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Original Article

IN SILICO STUDY OF *BASELLA ALBA* BIOACTIVE COMPOUNDS AS POTENTIAL THERAPY FOR PSORIASIS AGAINST TUMOR NECROSIS FACTOR-*α* (TNF-*α*) RECEPTOR

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ABSTRACT

Objective: This in silico study aims to explore the bioactive compound of *Basella alba* as a potential natural alternative by examining its molecular interactions with Tumor Necrosis Factor-α (TNF-α) receptors. While established biological receptors, such as adalimumab, are currently available and provide effective treatment for psoriasis, they are associated with high costs and potential adverse effects. This research emphasizes the novel potential of underexplored *Basella alba* compounds for psoriasis therapy, potentially offering safer and more affordable alternatives via plant-based compounds, focusing on receptor targets and interactions through molecular docking against the (TNF-α) receptor.

Methods: The active compounds of *Basella alba* were identified and analyzed using Simplified Molecular Input Line Entry System (SMILES) format via the PubChem database. The prediction on anti-psoriatic agents was performed by using Prediction of Activity Spectra for biologically active Substances (PASS). Structure-Activity Relationship (SAR) approach for predicting the bioactive compound activity. Followed by molecular docking using AutoDock Vina to assess binding affinity with the TNF-α receptor (PDB ID: 2AZ5).

Results: *Basella alba* contains 22 active compounds predicted to exhibit antipsoriatic properties based on computational analysis. Based on the structure-activity relationship (SAR) and molecular docking analyses, acacetin, kaempferol, and beta-carotene were selected as key focus compounds due to their promising pharmacological profiles and strong binding affinities to the TNF-α receptor, a central target in psoriasis pathogenesis. PASS prediction revealed that these compounds possessed high Pa values across critical biological activities, including apoptosis agonist, anti-inflammatory, antioxidant, and antipsoriatic properties. Notably, beta-carotene exhibited the highest predicted antipsoriatic potential with a Pa value of 0.910. Molecular docking studies further confirmed their potential, with acacetin demonstrating the strongest binding affinity (-7.5 kcal/mol) among the tested compounds, followed closely by kaempferol and beta-carotene. These ligands also formed stable interactions with key TNF-α residues, such as TYR59, TYR119, and GLY121, indicating their ability to mimic the control ligand's interaction profile.

Conclusion: The findings indicate that certain compounds from *Basella alba*, including acacetin, kaempferol, and beta-carotene, may be viable candidates for antipsoriatic agents and natural alternatives to conventional TNF-α inhibitors for psoriasis management. Further experimental validation is necessary to confirm these computational predictions.

Keywords: In silico study, *Basella alba*, Psoriasis, TNF-α

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INTRODUCTION

Psoriasis is a chronic, complicated, immune-mediated inflammatory disease [1], affecting approximately about 2-3% of the global population [2]. The clinical manifestations are characterized by erythema, epidermal hyperplasia and scaling. Histological analysis reveals epidermal hyperplasia, parakeratosis, and neutrophilic infiltration, often accompanied by features like Munro's microabscesses and spongiform pustules of Kogoj with inflammatory infiltrates and capillary angiogenesis in dermis [3]. Psoriasis is characterized by aberrant keratinocyte proliferation, vascular abnormalities, immune cell infiltration and elevated levels of inflammatory cytokines, particularly TNF-α [3]. Tumor necrosis factor-α (TNF-α) plays an important role as crucial mediator in the initial phase of pathogenesis of psoriasis and can contribute to its chronicity, as evidenced by the effectiveness of therapies targeting TNF-α [4]. In psoriasis, TNF-α stimulates cell proliferation, neovascularization, apoptosis, and regulates immune cell aggregation at the lesion site [5].

During the past decade, injectable biologics targeting specific molecules involved in the pathogenesis of psoriasis have gradually been developed or studied. One of the current treatment strategies for psoriasis often target pro-inflammatory cytokines, such as TNF-α inhibitors, with biological therapies such as adalimumab, etanercept, infliximab [4]. Adalimumab, an anti-TNF-α agent, showing high efficacy due to their efficacy and safety profiles, enabling long-term treatment. However, adalimumab is not suitable for all patients and these are associated with high cost, adverse drug reactions, long-term toxicity risks, and the need for clinical supervision, which limits their accessibility and usability in resource-limited settings [6]. Several attempts have been made in overcoming psoriasis with prolonged treatment duration and high cost [4]. Psoriasis, a chronic condition, requires a prolonged treatment protocol to mitigate its severity and scope, enhance patient care, and improve health-related quality of life [1]. Pharmacological management for psoriasis includes topical agents, oral medications, biologic therapies, and ultraviolet phototherapy [6] have severe long-term adverse effects and limited efficacy [7]. While no therapy can completely cure psoriasis, it can control symptoms and reduce comorbidities [8].

In recent years, there has been a shift towards investigating natural herbal medicines and a growing focus on plant-derived therapies as cost-effective and safer supplemental or alternative treatments alternatives to conventional treatments for psoriasis [1, 9]. Herbal compounds exhibit a wide range of pharmacological activities with a reduced incidence of adverse effects. While numerous plants, such as *Curcuma longa (turmeric)* [12] and *Aloe vera* [13], have been extensively investigated and commercialized for their antipsoriatic properties. *Basella alba* or Malabar spinach—a nutrient-dense,

medicinal plant traditionally utilized in Ayurveda and ethnomedicine [14]-remains largely unexplored in this context. *Basella sp*. is native to tropical Asia, likely originating from India or Indonesia [10]. Basella alba is one of the brightest candidates belonging to pharma-herb because

of its considerably enriched pharmacologically important product stocks like vitamin C, flavonoid compounds, carotenoids, saponins as well as a large number of different minerals and numerous amino acids [14].

In the traditional system like Ayurveda, *Basella alba* plants are used as medicines for primary health care and provide many novel compounds used for preventing and curative treatment to modern science. *Basella alba,* rich in essential nutrients and antioxidants, demonstrates considerable anti-inflammatory and antioxidant effects such as betacyanin, carotenoids, bioflavonoids, β-sitosterol, and lupeol. These compounds have been used to treat cancer, viral infections, oxidative stress, inflammation, hypercholesterolemia, ulcers, microbial infections, hypoglycemia, wound healing, and androgenic diseases [12]. *Basella alba* possesses a distinctive array of phytochemicals, including as flavonoids (e. g., kaempferol), carotenoids (e. g., beta-carotene), and flavones (e. g., acacetin), which exhibit anti-inflammatory, antioxidant, and immunomodulatory properties. The bioactivities are significantly related to the pathogenesis of psoriasis, rendering *Basella alba* an intriguing subject for examination [11]. Unlike more extensively studied botanicals, *Basella alba* offers the novelty of untapped bioactive compounds with potential antipsoriatic mechanisms. Moreover, medicinal plants are less expensive than current drugs and have no toxic effect [14].

Several studies have optimized and accelerated medication discovery. In herbal medicine study, ligand design and basic pharmacological qualities like absorption, distribution, metabolism, excretion, and side effects can define active compounds. In silico study can identify bioactive compounds in pharmacological test materials to optimize drug development and decrease animal testing [13]. The experimental evaluation of organic compounds for numerous biological activities is challenging; therefore, computational approaches are essential for identifying and optimizing novel pharmacologically active molecules [14]. This molecular docking and in silico study was conducted to identify the phytochemical bioactive compounds of *Basella alba* and their potential therapeutic effects on critical pathways and targets associated with psoriasis, the effectiveness of *Basella alba* bioactive compounds in inhibiting the TNF-α, thereby exploring their feasibility as alternative or adjunct therapies in psoriasis treatment.

MATERIALS AND METHODS

Analysis of the bioactive compound of *Basella alba*

The PubChem database is used to search for Simplified Molecular Input Line Entry system (SMILES) and bioactive structures found in *Basella alba* based on literature studies. SMILES is a simple sequence that describes the structural profile of a compound and needed in silico analysis, particularly to predict the role of a compound and to predict the target protein of the compound based on structural similarity.

Analysis of the potential prediction of bioactivity of *Basella alba* active compounds

The analysis data of *Basella alba* was obtained from Prediction of Activity Spectra for Biologically Active Substances (PASS) server/prediction by downloading PASS Online website. The active compound of *Basella alba* was extracted from database with Simplified Molecular Input Line Entry system (SMILES). Prediction of Bioactive Compound Activity using Structure-Activity Relationship (SAR) Approach. The bioactive *Basella alba* was subsequently evaluated for its potential as an antipsoriatic medication using the Way2Drug PASS prediction tool. Way2Drug PASS Prediction uses SAR (Structure-Activity Relationship) analysis to compare the input compound of *Basella alba* with compounds that are already known to have certain potential. The more similar the structure of the compounds, the higher the predictive value obtained. Compounds that have a high similarity generally have similar potentials. The Pa value (Probability to be Active) is a predictive value from Way2Drug PASS that describes the potential of a tested compound, with a score range of 0-1. The Pa value indicates the accuracy of the predictive function obtained; the higher the Pa value of a function, the better its accuracy [15].

Prediction of absorption, distribution, metabolism, excretion and toxicity of *Basella alba* bioactive compound

A medication's effectiveness depends on a balanced combination of pharmacokinetics, biochemical activity, and safety. An optimal absorption, distribution, metabolism, excretion, and toxicity (ADMET) profile is equally critical to the success of a drug candidate as high potency and selectivity. The RO5 approach or drug-likeness is employed by ADMET to predicate whether a bioactive compound has similarities to orally consumed pharmaceuticals [20, 21]. To predict the pharmacokinetics and toxicity properties of chemicals, we employed ADMETlab 2.0, a completely redesigned version of the widely used ADMETlab web server (https://admetmesh. scbdd. com/) [20]. Compounds that do not meet Lipinski's criteria are more likely to have problems accessing blood circulation, as demonstrated by the extra bioavailability score.

Molecular docking of *Basella alba*

Molecular docking is a computational method used to simulate the formation of stable protein-ligand complexes within the active site of a protein [16]. The web server used is the Research Collaboratory for Structural Bioinformatics Protein Data Bank (RCSB PDB) is an information resource that provides data related to the three-dimensional (3D) structure of biological molecules, specifically proteins and nucleic acids, to understand the structure and function of molecules by providing access and tools for the exploration, visualization, and analysis of experimentally defined 3D structures from the Protein Data Bank (PDB). The 3D macromolecule TNF-α was downloaded from the Protein Data Bank (PDB) at https://www. rcsb. org using the receptor TNF-α with the PDB ID: 2AZ5. Protein preparation was carried out using the PyMOL 2.5.2 software, while ligand energy minimization was performed using the Open Babel software on PyRx V.1.0. Molecular Docking was performed using Auto Dock Vina integrated in PyRx V.1.0. Visualization was conducted to observe the interactions occurring in the docking results between the receptor and ligands.

RESULTS AND DISCUSSION

Analysis of the bioactive compounds of *Basella alba*

The examination of bioactive compounds in *Basella alba* has identified 22 potential active compounds, as shown in table 1.

Analysis of the potential prediction of bioactivity of *Basella alba* compound

The present investigation utilized an in silico analysis to assess probable active compounds and investigate the bioactivity of *Basella alba* as a potential therapy for psoriasis, as illustrated in table 2**.** The Pa value (probable to be active) is a value that describes the potential of a tested compound, and if the Pa value assessment is ≥ 0.7, it indicates that the compound is predicted to have high potential both computationally and in laboratory tests. A Pa value of 0.3-0.7 means that the compound has computational activity in the tested activity but has not yet been proven in laboratory tests or has low potential, whereas a Pa value of ≤ 0.3 indicates that the compound has low potential both computationally and in laboratory tests.

Based on the SAR analysis, it shows that *Basella alba* has quite good potential as an apoptosis agonist (0.585), anti-inflammatory (0.573), antioxidant (0.470), proliferative disease therapy (0.431), and anti-psoriasis (0.415). The most promising compounds for further study are *Basella alba* compounds with an average activity value above 0.4 for apoptosis agonist, anti-inflammatory, antioxidant, proliferative disease treatment, and antipsoriatic.

Beta-carotene molecule in *Basella alba* exhibits the highest potential for bioactivity as an apoptotic agonist, with a probable activity (Pa) value of 0.943. This chemical is expected to show substantial potential in both computational and laboratory studies. Basella saponin C exhibits the best anti-inflammatory activity, with a Pa value of 0.831. The most potent antioxidant in *Basella alba* is

bioflavonoid (rutin), with a Pa value of 0.923, whereas stigmasterol glucoside, with a Pa value of 0.959, plays the most significant antiproliferative role. Beta-carotene, which is an apoptotic agonist and has a Pa value of 0.91, is the primary active component of *Basella alba* as an antipsoriatic. Based on the findings of this investigation, *Basella alba* is projected to act as an antipsoriatic agent by targeting apoptosis and inflammation pathways, which are frequently linked to the treatment of psoriasis.

Table 1: Bioactive compounds of *Basella*

No.	Active compounds	Formulation	PubChem ID
1	Betacyanin	C24H26N2O13	6324775
2	Gomphrenin I	C24H26N2O13	90658633
3	Gomphrenin III	C34H34N2O16	101105498
4	Niacin	C6H5NO2	938
5	Beta sitosterol	C29H50O	222284
6	Basellasaponin B	C47H68O21	101720818
7	Stigmasterol glucoside	C35H58O6	6602508
8	Basellasaponin A	C47H70O21	101720817
9	Anthraquinone	C14H8O2	6780
10	Basellasaponin D	C47H68O22	101720820
11	Basellasaponin C	C47H68O22	101720819
12	Salicylic acid	C7H6O3	338
13	Lupeol	C30H50O	259846
14	Linoleic acid	C18H32O2	5280450
15	Syringic acid	C9H10O5	10742
16	Momordin II C	C47H74O18	14162557
17	Bioflavonoid(Rutin)	C27H30O16	5280805
18	Gallic acid	C7H6O5	370
19	Kaempherol	C15H10O6	5280863
20	Acacetin	C16H12O5	5280442
21	Ferulic acid	C10H10O4	445858
22	Beta-carotene	C40H56	5280489

Table 2: Potential prediction of bioactivity of *Basella alba* active compounds

No.	Active compounds	Apoptosis agonist	Anti inflammatory	Anti oxidant	Proliferative diseases treatment	Anti psoriatic
1	Betacyanin	0	0	0.326	0.191	0
2	Gomphrenin I	0	0	0.431	0.213	0
3	Gomphrenin III	0.301	0.281	0.475	0.314	0.181
4	Niacin	0	0.459	0	0.161	0.548
5	Beta sitosterol	0.558	0.467	0.178	0	0.643
6	Basellasaponin B	0.769	0.721	0.586	0.381	0.448
7	Stigmasterol glucoside	0.702	0.599	0.379	0.959	0.644
8	Basellasaponin A	0.814	0.816	0.598	0.449	0.498
9	Anthraquinone	0.584	0.41	0.189	0.263	0.318
10	Basellasaponin D	0.811	0.818	0.642	0.449	0.543
11	Basellasaponin C	0.826	0.831	0.611	0.449	0.497
12	Salicylic acid	0.392	0.713	0.318	0,268	0.491
13	Lupeol	0.883	0.708	0.28	0.462	0.546
14	Linoleic acid	0.545	0.73	0.314	0.519	0.536
15	Syringic acid	0.538	0.498	0.403	0.317	0.494
16	Momordin II C	0.85	0.83	0.68	0,675	0.478
17	Bioflavonoid (Rutin)	0.747	0.728	0.923	0,952	0.32
18	Gallic acid	0.562	0.548	0.52	0,324	0.571
19	Kaempherol	0.881	0.676	0.856	0,602	0.181
20	Acacetin	0.827	0.595	0.628	0,538	0.179
21	Ferulic acid	0.702	0.604	0.54	0,558	0.596
22	Beta-carotene	0.943	0.69	0.775	0,639	0.91
	Pa average	0.585	0.573	0.47	0.431	0.415

Prediction of absorption, distribution, metabolism, excretion and toxicity of *Basella alba* bioactive compound

The ADMETLab database [21] can be used to predict the toxicity of compounds and the potential for compounds to be absorbed in accordance with the Lipinski rule of five (Rule of five/RO5/Druglikeness). The Lipinski rule of five is applied to predict the physicochemical properties of a compound when it is administered orally. The RO5 parameters are as follows: The molecular weight must not exceed 500 Da, the log P coefficient must not exceed 5, and the hydrogen bond donors and acceptors must not exceed five or ten. The SwissADME database (http://www.swissadme.ch/) is used to obtain the bioavailability data [22]. The selected compound is a predictive potential anti-psoriatic therapy that exceeds Lipinski's rule of five and exhibits high bioavailability.

Molecular docking of *Basella alba*

Before conducting molecular docking on test ligands, it is essential to conduct a preliminary test to validate the molecular docking method. The process at this stage entails the re-docking of the native ligand to the target protein, which has been removed, using AutoDock Tools. The objective of this validation procedure is to observe the discrepancies between the native ligand's conformation prior to and following re-docking. The RMSD (Root mean Square

Deviation) value is the validation parameter employed for anchoring. RMSD is a critical metric for the validation of docking programs, as it quantifies the degree of correspondence between the crystallography coordinates of the ligand and the coordinates of the tested ligand. Molecular Docking is performed using the targeted docking method. The size of the gridbox is adjusted according to the positions of the amino acid residues bound to the control from previous research [17] as follows: TNF-α: 307 (PDB 2AZ5). Molecular docking of the constituents of *Basella alba* was performed against the target protein of TNF-α (fig. 1).

Table 3: Prediction of absorption, distribution, metabolism, excretion and toxicity of *Basella alba* bioactive compound

No	Compounds	nHD	nHA	MW	LogP	Number of violation	Bioavailability score	Passes lipinski
1	Gallic acid	4	5	170.02	0.645	0	0.56	√
2	Salicylic acid	2	3	138.03	2.221	0	0.85	√
3	Ferulic acid	2	4	194.06	1.803	0	0.85	√
4	Betacyanin	7	15	550.14	2.599	3	0.11	×
5	Acacetin	2	5	284.07	3.645	0	0.55	√
6	Anthraquinone	0	2	208.05	3.414	0	0.55	√
7	Basellasaponin A	10	21	970.44	2.003	3	0.55	×
8	Basellasaponin B	9	21	968.43	1.848	3	0.11	×
9	Basellasaponin C	10	22	984.42	2.046	3	0.11	×
10	Basellasaponin D	10	22	984.42	2.038	3	0.11	×
11	Beta sitosterol	1	1	414.39	7.663	1	0.55	√
12	Beta-carotene	0	0	536.44	11.15	2	0.17	×
13	Bioflavonoid (Rutin)	10	16	610.15	0.763	3	0.17	×
14	Gomphrenin I	9	15	550.14	1.131	3	0.11	×
15	Gomphrenin III	9	18	726.19	0.681	3	0.11	×
16	Kaempherol	4	6	286.05	2.656	0	0.55	√
17	Linoleic acid	1	2	280.24	6.652	0	0.85	√
18	Lupeol	1	1	426.39	7.291	0	0.55	√
19	Momordin II C	10	18	926.49	2.414	3	0.11	×
20	Niacin	1	3	123.03	0.405	0	0.85	√
21	Stigmasterol glucoside	4	6	574.42	5.738	2	0.55	×
22	Syringic acid	2	5	198.05	1.212	0	0.56	√

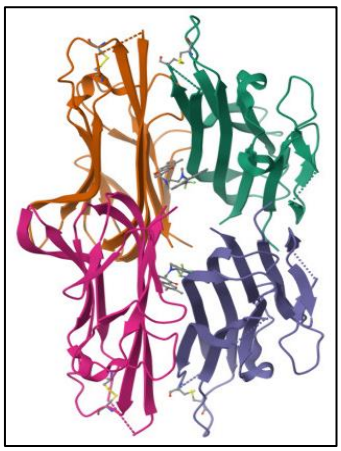

Fig. 1: Structure of tumor necrosis factor protein, (PDB ID: 2AZ5) (https://www.rcsb.org)

Based on the analysis of the RCSB PDB database, namely: TNF-α (PDB ID: 2AZ5), the 3D structure of the selected target protein was obtained from the 5 highest 3D structures of bioactive ligands of *Basella alba* (table 4) from the previous SAR PASS analysis obtained from the PubChem database (https://pubchem.ncbi.nlm.nih.gov/) with the following IDs:

Table 4: Bioactive compounds of *Basella alba* related to its potential

Bioactive compounds	PubChem ID
Acacetin	5280442
Kaempferol	5280863
Beta carotene	5280489
Ferulic acid	445858
Gallic acid	370

The results of the Molecular Docking are obtained in the form of binding affinity or interaction energy of the compound with the protein. Subsequently, the interaction between the compound and the protein from the docking is visualized using the BioVia Discovery Studio 2024 software. The docking results will be validated based on:

- The RMSD (Root mean Standard Deviation) value by comparing the redock results and the crystallography (experimental) results.
- The Molecular Docking results that can be used must be less than<2 Å if RMSD<2 Å indicates that there is the conformational similarity between the docking structure and the experimental control results.
- The docking position between the reference ligand and the control must be in the same cavity (location).
- Identical protein residues must be present in both the control and the comparative ligand to demonstrate that the comparative ligand serves a function analogous to that of the control in the experimental outcomes.

One of the requirements that must be met for the docking results to be accepted is to have an RMSD value<2 Å [25]. A low RMSD (e. g.,<2 Å) indicates structural stability, while a high RMSD (>3 Å) suggests major conformational changes. If RMSD>2, it indicates a lack of similarity between our data and the experimental data being imitated [26].

The Molecular Docking conducted in this study has an RMSD value of 0.595 Angstrom (TNF), thus the docking performed meets the requirements. Fig. 2 shows that *Basella alba* ligand interacts near position 307 with TNF-α as the inhibitor control, excluding beta carotene. Based on the binding affinity values, the binding affinity score of acacetin (-7.5 kcal/mol) is the highest among the top 5 bioactive ligands of *Basella alba* compared to others (table 3). The more negative the binding affinity value, the stronger the interaction between the ligand and the protein. Although the value of the *Basella alba* ligand is quite good, it is not as good as 307, which is-8.9 kcal/mol.

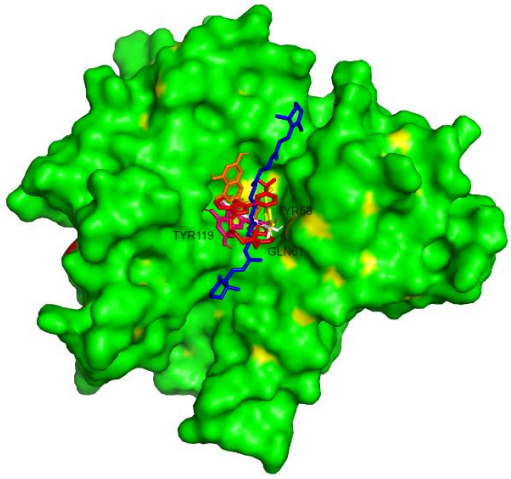

Fig. 2: Interaction of TNF-α (green color) and Ligand a) control inhibitor (red), b) beta carotene (blue), c) acacetin (orange), d) kaempferol (pink), e) gallic acid (yellow), f) ferulic acid (white). The test ligand interacts at the same cavity position as the control and TNF-α interaction. Beta carotene has a larger size, so its binding area is broader

Based on the molecular docking analysis, the affinity of the ligand and protein binding was obtained as shown in table 5 below:

Based on the exploration of protein and bioactive interactions, it shows that the top 3 ligands of *Basella alba*, namely acacetin, kaempferol, and beta carotene, are capable of interacting with TNF amino acids similar to control and TNF interactions. Acacetin is a bioactive compound from *Basella alba* that has the most similar residue to the control in interacting with TNF, TYR59, while TYR119 is the active residue of TNF that interacts the most with the bioactive compounds of *Basella alba*. Hydrogen interactions contribute to the bond strength between the ligand and the protein, while hydrophobic interactions are responsible for the stability of the interaction, making it less prone to degradation (table 6).

Although beta-carotene exhibited the highest Pa value for apoptosis agonist (0.943) and antipsoriatic potential (0.91), its binding affinity to TNF-α was relatively weak (-6.5 kcal/mol). This disparity underlines a known weakness of the PASS prediction system: it is based entirely on structural similarity (SAR) and does not take into consideration 3D spatial fit or particular interaction energy. A high Pa value paired with a less favorable docking score may also suggest that β-carotene acts via multi-target mechanisms, not limited to TNF-α inhibition. To assess the risk of false positives, the Pi (Probability to be Inactive) value was also considered. For beta-carotene, the Pi value was 0.01, suggesting a low false-positive risk despite the weaker binding affinity. Conversely, acacetin had a Pa of 0.827 and Pi of 0.05, indicating strong confidence in its predicted bioactivity and observed docking result (-7.5 kcal/mol). For context, clinical TNF-α inhibitors like etanercept have docking scores in the range of-9.5 to-10.2 kcal/mol. While acacetin's docking score (-7.5 kcal/mol) is lower, it is significant for a small natural molecule and supports its potential as a lead compound for further development.

Table 5: Molecular docking analysis on ligand-protein binding affinity

Ligand	ID	Binding Affinity (kcal/mol)
Kontrol	2az5	-8.9
Acacetin	5280442	-7.5
Kaempferol	5280863	-7.2
Beta carotene	5280489	-6.5
Ferulic acid	445858	-5.9
Gallic acid	370	-5.5

Table 6: Bioactive interactions and TNF amino acid residues

Ligand	Hydrofobic bond	Hydrogen bond	Van der waals bond	Others
Control	TYR119 (π-π T-shaped)	GLN61	LEU120 GLY122 TYR59 SER60 TYR151	GLY121 (Halogen)
Acacetin	LEU120 (π-π stacked) TYR59 (π-π stacked)	TYR151	GLY121	
Kaempferol	TYR119 (π-π stacked)	GLN61		
Beta carotene	TYR119 (π-alkyl stacked), LEU157 (alkyl), LEU57 (alkyl)			

Note: Green: amino acid residues that are the same between the control and the bioactive ligand *Basella alba;* Red: amino acid residues that are the same as the control but have different types of interactions.

Detailed analysis using PLIP (Protein-Ligand Interaction Profiler) revealed that acacetin forms two hydrogen bonds (TYR151 and GLY121), one π-π stacking interaction (with TYR59), and van der Waals contacts with LEU120 and TYR119. Kaempferol also showed π-π stacking with TYR119, contributing to moderate affinity (-7.2 kcal/mol). Beta-carotene, due to its bulky and rigid structure, lacked specific directional interactions (e. g., H-bonds), relying mostly on hydrophobic contacts (e. g., LEU157, TYR119), which might explain its weaker affinity.

Acacetin exhibited the strongest binding to the TNF-α receptor (-7.5 kcal/mol), forming multiple key interactions including hydrogen bonds and π-π stacking, although this is less potent than clinical TNF-α inhibitors (etanercept: ∼-10 kcal/mol). While β-carotene displayed the highest Pa value, its weaker docking score and lack of directional bonding suggest it may operate through alternate or multi-target mechanisms, emphasizing the need for comprehensive in vitro and in vivo validation. The objective of two-dimensional visualization is to determine the types of bonds that exist between the ligand and receptor during interaction, thereby facilitating the prediction of the bond strength. The binding free energy (ΔG), predicted inhibition constant (ki), amino acid residues, and the number of hydrogen bonds are the parameters that are observed to determine ligand affinity to the receptor. Ligand affinity to the receptor is determined by the ki and ΔG values. A higher ligand affinity is associated with a negative ΔG value and a smaller ki value. The presence of test ligands with amino acid residues and hydrogen bonds that are similar to the native ligand suggests that they exhibit similar interaction types, which is indicative of comparable biological activity [18, 19]. Here are the molecular docking modes of the TNF interaction with the control (fig. 3), acacetin (fig. 4), kaempferol (fig. 5), and beta carotene (fig. 6):

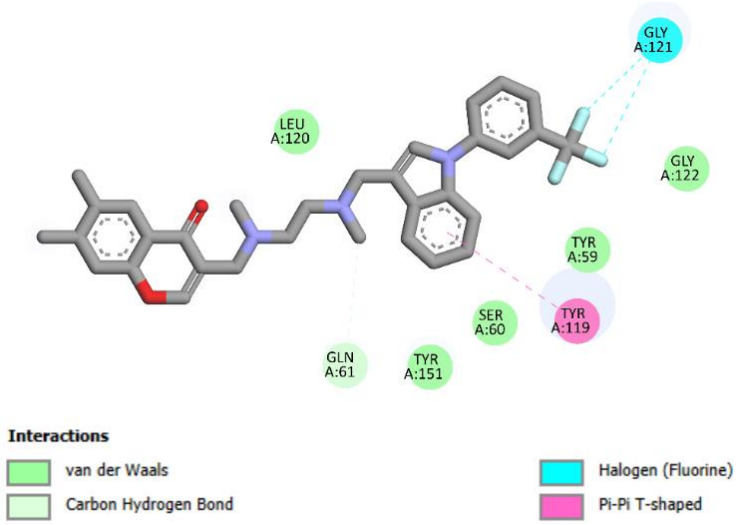

Fig. 3: Control Interaction with TNF

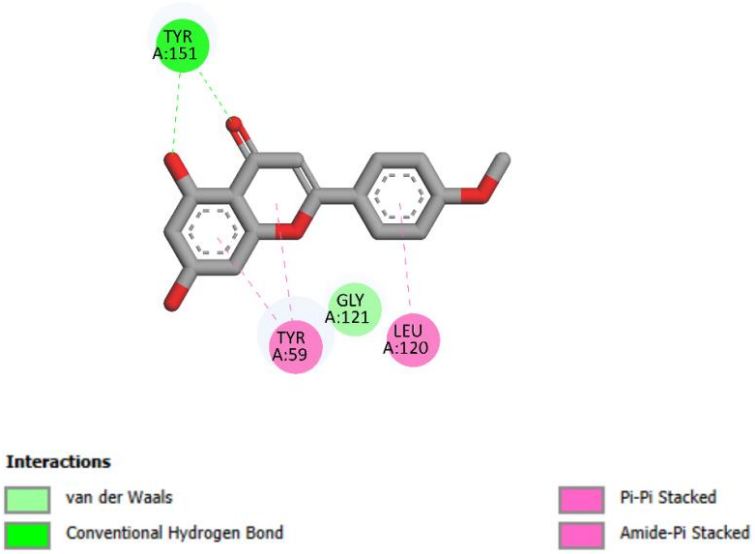

Fig. 4: Interaction of acacetin with TNF

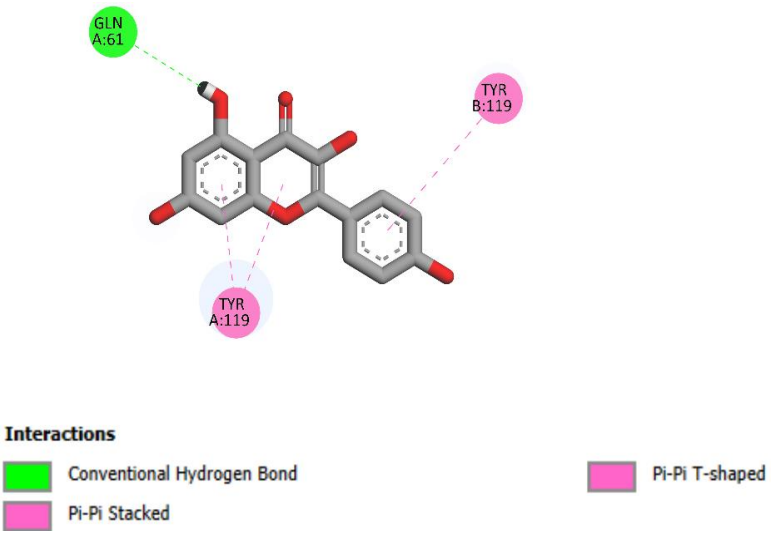

Fig. 5: Interaction of kaempferol with TNF

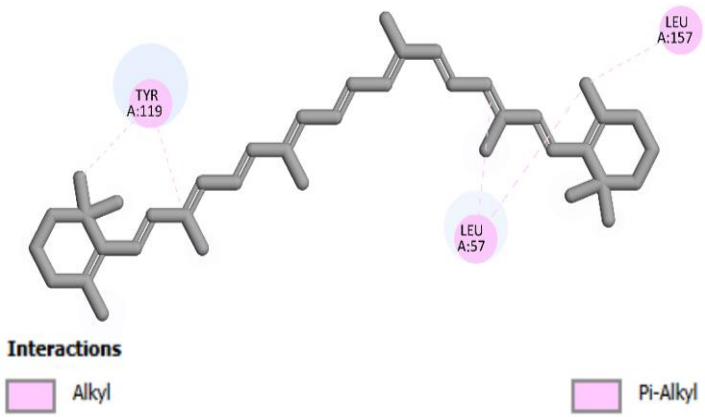

Fig. 6: Interaction of beta carotene with TNF

CONCLUSION

Through in silico analysis, *Basella alba* contains 22 active compounds. *Basella alba* as apoptosis agonists, anti-inflammatory agents, antioxidants, antiproliferative substances, and antipsoriatic properties are computationally predicted to have the ability on the activity being tested, but laboratory tests have not been proven or have little potential. The highest bioactivity potential of the active compound of *Basella alba* as apoptosis agonists and the active compound that plays the most dominant role is Beta-carotene which is predicted to have a computationally high potential and in the laboratory tests. The molecular docking of three bioactive compounds from *Basella alba* with the TNF receptor yielded the most favorable docking result for acacetin, which demonstrated a binding free energy of-7.5 kcal/mol and established two hydrogen bonds with TYR151 and GLY121. According to these findings, the bioactive molecule acacetin interacting with the TNF receptor is regarded as a promising option for the development of anti-psoriatic therapy. It's important to note that while these are promising findings, more research is needed to fully understand the mechanisms of action and clinical efficacy of these herbal medicines in treating psoriasis. Additional research is required to further refine the results of this investigation. This can be accomplished by conducting in vitro studies, such as enzyme-linked immunosorbent assays (ELISA) for the measurement of TNF-α secretion. Additionally, in vivo models, such as the induction of murine psoriasis with imiquimod (IMQ), may be implemented. Furthermore, additional research is necessary to investigate the synergistic effects of combinations, such as acacetin and kaempferol, on multi-target synergy.

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Nil

AUTHORS CONTRIBUTIONS

TO: conceptual or design of the work, collected data, analysis, interpretation of data, critical for important intellectual content, and final approval of the version to be published. HK: consultant and final approval. BP: consultant and final approval. VW: drafted the work analyzed, interpretation of data, revised and final approval of the version to be published. BW: consultant and analyzed data. MEI: consultant and final approval of the version to be published. PD: consultant, revised, and gave final approval for the version to be published.

CONFLICT OF INTERESTS

Declared none

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