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Original Article

Exploring Phytochemicals and Anti-bacterial Properties of *Bougainvillea glabra*: A Systematic Review with an *in silico* Perspective

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ABSTRACT

Background: Anti-microbial resistance is a major global hazard to human health, which is exacerbated by high costs and low returns associated with bringing new antibiotics to market. Plants have a diverse array of bioactive secondary metabolites, representing an exciting new option for drug discovery. **Materials and Methods:** We used a systemic review of the phytochemical composition of *Bougainvillaea glabra* flower extracts and computational analysis of its antibacterial activity. SwissADME and STRING are used to identify effective medications like phytochemicals and their targets. **Results:** Totally 36 bioactive compounds were identified in *B. glabra* among the 467 investigations. We used SwissADME to test these compounds for possible drug-like properties and to find their specific target. The N-(1-Deoxy-1-fructosyl) phenylalanine was virtual docked with a bacterial target protein, tryptophanyl-tRNA synthetase. We examined binding affinity and interactions in these models to estimate their anti-bacterial potential. The *in silico* study found solid evidence for specific phytochemicals anti-microbial activities. Notably, quercetin had a binding affinity of -7.83 and was crucial in inhibiting the translational process of protein synthesis. **Conclusion:** This computational investigation gives information on the potential anti-bacterial properties of phytochemicals produced from *B. glabra*. Our findings not only call for additional testing but also point to the possibility of synthesising novel anti-bacterial drugs derived from nature. This study helps the ongoing battle against antibiotic resistance by clearing the path for the development of novel therapeutic alternatives to combat bacterial infections through the use of computational approaches.

Keywords: *Bougainvillaea glabra*, Phytochemical, Anti-bacterial activity, N-(1-Deoxy-1-fructosyl) phenylalanine, Tryptophanyl-tRNA synthetase

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INTRODUCTION

Anti-microbial Resistance (AMR) is a rising global health concern that jeopardises our ability to effectively combat bacterial diseases. The World Health Organisation (WHO) has proclaimed AMR to be one of the most serious risks to world health, emphasising the urgent need for novel anti-microbial drugs to address drug-resistant diseases.[1] The increase of resistant bacterial strains, along with a lack of new antibiotics in the pharmaceutical pipeline, created an urgent need for newer antibacterial treatments. The pharmaceutical industry's antibiotic pipeline, on the other hand, remains disturbingly dry, owing to the enormous challenges and high costs connected with researching and producing new medicines.[2] The development process of a novel antibiotic from discovery to market approval is a long and costly one, filled with clinical setbacks and questionable returns on investment. This depressing environment has caused pharmaceutical companies to be hesitant to invest in antibiotic research, aggravating the AMR epidemic.[3] One intriguing path is in the diverse variety of plant secondary metabolites, which have shown amazing bioactivity and potential medicinal applications.

Phytochemicals include a wide spectrum of compounds with distinct chemical structures and biological functions, including flavonoids, alkaloids, phenolic compounds, and terpenoids. Some phytochemicals have already found their way into therapeutic use, such as quinine, which is produced from the cinchona tree and has been used to treat malaria for centuries.[4] These natural chemicals have cleared the path for the investigation of other plant-derived molecules with medicinal potential. *Bougainvillaea glabra* has long been known for its brightly coloured blooms and rich foliage. Aside from its visual appeal, this plant has piqued the scientific community's interest due to its rich phytochemical

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composition. *B. glabra* is known to produce a profusion of bioactive secondary metabolites, such as flavonoids, alkaloids, and phenolic compounds, which have been linked to a variety of biological activities such as antioxidant, anti-inflammatory, and antibacterial characteristics.[5,6] While the phytochemical elements of *B. glabra* have attracted curiosity, a thorough assessment of its potential as a source of novel antibacterial agents remains an unexplored area. Given the importance of the AMR issue and the potential therapeutic benefit of plant-derived substances, studying the anti-bacterial activity of *B. glabra* phytochemicals is both topically and relevant.[7]

Computational techniques have gained significance in the search for novel anti-bacterial drugs due to their ability to speed up the drug discovery process and provide useful insights into molecular interactions.[8] Molecular docking simulations, in particular, are a strong tool for predicting the binding affinities and interactions of small compounds with target proteins, assisting in the discovery of possible therapeutic candidates.[9] The antibacterial potential of *B. glabra* phytochemicals is assessed using computational techniques in this study. We hope to accelerate the identification of interesting chemicals and explain their mechanisms of action by utilising *in silico* approaches. Integrating computational analysis into the drug development pipeline not only speeds up the research process but also allows for the rational design of novel antibacterial medicines based on natural compounds.

MATERIALS AND METHODS

Literature search

This review was carried out in accordance with the review process and in accordance with the PRISMA criteria.[10] Two bibliographic databases (PubMed and Google Scholar) were utilised to locate published research that investigated the nutritional and bioactive composition of *B. glabra* until August 25, 2023 (date latest searched). We utilised search phrases linked to bioactive compounds (phytochemicals) and plants (*Bougainvillaea glabra*; Paper plant). However, conference abstracts, letters to the editor, and editorials were not included. We searched the reference lists of the research included in the current review for additional publications.

Study selection criteria

Studies were considered if they matched the following criteria: (i) utilised *B. glabra* and/or Paper plant samples; (ii) assessed bioactive substances. Two reviewers evaluated the titles and abstracts separately based on the selection criteria. Two reviewers evaluated the full-text publications for each possibly eligible study.

Computational screening of phytochemicals and antibacterial activity

Phytochemicals identified from the literature review were screened for drug-like properties using the SwissADME web tool.[11] Phytochemicals meeting the criteria for drug-likeness were selected for target identification. To find antibacterial activity, the canonical smiles of the selected phytochemicals were entered into the AntiBacPred database, "a public, online-accessible, and experimentally determined antibacterial activity database," with a probability score of 0.4.[12]

Target identification

The SwissTarget Prediction method was used to determine the most likely macromolecular targets of the tested compounds, which were presumed to be bioactive.[13] PubChem SMILES of N-(1-Deoxy-1-fructosyl) Phenylalanine (DFP) were obtained and placed into the Swisstarget prediction system to predict their chemical targets.

Network Analysis

The STRING 11.0v was used to identify biochemical pathways and protein-protein interactions.[14] STRING received a collection of proteins (gene IDs) to better understand how proteins interact with one another.

Molecular docking

In the current study, bioactive phytochemicals DFP (101039148) 3D structure retrieved from PubChem. The RCSB Protein Data Bank (https://www.rcsb.org/) provided the X-ray crystal structure of tryptophanyl-tRNA synthetase (tyrZ) (PDB ID: 3BRH). Molecular docking is a computer approach that can be utilised to construct an atomic-level interaction between phytochemicals and target proteins before predicting the best confirmation that suits the protein binding site. AutoDock Vina was used to conduct molecular docking experiments with potential targets.[15] POAP and 5000 minimization steps with the MMF94 force field were used to construct the compounds. The molecular docking method exhaustiveness was set at 50. Increased exhaustiveness enhances accuracy by increasing the number of steps taken in the search for the best-docked location with the lowest binding energy.

RESULTS

Literature Search and Phytochemical Composition

Totally 467 potentially relevant citations were identified after scanning the electronic databases PubMed and Google Scholar, 464 abstracts and titles were reviewed according to inclusion and exclusion criteria (Figure 1). The full texts and reference lists of 37 studies were reviewed, and two of them were eligible for inclusion in the current review. In the two investigations that were included, these studies collectively reported a total of 36

Table 1: List of *Bougainvillea glabra* phytochemicals retrieved from PRISMA screened research articles.

IUPAC name	Molecular formula	Pubchem ID	Smile
4-(2-hydroxypropoxy)-3,5-dimethyl-Phenol	$C_{11}H_{16}O_3$	10420209	CC1=CC(=CC(=C1OCC(C)O)C)O
12-Hydroxyjasmonic acid	$C_{12}H_{18}O_4$	5497122	C1CC(=O)[C@@H]([C@H]1CC(=O)O)C/C=C\CCO
Annuionone B	$C_{13}H_{18}O_3$	24776721	CC(=O)/C=C/[C@@H]1[C@@]2(CC(=O)C[C@]1(OC2)C)C
Geigerin	$C_{15}H_{20}O_4$	101676	C[C@H]1C[C@@H]2[C@@H]([C@H](C(=O)O2)C)[C@@H](C3=C(C(=O)C[C@H]13)C)O
Emmotin A	$C_{16}H_{22}O_4$	42608142	CC1=C2C[C@@H]([C@H](C(=O)C2=C(C=C1)COC)O)C(C)(C)O
9-Acetoxyfukinanolide	$C_{17}H_{24}O_4$	5320805	C[C@H]1CCC[C@H]2[C@@]1(C[C@]3([C@@H]2OC(=O)C)C(=C)COC3=O)C
Uplandicine	$C_{17}H_{27}NO_7$	156778	C[C@@H]([C@](C(=O)OCC1=CCN2[C@H]1[C@@H](CC2)OC(=O)C)(C(C)(C)O)O)O
Methylgingerol	$C_{18}H_{28}O_4$	5312877	CCCCCCC(C/C=C/C(CCC(CCCC(=O)O)O)O)O
5,8,12-trihydroxy-9-octadecenoic acid	$C_{18}H_{34}O_5$	5312877	CCCCCCC(C/C=C/C(CCC(CCCC(=O)O)O)O)O
Ethyl 7-epi-12-hydroxyjasmonate glucoside	$C_{20}H_{32}O_9$	131751966	CCOC(=O)CC1CCC(=O)C1C/C=C/CCOC2C(C(C(C(O2)CO)O)O)O
N-(1-Deoxy-1-fructosyl) phenylalanine	$C_{15}H_{21}N$	101039148	C1=CC=C(C=C1)C[C@@H](C(=O)O)NCC2([C@H]([C@@H] ([C@H](O2)CO)O)O)O
Oenanthoside A	$C_{16}H_{20}$	54446769	C=CCC1=CC2=C(C(=C1)O[C@H]3[C@@H]([C@H]([C@@H] ([C@H](O3)CO)O)O)O)OCO2
Lucuminic acid	$C_{19}H_{26}O_{12}$	85260329	C1C(C(C(C(O1)OCC2C(C(C(C(O2)OC(C3=CC=CC=C3)C(=O)O)O)O)O)O)O)O)O
6-Hydroxyluteolin 5-rhamnoside	$C_{21}H_{20}O_{11}$	44258477	CC1[C@@H]([C@@H](C([C@@H](O1)OC2=C(C(=CC3=C2C(=O)C=C(O3)C4=CC(=C(C=C4)O)O)O)O)O)O)O)O
Laricitrin 3-rhamnoside	$C_{22}H_{22}O_{12}$	44259482	CC1[C@@H](C([C@@H]([C@@H](O1)OC2=C(OC3=CC(=CC(=C3C2=O)O)O)O)C4=CC(=C(C(=C4)OC)O)O)O)O)O
Tomentin 4'-glucoside	$C_{23}H_{24}$	44259811	COC1=C(C(=C2C(=C1)OC(=C(C2=O)OC)C3=CC(=C(C=C3)O[C@H]4C(C([C@@H](C(O4)CO)O)O)O)O)O)O)O
Robinetin 3-rutinoside	$C_{27}H_{30}O_{16}$	44258688	CC1[C@@H](C([C@@H]([C@@H](O1)OCC2[C@H]([C@@H](C([C@@H](O2)OC3=C(OC4=C(C3=O)C=CC(=C4)O)C5=CC(=C(C(=C5)O)O)O)O)O)O)O)O)O)O)O
Luteolin 7-rhamnosyl(1->6) galactoside	$C_{27}H_{30}O_{15}$	44258135	CC1[C@@H](C([C@@H]([C@@H](O1)OCC2[C@@H]([C@@H](C([C@@H](O2)OC3=CC(=C4C(=C3)OC(=CC4=O)C5=CC(=C(C=C5)O)O)O)O)O)O)O)O)O)O)O
Viscumneoside III	$C_{27}H_{32}O_{15}$	195287	COC1=C(C=CC(=C1)C2CC(=O)C3=C(C=C(C=C3O2)OC4C(C(C(C(O4)CO)O)O)OC5C(C(CO5)(CO)O)O)O)O

IUPAC name	Molecular formula	Pubchem ID	Smile
6-C-Rhamnopyranosylrhamnetin 3-O-glucopyranoside	$C_{28}H_{32}O_{16}$	44258375	CC1[C@@H](C([C@@H]([C@@H](O1) C2=C(C=C3C(=C2O)C (=O)C(=C(O3)C4=CC(=C(C=C4) O)O)O[C@H]5C([C@H]([C@@H] (C(O5)CO)O)O)O)OC) O)O)O
Tricetin 7-methyl ether 3'-glucoside-5'-rhamnoside	$C_{28}H_{32}O_{16}$	44258393	CC1[C@@H](C([C@@H]([C@@H](O1) OC2=C(C(=CC(=C2)C3=CC(=O)C4=C(C=C(C=C4O3) OC)O)O[C@H]5C([C@H]([C@@H](C(O5)CO)O)O)O)O) O)O)O
Isorhamnetin 3-rhamnosyl-(1->2)-gentiobiosyl-(1->6)-glucoside	$C_{28}H_{32}O_{17}$	44259397	CC1[C@@H](C([C@@H]([C@@H](O1) OC2[C@H]([C@@H](C(O[C@H]2OCC3 [C@H]([C@@H] (C([C@@H](O3)OC4=C(OC5=CC(=CC (=C5C4=O)O)O)C6=CC(=C(C=C6)O)OC)O)O)O) CO[C@H]7C([C@H]([C@@H] (C(O7)CO) O)O)O)O) O) O)O)O
6-Methoxykaempferol 3-rhamnoside-7-(4'''-acetylrhamnoside)	$C_{30}H_{34}O_{16}$	44259757	C[C@H]1[C@@H](C(C([C@@H](O1) OC2=C(C(=C3C(=C2)OC (=C(C3=O) O[C@H]4[C@H](C([C@H](C(O4)C)O)O)O)C5=CC=C (C=C5)O)O)OC)O)O)OC(=O)C
Egonol gentiobioside	$C_{31}H_{38}$	74960882	COC1=CC(=CC2=C1OC(=C2)C3=CC4=C(C=C3)OCO4) CCCOC5C(C(C(C(O5)COC6C(C(C(C(O6)CO) O)O)O) O)O)O
Robinin	$C_{33}H_{40}O_{19}$	5281693	C[C@H]1[C@@H]([C@H]([C@H]([C@@H](O1) OC[C@@H]2[C@@H]([C@@H]([C@H]([C@@H](O2) OC3=C(OC4=CC (=CC(=C4C3=O)O) O[C@H]5[C@@H]([C@@H] ([C@H]([C@@H](O5)C)O) O)O)C6=CC=C(C=C6)O)O)O)O)O)O)O
Kaempferol 3-(2G-glucosylrutinoside)	$C_{33}H_{40}O_{20}$	44258825	CC1[C@@H]([C@@H](C([C@@H](O1)OCC2[C@H](C(C([C@@H](O2)OC3=C(OC4=CC(=CC(=C4C3=O)O)O) C5=CC=C(C=C5)O)O[C@H]6[C@@H](C([C@@H](C(O6) CO)O)O)O)O)O)O)O)O
Isorhamnetin 3-rhamnosyl-(1->2)-gentiobiosyl-(1->6)-glucoside	$C_{34}H_{42}O_{21}$	44259397	CC1[C@@H](C([C@@H]([C@@H](O1) OC2[C@H]([C@@H](C(O[C@H] 2OCC3[C@H] ([C@@ H](C ([C@@H](O3) OC4=C(OC5= CC(=CC(=C5C4=O) O)O)C6=CC(=C(C=C6) O)OC)O)O)O)CO[C@H]7C([C @H]([C@@H] (C(O7) CO)O)O)O)O)O)O) O)O
Brassicoside	$C_{34}H_{42}O_{22}$	12302038	COC1=C(C=CC(=C1)C2=C(C(=O)C3=C(C=C(C=C3O2) O[C@H]4[C@@H]([C@H]([C@@H]([C@H](O4)CO)O)O) O)O)O[C@H]5[C@@H]([C@H]([C@@H]([C@H](O5)CO) O)O)O[C@H]6[C@@H]([C@H]([C@@H]([C@H](O6)CO) O)O)O)O
oleanolic acid 3-O-beta-D-glucosiduronic acid	$C_{36}H_{56}O_{9}$	176079	C[C@]12CC[C@@H](C([C@@H] 1CC[C@@]3 ([C@@ H]2CC=C4[C@]3(CC[C@@]5([C@H]4CC (CC5)(C) C) C(=O)O)C)C)(C)C)O[C@H]6[C@@H]([C@H]([C@@H]([C@H] (O6)C(=O)O)O)O)O
Isorhamnetin 3-rhamnosyl-(1->2)-gentiobiosyl-(1->6)-glucoside	$C_{40}H_{52}O_{2}$	4259397	CC1[C@@H](C([C@@H]([C@@H](O1) OC2[C@H]([C@@H](C(O[C@H] 2OCC3[C@H]([C @@H](C([C@@H](O3)OC4=C(OC5=CC(=CC(=C5C4=O) O)O)C6=CC(=C(C=C6)O)OC)O)O)O) CO[C@H]7C([C@H]([C@@H](C(O7)CO) O)O)O) O)O) O)O)O

IUPAC name	Molecular formula	Pubchem ID	Smile
Isovitexin 2"-O-(6"'-(E)-p-coumaroyl)glucoside 4'-O-glucoside	$C_{42}H_{46}O_{22}$	44257785	C1=CC(=CC=C1/C=C/C(=O)OCC2[C@H]([C@@H](C([C@@H](O2)OC3[C@H]([C@@H](C(O[C@H]3C4=C(C5=C(C=C4O)OC (=CC5=O)C6=CC=C(C=C6)O[C@H]7C([C@H]([C@@H](C(O7) CO)O)O)O)O)CO)O)O)O)O)O
Kaempferol3-rhamnoside-7-[6"'-ferulyglucosyl-(1->3)-rhamnoside]	$C_{43}H_{48}O_{22}$	44258974	C[C@H]1[C@@H]([C@H]([C@H]([C@@H](O1)OC2=C(OC3=CC(=CC(=C3C2=O)O)O[C@H]4[C@@H]([C@@H]([C@H]([C@@H](O4)C)O)O[C@H]5[C@@H]([C@H]([C@@H]([C@H](O5)COC (=O)/C=C/C6=CC(=C(C=C6)O)OC)O)O)O)O)C7=CC=C(C=C7)O)O)O)O
Kaempferol 3-(2G-glucosylrutinoside)	$C_{43}H_{48}O_{23}$	44258825	CC1[C@@H]([C@@H](C([C@@H](O1)OCC2[C@H](C(C([C@@H](O2)OC3=C(OC4=CC(=CC(=C4C3=O)O)O)C5=CC=C(C=C5)O)O[C@H]6[C@@H](C([C@@H](C(O6)CO)O)O)O)O)O)O)O)O)O
Isovitexin 2"-O-(6"'-(E)-p-coumaroyl) 4'-glucoside	$C_{44}H_{50}O_{24}$	44257785	C1=CC(=CC=C1C=CC(=O)OCC2C(C(C(C(O2)OC3C(C(C(OC3C4=C(C5=C(C=C4O)OC(=CC5=O)C6=CC=C(C=C6)OC7C(C(C(C(O7)CO)O)O)O)O)CO)O)O)O)O)O)O
Vitisifuran A	$C_{56}H_{40}O_{12}$	131751783	C1=CC(=CC=C1C2C(C3=C(C=C(C=C3O2)O)/C=C/C4=CC5=C(C=C4)OC(=C5C6=C7C(C(OC7=CC(=C6)O)C8=CC=C(C=C8)O)C9=CC(=CC(=C9)O)O)C1=CC=C(C=C1)O)C1=CC(=CC(=C1)O)O)O
N-Carboxyethyl-?-aminobutyric acid	$C_7H_{13}NO_4$	2572	C(CC(=O)O)CNCCC(=O)O

distinct phytochemicals present in *B. glabra*, marking a significant step in understanding the chemical constituents of this plant. Phytochemicals, as evidenced by their diversity, hold promise for various pharmacological applications. The compilation of these compounds in Table 1 serves as a valuable resource for researchers and underscores the potential therapeutic significance of *B. glabra*.

Pharmacokinetics and Drug-Likeness Assessment

Moving beyond the identification of phytochemicals, we sought to assess their suitability for drug development. In this pursuit, we employed predictive models and computational tools to evaluate crucial pharmacokinetic parameters, bioavailability, and drug-likeness of the 36 phytochemicals. The selection of effective phytochemicals was driven by a multifaceted approach, including bioavailability predictions and consideration of parameters (Figures 2 and 3). Notably, DFP emerged as a promising candidate based on these criteria. Its potential as an antibacterial agent was further explored through the AntiBacPred database.

Antibacterial Activity Assessment

The AntiBacPred database results on the antibacterial activity of individually identified phytochemicals against a wide range of bacterial strains. The anti-bacterial action of DFP structures has been anticipated. AntiBacPred determined potential action against various bacterial strains and species with a confidence value of greater than 0.500. Some micro-organisms were projected to be targets for discovered phytochemicals. These ratings were obtained for compounds anti-microbial activity against *Clostridium ramosum, Actinomyces meyeri, Clostridium cadaveris, Porphyromonas asaccharolytica, Acinetobacter pittii, Mycobacterium ulcerans*, and *Bacillus subtilis* (Table 2).

Target Identification and Molecular Docking

Potential targets were obtained by SwissTarget servers, using the aforementioned method. The threshold value of the similarity value was set as 0.85 and the value of 2D was 0.65. Finally, to increase the accuracy of the target prediction process, the top-ranked tyrZ was selected for further studies. To gain a deeper understanding of the molecular mechanisms underlying the anti-bacterial activity of DFP, computational molecular

Table 2: Effective *Bougainvillea glabra* phytochemicals anti-bacterial activity analysed by AntiBacPred database.

Organism name	Confidence score
Clostridium ramosum	0.6618
Actinomyces meyeri	0.6537
Clostridium cadaveris	0.5746
Porphyromonas asaccharolytica	0.5726
Acinetobacter pittii	0.5485
Mycobacterium ulcerans	0.5200
Bacillus subtilis	0.3824

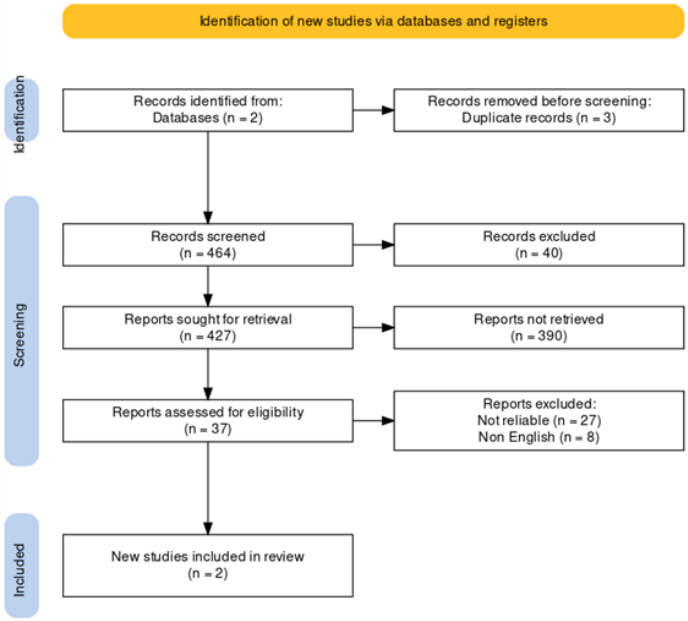

Figure 1: PRISMA for the scrutinizing of research articles to include in the study according to appropriate criteria.

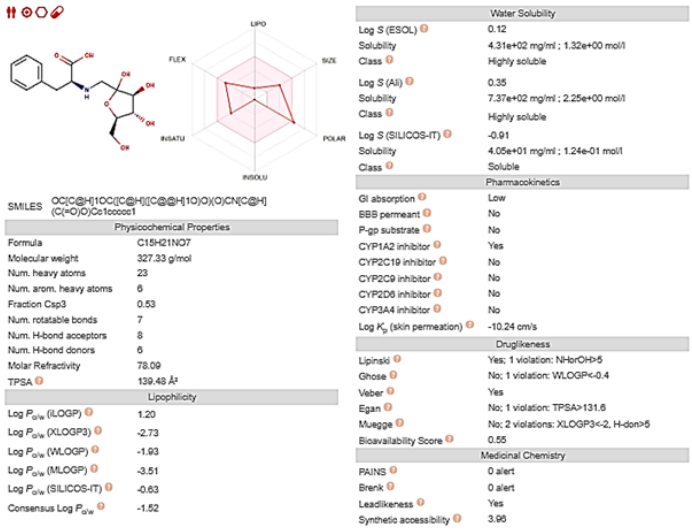

Figure 2: Analysis of N-(1-Deoxy-1-fructosyl) phenylalanine Properties Using SwissADME results.

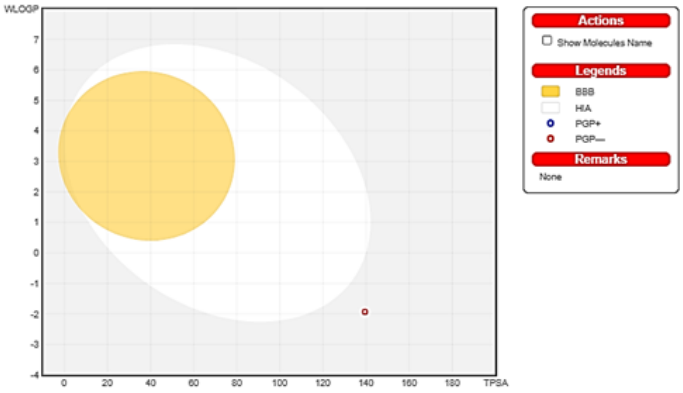

Figure 3: ADME Analysis of Efficacious Phytocompounds using the Boiled Egg Method.

docking was employed. This approach allowed for the prediction of ligand-target interactions and provided insights into intermolecular energies. The interaction of DFP with the selected target, tyrZ was characterized by a strong binding energy of -7.83 kcal/mol (Figure 4). Hydrogen bonds were observed with PHE 6, SER 7, GLY 8, and GLN 10, while van der Waals interactions were identified with ILE 9, HSD 44, GLN 148, PRO 144, ASP 133, GLU 146, GLY 145, PRO 143, VAL 142, and ILE 134.

Network Analysis and Functional Associations

In parallel, network analysis provided additional insights into the potential interactions and functional associations of the target protein tyrZ. The generated network illustrated the predicted associations between tyrZ and other proteins, shedding light on potential pathways and interactions relevant to the antibacterial activity of DFP. STRING generates a list of proteins with activities similar to the query protein and builds an interactive functional association network to show relationships between proteins and datasets. The projected tyrZ target network (Figure 5).

DISCUSSION

The present study embarked on an exploration of the antibacterial potential of phytochemicals derived from *B. glabra* through a comprehensive and systematic approach. The findings, as summarized from the results, provide valuable insights into the pharmacological and antibacterial properties of these natural compounds.

This comprehensive literature search compilation not only provides a consolidated inventory of the phytochemicals but also offers a foundation upon which future research can be built. It offers researchers a starting point for investigations into the therapeutic significance of these compounds, potentially leading to the development of novel pharmaceuticals or therapeutic agents. The findings of this systematic review underscore the

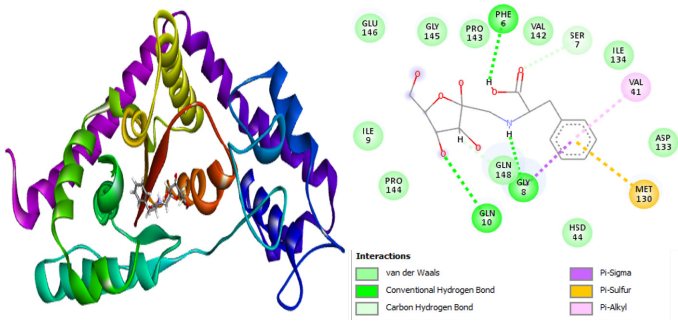

Figure 4: The bioactive compounds from *B. glabra* extract N-(1-Deoxy-1-fructosyl) phenylalanine docked with targeted protein tryptophanyl-tRNA synthetase.

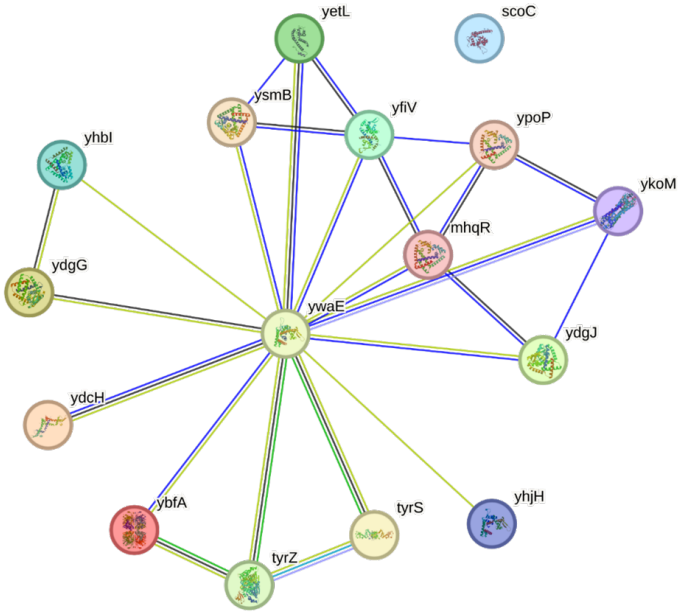

Figure 5: Network of target protein interactions. Colored nodes depict candidate proteins, while the colored lines represent interactions between proteins.

importance of continued research into natural sources of bioactive compounds like *B. glabra*. By unveiling the phytochemical diversity within this plant, this study not only contributes to the scientific understanding of its chemical composition but also highlights its potential as a valuable resource in the development of pharmaceuticals and therapeutics.[16,17]

Experiments in anti-bacterial assays could shed light on the selectivity of the phytochemicals action on specific bacteria. In turn, docking the investigated chemical structures to the targets could shed light on the molecular mechanism of their activity. However, it is crucial to note that these predictions are theoretical and require experimental validation through antibacterial assays. The use of predictive models and computational tools to evaluate these parameters is pivotal in streamlining the process of identifying phytochemicals with the greatest potential for drug development.[18,19] Bioavailability predictions, provide critical insights into the likelihood of a compound being absorbed and utilized effectively in the human body. The study capitalizes on the AntiBacPred database to delve deeper into the antibacterial potential of DFP. This database offers valuable insights into the compounds ability to combat bacterial infections, adding another layer of evidence to support its therapeutic promise. This approach exemplifies the convergence of computational methodologies and predictive models with empirical research. By systematically evaluating phytochemicals based on critical pharmacokinetic parameters and bioavailability, the study not only identifies promising candidates but also optimizes the early stages of drug development.[20] DFP, as a standout candidate, serves as a testament to the potential of natural compounds like those found in *B. glabra* in the development of novel antibacterial agents.

The results of molecular docking and ligand-target interaction analysis shed light on the potential mode of action of DFP as an anti-bacterial agent. It belongs to the class of chemical compounds known as phenylalanine and derivatives and is also known as N-(D-fructos-1-yl)-L-phenylalanine. Phenylalanine and derivatives are compounds that contain phenylalanine or a derivative of phenylalanine originating from phenylalanine reactivity at the amino or carboxy group, or from the substitution of any hydrogen of glycine by a heteroatom.[21] The strong binding energy and the presence of hydrogen bonds and van der Waals interactions suggest a specific and stable interaction with the target protein tyrZ. It is a required enzyme that catalyses the aminoacylation of tryptophan to its corresponding $tRNA^{trp}$ during translation.[22] These findings have significant implications for future research and drug development efforts. Experimental studies, including *in vitro* assays and structural biology investigations, can validate the computational predictions and provide a deeper understanding of the antibacterial mechanisms.[23] Moreover, the selectivity of DFP for tyrZ and its potential impact on bacterial growth and survival warrant.

In the network analysis, each node indicates either a predicted target protein or a protein that is connected with these target proteins. The size of the node shows the strength of the interactions. The sorts of protein-protein interactions are represented by the inter-node connection lines, and colour of line denotes the type of interaction. The query protein tyrZ interacts with acetyltransferase-binding DNA and transcriptional regulator proteins.[24]

Implications and Future Directions

The results of this study collectively contribute to our understanding of antibacterial potential of phytochemicals derived from *B. glabra*. The identified compounds, particularly DFP, exhibit promise as antibacterial agents. However, it is imperative to validate these predictions through rigorous experimental investigations. Furthermore, future research may explore precise molecular mechanisms underlying the

antibacterial activity of these phytochemicals. Experimental validation of their efficacy, along with detailed studies on selectivity and safety, will be pivotal in advancing these natural compounds toward drug development.

CONCLUSION

This study emphasizes the significance of computational approaches in predicting the pharmacological properties of natural compounds and highlights the potential of *B. glabra* derived phytochemicals as a resource for anti-bacterial drug discovery. Experimental studies and further exploration of their mechanisms of action will pave the way for novel therapeutic interventions against bacterial infections.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

ABBREVIATIONS

AMR: Antimicrobial resistance; **WHO:** World Health Organisation; **SMILES:** Simplified Molecular Input Line Entry System; **STRING:** Search Tool for the Retrieval of Interacting Genes/Proteins; **KEGG:** Kyoto Encyclopedia of Genes and Genomes; **MMF94:** Merck Molecular Force Field; **POAP:** Parallelized Open babel and AutoDock suite pipeline; **tyrZ:** tryptophanyl-tRNA synthetase; **DFP:** N-(1-Deoxy-1-fructosyl) phenylalanine.

SUMMARY

In the context of the global challenge posed by antimicrobial resistance and the difficulties in developing new antibiotics, this study explores the potential of *B. glabra* flower extracts as a source of bioactive compounds for drug discovery. Through a systematic review and computational analysis, N-(1-Deoxy-1-fructosyl) phenylalanine was selected and virtually docked with the bacterial target protein tryptophanyl-tRNA synthetase. The *in silico* analysis revealed promising antibacterial potential with quercetin and playing a crucial role in inhibiting the translational process of protein synthesis. This computational investigation provides valuable insights into the potential antibacterial properties of phytochemicals derived from *B. glabra.*

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