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GC-MS analysis, molecular docking with Human TGF-β Receptor I, and the prediction of pharmacokinetic properties of active compounds isolated from *Musa balbisiana* Colla fruit pulp extracts

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Abstract

This study was aimed at identifying phytochemical compounds from the methanolic fruit extract of *Musa balbisiana* Colla, along with molecular docking of these compounds with the target protein transforming growth factor -beta type I receptor, responsible for hepatic and renal fibrosis. *Musa balbisiana* Colla is a plantain native to Southeast Asia, famous for nutritional and therapeutic properties. Gas chromatography-mass spectroscopy (GC-MS) was used to identify the phytochemical compounds of methanolic fruit pulp extract of *Musa balbisiana* Colla. The pharmacokinetic properties of these compounds were also evaluated to predict its drug-likeness via Swiss ADME. Toxicity profile of the short-listed compounds was assessed by Protox-II. Molecular docking of the compounds was carried out by the Autodock vina tool. Two best phytochemical compounds namely, Hexanoic acid, 1-cyclopentylethyl ester (binding affinity -6.4 kcal/ mol) and 5-hexenoic acid (binding affinity -8.3 kcal/ mol) exhibited an incredibly excellent binding affinity with transforming growth factor -beta type I receptor. Thus, Hexanoic acid, 1-cyclopentylethyl ester and 5-hexenoic acid from methanolic fruit pulp extract of *Musa balbisiana* Colla have the ability to bind with transforming growth factor -beta type I receptor and may play a protective role in hepatic and renal diseases associated with fibrosis.

Keywords: phytochemical compound, molecular docking, ADMET, TGF-β, pharmacokinetic

Full-length article **Corresponding Author*, e-mail: *baruahnabanita87@gmail.com*

1. Introduction

Transforming growth factor-beta (TGF-β) is a chief profibrogenic cytokine and also has anti-inflammatory and immunosuppressive effects [1]. It furthermore negatively regulates cell proliferation, induces apoptosis, and governs both hepatic and renal fibrosis [1,2]. It regulates chronic liver disease by mediation of hepatic stellate cells plus activation of fibroblast and deposition of extracellular matrix [3]. TGF-β signals in various phases of liver disease development, right from early hepatic injury to fibrosis and then cirrhosis, followed by hepatocellular carcinoma (HCC). During chronic liver injury, inflammation occurs and macrophage releases TGF-β that aid in transdiffrentiation of hepatic stellate cells toward myofibroblast and results in accumulation of extracellular matrix and thus mediate fibrogenesis. It also governs the process of epithelial -mesenchymal transition that mediate fibrogenesis by increasing myofibroblast. TGF-β behaves as a suppressor during the early stages of HCC, although contributes to tumor development and alters tumor cell plasticity [4].

TGF-β1 acts as a key pro-fibrotic mediator associated with different renal ailments. It drives chronic kidney disease featuring inflammation and renal fibrosis. TGF-β1 triggers generation of enormous extracellular matrix and drops in the tubule-interstitium and the glomeruli. It also brings about the transition of tubular and glomerular epithelial cell to mesenchymal cells. TGF-β1 along with latency-associated peptide (LAP) integrates with the TGF-β binding protein (LTBP) eventually forming an inactive superior complex in extracellular matrix (ECM) which is activated by reactive oxygen species (ROS) by releasing the TGF-β1 and it binds to Type II TGF-β receptor (TβRII) which in turn employs and activates Type I TGF-β receptor (TβRI) and downstream receptor-linked Smads, Smad2, plus Smad3. An oligomeric complex of the phosphorylated Smad2/3 with Smad4 is generated and its translocation to nucleus aids in regulation of inhibitory Smad7 that eventually provokes TGF-β-mediated renal fibrosis and other associated diseases [2]. Hence, development of strategies to inhibit TGF-β1 production or its action should be encouraged as a principal aim to prevent hepatic and renal fibrosis disease progression.

Phytochemical compounds are more efficient than conventional synthetic compounds as novel drug candidate because of their minimal toxicity, more bioavailability, and eminent chemical diversity. Phytochemical compounds are widely maneuvered as antioxidants, antimicrobial,

cardiovascular, immunomodulatory, hepatoprotective, renoprotective and anticancer drugs across the world. However, the innovation of a proficient Phytochemical compounds is a lengthy, laborious process depending on *in vitro* and *in vivo* selection method and this obstacle can be overcome alternatively by, the computational drug discovery approach via an online database, computational algorithm technique which reduces both time and the cost [5]. *Musa balbisiana* Colla is found in wild habitats and also cultivated in South East and Central Asia. It is a member of the family Musaceae. Its fruit is extensively used as food as it is enriched with essential nutrients such as vitamins, minerals, dietary fibers, flavonoids, polyphenols, and carotenoids and has abundant remedial properties [6]. It also has antioxidant, anti-gout, [7], anti-inflammatory and anti-diabetic effects [7,8]. Its fruit also prevents cardiac hypertrophy by modulating inflammation and oxidative stress in the hypertrophic heart [9].

Gas chromatography-mass spectroscopy (GC-MS) is a common investigative method used in the phytochemical analysis of medicinal plants that discovers and recognizes biologically active compounds present in a plant sample [10]. A computational tool called the Swiss ADME is used in the prediction of physicochemical and pharmacokinetic properties of the query compound [11]. The toxicity profile of a query compound can be assessed computationally by Protox II, a free web tool [12]. Molecular docking is an approach to drug designing that revolves around the interactions of drug compounds and target receptors [11].

The primary intention of this current study is to recognize phytochemical compounds from the methanolic extract of *Musa balbisiana* Colla unripe fruits, conduction of molecular docking with TGF-β type I receptor along with the scrutinizing of ADME as well as toxicity profile of the promising phytochemical compounds. This study could open a door for further exploration of the selected phytochemical compounds as novel drug or therapeutic interface for the remedial purpose of protecting the liver and kidneys from hepatic and renal diseases associated with fibrosis.

2. Materials and methods

2.1. Plant material and extract preparation

Unripe fruits of *Musa balbisiana* Colla were collected from Guwahati, Kamrup Metropolitan, Assam India, washed, cut, dried, powdered, and used in the current investigation. Its fine powder (10g) was added to methanol (1:10 ratio) and extracted by cold maceration extraction followed by filtration with Whattman No. 1 filter paper and the filtrate was dried via evaporation resulting in the methanolic extract of *Musa balbisiana* Colla unripe fruit pulp (MBME) and stocked up at 4°C for future use (13). A voucher specimen of the same was submitted to Herbarium of the department of Botany, Gauhati University, Assam, India, for identification and an accession number was provided for the same.

2.2. Gas Chromatography Mass Spectrometry (GC-MS) analysis of MBME

The GC-MS instrument Clarus 680 GC & amp; Clarus 600C MS comprising a liquid auto-sampler manufactured by Perkin Elmer (USA) was used to determine the chemical composition of MBME. TurboMass Ver. 5.4.2 software was used at the system. NIST-2014(data analysis software) was used to analyze the peaks. 'Elite- 5MS' is the capillary column possessing dimensions- length- 60 m, ID- 0.25 mm and film thickness- 0.25 µm and the stationary phase used during the analysis is 5% diphenyl 95% dimethyl polysiloxane. The carrier gas (i.e., mobile phase) was helium gas (99.99%) at 1 ml/minute flow rate. In split less mode, two micro liter injection volumes were utilized. Injector temperature and ion-source temperature were kept at 280 and 180°C correspondingly. The oven temperature was positioned at 60°C for one minute, with an increase at the rate of 7°C/minute to 200°C (held for three minutes) and then again amplified at 10°C /minute rate to 300°C (seized for five minutes). The entire run time was estimated to be ~ 39min. Solvent delay set for eight minutes.

Electron Impact positive (EI+) mode was put at 70 eV to get MS Protocol Mass Spectra. An eight minute's solvent delay was established for an MS scan. 50-600 amu was the mass range or m/z range. The peaks visible in the GC Chromatogram were inferred by the mass spectrum library search of consequent peaks using the National Institute Standard and Technology- 2014 (NIST-2014) database software. The mass spectrums of the unknown components were compared with the spectrum known components of the NIST library and thus the identification of the compounds with the name along with the molecular weight, empirical formula etc. was done successfully.

2.3. In-silico studies

2.3.1. Selection of compounds

A total of 22 compounds out of 58 compounds from the table of the GC-MS compound profiling (remaining compounds were not found in the NCBI database) were selected (Table 1). The phytochemical compounds were docked to Human TGF beta receptor I (PDB ID: 1VJY) using Autodock 4.2 [14].

2.3.2. Pharmacokinetic Properties

Hepatotoxicity, carcinogenicity, immunogenicity, and cytotoxicity of the compounds were analyzed using Protox II [12]. Lead likeliness of the compounds and their violations to drug ability rules, such as Lipinski, Ghose, and Veber, was studied using SwissADME tool [15]. ADME (Absorption, distribution, metabolism, and excretion) properties of the best interacted phytochemical compounds of MBME were analyzed by SwissADME [16].

2.3.3. Docking studies

2.3.3.1. Preparation of ligands for docking

The compounds listed in Table 1 were downloaded from the PubChem database of NCBI (https://www.ncbi.nlm.nih.gov). The compounds were extracted in SDF format and converted to PDB format by the OpenBabel tool [17].

2.3.3.2. Receptor protein preparation

TGF-beta receptor I (Transforming growth factor beta receptor I) is a membrane-bound protein of the TGF-beta receptor family for the TGF beta superfamily of signaling ligands [18]. As a cytokine associated with inflammatory responses in type 2 diabetes mellitus, TGF-β has been recognized as a central player in the diabetic nephropathy being involved in the development of glomerulosclerosis and interstitial fibrosis mostly observed in the case of renal disease. Multifunctional cytokine TGF-β1 controls immunity

related biological actions, differentiation, tumor suppression, and metastasis, senescence, migration, wound healing, apoptosis, cell division, adipogenesis, and osteogenesis [19]. The 3D structure file of the protein, TGF-beta receptor I was downloaded from the PDB database [20] and refined the structure by using the Pymol program [21].

2.3.3.3. Molecular Docking

The protein-ligand docking studies were performed using Autodock 4.2 [14]. The protein was reserved in rigid form, while the compounds (ligands) were kept flexible. Polar hydrogen plus Gasteiger charges were attached to the protein and ligands. AutoDock Tools (v.1.5.6) of the MGL software package were used to prepare PDBQT files for the ligands as well as proteins. The protein-ligand docking complexes were analyzed by the Lamarckian genetic algorithm (LGA) method [22].

The program was run for a total number of 100 genetic algorithms with default settings for all other parameters. Binding energy results of the molecular docking study described the binding affinity represented by the docking score and binding interaction of each ligand on the studied protein target. The binding interactions of the docking complexes were analyzed via the UCSF Chimera version 1.14 and Accelrys Discovery Studio Visualizer (Dassault Systèmes BIOVIA 2017) [23]. For the docking experiment, the grid box was generated with the following specification: X=27.275 Å, Y= 25.00 Å and Z=27.226 Å. The Center of the Grid Box was: X=13.785 Å, Y= -67.349 Å and Z= 3.961 Å.

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3. Results and Discussions

3.1. GC-MS analysis

The GC-MS analysis data of MBME resulted in a chemical spectrum and it was compared with the stored compound data of the NIST library associated with the GC-MS. It resulted in identification of 58 compounds. Among these compounds, leaving aside the non-relevant compounds as well as the compounds whose data are not available in the NCBI database for molecular docking studies, 22 compounds were contemplated for advance study and details are tabulated in the table 1. From the results (table 1), Two compounds out of these, Hexanoic acid, 1-cyclopentylethyl ester and 5-hexenoic acid, displayed a binding affinity to the TGF-β type I receptor, the target protein. These two compounds were observed at the retention time of 6.579.

The names of the selected phytochemical compounds, molecular formula, and weight, along with the PubChem ID and the 2D structure against the TGF-β type I receptor (PDB entry: 1VJY) involved in the development of hepatic plus renal tubulointerstitial fibrosis are revealed in the table 2. The GC–MS chromatogram of the methanolic fruit (unripe) extract of *Musa balbisiana* Colla and the two compounds targeted for the molecular docking study are revealed in the figure 1.

3.2. Docking studies

Molecular docking envisages the structure of the ligand-receptor complex. It implements virtual recognition of compounds and the results are set consistent with the scores. Factors such as bond width, bond angle, dihedral angle, and intermolecular forces affect the docking process [11]. The physiochemical along with pharmacokinetic properties of these compounds were analyzed thoroughly. The 3D structure of target protein TGF-β type I receptor is depicted in figure 2. Total 22 phytochemical compounds out of all the compounds recognized from the GC–MS analysis of MBME were docked with TGF-β type I receptor (excluding the compounds whose data are not available on NCBI database). Based on toxicity analysis, drug ability rule violations and binding affinity of compounds, two compounds were shortlisted. The shortlisted compounds were found with no toxicity, without violations of rules and low binding energy. Name of the shortlisted compounds, their structure, and other physiochemical properties were articulated in the Table 2 and 3, respectively. The binding energy of the shortlisted compounds to the target protein TGF-β type I receptor is given in Table 3. Two compounds showed excellent binding affinity with the TGF-β receptor I target protein. Considering the low binding energy, both the protein-ligand docking complexes, namely 1vjy_ Hexanoic acid, 1-cyclopentylethyl ester and 1vjy_5-Hexenoic acid, are revealed in the figure 3 and 4.

3.2.1. Hexanoic acid-1-cyclopentylethyl ester - Transforming Growth Factor Beta Receptor 1 (TGF β1) Complex

The 2D interaction showed that Hexanoic acid, 1-cyclopentylethyl ester maintained the interaction, co-ordinating with the conventional hydrogen bonds among Asp351 and Lys232 residues of the receptor protein and also favored alkyl coordination with Leu278, Tyr249, Phe262 and Ala350. The interaction also shows π interactions with Val219, Leu340, and Ile211 of the receptor protein (Figure 3).

3.2.2. 5-Hexenoic acid-Transforming Growth Factor Beta Receptor 1 (TGF β1) Complex

The 2D interaction showed that 5 Hexenoic acids maintained the interaction, co-ordinating with the conventional hydrogen bonds among Ser280, Ala 230, Lys232, Asp351 and His283 residues of the receptor protein. The interaction also shows π-sigma interactions with Leu 340 and Val219 of the receptor protein (Figure 4).

3.3. Physicochemical and Pharmacokinetic Properties of the selected compounds

ADMET physicochemical and pharmacokinetic properties of the two interacted phytochemical compounds of MBME were evaluated and documented in the table 4,5,6, and 7. The evaluation of the physicochemical properties is imperative for any phytochemical compound for the confirmation of its drug-likeness [11]. Compounds with molecular weight less than or equal to 500 g/mol are inclined to easier absorption, diffusion, and transport [24]. Lipophilicity is an imperative factor in the discovery and blueprint of drugs. It is an informative property defining solubility and permeability of a drug candidate through membranes, strength, and selectivity. It also affects the metabolism, pharmacokinetics, pharmacodynamic, and toxicity summary of a query compound. High lipophilicity of a compound leads to rapid metabolic turnover, low solubility, and poor absorption, toxicity, plus reduced solubility along with poor metabolic clearance. Low lipophilicity contributes to poor ADMET properties of a drug compound [25].

Table 1: Compound details from GC-MS study of methanolic fruit (unripe) extract of *Musa balbisiana* Colla

Serial no.	Compound name	Retention time	Area	Area%
1	butoxyacetic acid	6.044	7,091,060.5	4.108
2	2-propenoic acid, pentadecyl ester	19.239	1,964,857.2	1.138
3	docosanoic acid, docosyl ester	19.239	1,964,857.2	1.138
4	1r,2c,3t,4t-tetramethyl-cyclohexane	5.018	17,576,332.0	10.182
5	chloroacetic acid, tetradecyl ester	19.239	1,964,857.2	1.138
6	chloroacetic acid, 2-pentadecyl ester	19.239	1,964,857.2	1.138
7	3-trifluoroacetoxy-6-ethyldecane	13.362	2,507,840.2	1.453
8	trifluoromethyl t-butyl disulfide	20.450	7,017,373.5	4.065
9	hexanoic acid, 1-cyclopentylethyl ester	6.579	2,967,564.2	1.719
10	5-hexenoic acid	6.579	2,967,564.2	1.719
11	5-methyl-z-5-docosene	16.443	1,480,523.8	0.858
12	cis-1-chloro-9-octadecene	5.018	17,576,332.0	10.182
13	1-nonylcycloheptane	31.384	456,664.8	0.265
14	hexadecyl nonyl ether	12.591	1,788,469.0	1.036
15	tetracosanoic acid, isobutyl ester	20.650	2,260,703.0	1.310
16	nonyl octacosyl ether	13.147	1,470,638.6	0.852
17	isopropyl hexacosyl ether	19.239	1,964,857.2	1.138
18	heptadecafluorononanoic acid, nonyl ester	12.997	2,092,952.2	1.212
19	heptyl hexadecyl ether	13.362	2,507,840.2	1.453
20	isopropyl triacontyl ether	19.239	1,964,857.2	1.138
21	dotriacontyl isopropyl ether	19.239	1,964,857.2	1.138
22	heptyl octacosyl ether	12.591	1,788,469.0	1.036

Table 2: The phytochemical compounds identified from GC–MS analysis of the methanolic fruit (unripe) extract of *Musa balbisiana* Colla against liver plus renal fibrosis

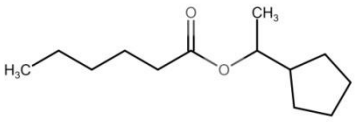
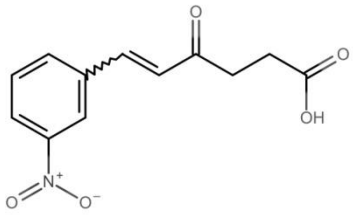
Sl. no	Compound name	PubChem (CID)	Molecular formula	Molecular weight (g/mol)	2D Structure of phytochemical compounds
1	Hexanoic acid, 1-cyclopentylethyl ester	567215	$C_{13}H_{24}O_2$	212.33 g/mol	
2	5-hexenoic acid	5357568	$C_{12}H_{11}NO_5$	249.22 g/mol	

Table 3: Interaction of phytochemical compounds from the methanolic fruit (unripe) extract of *Musa balbisiana* Colla with the target protein TGF-β receptor I

S. no	Compound name	Binding affinity (kcal/ mol)
1	Hexanoic acid, 1-cyclopentylethyl ester	-6.4
2	5-hexenoic acid	-8.3

Table 4: Physicochemical properties of the short-listed phytochemical compounds of MBME

Compound name	Molecular weight (g/mol)	X log P3	TPSA (Å)	Log S (ESOL)	Fraction Csp3	Rotatable bonds	Octanol/Water partition coefficient (logP)	H-bond acceptors	H-bond donors
Hexanoic acid, 1-cyclopentylethyl ester	212.33 g/mol	4.29	26.30 Å^2	-3.40	0.92	7	3.69	2	0
5-hexenoic acid	249.22 g/mol	1.31	100.19 Å^2	-2.06	0.17	6	2.57	5	1

Table 5: Pharmacokinetic properties of identified compounds from MBME

Compound name	Lipinski	Ghose	Veber	Leadlikeness	BBB	HIA	PGP-	Bioavailability score
Hexanoic acid, 1-cyclopentylethyl ester	0	0	0	2	yes	high	yes	0.55
5-hexenoic acid	0	0	0	1	yes	high	yes	0.56

Table 6: Toxicity model report of the selected compounds

Compound name	Predicted LD_{50} (mg/kg)	Toxicity class	Hepatotoxicity	Carcinogenicity	Immunogenicity	Cytotoxicity
Hexanoic acid, 1-cyclopentylethyl ester	5000	5	Inactive	Inactive	Inactive	Inactive
5-hexenoic acid	4400	5	Inactive	Inactive	Inactive	Inactive

Table 7: Cytochrome properties and skin permeation of the selected compounds from MBME

compound name	GI absorption	P-gp substrate	CYP1A2 inhibitor	CYP2C19 inhibitor	CYP2C9 inhibitor	CYP2D6 inhibitor	CYP3A4 inhibitor	Log Kp (skin permeation)
Hexanoic acid, 1-cyclopentylethyl ester	**High**	**no**	**no**	**no**	**yes**	**no**	**no**	**-4.55 cm/s**
5-hexenoic acid	**High**	**no**	**no**	**no**	**no**	**no**	**no**	**-6.89 cm/s**

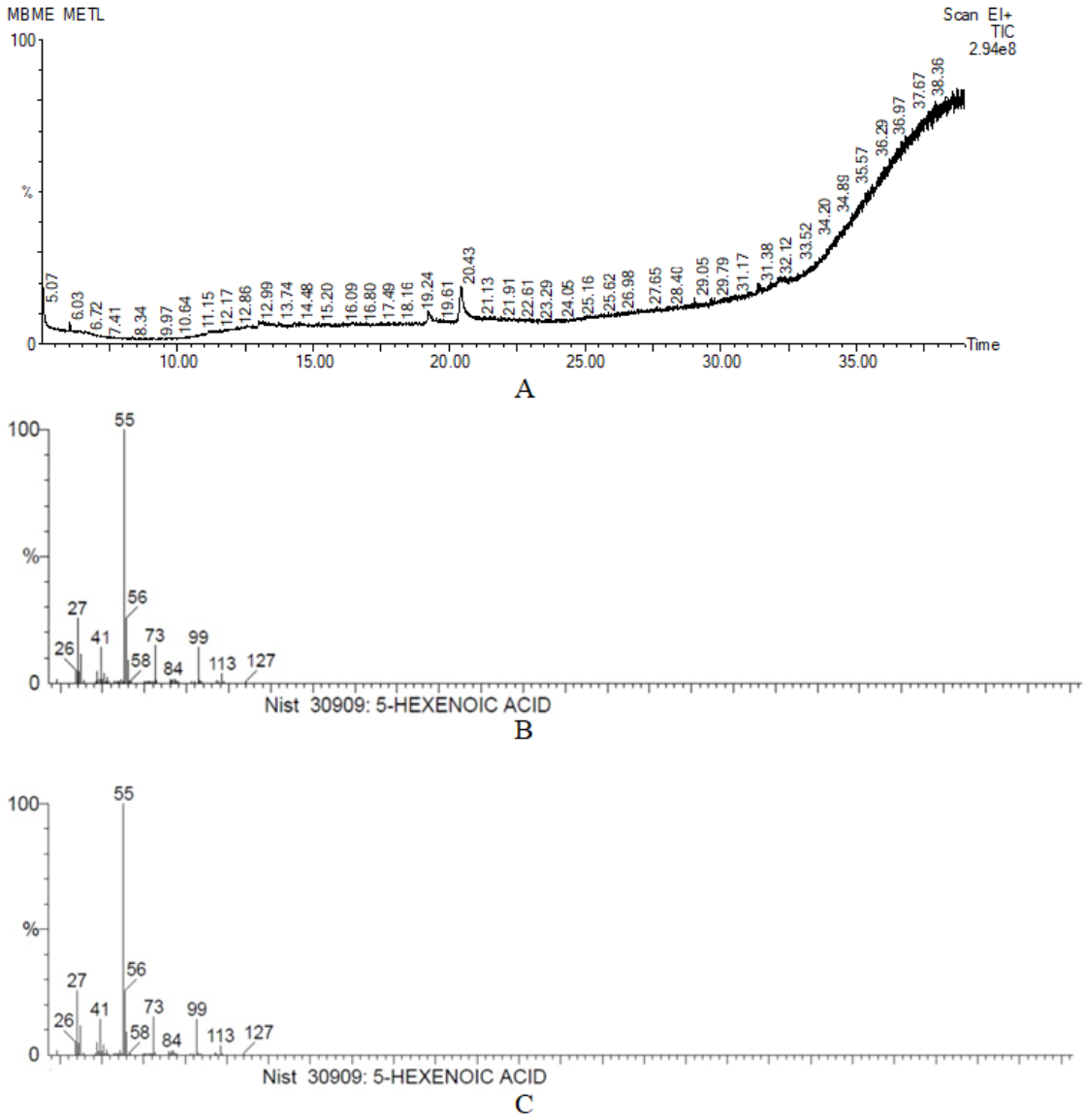


Figure 1: The GC–MS chromatograms: methanolic fruit (unripe) extract of *Musa balbisiana* Colla [A], Hexanoic acid, 1-cyclopentylethyl ester [B], and 5-hexenoic acid [C]

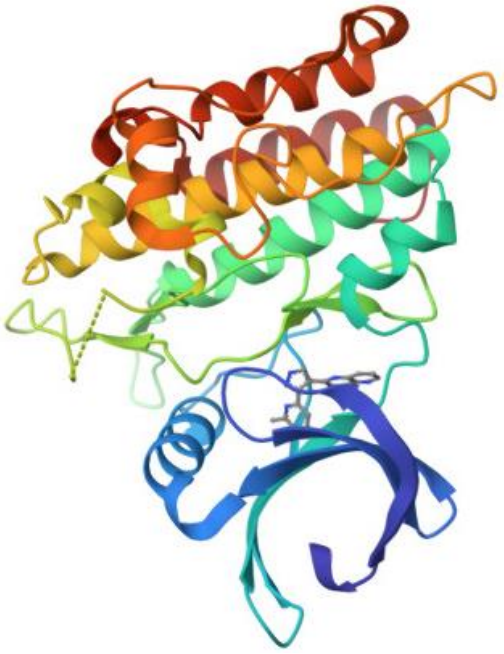


Figure 2: The 3D structure of target protein TGF-β type I receptor (PDB entry: 1VJY)

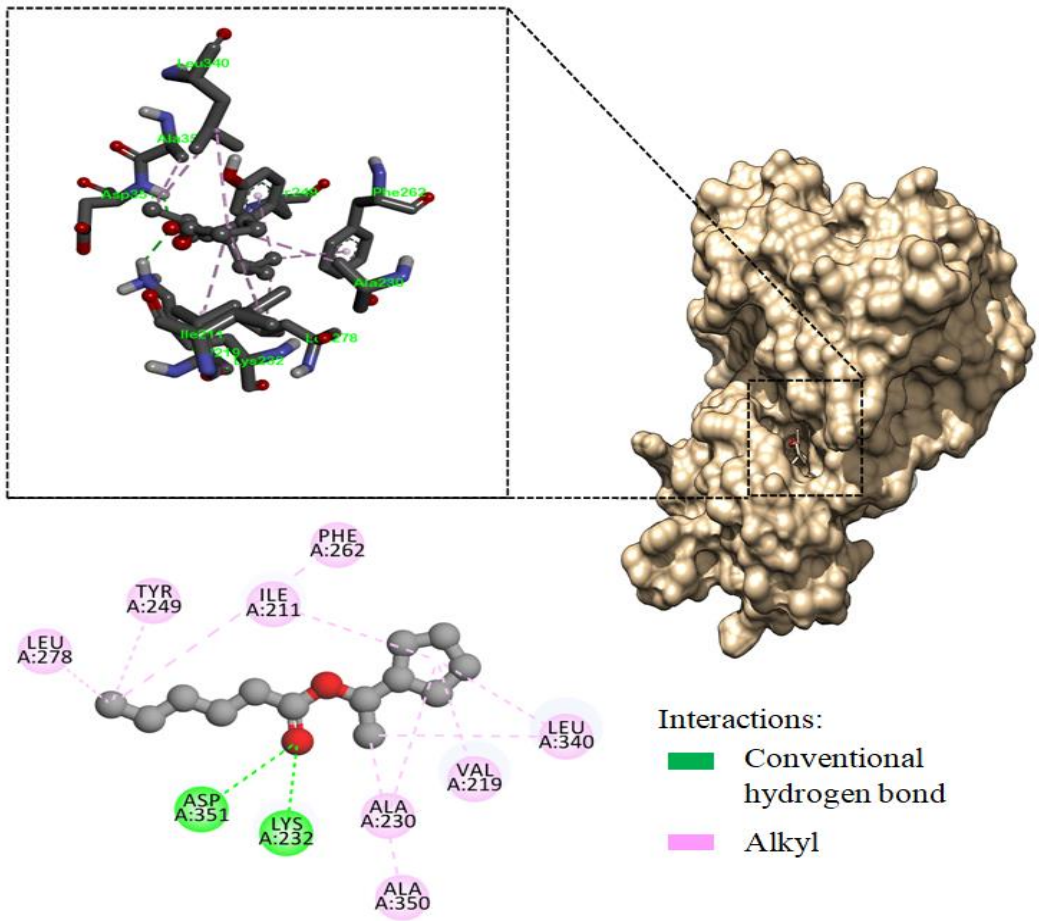


Figure 3: Molecular docking of Hexanoic acid-1-cyclopentylethyl ester with Transforming Growth Factor Beta Receptor 1 (TGF β1) Complex

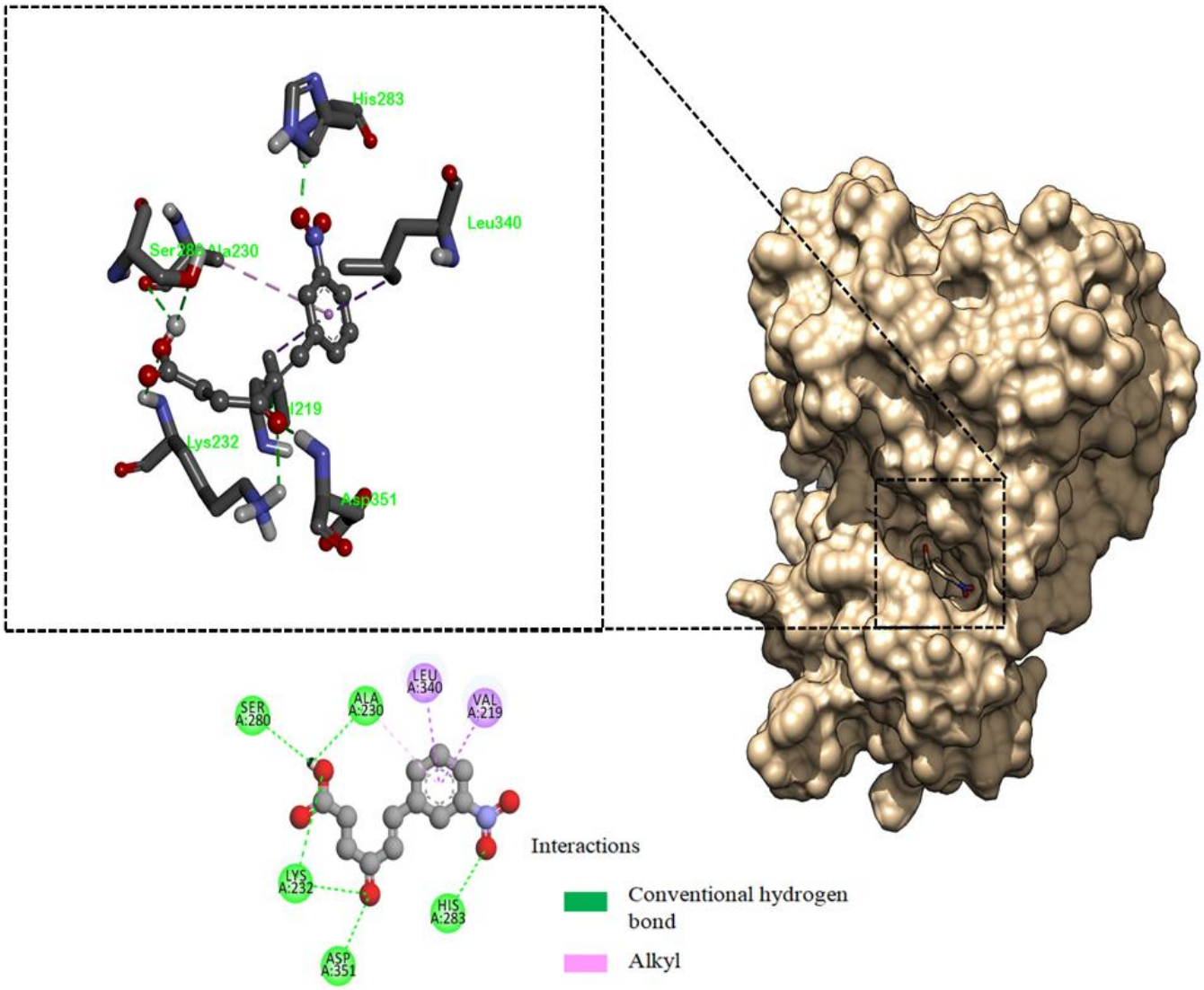


Figure 4: Molecular docking of 5-Hexanoic acid with Transforming Growth Factor Beta Receptor 1 (TGF β1) Complex

The calculated XlogP3 of a query compound in terms of lipophilicity should fall into the array of -0.7 to +6.0. Topological polar surface area (TPSA) is an important molecular descriptor, which is an expedient calculation of the polar surface area in the study of drug transport attributes [26]. The TPSA in regard to polarity of a query compound should be within the range of 20 to 130 Å. The log S (ESOL) determines the solubility of a drug compound which is supposed not to go beyond six. Fraction Csp3 is a molecular descriptor for determining saturation of a drug compound which is a ratio of sp^3 hybridized carbons over the total carbons of the molecule. Fraction Csp3 of a query compound should not be more than 0.25. The compound is also desired not to bear rotatable bonds for more than nine for flexibility [15].

The Octanol/Water partition coefficient (logP) of a compound should not be more than five, total hydrogen bond acceptors and donors not more than 10 and five respectively, consistent with the Lipinski rule of five [24]. This study reveals that both the short-listed compounds had the desired molecular weight, XlogP3, TPSA, log S (ESOL), the number of rotatable bonds, the Octanol/Water partition coefficient (logP), total hydrogen bond acceptor, and donor with the mentioned range. Fraction Csp3 of 5-hexenoic acid was less than 0.25 while in the case of Hexanoic acid, 1-cyclopentylethyl ester, it was beyond 0.25. “Rule of five” (Ro5) properties prepared by Lipinski are exploited as a colander for drug-like compound recognition. The phytochemical compounds selected for docking studies satisfied Lipinski’s rule of five.

The two selected query compounds did not violate the filters, which are Lipinski, Ghose, and Veber, though lead-likeness violation was observed. The Abbot Bioavailability score of the selected two compounds fell

within 55-56% class (Table 7). BBB (blood-brain barrier) separates brain and the bloodstream, which is made up of a layer of microvascular endothelial cells. Drug-like compounds intended to target the central nervous system must cross BBB [11]. Our study revealed that both the selected compounds comprise the potential to cross BBB. HIA (passive human gastrointestinal absorption) is also a key ADME factor that gives a hint about absorption capacity of the drug compound across the human gastrointestinal tract passively [15]. Both the selected compounds revealed high passive human gastrointestinal absorption (HIA). P-glycoproteins (P-gp) are the membrane transporters that help in drug absorption plus excretion. PGP- stands for P-gp non-substrate and the short-listed compounds were non-substrates for P-glycoproteins. It entails that these compounds will not be influenced by P-gp efflux [11,15]. The Abbot Bioavailability score predicts the likelihood of greater than 10% oral bioavailability within the animal models. It comprises four probability classes, which are 11%, 17%, 56%, and 85% [27]. The Abbot Bioavailability score of the selected two compounds fell within 55-56% probability class (Table 7).

Predicted LD_{50} (mg/kg) for Hexanoic acid, 1-cyclopentylethyl ester and 5-hexenoic acid (table 6) revealed the safety of these compounds as LD_{50} (mg/kg) of these compounds is greater than 2000 mg/kg. [28]. These compounds are also non hepato-toxic, non-cytotoxic, non-immunogenic, and non-carcinogenic (table 6). The selected phytochemical compounds also show high gastrointestinal absorption, an essential factor in drug designing, as it also decides the bioavailability of a query compound [11]. Cytochrome P450 monooxygenase enzyme exists in five isoforms: CYP1A2, CYP2C19, CYP2C9, CYP2D6 and CYP3A4 and this enzyme aids in metabolism and elimination of drugs in animals. Hexanoic acid, 1-cyclopentylethyl ester, is a substrate for each isoform except CYP2C9 and 5-hexenoic acid is a substrate for all isoforms of this enzyme. This implies that these compounds are mostly non-inhibitory to this enzyme, hence these become bioavailable when administered orally and produce no adverse effect compound [11].

For the assessment of transdermal administration of a drug, an important parameter called skin permeation expressed as log *K*p. Higher negative log *K*p value signifies less skin permeable capacity of the studied compound. Both the short-listed compounds are reported with the negative values of log *K*p, demonstrating that these are impermeable to the skin compound [11]. On the whole, both the selected compounds Hexanoic acid, 1-cyclopentylethyl ester and 5-hexenoic acid have the ADMET properties, along with drug-like attributes and possess potential binding interaction with the target protein TGF-β receptor I. So far, these two compounds have not been yet reported as anti-fibrotic drug against hepatic and nephrotoxicity.

4. Conclusions

The current investigation reveals that the phytochemical compounds Hexanoic acid, 1-cyclopentylethyl ester and 5-hexenoic acid identified from the *Musa balbisiana* Colla fruit pulp extracts by GC–MS analysis exhibit necessary ADMET properties and entail the potential capacity to prevent hepatic and renal fibrosis via binding with the target protein TGF-β receptor I. thus, it is predicted that these compounds are potential remedial alternative to prevent hepatic and renal ailment. The analyzed pharmacokinetic behavior of the studied compounds adjusts mostly within the tolerable range for human use. As a future prospect of this study, advance structural development, and exploration of these molecules via *in vitro* as well as *in vivo* experimental approaches would be indispensable to clarify whether these molecules represent a suitable therapeutic driving force against hepatic and renal fibrosis.

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