

Exploring the Therapeutic Potential of Danshen (*Salvia miltiorrhiza*) and Ginkgo Biloba in Coronary Heart Diseases: A Network Pharmacology Investigation

Muhammad Kashif Aslam [1], Noureen Ashraf [2], Shawana Ambreen [3*], Sehrish Jehan [4], Shehnaz Bibi [5], Abdul Arham [6], Zunera Iqbal [7], Minahil Ashraf [8], Mehwish Yousaf [9], Nayab Tahir [10], Farhana [11], Abeer Ilyas [12], Aleezah Shaukat ul Hassan [13]

[1,12,13] Department of Zoology, The University of Okara, Okara, Pakistan
[3,5] Department of Zoology, University of Mianwali, Mianwali Lahore, Pakistan
[2,4] Department of Biotechnology, Lahore College for Women University, Lahore, Pakistan
[6] Department of Biotechnology, University of Mianwali, Mianwali, Pakistan
[7,8,9] Department of Botany, Lahore College for Women University, Lahore, Pakistan
[10,11] Department of Chemistry, The University of Okara, Okara, Pakistan

* Corresponding Author: **Shawana Ambreen**

Article Info

ISSN (online): 3049-0421
Volume: 03
Issue: 06
Received: 06-09-2026
Accepted: 04-10-2026
Published: 02-11-2026
Page No: 01-11

Abstract

Traditional Chinese medicine (TCM) pattern is beneficial in complicated diseases such as CHD as a classification method. In the case of atherosclerosis, plaque builds up in the arteries, and can become a serious problem in various parts of the body. In China, Salvia miltiorrhiza and Ginkgo biloba have been employed as medicinal plants in treating some complex diseases such as CVD. But there are mechanisms that need to be explored for the particular treatments. The aim of this study was to use network pharmacology to clarify the molecular mechanism of GDHP in the therapy of CHD. Batman-TCM was used to investigate the targets and bioactive compounds that were part of the GDHP. The pharmaceutical databases were used to extract the targets for CHD disease. Next, the protein-protein interaction (PPI) network was constructed using Cytoscape software and STRING online tool. The DAVID online tool was used to perform the KEGG and GO analysis. Finally, to confirm GDHP's potential targets for CHD treatment, molecular docking of the active components was performed. After screening, 199 matching targets and 34 active compounds were discovered. There were 16 common targets between CHD and GDHP. According to the results obtained from the network analysis, it appears that tanshinone IIA, miltirone, and gallocatechin could be classified as three distinct therapeutic components. There were eight main potential targets according to enrichment analysis the majority of the discovered genes were engaged in CHD-related pathways. This implies that discovered compounds may be the main GDHP active substances for atherosclerosis. In the current experiment, the binding potential of active substances to target sites was determined by conducting the network pharmacology analysis to determine the target sites, mechanism and related signaling pathway of GDHP for the treatment of CHD. This indicates that the new substances obtained from GDHP may become the major drugs to treat atherosclerosis, and this can have a very high connection with inflammatory response, lipid metabolism and fluid shear stress. By conducting the network pharmacology, we give new insights into the possible mechanism of GDHP for the treatment of CHD.

DOI: https://doi.org/10.54660/IJPGRR.2026.3.6.01-11

Keywords: Coronary heart disease, Traditional Chinese medicine, Network pharmacology, Danshen (*Salvia Miltiorrhiza*), Ginkgo biloba, Databases, GO and KEGG, Cytoscape, Molecular docking, Gallocatechin, Miltirone, Tanshinone IIA

1. Introduction

The leading cause of death globally is cardiovascular disease (CVD), which takes the lives of around 17.9 million people annually. CVDs are a group of heart and blood vessel diseases, such as coronary heart disease, cerebrovascular disease, rheumatic heart disease and others [1]. Additionally, it has been shown that the frequency of CVD, such as atherosclerosis, stroke, and myocardial infarction increases with age in men and women [2]. Statins and antiplatelet drugs have greatly reduced the incidence of cardiovascular diseases. Still, it remains unclear whether chronic heart disease (CHD) as a result of using drugs is a concern or not in the long run [3]. Coronary heart disease (CHD) is a polyetiological disease. It is the most frequent type of heart

disease in the USA. WHO estimates that there are about 18 million adult Americans with coronary heart disease [4]. That's the combined populations of Houston, Chicago, Los Angeles and New York City. In the U.S., CHD resulted in 375,500 deaths in 2021 [5]. When referring to the same disorder, the words "coronary artery disease (CAD)" and "coronary heart disease (CHD)" are often used interchangeably. CHD is caused mainly by the build-up of plaque in the walls of the coronary arteries that are responsible for supplying blood to the heart and other parts of the body (Figure 1). Plaque is formed by the accumulation of some element, such as cholesterol, in the artery. The walls of the artery narrow over time due to plaque buildup, partially or completely closing off the artery. The process that is being described is called atherosclerosis. A chest pain called angina is a consequence of significant reductions in blood flow to the heart, a heart attack and damage to the heart tissue occur if blood flow is reduced excessively or is completely stopped by plaque accumulation or a clot.

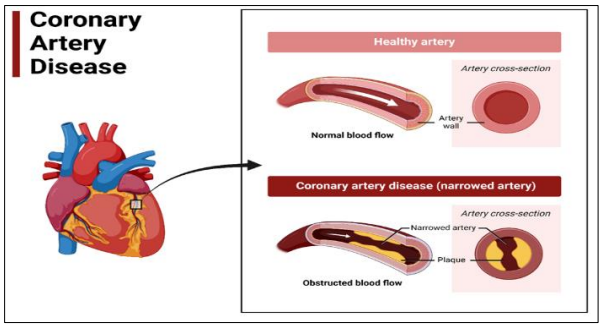


Fig 1: A comparison of arteries with coronary heart disease.

TCM has clear benefits for treating CHD. Danshen decoction, made from Salvia miltiorrhiza Bunge's root and rhizome, is mostly used in Traditional Chinese Medicine (TCM) to treat various abdominal and cardiac ailments [6]. It can improve blood flow, break up blood clots, encourage the flow of essential energy, and reduce discomfort. As such, it is widely used in the medical treatment of angina pectoris, coronary heart disease, and gastric and duodenal ulcers. Clinical studies have shown its efficacy in reducing atherosclerosis and thrombosis, as well as its capacity to inhibit blood clotting and improve fibrin breakdown [7]. Although studies on Salvia miltiorrhiza's potential for treating CHD, angina pectoris, and diabetic cardiomyopathy have been published, there is still a need to further investigate the processes by which Salvia miltiorrhiza treats CHD. The Ginkgo biloba L. plant's leaves are used to make Ginkgo biloba extract (GBE). The primary components of it are terpenoid lactones and flavonoids, which function as free radical accelerators and antioxidants. In addition, GBE promotes cognition, increases cerebral blood flow, and has other advantages. GBE is utilized as a pharmaceutical treatment for enhancing cardiovascular and cerebrovascular conditions in European nations [8]. In the United States and Japan, it is utilized as a dietary supplement. GBLs are widely used as a natural dietary supplement in a variety of industries, including food additives, health foods, pharmaceuticals, and functional drinks [9].

This study investigated the potential mechanisms of Ginkgo biloba and Salvia miltiorrhiza on CHD using network pharmacology techniques. In order to show the link between active ingredients in plants and diseases we have included the literature study which has provided us with an innovative way to prevent and treat CHD (coronary heart disease). As shown in Figure 2, the study employed a particular network pharmacology and bioinformatics technique.

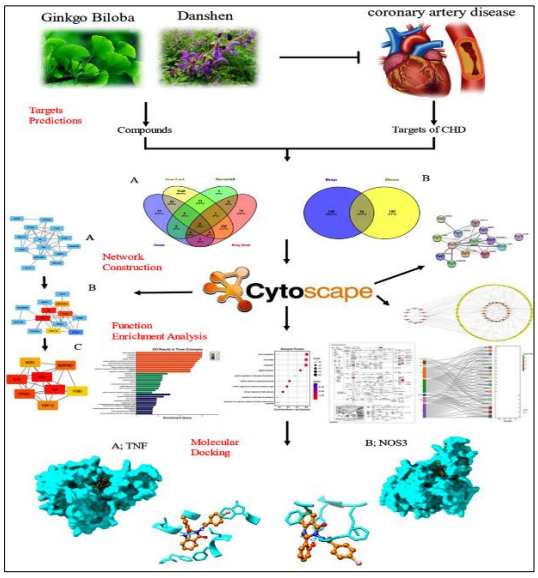


Fig 2: Workflow for investigating the mechanisms of CHD therapy through target screening, compound network analysis, core gene identification, and molecular docking.

2. Methodology

2.1 Screening of active compounds:

The chemical composition of Salvia miltiorrhiza Bunge and Ginkgo biloba was investigated using the TCMSP database (http://lsp.nwu.edu.cn/tcmsp.php). Drug-likeness (DL) score of at least 0.18 and oral bioavailability of at least 30% were set as the screening criteria for compounds. While DL indicates the resemblance between the active component and the recognized medicine, OB represents the relative amount of drug absorption once taken orally. Moreover, the TCMSP database was searched for verified target proteins that were shown to be affected by the active ingredients. The UniProt Knowledge Base was used to transform the active ingredient's target protein names to their conventional target gene names (UniProtKB, http://www.uniprot.org/).

2.2 Isolation of genes related to CHD:

The keyword "chronic heart disease" was used to obtain CHD-related genes from the Genecards database (https://www.genecards.org/), OMIM database (https://omim.org/), DrugBank database (https://www.drugbank.ca/) and PharmGkB database (https://www.pharmgkb.org/). The genes that were associated with CHD were then merged and any duplicate genes were removed. Furthermore, an online tool called Venny v2.1 (https://bioinfogp.cnb.csic.es/tools/venny/index.htm) was used to find common gene targets between the CHD and the herbs targets.

2.3 The development of Herbal Compound-Target Network:

“Herbal-compound-target” Network was developed with the help of Cytoscape Software version (3.10.1). Moreover, the protein interactome network has been constructed in the form of the network diagram. Several topological features have been considered to identify the most significant chemical compounds and CHD targets from the herbal data set. The process of protein-protein interaction (PPI) was performed through STRING database (https://string-db.org/cgi/input.pl). The core genes were identified based on compound score > 0.5 and “Homo sapiens” in PPI analysis.

2.4 Designing PPI Network of Common Targets genes.

The common genes of the CHD and herbs were loaded into the STRING 11.0 database (http://string-db.org/) for PPI analysis. Based on the total value of the protein, an interaction network was constructed with a value greater than 0.4. Moreover, Cytoscape 3.7.1 was used to visualize the network. The parameters of the PPI network were analyzed with the help of the network analyzer. The most important module in the PPI network was then selected by MCODE. A large-scale protein network's highly connected regions were identified by an MCODE module. Maximum depth was set to 100, K score to 2, degree cutoff to 2 and node score cutoff to 0.2 to evaluate the degree of protein link within the module.

2.5 GO and KEGG enrichment analysis

Database for Annotation, Visualization, and Integrated Discovery (DAVID) is an informative annotation tool that can be used to identify the biological relevance of a gene list. Common CHD targets were used to fill the DAVID database with the assumption of the organism being "Homo sapiens". For GO keywords and KEGG pathways, the P value was < 0.05 and FDR < 0.05, respectively.

2.6 Molecular Docking Studies

The protein structures targeted and the structures of drug compounds were obtained from the RCSB Protein Data Bank (https://www.rcsb.org/) and PubChem (https://pubchem.ncbi.nlm.nih.gov/), respectively. The Biovia Discovery Studio was used for hydrogenation and removal of water molecules for protein processing. PyRx was used to calculate the affinities and docking binding energy of each complex. Interactions between proteins and chemicals were analyzed using the Biovia Discovery Studio.

3. Results

3.1 Active Compounds and disease targets

The active compounds in herbs and target diseases were retrieved from TCM database. (Supplementary Table S1). In total, 34 active compounds were screened out from two herbs, 12 from Ginkgo Biloba and 22 from Danshen (Supplementary Table S2). One of the derivatives of gallocatechin, epigallocatechin gallate, exhibits anti-oxidative, anti-inflammatory, hypolipidemic, anti-thrombogenic and anti-hypertensive effects, which inhibit the canonical NF-κB pathway and prevent the development of CVDs. They both belong to the catechins family. The extract of Danshen has an anti-inflammatory and anti-oxidative effect due to the presence of a compound called miltirone. Miltirone is reportedly endowed with robust anti-microbial, neuroprotective and anti-tumor properties. The rhizome of Salvia miltiorrhiza Bunge plant contains a biologically active compound, called Tanshinone IIA (Tan-IIA). Many studies have been associated with the prevention and delay of different diseases such as cancer, neurological disorders, cardiovascular diseases, etc. with the use of Tan-IIA. Based on their medicinal qualities, the following drugs have also been identified as potential CHD treatments: miltirone, succinic acid, ginkgetin, quercitrin, hyproside, sciadopitisin, techtochrysin, astragalin, bilobetin, isoginkgetin, gallocatechin, isoguanosine, isoimperatorin, dauricine, hexadecanoic acid, and chyrophanol.

3.2 Herbal Compound-Targets Network

The active compounds from the TCM database and CHD disease genes from Genecards (9248 genes), OMIM (64 genes), PharmGkb (27 genes) and DrugBank (211 genes) were merged (Figure 3a). Total 176 targets were common among all databases. The data comprised 34 active compounds which matched 176 specific targets, 199 disease targets and 16 common target genes, as shown in Figure 3b. The active components and target genes were added to Cytoscape software. The segregated components were then removed since they failed to interact with the targets. The network of target genes and active ingredients of herbs was generated and is displayed in Figure 4. The degree indicates the number of target genes and herbal active compounds connected to each other. The more relevant the elements of a target point are, the higher its degree value.

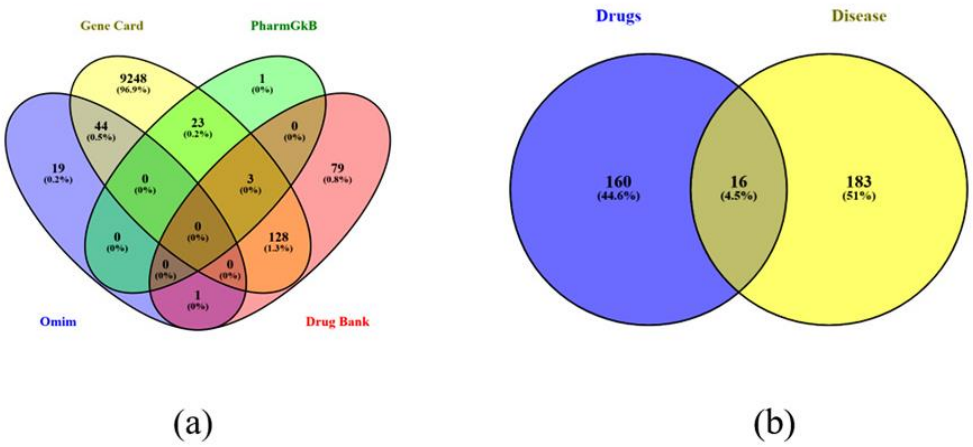


Fig 3: Venn Diagram of herbs targets **(a)** CHD disease targets **(b)** Common targets between CHD and herbs.

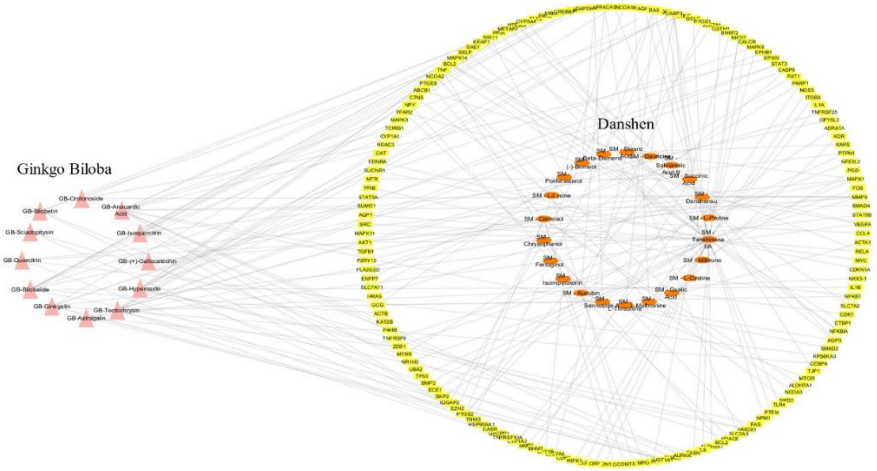


Fig 4: Interaction network between active compounds of Salvia miltiorrhiza and Ginkgo biloba and their target genes (pink: Danshen compounds; orange: Ginkgo biloba compounds; yellow: CHD-related gene targets).

3.3 Screening of Key Genes

Component target network was designed by using Cytoscape software (version 3.7.1). The data was collected through the online database STRING with 16 common targets. The PPI network was obtained by using CytoNCA after two screens. A total of 14 nodes were acquired during the 1st screening, and 10 nodes (MMP3, SERPINE1, IL6, TLR4, ITGB3, PTGS1, NOS3, TNF, SHARPIN, and P2RY12) were identified in 2nd screening and finally 8 key genes (TNF, IL6, ITGB3, PTGS1, NOS3, SERPINE1, TLR4, and P2RY12) were identified based on degree and central connectivity (Figure 6).

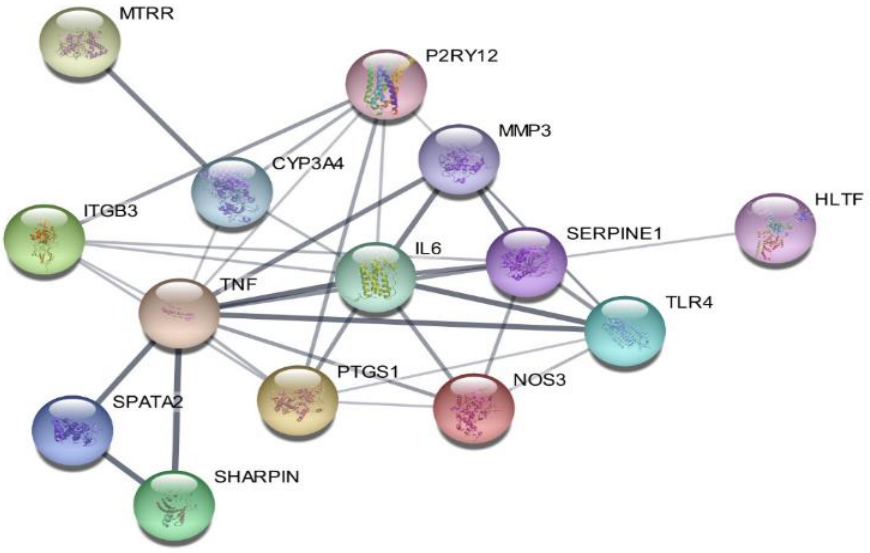


Fig 5: Common gene targets for CDH and the PPI network of herbs

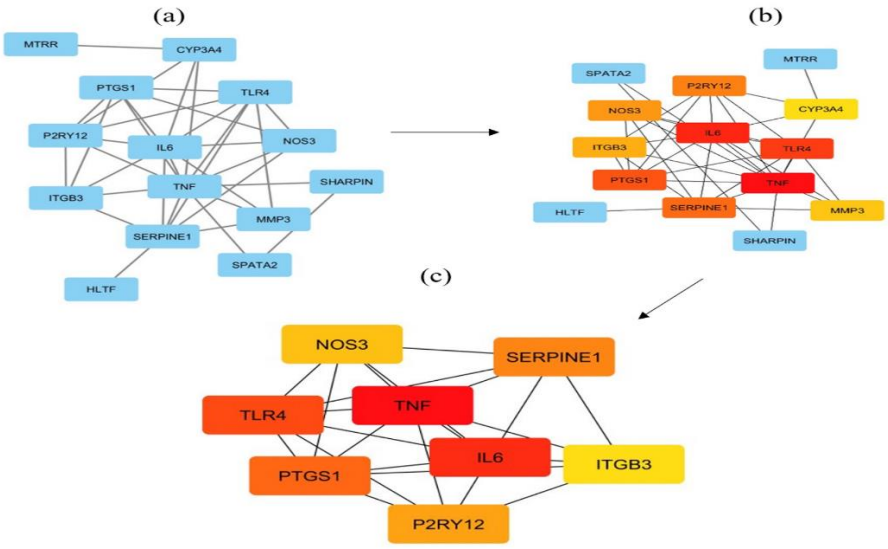


Fig 6: Screening of the key genes (a) 1st Screening (b) 2nd Screening (c) 8 key genes identified.

3.4 GO and KEGG Enrichment Analysis

An investigation of the 8 key targets in CHD treatment was performed using the DAVID. Using DAVID, the targets were investigated with respect to their cellular components (CC), biological processes (BP) and molecular functions (MF). We chose the top 30 results from the GO biological function analysis (Figure 7(a-d)) based on a P-value < 0.05. The most significant BP concepts that were found were: blood coagulation, hemostasis and platelet activation (Figure 7a). More CC terms existed in each of the membrane rafts, regions, micro domains, and the exterior area of the plasma membrane. MF keywords were highly enriched when it came to binding to cytokine receptors and proteases.

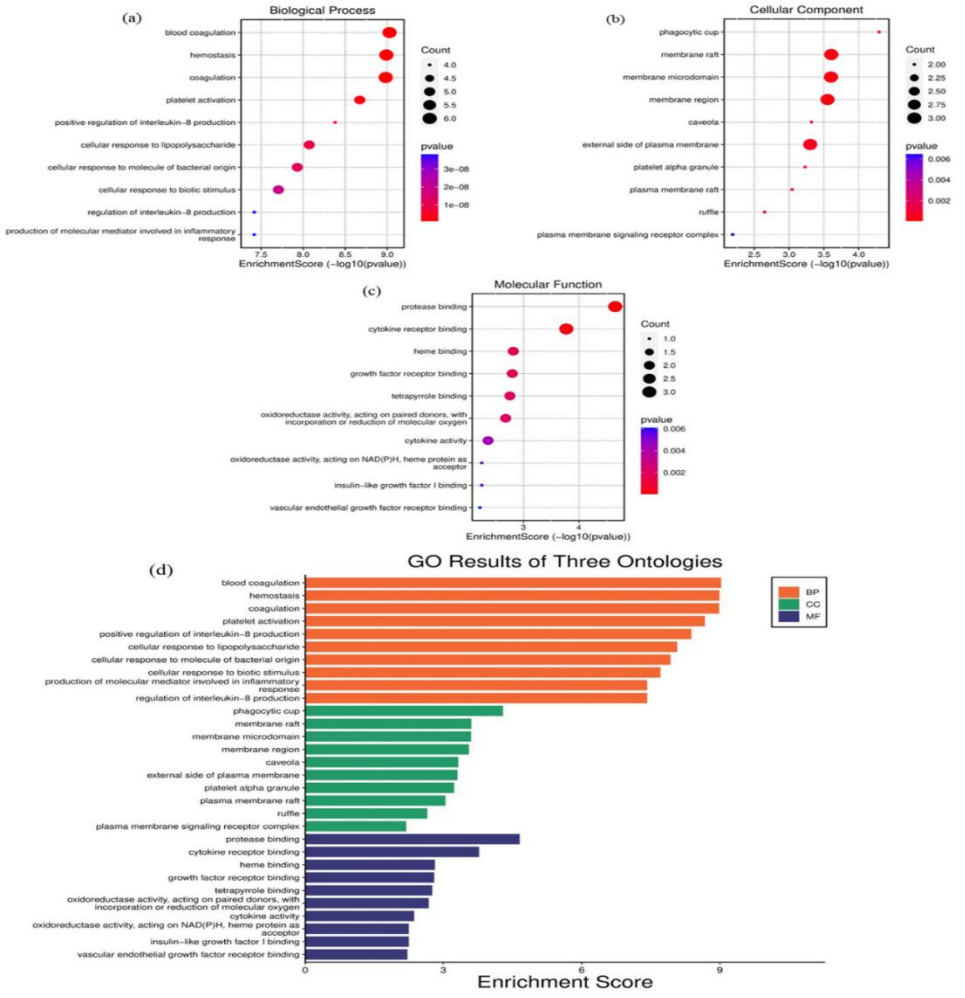


Fig 7: GO enrichment analysis of CHD-related gene targets, showing the top 10 terms for (a) biological process (BP, green), (b) cellular component (CC, orange), and (c) molecular function (MF, purple).

A KEGG pathway enrichment analysis was performed to assess the eight common targets at $P < 0.05$. The targets in forty-two pathways are highly enriched (Supplementary Table S3). The top 20 pathways that were significantly enriched were identified by gene counts (Table 1). The top 20 pathways, targets, and compounds were selected through the gene ratio and P-value derived from the KEGG enrichment analysis outcome in Cytoscape 3.7.1. It helped us develop the network of compound target pathways (Fig. 8A). In many cases, the targets of primary interest, IL6, TNF, TLR4, P2RY12, SERPINE1, ITGB3, NOS3, and PTGS1, were incorporated into the pathways in different ways. The Sankey Diagram (Fig. 8B) was developed via an open-source web tool (http://www.bioinformatics.com.cn) from the target gene links with enriched pathways. The GO and KEGG databases are significantly enriched for the TNF signaling pathway and for pathways related to fluid shear stress, suggesting that GDHP may act via these two pathways when treating CHD.

Table 1: Key genes' KEGG enrichment results.

IDs	Count	P values	Genes
hsa04933	4	5.05E-05	IL6, NOS3, SERPINE1, TNF
hsa05142	4	5.36E-05	IL6, SERPINE1, TNF, TLR4
hsa04066	4	6.54E-05	IL6, NOS3, SERPINE1, TLR4
hsa04611	4	9.61E-05	P2RY12, NOS3, ITGB3, PTGS1
hsa05417	4	9.61E-05	IL6, NOS3, TNF, TLR4
hsa04151	4	0.002182	IL6, NOS3, ITGB3, TLR4
hsa05144	3	6.73E-04	IL6, TNF, TLR4
hsa05134	3	8.44E-04	IL6, TNF, TLR4
hsa05321	3	0.001137	IL6, TNF, TLR4
hsa05133	3	0.001551	IL6, TNF, TLR4
hsa05323	3	0.002312	IL6, TNF, TLR4
hsa05410	3	0.002513	IL6, ITGB3, TNF
hsa04640	3	0.002616	IL6, ITGB3, TNF
hsa05146	3	0.002775	IL6, TNF, TLR4
hsa04931	3	0.003105	IL6, NOS3, TNF
hsa04620	3	0.003105	IL6, TNF, TLR4
hsa05135	3	0.004951	IL6, TNF, TLR4
hsa05418	3	0.005093	NOS3, ITGB3, TNF
hsa04936	3	0.00531	IL6, TNF, TLR4
hsa05161	3	0.006863	IL6, TNF, TLR4

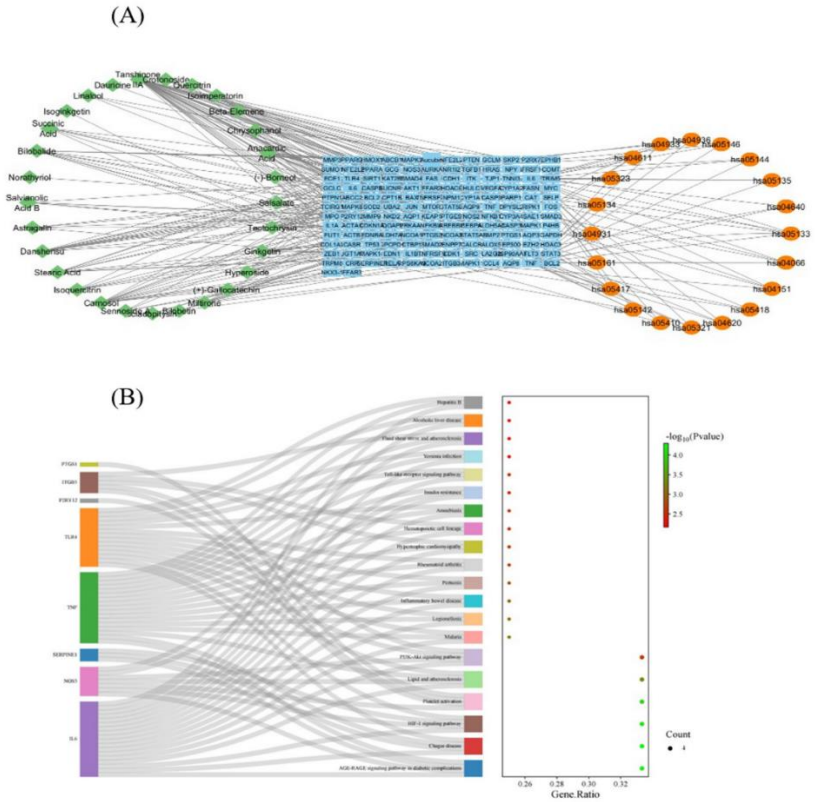


Fig 8: (A)Compound-target-pathway network for GDHP in CHD therapy (pink: compounds; purple: targets; green: pathways). (B)Sankey diagram of KEGG pathway analysis showing target–pathway associations (left: therapeutic targets; right: KEGG pathways).

3.5 Molecular Docking analysis

Molecular docking of the selected genes (IL6, TNF, TLR4, P2RY12, SERPINE1, ITGB3, NOS3, and PTGS1) was done to validate the research findings obtained from the network analysis. The molecular docking was performed using the key targets of CB along with the 19 compounds that had the highest degree values obtained from the network analysis of the herb-compound-target interaction based on the degree value of the PPI and KEGG networks. The ADME properties of the selected drugs were evaluated using the web-based software of the Swiss ADME (http://www.swissadme.ch/) and ADMET Lab (https://admet.scbdd.com/) (Supplementary Table S4). Following molecular docking, the 19 compounds (out of 34) from GDHP were selected according to their medicinal properties and binding affinity. These compounds included Gallocatechin, Carnosol, Tanshinone IIA Miltirone, Succinic Acid, Ginkgetn, Quercitrin, Hyproside, Sciadopitisin, Techtochrysin, Astragalin, Bilobetin, Isoginkgetin, Gallocatechin, Isoguanosine, Isoimperatorin, Dauricine, Hexadecanoic Acid, and Chrysophanol.

Target interactions and the binding modes of the interacting complexes having optimal values of free binding energy were illustrated using Discovery Studio 2020 (Fig. 9A-H). The values of free binding energies from the docking results ranged from -4 to -12 kcal/mol indicating that the binding is stable. Heat map in (Figure 10) illustrates the binding affinity of all compounds with target proteins. The red colour corresponds to the greatest binding values, the yellow colour to intermediate values, and the blue colour to lower binding values. One of the chosen compound called miltirone that exhibited the strongest binding value to every target protein and all binding interactions with every target protein is shown in (Figure 9). The binding of miltirone to TNF is due to several interactions. There is a PI-PI stacking between miltirone and the TYR-59 residue. Additionally, there is a hydrogen bond between miltirone and the TYR-151 residue. The molecule also interacts through van der Waals forces with the ILE-155, HIS-15, LEU-57, and TYR-119 residues. Hydrophobic small compounds generate stable complexes when they make hydrogen bonds with the active cavities of target proteins. After molecular docking and ADMET analysis, we found that GDHP's gallocatechin, miltirone, and tanshinone IIA exhibited potent binding activity with targeted proteins and shown less toxicity. These substances are therefore potential medication candidates. Molecular docking is a method used to study how herbal medicines bind to specific targets linked to diseases. However, it's important to note that more studies are needed to identify the exact active components in these herbs.

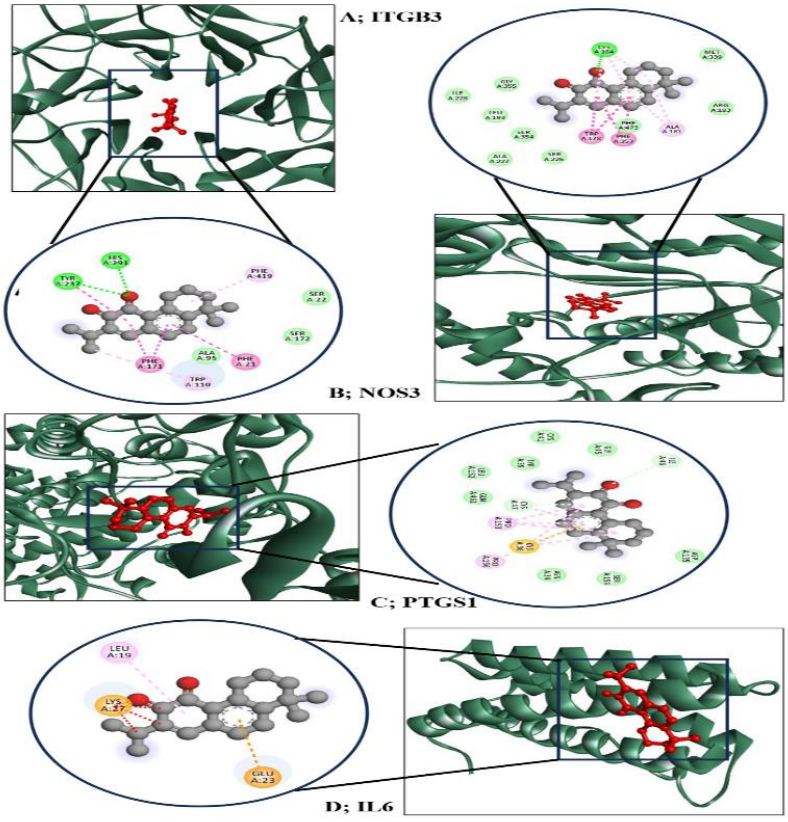


Fig 9: The docking simulation includes detailed interactions between target compounds.

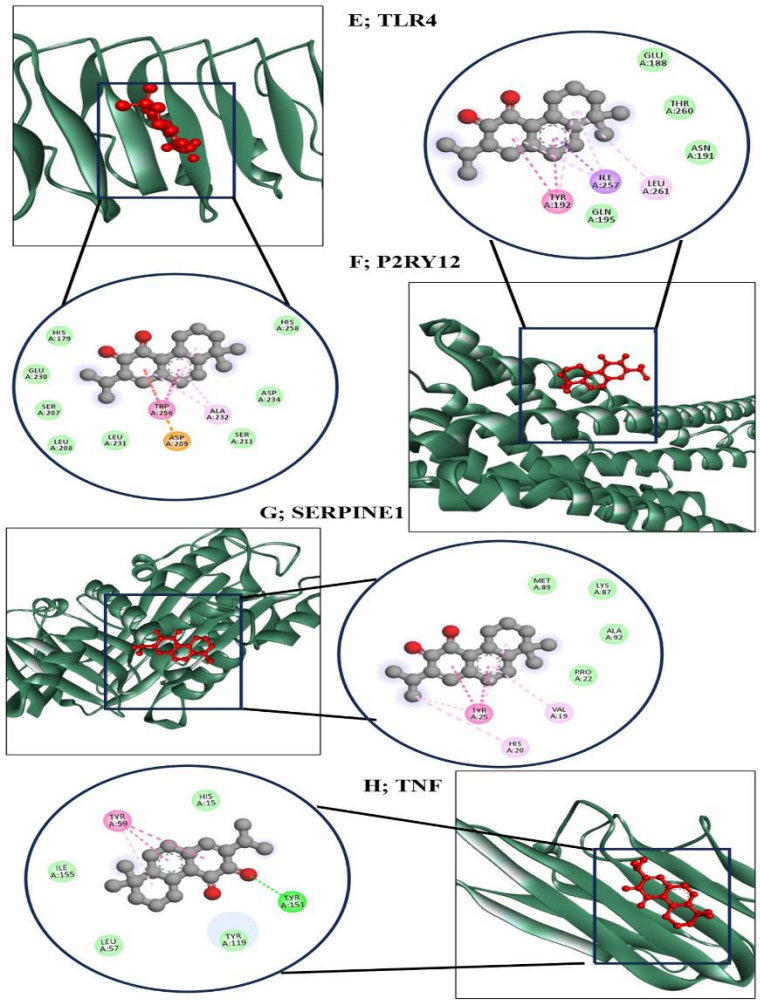


Fig 10: The docking simulation includes detailed interactions between target compounds.

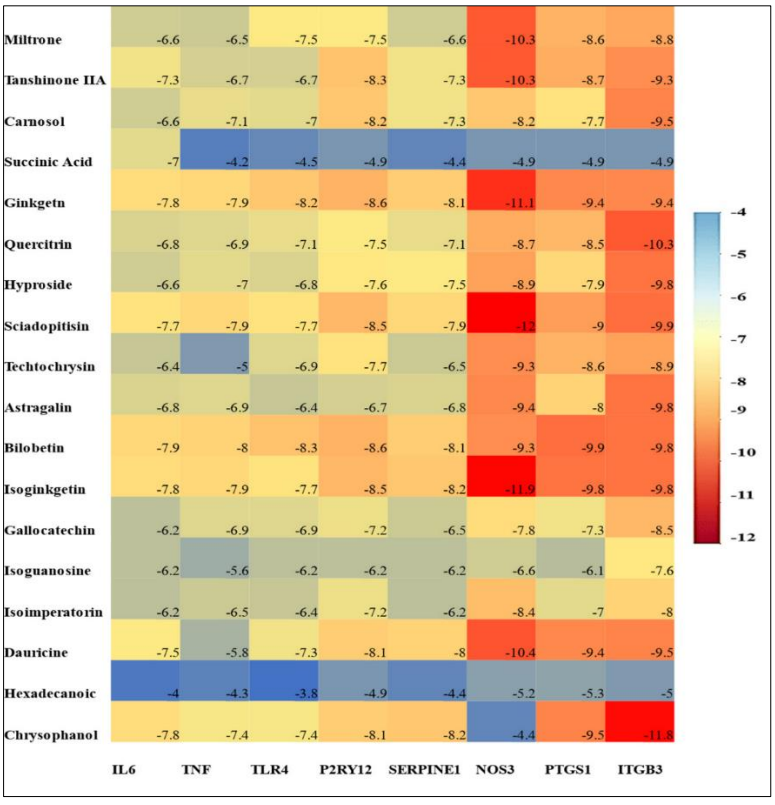


Fig 11: Heatmap of molecular docking binding affinities between compounds and proteins (red: highest; yellow: medium; blue: lowest binding values).

4. Discussion

Atherosclerosis is one of the main reasons people get coronary heart disease around the world. Among these therapies include angiotensin receptor blockers, antioxidants, anti-platelets, anti-coagulants, nicotine, and statins. Chinese herbal therapy frequently offers a multicomponent, multitarget, affordable therapeutic alternative without overtly harmful or adverse side effects. This study has shown pertinent evidence suggesting that Danshen (Salvia Miltiorrhiza) and ginkgo biloba may be compatible, with potential benefits for treating atherosclerosis and possibly coronary heart disease. Consequently, the underpinning was comprehensively evaluated in this study using the network pharmacology analysis technique. GDHP as a CHD treatment. In this scenario, the key molecules identified are IL6, TNF, TLR4, P2RY12, SERPINE1, ITGB3, NOS3, and PTGS1 according to the results obtained through the network analysis. Within the last decade and half, a considerable amount of studies has been conducted with regard to TNF-α's role in the heart. All of them confirmed the contradictory effect of TNF-α on the heart disease and heart physiology. TNF-α is produced by macrophages and monocytes located in atherosclerotic plaques and assisting in the atherosclerosis development. Two inflammatory mediators – TNF-α and IL-1 – are regulated by NF-κB.NF-κB regulates the activity of TNF-α and IL-1. The secretion of IL-1, TNF-α and other cytokines results in self-promotion circle which activates NF-κB and produces an increasing level of cytokines. Those cytokines participate in the development and progression of atherosclerosis. In a clinical study, the relationship between TNF-α and oxidative stress as well as coronary atherosclerosis severity was established. This relationship may be utilized for diagnosing of coronary chronic total occlusions (CCTO) in old patients suffering from congestive heart failure [10]. The prevention of atherosclerosis by GDHP was studied using two types of analysis: KEGG pathway functional analysis and Gene Ontology biological function analysis.

The main biological processes involved in the GO function analysis were blood pressure, hormone-related and intracellular receptor signaling, lipid and steroid metabolism, and controlling inflammation. The main focus of MF was on inflammation and lipids, especially how they bind to steroids, how steroid receptors work, and how nuclear receptors function. The significant locations at which CC has been located include the transcription regulator complex, RNA polymerase II transcription regulator complex, nuclear chromatin, and many other associated components. The KEGG pathway analysis indicated that the disorders associated with blood circulation, metabolism, and atherosclerosis treatment with respect to GDHP have mostly been associated with inflammatory signal transduction pathways. These include fluid shear stress, TNF signaling, and insulin signaling (Fig.12).

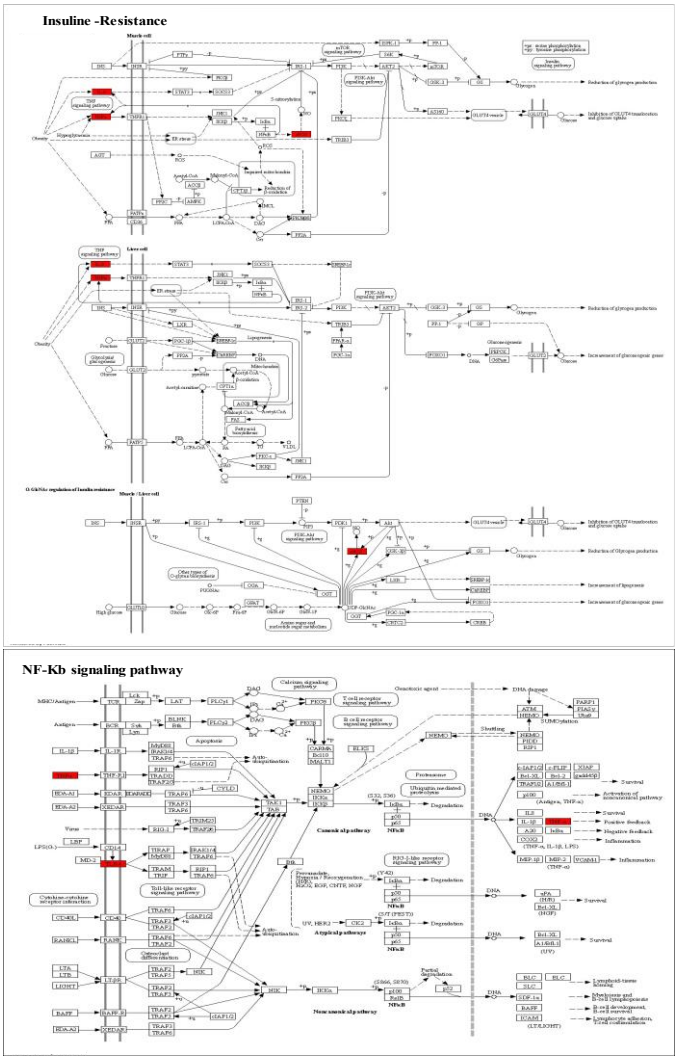


Fig 12: Signaling pathways in CHD.

Based on the findings from the network between compounds and targets and from the molecular docking studies, the potential therapeutics were gallocatechin, miltirone, and tanshinone IIA. Tanshinone IIA has various medicinal qualities such as anti-inflammatory and anti-tumor effects. It has been used traditionally to treat disorders such as arrhythmia, cardiomyopathy, and congenital heart problems. Tanshinone IIA is the major lipophilic constituent of Salvia miltiorrhiza referred to as tan-IIA. Various contemporary pharmacological studies have revealed that tan-IIA possesses anti-inflammatory and antioxidant activities. Tan-IIA is a potential treatment for CVD due to its ability to enhance angiogenesis. It has been demonstrated that tan-IIA is significant for immune cell growth and function and has a wide range of immunomodulatory actions. These include potentially harmful outcomes including the onset of atherosclerosis, reperfusion damage, hypertrophy, and heart failure, as well as advantageous benefits like cardioprotection against ischemia, myocarditis, and pressure overload. By controlling how immune cells act and function, tan-IIA reduces the production of substances that cause inflammation and helps fix wrong signals in the body. It can manage pathways like the TLR/NF-κB pathway, which helps in controlling signals inside cells. Because of this, tan-IIA has properties that reduce inflammation, prevent blood from clotting too much, stop blood clots from forming, and protect the nervous system. It also activates the MAPKs/NF-κB pathway. It has the ability to delay the onset of Alzheimer's disease and cardiovascular diseases such as hypertension and atherosclerosis. Through the death of various tumor cells, the activation of differentiation and apoptosis, and maybe the suppression of the development of carcinomas, tan-IIA has also been demonstrated to have anti-tumor capabilities.

Research has demonstrated that Salvia miltiorrhiza naturally possesses this intriguing polyphenol. Additionally, prior research has demonstrated that miltirone possesses a number of beneficial qualities, such as immunomodulatory effects, anti-oxidant, anti-microbial, anti-diabetic, anti-cancer, and modulation of peripheral pain signaling [11]. Epigallocatechin-3-gallate, the primary polyphenolic component of green tea, is a derivative of gallocatechin and has been demonstrated to have several impacts on cardiovascular health by altering various pathways [12]. Both gallocatechin and epigallocatechin-3-gallate belong to a family called catechins. Thus, Gallocatechin, Miltirone and Tanshinone IIA may be crucial elements in the treatment of CHD.

We checked more closely into the network pharmacology results, using our team's earlier studies and other research. Earlier studies showed that GDHP can stop the expression of inflammatory factors like IL-6 and block the TNF signaling pathway, which is linked to cholesterol and atherosclerosis. Lowering the levels of TG, TC, ApoB100, and Lp(a) in the blood is the main way GDHP does this. These results show how GDHP affects various signaling pathways, including lipid and atherosclerosis, fluid shear stress, TNF, insulin resistance, and atherosclerosis, as well as the expression of important genes. One key pro-inflammatory factor involved in inflammatory and immune responses is TNF.IL-1 and IL-6 not only naturally help control lipid metabolism and increase the production of adhesion molecules, but they also have anti-inflammatory effects and can speed up the development of atherosclerosis. Miltirone has an anti-inflammatory effect by reducing the production of TNF-α, IL-6, and IL-1β, which are major inflammatory cytokines [13]. It mainly affects the NF-κB-p65 pathway. These findings suggest that the anti-atherosclerotic effects of GDHP may involve shear stress and insulin resistance. Insulin resistance is the main pathway that connects different metabolic problems to congestive heart failure (CHD). It is closely tied to the start and progression of CHD. Insulin resistance may contribute to atherosclerosis by causing inflammation, oxidative stress, problems with lipid metabolism, damage to the endothelium, and other effects [14]. Insulin resistance activates JNK and IKK through increased ROS levels, leading to inflammation and problems with the endothelium. JNK stimulates the production of inflammatory factors such as matrix metalloproteinase, IL-2, and TNF-α. TNF-α and IL-6 stimulate the process of insulin signaling and the production of fatty acid (FFA). The pathways stimulated include MAPK pathways and DAG and PKC pathways in the endothelial cells and stimulation of movement of middle layer smooth muscle cells in the vascular endothelium [15]. They cause thrombosis due to an increase in the secretion and production of extracellular matrix proteins and fibrinolytic enzyme inhibitor 1.

5. Conclusion

This study used network pharmacology to predict the targets, mechanisms, and signaling pathways of GDHP in treating CHD. It also checked how well the active compounds in herbs bind to their targets. The study looked at the molecular docking effects of common GDHP compounds like tanshinone IIA, miltirone, and gallocatechin. As a result, it seems that GDHP plays a significant role in treating atherosclerosis, and its main way of working involves changing key targets related to insulin resistance, inflammation, blood flow shear force, and metabolic signaling pathways. More experiments are needed to confirm how effective GDHP is for CHD, and the study has some limitations in assessing the active components. Thus, additional research is required for gaining better insights into the potential benefits of GDHP.

Conflict of Interest

Authors declare no conflict of interest.

Funding Note

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Acknowledgment

The authors would like to acknowledge the support and resources provided by the Department of Zoology, University of Okara.

References

1. Hussain MM, *et al*. Risk factors associated with cardiovascular disorders. Pakistan BioMedical Journal. 2024:3-10.
2. Vakhtangadze T, *et al*. Gender differences in atherosclerotic vascular disease: from lipids to clinical outcomes. Front Cardiovasc Med. 2021;8:707889.
3. Kolanu ND, *et al*. The differential impact of medical therapy and lifestyle modification on cardiovascular health and risk of adverse cardiovascular events: a narrative review. Cureus. 2024;16(4).
4. Ralapanawa U, Sivakanesan R. Epidemiology and the

magnitude of coronary artery disease and acute coronary syndrome: a narrative review. J Epidemiol Glob Health. 2021;11(2):169-177.
5. Parsan SJ, *et al*. Advocating for early cardiovascular disease screening in Canada—the enormous economic burden in Canada and globally: change is necessary and urgent. 2025.
6. Nwafor EO, *et al*. Traditional Chinese medicine of Salvia miltiorrhiza Bunge: a review of phytochemistry, pharmacology and pharmacokinetics. Tradit Med Res. 2021;6(4):35-25.
7. Yuan MH, *et al*. Therapeutic effects and molecular mechanisms of natural products in thrombosis. Phytother Res. 2024;38(5):2128-2153.
8. Bhatti MA, *et al*. Exploring the therapeutic potential of Danshen (Salvia miltiorrhiza) and Ginkgo biloba in coronary heart diseases: a network pharmacology investigation. 2025.
9. Wang J, *et al*. Study on mechanism of Ginkgo biloba L. leaves for the treatment of neurodegenerative diseases based on network pharmacology. Neurochem Res. 2021;46(7):1881-1894.
10. Li X, *et al*. Interplay of TNF-α, soluble TNF receptors and oxidative stress in coronary chronic total occlusion of the oldest patients with coronary heart disease. Cytokine. 2020;125:154836.
11. Al-Shuhaib MBS, Al-Shuhaib JM. Assessing therapeutic value and side effects of key botanical compounds for optimized medical treatments. Chem Biodivers. 2025;22(1):e202401754.
12. Lei M, *et al*. Bioactivity and structure–activity relationship of epigallocatechin and epigallocatechin-3-gallate derivatives. Rev Bras Farmacogn. 2025;35(4):641-665.
13. Dai W, *et al*. Phytochemicals targeting Toll-like receptors 4 (TLR4) in inflammatory bowel disease. Chin Med. 2022;17(1):53.
14. Poznyak A, *et al*. The diabetes mellitus–atherosclerosis connection: the role of lipid and glucose metabolism and chronic inflammation. Int J Mol Sci. 2020;21(5):1835.
15. Weinberg Sibony R, *et al*. Overview of oxidative stress and inflammation in diabetes. J Diabetes. 2024;16(10):e70014.

How to Cite This Article

Aslam MK, Ashraf N, Ambreen S, Jehan S, Bibi S, Arham A, *et al*. Exploring the therapeutic potential of Danshen (*Salvia miltiorrhiza*) and Ginkgo biloba in coronary heart diseases: a network pharmacology investigation. International Journal of Pharma Growth Research Review. 2026;3(6):1-11. doi:10.54660/IJPGRR.2026.3.6.01-11.

Creative Commons (CC) License

This is an open access journal, and articles are distributed under the terms of the Creative Commons Attribution Non-Commercial-ShareAlike 4.0 International (CC BY-NC-SA 4.0) License, which allows others to remix, tweak, and build upon the work non-commercially, as long as appropriate credit is given and the new creations are licensed under the identical terms.