RESEARCH PAPER

Computational ADMET Assessment and Molecular Docking-Based Investigation of Phytoconstituents from *Sechium edule* as Potential Anthelmintic Agents

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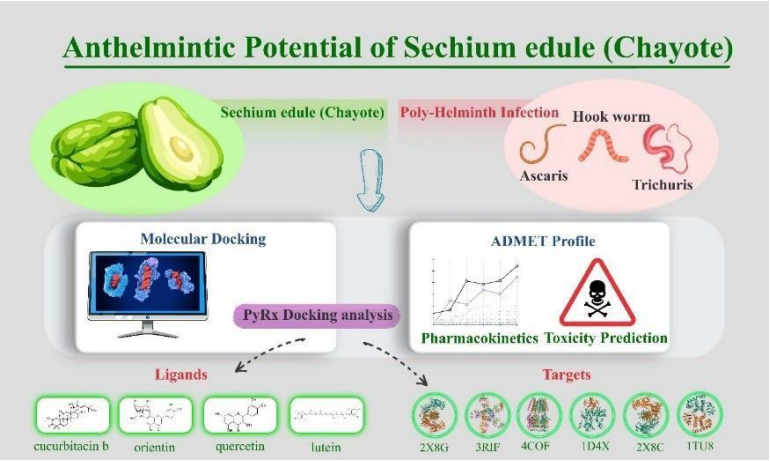
ABSTRACT

Poly-helminth infection is a worsening condition caused by the invasion of more than one soil transmitted helminths, affecting several biological functions in human. Chayote is the common name for *Sechium edule* fruit (SEF) possessing various medicinal properties such as anti-epilepsy, anticancer, antidiabetics, antihypertension, anti-urolithiasis, hepatoprotectives and anti-oxidant. This study employs an integrated in silico approach that merges molecular docking and ADMET profiling to evaluate the anthelmintic efficacy of specific phytoconstituents from SEF. The six critical molecular targets implicated in cytoskeletal integrity, detoxification, and redox processes are actin, glutathione S-transferase, thioredoxin glutathione reductase, Ivermectin-sensitive glutamate-gated chloride channel and GABA receptor. The docking study was performed by PyRx, found that some phytoconstituents had stronger binding affinities than the reference drugs. Cucurbitacin B, orientin, quercetin and lutein exhibited robust and enduring interactions with critical catalytic and binding site residues, as evidenced by multiple hydrogen bond configurations and favourable binding energy scores across various targets. In silico ADMET profile studied using ADMETlab 2.0. Pharmacokinetic profiles were analysed among the phytochemicals from that Kaempferol, quercetin, and lutein shows good results and have manageable toxicity predictions. In summary, the results show that the phytoconstituents of SEF are good candidates for the development of new anthelmintic agents.

GRAPHICAL ABSTRACT:



Keywords: *Sechium edule* fruit (SEF), Phytoconstituents, ADMET, PyRx, binding energy.

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INTRODUCTION:

Helminthiasis is the common name used to describe several chronic infections caused by helminths, known as macro-parasitic worms[1,2]. It has been stated that 2 billion individuals worldwide suffer from a variety of helmintic diseases caused by nematodes, trematodes, and cestodes, including Echinococcosis, Cysticercosis, Dracunculiasis, Schistosomiasis, Loiasis, Trichiniasis, and Ascariases[3]. Due to poor sanitation and a lack of psychomotor capabilities, it is a neglected tropical disease[4] that mainly impacts equatorial regions[5] and developing countries. By altering the host's immune system, the infected worm causes anemia, poor child development[6], vitamin and mineral shortages, and problems digesting lactose. In their mitochondria, helminths naturally contain a branching electron transport chain charged with enzymatic proteins that support respiration and energy production[7].

Fumarate reductase (FR), Triosephosphate isomerase (TPI)[8,9], β-tubulin[10,11], Glutathione S-transferase (GST)[12,13], Thioredoxin Reductase (TR)[14,15] and DNA-dependent RNA polymerase[16] are the common and essential molecular enzymes involved in various metabolic pathways in worms[8]. The conversion of fumarate to succinate is a terminal step of phosphor-enol-pyruvate carboxy kinase - succinate pathway[17] catalysed by NADH-FR in anaerobic conditions[8]. TPI is another enzymatic protein takes part in glycolysis in parasitic hooks for survival. Inhibition by targeting those two enzymes results in loss of energy causing static paralysis and death[18]. β-tubulin is an important cytoskeletal protein that is needed for intracellular transport, cell replication, and the formation of microtubules. Helminths need microtubules to take in nutrients, move around, and reproduce. Albendazole and other anthelmintics primarily target β-tubulin. The parasite is killed and rendered paralyzed when they attach to it and prevent microtubule assembly[10,11]. By connecting glutathione to toxic metabolites, GST detoxifies Helminths use GSTs to protect themselves from xenobiotics and oxidative stress caused by the host. This helps them stay alive and avoid the immune system. GSTs are important for protecting the body, which is why they are targets for drugs and vaccines against parasites like *Schistosoma* and *Fasciola*[12,13]. TR keeps the redox balance inside cells by making less thioredoxin. This enzyme is needed for helminths to live through oxidative damage caused by the immune system of the host. TR is a suitable target for anti-helminthic therapies, as its inhibition results in oxidative damage, redox imbalance, and the demise of parasites[14,15]. DNA-dependent RNA polymerase catalyses the transcription of genetic information from DNA into RNA, which is essential for the development and reproduction of parasites. All species, helminths included, have transcriptional machinery that is very similar. Inhibiting RNA polymerase is viewed as a potential method for interfering with vital biological processes in parasitic worms[16].

Chayote (*Sechium edule*, SE) is a green, viviparous fruit that is belongs to the Cucurbitaceae family that live for a long time. This nutrient-rich fruit has a lot of phytochemicals in it, such as alkaloids, flavonoids, saponins, carotenoids, phospholipids, triterpenoids, proteins, potassium, phosphorus, calcium[19], and gibberellins[20]. People use the edible parts of SE to treat a number of health problems, such as cancer[21], ulcers[20], convulsions[22], microbial infections[21], high blood pressure[23], headaches, anxiety, and nervousness[24]. Chayote is also used in a lot of personal care and beauty products, like deodorants, moisturizers, sun lotions, toothpastes, mouthwashes, cleansers, shaving creams, and shampoos[19]. It might keep fungus, bugs, and nematodes away[3]. There are many numbers of primary and secondary metabolites in *Sechium edule* fruit (SEF)[25–27]. Because of this, anthelmintics made from these chemicals might be a good alternative to chemical drug resistance and the problems that come with it[28]. Molecular docking and molecular dynamics simulation are two ways to design drugs that have also made it easier and faster to find new chemical entities and pharmacological activities. Modern tools can tell how many and what kinds of chemicals are in the things being studied. One of the most common things people do with computers is molecular docking (*in-silico*)[29–31]. It gives information about selected ligand and protein interaction with a 3D image, bond angle, number of hydrogen bond, and binding energy. This makes it easier to guess how well the ligand-protein interaction will work, which helps figure out if the compounds being studied are agonistic or antagonistic[4].

Absorption, Distribution, Metabolism, Excretion and Toxicity (ADMET) analysis and *in-silico* methods are very important to drug research right now because they can predict pharmacokinetic and toxicity profiles early on. Hence the objectives of our study were to identify the anthelmintic responsible compounds present in SEF. Pyrx software was used for molecular docking to find out how the ligand and target interactions[32]. Whereas ADMETlab 2.0 was used to predict ADMET characteristics[33]. By improving lead optimization and lowering expenses, time, and the necessary number of trials, these computational methods make it easier to choose safer and more effective drug candidates.

METHODS:

Ligand preparation

The docking ligands employed in this study were chosen from previously published literature. The study focused on bioactive chemicals found in *Sechium edule*. Despite the existence of numerous phytochemicals in SEF, only β-Carotene, Cucurbitacin B, Kaempferol, Lutein, Orientin, Quercetin and Vitexin were chosen for the present study. The standard inhibitors, Albendazole and piperazine were also selected for comparative studies. The structures of the ligands were retrieved in the spatial data file format from the PubChem Compound Database (National Centre for Biotechnology Information; https://pubchem.ncbi.nlm.nih.gov/).

Receptor preparation

The 3-dimensional structure of target proteins C. elegans Actin gene (PDB ID: 1D4X), Glutathione S transferase (PDB ID: 1TU8), Thioredoxin Glutathione Reductase (PDB ID: 2X8C, 2X8G), Ivermectin sensitive glutamate – gated chloride channel (PDB ID: 3RIF) and GABA-RB3 (PDB ID: 4COF) were retrieved from the RCSB Protein Data Bank. All water molecules were removed from protein files before the docking process. The 3-dimensional coordinates were unloaded and converted to PDBQT format in the python prescription virtual screening tool (PyRx) window and subjected to further assays[34].

Molecular docking

PyRx (AutoDock Vina) tool version 0.8 (The Scripps Research Institute) was used to conduct the docking studies. Selected compounds were docked to target proteins using a rigid body model with the molecule as the rigid body and the ligand as the flexible body. The search was widened to include the entire receptor protein that was using the AutoDock Vina scoring tool as negative Gibbs free energy (G) scores (kcal/mole). Post docking analyses were visualized using Discovery Studio Biovia 2021, which displayed the sizes and positions of binding sites, hydrogen-bond interactions and bond lengths as a measure of interaction[35,36].

In-silico predicted ADMET profiles

In-silico prediction of ADMET properties of the selected phytoconstituents were carried out using ADMETlab2.0. The SMILES approach was employed to evaluate the absorption, distribution, metabolism, excretion and toxicity (ADMET) and Lipinski's rule for all the seven compounds[37].

RESULTS:

Molecular docking:

Two standards and seven chosen phytoconstituents were docked to the target enzyme. The binding affinities of these phytoconstituents ranged from -7.3 to -8.7 kcal/mol, -7.2 to -8.9 kcal/mol, -8.6 to -10.6 kcal/mol, -7.4 to -8.8 kcal/mol, -7.7 to -10.1 kcal/mol, and -8.6 to -9.6 kcal/mol, respectively, as determined through molecular docking against 1D4X, 1TU8, 2X8C, 2X8G, 3RIF, and 4COF. Tables 1-6 and Figure 1-6 shows how the phytoconstituents interact with each other.

Table 1: The docking score of the phytoconstituents and their interactions with the enzyme C. elegans Actin gene (1D4X).

S.No.	Compounds	Binding affinity (kcal/mol)	No. of hydrogen bonds	Conventional Hydrogen Bond Amino acid residues
Standards				
1	Albendazole	-6.2	2	TYR A:133 (2)
2	Piperazine	-3.8	0	-
Phytoconstituents				
3	β-Carotene	-8.2	0	-
4	Cucurbitacin B	-8.1	1	TRP A:356
5	Kaempferol	-7.3	5	THR A:148, THR A:149, LYS A:326, TYR G:63, GLN G:94
6	Lutein	-8.4	0	-
7	Orientin	-8.7	7	THR A:148, LYS A:291, LYS A:328 (2), TYR G:63 (2), ARG G:96
8	Quercetin	-8.0	4	THR A:148, THR A:149 (2), ASP A:292
9	Vitexin	-8.4	4	THR A:148, THR A:149 (2), TYR G:63

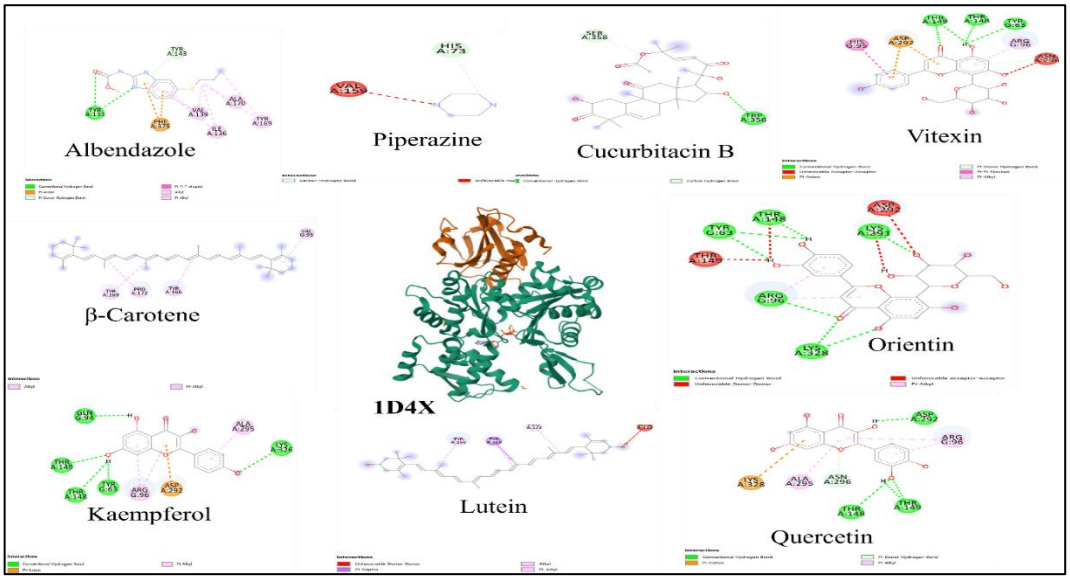

Figure 1: Schematic representation of molecular interaction of phytoconstituents with 1D4X. 1D4X = C. elegans Actin Gene

Table 2: The docking score of the phytoconstituents and their interactions with the enzyme Glutathione S transferase (1TU8).

S.No.	Compounds	Binding affinity (kcal/mol)	No. of hydrogen bonds	Conventional Hydrogen Bond Amino acid residues
Standards				
1	Albendazole	-6.3	1	GLN B:58
2	Piperazine	-3.5	1	LEU B:13
Phytoconstituents				
3	β-Carotene	-8.7	0	-
4	Cucurbitacin B	-8.6	2	TYR B:7, ARG B:95
5	Kaempferol	-7.4	3	VAL B:22, GLU B:190, LYS B:194
6	Lutein	-8.9	1	ASP B:36
7	Orientin	-7.6	2	TYR B:7, THR B:102
8	Quercetin	-7.2	1	ASP D:25
9	Vitexin	-7.4	7	TYR C:7 (2), LYS C:42, GLN C:49, ASP D:96 (2), ARG D:103

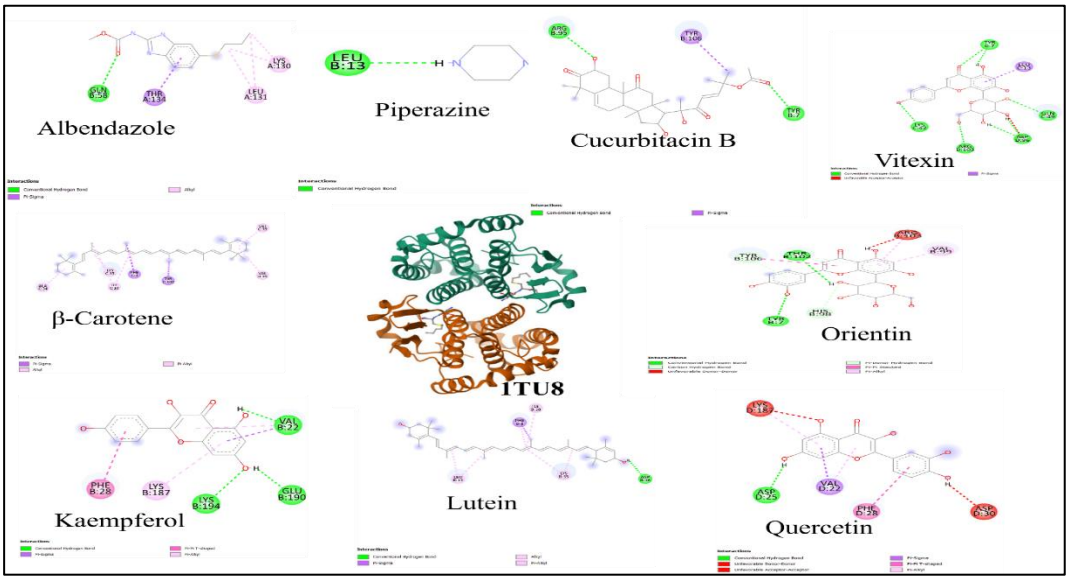

Figure 2: Schematic representation of molecular interaction of phytoconstituents with 1TU8. 1TU8 = Glutathione S transferase

Table 3: The docking score of the phytoconstituents and their interactions with the enzyme Thioredoxin Glutathione Reductase (2X8C).

S.No.	Compounds	Binding affinity (kcal/mol)	No. of hydrogen bonds	Conventional Hydrogen Bond Amino acid residues
Standards				
1	Albendazole	-6.8	3	SER A:117, GLY A:118, CYS A:159
2	Piperazine	-3.5	1	GLU A:478
Phytoconstituents				
3	β-Carotene	-8.6	0	-
4	Cucurbitacin B	-10.6	1	GLN B:167
5	Kaempferol	-8.8	3	GLU B:140, GLY B:228 GLN B:396
6	Lutein	-8.6	0	-
7	Orientin	-9.2	4	TYR A:212, LYS B:506, THR B:577, THR B:580
8	Quercetin	-9.4	3	GLU B:140, THR B:153 (2)
9	Vitexin	-9.0	4	SER B:503, ASN B:504, THR B:573, GLU B:576

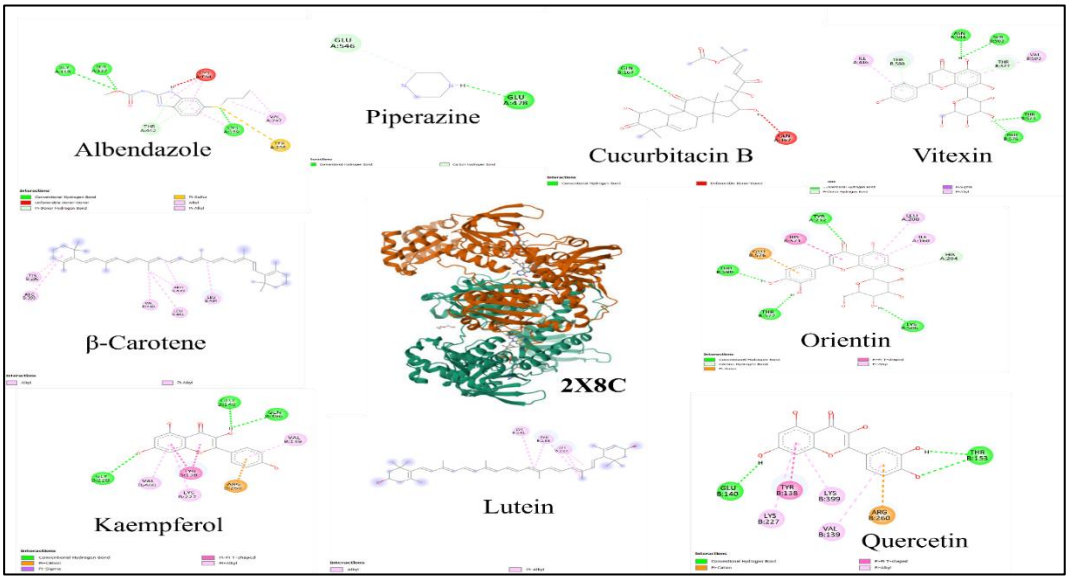

Figure 3: Schematic representation of molecular interaction of phytoconstituents with 2X8C. 2X8C = Thioredoxin Glutathione Reductase

Table 4: The docking score of the phytoconstituents and their interactions with the enzyme Thioredoxin Glutathione Reductase (2X8G).

S.No.	Compounds	Binding affinity (kcal/mol)	No. of hydrogen bonds	Conventional Hydrogen Bond Amino acid residues
Standards				
1	Albendazole	-5.7	1	ARG A:455
2	Piperazine	-3.6	1	THR A:442
Phytoconstituents				
3	β-Carotene	-8.4	0	-
4	Cucurbitacin B	-8.8	2	ALA A:294, SER A:295
5	Kaempferol	-7.4	6	ASP A:177, PRO A:476, GLU A:478, TRP A:510 (2), ASN A:543
6	Lutein	-8.4	0	-
7	Orientin	-8.6	5	LYS A:42, LYS A:44, THR A:133 (2), GLN A:220
8	Quercetin	-7.5	3	TYR A:335 (2), PRO A:476
9	Vitexin	-7.9	6	GLY A:323, VAL A:469, THR A:471 (2), ALA A:481, GLYA:483

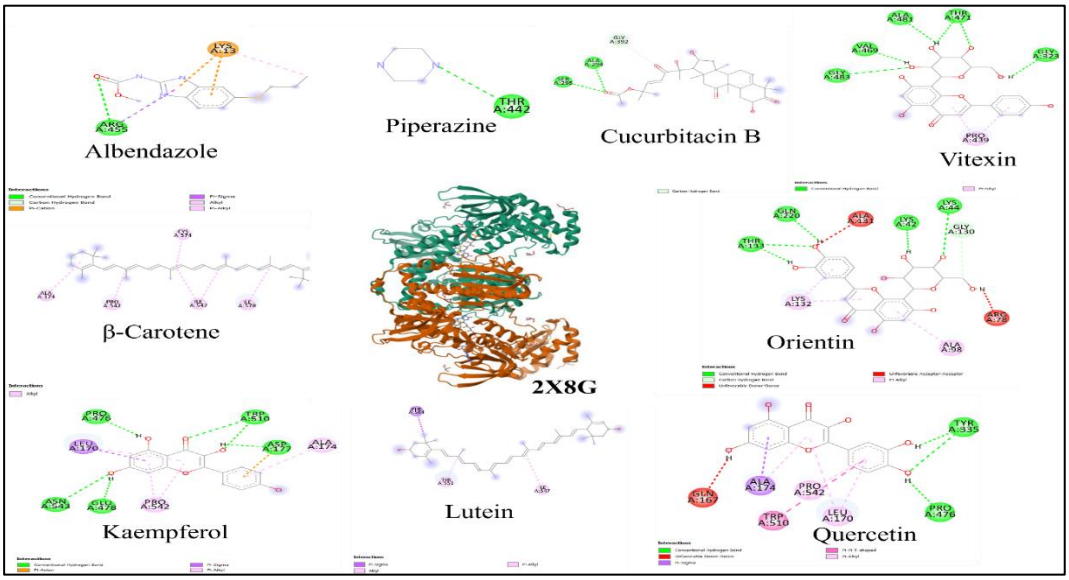

Figure 4: Schematic representation of molecular interaction of phytoconstituents with 2X8G. 2X8G = Thioredoxin Glutathione Reductase

Table 5: The docking score of the phytoconstituents and their interactions with the enzyme Ivermectin sensitive glutamate – gated chloride channel (3RIF).

S.No.	Compounds	Binding affinity (kcal/mol)	No. of hydrogen bonds	Conventional Hydrogen Bond Amino acid residues
Standards				
1	Albendazole	-7.1	1	SER B:260
2	Piperazine	-3.7	1	TYR I:105
Phytoconstituents				
3	β-Carotene	-9.0	0	-
4	Cucurbitacin B	-10.1	5	THR B:247, THR C:247, THR C:251, THR D:247, THR E:247
5	Kaempferol	-7.7	2	ARG C:211, GLN C:266
6	Lutein	-9.9	2	ASN A:264, THR D:247
7	Orientin	-9.3	5	VAL B:45, ASN B:46, ARG C:211, TYR C:216, TYR C:137
8	Quercetin	-7.9	4	VAL A:45, ASN A:46, ASP B:43, GLN B:266
9	Vitexin	-8.0	5	GLU K:40, LYS K:105, LEU K:106, PRO K:167, LYS K:169

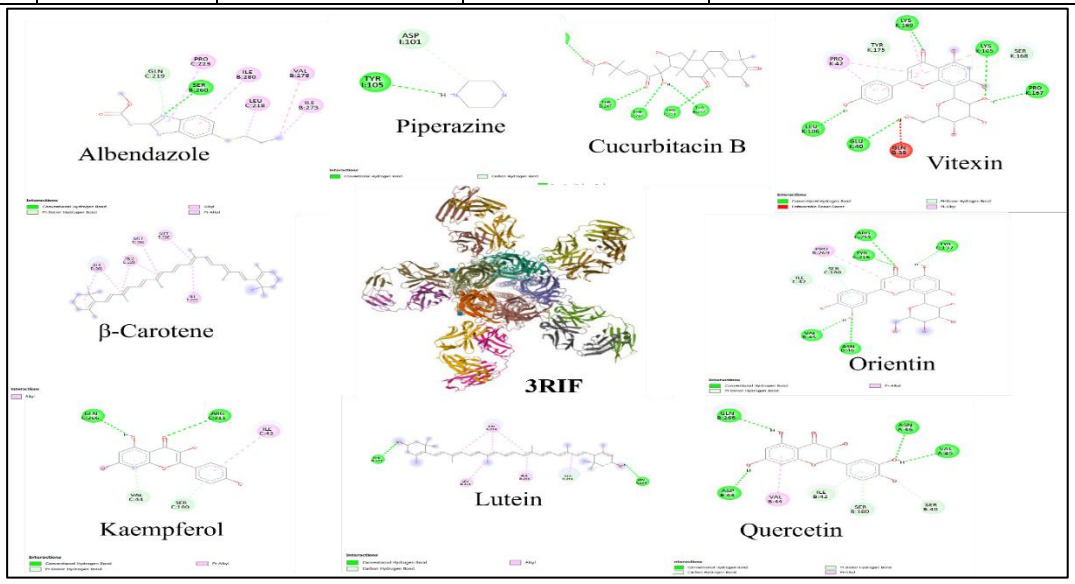

Figure 5: Schematic representation of molecular interaction of phytoconstituents with 3RIF. 3RIF = Ivermectin sensitive glutamate-gated chloride channel.

Table 6: The docking score of the phytoconstituents and their interactions with the enzyme GABA – RB3 (4COF).

S.No.	Compounds	Binding affinity (kcal/mol)	No. of hydrogen bonds	Conventional Hydrogen Bond Amino acid residues
Standards				
1	Albendazole	-7.0	2	ILE A:47 (2)
2	Piperazine	-3.8	3	TYR E:97, TYR E:157, THR E:202
Phytoconstituents				
3	β-Carotene	-9.5	0	-
4	Cucurbitacin B	-8.6	5	ALA A:248, THR A:260, THR B:256 (2), THR C:256
5	Kaempferol	-9.2	4	GLN D:64, THR D:176, TYR E:97, GLU E:155
6	Lutein	-9.6	1	TYR E:446
7	Orientin	-9.2	4	ASP D:43, ARG D:180, TYR E:97, VAL E:199
8	Quercetin	-9.6	6	ASN D:41, GLN D:64, TYR E:97, GLU E:155, SER E:156
9	Vitexin	-9.4	4	ASN D:41, ARG D:180, TYR E:97, GLU E:155

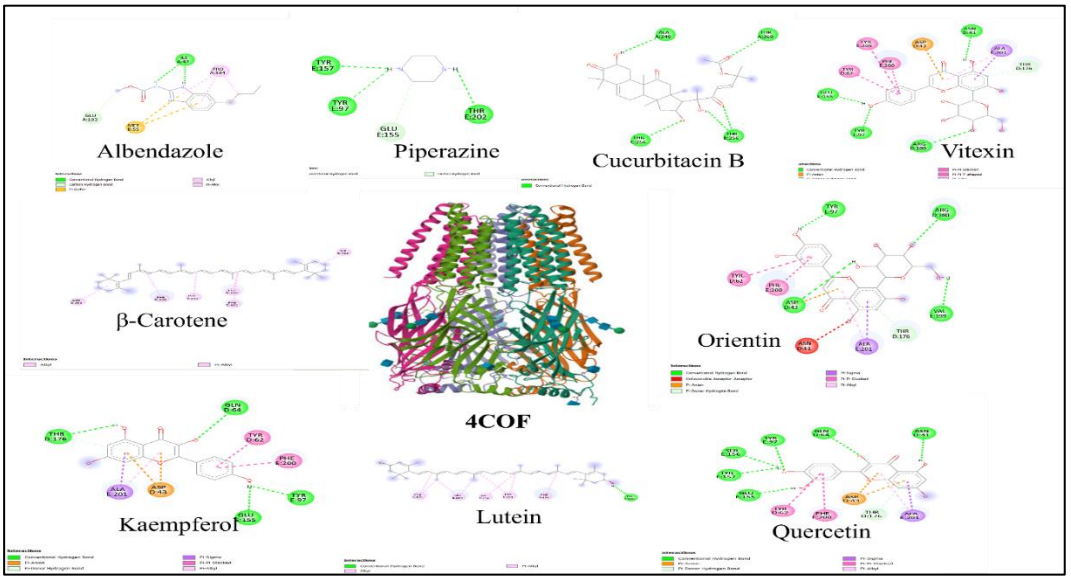

Figure 6: Schematic representation of molecular interaction of phytoconstituents with 4COF. 4COF = GABA-RB3

In-silico predicted ADMET profiles

In-silico prediction of ADMET properties of the selected phytoconstituents were carried out using ADMETlab2.0. The SMILES approach was employed to evaluate the absorption, distribution, metabolism, excretion and toxicity (ADMET) and Lipinski's rule for all the seven compounds. The physico-chemical properties of the phytoconstituents were given in the table 7 and the predicted toxicity level of the compounds were summarized in the table 8.

Table 7: Results of predicted ADME properties of the Phytoconstituents of SE

	β-Carotene	Cucurbitacin B	Kaempferol	Lutein	Orientin	Quercetin	Vitexin
M.W	536.44	558.32	286.05	568.43	448.1	302.04	432.11
NHA	0	8	6	2	11	7	10
NHD	0	3	4	2	8	5	7
TPSA	0	138.2	111.13	40.46	201.28	131.36	181.05
Log P	7.687	2.74	2.656	5.678	0.757	2.155	1.232
HIA	Yes	Yes	Yes	Yes	No	Yes	No
P-gp substrate	No	No	No	No	Yes	No	Yes
BBB penetration	No	No	No	No	No	No	No
PPB	105.8%	70.20%	97.86%	102.1%	88.77%	95.49%	89.60%
VD	1.175	0.746	0.522	1.19	0.842	0.579	0.9.3
CYP1A2 substrate	Yes	No	No	Yes	No	No	No
CYP3A4 inhibitor	Yes	Yes	Yes	Yes	No	No	No
CL	0.576	3.647	6.868	0.902	5.439	8.284	4.091
$T_{1/2}$	0.011	0.645	0.905	0.023	0.833	0.929	0.765

M.W = Molecular Weight (g); NHA = Number of Hydrogen bond Acceptors; NHD = Number of hydrogen bond Donors; TPSA = Topological Polar Surface Area ($A^{\circ 2}$); Log P = Log of the octanol/water partition coefficient; HIA = Human Intestinal Absorption; P-gp = P- glycoprotein; BBB = Blood-Brain Barrier; PPB = Plasma Protein Binding; VD = Volume of Distribution (L/kg); CYP = Cytochrome P; CL = Clearance (mL/min/kg); T1/2 = Biological Half Life (h).

Table 8: Results of predicted toxicity of the Phytoconstituents of SE

	Organ Toxicity				Genomic Toxicity	
	Acute Oral Toxicity	**H-HT**	**Eye Irritation**	**Eye Corrosion**	**Carcinogenicity**	**AMES Toxicity**
β-Carotene	-	-	+	-	-	-
Cucurbitacin B	+	-	-	-	+	-
Kaempferol	-	-	+	-	-	+
Lutein	-	-	-	-	-	-
Orientin	-	-	+	-	-	+
Quercetin	-	-	+	-	-	+
Vitexin	-	-	-	-	-	+

H-HT = Human Hepatotoxicity; AMES = Ames Salmonella/microsome Mutagenicity Assay

DISCUSSION

Molecular docking analysis

Molecular docking analysis was performed to find out how well some of the phytoconstituents in *Sechium edule* fruit (SEF) could bind to different Caenorhabditis elegans target proteins. We then compared the results to those of the standard anthelmintic drugs Albendazole and Piperazine[38,39].

C. elegans Actin (1D4X) is very important for muscle contraction and movement in nematodes; therefore, it might be a good target for anthelmintic treatment. In this work, albendazole had a moderate binding affinity (−6.2 kcal/mol) with two hydrogen bonds involving TYR A:133. On the other hand, piperazine had a weak binding affinity (−3.8 kcal/mol) with no hydrogen bond interactions. Conversely, phytoconstituents of SEF including orientin (−8.7 kcal/mol), lutein (−8.4 kcal/mol), vitexin (−8.4 kcal/mol), and β-carotene (−8.2 kcal/mol) had greater binding affinities. Orientin made the most hydrogen bonds[7] with important residues including THR A:148, LYS A:291, LYS A:328, TYR G:63, and ARG G:96. People know that these residues have a role in stabilizing actin filaments and binding ligands. Flavonoid glycosides like orientin, vitexin, and quercetin have a higher binding affinity and more hydrogen bonds than regular medicines. This suggests that they may be better at stopping actin dynamics[40].

Glutathione S-transferase (GST) (1TU8) involved in drug resistance in helminths. Piperazine had a small effect (−3.5 kcal/mol) and Albendazole had a big effect (−6.3 kcal/mol). Lutein (−8.9 kcal/mol), β-carotene (−8.7 kcal/mol), and Cucurbitacin B (−8.6 kcal/mol) were the phytoconstituents that stuck to the most. Vitexin formed the most hydrogen bonds[7] with active site residues like TYR C:7, LYS C:42, GLN C:49, ASP D:96, and ARG D:103. This shows that it is very stable inside the GST binding pocket. The fact that these substances stop GST from working may make detoxification less effective, which could make nematodes more sensitive to xenobiotics and oxidative stress[41,42].

Thioredoxin glutathione reductase (TGR) (2X8C and 2X8G) is a key redox enzyme that only helminths have. It is a good target for selective drugs. In both crystal structures (2X8C and 2X8G), phytoconstituents of SE had much stronger binding affinities than Albendazole and Piperazine. Quercetin (−9.4 kcal/mol) and Orientin (−9.2 kcal/mol) also had strong interactions through hydrogen bonding with residues that are important for catalysis. However, Cucurbitacin B had the strongest binding to 2X8C (−10.6 kcal/mol). In the same way, Orientin (−8.6 kcal/mol) and Cucurbitacin B (−8.8 kcal/mol) in 2X8G showed strong binding backed by many hydrogen bonds. These results suggest that polyphenolic and triterpenoid substances may be able to effectively stop helminth redox homeostasis, which would kill the parasite[14,43].

The glutamate-gated chloride channel (3RIF) is a well-known target for anthelmintics that causes paralysis of the nervous system. Albendazole had a weak binding affinity (−7.1 kcal/mol), and Piperazine had a low affinity again. Lutein (−9.9 kcal/mol), Orientin (−9.3 kcal/mol), and Cucurbitacin B (−10.1 kcal/mol) all had very strong binding affinities. Cucurbitacin B formed five hydrogen bonds with conserved THR residues from different chains. This shows that the interaction was still happening in the channel pore area. These interactions could keep the channel open or closed for a long time, which could stop the parasite from moving[44].

GABA-gated chloride channels (4COF) are primarily target for piperazine and other neuromuscular blockers. Lutein and Quercetin had the strongest binding affinities (−9.6 kcal/mol), which was better than Albendazole's (−7.0 kcal/mol). Quercetin made hydrogen bonds with six residues that are important for recognizing ligands: ASN D:41, GLN D:64, TYR E:97, and GLU E:155. These interactions suggest that flavonoids may be more effective than conventional anthelmintics in regulating GABAergic transmission[45].

ADMET analysis

In silico ADME analysis (Table 7) was done to look at the phytoconstituents of SE and see if they would work for pharmacokinetics. Since Quercetin and Kaempferol have molecular weights of less than 350 g/mol, they should act like drugs and be easy to swallow. But it might be hard to passively take in β-carotene, Lutein, Cucurbitacin B, Orientin, and Vitexin because their molecules are bigger[46,47]. TPSA measurements were also performed to back up these results. The levels of Orientin and Vitexin would be too high because the stomach doesn't absorb them well. Kaempferol (111.13 Å²), Lutein (40.46 Å²), and Quercetin (131.36 Å²) can be safely taken by mouth[48]. Lutein and β-carotene are very lipophilic, which means they stick to plasma proteins very tightly. Flavonoids, on the other hand, have low Log P values, which means they might be able to easily pass through and dissolve in other things[49,50].

No phytoconstituent was anticipated to traverse the blood-brain barrier, consequently diminishing the probability of central nervous system damage. It was found that Orientin and Vitexin are substrates for P-glycoprotein, which means that efflux may make them less available.

Based on toxicity prediction, Table 8 shows that most of the phytoconstituents were usually safe. When taken by mouth, Cucurbitacin B caused the short-term toxicity and cancer-causing effects that were expected, which means that the dosage needs to be very carefully controlled. Higher doses of Vitexin, Kaempferol, Quercetin, and Orientin may cause mutations because they all showed AMES toxicity[51]. Lutein was safer because it was not thought to harm organs or DNA. Kaempferol, quercetin, and lutein all have great ADME and toxicity profiles, which means they are good candidates for the best anthelmintic drugs[52,53].

CONCLUSION:

In conclusion, the molecular docking analysis revealed that the chosen phytoconstituents of SE exhibit strong and consistent binding to several essential C. elegans molecular targets involved in cytoskeletal maintenance, detoxification, redox regulation, and signal transmission between neuronal and muscular cells. These substances are often more effective than the standard anthelmintic drugs, albendazole and piperazine. Flavonoids like orientin, quercetin, vitexin, and kaempferol, along with cucurbitacin B and lutein, forms stable bonds with important amino acid residues of target protein through conventional hydrogen bonding. This means that they can affect more than one thing. ADMET profiling showed that some drugs have beneficial pharmacokinetic properties, such as being easily absorbed by the mouth, not being able to cross the blood-brain barrier, and having acceptable levels of toxicity. On the other hand, glycosylated flavonoids were not as easily absorbed in the intestines. It's also possible that some molecules interacted with CYP or were genotoxic, so keep that in mind. Both docking and ADMET profiling showed that phytoconstituents from SE could be considered as potential ligands to kill worms. Further, in vitro and in vivo testing is needed to prove the right pharmacokinetic properties of phytoconstituents.

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