lipinski rule without any violations and high GI absorption. The name of the selected phytocompounds which are passing the criteria are: Bufotenine, N, N-Dimethyl-5-methoxytryptamine, Serotonin, Dimethyltryptamine, 9H-Pyrido[3,4-B] indole, 6-Methoxyharman, Myristic Acid, Tryptamine, Coumarin, Nicotine, Vernolic acid, Levodopa, Dopamine, Acacetin, Luteolin, Gallic Acid, Genistein and Ascorbic Acid.

Table 2: ADME data of Phytocompounds (Source: SwissADME)

S. No.	Phytocompounds	BBB penetration	GI absorption	Silicos-IT LogSw (Solubility)	Pgp substrate	TPSA
1	Bufotenine	No	High	-0.08(Soluble)	39.26	197.62
2	N, N-Dimethyl-5-methoxytryptamine	No	High	-3.82(Moderately soluble)	28.26	111.13
3	Choline	No	Low	1.49 (Soluble)	20.23	107.22

4	Serotonin	No	High	-0.72 (Soluble)	62.04	103.78
5	Dimethyltryptamine	No	High	-0.04(Moderately soluble)	19.03	97.99
6	9H-Pyrido[3,4B] indole	No	High	-4.4 (Moderately soluble)	28.68	90.9
7	Levodopa	No	High	-5.1 (Soluble)	103.78	79.9
8	Dopamine	No	High	-1.68 (Soluble)	66.48	66.48
9	alpha-Amyrenyl acetate	Yes	Low	-3.16 (Poorly soluble)	26.3	62.04
10	Acacetin	No	High	-5.67 (Moderately soluble)	79.9	57.53
11	Luteolin	No	High	-5.7 (Soluble)	111.13	57.53
12	6-Methoxyharman	Yes	High	-4.41 (Moderately soluble)	37.91	49.83
13	Oleic Acid	Yes	High	-3.72 (Moderately soluble)	37.3	41.81
14	Ursolic Acid	Yes	Low	-3.63 (Moderately soluble)	57.53	39.26
15	Betulinic Acid	Yes	Low	-5.11 (Moderately soluble)	57.53	37.91
16	Beta-Sitosterol	No	Low	-5.39 (Poorly soluble)	20.23	37.3
17	Stigmasterol	Yes	Low	-4.51 (Moderately soluble)	20.23	37.3
18	Myristic Acid	No	High	-6.11 (Moderately soluble)	37.3	37.3
19	Tryptamine	Yes	High	-5.31 (Soluble)	41.81	37.3
20	Coumarin	No	High	-6.91 (Soluble)	30.21	37.3
21	Stearic Acid	Yes	High	-4.67 (Poorly soluble)	37.3	37.3
22	Nicotine	Yes	High	-3.59 (Soluble)	16.13	30.21
23	Palmitic Acid	Yes	High	-4.58 (Moderately soluble)	37.3	28.68
24	Arachidic Acid	Yes	Low	-4.34 (Poorly soluble)	37.3	28.26
25	Vernolic acid	No	High	-7.32 (Moderately	49.83	26.3

				soluble)		
26	Gallic Acid	No	High	-1.26 (Soluble)	97.99	20.23
27	Sterol	No	High	-6.19 (Soluble)	20.23	20.23
28	Glutathione	No	Low	-5.47 (Soluble)	197.62	20.23
29	Linoleic Acid	Yes	High	-2.41 (Moderately soluble)	37.3	20.23
30	Genistein	Yes	High	-4.21 (Moderately soluble)	90.9	19.03
31	Ascorbic Acid	Yes	High	-2.62 (Soluble)	107.22	16.13

Table3: Parameters showing Lipinski Filter criteria of ligands (Source: SwissADME)

S.No.	Phytocompounds	MW	H-Bond Acceptor	H-Bond Donor	LOGP	Lipinski violations
1	Bufotenine	204.27	2	2	1.92	0
2	N, N-Dimethyl-5-methoxytryptamine	218.29	2	1	2.54	0
3	Choline	104.17	1	1	-2.14	0
4	Serotonin	176.22	2	3	1.18	0
5	Dimethyltryptamine	188.27	1	1	2.21	0
6	9H-Pyrido[3,4B] indole	168.19	1	1	1.43	0
7	Levodopa	197.19	5	4	0.78	0
8	Dopamine	153.18	3	3	1.27	0
9	alpha-Amyrenyl acetate	468.75	2	0	4.89	1
10	Acacetin	284.26	5	2	2.56	0
11	Luteolin	286.24	6	4	1.86	0
12	6-Methoxyharman	212.25	2	1	2.03	0
13	Oleic Acid	282.46	2	1	4.27	1
14	Ursolic Acid	456.7	3	2	3.71	1
15	Betulinic Acid	456.7	3	2	3.79	1
16	Beta-Sitosterol	414.71	1	1	4.79	1
17	Stigmasterol	412.69	1	1	5.01	1
18	Myristic Acid	228.37	2	1	3.32	0
19	Tryptamine	160.22	1	2	1.54	0
20	Coumarin	146.14	2	0	1.75	0
21	Stearic Acid	284.48	2	1	4.3	1
22	Nicotine	162.23	2	0	2.14	0
23	Palmitic Acid	256.42	2	1	3.85	1
24	Arachidic Acid	312.53	2	1	4.56	1
25	Vernolic acid	296.44	3	1	4.12	0

26	Gallic Acid	170.12	5	4	0.21	0
27	Sterol	248.4	1	1	3.26	1
28	Glutathione	307.32	7	5	0.73	0
29	Linoleic Acid	280.45	2	1	4.14	1
30	Genistein	270.24	5	3	1.91	0
31	Ascorbic Acid	176.12	6	4	0.39	0

Molecular Docking

The binding affinity of all the selected ligands toward the α-syn protein as obtained by PyRx is enlisted in Table 4. For further analysis, the docking conformation that had the maximum binding energy was taken into consideration. The phytocompound luteolin was shown to have the highest binding energy in this investigation. Therefore, this is considered for further analysis. The DS BIOVIA Discovery Studio is used to produce the 3D diagram and the 2D diagram, as given in the figure 4 and 5 respectively, showing interaction between the α-syn protein and luteolin. The ligand luteolin established a strong interaction with the amino acids of 'A' chain with a binding affinityof-9. The ligand was interacting with ASP15, TRP63, ALA64, ASP66, GLU112, TYR156, GLU154 and MET331 amino acids of the target protein as clearly seen in the figure 5.

Table 4: Binding affinity of ligand with α-syn protein

S.No.	Ligand name	Ligand-Target interaction	Binding Affinity
1	Luteolin	Clean_3q27_5280445_uff_E=242.10	-9
2	Acacetin	Clean_3q27_5280442_uff_E=247.39	-8.9
3	Genistein	Clean_3q27_5280961_uff_E=356.74	-8.4
4	9H-Pyrido[3,4-B]indole	Clean_3q27_64961_uff_E=348.52	-8.2
5	6-Methoxyharman	Clean_3q27_5376026_uff_E=369.43	-7.9
6	N,N-Dimethyl-5-methoxytryptamine	Clean_3q27_1832_uff_E=373.32	-7.3
7	Bufotenine	Clean_3q27_10257_uff_E=360.39	-7.2
8	Levodopa	Clean_3q27_6047_uff_E=113.02	-7.2
9	Dimethyltryptamine	Clean_3q27_6089_uff_E=359.91	-7.2
10	Coumarin	Clean_3q27_323_uff_E=92.32	-7
11	Serotonin	Clean_3q27_5202_uff_E=323.58	-6.9
12	Vernolic acid	Clean_3q27_6449780_uff_E=1575.	-6.9

		85	
13	Tryptamine	Clean_3q27_1150_uff_E=319.68	-6.7
14	Nicotine	Clean_3q27_89594_uff_E=283.26	-6.3
15	Myristic Acid	Clean_3q27_11005_uff_E=51.08	-6.2
16	Gallic Acid	Clean_3q27_370_uff_E=77.82	-6.2
17	Ascorbic Acid	Clean_3q27_54670067_uff_E=200.65	-6.2
18	Dopamine	Clean_3q27_681_uff_E=104.20	-5.9

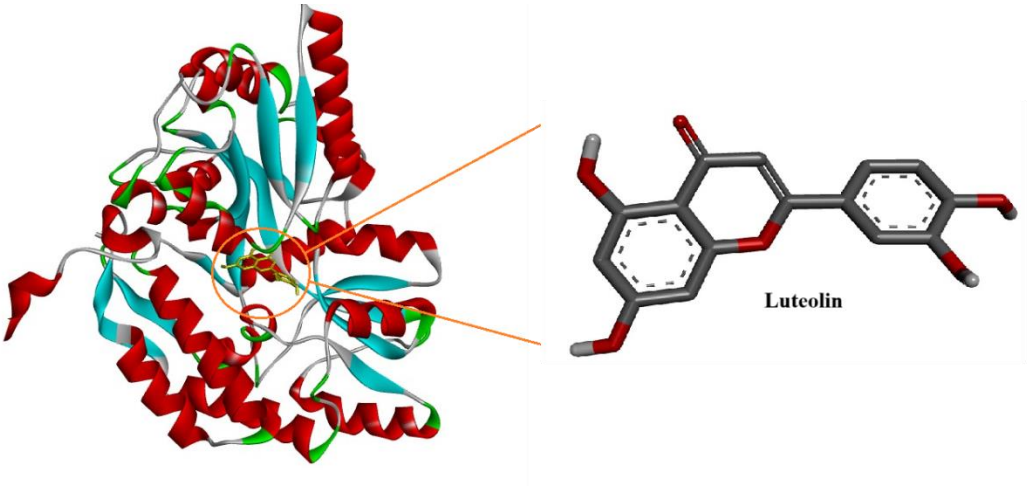

Figure 5: 3D diagram of interaction of the α-synand the Luteolin

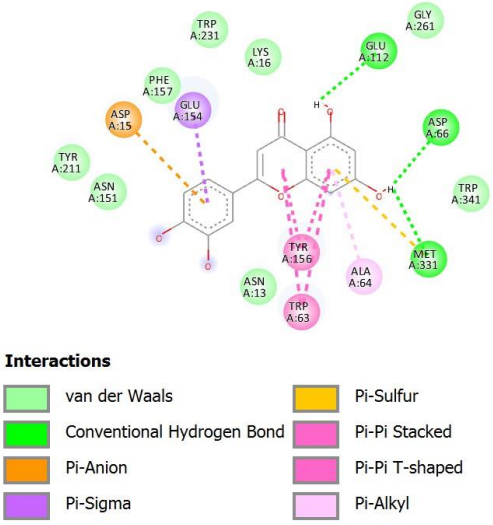

Figure 6: 2D diagram of interaction of the α-synand the Luteolin

DISCUSSION

Parkinson's disease (PD) is the world's second most common neurological disorder. Parkinson's disease is a nervous system ailment with unclear root cause that affects both the motor and non-motor systems. The complex pathological pathways underlying Parkinson's disease have not been successfully treated by the common medications and therapies currently on the market. On the other hand, it has been demonstrated that using the bioactive components of medicinal plants can alter or impede the progression of Parkinson's disease. Identification of novel bioactive chemicals becomes the need of the hour to produce new and effective medications.

Inflammation may be caused by the aggregation of the pathological proteins. Lewy bodies have insoluble fibrils, but the insoluble fibrils of α-syn are more deadly. There are several conditions that speed up the aggregation of α-syn. It is appropriate to use the therapeutic methods to stop the aggregation. Even though little is known about α-syn's normal function, it appears to interact with a wide range of signaling pathways, suggesting that it may take part in several signaling pathways. It might affect dopaminergic neurotransmission, synaptic plasticity, cell survival, and cell differentiation. It's also possible for pathways that disturb normal function[31].

The structure of α-syn protein (3Q27) was observed. The secondary structure of protein is important for its functionality, stability, and interactions with other molecules. The secondary structure of the 3Q27 protein suggests a compact, globular fold with a mix of alpha helices, beta strands, and turns. The Ramachandran plot analysis suggests that the protein structure 3Q27 has a good overall quality, with most residues adopting the most favorable conformations.

Since the human brain is an extremely complicated organ, not all medications may be used to treat brain related diseases. One current drug treatment for Parkinson's disease is seed of *M. pruriens*. Due to its high levodopa content, *M. pruriens* has been shown to treat Parkinson disease over an extended period of time. In PD patients, powdered seed showed a quick start of activity without any corresponding increase in dyskinesia during clinical trials[20].Taking this into consideration, this plant was used as a source for compounds in order to determine its potential resistance to PD.

The molecular weights of all the chosen compounds fall within the permissible range (MWT 500). In contrast to large molecular weight substances, low molecular weight molecules are more readily ingested, dissipated and transported [18]. There is zero violation of Lipinski rule in the selected ligands. In the study of drug transport characteristics such as intestinal absorption and blood-brain barrier (BBB) penetration, polar surface area (PSA) has been a frequently employed molecular descriptor. An extremely quick additive fragment approach for computing PSA is topological polar surface area (TPSA) for barrier crossing ADME predictionsto quickly assess the virtual bioavailability of a vast library of compounds [11].For the selected ligands, the TPSA value is within range of <120 and GI absorption is high[18].

We can characterize the behavior of small compounds in the binding sites of target proteins and clarify essential biochemical processes by using the molecular docking approach to describe the interaction between a small molecule and a protein at the atomic level. Two fundamental phases make up the docking process: determining the binding affinity and predicting the ligand conformation together with its pose, or location and orientation within these sites [25].

The binding affinity of the selected phyto compounds with the 3Q27 protein is predicted using Pyrx. The ligand luteolin was selected as it has the highest binding affinity score with the targeted protein and also passing the Lipinski rule and ADME analysis. With the selected ligand, the 2D and 3D diagram are predicted in the DS BIOVIA Discovery Studio which shows the amino acid binding with the ligand molecules. The successful binding shows that it can be the potential inhibitor of the α-syn protein.

Time and risk reduction, affordable, and ease of finding effective compounds with the chosen target were all made possible with the help of computational tools. It seems that with an improved comprehension of the drug and receptor interactions, current computational approaches can significantly support and facilitate the design of novel, more potent, and effective inhibitors of PD [20].

CONCLUSION

Parkinson's disease (PD) has increased in frequency in recent years and usually affects the old people. To address this condition, numerous medications are being developed.

It is also possible to create PD treatment from the medicinal herbs. Certain compounds have the ability to bind to the active sites of the PD-causing protein, hence blocking its activities.*M. pruriens* is one such plant with a variety of medicinal uses. The research results serve as a guide for the creation of novel, highly effective medication for PD. The plant *M. pruriens* has phytochemicals that can be utilized to make therapeutic treatment for PD. According to the computational study, the phytochemical with such potential is Luteolin, which is found in the roots of the plant. It can serve as a guide for the development of more effective and functioning medication with less side effects.

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