

# In-Silico Pharmacological Assessment of *Pueraria tuberosa* DC

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## ABSTRACT:

*Pueraria tuberosa* DC, a traditional medicinal herb, is widely recognised for its therapeutic benefits. The study aims to estimate the pharmacological probability of its phytochemicals through an extensive ADME (Absorption-Distribution-Metabolism-Excretion) investigation. We discovered substantial bioactive compounds in *Pueraria tuberosa* using the online database IMPPAT (Indian Medicinal Plants, Phytochemistry, and Therapeutics). Our analysis revealed a miscellaneous range of chemical constituents with excellent pharmacological profiles, indicating favourable absorption and distribution properties. The findings accentuate the therapeutic value of *Pueraria tuberosa*, validating its historic use in the management of various diseases. This study corroborates the foundation for further research and drug development efforts by emphasizing the pharmacological properties of its phytochemicals. We conducted a detailed examination of the phytochemicals discovered in *Pueraria tuberosa*, comparing fourteen compounds based on ADME features such as lipophilicity, water solubility, medicinal chemistry, pharmacokinetics, and drug-likeness. Overall, this study advocates for further exploration into *Pueraria tuberosa* as a potential candidate for the development of herbal-based medicines, thereby contributing to the emergent interest in phytomedicine and the quest for novel therapeutic agents.

**Keywords:** ADME, IMPPAT, Pharmacological, Phytomedicine, Phytochemicals, *Pueraria tuberosa*, Therapeutic agents.

## INTRODUCTION

India possesses a rich intellectual and textual inheritance that dates back several centuries. Ayurveda, the Indian aboriginal system of medicine, emanating from the Vedic period (circa 4500-1600 BC), has been an integral part of Indian culture. Plants have long been utilized as a rich source of effective and safe medicines due to their natural healing potential (Thorat and Mishra, 2016). Natural source of chemicals has continuously garnered substantial interest from scientists exploring disease treatments, as these compounds are accountable for the therapeutic properties of plants. Biochemical compounds synthesized by plants exhibit pharmacological activities (Mishra and Thorat, 2017; Bultum et al., 2022). Phytochemicals, exclusively, have been recognized for their multifaceted biological activities, including antioxidant, antimicrobial, anticancer, and anti-inflammatory properties (Sharma et al., 2018; Kowalska). These phytochemicals, along with other natural products, represent a biologically relevant chemical space produced by numerous organisms that have evolved to accomplish high levels of fitness under assorted

selective pressures. This characteristic of phytochemicals has intrigued scientists, inspiring them to identify and develop pharmacological agents for various health conditions (Varma et al., 2023).

*Pueraria tuberosa* DC, a perennial plant of the family Fabaceae, is scattered throughout Southeast Asia (Maji et al., 2014). It is known by numerous vernacular names, including Bhuikumbhada, Bīlaikānda, Surāl, Vidāri, Vidārīkand and Pātāl kohada. In ancient Ayurvedic texts, it is mentioned by different Sanskrit names such as Kṣhīrvallī, Sīta, Swādūkānda, Ikṣugandhā, Gajavājipriyā, Krośtri, Kāṇḍapalāśa, Kṣhīrśukla, Payśvini, Swādūkānda, and Vidārī (Thorat and Mishra, 2016). The plant's rhizome/tuber is extensively used in ethno-medicine as well as in traditional systems of medicine, principally in Ayurveda (Maji et al., 2014). *Pueraria* species are highly esteemed for their health and cosmetic benefits and are additionally utilized in agriculture to reduce soil erosion. They are used across numerous conventional practices to treat menopausal syndrome-related infirmities, with the tuber constituting the most often employed part of the plant in indigenous medicine (Wang et al., 2020). In Ayurveda, *P. tuberosa* is described as a plant with significant nutritional value and is also known for its diuretic, aphrodisiac, energizing and galactagogue properties (Kirtikar and Basu, 1935 and Maji et al., 2014). Extracts and purified compounds of *P. tuberosa* showed a range of pharmacological activities, including anti-stress, anti-inflammatory, antidiabetic, anticonvulsant, hepatoprotective, anticancer, antifertility, europrotective, hypolipidemic, antioxidant, nootropic, cardioprotective, antiulcerogenic, immunomodulatory, wound healing and nephroprotective properties. The plant is particularly used as a tonic, antitumor, antirheumatic, antiallergic, and for the treatment of malaria, typhoid fever, and cough (Anonym, 1978; Jeon et al., 2005; Sadguna et al., 2015; Bharti et al., 2021).

IMPPAT (Indian Medicinal Plants, Phytochemistry and Therapeutics) is a methodically curated database that encompasses the directory of naturally occurring medicinal plants, their phytochemicals and therapeutic potential. (Mohanraj et al., 2018). *In-silico* development of therapeutic preparations can be aided by the availability of a carefully maintained database including data on plants, their associated natural compounds, and a repository for their chemical structures (Jensen et al., 2014). ADME (Absorption - Distribution - Metabolism - Excretion) is an expeditious and convenient method used for predicting the pharmacological properties of innumerable chemical constituents, holding significant importance in the drug development process (Hou and Wang, 2008). The term ADME designates the pharmacokinetics of a drug, defining how the drug behaves in the human body after administration, including its transit across the membrane and body, metabolic processes, and routes of excretion or elimination (Doogue and Polasek, 2013). The properties such as P-glycoprotein substrate, Blood Brain Barrier influence the properties of absorption. The following phytochemical chemical metabolism have the ability to inhibit CYP450 enzymes, and several other properties helps in the designing of drugs (Shen et al., 2010, Cheng et al., 2011 and Wang et al., 2011).

Analyzing and anticipating the pharmacological basis of the therapeutic activity of *Pueraria tuberosa* using Swiss ADME analysis, considering the physiochemical properties of the phytoconstituents of the medicinal plant, which predict the pharmacokinetic properties, drug-like nature, solubility, lipophilicity, medicinal chemistry. The present study was designed in *Pueraria tuberosa* for *in-silico* ADMET screening

## METHODOLOGY

### *In-silico* Collection of Phytochemicals of *Pueraria tuberosa* DC

Indian Medicinal Plants-Phytochemicals-Therapeutics or IMPPAT is the most comprehensive database on phytochemicals of Indian medicinal plants. IMPPAT provides an integrative platform for using

cheminformatic<sup>30</sup> methods to accelerate natural product-based drug development. IMPPAT (Indian Medicinal Plants-Phytochemicals-Therapeutics) which helps in the curation of Indian Medicinal Plants their Phytochemicals and Therapeutic uses. With the help of IMPPAT we have curated the phytochemicals and computed physiochemical properties and predicted Absorption, Distribution, Metabolism, Excretion (ADME) properties using cheminformatic tools. At present, IMPPAT has about 9500 phytocompounds with their physiologically relevant data (Mohanraj et al., 2018 and Roshni et al., 2022).

### **Swiss ADME- an online resource**

Swiss ADME, produced by the Swiss Institute of Bioinformatics, is an online resource that offers free access to a variety of parameters and predictive models. This online tool estimates the pharmacokinetics property, lipophilicity, physicochemical properties, drug-likeness, and medicinal chemistry of one or more compounds. Users can acquire findings in the form of tables or Excel sheets by submitting the compounds into the Simplified Molecular Input Line Entry System (SMILES). This aids in simplifying the analysis and comprehend critical pharmacokinetic data, facilitates medication development. (Daina et al., 2017, Fan and De Lannoy, 2014, Lipinski, 2000 and Tsopelas et al., 2017).

### **Structure and bioavailability radar**

The graphical representation of drug-likeness requirements is crucial when assessing the oral bioavailability of substances. A drug's biological activities is determined by 6 crucial physicochemical variables: lipophilicity, size, polarity, solubility, saturation, and flexibility. Specific thresholds are specified for all parameters in order to precisely assess drug-likeness. Molecular weight, a measurement of size, should range around 150 and 500 g/mol. Lipophilicity, estimated by XLOGP3, ought to lie within -0.7 and +6.0. For solubility, the logarithmic value for solubility (log S) ought to stay below an established limit. Saturation is determined by the percentage of sp<sup>3</sup> hybridised carbon to the overall carbon count of the molecule, which should be a minimum of 0.25. The topological polar surface area (TPSA) ranges from 20 to 130 Å and is utilised for evaluating polarity. The flexibility is determined by the number of rotatable bonds, which should not exceed nine (Delaney, 2004, Tian et al., 2015, Cheng et al., 2007 and Daina et al., 2017).

### **Physicochemical property**

Physicochemical characteristics furnish comprehensive explanations of molecules structures and behaviours. Relevant parameters include molecular weight, molecular refractivity, polar surface area (PSA), and the number of specific atom types such heavy atoms, aromatic heavy atoms, rotatable bonds, hydrogen bond acceptors, and hydrogen bond donors. These values have been obtained with Open Babel version 2.3.0 (Daina et al., 2017 and Boyle et al., 2011). Topological polar surface area (TPSA) is a fragmental methodology to estimate the polar surface area. This technique considers sulphur and phosphorus as polar atoms, which contributed to the overall calculations of PSA (Ertl et al., 2000).

### **Lipophilicity**

Lipophilicity is a significant consideration in drug discovery and design, influencing solubility, cell membrane penetration, transport to molecular targets, receptor binding, potency, selectivity, and overall impact on metabolism and pharmacokinetics. It is essential in defining the ADMET (Absorption, Distribution, Metabolism, Excretion, and Toxicity) qualities of a drug (Arnott and Planey, 2012). Lipophilicity is often determined using log P and log D. Log P, additionally referred to as the logarithmic n-octanol-water partition coefficient, quantifies the partition equilibrium of a unionised solute between water and an immiscible organic solvent. The distribution coefficient, log D, indicates the ratio of the compound's complete forms in each phase. A higher log P value demonstrates additional lipophilicity,

which typically correlates with improved ability to cross cell membranes and interact with target receptors (Testa et al., 2000). Swiss ADME has five openly accessible models to determine the lipophilicity of compounds: XLOGP3, WLOGP, MLOGP, SILICOS-IT, and iLOGP. Among these, the logarithmic partition coefficient between n-octanol and water ( $\log P_{o/w}$ ) is regarded as an essential indicator of lipophilicity (Cheng et al., 2007 and Mannhold et al., 2009).

XLOGP3 is an atomistic, knowledge-based approach calculated using the XLOGP program, incorporating correction aspects (Cheng et al., 2007). WLOGP remains entirely reliant on an atomic approach that employs the fragmentation mechanism established by Wildman and Crippen (Wildman and Crippen, 1999). MLOGP employs a topological technique, as implemented by Moriguchi et al. (Moriguchi et al., 1992). SILICOS-IT offers a hybrid approach that combines fragmental and topological methodologies, as predicted according to the FILTER-IT program, and comprises 27 fragments and 7 topological descriptors. iLOGP is an in-house, physics-based approach for assessing lipophilicity based on free energies of solvation in water and n-octanol using the Generalized-Born and Solvent Accessible Surface Area (GB/SA) model (Daina et al., 2017).

### **Solubility**

Solubility is a significant factor in drugs development, because it significantly impacts drug bioavailability following oral delivery. It is essential to drugs absorption. A compound's water solubility and lipophilicity are highly linked (Ottaviani et al., 2010). Factors like temperature, pressure, and the type of solvent used can impact solubility. The saturation concentration measures the extent of solubility by identifying the point at which the concentration of the solute in the solution reaches equilibrium and no longer increases with more solute (Lachman et al., 1986). Water solubility is determined using the following approaches: Log S (ESOL), Log S (Ali), and Log S (SILICOS-IT). The ESOL and Ali models, both topological methods readily available in Swiss ADME, are frequently utilised to predict water solubility. The ESOL model characterises solubility as follows: Insoluble ( $< -10$ ), Poorly soluble ( $< -6$ ), Moderately soluble ( $< -4$ ), Soluble ( $< 2$ ), and Highly soluble ( $< 0$ ) (Yalkowsky and Valvani, 1980). The Ali model, inspired by the ESOL model, applies a similar scale with slightly distinct thresholds: insoluble ( $< -10$ ), poorly soluble ( $< -6$ ), moderately soluble ( $< -4$ ), soluble ( $< -2$ ), and highly soluble ( $< 0$ ). Both models diverge from the fundamental universal solubility equation by exhibiting variable linear relationships with experimental results. The ESOL and Ali models display substantial linear correlations, with  $R^2$  values of 0.69 and 0.81, respectively. The SILICOS-IT model's fragmental approach provides a linear correlation coefficient of  $R^2 = 0.75$ . (Ali et al., 2012, Delaney, 2004 and Mahanthesh et al., 2020)

### **Pharmacokinetics**

The pharmacokinetics section compiles all predictions regarding a molecule's ADME characteristics, aiding with estimating its absorption, distribution, metabolism, and excretion characteristics. The second section captures data on all absorbed molecules to assist in an evaluation of their ADME properties. The BOILED Egg model, an elliptical visualisation tool, has been utilised to explain the absorption properties of these compounds. This model presents a quick and effective prediction of passive human gastrointestinal absorption and the ability to cross the blood-brain barrier (Daina and Zoete, 2016 and Di et al., 2011). Understanding the functioning of P-glycoprotein (P-gp) becomes essential given that it safeguards the central nervous system (CNS) by aggressively pumping foreign chemicals back into the intestinal lumen and capillaries from the brain's capillary endothelial cells (Szaka et al., 2008). Knowing whether a chemical is a substrate or non-substrate of P-gp is crucial for assessing its ability to penetrate

biological barriers, such as the blood-brain barrier or the gastrointestinal wall (Montanari and Ecker, 2015).

Understanding drug metabolism requires an analysis of how chemicals interact with cytochrome P450 enzymes. Among these enzymes, CYP3A4 and CYP2D6 play significant functions in drug biotransformation, regulating metabolic pathways and excretion (Testa et al. 2009). Inhibition of these isoenzymes is the primary cause of drug-drug interactions, which can lead to undesirable side effects, suboptimal drug clearance, and excessive drug accumulation (Kirchmair et al., 2015). Swiss ADME employs a binary classification technique and applies the support vector machine (SVM) algorithm to datasets comprising known substrates, non-substrates, inhibitors, and non-inhibitors. The model anticipates whether the substance under research is a substrate for P-gp and cytochrome P450 enzymes, giving insights into possible relationships and metabolic behaviour (Mitchell, 2014).

### Drug likeness

The qualitative characterisation of a molecule's bioavailability is essential to its development as an oral medicine. In order to simplify the chemical libraries and eliminate substances that fail to meet the acceptable pharmacokinetic profiles, five rule-based filters were used (Daina et al., 2017). Swiss ADME offers five different rule-based filters: Lipinski, Veber (GSK), Egan (Pharmacia), Muegge (Bayer), and Ghose (Amgen). Each set of filters evaluated various factors to determine a molecule's suitability as a drug. The Lipinski filter, also referred to as the Rule of Five, divides smaller molecules based around their physicochemical attributes, such as molecular weight (MW) less than 500, MLOGP less than 4.14, and nitrogen or oxygen atom count < 5 (Lipinski et al., 2001). The Veber filter classifies drug-like molecules as those that possess a topological polar surface area (TPSA) of 140 Å<sup>2</sup> or less and 10 or fewer rotatable bonds (Veber et al., 2002). The Egan filter necessitates WLOGP of 5.88 or less and TPSA of 13.6 Å<sup>2</sup> or less. This filter evaluates chemicals based on the physicochemical processes and permeability of the membrane (Egan et al., 2000). The Muegge and Ghose filters consider additional variables such as the bioavailability score, which is determined by total charge, TPSA, and compliance with the Lipinski filter. These filters classify compounds based on their bioavailability, assigning probabilities of 11%, 17%, 56%, or 85% (Martin and Park, 2005).

### Medicinal Chemistry

Medicinal chemists play a substantial part in leading the pursuit for novel medications, and countless essential features impact the drug development process. One of these characteristics is PAINS (Pan Assay Interference Compounds), a group of compounds which demonstrate robust assay reactions but have no relationship with protein targets. If PAINS has been identified during the examination, SWISS ADME gives a warning (Baell and Holloway, 2010). Another significant attribute is Brenk, which recognises chemicals that are chemically reactive, metabolically unstable, or have poor pharmacokinetic characteristics, causing structural alerts. Brenk's molecules tend to be smaller and less hydrophobic, rendering Lipinski's rule of five less applicable. In addition, lead-likeness describes molecules having 10 to 27 heavy atoms, a maximum of four hydrogen bond donors, and less than seven hydrogen bond acceptors. These variables contribute in the assessment of molecules as lead candidates in drug development (Brenk et al., 2008).

## RESULTS



**IMPPAT data base**
**Table 1: Phytochemical data of *Pueraria tuberosa* DC from IMPPAT database.**

S r . N o .	Pla nt par t	IMPPAT Phytoche mical identifier	Phytochemical name	SMILE
1	Tuber	IMPHY01 4037	1,14-Dihydroxy-7,7-Dimethyl- 8,12,20- Trioxapentacyclo[11.8.0.02,11.04,9.0 14,19]Henicosa-2(11),3,5,9,15,18- Hexaen-17-One	<chem>O=C1C=CC2(C(=C1)OCC1(C2Oc2c1cc1c(c2)OC(C=C1)(C)C)O)O</chem>
2	Tuber	IMPHY00 5114	Anhydrotuberosin	<chem>Oc1ccc2c(c1)OCc1c2oc2c1cc1c(c2)OC(C=C1)(C)C</chem>
3	Tuber	IMPHY01 4836	Beta-Sitosterol	<chem>CC[C@@H](C(C)C)CC[C@H]([C@H]1CC[C@@H]2[C@]1(C)CC[C@H]1[C@H]2CC=C2[C@]1(C)CC[C@@H](C2)O)C</chem>
4	Root	IMPHY01 4836	Beta-Sitosterol	<chem>CC[C@@H](C(C)C)CC[C@H]([C@H]1CC[C@@H]2[C@]1(C)CC[C@H]1[C@H]2CC=C2[C@]1(C)CC[C@@H](C2)O)C</chem>
5	Whole plant	IMPHY00 4566	Daidzein	<chem>Oc1ccc(cc1)c1coc2c(c1=O)ccc(c2)O</chem>
6	Root	IMPHY00 4566	Daidzein	<chem>Oc1ccc(cc1)c1coc2c(c1=O)ccc(c2)O</chem>
7	Tuber	IMPHY00 4566	Daidzein	<chem>Oc1ccc(cc1)c1coc2c(c1=O)ccc(c2)O</chem>
8	Tuber	IMPHY00 4643	Genistein	<chem>Oc1ccc(cc1)c1coc2c(c1=O)c(O)cc(c2)O</chem>
9	Tuber	IMPHY00 4138	Genistin	<chem>OC[C@H]1O[C@@H](Oc2cc(O)c3c(c2)occ(c3=O)c2ccc(cc2)O)[C@@H]([C@H]([C@@H]1O)O)O</chem>
10	Whole plant	IMPHY01 0265	Gluconic Acid	<chem>OC[C@H]([C@H]([C@@H]([C@H](C(=O)O)O)O)O)O</chem>
11	Not men	IMPHY00 7169	Pterocarpan	<chem>c1ccc2c(c1)C1Oc3c(C1CO2)cccc3</chem>

	tion ed			
1 2	Not men tion ed	IMPHY00 4578	Puerarin	<chem>OC[C@H]1O[C@H]([C@@H]([C@H]([C@@H]1O)O)O)c1c(O)ccc2c1oc(c2=O)c1ccc(cc1)O</chem>
1 3	Wh ole plan t	IMPHY00 4578	Puerarin	<chem>OC[C@H]1O[C@H]([C@@H]([C@H]([C@@H]1O)O)O)c1c(O)ccc2c1oc(c2=O)c1ccc(cc1)O</chem>
1 4	Roo t	IMPHY00 4578	Puerarin	<chem>OC[C@H]1O[C@H]([C@@H]([C@H]([C@@H]1O)O)O)c1c(O)ccc2c1oc(c2=O)c1ccc(cc1)O</chem>
1 5	Tub er	IMPHY00 4578	Puerarin	<chem>OC[C@H]1O[C@H]([C@@H]([C@H]([C@@H]1O)O)O)c1c(O)ccc2c1oc(c2=O)c1ccc(cc1)O</chem>
1 6	Tub er	IMPHY01 3046	Puerarone	<chem>Oc1ccc2c(c1)oc(c2=O)c1cc2C=CC(Oc2cc1O)(C)C</chem>
1 7	Tub er	IMPHY01 3182	Puerarostan	<chem>COc1c(O)ccc2c1oc(=O)c1c2oc2c1cc(c2)O)CC=C(C)C</chem>
1 8	Tub er	IMPHY01 4842	Stigmasterol	<chem>CC[C@@H](C(C)C)/C=C/[C@H]([C@H]1CC[C@@H]2[C@]1(C)CC[C@H]1[C@H]2CC=C2[C@]1(C)CC[C@@H](C2)O)C</chem>
1 9	Roo t	IMPHY01 4842	Stigmasterol	<chem>CC[C@@H](C(C)C)/C=C/[C@H]([C@H]1CC[C@@H]2[C@]1(C)CC[C@H]1[C@H]2CC=C2[C@]1(C)CC[C@@H](C2)O)C</chem>
2 0	Not men tion ed	IMPHY00 2579	Tuberosin	<chem>Oc1ccc2c(c1)OC[C@]1([C@@H]2Oc2c1cc1c(c2)OC(C=C1)(C)C)O</chem>
2 1	Wh ole plan t	IMPHY00 2579	Tuberosin	<chem>Oc1ccc2c(c1)OC[C@]1([C@@H]2Oc2c1cc1c(c2)OC(C=C1)(C)C)O</chem>
2 2	Roo t	IMPHY00 2579	Tuberosin	<chem>Oc1ccc2c(c1)OC[C@]1([C@@H]2Oc2c1cc1c(c2)OC(C=C1)(C)C)O</chem>
2 3	Tub er	IMPHY00 2579	Tuberosin	<chem>Oc1ccc2c(c1)OC[C@]1([C@@H]2Oc2c1cc1c(c2)OC(C=C1)(C)C)O</chem>
2 4	Tub er	IMPHY01 0858	Tuberostan	<chem>COc1ccc2c(c1)oc(=O)c1c2oc2c1cc1c(c2)OC(C=C1)(C)C</chem>

IMPPAT was used to identify all 24 phytoconstituents from plant components, including the roots, tubers, and whole plant, as shown in the above table. Nevertheless, certain phytoconstituents were discovered to be common, For example, it has been found that Daidzein, Tuberosin, and Puerarin were shared by all three sections. 14 compounds were chosen for Swiss ADME investigation out of the twenty-four compounds.

**Table 2: Physicochemical Properties of select phytochemicals of *P. tuberosa***

Mol ecul e	Name of the Phytochemical	Form ula	Mole cula r weig ht	No . he av y at o ms	No . ar o m. he av y at o ms	Fra ctio n Csp 3	Nu m. rota tabl e bon ds	Nu m. H- bon d acce ptor s	Nu m. H- bon d no rs	Mola r Refra ctivit y	TP SA
Mol ecul e 1	1,14-Dihydroxy-7,7- dimethyl-8,12,20- trioxapentacyclo[11.8.0.0 2,11.04,9.014,19]henicosa -2(11),3,5,9,15,18- hexaen-17-one	C <sub>20</sub> H 18O <sub>6</sub>	354. 35	26	6	0.35	0	6	2	91.91	85. 22
Mol ecul e 2	Anhydrotuberosin	C <sub>20</sub> H 16O <sub>4</sub>	320. 34	24	15	0.2	0	4	1	92.33	51. 83



Molecule 3	Beta-sitosterol	C <sub>29</sub> H <sub>50</sub> O	414.71	30	0	0.93	6	1	1	133.23	20.23
Molecule 4	Daidzein	C <sub>15</sub> H <sub>10</sub> O <sub>4</sub>	254.24	19	16	0	1	4	2	71.97	70.67
Molecule 5	Genistein	C <sub>15</sub> H <sub>10</sub> O <sub>5</sub>	270.24	20	16	0	1	5	3	73.99	90.9
Molecule 6	Genistin	C <sub>21</sub> H <sub>20</sub> O <sub>10</sub>	432.38	31	16	0.29	4	10	6	106.11	170.05

Molecule 7	Gluconic acid	C <sub>6</sub> H <sub>12</sub> O <sub>7</sub>	196.16	13	0	0.83	5	7	6	38.54	138.45
Molecule 8	Pterocarpan	C <sub>15</sub> H <sub>12</sub> O <sub>2</sub>	224.25	17	12	0.2	0	2	0	64.65	18.46
Molecule 9	Puerarin	C <sub>21</sub> H <sub>20</sub> O <sub>9</sub>	416.38	30	16	0.29	3	9	6	104.59	160.82
Molecule 10	Puerarone	C <sub>20</sub> H <sub>16</sub> O <sub>5</sub>	336.34	25	16	0.15	1	5	2	96.09	79.9

Molecule 11	Puerarostan	C <sub>21</sub> H <sub>18</sub> O <sub>6</sub>	366.36	27	17	0.19	3	6	2	104.02	93.04
Molecule 12	Stigmasterol	C <sub>29</sub> H <sub>48</sub> O	412.69	30	0	0.86	5	1	1	132.75	20.23
Molecule 13	Tuberosin	C <sub>20</sub> H <sub>18</sub> O <sub>5</sub>	338.35	25	12	0.3	0	5	2	91.84	68.15
Molecule 14	Tuberostan	C <sub>21</sub> H <sub>16</sub> O <sub>5</sub>	348.35	26	17	0.19	1	5	0	100.38	61.81

**Table 3: Lipophilicity of the select phytochemicals of *P. tuberosa***

Name of the phytochemicals	iLOGP	XLOGP3	WLOGP	MLOGP	Silicos-IT Log P	Consensus Log P
1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo[1.1.8.0.0.2,11.0.4,9.0.1.4,19]henicosa-2(11),3,5,9,15,18-hexaen-17-one	2.49	0.68	1.39	0.55	2.02	1.43
Anhydrotuberosin	3.26	4.1	4.62	2.58	4.35	3.78
Beta-sitosterol	5.05	9.34	8.02	6.73	7.04	7.24
Daidzein	1.77	2.47	2.87	1.08	3.02	2.24
Genistein	1.91	2.67	2.58	0.52	2.52	2.04
Genistin	2.44	0.86	0.05	-1.61	0.35	0.42
Gluconic acid	-0.06	-3.37	-3.49	-2.9	-2.26	-2.42
Pterocarpan	2.51	3.15	2.97	2.81	3.28	2.95
Puerarin	1.77	0.01	0.06	-1.52	0.81	0.23
Puerarone	2.62	3.39	3.95	1.64	3.9	3.1
Puerarostan	3.51	4.66	4.62	2.55	4.62	3.99
Stigmasterol	5.08	8.56	7.8	6.62	6.86	6.98
Tuberosin	3.09	3.36	2.75	1.9	3.1	2.84
Tuberostan	3.74	4.37	4.78	3.1	4.78	4.15

The table above displays high values for iLOGP, XLOGP3, WLOGP, MLOGP, and Silicos-IT Log P. Beta-sitosterol represents the Consensus Log P value, while glutamic acid represents the low value.

**Table 4: Solubility of the phytochemicals of *P. tuberosa***

Name of the phytochemical	ESOL				Ali				SILICOS-IT			
	E S O L	E S O L	E S O L	E S O L	A l i	A l i	A l i	A l i	S i l i	S i l i	S i l i	S i l i
1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo[1.1.8.0.0.2,11.0.4,9.0.1.4,19]henicosa-2(11),3,5,9,15,18-hexaen-17-one	-2.64	8.1901	2.3103	Soluble	-2.64	3.1800	8.9903	Soluble	-2.96	3.8901	1.1003	Soluble

.02,11.04,9.014,19]heni cosa-2(11),3,5,9,15,18- hexaen-17-one					0 5							
Anhydrotuberosin	- 4. 87	4.31 E- 03	1.34 E- 05	Mod erate ly solu ble	- 4. 8 9	4.09 E- 03	1.28 E- 05	Mod erate ly solu ble	- 6.0 9	2.63 E- 04	8.20 E- 07	Poor ly solu ble
Beta-sitosterol	- 7. 9	5.23 E- 06	1.26 E- 08	Poor ly solu ble	- 9. 6 7	8.90 E- 08	2.15 E- 10	Poor ly solu ble	- 6.1 9	2.69 E- 04	6.49 E- 07	Poor ly solu ble
Daidzein	- 3. 53	7.51 E- 02	2.95 E- 04	Solu ble	- 3. 6	6.41 E- 02	2.52 E- 04	Solu ble	- 4.9 8	2.64 E- 03	1.04 E- 05	Mod erate ly solu ble
Genistein	- 3. 72	5.11 E- 02	1.89 E- 04	Solu ble	- 4. 2 3	1.59 E- 02	5.88 E- 05	Mod erate ly solu ble	- 4.4	1.07 E- 02	3.94 E- 05	Mod erate ly solu ble
Genistin	- 3. 18	2.85 E- 01	6.60 E- 04	Solu ble	- 4. 0 1	4.18 E- 02	9.67 E- 05	Mod erate ly solu ble	- 2.6 9	8.77 E- 01	2.03 E- 03	Solu ble
Gluconic acid	1. 4	4.89 E+0 3	2.49 E+0 1	High ly solu ble	1. 0 4	2.14 E+0 3	1.09 E+0 1	High ly solu ble	3.0 2	2.04 E+0 5	1.04 E+0 3	Solu ble
Pterocarpan	- 3. 74	4.11 E- 02	1.83 E- 04	Solu ble	- 3. 2 1	1.39 E- 01	6.20 E- 04	Solu ble	- 4.7 6	3.86 E- 03	1.72 E- 05	Mod erate ly solu ble
Puerarin	- 2. 62	9.89 E- 01	2.37 E- 03	Solu ble	- 2. 9 4	4.79 E- 01	1.15 E- 03	Solu ble	- 2.9 7	4.49 E- 01	1.08 E- 03	Solu ble

Puerarone	- 4. 47	1.14 E- 02	3.40 E- 05	Mod erate ly solu ble	- 4. 7 5	6.02 E- 03	1.79 E- 05	Mod erate ly solu ble	- 5.8 1	5.17 E- 04	1.54 E- 06	Mod erate ly solu ble
Puerarostan	- 5. 32	1.77 E- 03	4.84 E- 06	Mod erate ly solu ble	- 6. 3 4	1.67 E- 04	4.56 E- 07	Poor ly solu ble	- 6.3 7	1.56 E- 04	4.25 E- 07	Poor ly solu ble
Stigmasterol	- 7. 46	1.43 E- 05	3.46 E- 08	Poor ly solu ble	- 8. 8 6	5.71 E- 07	1.38 E- 09	Poor ly solu ble	- 5.4 7	1.40 E- 03	3.39 E- 06	Mod erate ly solu ble
Tuberosin	- 4. 41	1.32 E- 02	3.89 E-15	Mod erate ly solu ble	- 4. 4 7	1.15 E- 02	3.40 E- 05	Mod erate ly solu ble	- 4.6 6	7.40 E- 03	2.19 E- 05	Mod erate ly solu ble
Tuberostan	- 5. 17	2.35 E- 03	6.75 E- 06	Mod erate ly solu ble	- 5. 3 8	1.44 E- 03	4.13 E- 06	Mod erate ly solu ble	- 7.1 3	2.58 E- 05	7.40 E- 08	Poor ly solu ble

In the table given above high solubility was shown by Gluconic acid for ESOL and Ali, while in SILIOCS-IT none of the compound showed high solubility. 1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo [11.8.0.02,11.04,9.014,19] henicosa-2(11),3,5,9,15,18-hexaen-17-one, Daidzein, Pterocarpan, Puerarin these compounds are the common molecules that are soluble according to ESOL and Ali characteristics, other compounds that showed solubility in ESOL are Genistein and Genistin. According to SILICOS-IT, 1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo[11.8.0.02,11.04,9.014,19]henicosa-2(11),3,5,9,15,18-hexaen-17-one, Genistin and Gluconic acid showed solubility. Anhydrotuberosin, Puerarone, Tuberosin and Tuberostan are the common compounds that are moderately soluble according to ESOL and Ali. Other compounds that showed moderate solubility according to Ali are Genistein, Genistin. According to SILICOS-IT the compounds that showed moderate solubility are Daidzein, Genistein, Pterocarpan, Puerarone, Stigmasterol, Tuberosin. The common compounds that showed poor solubility according to ESOL and Ali characteristics is Stigmasterol, Beta-sitosterol. Compounds that showed poor solubility according to SILICOS-IT are Tuberostan, Puerarostan, Beta-sitosterol, Anhydrotuberosin.

**Table 5: Pharmacokinetic properties of the phytochemicals of *P. tuberosa***



Name of the phytocompounds	GI absorption	BBB permeant	Pgp substrate	CYP 1A2 inhibitor	CYP 2C19 inhibitor	CYP 2C9 inhibitor	CYP 2D6 inhibitor	CYP 3A4 inhibitor	log Kp (cm/s)
1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo[11.8.0.0.02,11.04,9.014,19]henicosane-2(11),3,5,9,15,18-hexaen-17-one	High	No	Yes	No	No	No	No	No	-7.98
Anhydrotuberosin	High	Yes	Yes	Yes	Yes	No	No	Yes	-5.34
Beta-sitosterol	Low	No	No	No	No	No	No	No	-2.2
Daidzein	High	Yes	No	Yes	No	No	Yes	Yes	-6.1
Genistein	High	No	No	Yes	No	No	Yes	Yes	-6.05
Genistin	Low	No	Yes	No	No	No	No	No	-8.33
Gluconic acid	Low	No	No	No	No	No	No	No	-9.89
Pterocarpan	High	Yes	Yes	Yes	No	No	Yes	No	-5.43
Puerarin	Low	No	No	No	No	No	No	No	-8.83
Puerarone	High	No	No	Yes	No	Yes	No	Yes	-5.94
Puerarostan	High	No	No	No	Yes	Yes	No	No	-5.23
Stigmasterol	Low	No	No	No	No	Yes	No	No	-2.74

Tuberosin	High	Yes	Yes	Yes	Yes	Yes	Yes	Yes	-5.98
Tuberostan	High	Yes	No	Yes	Yes	Yes	No	No	-5.32

Compounds that showed GI absorption are 1,14-Dihydroxy-7,7-dimethyl-8,12,20 trioxapentacyclo[11.8.0.02,11.04,9.014,19]henicosa-2(11),3,5,9,15,18-hexaen-17-one, Anhydrotuberosin, Daidzein, Genistein, Pterocarpan, Puerarone, Puerarostan, Tuberosin, Tuberostan and the compounds that does not depict GI absorption are Stigmasterol, Puerarin, Gluconic acid, Genistin, Beta-sitosterol. Compounds that exhibit BBB permeant Anhydrotuberosin, Daidzein, Pterocarpan, Tuberosin, Tuberostan and compounds that does not display BBB permeant are 1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo[11.8.0.02,11.04,9.014,19]henicosa-2(11),3,5,9,15,18-hexaen-17-one, Beta-sitosterol, Genistein, Genistin, Gluconic acid, Puerarin, Puerarone, Puerarostan, Stigmasterol.

**Table 6: Drug likeness properties of the phytochemicals of *P. tuberosa***

Name of the phytochemicals	Lipinski #violations	Ghose #violations	Veber #violations	Egan #violations	Muegge #violations	Bioavailability Score
1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo[11.8.0.02,11.04,9.014,19]henicosa-2(11),3,5,9,15,18-hexaen-17-one	0	0	0	0	0	0.56
Anhydrotuberosin	0	0	0	0	0	0.55
Beta-sitosterol	1	3	0	1	2	0.55
Daidzein	0	0	0	0	0	0.55
Genistein	0	0	0	0	0	0.55
Genistin	1	0	1	1	2	0.55
Gluconic acid	1	2	0	1	3	0.56
Pterocarpan	0	0	0	0	0	0.55
Puerarin	1	0	1	1	2	0.55
Puerarone	0	0	0	0	0	0.55
Puerarostan	0	0	0	0	0	0.55
Stigmasterol	1	3	0	1	2	0.55
Tuberosin	0	0	0	0	0	0.55
Tuberostan	0	0	0	0	0	0.55

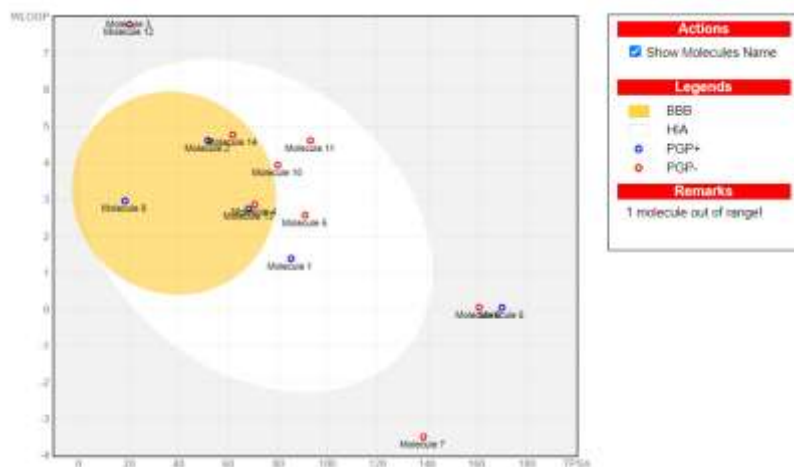
1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo[11.8.0.02,11.04,9.014,19]henicosa-2(11),3,5,9,15,18-hexaen-17-one, Daidzein, Genistein, Pterocarpan, Puerarone, Puerarostan, Tuberosin and Tuberostan these nine compounds are follow the Lipinski rule of 5, which is essential for the compound to be druggable.

**Table 7: Medicinal chemistry properties of the phytochemicals of *P. tuberosa***

Name of the phytocompounds	PAINS #alerts	Brenk #alerts	Leadlikenes #violations	Synthetic Accessibility
1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo[11.8.0.02,11.04,9.014,19]henicosa-2(11),3,5,9,15,18-hexaen-17-one	0	0	1	4.82
Anhydrotuberosin	0	0	1	3.83
Beta-sitosterol	0	1	2	6.3
Daidzein	0	0	0	2.79
Genistein	0	0	0	2.87
Genistin	0	0	1	5.12
Gluconic acid	0	0	1	3.33
Pterocarpan	0	0	1	3.29
Puerarin	0	0	1	4.98
Puerarone	0	0	0	3.71
Puerarostan	0	2	2	3.66
Stigmasterol	0	1	2	6.21
Tuberosin	0	0	0	4.31
Tuberostan	0	1	1	3.77

All of these compounds don't show any PAINS alerts.

**Figure 1: BOILED-Egg representation of the phytochemicals found in *P. tuberosa***



## DISCUSSION

Ayurveda, one of the world's oldest medical systems, utilized natural sources with no known adverse effects for discovering medicinally useful and efficient chemicals obtained from botanicals for drug development. Today, treatment with herbs is used extensively in developed as well as developing nations (Ekor, 2014, Thorat and Mishra, 2016). The characteristics of these chemicals can be easily obtained using numerous resources and websites, such as Swiss ADME (Daina et al., 2017). Reports from the World Health Organization (WHO) indicate that more than 30% of all plant species have been utilized for medicinal purposes at some point (Uniyal et al., 2006). The first phase of drug discovery is the prediction of ADMET (Absorption, Distribution, Metabolism, Excretion, and Toxicity) characteristics, which can be performed easily using computer-based drug design (Lombardo et al., 2003). In silico compound profiling delivers significant advantages over traditional approaches in terms of time and expense. While wet screen examination of chemical characteristics is tedious and costly, ADMET screening may evaluate over 20,000 compounds in one minute (Hodgson, 2001). This fast screening capability helps to speed the drug discovery process and identify feasible medication candidates.

In this study, we used the free online Swiss ADME software application for evaluating the ADME features of *Pueraria tuberosa* DC. Tuberosin, Daidzein, Puerarin, beta-Sitosterol, Stigmasterol, Genistin, Anhydrotuberosin, Tuberosan, Puerarone, Puerarostan, 1,14-Dihydroxy-7,7-dimethyl-8,12,20-trioxapentacyclo[11.8.0.02,11.04,9.014,19] henicosa-2(11),3,5,9,15,18-hexaen-17-one, Gluconic acid, and Pterocarpan were identified by the software. Those phytochemicals are obtained from various parts of plants, including the root, tuber, and whole plant. Certain phytochemicals, such as Tuberosin, Daidzein, and Puerarin, are found in all three plant parts. The ADME features of these phytoconstituents were thoroughly studied and summarised in relevant tables. This information is crucial to researchers and scientists, since it provides a foundation for the discovery of possible synthetic and semisynthetic drugs with a wide range of applications. The use of computational silico techniques into the drug development pipeline improves the efficiency of identifying new therapeutic compounds from sources that are natural. Researchers can accelerate the development of novel, safe, and effective herbal-based drugs by combining the best features of traditional wisdom and modern technology. This integrative strategy has significant possibilities for treating contemporary health issues and enhancing the medicinal potential of naturally occurring substances.

## CONCLUSION

Computational techniques significantly accelerate the drug discovery process. By simulating and analysing millions of compounds, researchers can identify potential drug candidates more quickly and efficiently, thereby reducing the cost and resources required for experimental testing. These techniques allow scientists to explore a vast and multifaceted range of chemical space, facilitating the identification of compounds with desirable properties. Additionally, computational methods help in predicting the possible side effects and toxicity of candidate compounds. By analysing molecular structures and properties, researchers can assess the safety profile of drugs before they proceed to clinical trials. This approach enhances the efficiency of the drug development pipeline and ensures that only the most promising candidates advance to further stages, ultimately leading to the discovery of safe and effective new medications.

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