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# **INTEGRATING TAXONOMY AND DRUG DISCOVERY: LILIOPSIDA FLORA OF RAJBARI, BANGLADESH TARGETING** *AMORPHOPHALLUS PAEONIIFOLIUS* **FOR COLORECTAL CANCER THERAPY**

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## **Abstract**

The present study explores the angiosperm flora belonging to the class Liliopsida in Rajbari district, seamlessly integrating taxonomy with phytocompound-based drug discovery through advanced computational biology approaches. The study covered all five upazilas (sub-districts) of the district. A total of 201 taxa across 118 genera and 24 families of Liliopsida were identified. The flora is predominantly composed of herbs (79.06%), followed by climbers (7.96%), trees (7.46%), shrubs (2.98%), and a minimal occurrence of epiphytes (1.99%). Poaceae emerged as the largest family, comprising 58 taxa across 36 genera, followed by Araceae (26 taxa) and Cyperaceae (17 taxa). Notably, the study identified 25 medicinal plant species under Liliopsida. Some rare species within Liliopsida, such as *Coix aquatica, Wolffia arrhiza, Typha domingensis,* and *Schumannianthus benthamianus* were also recorded in the study area. Among the medicinal plants identified, *Amorphophallus paeoniifolius* (Dennst.) Nicolson was selected for further investigation into colorectal cancer drug discovery. The computational therapeutics design endeavor unveiled two lead compounds: Riboflavin (- 7.9 kcal/mol) and Lupeol (-6.1 kcal/mol), both of which demonstrated promising favorable drug-likeness properties. Molecular dynamics simulation spanning 100 ns revealed structural stability of the identified leads. PCA and Gibbs free energy landscape study further corroborated the drug-candidacy of the leads. DFT-based molecular reactivity study unveiled Lupeol as the most kinetically stable compound (6.915 eV). The findings highlight the significance of multi-disciplinary approach integrating classical taxonomy with bioinformatics and pave the way for future colorectal cancer therapeutics.

## **Introduction**

The Convention on Biological Diversity (CBD) has underscored the pivotal role of taxonomic and vegetation studies in ensuring effective biodiversity conservation. Such studies provide fundamental data on species identification, distribution, and classification, which are crucial for crafting well-informed conservation strategies. The CBD highlights that a lack of comprehensive taxonomic knowledge, coupled with a shortage of trained taxonomists and inadequate infrastructure, creates a significant "taxonomic impediment" that hampers efforts to assess and safeguard global biodiversity. Addressing this impediment is vital for achieving the CBD's objectives, as it facilitates precise documentation of species diversity, helps identification of conservation priorities, and allows for effective monitoring of ecosystem changes over time. The CBD thus advocates for enhanced investment in taxonomic research and capacity building to support sustainable biodiversity management and policy development (Heywood, 2004).

Rajbari district is geographically positioned between 22°40` and 23°50` N latitudes and between  $89^{\circ}19$ ` and  $90^{\circ}40$ ` E longitudes, covering an area of 1,119 sq. km. The district enjoys a

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moderate tropical monsoon climate characterized by three distinct seasons: a hot summer, a rainy season, and a dry winter. The annual average temperature ranges from a minimum of 9.8°C to a maximum of 30.1°C. Relative humidity remains fairly consistent throughout year, fluctuating from 77 to 79%. The annual rainfall is approximately 3742 mm (BBS, 2022). Rajbari district comprises 5 upazilas, namely Rajbari Sadar, Pangsha, Baliakandi, Kalukhali and Goalanda with an area of 347.1, 313, 242.53, 157.14 and 149 sq. km, respectively. Rajbari district encompasses a variety of habitats, including wetlands, cultivated land, charland, fallow land, scrub jungles and homestead areas. As an agriculturally rich region, its plant genetic, species and ecosystem diversity significantly influence the local environment. However, the floristic compositions are declining due to increasing urbanization, industrialization, habitat fragmentation, road construction, agricultural expansion, mismanaged brickfields as well as other human activities. Given the ongoing trend of habitat degradation and fragmentation, many species could disappear from the region before they are even documented and studied.

Building upon the foundational works of Hooker (1872–1897) and Prain (1903), numerous floristic endeavors have been conducted within the present political boundaries of Bangladesh, including different upazilas and protected areas (Rahman *et al*., 2012, 2013, 2019a,b; Rahman and Alam, 2013; Sarker *et al*., 2013; Rahman and Hassan, 1995; Islam *et al*., 2009; Uddin and Hassan 2010, Arefin *et al*., 2011; Rahman *et al*., 2015; Haque *et al*., 2018). Despite these efforts, only a few district-level floras have been produced, such as those for Gazipur (Tabassum 2015), Patuakhali (Sultana, 2012), Bagerhat (Hossain *et al*., 2022), Satkhira (Hossain *et al*., 2021) and Narsingdhi (Khanam and Khan, 2020; Khanam *et al*., 2020). However, the floral diversity of Rajbari district has yet to be explored through detailed field inventories and specimen examination, leaving much of its flora unexplored.

Plant taxonomy and floristics are essential for the precise detection of medicinal taxa, forming the foundation for exploring their therapeutic potential. By systematically classifying plants and understanding their distribution, taxonomists can identify species traditionally used in medicine or those possessing bioactive compounds, thus providing a gateway to drug discovery. This taxonomic accuracy is critical in ensuring the correct selection of plants for phytochemical analysis, driving the development of novel drugs through natural compounds. Compared to synthetic drugs, natural products offer several advantages, such as greater structural diversity, better biocompatibility, lower toxicity, and improved efficacy in targeting biological systems. These compounds, refined by evolution over thousands of years, are inherently optimized for biological interactions, making them a valuable resource in modern drug discovery (Ahmed and Rahman, 2024; Ahmed *et al*., 2024).

Structure-based drug design (SBDD) integrates this taxonomic knowledge by leveraging advanced computational techniques to accelerate the drug discovery process. SBDD focuses on analyzing the three-dimensional structure of target proteins and identifying compounds, such as phytochemicals, that can effectively bind to them. This approach greatly minimizes the trial-anderror nature of traditional drug development by allowing precise predictions of compound-protein interactions. Key techniques in SBDD include molecular docking, which predicts the binding affinity and orientation of drug candidates targeting key protein; ADMET (absorption, distribution, metabolism, excretion, and toxicity) analysis, which assesses the pharmacokinetic and safety profiles of compounds; and molecular dynamics (MD) simulation, which evaluates the stability and flexibility of compound-receptor interactions over time. Additionally, DFT (Density functional theory)-based molecular reactivity analysis aids in understanding the electronic structure and kinetic stability of the lead compounds. Together, these methods streamline the drug discovery process, reducing time and costs, while enhancing the precision of selecting potential drug candidates from natural sources (Bajad *et al*., 2021; Ahmed *et al*., 2023a).

MMP-9 (Matrix Metalloproteinase-9) is a crucial enzyme involved in the degradation of the extracellular matrix (ECM), and plays a significant role in cancer progression, invasion, and metastasis across various types of cancers, including colorectal cancer (CRC) (Bendardaf *et al.*, 2010; Said *et al.*, 2014). MMP-9 is frequently overexpressed in CRC and is associated with poor prognosis due to its involvement in tumor growth, angiogenesis, and the spread of cancer cells to other tissues. Inhibiting MMP-9 has been suggested to reduce tumor invasiveness and slow metastasis, making it a viable target for therapeutic agents aimed at improving CRC outcomes (Rashid and Bardaweel, 2023; Sarkar *et al.*, 2024). Therefore, this MMP-9 protein serves as a promising target for structure-based drug design endeavors.

The study aims to identify, document, and analyze the angiosperm flora, particularly Liliopsida taxa of Rajbari district, assessing their current distribution, and medicinal significance. Consequently, it is crucial to identify, and document the plant species, providing a comprehensive taxonomic treatment of the angiosperm flora of Rajbari district, and to implement conservation measures to safeguard the region's plant resources for the benefit of future generations. In addition, the study further aims to bridge the gap between taxonomy and drug design endeavor by identifying potential colorectal cancer drug candidates targeting MMP-9 protein from a medicinal plant of Rajbari district. This multi-disciplinary endeavor, therefore aims not only to deepen the understanding of Liliopsida diversity in Rajbari district but also to investigate novel anticancer therapeutics derived from the selected medicinal plant.

### **Materials and Methods**

## *Botanical expedition, plant sample collection and identification*

A total of 128 field expeditions were conducted between 2019 to 2023 to collect plant specimens from Rajbari district covering all five upazilas: Rajbari Sadar, Pangsha, Baliakandi, Kalukhali and Goalanda (Fig. 1).



Fig. 1. Map of Rajbari district showing the area of investigation (Source: Banglapedia).

The collected plant samples were processed following standard herbarium procedures (Singh and Subramaniam, 2008) and underwent thorough examination and identification at the Dhaka University Salar Khan Herbarium (DUSH). Identifications were ensured by consulting standard literatures (Khan and Alam, 1977; Khan and Halim, 1985; Ara and Hassan, 2019; Siddiqui *et al*., 2007; Ahmed *et al*., 2008) and were cross-referenced with previously identified specimens housed at DUSH and DACB. For updated nomenclature, the authoritative database Plants of the World Online (POWO, 2024) was consulted. Local names were sourced from Huq (2019), and the families were arranged following Cronquist (1981). The voucher specimens for the identified taxa are deposited at DUSH.

### *Drug Design endeavor*

*Amorphophallus paeoniifolius* (Dennst.) Nicolson was chosen for designing colorectal cancer drug candidates due to its novelty, ethnomedicinal significance, and consent of local population in the study area. The drug design endeavor was accomplished in the following steps:

## *Preparation of receptor macromolecule*

The structure of the Matrix Metalloproteinase 9 (MMP-9) protein, identified by the PDB ID "1GKC," was retrieved from the Protein Data Bank (Rowsell *et al*., 2002). Receptor preparation was carried out using AutoDockTools v.1.5.6 and SWISS-PDB Viewer v.4.10. Subsequently, OpenBabel v.3.1.1.1 was employed to convert the energy-minimized protein from PDB to PDBQT format for further analysis (Guex and Peitsch, 1997; O'Boyle *et al.*, 2008; Rizvi *et al.*, 2013).

## *Preparation of ligands*

Phytochemicals from *A. paeoniifolius* were identified and retrieved in 3D SDF format from relevant literature and the IMPPAT database (Shrivastava *et al.*, 2023; Vivek-Ananth *et al.*, 2023). Doxycycline, a known inhibitor of the MMP-9 receptor, was selected as the control drug and obtained from the PubChem database (Kim *et al.*, 2005). All ligands were then energy-minimized and converted to PDBQT format using OpenBabel v.3.1.1.1 for further analysis.

#### *Active site determination*

For site-specific molecular docking, the receptor's active site was determined via the CASTp v.3.0 (Tian *et al.*, 2018). The protein, uploaded in PDB format, was analyzed, and the active site with the highest surface area and volume was selected as the optimal site for docking simulations.

#### *Molecular docking*

A grid box for molecular docking was defined using the output from CASTp v.3.0, with dimensions of  $68 \times 64 \times 66$  and center coordinates set to  $61.125 \times 29.614 \times 113.283$  along the X, Y, and Z axes, respectively. Molecular docking was conducted using EasyDock Vina v.2.237 (Minibaeva *et al.*, 2023). The receptor-ligand complexes were visualized with Discovery Studio (Islam *et al.*, 2023). Following docking, the selected phytocompounds were evaluated through ADMET analysis for further assessment.

### *ADMET properties evaluation*

The ADMET evaluation was performed using SwissADME to evaluate the drug-likeness of the compounds (Daina *et al.*, 2017). Toxicity parameters were then analyzed using the STopTox server (Borba *et al.*, 2022). For both analyses, the compounds were provided in SMILES format.

## *Molecular dynamics (MD) simulation*

To examine the thermodynamic behavior of the control drug and lead compounds, molecular dynamics (MD) simulations were performed on an Ubuntu 22.04 (Jammy Jellyfish) operating system using the Desmond module of the Schrödinger 2020-1 package, over a duration of 100 ns (Rahman *et al.*, 2024). The simulated systems were solvated with the SPC water model in orthorhombic periodic boundary boxes. The OPLS4 force field was applied for energy optimization of the solvated framework, with the default settings in Desmond. Simulations were processed using the NPT ensemble, with Nose–Hoover temperature coupling and isotropic pressure scaling. The trajectories were sampled at 100 ps intervals, resulting in approximately 1000 frames for subsequent analysis, while energy data were recorded at 1.2 ps intervals.

## *Principal component analysis and Gibbs FEL*

To analyze the essential dynamics of the top selected leads and the control drug, principal component analysis (PCA) was conducted using the Statistics Kingdom server [\(https://www.statskingdom.com/\).](https://www.statskingdom.com/).) RMSD and Rg coordinates for all simulated frames were input as two series to perform PCA using a covariance matrix. For Gibbs free energy landscape (FEL) analysis, a Python script was employed on Ubuntu Focal Fossa 20.04.6 LTS. The PCA data was saved in a CSV file for easy manipulation via the Pandas library. The script utilized essential libraries such as NumPy for numerical operations, facilitating the efficient computation of statistical metrics, and Matplotlib for data visualization. A 2D histogram of the PCA results was generated to estimate the probability distribution of data points, enabling the calculation of Gibbs free energy based on Boltzmann statistics (Ahmed and Rahman, 2024).

#### *Molecular reactivity analysis*

Quantum mechanics-based DFT calculation was performed to estimate molecular reactivity for the lead compounds and control drug employing Avogadro and ORCA v.4.1.1 software packages (Snyder and Kucukkal, 2021; Paul *et al.*, 2023). Input files were prepared in Avogadro for subsequent processing in ORCA. Geometry optimization was performed, employing the B3LYP-D3 functional and the 6-31G (d, p) basis set to estimate the HOMO-LUMO (Highest Occupied Molecular Orbital-Lowest Unoccupied Molecular Orbital) energy gap.

### **Results and Discussion**

#### *Angiosperm flora: Annotation of Liliopsida*

The present study identified 201 taxa across 46 genera and 25 families within the class Liliopsida (monocotyledons) from Rajbari district (Table 1). Among the families, Poaceae emerged as the largest, comprising 58 taxa under 36 genera, followed by Araceae (26 species) and Cyperaceae (17 species). Figure 2 illustrates the ten largest families along with the number of genera and species. Agavaceae and Dioscoraceae each contribute 9 species, while the Liliaceae includes 8 species. The families Aponogetonaceae, Heliconiaceae, Lemnaceae, Orchidaceae, and Pontederiaceae each contain 3 species. Eight families, including Aloaceae, Cannaceae, Costaceae, Marantaceae, Musaceae, Smilacaceae, Strelitziaceae and Typhaceae are represented by a single species each. Among the genera, *Cyperus* stands out as the largest with 17 species, followed by *Dioscorea* with 10 species. The genera *Colocasia, Commelina* and *Digitaria* each contain 5 species, while *Alocasia, Bambusa, Eragrostis, Fimbristylis* and *Paspalum* are represented by 4 species each.

Vegetation analysis shows that the majority of the species are herbs, representing 79.6% (140 species) of the total, followed by climbers (7.96%), trees (7.46%), shrubs (2.98%), and epiphytes (1.99%). Habitat analysis reveals that fallow lands (open fields) constitute 24.38% of the identified species, followed by homestead (22.89%), scrub jungles (16.91%), agricultural fields (14.93%), aquatic (11.44%), and road sides (9.45%).

Taxa	Local name			Habit Habitat Distribution	Vouchers
<b>Alismataceae</b>					
Sagittaria guayanensis subsp. lappula (D. Don) Bogin	Muamia	Her	Aqu	Rs, Ka, Ba, Go, Pa	Miruna 1482
S. sagittifolia L.	Muamia	Her	Aqu	Rs, Ka, Ba, Go, Pa	Miruna 242
Hydrocharitaceae					
Hydrilla verticillata (L.f.) Royle	Kureli	Her	Aqu	Rs, Ka, Ba, Go, Pa	Miruna 2097
Nechamandra alternifolia (Roxb.) Thw.	Sheola	Her	Aqu	Rs, Ka, Ba, Go, Pa	Miruna 1749
Ottelia alismoides (L.) Pers.	Kuchkalai	Her	Aqu	Rs, Ka, Ba, Go, Pa	Miruna 1438
Vallisneria spiralis L.	Pata seola	Her	Aqu	Rs, Ka, Ba, Go, Pa	Miruna 1779
Aponogetonaceae					
Aponogeton appendiculatus Bruggen	Ghetu	Her	Aqu	Rs, Ba, Ka, Go, Pa	Miruna 185
Aponogeton crispus Thunb.	Ghechu	Her	Aqu	Rs, Ba, Ka, Go, Pa	Miruna 231
Aponogeton natans (L.) Engl. & Krause	Apanogeton	Her	Aqu	Rs, Ba, Ka, Go, Pa	Miruna 205
Arecaceae					
Areca catechu L.	Supari	Tre	Hom	Rs, Ka, Ba, Go, Pa	Miruna 1595
Borassus flabellifer L.	Tal	Tre	Roa	Rs, Ka, Ba, Go, Pa	Miruna 1673
Calamus viminalis Willd.	Bet	Cli	Scr	Rs, Ka, Ba, Go, Pa	Miruna 61
Caryota mitis Lour.	Bottle palm	Tre	Hom	Rs, Ka, Ba, Go, Pa	Miruna 1759
Caryota urens L.	Sagu palm	Tre	Hom	Rs, Ka, Ba, Go, Pa	Miruna 1663
Chrysalidocarpus lutescens (Bory) H. Wen.	Holud palm	Tre	Hom	Rs, Ba, Ka, Go, Pa	Miruna 1673
Cocos nucifera L.	Narikel	Tre	Hom	Rs, Ka, Ba, Go, Pa	Miruna 320
Corypha taliera Roxb.	Tali	Tre	Hom	Rs	Miruna 1449
Elaeis guineensis Jacq.	Oil Palm	Tre	Hom	Rs, Ka, Ba, Go, Pa	Miruna 1565
Licuala spinosa Wurmb	Unknown	Shr	Hom	Rs, Ka, Ba, Go, Pa	Miruna 1774
Phoenix sylvestris (L.) Roxb.	Khejur	Tre	Roa	Rs, Ka, Ba, Go, Pa	Miruna 1593
<b>Araceae</b>					
Adelonema wallisii (Regel) S.Y. Wong & Croat	Jongli kachu	Her	Scr	Rs, Go, Bal, Pa, Ka Miruna 1015	
Aglaonema costatum N.E. Brown	<b>Nemacos</b>	Her	Hom	Rs, Ka, Ba, Go, Pa	Miruna 1658
Aglaonema robeleynii (Van Geert) Pitcher & Manda	Nemacris	Her	Hom	Rs, Ka, Ba, Go, Pa	Miruna 1659
Alocasia cucullata (Lour.) G. Don	Bish kachu	Her	Scru	Rs, Ka, Ba, Go, Pa	Miruna 584
Alocasia fornicata (Roxb.) Schott	Salu kachu	Her	Hom	Rs, Ka, Ba, Go, Pa	Miruna 976
Alocasia macrorrhizos (L.) G. Don	Man kachu	Her	Scr	Rs, Ka, Ba, Go, Pa	Miruna 975
Alocasia portei Schott	Puti kachu	Her	Scr	Rs, Ka, Ba, Go, Pa	Miruna 977
Amorphophallus bulbifer (Schott) Blume	Jongle ol	Her	Scr	Rs, Ka, Ba, Go, Pa	Miruna 978
Amorphophallus paeoniifolius (Dennt.) Nicol.	Olkachu	Her	Agr	Rs, Ka	Miruna 586
Caladium bicolor (Ait.) Vent.	Diranga kachu Her		Hom	Rs, Ka, Ba, Go, Pa	Miruna 979
Caladium humboldtii (Raf.) Schott	Befula kachu	Her	Hom	Rs, Ka, Ba, Go, Pa	Miruna 980
Colocasia esculenta (L.) Schott	Kachu	Her	Agr	Rs, Ka, Ba, Go, Pa	Miruna 981
Colocasia fallax Schott	Ranga kachu	Her	Hom	Rs, Ka, Ba, Go, Pa	Miruna 982
Colocasia mannii Hook. f.	Mani kachu	Her	Scr	Rs, Ka, Ba, Go, Pa	Miruna 1719
Epipremnum aureum (Linden & Andr.) G.S. Pargacha		Cli	Roa	Rs, Go, Bal, Pa, Ka Miruna 1723	
Bunting					
Lasia spinosa (L.) Thw.	Kanta kachu	Her	Scru	Rs, Go, Bal, Pa, Ka Miruna 329	

**Table 1. List of Liliopsida taxa in Rajbari district with local name, habit, habitat, distribution and voucher numbers.**





## **Table 1 contd.**







## **Table 1 contd.**







**Habit:** Her: Herb, Shr: Shrub, Tre: Tree, Cli: Climber, Epi: Epiphyte; **Habitat**: Aqu: Aquatic, Scr: Scrub jungles, Roa: Roadside, Hom: Homestead, Agr: Agricultural field, Ope: Open field; **Distribution**; Rs: Rajbari sadar, Ba: Baliakandi, Go: Goalondo, Ka: Kalukhali, Pa: Pangsha.



Fig. 2. Ten dominant families of Liliopsida illustrating the number of genera and species in Rajbari.

The study area supports a variety of aquatic habitats including ponds, beels, lowlands, and rivers, where many monocot species are found, and some of the common aquatic species are *Aponogeton appendiculatus*, *Aponogeton natans, Eichhornia crassipes, Hydrilla verticillata, Ottelia alismoides, Pistia stratiotes, Sagittaria sagittifolia, Typha elephantina*, *Vallisneria spiralis, Wolffia arrhiza* etc. A total of 25 medicinal plants used by traditional healers in the study area for treatment of different diseases, and notable species are *Aloe vera, Amorphophallus paeoniifolius, Colocasia esculenta*, *Hellenia speciosa*, *Curcuma amada*, *Cyperus rotundus, Dioscorea alata, Kaempferia galanga, Lasia spinosa, Pontederia hastata*, *Vanda tessellata* and *Zingiber zerumbet.* Some medicinally important and rare species are shown in Figure 3. Field observations have identified several rare species, such as *Coix aquatica*, *Schumannianthus benthamianus*, *Bulbostylis barbata* and *Bambusa salarkhanii*, which warrants further attention for conservation efforts.

While numerous studies have focused on the angiosperm flora of several upazilas in Bangladesh (Islam *et al*., 2009; Rahman *et al*., 2019a,b; Sarker *et al*., 2013; Sajib *et al*., 2014; Mahmudah *et al*., 2017), little effort has been made to produce comprehensive district-level flora. Khanam and Khan (2020) documented 168 species of Liliopsida (monocotyledons) from Narsinghdi district, whereas Hossain *et al.* (2021) identified 144 taxa from Liliopsida in the coastal district Satkhira, and Islam *et al.* (2022) reported a mere 133 taxa from Borguna district. In contrast, higher numbers of monocotyledonous taxa were recorded in Chapai Nawabganj and Rangpur districts, with 224 and 211 taxa, respectively (Islam and Khan, 2024; Khan *et al*., 2021).



Fig. 3. Some medicinal and rare plants of Rajbari district. A. *Amorphophallus paeoniifolius*, B. *Bambusa salarkhanii,* C. *Corypha taliera,* D. *Curcuma amada,* E. *Cyanotis cristata*, F. *Cyperus michelianus,* G. *Cyrtococcum accrescens,* H. *Dactyloctenium aegyptium,* I. *Heliconia rostrata,* J. *Hellenia speciosa,* K. *Kaempferia galanga,* L. *Nechamandra alternifolia*, M. *Pontederia hastata*, N. *Schumannianthus benthamianus*, O. *Syngonium podophyllum*, P. *Zingiber zerumbet*.

Compared to the earlier reports, our study, with 201 monocotyledonous taxa from Rajbari, surpasses the figures reported for Narsinghdi, Borguna, Satkhira, and Patuakhali (Sultana, 2012; Khanam and Khan, 2020; Hossain *et al*., 2021; Islam *et al*., 2022), yet falls slightly short compared to the monocot floras of Rangpur and Chapai Nawabganj flora (Khan *et al*., 2021; Islam and Khan, 2024).

### *Molecular docking analysis*

A total of 27 unique active site residues were identified in the MMP-9 receptor (Fig. 4). The surface area (SA) was calculated as 205.130 Å<sup>2</sup>, with a volume of 102.572 Å<sup>3</sup>, making the active site as a significant binding region for molecular docking analysis. Performing site-specific docking with active site residues is crucial in accurately predicting the binding interactions between ligands and their target proteins. Unlike blind docking, which assesses potential binding across the entire protein surface, site-specific docking focuses on predefined active sites, enhancing the precision of ligand placement. This targeted approach allows for a more refined understanding of ligand-receptor interactions, increasing the likelihood of identifying effective drug candidates (Ahmed and Rahman, 2024).



Fig. 4. Determination of the best ranked binding site in MMP-9 receptor. Rank 1 cavity was determined as the final binding site for its highest surface area and volumetric features. A. Rank 1 cavity, B. Rank 2 cavity.

Molecular docking of 22 phytocompounds of *A. paeoniifolius* revealed binding affinity ranged from -4.1 to -8.1 kcal/mol (Table 2). Alpha-carotene showed the highest affinity (-8.1 kcal/mol), while Oxalic acid demonstrated the lowest affinity (-4.1 kcal/mol). Doxycycline, as a control, scored -6.0 kcal/mol and comparing with it, a total of nine phytocompounds scored better than the control. These nine compounds were put forward for second-step screening via ADMET assay that revealed two lead compounds such as Riboflavin and Lupeol. The docked complexes of the leads and control drug are visualized in the Figure 5.

	No. Ligands	<b>IMPAAT ID/</b>	Chemical	Molecular	Binding affinity
		PubChem CID	formula	weight $(g/mol)$	(kcal/mol)
$\mathbf{1}$	Alpha-carotene	IMPHY011609	$C_{40}H_{56}$	536.9	$-8.1$
2	Riboflavin	IMPHY000846	$C_{17}H_{20}N_4O_6$	376.4	$-7.9$
3	Stigmasterol	IMPHY014842	$C_{29}H_{48}O$	412.7	$-7.6$
$\overline{4}$	Quercetin	IMPHY004619	$C_{15}H_{10}O_7$	302.2	$-7.2$
5	Beta-sitosterol	IMPHY014836	$C_{29}H_{50}O$	414.7	$-6.9$
6	Retinol	IMPHY001308	$C_{20}H_{30}O$	286.5	$-6.3$
7	Amylotetraose	<b>IMPHY008888</b>	$C_{24}H_{42}O_{21}$	666.6	$-6.3$
8	Betulinic acid	IMPHY012003	$C_{30}H_{48}O_3$	456.7	$-6.1$
9	<b>Lupeol</b>	IMPHY012473	$C_{30}H_{50}O$	426.7	$-6.1$
10	1-ethoxy-4- $[(Z)-2$ -nitroprop-1-	5373673	$C_{11}H_{13}NO_3$	207.2	$-5.9$
	enyl] benzene				
11	Palmitic acid	IMPHY007327	$C_{16}H_{32}O_2$	256.4	$-5.9$
12	D-xylose	IMPHY015116	$C_5H_{10}O_5$	150.1	$-5.9$
13	4,6-Di-tert-butylresorcinol	79337	$C_{14}H_{22}O_2$	222.3	$-5.7$
14	D-galactose	IMPHY012050	$C_6H_{12}O_6$	180.1	$-5.7$
15	Nicotinic acid	IMPHY007357	$C_6H_5NO_2$	123.1	$-5.6$
16	L-rhamnose	IMPHY015056	$C_6H_{12}O_5$	164.1	$-5.6$
17	Thiamine	IMPHY000005	$C_{12}H_{17}N_4OS^+$	265.3	$-5.5$
18	Phytic acid	IMPHY007365	$C_6H_{18}O_{24}P_6$	660.0	$-5.5$
19	Beta-sitosterol palmitate	IMPHY003933	$C_{45}H_{80}O_2$	653.1	$-5.4$
20	Triacontane	IMPHY009413	$C_{30}H_{62}$	422.8	$-5.0$
21	Calcium oxalate	IMPHY003530	$C_2$ CaO <sub>4</sub>	128.1	$-4.2$
22	Oxalic acid	IMPHY007450	$C_2H_2O_4$	90.0	$-4.1$
23	Doxycycline (control)	54671203	$C_{22}H_{24}N_2O_8$	444.4	$-6.0$

**Table 2. Binding affinities of** *A. paeoniifolius* **phytocompounds against the receptor MMP-9.**

### *Molecular interaction analysis*

The molecular interaction study revealed similar interaction patterns between the lead compounds and Doxycycline. Among the two leads and control, conventional hydrogen bonds (CHBs) were observed only in Riboflavin, supporting its superiority as potential anticancer drug candidate (Table 3). Riboflavin interacted with residues Gly186, Leu187, Leu188, His401, Glu402, His405, His411 and Met422 (Fig. 6A), forming CHBs with Gly186 and Met422 residues, while other residues were involved in hydrophobic interactions. Lupeol showed interactions with Leu187, Leu188, His401, His411, and Pro421 residues (Fig. 6B) where all residues formed hydrophobic interactions. Doxycycline interacted with Phe110, Leu187, His190, and His411 residues with hydrophobic bonding only (Fig. 6C). Hydrogen bonding and hydrophobic interactions are very important for drug binding and efficacy. Hydrogen bonds stabilize ligandreceptor complexes, enhancing specificity and orientation, which improves binding affinity.



Fig. 5. Two lead compounds and control drug showing docked complexes after molecular docking analysis. A. Riboflavin, B. Lupeol, C. Doxycycline (control).

These interactions often dictate the orientation of the ligand within the binding cavity, facilitating effective biological activity. On the contrary, hydrophobic interactions promote the exclusion of water molecules from the binding site, further increasing the stability of the ligandreceptor complex. These interactions occur between nonpolar residues and contribute significantly to the overall binding energy (Ahmed *et al.*, 2023b).



Fig. 6. Two-dimensional molecular interaction analysis of the two leads and control drug targeting MMP-9 protein. A. Riboflavin, B. Lupeol, C. Doxycycline.

**Table 3. Evaluation of molecular interaction between the leads and the control drug targeting MMP-9 protein.**

Ligands	Binding sites	Hydrogen-		Hydrogen Hydrophobic-	Binding
		bonding residues	<b>bonds</b>	interaction	affinity
		(Distance in $\AA$ )	number		(kcal/mol)
Riboflavin	Gly186, Leu187, Leu188, Gly186 <sup><math>(2.54)</math></sup> ,			Leu187, Leu188,	$-7.9$
	His401, Glu402, His405, Met422 <sup>(2.59)</sup>			His401, Glu402,	
	His411, Met422			His405, His411	
Lupeol	Leu187, Leu188, His401, No residues		$\Omega$	Leu187, Leu188,	$-6.1$
	His411, Pro421			His401, His411, Pro421	
	Doxycycline Phe110, Leu187, His190, No residues		$\Omega$	Phe110, Leu187,	$-6.0$
(control)	His411			His190, His411	

#### *ADMET evaluation*

ADMET study revealed drug-likeness of Riboflavin and Lupeol in comparison with Doxycycline (Table 4, Fig. 7). Among the lead compounds, Lupeol exhibited the highest molecular weight (426.7 g/mol). The H-bond accepting and donating profiles of Riboflavin was closely comparable to those of Doxycycline, while Lupeol demonstrated only one H-bond donor and acceptor. Lupeol had the highest molar refractivity score, while Riboflavin had the lowest. TPSA was lowest for Lupeol, while it was highest for Doxycycline. The gastrointestinal absorption capacity of the two lead compounds were very similar to that of the control drug. The CYP isoform inhibition profiles of both leads and Doxycycline were alike, with none showing inhibition against various CYP isoforms (Table 4). In terms of solubility, Riboflavin was highly soluble, Doxycycline was soluble and Lupeol exhibited poor solubility. Riboflavin adhered to Lipinski's rule of five with zero violation, while Lupeol and Doxycycline demonstrated one violation each which is acceptable. In toxicity analysis, Riboflavin and Lupeol revealed satisfactory results with no major undesirable complications, similar to the control drug Doxycycline. The ADMET results of the present investigation were consistent with previous SBDD studies (Rahman *et al*., 2024; Ahmed *et al*., 2023a,b; Ahmed *et al*., 2024).



Fig. 7. Drug-likeness and oral bioavailability evaluation of the leads and Doxycycline. LIPO indicates lipophilicity, INSOLU depicts insolubility, INSATU suggests insaturation index, FLEX points flexibility, SIZE implies molecular weight, and POLAR denotes polarity. Pink region reflects the best zone while red line denotes best fit. A. Riboflavin, B. Lupeol, C. Doxycycline.

#### *Molecular dynamics simulation*

The MD simulation analysis unveiled structural stability and compactness of Riboflavin and Lupeol (Table 5). Both the leads showed similar mean values in RMSD (root mean square deviation), RMSF (root mean square fluctuation), Rg (radius of gyration), and SASA (solvent accessible surface area). The RMSD analysis showcased the stability of Riboflavin and Lupeol after 30 ns and continued to stable until 100 ns (Fig. 8A). Riboflavin and Lupeol closely followed each other than Doxycycline. The control drug exhibited a minor fluctuation between 12 to 18 ns, stabilized until 85 ns, and then showed a slight upward movement, becoming stable again with a downward movement near 100 ns. The RMSF analysis showed fluctuations in a narrow range (Fig. 8B). The mean RMSF varied from  $1.05 \pm 0.78$  to  $1.40 \pm 1.07$  Å, where Doxycycline scored the lowest and Riboflavin scored the highest. Although the RMSF graph begins with residue index 1, this corresponds to the actual sequence of the protein. Specifically, the first residue in the graph (index 1) corresponds to Phe110 in the protein sequence, the second residue (index 2) corresponds to Val111, and so on. This consistent pattern ensures that the fluctuations observed in the RMSF graph can be directly mapped to the biologically relevant residue positions, despite the indexing convention used by the simulation software.

Parameters	Molecule	Riboflavin	Lupeol	Doxycycline
Physicochemical	Formula	$C_{17}H_{20}N_{4}O_{6}$	$C_{30}H_{50}O$	$C_{22}H_{24}N_2O_8$
properties	Molecular weight $(g/mol)$	376.4	426.7	444.4
	H-bond acceptors	8	1	9
	H-bond donors	5	1	6
	Molar refractivity	96.99	135.14	110.91
	<b>TPSA</b>	$161.56 \, \text{\AA}^2$	$20.23 \text{ Å}^2$	181.62 $\AA^2$
Lipophilicity	<b>iLOGP</b>	1.63	4.72	1.82
	XLOGP3	$-1.46$	9.87	0.54
	<b>WLOGP</b>	$-1.68$	8.02	$-0.50$
	<b>MLOGP</b>	$-0.54$	6.92	$-2.08$
	Silicos-IT Log P	1.09	6.82	$-0.98$
	Consensus Log P	$-0.19$	7.27	$-0.24$
Pharmacokinetics	GI absorption	Low	Low	Low
	CYP1A2	N <sub>0</sub>	N <sub>0</sub>	No
	CYP2C19	No	N <sub>0</sub>	N <sub>0</sub>
	CYP2C9	No	N <sub>0</sub>	N <sub>0</sub>
	Log Kp	$-9.63$ cm/s	$-1.90$ cm/s	$-8.63$ cm/s
Water solubility	Log S	$-1.31$	$-8.64$	$-2.94$
(ESOL)	Solubility (mg/ml)	$1.85E + 01$	9.83E-07	5.07E-01
	Solubility (mol/l)	4.93E-02	2.30E-08	1.14E-03
	Class	Very soluble	Poorly soluble	Soluble
Drug likeness	Lipinski (violations)	$\Omega$	1	1
	Bioavailability score	0.55	0.55	0.11
Medicinal	PAINS (alerts)	$\theta$	$\theta$	$\theta$
chemistry	Synthetic accessibility	3.84	5.49	5.25
Toxicity	Acute inhalation toxicity	N <sub>0</sub>	N <sub>0</sub>	N <sub>o</sub>
	Acute oral toxicity	N <sub>o</sub>	Yes	No
	Acute dermal toxicity	N <sub>o</sub>	N <sub>0</sub>	No
	Eye irritation and corrosion	Yes	N <sub>0</sub>	Yes
	Skin sensitization	N <sub>0</sub>	N <sub>0</sub>	N <sub>0</sub>
	Skin irritation and corrosion	N <sub>o</sub>	Yes	No

**Table 4. ADMET properties evaluation of the lead candidates and Doxycycline.**

Tested systems	PL RMSD $(\AA)$	$RMSF(\AA)$	$Rg(\AA)$	$SASA(\AA^2)$
Riboflavin	$2.92 + 0.41$	$1.40 + 1.07$	$3.96 + 0.09$	$183.01 \pm 39.93$
Lupeol	$3.04 + 0.55$	$1.23 + 1.03$	$4.26 + 0.03$	$235.24 + 38.18$
Doxycycline (control)	$2.11 + 0.43$	$1.05 + 0.78$	$3.85 + 0.04$	$260.95 + 30.59$

**Table 5. Molecular dynamics simulation trajectory analysis of the leads and Doxycycline.**

The radius of gyration (Rg) study further corroborated the drug candidacy of the two lead compounds, as both exhibited stability without any drastic fluctuations (Fig. 8C). Lupeol maintained a very steady trajectory, with fluctuations less than (0.2 Å). Riboflavin also maintained steady trajectory but at around 35 to 52 ns, it showed a minor downward movement, during which it intersected with Doxycycline. From 52 ns onwards, Riboflavin stabilized, maintaining a steady distance from both Doxycycline and Lupeol. Doxycycline demonstrated a few initial movements from 0 to 5 ns, but after 5 ns, it remained stable throughout the 100 ns. The SASA analysis bolstered the drug candidacy of the two leads as mean SASA score was lower for the two leads compared to Doxycycline (Table 5). The lowest mean SASA score was found in Riboflavin  $(183.01 \pm 39.93)$   $\AA^2$ , followed by Lupeol (235.24  $\pm$  38.18)  $\AA^2$ , and Doxycycline (260.95  $\pm$  30.59)  $\AA^2$ . The trajectory graph elucidated the compactness of the two leads with the progression of time (Fig. 8D). Riboflavin and Lupeol showed minor primary movements from 0 to 55 ns, after which they maintained a consistent distance with each other and demonstrated a steady downward trend until 100 ns. Doxycycline also displayed a downward stabilization trend from around 50 ns until 88 ns, after which it showed a slight upward movement from 88 to 96 ns, and became stabilized again near 100 ns.



Fig. 8. Molecular dynamics simulation study showing dynamic stability of the tested systems. A. Trajectory based on protein-ligand RMSD, B. Trajectory based on RMSF, C. Trajectory based on Rg, D. Trajectory based on SASA.

The protein-ligand contact analysis revealed that Riboflavin formed the most extensive protein-ligand interactions, surpassing both Doxycycline and Lupeol (Fig. 9). Riboflavin exhibited the highest interaction fraction with Phe110, followed by His175, His190, and other residues (Fig. 9A), signifying its robust binding potential. Lupeol, which showed predominant hydrophobic interactions, formed its strongest contacts with Tyr393, followed by Asp185 and Leu188 (Fig. 9B), underscoring the role of nonpolar interactions in its binding affinity. Doxycycline demonstrated the highest interaction with Tyr420, followed by Asp185 and Leu187 (Fig. 9C), reflecting its distinct interaction pattern. These variations in binding profiles suggest differential stability and affinity of the compounds within the active site, emphasizing the importance of diverse interactions, especially hydrophobic and hydrogen bonding, in determining the efficacy of ligand binding.



Fig. 9. Evaluation of protein-ligand contacts during molecular dynamics simulation. A. Riboflavin, B. Lupeol, C. Doxycycline.

## *PCA and Gibbs FEL*

The PCA and Gibbs FEL analyses provided crucial insights into the essential dynamics and conformational stability of Riboflavin and Lupeol compared to Doxycycline (Fig. 10).



Fig. 10. Evaluation of essential molecular dynamics based on principal components analysis and Gibbs free energy landscapes. A. Riboflavin, B. Lupeol, C. Doxycycline, D. Superimposition of the two leads and Doxycycline.

The PCA phase-space distribution indicated that Riboflavin exhibited the highest degree of compactness, followed by Lupeol and Doxycycline, suggesting that Riboflavin maintains the most stable conformation during simulation. This was further corroborated by the Gibbs FEL analysis, which underscored the stability of Riboflavin by displaying a more centralized and extensive lowenergy region (denoted by blue space), reflecting its preference for energetically favorable conformations (Fig. 10). Lupeol showed moderate stability, with a relatively smaller low-energy region, while Doxycycline displayed the least stable dynamics, with more dispersed energy states. These findings suggest that both Riboflavin and Lupeol demonstrate superior conformational stability compared to Doxycycline, potentially enhancing their suitability as drug candidates. The PCA and Gibbs FEL analyses align with previously published structure-based drug design study on *Chamaecostus cuspidatus* targeting DPP4 (Ahmed and Rahman, 2024).

#### *Molecular reactivity evaluation*

Molecular reactivity analysis revealed the energy levels of the electrons in the HOMO and LUMO states (Fig. 11). The energy of the HOMO state was the highest for Riboflavin (-6.496 eV), followed by Lupeol (-6.344 eV), and Doxycycline (-5.748 eV). For the LUMO state, the



Fig. 11. DFT-based molecular reactivity analysis of the lead compounds and control drug. A. Riboflavin, B. Lupeol, C. Doxycycline (control).

highest energy was recorded for Riboflavin (-3.009 eV), followed by Doxycycline (-2.370 eV), and Lupeol (0.571 eV). The band energy gap ( $\Delta E$ ) was 3.487, 6.915, and 3.378 eV for Riboflavin, Lupeol, and Doxycycline, respectively (Fig. 11). The HOMO represents the orbital with the highest energy-containing electrons in a molecule. The electrons in the HOMO are generally the most reactive due to their high energy state and are thus the easiest to excite or donate to another molecule. The LUMO is the lowest energy orbital that does not contain electrons but can accept them. The LUMO is critical for understanding molecular interactions, as it is the orbital most likely to accept electrons (Paul *et al.,* 2023). The energy difference between HOMO and LUMO plays a critical role in understanding the molecular reactivity and kinetic stability of the lead compounds (Ahmed *et al.*, 2023a). Doxycycline revealed the highest molecular reactivity with its lowest ΔE score of 3.378 eV. Riboflavin demonstrated closely similar results to Doxycyline with band energy gap of 3.487 eV. Lupeol showed the highest band energy gap of 6.915 eV and became the least reactive and most kinetically stable compound. The molecular reactivity results of the present investigation were congruent to the DFT analysis of *Amberboa ramosa*  phytocompounds (Paul *et al.*, 2023).

With advanced computational biology techniques, our current investigation integrates classical plant taxonomy with drug design endeavor. This study would enrich the floristics knowledge of Liliopsida in Rajbari district and promote the discovery of anticancer agents targeting colorectal cancer. Furthermore, the study will encourage future floristics research to integrate taxonomic insights with bioinformatics, facilitating successful drug discovery from natural compounds and paving the way for exploring alternative medicines.

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