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In Silico Screening and Molecular Docking of *Cynodon dactylon* Phytochemicals Against COPD-Associated Proteins

Namita Krishnakumar[1,*], Deekshitha M.[2]

Abstract

Chronic Obstructive Pulmonary Disease or COPD is a pulmonary disease that obstructs airways and alveoli accompanied by respiratory issues like emphysema and bronchitis. This disease is caused mainly by inflammatory responses of the body to foreign particles that enter the respiratory path including tobacco smoke, air pollutants and irritants. The hallmark of COPD is excessive inflammation caused by imbalance in protease anti-protease activity. Proteases – like elastase – breakdown the ECM of alveoli in lung and the antiproteases, like alpha-1-antitrypsin, help curb the protease activity protecting the lung tissue. The imbalance here causes excessive elastase activity leading to deterioration of lung tissue. Drugs have been administered for the treatment of COPD – such as short- and long-acting β2-agonists (SABA and LABA) – but these primarily target specific pathways. To help in effective COPD management, research is being pursued on drugs and lead molecules that can target multiple COPD pathways with less side effects. Cynodon dactylon or Durva is used in traditional Ayurvedic and folk medicine for its anti-inflammatory, wound healing and anti-oxidant properties. Owing to the inflammatory response in COPD, Bermuda grass (Durva) seemed to be a viable subject of study to investigate its COPD targets and the properties of its phytocompounds. This in silico study aimed to understand the potential of phytocompounds present in Durva for multiple pathway COPD treatment. It includes molecular docking of Durva phytocompounds with proteins, like MMP9, IL-8, and TNF alpha, proteins involved in major COPD pathways to evaluate binding affinity and potential for lead molecules.

Keywords: COPD, emphysema, bronchitis, tobacco smoke, inflammation, *Cynodon dactylon*, anti-inflammatory, in silico, molecular docking

INTRODUCTION

COPD, also known as Chronic Obstructive Pulmonary Disease, is a chronic disease which is caused due to severe inflammation of lung tissue. This characteristic inflammation in the lungs is a significant marker in COPD; it occurs due to excessive production of neutrophils and macrophages owing to the foreign particles that enter the lungs and respiratory tract [1]. These foreign particles usually include cigarette smoke, air pollutants, irritants, etc. COPD essentially comprises of 2 types of severe diseases – emphysema and bronchitis [2, 3]. Emphysema mainly damages the alveoli in the lungs. In normal conditions, alveoli usually expand and relaxes to allow movement of air in them. In emphysema, neutrophils are in surplus and produce excessive elastase and reactive oxygen species (ROS) which destroy the alveolar walls [4].

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Chronic bronchitis is another severe disease associated with COPD. Bronchitis refers to inflammation of bronchi, which leads to difficulty in breathing, accompanied by emphysema. This condition could be potentially fatal as patients cannot inhale properly and the gaseous exchange is impaired in lungs [5]. Goblet cells and submucosal glands present in the bronchi are affected by irritants and secrete more mucous leading to severe bouts of cough and airflow obstruction due to narrowing of pathway [6]. In COPD, these 2 diseases usually occur in a combined form making it chronic [7]. In COPD multiple pathways are involved, in this study we focus on proteins of 3 main pathways: NF-κB Signaling Pathway, Protease–Antiprotease Imbalance Pathway and TNF-α / MAPK Pathway [8–10].

NF-κB Signaling Pathway which is Nuclear Factor kappa light-chain-enhancer of activated B cells. This pathway is initiated by TNF alpha molecules. TNF alpha molecules not only have apoptosis function but also allow for cell survival using their inflammation pathway by cytokine production in NF kB pathway [6]. In a cell, when TNF-α binds to TNFR1, the NF-κB pathway is activated, which results in TRADD replacing SODD. RIP activates IKK and TRAF2 recruits IAP to prevent apoptosis and trigger inflammation. IKK phosphorylates the NF-κB–IκBα complex leading to IκBα degradation and NF-κB activation, which then enters the nucleus to induce cytokines like IL-6 and IL-8 [5, 11]. COPD is also characterized mainly by protease–antiprotease imbalance driven by MMP9. The imbalance is characterized by high amounts of elastase and lesser concentrations of antiproteases like α-1 antitrypsin and Tissue Inhibitors of Metalloproteinases (TIMPs) [12]. In emphysema, excessive secretion of MMP9 overwhelms the antiproteases leading to MMP9 mediated destruction of alveolar sacs, unregulated ECM regulation and thus gaseous exchange is hampered [13]. In normal conditions, MAPKs maintain immune responses without causing tissue damage. ERK promotes controlled cell proliferation and survival, p38 governs moderate inflammatory responses and stress adaption, while JNK manages apoptosis and tissue homeostasis [14].

In COPD, triggers – like cigarette smoke and TNF-α – activate cell surface receptors, initiating the MAPK cascade (ERK, JNK, p38). Activated MAPKs stimulate transcription factors, increasing inflammatory cytokines and MMP-9, leading to protease–antiprotease imbalance and alveolar destruction.

COPD treatments have primarily aimed to reduce inflammation and improve protease–antiprotease balance. Previous studies have inferred that anti-inflammatory compounds are effective in managing COPD [15]. Current treatments – like Bronchodilators, corticosteroids, PDE4 inhibitors – are used in combinations and usually target inflammation. Currently, no single therapy effectively targets the multiple molecular pathways driving COPD, highlighting the need for multi-targeted approaches. Hence, there's increased research in multi-pathway targeting drug to treat COPD. This study tries to learn if the compound from one plant can target the 3 main pathway proteins of COPD. In this study, the focus is mainly on 3 proteins – MMP9, IL-8 and TNF alpha.

Cynodon dactylon popularly known as Durva grass or Bermuda grass is an herb that is native to tropics along Asia, Africa and Americas [16]. This plant has been used in traditional medicines including Ayurveda for its anti-inflammatory, anti-oxidant, wound healing and hepato-curing properties. Durva has been used for bleeding, infections and inflammatory conditions, showing huge pharmacological potential. Modern phytochemical analyzes have revealed that *Cynodon dactylon* contains a diverse array of bioactive compounds including flavonoids, alkaloids, terpenoids, and phenolic acids, many of which exhibit strong anti-inflammatory and antioxidant activities [17]. These features provide a scientific basis for investigating its potential in respiratory diseases characterized by chronic inflammation and oxidative stress such as COPD. Durva phytocompounds are expected to help in restoring protease–antiprotease imbalance, lowering MMP9 activity, reducing alveolar wall loss. Additionally, also blocking activation of proinflammatory signalling pathways like NFkB and MAPK pathways. These phytocompounds inhibit excessive cytokine production, decrease neutrophil influx, and lessen tissue damage caused by ROS and elastase [18]. Durva thus is a viable option for this study as it affects both pro-inflammatory and proteolytic pathways. To assess how *C. dactylon* phytocompounds

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interact with important COPD targets (such as MMP-9, TNF-α, and MAPKs), we chose them for in silico molecular docking experiments. The goal of this study was to find potential lead compounds that might be further developed for pharmacological validation of COPD.

METHODOLOGY

In silico Retrieval of Phytocompounds from Durva Plant

All the phytocompounds present in Durva (*Cynodon dactylon*) were retrieved using IMPPAT database (Indian Medicinal Plants, Phytochemistry and Therapeutics – https://cb.imsc.res.in/imppat/). PubChem database (https://pubchem.ncbi.nlm.nih.gov/) was used to retrieve the canonical smiles and PubChem ID of compounds. IMPPAT consists of the concise list of phytochemicals present in traditional Indian plants including *Cynodon dactylon* [18]. IMPPAT also specifies the part of the plant where certain phytochemicals are found. PubChem provides accurate information about compounds and their properties.

Retrieval of Target Proteins from COPD Pathways

Using RCSB PDB (https://www.rcsb.org/), the tertiary structures of proteins were retrieved. All the proteins were determined using X-ray diffraction method. RCSB PDB (Research Collaboratory for Structural Bioinformatics Protein Data Bank) is a database that is used to retrieve tertiary structure of protein in the standard PDB format [19]. This database also gives information about the protein structure including the resolution of the experimentally determined structure. The proteins retrieved were – Tumor Necrosis Factor-α (TNF-α)-5TSW (2.50 Å), Matrix Metalloproteinase-9 (MMP-9)-6ESM (1.10 Å), Interleukin-8 (IL-8)-4XDX (0.95 Å).

Insilico Pharmacological Screening of Retrieved Plant Compounds

Using SwissADME tool (http://www.swissadme.ch/), the compounds previously extracted are analyzed for their ADME properties which include certain conventions like Lipinski rule, GI absorption, BBB permeation, Bioavailability, PAINS and BRENK, and solubility. Solubility of drug in water must be high. Toxicity prediction is carried out by using ProTox tool (https://tox.charite.de/protox3/index.php?site=compound_input) [17]. Accepted classes of toxicity for this study are 4,5 and 6. ProTox tool is used as it is developed using machine learning. The input compounds are compared with the training datasets previously uploaded to tool giving valid results. The screened compounds were retrieved in SDF format from PubChem database.

Protein Purification and Structural Analysis

Protein purification is done using BioVia Discovery studio tool. Removal of water, hetero atoms and ligand group from the protein retrieved from RCSB PDB is carried out to get purified protein, retaining only chain A for each protein. The purification step is done to reduce structural complexity. Protein secondary structure is visualized using PDBsum generate (https://www.ebi.ac.uk/thornton-srv/databases/pdbsum/Generate.html) to analyze the components and to view and analyze the Ramchandran plot of the protein. This helps to validate the structure of the protein.

Molecular Docking and Visualization of Receptor Ligand Complex

In this study, molecular docking is the primary investigative method to validate the receptor ligand binding [20]. PyRx is the bioinformatics tool used in this study for molecular docking. It is based on AutoDock Vina software and has a user-friendly GUI. The molecular docking of the retrieved proteins and ligands were performed. Later, the top interactions were saved as .PDB files. These interactions were viewed in BioVia software. BioVia is used to visualize the receptor ligand interactions too. This tool is used for analyzing the structures and visualization of complexes.

RESULTS

In silico Retrieval of Phytocompounds

The phytocompounds of *Cynodon dactylon* were retrieved from IMPPAT database and cross-referenced with PubChem to obtain – compound name, canonical SMILES and PubChem ID. 53 compounds were retrieved from IMPPAT. These compounds were used for further in silico analysis.

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Retrieval of Target Proteins from COPD Pathways

Three COPD-related target proteins: The proteins retrieved were – Tumor Necrosis Factor-α (TNF-α)-5TSW (2.50 Å), Matrix Metalloproteinase-9 (MMP-9)-6ESM (1.10 Å), Interleukin-8 (IL-8)-4XDX (0.95 Å). 4XDX, 5TSW, and 6ESM, were retrieved from the RCSB Protein Data Bank, as these are major proteins implicated in COPD pathways. They were retrieved from RCSB in the .PDB standard format.

In Silico Pharmacological Screening of Retrieved Plant Compounds

The retrieved 53 compounds were screened for ADME properties using SwissADME tool. This output is downloaded in the .csv format. Further, as shown in Table 1, applying conventions – like Lipinski rule, GI absorption, bioavailability, solubility, PAINS and BRENK – resulted in a total of 7 compounds. After removal of repeated compounds, 5 promising ligands were finalized for further molecular docking.

For the toxicity profile, compounds classified in toxicity classes 4, 5, or 6 are preferred, as these correspond to higher LD50 values, indicating a larger dose required to reach lethality and hence greater safety for human consumption. Syringic acid exhibited an LD50 of 1700 mg/kg (class 4), Apigenin 2500 mg/kg (class 5), Ascorbic acid 3367 mg/kg (class 5), Vanillic acid 2000 mg/kg (class 4), and Tricin 4000 mg/kg (class 5). These results, as observed in Table 2, suggest that all tested compounds fall within moderately low toxicity ranges and thus can be used for further analysis.

Following the in-silico screening, protein purification is carried out.

Table 1. Seven (7) Compounds after SwissADME screening.

Molecule	ESOL class	GI absorption	Lipinski violations	Bioavailability Score	PAINS alerts	Brenk alerts
Syringic acid	Very soluble	High	0	0.56	0	0
Apigenin	Soluble	High	0	0.55	0	0
Ascorbic acid	Highly soluble	High	0	0.56	0	0
Vanillic acid	Soluble	High	0	0.85	0	0
Ergometrine	Soluble	High	0	0.55	0	0
Ergometrinine	Soluble	High	0	0.55	0	0
Tricin	Moderately soluble	High	0	0.55	0	0

Table 2. The 5 ligands after screening and toxicity analysis.

Molecule	Canonical SMILES	Toxicity class	LD50 mg/kg
Syringic acid	COc1cc(cc(c1O)OC)C(=O)O	4	1700
Apigenin	Oc1ccc(cc1)c1cc(=O)c2c(o1)cc(cc2O)O	5	2500
Ascorbic acid	OC[C@@H]([C@H]1OC(=O)C(=C1O)O)O	5	3367
Vanillic acid	COc1cc(ccc1O)C(=O)O	4	2000
Tricin	COc1cc(cc(c1O)OC)c1cc(=O)c2c(o1)cc(cc2O)O	5	4000

Protein Purification and Structural Analysis

The retrieved protein structures were purified using BioVia Discovery Studio as displayed in Figure 1. All water molecules, heteroatoms, and pre-bound ligands were removed and only chain A was retained for docking.

Ramchandran Plot Analysis

Secondary structure analysis of proteins was performed using the PDBSumgenerate tool. Ramachandran plots of proteins were observed as depicted in Figure 2. Secondary structure, Ramachandran plot and purified primary protein structure of each of the proteins were observed as shown in Figures 3, 4 & 5. These results provided information on favorable and unfavorable regions of the proteins and hence confirmed structural quality as shown in Table 3(a).

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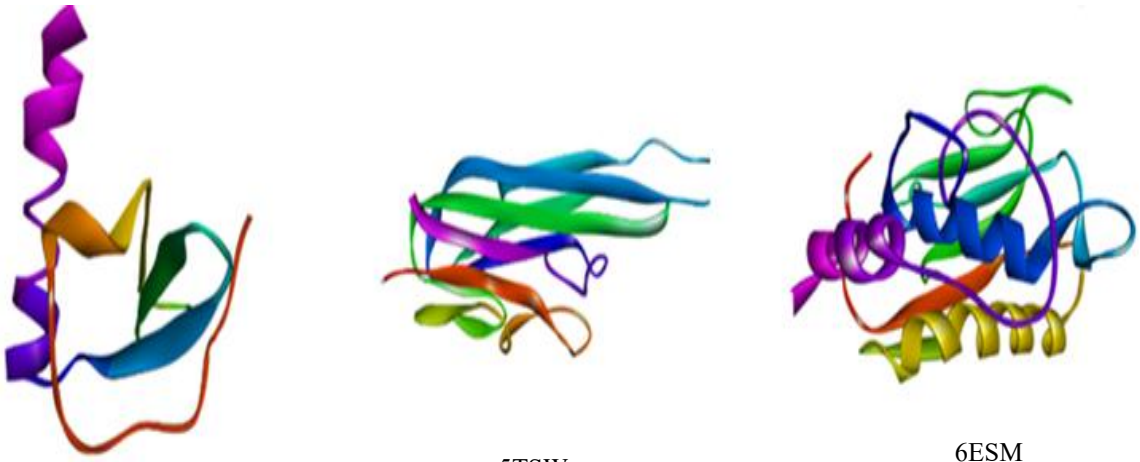


Figure 1. Purified proteins 4XDX (Intrleukin-8), 5TSW (TNF alpha), 6ESM (Metal metalloproteinase 9-MMP9).

Favorable and unfavorable regions in the proteins:

- 4XDX has 91.9% favorable regions, additionally allowed regions being 8.1% and generously allowed and disallowed regions being 0.0%.
- *5TSW:* 78.0% most favored regions, 14.2% additionally allowed regions, 5.5% generously allowed regions and 2.4% disallowed regions.
- *6ESM:* 90.8% most favored regions, 8.4% additional allowed regions, 0.8% generously allowed regions and 0.0% disallowed regions.

The secondary structure of proteins, as depicted in Table 3(b), includes the following:

- *4XDX (Intrleukin-8):* The PDBSum reslts for this protein has 1 sheet, 2 beta hairpins, 2 beta bulges, 3 strands, 2 helices and 2 disulphide bonds.
- *5TSW (TNF alpha):* The PDBSum results for this protein have 2 sheets, 3 beta hairpins, 2 beta bulges, 11 strands, 14 beta turns, 3 gamma turns, and 1 disulphide bond.
- *6ESM (Metal metalloproteinase 9-MMP9):* The PDBSum results for this protein have 2 sheets, 1 beta alpha beta unit, 1 beta hairpin, 1psi loop, 7 strands, 3 helices,12 beta turns and 2 helix–helix interactions.

Table 3. (a) Ramachandran plot analysis of proteins indicating favorable regions, additionally allowed regions, generously allowed regions and disallowed regions from PDBSum generate tool.
(b) Analysis of secondary structure of the purified proteins from PDBSum generate tool.
(a) Ramachandran plot analysis of proteins.

Protein name	Most favored regions	Additional allowed regions	Generously allowed	Disallowed regions
4XDX	91.9%	8.1%	0.0%	0.0%
5TSW	78.0%	14.2%	5.5%	2.4%
6ESM	90.8%	8.4%	0.8%	0.0%

(b) Analysis of secondary structure of the purified proteins.

Prot. name	Sheet	Beta alpha beta unit	Beta hairpins	Psi loop	Beta bulges	Strand	Helices	Beta turns	Helix–helix	Gamma turns	Disulphides
4XDX	1	0	2	0	2	3	2	4	0	0	2
5TSW	2	0	3	0	2	11	0	14	0	3	1
6ESM	2	1	1	1	0	7	3	12	2	0	0

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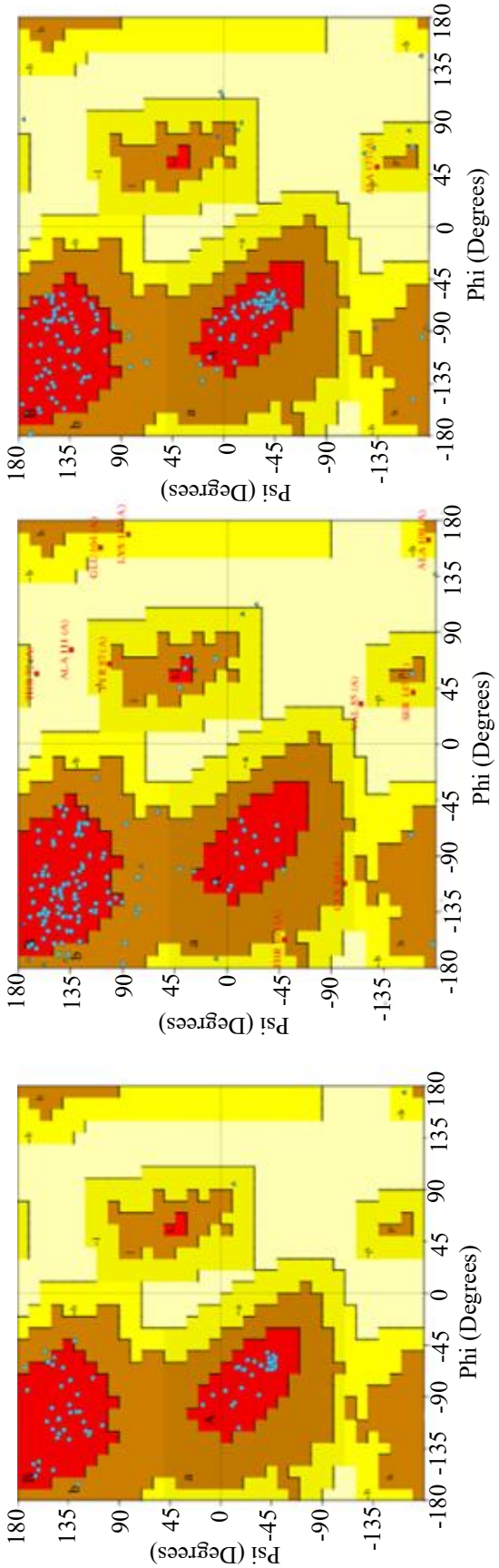


Figure 2. Ramachandran plot for 4XDX, 5TSW, and 6ESM (left to right).

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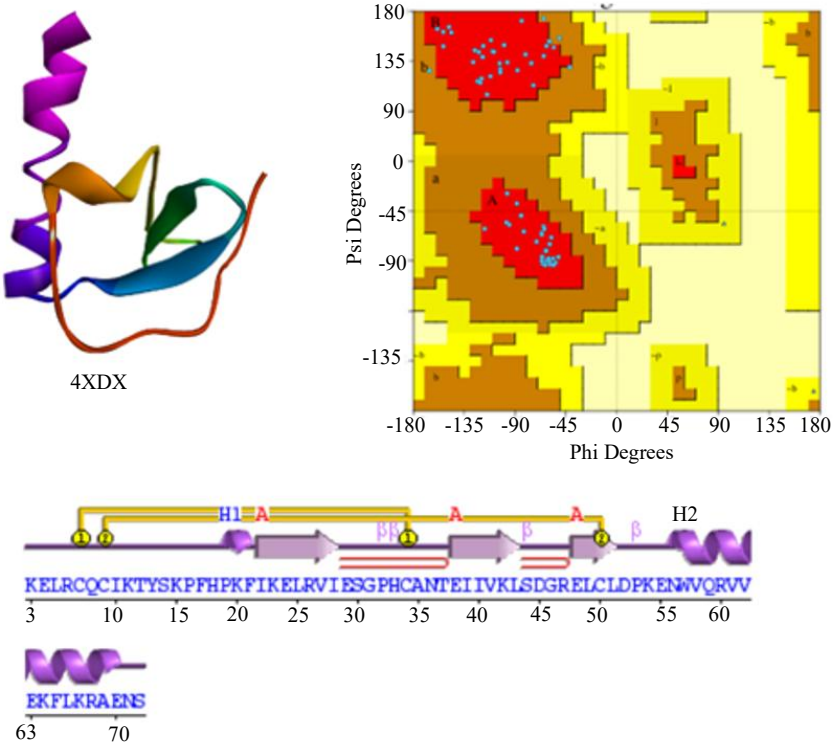


Figure 3. Protein 4XDX with its Ramachandran plot and secondary structure.

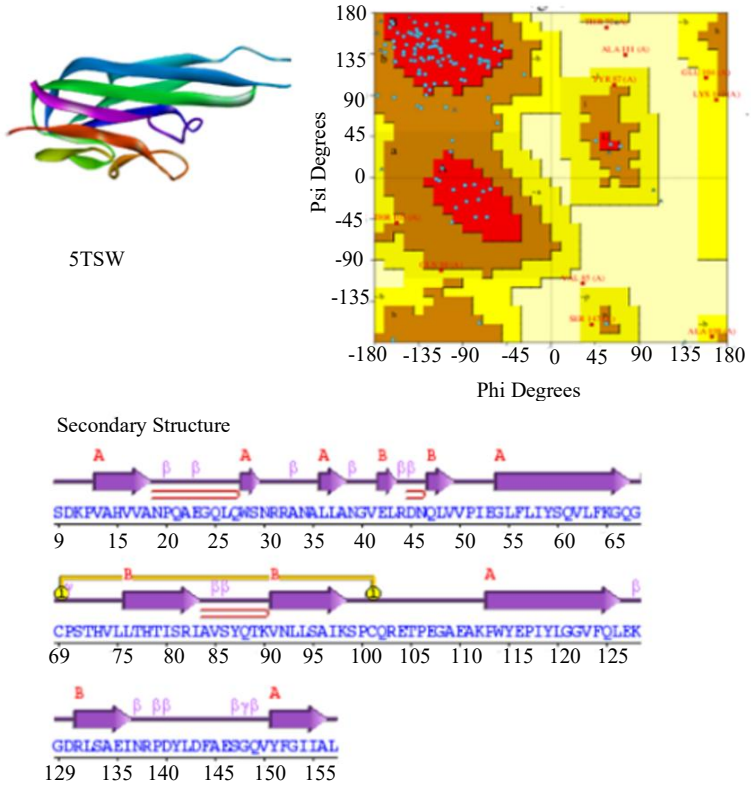


Figure 4. Protein 5TSW with its Ramachandran plot and secondary structure.

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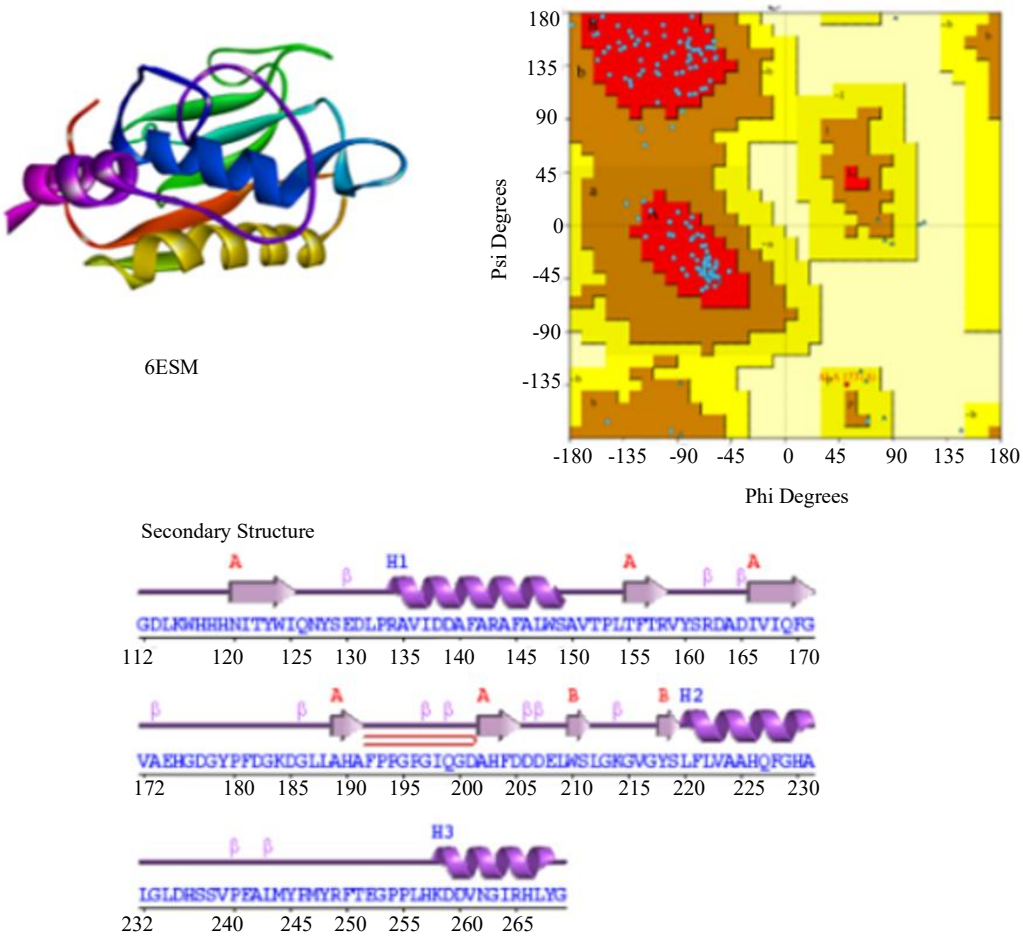


Figure 5. Protein 6ESM with its Ramachandran plot and secondary structure.

Molecular Docking and Visualization of Receptor Ligand Complex

Molecular docking was performed using PyRx. Each of the three purified proteins was docked individually with the five selected ligands. A total of 45 docking poses were generated for 4XDX, 45 poses for 5TSW, and 44 poses for 6ESM. The x, y and z coordinates for 4XDX was: X = 36.3560 angstrom, Y = 33.5761 angstrom, Z = 37.2448 angstrom, for 5TSW was 5TSW: X=44.2087 angstrom, Y == 43.3437 angstrom, Z = 50.1647 angstrom and for 6ESM was: 6ESM: X = 40.1697 angstrom, Y = 30.7065 angstrom, Z = 43.9544 angstrom.

To identify the top 3 best interactions, two parameters were considered: lowest binding affinity and an RMSD value of zero as shown in Table 4(a–c). Based on these criteria, the top three ligand–receptor interactions were shortlisted for each protein. The best overall interaction was observed between 6ESM and apigenin (PubChem ID: 5280443), which exhibited a binding affinity of –10.3 kcal/mol and an RMSD of zero.

Visualization of the top three receptor–ligand complexes for each protein was carried out using BioVia Discovery Studio. The docked protein–ligand complexes obtained from PyRx were imported and interactions were visualized in both 2D and 3D formats (as observed in Figures 6, 7, & 8). Distinct coloring schemes were applied to differentiate proteins and ligands clearly. The interaction images were documented for further analysis.

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Table 4. Molecular docking results with least Binding affinity.

(a) 4XDX.

Ligand	Binding affinity
Ascorbic acid	–5.2
Syringic acid	–5.6
Vanillic acid	–5.7
Tricin	–7.1
Apigenin	–7.5

(b) 5TSW.

Ligand	Binding affinity
Ascorbic acid	–4.4
Syringic acid	–4.6
Vanillic acid	–4.8
Tricin	–6
Apigenin	–6.2

(c) 6ESM.

Ligand	Binding affinity
Syringic acid	–5.8
Ascorbic acid	–6.7
Vanillic acid	–6.8
Tricin	–8.7
Apigenin	–10.3

Visualization

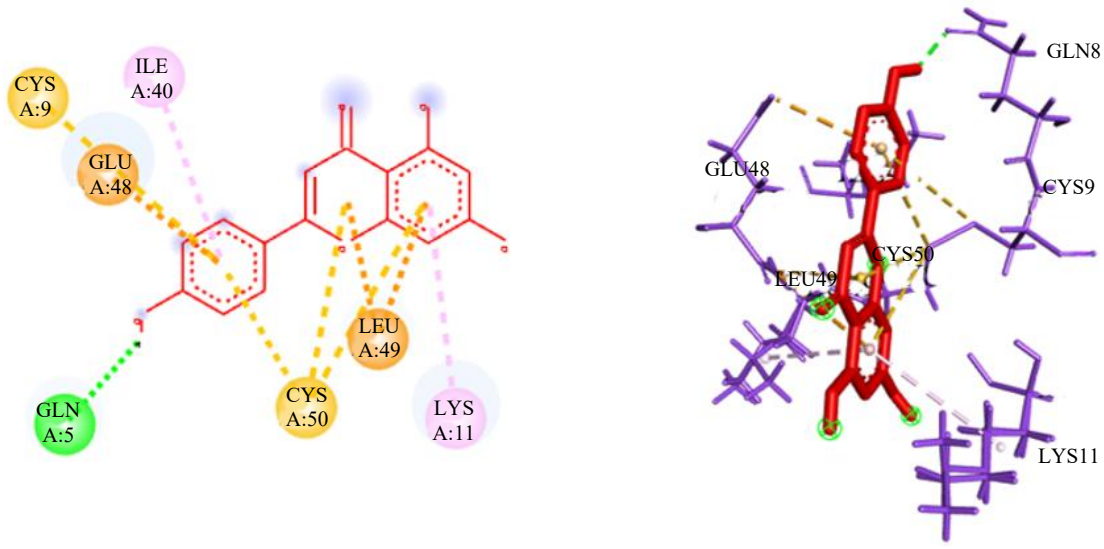


Figure 6. 2D and 3D structure of Protein 4XDX docking with top affinity ligand (apigenin).

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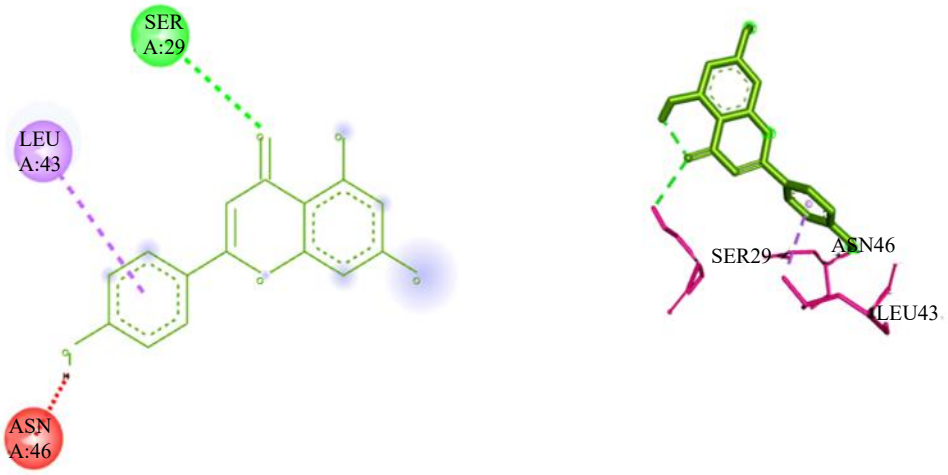


Figure 7. 2D and 3D structure of Protein 5TSW docking with top affinity ligand (apigenin).

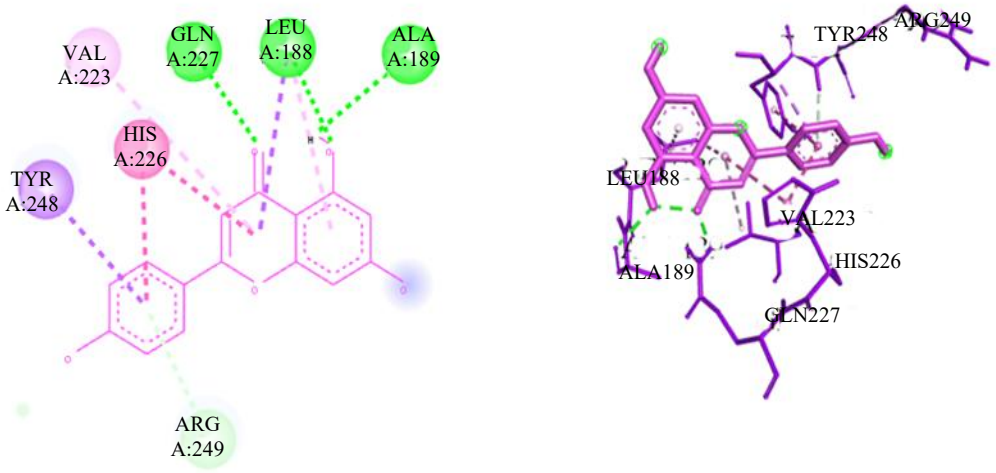


Figure 8. 2D and 3D structure of protein 6ESM docking with top affinity ligand (apigenin).

DISCUSSION

COPD is one of the leading causes of mortality around the world. About 25–45% of COPD patients are non-smokers. This suggests that passive smoking also can lead to severe health issues. Current COPD treatments target the symptoms of COPD including swelling of bronchi, damage to alveoli, etc. COPD can only be treated and not cured completely. Efficient COPD management can be achieved by suppressing the inflammatory response [21]. The primary treatment approaches include complete stoppage on smoking, pulmonary rehabilitation and surgical methods. The drugs for COPD treatment include Bronchodilators like SABA, LABA, and combination therapy [22]. SABA stands for short-acting β2 agonists and LABA stands for Long-acting β2 agonists. These are used in the form of inhalers and can be used in combination too. Salbutamol and other short-acting β2 agonists (SABA) quickly activate β2-adrenergic receptors, raising cAMP and relaxing smooth muscle in the airways. Salmeterol and formoterol are examples of long-acting β2 agonists (LABA) that function on the same route but hold their binding longer because of their increased lipophilicity [23]. When combined, they offer sustained bronchodilation (LABA) and immediate relief (SABA) for the treatment of COPD. PDE4 inhibitors – like roflumilast – are considered for more severe cases. Despite these options COPD treatment methods usually target single pathways, highlighting the need for multi-pathway therapeutic strategies.

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Cynodon dactylon is found in the tropics. This herb is used in traditional medicine for its anti-inflammatory properties. Its properties are largely attributed to its rich phytochemical profile, including flavonoids, alkaloids, terpenoids, and glycosides [23]. Several studies have shown its potential in being an anti-inflammatory and anti-oxidant agent. Traditionally, Bermuda grass or *Cynodon dactylon* has been used in Ayurveda and folk medicine for treating wounds, inflammations and hepatic diseases. Some studies have demonstrated the ability of Durva to modulate oxidative stress and potentially target pathways that induce inflammation. Owing to its broad bioactive potential*, C. dactylon* is increasingly being investigated as a source of natural compounds for drug discovery.

The anti-inflammatory properties of *Cynodon dactylon* are of particular interest in the context of COPD which is driven by chronic inflammation of the airways, bronchi and oxidative stress [24]. The phytochemicals present in Durva – like flavonoids, alkaloids, terpenoids, etc. – have shown anti-inflammatory tendencies and have also shown promising results with respect to oxidative stress and inhibition of pro-inflammatory mediators. It has also shown to modulate pathways, like NF-κB and IL-6, IL-8 pathways, which are highly involved in COPD pathogenesis [25].

In this study, 53 compounds of *Cynodon dactylon* were extracted from IMPPAT database. These compounds were verified in PubChem and their compound name, canonical smiles and PubChem ID were recorded. Further, ADME analysis and toxicity profiling was carried out and 53 phytocompounds were screened resulting in 5 phytocompounds that could serve as ligands for the molecular docking studies. The parameters for screening included – Lipinski rule, GI absorption, PAINS and BRENK, Bioavailability and solubility of compound. Lipinski rule states that the molecular weight of the ligand must be at least 500kDa or greater, should have at most 5 hydrogen bond acceptors, should have at most 10 hydrogen bond donors and value of Log P must be at most 5. Ideally ligands must have no deviation from Lipinski rule. GI absorption refers to gastro-intestinal absorption, this GI absorption must be high as the ligand must travel through this GI barrier to enter the blood stream and reach the target of interest, in this case proteins like MMP9, IL-8, and TNF alpha [26]. Bioavailability of the drug refers to the concentration of drug present in the body, and this should be above 0.55 or 55%. PAINS stands for Pan Assay Interference Compounds; these are compounds that give false positives. BRENK helps identify structural discrepancies. Thus, ideally PAINS and BRENK must have no violations indicating that there are no false positives and that there are no problematic features. Solubility must be high.

Toxicity profile checked for the class of toxicity and the lethal dosage 50. Toxicity class must be 4, 5, or 6 for safe drug use. The ligands got after screening were – Syringic acid, Apigenin, Ascorbic acid, Vanillic acid, and Tricin. Further, molecular docking of these ligands was carried out with the purified proteins.

Molecular docking is a computational technique used to predict the preferred orientation of small molecules when bound to a target protein, thereby estimating binding affinity and interaction stability. It offers significant advantages, including cost-effectiveness, reduced experimental workload, and the ability to screen large libraries of compounds in silico [27]. Thus, docking serves as a powerful tool in early-stage drug discovery and rational therapeutic design. After the molecular docking was carried out with the purified proteins – 4XDX,5TSW and 6ESM. The results were documented and analyzed. The binding affinity exhibited by apigenin was –10.3 with respect to 6ESM. This interaction had the lowest binding affinity and also had zero RMSD value. This receptor–ligand binding was the most favorable binding among all the docked compounds. An overall analysis of the 3D and 2D structures of the receptor–ligand interactions were recorded for further study.

Thus, apigenin has been found to potentially target the metal metalloproteinase-9 (MMP9) which causes inflammation and disrupts the protease–antiprotease balance in the lungs. This potential interaction can be further studied in future to assess the therapeutic potential. This suggests that the bioactive compounds of *Cynodon dactylon* could serve as promising leads for developing multi-targeted therapies for COPD management.

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Apigenin – Therapeutic Effects and API Status

Apigenin (4′,5,7-trihydroxyflavone) is a naturally occurring flavone widely distributed in fruits, vegetables, and medicinal plants [28]. It has been extensively studied for its anti-inflammatory, antioxidant, anticancer and hepatoprotective properties. Studies have shown its potential in targeting diseases such as cancer, neurodegenerative, liver disorders, and chronic inflammatory diseases. The findings from this study aligns with the results from previous studies showing that apigenin can be a potential lead molecule for treatment of chronic inflammatory diseases – like COPD – that involves proteins like MMP9, IL-8, and TNF alpha [29].

Thus, it shows interesting potential for further drug testing and COPD studies [30].

CONCLUSION

In this study, the proteins related to COPD pathway were docked with 5 ligands from *Cynodon dactylon*. The most favorable binding result was of apigenin and MMP9, with binding affinity of –10.3 kcal/mol and RMSD value of 0Å. Apigenin also showed favorable binding with the other COPD proteins in the study: IL-8 and TNF alpha. These multitarget effects and effects on oxidative stress pathways can thus present apigenin as a potential therapeutic lead compound for further COPD and anti-inflammatory studies.

Future research can focus on in vitro validation and pharmacokinetic profiling. Thus, the traditionally used plant has shown actual potential in being used as an anti-inflammatory and anti-oxidant.

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Abbreviations

Abbreviation	Full form
ADME	Absorption, Distribution, Metabolism and Excretion
BBB permeation	Blood Brain Barrier
BRENK	Brenk Structural Alert
C. dactylon	*Cynodon dactylon*
COPD	Chronic Obstructive Pulmonary Disease
ECM	Extracellular Matrix
ERK	Extracellular Signal-Regulated Kinase
GI absorption	Gastrointestinal Absorption
IAP	Inhibitor of Apoptosis Protein
IKK	IκB Kinase
IL-6	Interleukin-6
IL-8	Interleukin-8
IMPPAT	Indian Medicinal Plants Phytochemistry and Therapeutics Database
IκBα	Inhibitor of Kappa B Alpha
JNK	c-Jun N-terminal Kinase
LABA	Long-Acting β2 Agonist
MMP9	Matrix Metalloproteinase-9
NF-κB Signaling Pathway	Nuclear Factor Kappa-Light-Chain-Enhancer of Activated B Cells Signaling Pathway
NF-κB–IκBα	Complex of Nuclear Factor Kappa B Bound to Its Inhibitor IκBα

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PAINS	Pan-Assay Interference Compounds
PDE4 inhibitors	Phosphodiesterase-4 Inhibitors
PubChem	Public Chemical Database
RCSB PDB	Research Collaboratory for Structural Bioinformatics Protein Data Bank
RIP	Receptor-Interacting Protein
RMSD value	Root Mean Square Deviation Value
ROS	Reactive Oxygen Species
SABA	Short-Acting β2 Agonist
SMILES	Simplified Molecular Input Line Entry System
SODD	Silencer of Death Domains
TIMPs	Tissue Inhibitors of Metalloproteinases
TNF alpha / TNF-α	Tumor Necrosis Factor-Alpha
TNFR1	Tumor Necrosis Factor Receptor 1
MAPK Pathway	Mitogen-Activated Protein Kinase Pathway
TRADD	TNF Receptor-Associated Death Domain
TRAF2	TNF Receptor-Associated Factor 2

REFERENCES

1. Parris BA, O'Farrell HE, Fong KM, Yang IA. Chronic obstructive pulmonary disease (COPD) and lung cancer: common pathways for pathogenesis. J Thorac Dis. 2019;11(Suppl 17):S2155–S2172.
2. Che L, Yu C, Chen G, Lin J, Xie Z, Xia T, et al. The inflammatory response induced by RELMβ upregulates IL-8 and IL-1β expression in bronchial epithelial cells in COPD. Int J Chron Obstruct Pulmon Dis. 2021;16:2503–2513.
3. Dang X, He B, Ning Q, Liu Y, Guo J, Niu G, et al. Alantolactone suppresses inflammation, apoptosis and oxidative stress in cigarette smoke-induced human bronchial epithelial cells through activation of Nrf2/HO-1 and inhibition of the NF-κB pathways. Respir Res. 2020;21(1):95.
4. Zhang Y, Li Y, Ye Z, Ma H. Expression of matrix metalloproteinase-2, matrix metalloproteinase-9, tissue inhibitor of metalloproteinase-1, and changes in alveolar septa in patients with chronic obstructive pulmonary disease. Med Sci Monit. 2020;26.
5. Kubysheva N, Boldina M, Eliseeva T, Soodaeva S, Klimanov I, Khaletskaya A, et al. Relationship of serum levels of IL-17, IL-18, TNF-α, and lung function parameters in patients with COPD, asthma-COPD overlap, and bronchial asthma. Mediators Inflamm. 2020;2020:4652898.
6. Ding Y, Wang Z, Zhang Z, You R, Wu Y, Bian T. GLUT3-mediated cigarette smoke-induced epithelial-mesenchymal transition in chronic obstructive pulmonary disease through the NF-κB/ZEB1 pathway. Respir Res. 2024;25(1):158.
7. Huang Y, Niu Y, Wang X, Li X, He Y, Liu X. Identification of novel biomarkers related to neutrophilic inflammation in COPD. Front Immunol. 2024;15.
8. Shyam Prasad Shetty B, Chaya SK, Kumar VS, Mahendra M, Jayaraj BS, Lokesh KS, et al. Inflammatory biomarkers interleukin 1 beta (IL-1β) and tumour necrosis factor alpha (TNF-α) are differentially elevated in tobacco smoke associated COPD and biomass smoke associated COPD. Toxics. 2021;9(4):72.
9. Ahmadi A, Ahrari S, Salimian J, Salehi Z, Karimi M, Emamvirdizadeh A, et al. p38 MAPK signaling in chronic obstructive pulmonary disease pathogenesis and inhibitor therapeutics. Cell Commun Signal. 2023;21(1):314.
10. Ma C, Liao K, Wang J, Li T, Liu L. L-Arginine, as an essential amino acid, is a potential substitute for treating COPD via regulation of ROS/NLRP3/NF-κB signaling pathway. Cell Biosci. 2023;13(1):152.
11. Ding Q, Sun S, Zhang Y, Tang P, Lv C, Ma H, et al. Serum IL-8 and VEGFA are two promising diagnostic biomarkers of asthma-COPD overlap syndrome. Int J Chron Obstruct Pulmon Dis. 2020;15:357–365.

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12. Dimic-Janjic S, Hoda MA, Milenkovic B, Kotur-Stevuljevic J, Stjepanovic M, Gompelmann D, et al. The usefulness of MMP-9, TIMP-1 and MMP-9/TIMP-1 ratio for diagnosis and assessment of COPD severity. Eur J Med Res. 2023;28(1):127.
13. Christopoulou ME, Papakonstantinou E, Stolz D. Matrix metalloproteinases in chronic obstructive pulmonary disease. Int J Mol Sci. 2023;24(4):3786.
14. Suzuki R, Kamio N, Sugimoto K, Maruoka S, Gon Y, Kaneko T, et al. Periodontopathic bacterium Fusobacterium nucleatum affects matrix metalloproteinase-9 expression in human alveolar epithelial cells and mouse lung. In Vivo. 2022;36(2):649–656.
15. Maboudian M, Amjad E, Asnaashari S, Dastmalchi S, Sokouti B, Javadzadeh Y. Evaluation of the effects of curcumin on chronic obstructive pulmonary disease with a bio-computational approach. Egypt J Med Hum Genet. 2024;25(1):13.
16. Poojary R, Kumar NA, Kumarchandra R, Vinodini NA, Bhagyalakshmi K, Sanjeev G. Cynodon dactylon extract ameliorates cognitive functions and cerebellar oxidative stress in whole body irradiated mice. Asian Pac J Trop Biomed. 2019;9(7):278.
17. Balasundari T, Boominathan M. Screening of bioactive compounds by GC-MS, antimicrobial activity and in silico studies in Cynodon dactylon L. Pers. leaves. 2018.
18. Savadi S, Vazifedoost M, Didar Z, Nematshahi MM, Jahed E. Phytochemical analysis and antimicrobial/antioxidant activity of Cynodon dactylon (L.) Pers. rhizome methanolic extract. J Food Qual. 2020;2020:5946541.
19. Srivastava A, Subhashini, Pandey V, Yadav V, Singh S, Srivastava R. Potential of hydroethanolic leaf extract of Ocimum sanctum in ameliorating redox status and lung injury in COPD: An in vivo and in silico study. Sci Rep. 2023;13(1):1131.
20. Habib T, Rahman A, Nair AB, Islam SMS. Application of three compounds extracted from Cynodon dactylon against Streptococcus mutans biofilm formation to prevent oral diseases. Biomolecules. 2023;13(9):1292.
21. Sindhoora B, Singh V, Mungamuri SK, Bharatraj DK. Pharmacological benefits of durva swaras (Cynodon dactylon L. Pers.) administration in APAP-induced liver injury model of mice–assessment by metabolic and inflammatory markers. Indian J Pharmacol. 2024;56(4):260.
22. Yuan J, Li X, Fang N, Li P, Zhang Z, Lin M, et al. Perilla leaf extract (PLE) attenuates COPD airway inflammation via the TLR4/Syk/PKC/NF-κB pathway in vivo and in vitro. Front Pharmacol. 2022;12.
23. Gokul M, Nayanatara AK, Kini RD, Sheryl R. The LC-MS analysis of bioactive compounds in Cynodon dactylon: A step towards therapeutic drug development: Bioactive compounds in Cynodon dactylon: A step toward therapeutic applications. Clin Ter. 2025;176(4).
24. Cai SY, Liu A, Xie WX, Zhang XQ, Su B, Mao Y, et al. Esketamine mitigates mechanical ventilation-induced lung injury in chronic obstructive pulmonary disease rats via inhibition of the MAPK/NF-κB signaling pathway and reduction of oxidative stress. Int Immunopharmacol. 2024;139:112725.
25. Strickson S, Houslay KF, Negri VA, Ohne Y, Ottosson T, Dodd RB, et al. Oxidised IL-33 drives COPD epithelial pathogenesis via ST2-independent RAGE/EGFR signalling complex. Eur Respir J. 2023;62(3).
26. Usmani OS, Scichilone N, Mignot B, Belmans D, Holsbeke CV, Backer JD, et al. Airway deposition of extrafine inhaled triple therapy in patients with COPD: A model approach based on functional respiratory imaging computer simulations. Int J Chron Obstruct Pulmon Dis. 2020;15:2433–2440.
27. Wang C, Zhou J, Wang J, Li S, Fukunaga A, Yodoi J, et al. Progress in the mechanism and targeted drug therapy for COPD. Signal Transduct Target Ther. 2020;5(1):248.
28. Ding F, Li X. Apigenin mitigates intervertebral disc degeneration through the amelioration of tumor necrosis factor α (TNF-α) signaling pathway. Med Sci Monit. 2020;26:e924587.
29. Jiang X, Huang H. The therapeutic potential of apigenin against atherosclerosis. Heliyon. 2024;11(1):e41272.
30. Department of Biotechnology, Chemistry and Pharmacy at University of Siena, Italy, Reza P. Features of apigenin, luteolin, hesperetin and naringenin in crop and body. Int J Food Sci Nutr Diet. 2016;300–304.

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