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Research Article

GC-MS Analysis and Molecular Docking of Plant-based Compounds from Medicinal Plant *Sida acuta* Burm F. for Antibacterial Potential

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ABSTRACT

Antimicrobial-resistant bacteria cause severe public health issues and mortalities. The evolution of multi-drug resistant bacteria shifted the focus of researchers towards traditional medicine involving bioactive compounds. Plants with bioactive compounds play a pivotal role in treating human diseases. Many of the plant-based bioactive compounds were proven to have the ability to inhibit bacterial growth through different modes of action. Thus, plant-based compounds have been focused on finding potential molecules with antibacterial efficiency to overcome bacterial infection problems. So, in the present study, phytochemicals of *Sida acuta* Burm F. leaf extract were identified using GC-MS technique and phytochemicals with antibacterial potential were identified through a molecular docking study. The qualitative test carried out indicated the presence of carbohydrates, alkaloids, phenols, terpenoids, flavonoids, amino acids, steroids, glycosides, saponins, quinones and coumarins in the extract. The GC-MS analysis showed the presence of 30 phytochemicals and molecular docking studies revealed the best binding affinity of the phytochemicals Pyrido[1,2-a]pyrimidine, Acetonitrile, 2-(6-phenanthridinyl), 5H-Imidazo[2,1-a]isoindole, 2-phenyl and Pyrido[1,2-a]pyrimidine towards *E. coli* biomolecules- 1PHO, 5I5H, 5UW2 and 6NTW respectively. The present study concludes that the phytochemicals of *S. acuta* have appreciable antibacterial efficiency.

INTRODUCTION

Public health has been threatened at the global level by number of infectious diseases. Even after the availability of many synthetic drugs for the treatment of the infection, there is still rise in the rate of infection day by day. The rise of microbial infection is due to the evolution of resistance in the microbes toward the antimicrobial drugs available.^[1-3] World Health Organization reported antimicrobial resistance as one of the top ten world public health threats.^[1-4] Among microbial infection, the infections caused by gram-negative bacteria have great clinical importance as they are highly resistant to antibiotics and causes high morbidity and mortality.^[5,6] The microbes alter some of their mechanisms, including the drug binding site and membrane permeability, efflux pumps, enzyme

degradation and the conformational alteration of the drug culminating in its activation to gain resistance against commercial antibiotics.^[7-10] This has become a major problem and a great challenge for researchers to knock down the microbes' resistance and find the clinical efficient drugs to get rid of microbial infections. The researchers recommended Many strategies, in that one of the suggested strategies, was to derive plant-based compounds of antibacterial potential. As plant-based compounds belong to nature, they have numerous benefits and no side effects over synthetic drugs.^[11-15]

The plant-based compounds such as alkaloids, phenols, flavonoids, tannins, steroids, fatty acids and the like, have already been proven to exhibit unique pharmacological properties of antimicrobial, anticancer, anti-inflammatory and antioxidant. Different plant species possess unique

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activities; only a small proportion have been investigated. Still there are more new compounds to be discovered.^[15-18] A suitable screening method is very important in discovering biologically active compounds. The high activity of the compounds depends upon the extraction and characterization methods used.^[19,20] Generally, the GC-MS technique has been used to identify compounds and detect functional groups.^[21-23] This technique is one of the best and most accurate method to detect different compounds, including alkaloids, alcohols, nitro compounds, long-chain hydrocarbons, steroids, esters, amino acids and organic acids in a small fraction of plant extract.^[22] Also, computer-based tools have been used to screen medicinally active compounds, making drug discovery approaches much easier and more cost-effective.^[24] Tools like molecular docking techniques give knowledge on the interaction of drug and receptors, which anticipate ligand binding to the target protein's stable binding sites.^[25,26]

The medicinal plant *S. acuta* of family Malvaceae is an erect perennial shrub.^[27] It is found along the roadside, fields, forests, coastal areas of India and Nepal. From ancient times, the tribal populations have been using the different parts of *S. acuta* plant as a remedy for dandruff, liver problems, kidney stones, rheumatism, nervous disorders, testicular swelling and elephantitis.^[28-31] It is also used as a medication for fever, asthma, ulcers, dysentery, malaria, venereal diseases and renal inflammations.^[32] Fresh leaf juices have been extensively used as anti-helminthic medicines and in treating gastric disorders.^[33-35] The presence of phytochemical constituents such as saponins, tannins, alkaloids, flavonoids, phytates, phenols, oxalate, terpenoids, glycosides and steroids were reported in *S. acuta*.^[36] The plant extract of *S. acuta* reported to have an antimicrobial property and several studies have proved the significant activity against the microorganism *Staphylococcus aureus*, *Escherichia coli*, *Bacillus subtilis* and *Mycobacterium phlei*.^[37] It was also indicated that the property of antibacterial and antimalarial of the methanolic leaf extract of *S. acuta* are due to the presence of phytoconstituents such as alkaloids, flavonoids, terpenoids and glycosides.^[38] Also, several studies have reported the use of ethanol as relatively safer solvent in the extraction process and useful in extracting wide class of compounds.^[39,40] Therefore, the present study focuses on extracting compounds using ethanol and identifying the phytocomponents from ethanolic leaf extract of *S. acuta* using GC-MS techniques. Further, *in-silico* molecular docking was performed to identify the functionally active compounds with antibacterial potentials on *E. coli* protein. However, to the best of our knowledge, there is no report on the molecular docking studies of bioactive compounds of *S. acuta* on *E. coli* protein.

MATERIALS AND METHODS

Collection of Plant Material

The plant *S. acuta* was collected in and around Nagercoil, Kanyakumari district, Tamil Nadu, India. The plant was

identified by Dr. S. Jeeva, Department of Botany, Scott Christian College (Autonomous), Nagercoil and the leaves collected were brought to Department of Zoology and Research Centre, Scott Christian College (Autonomous), Nagercoil for further analysis.

Preparation of Plant Extract

The leaves were washed thoroughly in tap water and rinsed once with sterile water. The leaves were shade dried at room temperature for 14 days and dried leaves were powdered. Exactly 20 g of leaf powder were extracted by using 200 mL of ethanol solvent in soxhlet apparatus at a moderate temperature of 35 to 50°C. At the end of 18th cycle, the extract was collected, filtered and evaporated with rotary evaporator. For further analysis, the residue was stored at 4°C in the refrigerator.

Preliminary Phytochemical Screening

The ethanolic extract of *S. acuta* was screened for phytochemicals, including carbohydrates, alkaloids, phenols, terpenoids, flavonoids, amino acids, steroids, glycosides, saponins, tannins, quinones, coumarins, anthraquinones, phlobatannins and anthocyanine by using the standard procedure.^[41-49]

Gas Chromatography-Mass Spectrometry (GC-MS) Analysis

The phytoconstituents of the ethanolic leaf extract of *S. acuta* was analyzed by GC-MS analyzer of Thermo Scientific Co., Thermo GC-TRACE ultra, version 5.0, Thermo MsDsQII. About 100 µL of the extract was dissolved in 1-mL of solvent, thoroughly mixed and filtered using a membrane filter. The instrument included DB 35-MS capillary standard non-polar column with dimension, film thickness and ID of 30 m × 0.25 µm × 0.25 mm and carrier gas, helium at flow rate of 1.0 mL/min was used. The plant sample was injected in the split mode at a ratio of 1:10. The injector temperature was maintained at 240°C and the transfer line at 280°C. In the starting the instrument column was programmed at 50°C for 2 minutes, then slowly increased by 5°C/ min to 260°C and finally stabilized at 260°C for 10 minutes. The electron impact mode of the instrument was operated at 70eV. Mass spectral range was set at 42 to 350 (*m/z*). The spectrum obtained in GC-MS were matched and compared with standard spectrum available in the NIST (National Institute of Standards and Technology) library to identify the compounds.^[50]

Molecular Docking

Ligand Selection and Drug Docking

About nine phytocompounds identified through the GC-MS analyzer were taken as ligand based on Lipinski rule of five parameter for the docking studies. The chemical structure of phyto-ligands were retrieved from the PubChem-NCBI database and converted into 3D structure by using online smiles translator.



Selection of Target Protein

About four biomolecules of *E. coli* were selected in order to perform protein modeling studies, 3D structure of *E. coli* biomolecules includes outer membrane porin PhoE protein (PDB-1PHO), inner membrane protein YejM protein (PDB-5I5H), intermembrane phospholipid transport system binding protein MlaD (PDB-5UW2) and probable L,D-transpeptidase YcbB protein (PDB-6NTW) were retrieved from Protein Data Bank and viewed through Discovery Studio software.

Docking Studies

Finally binding affinity for the target protein of *E. coli* and phytocompounds (ligands) of *S. acuta* were performed using Auto Dock Vina (version 4).

RESULTS

Preliminary Phytochemical Screening

The qualitative phytochemical study revealed the presence of carbohydrates, alkaloids, phenols, terpenoids, flavonoids, amino acid, steroids, glycoside, saponins, quinones and coumarins in *S. acuta* (Table 1).

Gas Chromatography-Mass Spectrometry (GC-MS) Analysis

The GC-MS chromatogram of the ethanolic extract of *S. acuta* recorded a total of 30 peaks, each peak designated the phytocompounds corresponding to their retention time, peak area, height, molecular weight, molecular formula and mass spectral records of the known compounds recorded by the National Institute of Standards and Technology (NIST) library (Table 2) (Fig. 1).

Table 1: Preliminary phytochemical screening of *S. acuta* leaves

Phytochemicals	<i>S. acuta</i>
Carbohydrates	+
Alkaloids	+
Phenols	+
Terpenoids	+
Flavonoids	+
Amino acid	+
Steroids	+
Glycoside	+
Saponins	+
Tannins	-
Quinones	+
Coumarins	+
Anthraquinones	-
Phlobatannins	-
Anthocyanine	-

In-silico Molecular Docking Studies

Further, based on the Lipinski's rule of five parameters, 9 bioactive compounds were identified from the GC-MS analysis of *S. acuta* and were used for molecular docking with biomolecules 1PHO, 5I5H, 5UW2 and 6NTW of *E. coli*. The *E. coli* protein 1PHO, 5I5H, 5UW2 and 6NTW retrieved from Protein Data Bank, <http://www.rcsb.org/> were shown in Fig. 4. The selected bioactive compounds 2D structure were retrieved from PubChem database. Structures of 9 bioactive compounds were shown in Fig. 2. Ciprofloxacin and Levofloxacin were used as standard controls and the chemical structure were shown in Fig. 3. The binding pattern of 1PHO, 5I5H, 5UW2 and 6 NTW protein with ligands varies according to the nature of ligand (Fig. 4). The docking score result of bioactive compounds were shown in Table 3 and the best four interaction complex for each protein target and the residues involved in the bonded interactions and non-bonded interactions are given in Table 4. 2D and 3D interaction between protein and ligand are shown in Fig. 5.

DISCUSSION

Gram-negative bacteria are highly resistant to antibiotics due to the asymmetrical composition of lipids in cytoplasmic membrane, peptidoglycan layer and the outer membrane of the cell envelope.^[51] Gram negative bacteria are known to possess high resistance against synthetic drugs and are the major causes for heavy causalities than gram-positive bacteria.^[52,53] Recently, phytochemical compounds replace synthetic drugs and antibiotics in the management of gram-negative organisms that causes human diseases. The Gram-negative bacterium *E. coli* protein, which have been used in the present docking study, is a food-borne pathogen causing diarrhea, gastro-intestines, and a series of other problems.^[54] A study in South Africa reported 85.7% of *E. coli* isolated from HIV-infected kids was resistant to the prophylactic drug, cotrimoxazole.^[55] The resistance developed by *E. coli* and similar gram-negative bacteria against synthetic drugs made researchers to opt for alternative medicines with less side effects and

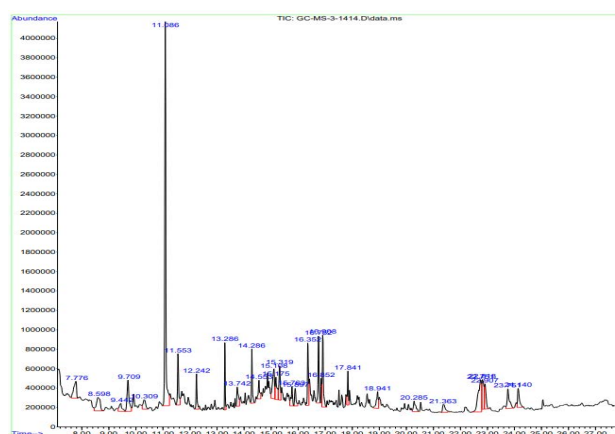


Fig. 1: GC-MS chromatogram of ethanolic leaf extract of *S. acuta*

Table 2: The phytochemicals identified from GC-MS analysis of the ethanolic extract of *S. acuta* leaves

S. No.	Retention Time (min)	Compound Name	Molecular Formula	Molecular Weight (g/mol)	Percent area	PubChem (CID)
1	7.776	Methanaminium, 1-carboxy-N,N,N-trimethyl-, hydroxide, inner salt	C ₅ H ₁₁ NO ₂	117.15	2.92	247
2	8.598	4H-Pyran-4-one, 2,3-dihydro-3,5-dihydroxy-6-methyl	C ₆ H ₈ O ₄	144.12	3.06	119838
3	9.442	Cyclohexanol, 3,5-dimethoxy-, stereoisomer	C ₈ H ₁₆ O ₃	160.21	1.29	547125
4	9.709	Benzofuran, 2,3-dihydro-	C ₈ H ₈ O	120.15	3.76	10329
5	10.309	1-Buten-3-yne, 2-methyl-	C ₅ H ₆	66.10	1.43	62323
6	11.086	2-Methoxy-4-vinylphenol	C ₉ H ₁₀ O ₂	150.17	24.88	332
7	11.553	Phenol, 2,6-dimethoxy-	C ₈ H ₁₀ O ₃	154.16	3.39	7041
8	12.242	1-(3,6,6-Trimethyl-1,6,7,7a-tetrahydrocyclopenta[c]pyran-1-yl)ethanone	C ₁₃ H ₁₈ O ₂	206.28	2.03	605654
9	13.742	2-Ethyl-5-propylcyclopentanone	C ₁₀ H ₁₈ O	154.25	1.88	574441
10	14.286	2,3,5,6-Tetrafluoroanisole	C ₇ H ₄ F ₄ O	180.1	2.60	75351
11	14.553	Tricyclo[4.2.2.0(2,5)]dec-7-ene, 7-butyl	C ₁₄ H ₂₂	190.32	1.54	561940
12	15.108	d-Glycero-l-gluco-heptose	C ₇ H ₁₄ O ₇	210.18	3.65	21139463
13	15.175	Methyl. beta.-d-galactopyranoside	C ₇ H ₁₄ O ₆	194.18	2.33	2108
14	15.319	Methyl-(2-hydroxy-3-ethoxy-benzyl)ether	C ₁₀ H ₁₄ O ₃	182.22	2.74	586449
15	15.897	1H-Indole, 2-(2-pyridinyl)-	C ₁₃ H ₁₀ N ₂	194.23	1.50	270302
16	16.352	4-((1E)-3-Hydroxy-1-propenyl)-2-methoxyphenol	C ₁₀ H ₁₂ O ₃	180.20	4.07	91753526
17	16.752	5-Ethylcyclopent-1-ene-1-carboxylic acid	C ₈ H ₁₂ O ₂	140.18	3.89	574024
18	16.852	2-(2-Bromoethyl)-3-methyl-oxirane	C ₅ H ₉ BrO	165.03	1.27	558912
19	16.908	Guaifenesin	C ₁₀ H ₁₄ O ₄	198.22	4.40	3516
20	18.941	3-Phenylbicyclo(3.2.2)nona-3,6-dien-2-one	C ₁₅ H ₁₄ O	210.27	1.86	610888
21	20.285	1H-Cyclopropa[a]naphthalene, 1a,2,3,5,6,7,7a,7b-octahydro-1,1,7,7a-tetramethyl-, [1aR-(1a.alpha.,7a.alpha.,7b.alpha.)]-	C ₁₅ H ₂₄	204.35	1.41	6432176
22	21.363	Methyl 2-O-benzyl-d-arabinofuranoside	C ₁₃ H ₁₈ O ₅	254.28	1.35	22215008
23	22.751	beta.-Sitosterol	C ₂₉ H ₅₀ O	414.7	6.46	222284
24	22.907	7-Methoxy-1,2,3-trimethylindole	C ₁₂ H ₁₅ NO	189.25	2.26	605096
25	23.751	4-Pyridinamine, N-(1-naphthalenylmethylidene)-	C ₁₆ H ₁₂ N ₂	232.28	2.56	6425626
26	23.751	5H-Imidazo(2,1-a)isoindole, 2-phenyl-	C ₁₆ H ₁₂ N ₂	232.28	2.56	162928
27	23.751	Phenol, 3,5-bis(1-pyrrolidinyl)-	C ₁₄ H ₂₀ N ₂ O	232.32	2.56	616044
28	24.140	Acetonitrile, 2-(6-phenantridinyl)-	C ₁₅ H ₁₀ N ₂	218.25	2.09	612758
29	24.140	Benzimidazo[2,1-a]isoquinoline	C ₁₅ H ₁₀ N ₂	218.25	2.09	612818
30	24.140	Pyrido[1,2-a]pyrimidine	C ₁₅ H ₁₀ N ₂	218.25	2.09	612675

cost. Many studies on traditional medicines reported the availability of a wide spectrum of phytoconstituents as antimicrobial agents against pathogenic microbes.^[56] Though the exact mechanisms of plant compounds in inhibiting the growth of microbes are undetermined, few studies have reported that the antimicrobial property of the plant compounds are due to their ability to inhibit nucleic acid synthesis, restrict the function of the cytoplasmic membrane and non-detrimental role in energy metabolism.^[57] Phytochemicals are known to have a broad spectrum of antibacterial properties.^[58]

The present study's qualitative phytochemical test of *S. acuta* leaves revealed the presence of carbohydrates, alkaloids, phenols, terpenoids, amino acids, steroids, glycoside, saponins, quinones, flavonoids and coumarins. Palaksha *et al.*^[59] reported the presence of phytoconstituents such as alkaloids, carbohydrates, phytosterols, saponins, fixed oils, tannins, and flavonoids in the ethanolic leaf extract of *S. acuta* from East Godavari district, Andhra Pradesh, India. Tannins were found to be absent in the ethanolic leaf extract of *S. acuta*. This variation in the phytoconstituent compositions might be attributed to the difference in



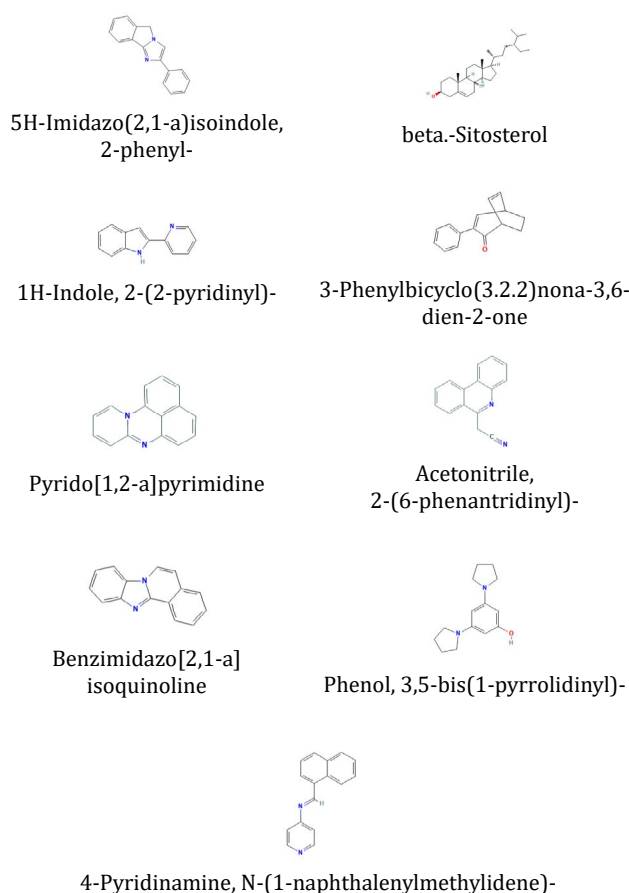


Fig. 2: Structure of bioactive compounds identified from *S. acuta* for the analysis of molecular docking. (Photo Courtesy: <http://www.pubchem.ncbi.nlm.nih.gov/>)

climatic conditions under which the plant grew or due to the stage of the plant.^[60,61] Multiple factors are involved in the extraction of bioactive compounds from plants such as solvent selection, phytoconstituents chemistry, extraction technique, time and temperature.^[62] Major phytoconstituents, such as flavonoids, possess antioxidant, antibacterial, antifungal, antiviral, antiallergic, antitumor and antithrombotic properties, whereas the phenols were observed to have potential antioxidant and free radical scavenging activities. The alkaloids act as analgesic and antimicrobial agents.^[63,64] Saponins contribute to antibacterial, antidiabetic, anti-inflammatory and anticancer activities.^[65] Tannins are reported to have inhibitory action on bacterial growth of *E. coli*, *Vibrio cholera*, *S. aureus*, *Bacillus cereus* and *Streptococcus faecalis*.^[66-68] The presence of these phytoconstituents in the extracts of *S. acuta* might be responsible for contributing therapeutic value to the plant.

The GC-MS analysis of the ethanolic leaf extract of *S. acuta* led to the identification of 30 components, many of which with therapeutic properties. Based on Dr. Duke's Phytochemical and Ethnobotanical Databases, Methanaminium, 1-carboxy-N,N,N-trimethyl-, hydroxide,



Fig. 3: Structure of Ciprofloxacin and Levofloxacin used for the analysis of molecular docking. (Photo Courtesy: <http://www.pubchem.ncbi.nlm.nih.gov/>)

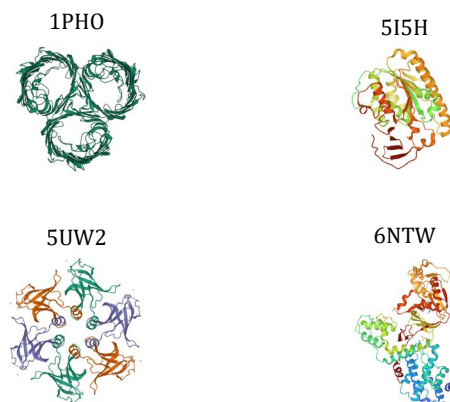


Fig. 4: The target Protein 1PHO, 515H, 5UW2 and 6NTW (Photo Courtesy: Protein Data Bank, <http://www.rcsb.org/>)

inner salt, a nitrogen compound have been reported to possess antimicrobial property, 1-(3,6,6-Trimethyl-1,6,7,7a-tetrahydrocyclopenta[c]pyran-1-yl)ethenone has antihistamine activity, 4-((1E)-3-Hydroxy-1-propenyl)-2-methoxyphenol, a phenolic compound, possesses antimicrobial, antioxidant, anti-inflammatory and antifungal activities. Similarly, beta-sitosterol possesses antimicrobial, anti-inflammatory, anticancer, antiasthma, diuretic and hepatoprotective activities. A study reported that beta-sitosterol with hypoglycemic activity promotes the synthesis of serum insulin with an inhibitory effect on the α -amylase enzyme.^[69,70] The phenolic compound, phenol,2,6-dimethoxy isolated from *Rhizophora apiculata* is reported to have significant antioxidant activity.^[71] A previous study suggested that the antibacterial and antioxidant effect of *Litchi chinensis*, wood vinegar is due to phenol,2,6-dimethoxy.^[72] Through the suppression of NF- κ B and MAPK activation, and histone acetylation proved that 2-methoxy-4-vinylphenol isolated from pine needles have anti-inflammatory activity.^[73] A study reported the antineoplastic activity associated with ellipticine retained with heterocyclic compound, Benzimidazo[2,1-a]isoquinoline. Pyrido[1,2-a]pyrimidine with insecticidal activity against *Aphis craccivora* and *Sogatella furcifera*.^[74]

The identification of bioactive compounds with antimicrobial properties and less toxicity is an elaborated study that would consume more time. Hence, utilizing *in-silico* computational approaches such as molecular docking, chemo informatics and artificial intelligence has

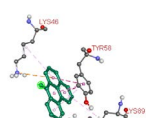
Table 3: Molecular docking score for bioactive compounds of *S. acuta* with 1PHO, 5I5H, 5UW2 and 6NTW

S.No.	Compound Name	Pubchem ID	1PHO	5I5H	5UW2	6NTW
			Docking score in Kcal/mol			
1	5H-Imidazo(2,1-a)isoindole, 2-phenyl-	162928	-7.6	-7.2	-6.4	-7.1w
2	beta.-Sitosterol	222284	-7.8	-7.3	-5.8	-7.2
3	1H-Indole, 2-(2-pyridinyl)-	270302	-6.9	-7.3	-6.2	-6.7
4	3-Phenylbicyclo(3.2.2)nona-3,6-dien-2-one	610888	-6.6	-7.9	-5.9	-6.6
5	Pyrido[1,2-a]pyrimidine	612675	-8.1	-7.6	-6.1	-7.5
6	Acetonitrile, 2-(6-phenantridinyl)-	612758	-7.5	-8	-6.1	-6.5
7	Benzimidazo[2,1-a]isoquinoline	612818	-7.8	-7.6	-6.3	-7.4
8	Phenol, 3,5-bis(1-pyrrolidinyl)-	616044	-6.3	-6.6	-5.7	-6.2
9	4-Pyridinamine, N-(1-naphthalenylmethylidene)-	6425626	-7.9	-7.3	-6.2	-7.4
Standard Drugs						
10	Ciprofloxacin	2764	-7.6	-7.2	-6.1	-7.5
11	Levofloxacin	149096	-7.6	-7.9	-7.1	-7.6

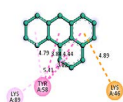
Table 4: The best four interaction complex for each protein with residues involved in bonded and non-bonded interactions

S.No	Complex	Docking Score (-kcal/mol)	No of H Bonds	No of Alkyl Bonds	Residues involved in Bonded Interactions	Residues involved in Non-Bonded Interactions
1	1PHO-612675	-8.1	-	3	-	Lys46, Tyr58, Lys89
2	1PHO -6425626	-7.9	1	4	Lys10	Lys46, Glu48, Tyr58, Lys89
3	1PHO-222284	-7.8	-	4	-	Lys46, Tyr58, Arg60, Phe85
4	1PHO-612818	-7.8	-	2	-	Tyr58, Asp97
5	5I5H-612758	-8.0	1	2	Asp406	Phe412, Ile453
6	5I5H-610888	-7.9	-	2	-	Phe412, Ile453
7	5I5H-612675	-7.6	1	3	Pro454	Asp406, Phe412, Ile453
8	5I5H- 612818	-7.6	1	1	Asp406	Phe412
9	5UW2 - 162928	-6.4	1	3	Ile101	Arg102, Ala140, Met141
10	5UW2-612818	-6.3	1	4	Asn91	Tyr40, Gln88, Ile127, Lys129
11	5UW2- 270302	-6.2	2	4	Asn91, Leu128	Tyr40, Gln88, Ile127, Lys129
12	5UW2- 6425626	-6.2	1	3	Gln88	Tyr40, Gln88, Lys129, Asp130
13	6NTW- 612675	-7.5	1	3	Asp230	Ala226, Leu227, Pro352
14	6NTW- 612818	-7.4	1	4	Asp230	Ala226, Leu227, Trp234, Pro352
15	6NTW-6425626	-7.4	-	4	-	Ala226, Leu227, Pro352, Arg586
16	6NTW-222284	-7.2	-	3	-	Ala343, Trp347, Pro599
17	1PHO- 2764	-7.6	2	4	Ser95, Arg140	Lys46, Glu48, Tyr58, Phe85
18	5I5H- 2764	-7.2	2	3	Ser407, Arg451	Asp406, Phe412, Pro454
19	5UW2- 2764	-6.1	3	-	Gly51, Gln110, Met141	-
20	6NTW- 2764	-7.5	2	3	Tyr446, Arg490	Asp435, Pro512
21	1PHO- 149096	-7.6	5	1	Lys46, Tyr58, Ser95, Asp97, Arg140	Glu48
22	5I5H- 149096	-7.9	1	5	Arg451	Ile404, Asp406, Phe412, Gly452, Ile453
23	5UW2- 149096	-7.1	1	4	Gly51	Ile101, Thr103, Ala140, Gln110
24	6NTW- 149096	-7.6	-	1	-	Pro512

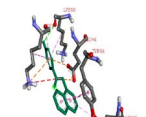
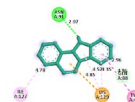




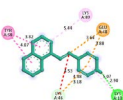
Pyrido[1,2-a]pyrimidine with 1PHO (- 8.1 Kcal/mol)



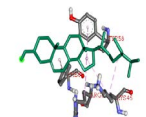
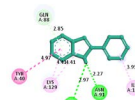
Benzimidazo[2,1-a]isoquinoline with 5UW2 (- 6.3 Kcal/mol)



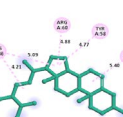
4-Pyridinamine, N-(1-naphthalenylmethylidene) with 1PHO (- 7.9 Kcal/mol)z



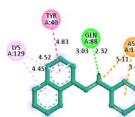
1H-Indole, 2-(2-pyridinyl) with 5UW2 (- 6.2 Kcal/mol)



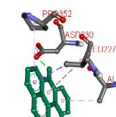
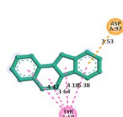
beta-Sitosterol with 1PHO (- 7.8 Kcal/mol)v



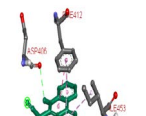
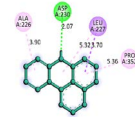
4-Pyridinamine, N-(1-naphthalenylmethylidene) with 5UW2 (- 6.2 Kcal/mol)



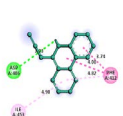
Benzimidazo[2,1-a]isoquinoline with 1PHO (- 7.8 Kcal/mol)



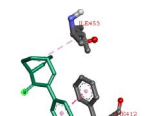
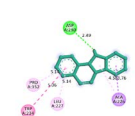
Pyrido[1,2-a]pyrimidine with 6NTW (- 7.5 Kcal/mol)



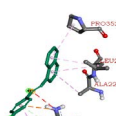
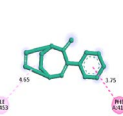
Acetonitrile, 2-(6-phenantridinyl) with 515H (- 8.0 Kcal/mol)



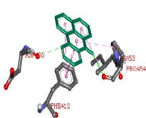
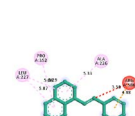
Benzimidazo[2,1-a]isoquinoline with 6NTW (- 7.4 Kcal/mol)



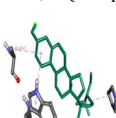
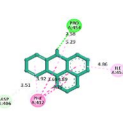
3-Phenylbicyclo[3.2.2]nona-3,6-dien-2-one with 515H (- 7.9 Kcal/mol)



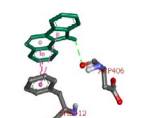
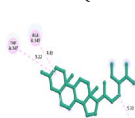
4-Pyridinamine, N-(1-naphthalenylmethylidene) with 6NTW (-7.4 Kcal/mol)



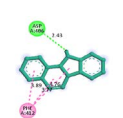
Pyrido[1,2-a]pyrimidine with 515H (- 7.6 Kcal/mol)



beta-Sitosterol with 6NTW (-7.2 Kcal/mol)



Benzimidazo[2,1-a]isoquinoline with 515H (- 7.6 Kcal/mol)



5H-Imidazo[2,1-a]isoindole, 2-phenyl with 5UW2-162928 (- 6.4 Kcal/mol)

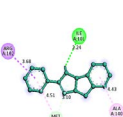


Fig. 5: The 2D interaction and 3D docked complex of the ligands with *E. coli* proteins

greatly increased during the last decade in the sector of design, development, and discovery of medicine.^[75,76] The molecular docking studies makes it easier and provides

in depth understanding about the molecular interactions along with docking score to know the affinity of the ligands with proteins.^[77,78] Several molecular docking approaches have enabled virtual screening of protein and ligand interactions which would help discover suitable pharmaceutical agents with high output, within a short duration and in a cost-effective manner.^[75,79] In the present investigation, 9 phytocompounds from *S. acuta* have been docked against four *E. coli* protein- 1PHO, 515H, 5UW2, 6NTW to find out potential phytocompounds with good

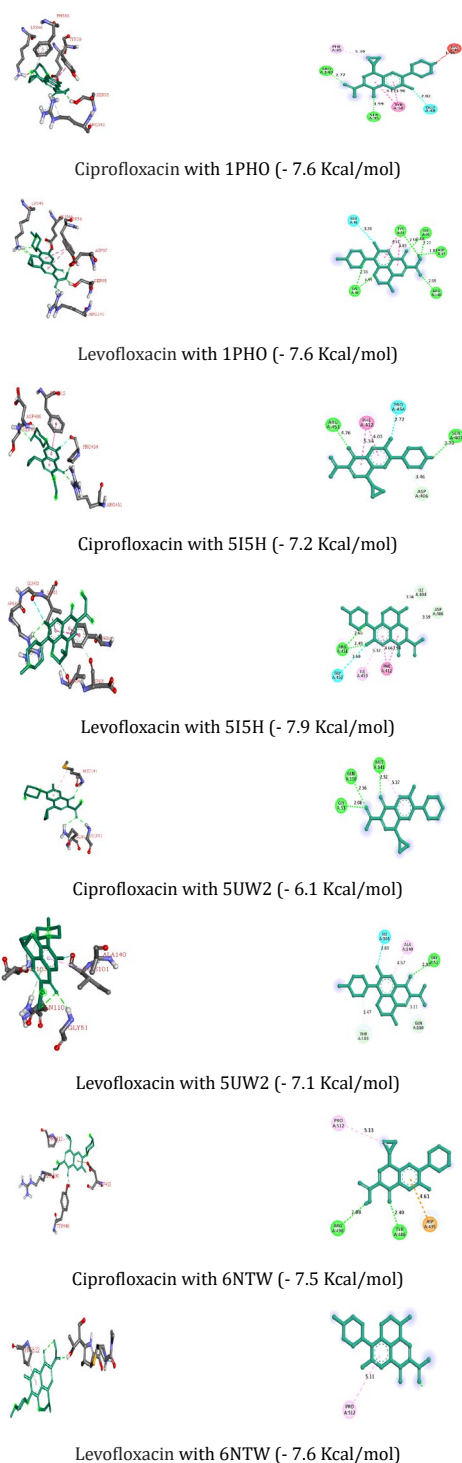


Fig. 6: The 2D interaction and 3D docked complex of the ligands (Standard drugs Ciprofloxacin and Levofloxacin) with *E. coli* proteins

binding affinities. The result has been compared with antibiotic compounds, ciprofloxacin and levofloxacin. 1PHO shows higher binding affinity of -8.1 Kcal/mol with a ligand, pyrido[1,2-a]pyrimidine by non-bonded interaction with amino acid residues Lys46, Tyr58

and Lys89. Ciprofloxacin showed binding affinity of -7.6 Kcal/mol with 1PHO by hydrogen bonds with amino acid residues Ser95 and Arg140, and four non-bonded interaction with amino acid residues Lys46, Glu48, Tyr58 and Phe85. Another antibiotic compound, levofloxacin showed docking score of -7.6 Kcal/mol when interacting with 1PHO. The interaction led to the formation of five bonded interactions with Lys46, Tyr58, Ser95, Asp97 and Arg140, and one non-bonded interaction with Glu48. 5I5H showed higher binding affinity of -8.0 Kcal/mol with ligand acetonitrile, 2-(6-phenantridiny)- (Fig. 3) than the control which showed -7.2 Kcal/mol. 5I5H formed a hydrogen bond interaction with the amino acid residue Asp406 and non-bonded interaction with amino acid residues Phe412 and Ile453. Ciprofloxacin interacting with 5I5H, showed two hydrogen bonds with amino acid residues Ser95 and Arg140, and three alkyl bonds with amino acid residues such as Asp406, Phe412 and Pro454, the docking score was -7.2 kcal/mol but levofloxacin showed docking score of -7.9 with bonded interaction with amino residue Arg451 and non-bonded interaction with amino residues Ile404, Asp406, Phe412, Gly452 and Ile453. One hydrogen bond was formed with Ile101 and three alkyl bonds were formed with amino acid residues such as Arg102, Ala140, Met141 when 5UW2 interacted with 5H-Imidazo(2,1-a)isoindole, 2-phenyl- (Fig. 4). The docking score was -6.4 Kcal/mol. The antibiotic compound, Ciprofloxacin interacted with amino acid residues such as Gly51, Gln110 and Met141 by forming three hydrogen bonds but Levofloxacin showed non-bonded interaction with Ile101, Thr103, Ala140 and Gln110, and hydrogen bond interaction with amino acid Gly51. The protein of *E. coli*, 6NTW interacted with pyrido[1,2-a]pyrimidine by forming one hydrogen bond and three alkyl bond with amino acid residues Asp230 and Ala226, Leu227, Pro352, respectively, the docking score was -7.5 Kcal/mol, where the interaction of ciprofloxacin with 6NTW also showed the same docking score (Fig. 5). Ciprofloxacin showed bonded interaction with two amino acid residues (Tyr446 and Arg490) and two non-bonded interactions with residues Asp435 and Pro512. Levofloxacin showed affinity of -7.6 Kcal/mol by the formation of an alkyl bond with Pro512. The phytocompounds of *S. acuta* showed better affinity towards the *E. coli* protein than the antibiotic compounds which was similar to the molecular docking study reported on the phytocompounds of *Lantana camara* towards *E. coli* protein 1PHO, 5I5H, 5UW2 and 6NTW.^[80]

CONCLUSION

The present investigation clearly revealed that phytochemical of ethanolic leaf extract of *S. acuta* has considerable antimicrobial activity. The GC-MS result of the *ethanolic leaf extract* of *S. acuta* provided tentative identification of antibacterial compounds such as methanaminium, 1-carboxy-N,N,N-trimethyl-,



hydroxide, inner salt; 4-((1E)-3-Hydroxy-1-propenyl)-2-methoxyphenol; beta-Sitosterol; phenol, 2,6-dimethoxy and other potential biologically active secondary metabolites. The molecular docking showed that the phytoconstituents of this plant has antibacterial potential. The phytochemicals pyrido[1,2-a]pyrimidine possessed highest binding affinity with 1PHO, acetonitrile, 2-(6-phenantridinyl) showed best binding affinity with 5I5H, 5H-Imidazo(2,1-a)isoindole, 2-phenyl has still better affinity with 5UW2 and Pyrido[1,2-a]pyrimidine showed good binding affinity with 6NTW. Thus, our study suggests that ethanolic leaf extract of *S. acuta* contains many phytochemical compounds with antibacterial property and may be utilized as a therapeutical source for developing beneficial drugs. However, further research on *in-vitro* screening of pharmacological activities, fractionation, isolation of pure compounds from the extract of *S. acuta* is in progress.

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CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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