Research Article

A systems pharmacology approach for targeted study of potential inflammatory pathways and their genes in atherosclerosis

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Abstract: Atherosclerosis is a widespread and chronic progressive arterial disease that has been regarded as one of the major causes of death worldwide. It is caused by the deposition of cholesterol, fats, and other substances in the tunica intima which leads to narrowing of the blood vessels, loss of elasticity, and arterial wall thickening, thus causing difficulty in blood flow. For a long time, one of the most crucial approaches to the treatment and prevention of cardiovascular illnesses has been the use of natural products. Numerous studies on natural chemicals that are beneficial against atherosclerosis have been carried out in recent decades due to the growing interest in natural products, including medicinal herbs. The primary cause of coronary heart disease, a chronic inflammatory condition marked by fat buildup in the artery wall, is atherosclerosis. Since inflammation is its precursor, seaweed-derived polysaccharides that target inflammatory genes are a viable source of anti-inflammatory drugs. After preparing the list of herbal medications and predicting the suspected indicators for atherosclerosis, we looked for possible binding targets. The binding model of fucoidan and alginate with targeting genes was predicted using computational methods such as molecular docking and Swiss-ADME. Molecular docking experiments showed that Fucoidan could block genes involved in inflammation. Furthermore, Fucoidan's sulphate group gives it unique properties in the GI tract and molecular dynamics. These findings suggest that sulphate polysaccharides may have anti-atherogenic properties. We used the publicly available dataset to investigate the top-ranked genes based on network-level understanding of gene expression patterns and their effects on functions. The pathways that were most affected were phagosomes, cell adhesion molecules, haematopoietic cell lineage, cytokine-cytokine receptor interaction, osteoclast differentiation, antigen processing and presentation, and critical immune signalling pathways. Additionally, based on networks of DEGs, the genes that were most connected were PTPRC, ITGB2, HCLS1, RAC2, LAPTM5, CD37, CD53, CD48, SYK, HCK, TYR0BP, FERMT3, COR01A, LCP1, and phagosome. Here, we have investigated the possible connections between the marine medications Fucoidan and Alginate-N, as well as their possible targets in atherosclerosis.
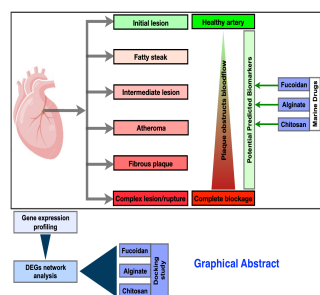
Keywords: Natural drugs (NDs)/Herbal drugs (HDs); Fucoidan and Alginate-n; atherosclerosis; metabolic disorders; genes and pathways; biological networks

Graphical Abstract

1. Introduction

One of the main causes of death and morbidity worldwide is atherosclerosis. Peripheral vascular disease, myocardial ischaemia, heart failure, heart attacks, and strokes are all caused by it. Inflammation, damage, and malfunction of endothelial cells in the heart are hallmarks of atherosclerosis. Acute cardiovascular disease is brought on by unstable atherosclerotic plaque rupture, arterial stenosis, or occlusion brought on by platelet aggregation and thrombosis. Atherosclerosis is a chronic inflammatory disease[1-6]. Proinflammatory cytokines, inflammatory signalling pathways, adhesion molecules, and bioactive lipids all contribute to the inflammation associated with atherosclerosis. The impact of inflammation and the systemic inflammatory signalling pathway on atherosclerosis, the part related signalling pathways play in inflammation, the development of atherosclerosis plaques, and the potential for atherosclerosis treatment through inflammation inhibition are all covered in this

review. Plaque accumulation in the wounded area, arterial constriction, cholesterol deposition on the arterial wall, and monocyte adhesion to the endothelium are all consequences of endothelial injury. This mechanism causes chronic inflammation, which ultimately results in thrombosis or stenosis. The lipid-driven, multifocal, smouldering immuno-inflammatory illness known as atherosclerosis affects the medium and large arteries. Leukocytes, intimal smooth muscle cells, and endothelial cells are the primary players in the development of this disease. The most severe consequences of atherosclerosis, including heart attacks and strokes, are brought on by superimposed thrombosis. Therefore, the important topic is not why atherosclerosis starts, but rather why, after years of slow progression, atherosclerosis becomes complicated by luminal thrombosis. If thrombosis-prone plaques could be identified and prevented, atherosclerosis would be a far less dangerous condition. The vast majority of deadly coronary thrombi are caused by plaque rupture. Compared to women, coronary thrombosis is more frequently caused by plaque rupture in men[3, 4, 7-18].

As blood pressure, smoking, and low-density lipoprotein (LDL) cholesterol levels have dropped, the risk factor profile has changed. The preventive properties of high-density lipoprotein have been questioned by recent research, which now focusses on triglyceride-rich lipoproteins as well as low-density lipoproteins as the causes of atherosclerosis[9-11, 16, 19-21]. Atherosclerosis's non-traditional causes, like sleep disturbances, sedentary lifestyles, the microbiota, air pollution, and environmental stress, have also drawn more attention. Leukocytes and inflammatory pathways connect both established and new risk factors to the changed behaviour of arterial wall cells. Investigating the pathophysiology of atherosclerosis has brought attention to the bone marrow's role: clonal haemopoiesis, a previously unknown but frequent and significant age-related contributor to the risk of cardiovascular disease, can result from somatic mutations in stem cells. The idea of "vulnerable plaque" has given way to more detailed descriptions of the mechanisms behind the thrombotic consequences of atherosclerosis. These developments in our knowledge of the biology of atherosclerosis have made it possible to develop therapeutic approaches that could enhance the prevention and management of the now common atherosclerotic conditions. Ruptured plaques exhibit angiogenesis, adventitial inflammation, and outward remodelling. They consist of a big, lipid-rich core, angiogenesis, adventitial inflammation, outward remodelling, and a thin, fibrous cap with many macrophages and few smooth muscle cells. Plaque rupture is the most common cause of coronary thrombosis. Distinct patho-anatomical features of ruptured plaques, and consequently, rupture-prone plaques, may help with in vivo image recognition[8, 10, 12, 13, 16, 18, 19, 22, 23].

Atherosclerosis is by far the most prevalent underlying cause of peripheral arterial disease, carotid artery disease, and coronary artery disease. Thrombosis, which happens when a ruptured or eroded atherosclerotic plaque is superimposed on another ruptured or eroded atherosclerotic plaque, is what causes life-threatening clinical events including acute coronary syndromes and stroke. Atherosclerosis by itself is rarely fatal. Therefore, the key question is not why atherosclerosis develops, but rather why none or a small number of plaques out of many in a particular person seem to experience a thrombosis-prone and fatal phase over their lifetime. Atherosclerosis, a chronic inflammatory blood artery disease, is the primary cause of cardiovascular disease, a major cause of death globally. Along with cholesterol that enters from the circulation, atherosclerotic lesions also contain macrophages, T lymphocytes, and other immune response cells. While interfering with regulatory immunity speeds up disease, targeted ablation of genes expressing proinflammatory cytokines and costimulatory factors reduces disease in mice models. Atherosclerosis has been linked to both innate and adaptive immunological responses, with elements of low-density lipoprotein that carry cholesterol causing inflammation, T cell activation, and antibody formation as the illness progresses[3, 5, 8, 12, 13, 16, 17, 19, 21, 24-29].

Since the beginning of civilisation, natural goods have been prized for a number of uses, including medicinal ones. As they have been used to treat numerous other conditions, medicinal herbs have also been used to cure atherosclerosis. The mechanisms of action of several herbs used to prevent atherosclerosis have only lately been clarified by the use of cellular models for anti-atherogenic natural product screening or in-depth research on certain plants. To better comprehend these plants, recent studies on natural products—particularly medicinal herbs—were categorised and described based on their mechanisms of action (MOAs) against atherosclerosis.

2. Methods

In order to find possible targets and herbal medications that can interfere with the activated signalling pathways, we proposed to examine the activated signalling pathways of individual atherosclerosis. In particular, we use an integrated method to first discover the genes that are up- or down-regulated in patients with atherosclerosis, and then we identify the components of the pathway. Lastly, we mapped the upstream/downstream signalling for the medicines alginate and fucoidan.

The project's objective was to identify genes with altered expression in macrophages from atherosclerosis patients compared to macrophages from healthy individuals. To that end, we first selected the data we were interested in (raw expression datasets) GSE9874 (total 60 samples, 30 normal and 30 atherosclerosis)

(https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9874). They used baseline macrophages, monocyte-derived macrophages from peripheral blood, and foam cells cultured with or without oxidised LDL. Fifteen individuals with subclinical atherosclerosis and a family history of coronary heart disease (CHD) provided the macrophages. 15-year-olds' macrophages and sex-matched individuals without atherosclerosis or a family history of CHD served as controls. Four lists of differentially expressed genes (DEGs) were obtained by comparing the atherosclerosis samples with normal samples of the corresponding samples for the purpose of differential gene expression analysis[30-39].

In conclusion, processing raw files, calculating intensity, and normalisation are the fundamental procedures for the majority of the study. The most popular methods for normalisation are EB, RMA, and GCRMA. Here, we have normalised raw intensity using EB. Following normalisation, we move forward with our objective, which is to comprehend the patterns of gene expression and their deduced roles. The built-in function GEO2R has been utilised for statistical analysis and differential gene expression prediction. In this instance, a matrix of gene expression levels is required, where each row corresponds to a gene and each column to a replication. The number of rows in both the normal and target data categories must be equal, and each class's variances must be equal. We created our own algorithm for pathway and network analysis and conducted pathway research using the KEGG database.

Throughout the work, FunCoup2.0 was utilised to generate the DEGs networks, and Cytoscape was utilised to visualise the networks. We have used MATLAB for the majority of our coding and computations. Four sorts of functional couplings or linkages, including protein complexes, physical interactions between proteins, metabolic processes, and signalling pathways, are predicted by FunCoup.

Docking approach details:

ACVR1B, COL1A, CR2, GP5, IFNA21, IGF1, IL5RA, IL20RA, MAP2K6, RAPGEF3, RRM2; and BCL3, BMPRB1, CCL4, CCL5, CD14, CIITA, CSF2RA, CXCL5, HLA-DRB4, IL7R, IL15RA protein sequences were obtained from the UniProt database (www.uniprot.org). PubChem was used to obtain the 3D structures of marine drugs i.e., Alginate-n (Pubchem CID: 91666318) and Fucoidan (Pubchem CID: 129532628) in SDF format. The structure of proteins and ligands was visualized using PyMol.

The Swiss Model website (www.swissmodel.org) was used to model the homology of the proteins listed above. The GMQE, QMEANDisCo, and QMEAN Z-score analyses were used to choose the simulated structures. A scale of 0 to 1 for overall model quality is provided by GMQE (Global Model Quality Estimate) and QMEANDisCo global, where larger numbers denote higher expected quality. With all options set to default, the Swiss PDB Viewer was used to minimise the energy of the proteins' three-dimensional structure after hydrogen atoms were introduced[38, 40].

The total number of active sites, together with information on their amino acid sequence, cavity locations, and cavity average volume, were found using a search tool. Therefore, using the Discovery Studio and CASTp server with the default probe radius (1.4 Å), the binding pocket of each of the proteins listed above was predicted.

PyRx was used for the molecular docking experiment (AutoDock Vina). For docking, the atomic coordinates of the protein and ligand were converted to pdbqt files. AutoDock Vina and grid box dimensions with specified spacing and size pointing in the x, y, and z directions were used to build the binding pocket[38, 39, 41-47]. The docking trials were conducted using the default parameters. To identify the best binding configurations for the compounds, the lowest binding free energy (delta G), the quantity of hydrogen bonds, and other hydrophobic interactions were also taken into consideration. Discovery Studio and PyMol examined a wide range of interactions, including hydrogen bonds, carbon-hydrogen bonds, van der Waals interactions, pi-sigma, pi-sulfur, alkyl, pi-alkyl, pi-pi T-shaped, and halogen connections.

3. Results

3.1. Comparative gene expression profiling: We looked at the total gene expression profile as well as the important pathways that are enriched at a very high fold change threshold, not only the atherosclerotic genes. Genes that are upregulated, genes that are downregulated, and pathways are shown as nodes that are connected by strings (Figure 1a-1c). Here are the patterns of top upregulated genes' interactions with other overexpressed genes and functional pathways. Upregulated genes that interact with important pathways include COL1A2, MAP2K6, RRM2, IL20RA, RAPGEF3, ITGB1, GP5, ACVR1B, CR2, IL5RA, IFNA21, IGF1, EGF, and others. In the meantime, EGF has been discovered to interact directly with FoxO signaling, cytokine-cytokine receptor interaction, ErbB signaling, and HIF-1 signaling pathways, as well as indirectly with complement and coagulation cascades, hematopoietic cell lineage, and B-cell receptor signaling pathways through upregulated CR2. Through MAP2K6, IFNA21 is linked to neuroactive ligand receptor interaction, toll-like receptor signaling, cytokine-cytokine receptor interaction pathways, and TNF signaling (Figure 1a—1c).

3.2. Functional profiling: We evaluated the impact of gene expression changes at the functional level using pathway enrichment analysis after creating the list of differentially expressed genes. We acquire a list of routes with their p-values from pathway enrichment analysis, which we utilize to determine statistical significance. Following the compilation of a list of differentially expressed genes, we used pathway enrichment analysis to assess the functional significance of gene expression variations. Pathway enrichment analysis provided us with a list of pathways and their p-values, which we used to establish statistical significance. The top 13 and 25 DEGs down and upregulated genes that were significantly modified in atherosclerosis were found using the Enriched KEGG pathways, as shown in Figure 1d—1e. The cytokine-cytokine receptor interaction signaling, PI3K—Akt signaling pathway.
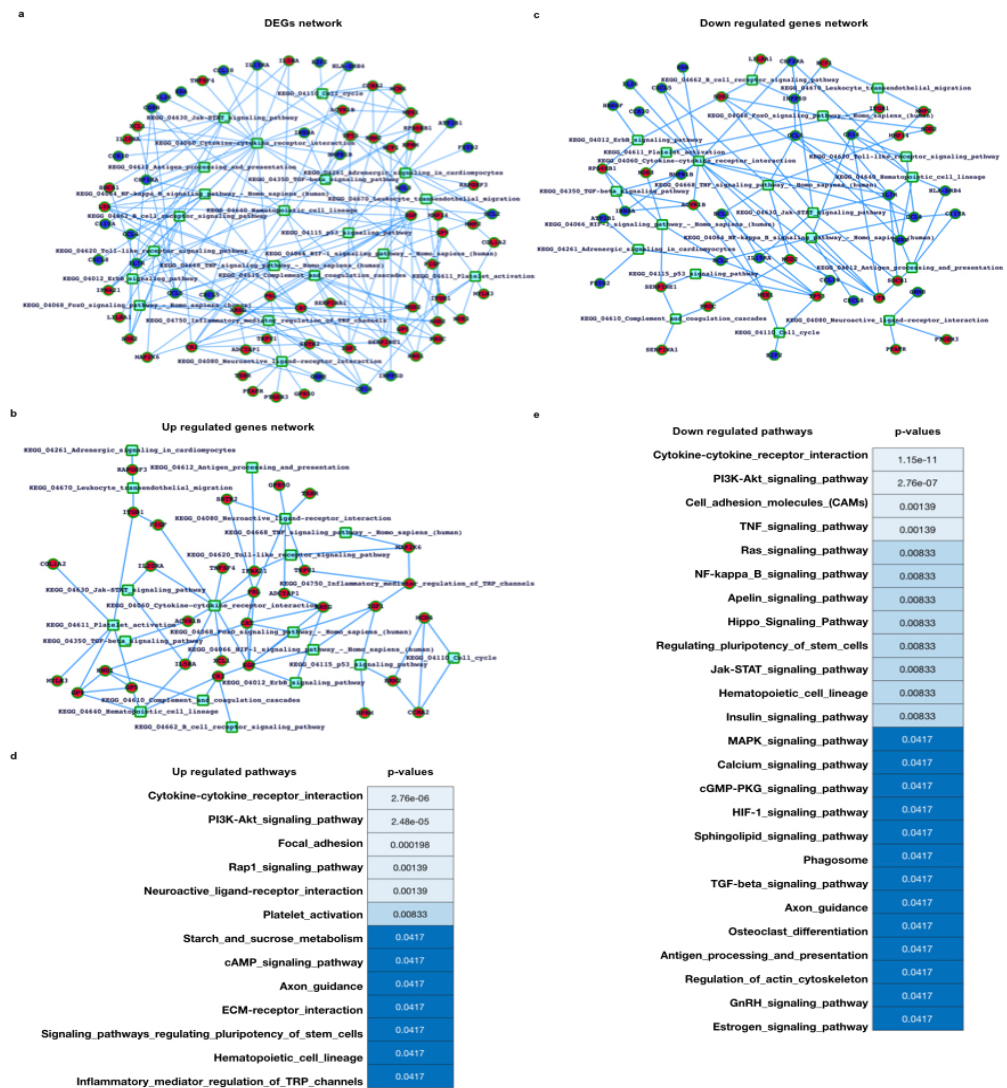

Figure 1. Atherosclerosis gene expression profiling, functional analysis, and network level understanding. (a) DEGs and the inferred pathways network. (b) Up-regulated genes and (c) down-regulated genes and inferred pathways network. (d) Pathways enriched for up-regulated genes and (e) the pathways enriched for down-regulated genes.

3.3. Critical infectious and inflammatory pathways are dominantly affected as a result of atherosclerosis progression: To analyze the detailed role of the altered genes in terms of expression at functional level, we have performed the individual pathway level analysis followed by their pathway components. Here, we observed the significantly altered pathways and majority of the genes belong to cytokine, TLR, NF--kB, ubiquitin proteasomal system, and some more pathways also as potential components of immune system (Figure 1). Furthermore, we have also performed gene ontology (GO) terms enrichment analysis and protein classification by using panther database as shown in Figure 2. In molecular functions, binding and catalytic activity appear dominantly enriched followed by molecular transducer activity, molecular function regulator, transcription regulator activity, and transporter activity. In cellular components terms, cellular anatomical entity and protein-containing complex terms were enriched. The potential biological processes terms which were enriched potentially are: cellular process, biological regulation, metabolic process, response to stimulus, signaling, localization, multicellular organismal process, localization, and immune system process. In panther protein classification, metabolic interconversion enzyme, protein modifying enzyme, gene-specific transcriptional regulator, defense/immunity protein, protein modifying enzyme, transporter, transmembrane signal receptor, scaffold/adaptor protein, and protein-binding activity modulator (Figure 2).

3.4. Docking profiling reveals potential putative targets against atherosclerosis:

Finally, we looked at herbal medicines as prospective treatments for such globally prevalent human disorders. This research not only provides prospective herbal medications, but also possible indicators.

3.4.1. Modelled structure of proteins:

Supplementary Table 1 lists the modelled structures of BCL3, BMPRB1, CCL4, CCL5, CD14, CIITA, CSF2RA, CXCL5, HLA-DRB4, IL7R, IL15RA: and ACVR1B, COL1A, CR2, GP5, IFNA21, IGF1, IL5RA, IL20RA, MAP2K6, RAPGEF3, RRM2 based on GMQE and QME The fraction of residues present in most favorable areas, extra allowed regions, generously allowed regions, and banned regions are depicted by the Ramachandran plot (Suppl. Figure 1 & Supplementary Table 1). These results revealed that the modelled structures were of sufficient quality to be used in subsequent molecular docking research.

3.4.2. Binding patterns of proteins with marine drugs:

Molecular docking findings revealed that the marine medicines Alginate-n and Fucoidan bind to the proteins' expected binding site (Figures 3 and 4). Table 1 shows the minimal binding energies of proteins with marine pharmaceuticals in kcal/mol. The majority of proteins have a strong affinity for Fucoidan (Figure 3). The maximum binding affinity was found in BMPRB1, CSF2RA, MAP2K6, CIITA, and ACVR1B, with binding energies of -6.5kcal/mol, -6.3kcal/mol, -6.2kcal/mol, and -

Figure 2. Functional analysis and protein classification by using Panther database. Molecular functions, cellular components, biological processes, and panther protein classes.

6.0kcal/mol, respectively. Except for CIITA, which displayed a binding affinity for Alginate-n, they all showed affinity for Fucoidan. We looked into the generated complexes with Discovery studio and PyMol to discover what was causing the differences in binding energies (Figure.). In terms of traditional hydrogen bonds, CSF2RA, MAP2K6, CIITA, and ACVR1B bound to Alginate-n and Fucoidan in the following order: 4, 5, 7, 8, and 2. (Table 1 and Figure 3 and 4). BMPRB1 formed substantial hydrogen connections with Tyr248, Asp350, and Lys336 with bond lengths ranging from 2.16--3.07nm. With Arg43, Thr44, Met45, and Arg155, CSF2RA demonstrated typical hydrogen bonds with bond lengths ranging from 2.11--2.69Å. Gly65, Lys82, Lys181, Ser201, and Lys210 formed conventional hydrogen bonds with Gly65, Lys82, Lys181, Ser201, and Lys210, with bond lengths ranging from 2.03Å--2.89Å (Figure 3 and 4). With Glu565, Ser567, Arg839, Thr866, and Trp896, C II TA formed conventional hydrogen bonds with lengths ranging from 2.14 Å to 2.77 Å. ACVR1B established conventional hydrogen bonds with Lys234
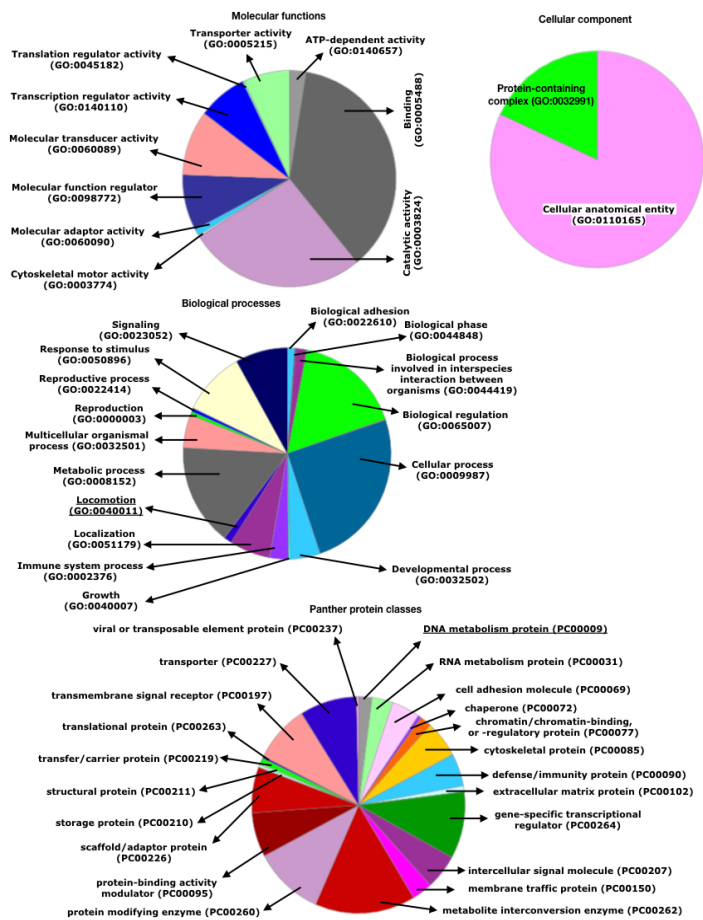
and Ser282 with bond lengths 2.18Å to 2.37Å, respectively (Figure 3 and 4). Furthermore, the respective Ramachandran plots have been presented in supplementary Figure 1.
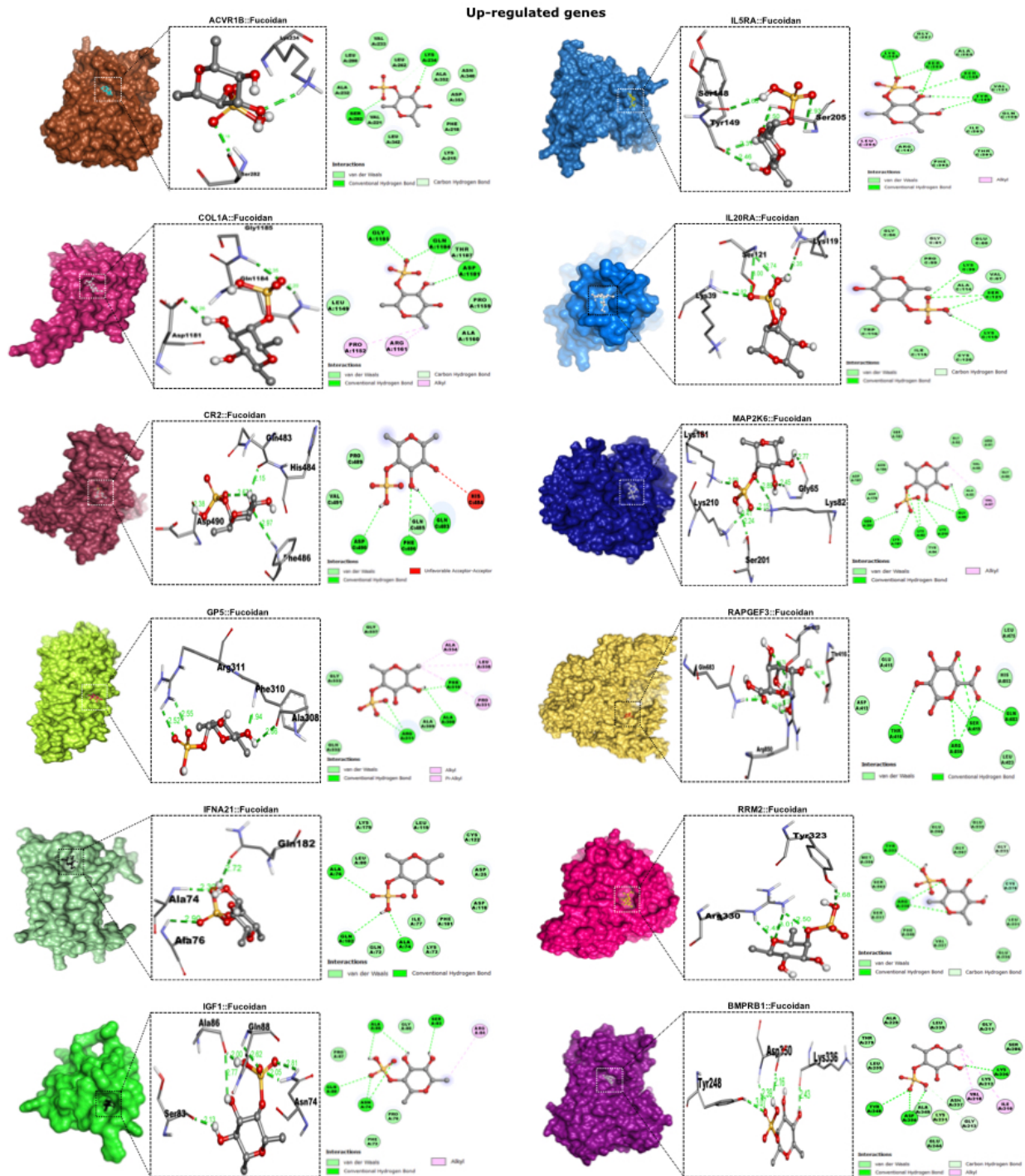

Figure 3. Docking profiling of up-regulated genes (inferred proteins). It represents the respective protein structures with the binding sites as enlarged view.

Table 1: List of top enzyme-ligand complex showing remarkable binding energies (Up and down regulated genes' respective proteins).

S. No.	Enzyme-ligand complex	Binding energy (Kcal/mol)	Number of HBs
1.	ACVR1B_Fucoidan	-6.0	2
2.	COL1A_Fucoidan	-5.4	3
3.	CR2_Fucoidan	-4.7	3
4.	GP5_Fucoidan	-5.1	4
5.	IFNA21_Fucoidan	-5.9	3
6.	IGF1_Fucoidan	-4.9	6
7.	IL5RA_Fucoidan	-5.6	6
8.	IL20RA_Fucoidan	-5.1	4
9.	MAP2K6_Fucoidan	-6.3	7
10.	RAPGEF3_Fucoidan	-5.8	6
11.	RRM2_Fucoidan	-5.9	3
	⬇	Down regulated genes	
1.	BCL3_Fucoidan	-5.1	5
2.	BMPRB1_Fucoidan	-6.5	4
3.	CCL4_Fucoidan	-5.1	3
4.	CCL5_Fucoidan	-4.3	5
5.	CD14_Alginate-n	-5.0	4
6.	CⅡTA_Alginate-n	-6.2	7
7.	CSF2RA_Fucoidan	-6.5	4
8.	CXCL5_Fucoidan	-4.3	3

9.	HLA-DRB4_Fucoidan	-4.6	5
10.	IL7R_Fucoidan	-4.8	6
11.	IL15RA_Alginate-n	-4.8	4

4. Discussion

In order to identify potential targets and herbal remedies that can interfere with the signalling pathways, we proposed in this study to examine signalling pathways, especially inflammatory pathways, and their constituents in individual atherosclerosis patients and subgroups. In particular, we identify the genes that are up- or down-regulated in each patient with atherosclerosis using a machine learning technique, and then we search for likely activated transcription factors. After dividing atherosclerosis patients and controls into groups, we were able to identify the upstream/downstream signalling pathways of inflammatory signalling pathways. Lastly, we determined the medicines' upstream and downstream signalling targets for alginate-N and fucoidan.

Multifocal, smouldering, immunoinflammatory atherosclerosis affects both big and medium-sized arteries and is driven by lipids. Leukocytes, intimal smooth muscle cells, and endothelial cells are the main contributors to the development of this illness. Superimposed thrombosis is responsible for the most severe effects of atherosclerosis, including heart attacks and strokes. Therefore, the key question is not why atherosclerosis occurs but rather why it abruptly becomes complex with luminal thrombosis after years of indolent progression. Atherosclerosis would be a far less dangerous condition if thrombosis-prone plaques could be identified and prevented. Plaque rupture is the cause of about 76% of all fatal coronary thrombi. Approximately 80% of coronary thrombosis in men is caused by plaque rupture, compared to 60% in women. Large lipid-rich core, thin fibrous cap with many macrophages and few smooth muscle cells, angiogenesis, adventitial inflammation, and outward remodelling are the hallmarks of ruptured plaques. The most frequent cause of coronary thrombosis is plaque rupture. The pathoanatomical characteristics of ruptured plaques and, thus, rupture-prone plaques may be helpful for imaging-based in vivo detection[1, 3, 4, 7, 13, 14].

The primary cause of cardiovascular disease, a major global cause of death, is atherosclerosis, a chronic inflammatory condition of the blood vessels. Macrophages, T lymphocytes, and other immune response cells are present in atherosclerotic lesions together with blood-borne cholesterol. In mouse models, disease is accelerated by interfering with regulatory immunity, while it is reduced by targeted deletion of genes encoding costimulatory factors and proinflammatory cytokines. Both innate and adaptive immunological responses have been linked to atherosclerosis; along the course of the illness, components of low-density lipoprotein that carry cholesterol cause inflammation, T cell activation, and antibody formation. Normal arterial defence relies on endothelial cells mounting innate immune responses and, following an inflammatory challenge, on macrophages and other immune response cells attracted to the artery wall. The development of atherosclerosis is also significantly influenced by these innate immune responses. Both internalising and signalling pattern-recognition receptors are involved[7, 9, 11, 48-52].

Numerous processes, including LDL oxidation, endothelial cell dysfunction, lipoprotein level variation, molecule adhesion, SMC migration, plaque formation, and others, are part of the intricate pathophysiology of atherosclerosis. The therapeutic medications used to treat atherosclerosis function in one or more ways. Plants have a wide range of chemical components, and these components work in different ways. Although phytochemicals and herbal remedies are a fantastic way to combat the risk of atherosclerosis, their application in the disease's therapy is still quite limited. Traditional medicine is currently receiving attention due to the research and development of several herbal remedies for the treatment of atherosclerosis. Additionally, we found that medicinal compounds produced from herbal sources offer a larger benefit due to less side effects when compared to synthetic drugs in terms of risk and benefit ratios. Depending on how they work, using herbal medicines sparingly can provide an alternate platform for the treatment of atherosclerosis[5, 21, 53-55].

Based on the previous scientific research, this study may have concentrated on phytomedicines that have the ability to affect the cardiovascular system, specifically atherosclerosis, in terms of their safety and effectiveness. Conversely, the majority of phytomedicines have a range of cardiovascular effects that frequently overlap. This classification is not intended to assign herbs to particular illnesses, but rather to make things simpler. The dilution of active ingredients in herbal medicines has less harmful and unwanted effects than the concentration of active

ingredients in allopathic treatments. Cardiovascular disease is a serious health risk, thus it is important to pay attention to these side effects and drug interactions. No herbal medicine program should be initiated without carefully assessing the possible outcomes.

5. Conclusions

The goal of this research is to identify potential targets and herbal remedies that may interfere with the active signaling pathways that lead to individual atherosclerosis. In particular, we have identified the genes that are up- or down-regulated in particular atherosclerosis patients using a machine learning technique, and then we search for likely activated transcription factors. We identified several subgroups of atherosclerosis patients with similar transcription factors based on their upstream/downstream signaling pathways. Lastly, we determined which upstream and downstream signaling targets the medications alginate-n and fucoidan target.

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