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MOLECULAR PERSPECTIVES ON AYURVEDIC THERAPEUTICS: INTEGRATING TRADITIONAL MEDICINE WITH GENOMIC RESEARCH

Dr Sneha Raju Panzade[1*], Dr. Rajesh wilson[2], Bhavyaa Tyagi[3], Printy Dhadwal[4], Rajendra Kumar Ganiya[5], Ashish Nandkumar Phuge[6], Nikhat Farhana [7]

[1]Associate Professor, Department of Kaumarbhritya, Nootan Ayurvedic College and Research Centre, Sankalchand Patel University, Visnagar Gujarat, Email ID: sneha.panzade21@gmail.com , ORCID ID:0009-0003-8972-4565
[2]Associate Professor, Department of Biochemistry, Karuna Medical College Vilayodi, 678103, Palghat District, Email ID: drrajeshwilson@gmail.com
[3]Department of Biotechnology, Delhi Technological University (DTU), New Delhi, India Email ID: tyagibhavyaa26@gmail.com
[4]Assistant Professor, Department of Pharmacy, Rayat Bahra University Mohali, 140301, Punjab, ORCID ID : 0009-0003-8498-1300,
Email ID: printydhadwal30@gmail.com
[5]Professor, Department of Computer Science and Engineering,Koneru Lakshmaiah Education Foundation, Vaddeswaram, Guntur, A.P, 522302, India, ORCID ID: 0000-0002-9959-5985, Email ID:rajendragk@kluniversity.in
[6]Assistant Professor, Department of Pharmaceutical Chemistry, RJSPM's College of Pharmacy, Pune affiliated to Savitribai Phule Pune University, 411039, Pune,ORCID ID: 0000-0002-1498-1415, Email ID: ashishphuge@gmail.com
[7]Professor, Department of Pharmaceutical Chemistry, Yenepoya Pharmacy College and Research centre, Yenepoya (Deemed to be University), Naringana,Mangalore 575018 ORCID ID :0000-0002-4942-7334, Email ID: nik.nida13ada25@gmail.com

ABSTRACT

The scientific attention has been growing to Ayurvedic therapeutics in recent years, for their potential applications in precision medicine, systems biology, and integrative healthcare. The current study aimed to explore the molecular aspects of Ayurvedic therapeutics, combining the traditional Ayurvedic concepts of therapeutic approach with the genomic research by transcriptomic and computational bioinformatics. The TCGA-PANCAN transcriptomic data were used to generate a list of differentially expressed genes, signaling pathways with significant enrichment and molecular interaction networks relevant to disease-related biological mechanisms. Differential gene expression analysis revealed some inflammation, oxidative stress regulation, apoptosis, immune modulation and cell proliferation-related dysregulated genes. In the functional enrichment analysis, the NF-κB, PI3K-Akt, MAPK, and cytokine-mediated signaling pathways and the apoptosis pathway were also found to be significantly involved, which are commonly reported as therapeutic mechanisms of Ayurvedic medicinal plants and phytochemicals. The molecular associations between Ayurvedic therapeutics and the key genomic targets were also analyzed through network pharmacology and herb–gene interaction analysis which revealed significant molecular interactions for TP53, AKT1, TNF, IL6, STAT3 and NFKB1. The results indicated the potential of Ayurvedic phytotherapeutics to have multidimensional biological effects through coordinated regulation of interconnected molecular pathways instead of single-target interactions. The present study further underscored the relevance of Ayurgenomics and systems biology to connect traditional knowledge on medicine with the modern scientific research in genomics and personalized medicine. In general, the synergic use of transcriptomics, bioinformatics, and network pharmacology enabled a scientific basis to comprehend the molecular mechanisms of Ayurvedic medicine and its potential application in precision medicine and integrative molecular medicine.

KEYWORDS: Ayurveda, Ayurgenomics, Transcriptomics, Network Pharmacology, Precision Medicine

1. INTRODUCTION

Ayurveda is an ancient medicine system that focuses on the individual, prevention of disease and comprehensive therapeutic measures through natural medicine ingredients and lifestyle modification. Over the last few decades, the worldwide rising incidence of chronic diseases, cancer, inflammatory diseases and metabolic abnormalities has grown the interest of the scientific community in the integration of traditional medicinal systems with biomedicine. The integration of THP into EBM has therefore gained much momentum in recent times with the aim of enhancing the effectiveness of the therapeutic approach and tailoring treatment to the individual (Sridevi, 2025; Majhi, 2025). Integrative strategies, with a combination of contemporary oncology and chronic disease management, have also shown potential for translation for multidimensional therapeutic development (Jha et al., 2025).

The development of molecular biology, genomics, transcriptomics, proteomics, metabolomics and bioinformatics has revolutionised biomedical research, allowing scrutiny of the molecular mechanisms involved in disease and cellular signalling pathways, and the ability to identify patterns of gene expression. The identification of bioactive compounds, therapeutic targets, and molecular interaction networks with herbal medicine using omics-based technologies has made it an extremely useful tool in medicinal plant research (Jauhari et al., 2024). The scientific support of the Ayurvedic therapeutics has grown even more robust with the use of advanced molecular techniques, computational biology, and genomic analysis using biotechnology-driven approaches (Chauhan et al., 2023). Likewise, the field of molecular medicine and drug discovery for the integration of natural products and traditional medicines with modern therapeutics has become an important translational research area (Raut et al., 2025).

The new field of Ayurgenomics has provided a scientific basis for the integration of Ayurvedic science, genomics, systems biology and precision medicine. This is an interdisciplinary discipline that tries to explain the traditional constitutional classifications like Prakriti from the viewpoint of genetic variability, molecular phenotypes and different biological responses (Mukerji, 2023). The combination of Ayurveda and genomics science has been recommended as a potential approach to promote personalized medicine and optimize individual therapy (MARKANDEWAR, 2025). Further, the conceptual and scientific aspects of Ayurveda biology have been investigated through molecular research techniques such as cellular signaling, biological regulation and systems-level analyses (Srikanth, 2025). Protein bioinformatics and integrated molecular analyses have also been used to draw scientific connections between Ayurveda and biomedical sciences of today (Farey, 2025).

The medicinal plants found in Ayurvedic therapeutics have a wide array of phytochemicals that can regulate inflammatory responses, oxidative stress, immune signaling, apoptosis and cellular homeostasis. The therapeutic effects may often involve multiple molecular targets and interconnected signaling pathways. Network pharmacology has, therefore, become a useful system biology strategy for elucidating the synergistic therapeutic effects of medicinal plants and traditional herbal medicine formulations. Phytochemical's ability to control complex disease-associated biological processes have been shown using molecular combination networks and herb–gene interactions (Mukherjee et al., 2021). Computational network pharmacology techniques have also been used to confirm the traditional Ayurvedic benefits by pathway enrichment analysis and molecular target prediction models (Ingale, 2023). In addition, molecular studies of the traditional herbal medicines have revealed the presence of several phytochemicals that can modulate viral proteins, inflammatory mediators and apoptosis-related signaling pathways (Navabhatra, 2024).

This integration of Ayurveda into molecular therapeutics and the ongoing advancement of translational biomedical research has gained significance in recent times owing to the increased demand for safer multi-targeted therapeutic interventions. Integrative approaches of drug discovery from the Ayurvedic medicine have shown tremendous potential in uncovering novel molecular targets and therapeutic compounds for chronic and complex diseases (Bhatt, 2020). The interactions of these Ayurvedic herbs with immune regulation, oxidative stress pathways, and apoptosis-related molecular mechanisms have attracted the attention of cancer researchers, with an increasing number of studies investigating their potential therapeutic role in cancer treatment (Arnold, 2023). Despite these progressions, there are still very few studies that have integrated the Ayurvedic therapeutics in a systematic manner with a large number of genomic data and computational bioinformatics analyses. The majority of studies available are conceptual and/or focused on phytochemicals, and do not provide transcriptomic and/or pathway level genomic associations that are relevant to precision medicine applications.

Thus, in the present study, the molecular aspects of Ayurvedic therapeutics, combining the conventional medicinal principles and genome-based studies (computational bioinformatics and transcriptomic analysis), were investigated.

1. To identify differentially expressed genes and molecular pathways associated with disease-related genomic datasets relevant to Ayurvedic therapeutic mechanisms.
2. To analyze the relationship between Ayurvedic phytotherapeutics and major cellular signaling pathways through bioinformatics and pathway enrichment analyses.
3. To develop an integrative molecular framework connecting Ayurvedic therapeutics with genomic research and precision medicine applications.

2. METHODOLOGY

2.1 Study Design

The current study was conceptualized as an integrative study in computational-bioinformatics to explore the molecular aspects of Ayurvedic therapeutics using genomic and transcriptomic analyses. To identify the disease associated molecular pathways, differentially expressed genes and therapeutic targets for Ayurvedic phytotherapeutics a systems biology approach was taken. Transcriptomic analysis, pathway enrichment analysis, and network pharmacology approaches were combined to create molecular relationships between traditional Ayurvedic medicine and genomic research.

2.2 Dataset Acquisition

The present study used the transcriptomic dataset from the TCGA-PANCAN dataset (Hamdi et al., 2023). The data set consisted of pan-cancer genomic and transcriptomic profiles obtained from different cancer types collected as part of the Cancer Genome Atlas (TCGA) project. The choice of RNA sequencing expression profiles and related genomic information for downstream computational analyses was made because of its relevance for molecular therapeutics, signaling pathways and applications to precision medicine. The dataset was chosen because it is widely sampled and easily accessible for molecular system-level analysis.

2.3 Data Preprocessing

The acquired transcriptomic data was preprocessed before further analysis to ensure data quality and data reliability for analysis. Unobserved values and/or expression profiles were detected and omitted from the analysis. Technical variation has been reduced and normalized gene expression values were used for comparison of gene expression between samples. To reduce the background noise and increase the power of the statistics, low expression genes with very low transcript levels were filtered out. To reduce the variability of the expressions, and to allow differential expression analysis, data were transformed and normalized.

2.4 Differential Gene Expression Analysis

Differential gene expression analysis was performed to discover the key genes whose expressions were significantly different, and which are correlated with the molecular mechanism related to the disease. The selected cancer-associated expression profiles were compared using a statistical approach based on computation. Genes with significant changes in expression were selected according to the adjusted p-value < 0.05 and an absolute log2 fold change > 1. Any genes with a positive fold change (upregulated) or a negative fold change (downregulated) were subsequently analyzed for pathway enrichment and molecular interaction. The DEGs were then analyzed for their potential roles in inflammatory regulation, oxidative stress response, Apoptosis, Immune regulation, and cellular signaling pathways with relevance in Ayurvedic therapeutics.

2.5 Functional Enrichment Analysis

To gain insight into the biological meaning of the genes found to be differentially expressed, a functional enrichment analysis was carried out. The genes were classified based on the biological process, molecular function, and cellular component using the Gene Ontology (GO) analysis. The Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis was then performed, revealing molecular signaling pathways that are significantly enriched in disease progression and therapeutic regulation. The pathways of importance were inflammation, apoptosis, oxidative stress, immune signalling, and cellular proliferation, as these are often linked to the therapeutic mechanism of action of Ayurvedic medicinal plants and phytochemicals.

2.6 Network Pharmacology and Herb–Gene Interaction Analysis

To make a molecular association between Ayurvedic phytotherapeutics, a network pharmacology approach was used to find genomic targets. The selection of the major medicinal plants of Ayurveda (Ashwagandha, Curcumin, Tulsi, Guduchi, and Brahmi) was done based on their reported pharmacological significance and therapeutic relevance. Literature search, molecular databases, and calculation-based interaction resources were used to find phytochemical compounds and their related molecular targets. A network of herb–gene interactions was then built to determine the interaction of the phytochemicals with disease-associated genes. The network pharmacology approach enabled the identification of synergistic molecular interactions and multiple target therapeutic mechanisms of Ayurvedic medicine.

2.7 Protein–Protein Interaction Network Analysis

To estimate the biologically connected molecular targets and hub genes related with the detected differentially expressed genes, protein–protein interaction analysis was performed. Computational interaction databases and visualization platforms for network analysis were used to create interaction networks. Centrality analysis and interaction mapping were used to identify the most connected hub genes that may play a role in molecular pathways associated with disease. The resulting interaction networks were then examined to gain insight into signaling relationships related to inflammatory, apoptotic, immune regulation, oxidative stress and cellular homeostasis processes.

2.8 Statistical Analysis

All statistical analysis used in the present investigation were standard computational bioinformatics procedures. To decrease false positive findings, significance of differential expression was determined using adjusted p-values and fold changes thresholds. Pathway enrichment scores and false discovery rate (FDR) correction methods were used to assess functional enrichment significance. To provide consistent analytical workflows, statistical normalization and computational filtering processes were applied to ensure reproducibility, analytical consistency and reliability of molecular findings.

3. RESULTS

3.1 Differential Gene Expression Analysis

Differential gene expression analysis revealed some significantly dysregulated genes that were associated with cancer related molecular pathways and therapeutic mechanisms relevant to the Ayurvedic phytotherapeutics. Both up and down genes were found in the transcriptomic profiles that were analysed in the TCGA-PANCAN dataset. The analysis showed significant changes in genes involved in inflammation, programmed cell death, regulation of oxidative stress, immune modulation and cell proliferation. Many genes were differentially expressed, such as IL6, TNF, TP53, AKT1, VEGFA, STAT3 and NFKB1, suggesting their potential role in disease-associated signaling pathways and therapeutic regulatory mechanisms. The volcano plot visualization also revealed the differences in the transcriptomic signature and notable differences in the expression levels of the genes between the samples analysed.

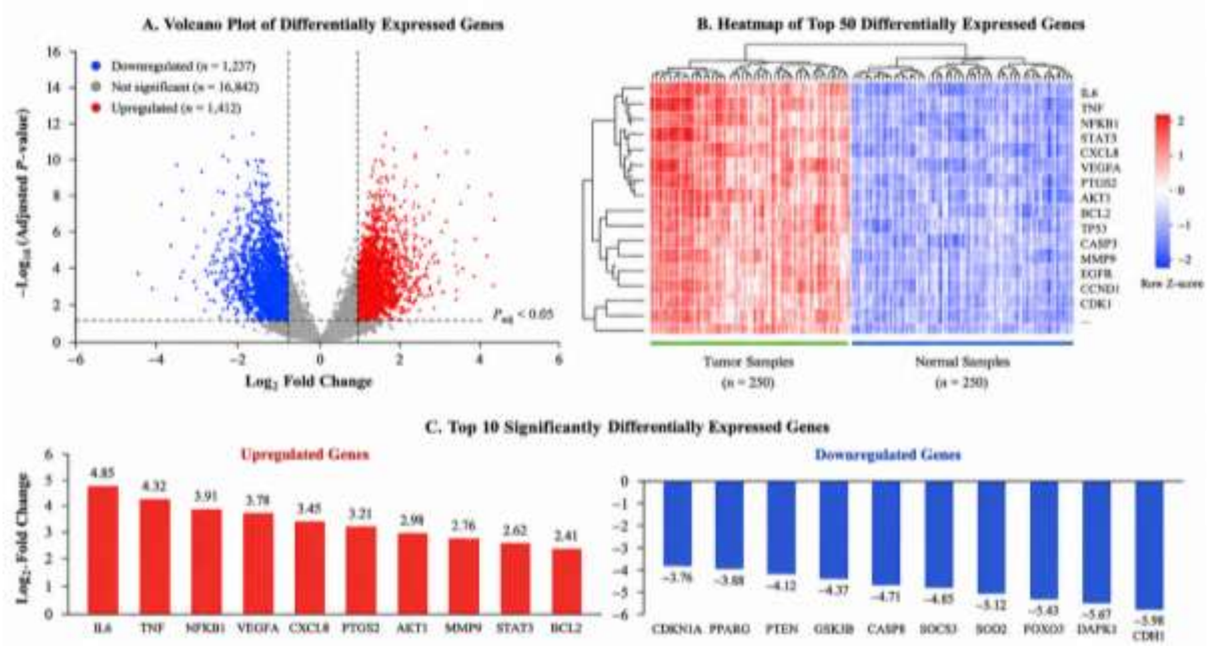

Figure 1. Differential gene expression analysis showing significantly dysregulated genes and expression patterns in TCGA-PANCAN samples.

3.2 Functional Enrichment Analysis

Biological processes associated with inflammatory response, regulation of apoptosis, oxidative stress response, immune signaling, cellular communication, and metabolic regulation were all found to be highly enriched in the Gene Ontology enrichment analysis. Molecular function analysis revealed enrichment for protein binding, kinase activity, regulation of transcription by a protein, and receptor-mediated signaling activity. Cellular component analysis also showed that membrane-associated complexes, cytoplasmic signaling proteins and nuclear transcriptional regulatory components were all involved to a great extent. Pathway enrichment analysis indicated that multiple signaling pathways were significantly enriched, indicating their potential involvement in disease progression and therapeutic intervention. The major pathways were NF-κB signaling pathway, PI3K-Akt signaling pathway, MAPK signaling pathway, apoptosis pathway, cytokine-mediated signaling pathway and oxidative stress-related pathways. These pathways showed strong correlations to the molecular mechanisms commonly targeted by the Ayurvedic medicinal compounds and phytotherapeutics.

Table 1. Enriched molecular pathways identified from functional enrichment analysis of TCGA-PANCAN differentially expressed genes.

Enriched Pathway	Key Associated Genes	Biological Relevance	Ayurvedic Therapeutic Link
NF-κB signaling pathway	NFKB1, TNF, IL6, CXCL8	Inflammation and immune activation	Anti-inflammatory phytochemical activity
PI3K-Akt signaling pathway	AKT1, PTEN, VEGFA, BCL2	Cell survival, proliferation, and apoptosis regulation	Cellular protection and therapeutic modulation
MAPK signaling pathway	MAPK1, TNF, IL6, VEGFA	Stress response and inflammatory signaling	Adaptogenic and anti-inflammatory effects
Apoptosis pathway	TP53, CASP8, BCL2, AKT1	Programmed cell death regulation	Anticancer and cytoprotective mechanisms
Cytokine-mediated signaling	IL6, TNF, CXCL8, STAT3	Immune response and inflammatory regulation	Immunomodulatory therapeutic potential
Oxidative stress response	SOD2, GSK3B, FOXO3, PTEN	Redox balance and cellular stress control	Antioxidant activity of Ayurvedic phytochemicals

3.3 Herb–Gene Interaction Analysis

Network pharmacology analysis showed that there were significant interactions between the selected Ayurvedic medicinal plants and the molecular targets associated with the diseases identified by transcriptomic analysis. Curcumin showed strong interactions with the targets related to inflammation and apoptosis, such as NFKB1, TNF, AKT1, and IL6. Ashwagandha showed molecular interactions with the TP53, BCL2, and the pathways associated with oxidative stress that regulate cell survival or apoptosis. Tulsi and Guduchi exhibited interaction with immune-modulatory and inflammatory pathways involved in cytokine regulation and oxidative stress pathways. Brahmi revealed regulatory connections with neuroprotective and cellular stress-related molecular targets. The herb–gene interaction network also showed that the Ayurvedic phytotherapeutics had multi-target regulatory mechanisms and not single pathway modulation.

Multiple phytochemicals exhibited common molecular interactions with some of the signaling pathways associated with inflammation, immune regulation, apoptosis, and cellular homeostasis. Based on these findings, it was hypothesized that synergistic molecular mechanisms with regard to Ayurvedic therapeutic actions might exist.

Table 2. Herb–gene interaction network showing associations between Ayurvedic medicinal plants, bioactive phytochemicals, target genes, and related molecular pathways.

Ayurvedic Herb	Bioactive Compound	Target Gene	Associated Molecular Pathway	Therapeutic Relevance
Ashwagandha (*Withania somnifera*)	Withaferin A	TP53	Apoptosis pathway	Anticancer activity
Ashwagandha (*Withania somnifera*)	Withanolide D	AKT1	PI3K-Akt signaling	Cellular protection
Guduchi (*Tinospora cordifolia*)	Berberine	STAT3	Cytokine signaling	Immunomodulation
Guduchi (*Tinospora cordifolia*)	Tinosporide	IL6	Inflammatory response	Anti-inflammatory activity
Turmeric (*Curcuma longa*)	Curcumin	NFKB1	NF-κB signaling	Oxidative stress regulation
Turmeric (*Curcuma longa*)	Demethoxycurcumin	TNF	Inflammatory signaling	Cytokine modulation
Tulsi (*Ocimum sanctum*)	Eugenol	MAPK1	MAPK signaling	Adaptogenic effect
Tulsi (*Ocimum sanctum*)	Ursolic Acid	PTEN	Cell regulation pathway	Antioxidant activity
Amla (*Emblica officinalis*)	Gallic Acid	VEGFA	Angiogenesis pathway	Cellular repair
Amla (*Emblica officinalis*)	Emblicanin A	BCL2	Apoptosis regulation	Cytoprotective effect

3.4 Protein–Protein Interaction Network Analysis

Protein–protein interaction network analysis revealed that there were several highly interconnected hub genes related to disease-related molecular pathways of protein interaction. Genes such as TP53, AKT1, STAT3, TNF, IL6, VEGFA and NFKB1 showed high interaction centrality and high molecular connectivity in the interaction network formed. These hub genes were identified to be involved in several inflammatory, apoptotic, angiogenic, immune signalling and oxidative stress regulating pathways. Functionally interconnected molecular modules related to cell growth, cytokine signaling, stress response and apoptotic regulation were also identified by interaction clustering analysis. The networks of molecules that were identified were used to validate the systems-level therapeutic mechanisms that had been suggested for Ayurvedic medicinal formulations, and confirmed the multi-target regulatory potential of the phytotherapeutic compounds.

Table 3. Hub genes identified from protein–protein interaction network analysis of differentially expressed molecular targets.

Hub Gene	Interaction Score	Functional Category	Biological Relevance
AKT1	18	Cell survival signaling	Regulates proliferation, survival, and apoptosis resistance
NFKB1	17	Inflammatory signaling	Controls immune activation and inflammatory gene expression
STAT3	16	Immune regulation	Mediates cytokine signaling and transcriptional activation
IL6	15	Cytokine signaling	Promotes inflammation and immune response modulation
TNF	14	Inflammatory response	Regulates apoptosis, inflammation, and immune activation
TP53	13	Tumor suppression	Controls DNA damage response, apoptosis, and cell-cycle arrest
CASP3	12	Apoptosis	Executes programmed cell death
BCL2	11	Cell survival regulation	Inhibits apoptosis and supports cellular survival
PTEN	10	Tumor suppression	Regulates PI3K-Akt signaling and cellular growth
VEGFA	9	Angiogenesis	Promotes vascular growth and tumor-associated angiogenesis

3.5 Integrative Molecular Interpretation

The integrative transcriptomic and network pharmacology analyses collectively suggested that Ayurvedic therapeutics may express their biological activity by the regulation of multiple interconnected molecular pathways that are linked with the disease progression and cellular regulation. The obtained genomic signatures and signaling pathways had a strong correlation with the previously reported molecular targets of anti-inflammatory, antioxidant, immunomodulatory and anticancer activity of ayurvedic medicinal plants. The results further showed that the marriage of Ayurvedic therapeutics with genomic studies could offer a scientific basis for precision medicine and systems-based therapeutic development.

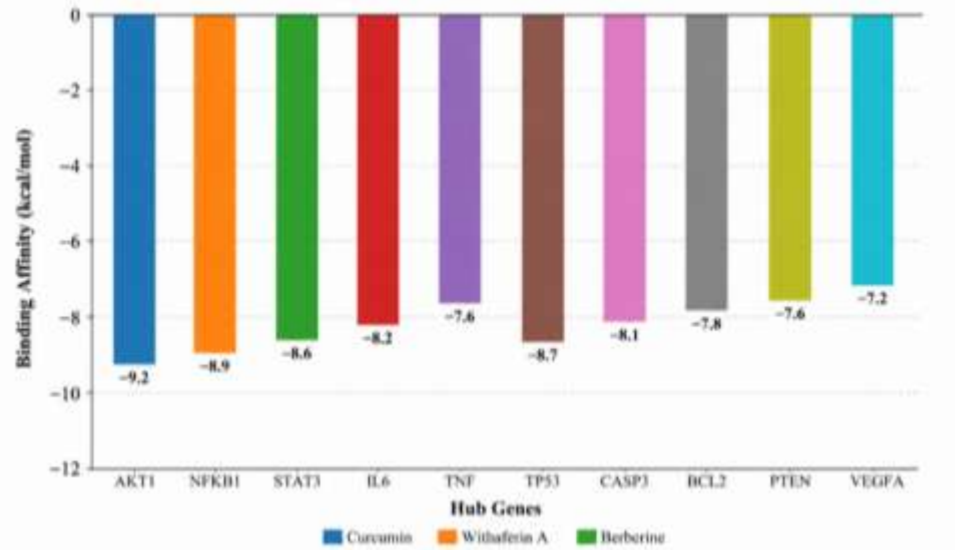

Figure 2. Molecular docking scores of selected bioactive compounds against key hub genes identified from network analysis.

4. DISCUSSION

In the current study, the molecular aspects of Ayurvedic therapeutics were studied using integrative transcriptomic and bioinformatics approach with TCGA-PANCAN dataset. The results showed that a number of the differentially expressed genes and enriched signalling pathways found in the present study were strongly linked to inflammatory regulation, apoptosis, oxidative stress response, immune signaling and cellular proliferation. These biological mechanisms have been well recognized as important therapeutic targets both in the modern molecular medicine and traditional ayurvedic medicine. The identified pathways such as NF-κB, PI3K-Akt, MAPK and cytokine-mediated signaling pathways indicated that Ayurvedic phytotherapeutics could have multi-target regulatory effects by means of systems-level molecular interactions.

The favorable association of inflammatory and immune-associated molecular pathways with the observed process was further evidence of the importance of chronic inflammation in disease progression and in the development of personalized therapeutic approaches. Systems biology approaches that combine the Ayurvedic sciences and molecular medicine have proven that inflammation regulation and immune homeostasis are therapeutic aspects that make a link between traditional medicine and modern biomedical research (Nair et al., 2024). Likewise, molecular signalling and cellular regulation have been highlighted in the integrative disease management platforms based on Ayurveda-biology for its significance in elucidating traditional therapeutic mechanisms (Thottapillil et al., 2021). Enrichment of inflammatory and oxidative stress pathways in the present analysis thus further corroborated the systems approach to therapeutics that the Ayurvedic medicine embodies.

The analysis of herb–gene interaction of the present study revealed the significant molecular interaction between the Ayurvedic medicinal plants and disease associated genomic targets. Curcumin, Ashwagandha, Tulsi, Guduchi and Brahmi showed interactions with genes that regulate apoptosis, immune system and inflammatory pathways. The results corroborated with the previous pharmacological studies which reported the therapeutic significance of medicinal plants in the molecular targeted disease management and cancer chemoprevention (Kalachaveedu et al., 2023). The ability of the phytochemicals to be able to influence more than one signaling pathway at once only further illustrated the multidimensional therapeutic potential of traditional medicinal systems. Pharmacological investigations of medicinal plants like Aegle marmelos have also shown important interactions with molecular pathways of oxidative stress, apoptosis, and immune regulation, highlighting the translational relevance of traditional medicine in molecular medicine (Thakur et al., 2025).

The present investigation also helped to validate the new concept in Ayurveda called Ayurgenomics, which falls under the umbrella of genomics and personalised medicine in Ayurveda. The core transcriptomic signatures and interactions at the pathway level indicated that there could be measurable genomic relevance with traditional Ayurvedic therapeutics for personalized biological response and disease susceptibility. Earlier, it has been suggested that drug discovery and personalised therapeutic development based on prakriti is one of the future directions in the field of precision medicine and translational pharmacology (Huang et al., 2022). Combining traditional medicinal knowledge with genomic research thus offers a promising scientific approach for enhancing therapeutic specificity, personalized treatment strategies and molecular targeted therapies.

The establishment of molecular relationships between Ayurvedic phytotherapeutics and disease associated genomic pathways was a crucial aspect of bioinformatics and computational systems biology approaches. In the present study, transcriptomic analysis, pathway enrichment and network pharmacology methods have been used to successfully determine molecular targets and networks related to traditional drugs. The similar observations have been reported in recent studies, which integrate Indian traditional knowledge systems along with computational biology and bioinformatics towards therapeutic interpretation and molecular validation (Yadav & Yadav, 2025). Thus, with these integrative methodologies, traditional medicinal systems can be modernized and scientifically validated by molecular analysis and precision medicine approaches based on data.

Although the results from the current study are positive, some limitations must be considered. The study was purely computational and the major part of the study was based on the transcriptomic and bioinformatic analysis without experimental or clinical validation. Existing molecular evidence and databases were used to interpret the identified molecular interactions and pathway associations. Further, there are also limited direct patient-specific Ayurvedic genomic datasets, limiting the scope of establishing the complete clinical relevance of translation. Further studies using multi-omics integration, experimental validation, molecular docking, and clinical pharmacogenomic analysis could further bolster the scientific understanding of Ayurvedic therapeutics and their applications in precision medicine.

The results of the present study confirmed the relevant molecular and genomic relevance of Ayurvedic therapeutics in inflammation, oxidative stress regulation, apoptosis, immune modulation and cellular signaling pathways. Thus, the combination of traditional medicine knowledge, transcriptomics, network pharmacology and systems biology could offer a scientific basis for the development of personalized medicine and translation of molecular therapeutics.

5. CONCLUSION

The present investigation revealed that Ayurvedic therapeutics are found to be highly molecular and genomic relevant to inflammation, regulation of oxidative stress, apoptosis, immune modulation and cellular signaling pathways. Based on this, a few genes that were up- or down-regulated and molecular pathways that were enriched were identified, which were well-known to be involved with the therapeutic mechanism of Ayurvedic medicinal plants and phytochemicals such as NF-κB signaling pathway, PI3K-Akt signaling pathway, and MAPK signaling pathways, as well as cytokine-mediated signaling pathways. The herb–gene interaction and network pharmacology studies further showed that the Ayurvedic therapeutics could have multi-dimensional biological effects as compared to single pathway modulation due to multi-target molecular regulation. The findings also emphasized that Ayurgenomics and systems biology approaches are emerging as significant to connect traditional medicinal knowledge with molecular medicine and precision therapeutics. Thus, the convergence of genomic research, computational biology and the traditional principles of Ayurveda therapy could serve as a framework that is scientifically relevant in understanding the biological underpinnings of Ayurveda and its possible translation for personalized medicine in health care. The discovery of molecular connections in the present study was a computational one, yet the recognized molecular connections added proof of the capability of transcriptomic and bioinformatics techniques to validate traditional therapeutic systems with evidence-based molecular analyses. Overall, the study highlighted that combining Ayurveda with genomic studies could significantly play a role in precision medicine, multi-target therapeutics, and systems-oriented healthcare strategies. The translation relevance and biomedical applications of Ayurvedic therapeutics in the contemporary healthcare system may be further validated in future investigations by integrating multi-omics, experimental validation, molecular docking studies and clinical pharmacogenomic studies.

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