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Systems Biology Approaches for Understanding the Therapeutic Mechanisms of Medicinal Plants

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ABSTRACT: Multi-omics technologies, computational biology, network pharmacology, and artificial intelligence are combined to create a comprehensive view of the therapeutic mechanisms of medicinal plants, making systems biology a transformative way of understanding complex therapy mechanisms. In contrast to traditional single-target strategies, systems biology studies complex interactions between genes, proteins, metabolites and biological pathways to gain insight into multi-target mechanisms of phytochemicals. When combined with computational approaches, genomics, transcriptomics, proteomics, metabolomics and microbiome analysis provide a comprehensive understanding of molecular targets, biomarkers, and signaling pathways involved in disease treatment. Moreover, AI, machine learning and network pharmacology improve target prediction, elucidation of drug mechanisms and drug discovery and facilitate precision phytomedicine. Although data integration, experimental validation and standardisation are some of the challenges encountered in systems biology, it offers a solid basis for the development of evidence based phytopharmaceuticals. This holistic approach speeds up medicinal plant research, aids in the development of personalized treatment strategies, and supports the conversion of traditional herbal remedies into scientifically proven and clinically effective treatments for complex diseases affecting human health.

1. INTRODUCTION TO SYSTEMS BIOLOGY AND MEDICINAL PLANTS

Systems biology is an interdisciplinary scientific approach that studies a biological system not in terms of its molecules but as a whole and dynamic network. In contrast to the reductionist approach of studying individual genes, proteins, and metabolites, systems biology is a new way of studying biology that incorporates genomics, transcriptomics, proteomics, metabolomics, epigenomics, bioinformatics, computational modelling, and network analysis to gain a deeper understanding of the complex interactions that regulate cellular and physiological function. Current development of high-throughput technologies, computers, artificial intelligence, and large-scale bio-databases is driving the shift from reductionist biology to systems biology to study molecular interactions at multiple biological levels simultaneously(1). The paradigm shift has resulted in improved understanding of disease mechanisms, biological pathways, and how a disease responds to therapy by gaining insight into networks of genes, proteins, metabolites, and signaling pathways and their interactions to regulate health and disease(2). Since medicinal plants typically contain multiple bioactive molecules and their therapeutic properties are often exerted by targeting several molecular targets and interacting biological pathways, instead of one receptor or enzyme, systems biology is a radical approach in medicinal plant research(3). These complex synergic interactions are hard to explain using traditional pharmacology techniques, but they can be explained using the systems biology approach that allows to identify the active phytochemicals, predict molecular targets, identify the signaling network, and understand the mechanism behind the pharmacology effect of herbal medicines. This is enhanced by the use of phytochemistry in conjunction with systems pharmacology, which combines the chemical analysis of plant metabolites with computational analyses of biological networks, drug–target interactions, pathway enrichment and disease-associated molecular mechanisms(3). The integration supports the identification of bioactive compounds, the possibility of predicting multiple target interventions, optimization of herbal formulations, the discovery of biomarkers and prioritization of bioactive compounds for drug discovery. Combined with artificial intelligence, machine learning, molecular docking, and network pharmacology, systems biology can accelerate the process of drug discovery and help to predict efficacy, safety, pharmacokinetics, toxicity, etc(4). And it is an integral part of the research framework of modern medicinal plants, providing a comprehensive approach that integrates traditional herbal medicine with the current disciplines of precision medicine, computational biology, and translational pharmacology, and can support the development of evidence-based phytopharmaceuticals and new prevention and treatment methods for complex diseases in humans(5).

2. BIOLOGICAL DATA RESOURCES AND MULTI-OMICS TECHNOLOGIES

The biological data resources and Multi-omics technologies provide the backbone of systems biology, which can be used to explore the molecular mechanisms in the therapeutic action of medicinal plants(6). New advances in high-throughput sequencing, mass spectrometry, bioinformatics, and computational biology have resulted in a flood of biological data, which can be brought together in a single systems-level view of genomics, transcriptomics, proteomics, metabolomics, epigenomics, and microbiome(7). The integrated view of the interaction of these plant-derived bioactive compounds with biological systems and the modulation of disease pathways with complex structures (as depicted in Figure 1), is obtained from these complementary omics platforms. Genomics offers a way to identify genes, genetic variants and molecular targets associated with susceptibility to disease and response to therapeutic interventions, which will aid in the discovery of genes targeted by phytochemicals.

Transcriptomics involves the analysis of the levels of expression of a genome-wide set of genes by measuring the amount of messenger RNA (mRNA) present, which helps researchers to understand the changes in the cellular signaling pathways produced by the constituents of medicinal plants under physiological and pathological conditions(8). Proteomics goes one step further and gives information on the quantities of proteins, the degree of post-translational modifications, the activity of enzymes, and protein-protein interactions, which directly affect biological functions and pharmacological effects(9). Comprehensive profiling of endogenous metabolites and plant secondary metabolites can be achieved by metabolomics, which could be used to find disease-related metabolic changes associated with disease progression and treatment, as well as to find bioactive phytochemicals and disease markers(10).

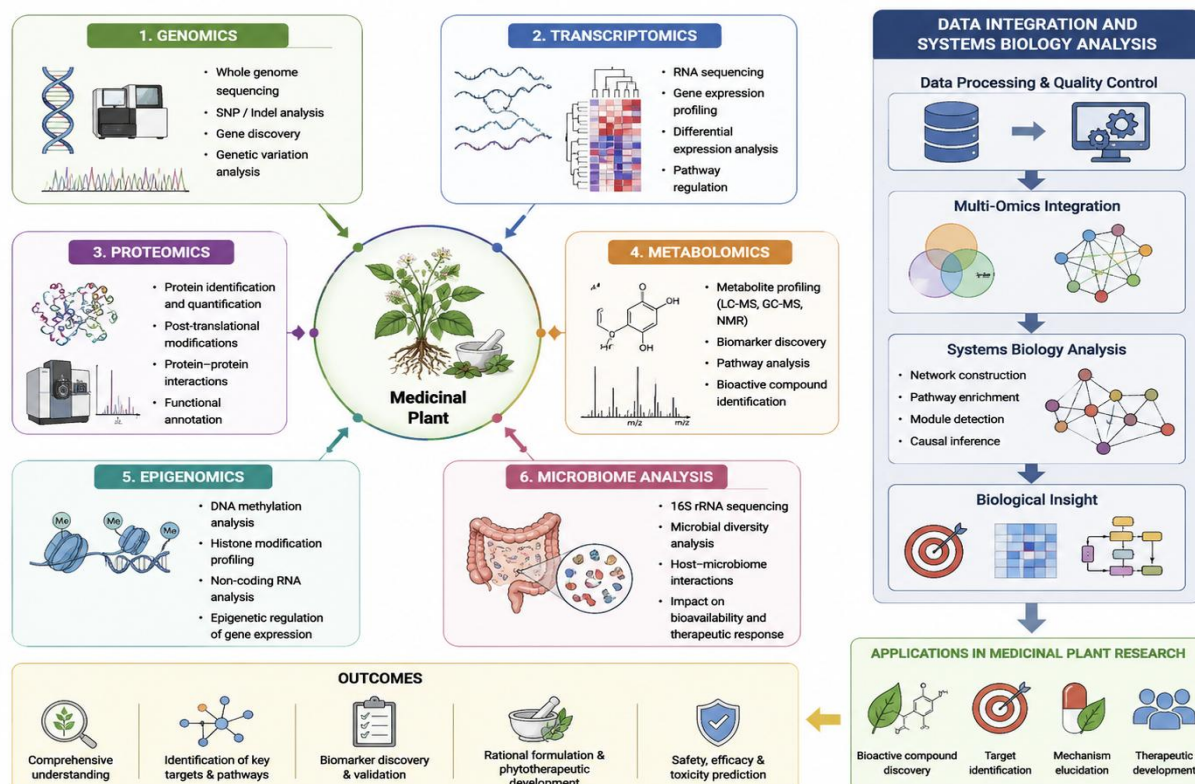


Figure 1. Integrated Multi-Omics Framework for Systems Biology-Based Investigation of Medicinal Plants

Epigenomics is an exploration of the mechanisms by which genes are regulated, including DNA methylation, histone modification, chromatin remodeling, and non-coding RNA regulation, and the way in which medicinal plant compounds affect gene expression without changing DNA sequences. Moreover, the analysis of the microbiome has become a key aspect of systems biology due to the vital roles of host-microbe interactions in influencing the metabolism, bioavailability, activity, and side effects of phytochemicals(11). By combining these multi-omics data in an integrated manner with the help of Artificial Intelligence, Machine Learning, Network Pharmacology and Computational Modeling, one can obtain a more comprehensive biological interaction network, which can be used for better target identification, biomarker discovery, pathway enrichment analysis and prediction of therapeutic mechanism. Thus, multi-omics technologies offer a powerful systems level approach to accelerate medicinal plant research, to guide precision phytomedicine, and to facilitate rational discovery and development of safe, effective and evidence-based plant-based medicines for complex human diseases(12).

3. NETWORK PHARMACOLOGY IN MEDICINAL PLANT RESEARCH

Network pharmacology, an interdisciplinary approach integrating pharmacology, bioinformatics, systems biology and computational science, is a powerful systems biology approach to elucidating the complex therapeutic mechanisms of medicinal plants. In the traditional 'one drug – one target – one disease' scheme, a network pharmacology approach offers the perspective that, in medicinal plants, multiple bioactive phytochemicals may simultaneously target multiple molecular targets and biological pathways(13). This is a holistic approach that enables the generation of compound-target interaction networks in which the phytochemicals are clustered with their predicted or experimentally confirmed protein targets, and thus revealing important bioactive components of the plants that contribute to their therapeutic benefits(14). These interactions are then combined with protein-protein interaction (PPI) networks to uncover functional relationships between proteins that play a role in cellular signaling, metabolism, immune regulation, and progression of disease(15). PPI network can be used to detect hub proteins, key signaling molecules, and regulatory modules which could be potential therapeutic targets for complex diseases via the PPI network. Gene-disease association networks also connect disease-associated genes to medicinal plant targets to discover common molecular mechanisms and prioritise candidate genes for preventing and treating diseases(16). The pathway enrichment analysis explains how these integrated biological networks are used to identify the biological pathways that are

significantly enriched by the phytochemicals with the use of databases such as KEGG, Reactome, and Gene Ontology. Pathway enrichment reveals the cell processes of medicinal plants, including those for inflammation, oxidative stress, apoptosis, immune modulation, cell proliferation, metabolic regulation, angiogenesis, and signal transduction, thus showing the multitarget therapeutic activity of medicinal plants(17). Finally, visualization and interpretation of network via computational platform such as Cytoscape and STRING transforms complex molecular data into visual models, which represent the interaction between compounds, genes, proteins, pathways and diseases in an intuitive way. These visual networks can be used to spot critical regulatory hubs, interaction clusters, functioning modules, and can be used to come up with hypotheses and test it out experimentally(18). In addition to molecular docking, multi-omics technologies, artificial intelligence and machine learning, network pharmacology greatly reduces the time for target identification, discovery of biomarkers, lead optimization and mechanism of action (MOA) studies. Therefore, the multi-target drug action of medicinal plants, the precision phytomedicine, and rational discovery and development of safe, effective, and evidence-based plant-based therapeutics for complex human diseases may all be understood by network pharmacology, which provides a whole-system level perspective to the study of medicinal plants(19).

4. SYSTEMS PHARMACOLOGY AND MECHANISTIC UNDERSTANDING

The use of systems biology, pharmacology, bioinformatics and computational biology in the study of medicinal plants, providing a global understanding of the mechanism(s) of action of medicinal plants through multiple molecular targets. In contrast to traditional pharmacology which is mostly concerned with single drug–target interactions, systems Pharmacology acknowledges that medicinal plants are rich with various bioactive phytochemicals that can exert multi-component, multi-target effects, involving a number of compounds that interact with multiple proteins, enzymes, receptors, transcription factors, and signaling molecules. These interactions are synergistic in nature and their synergistic regulation of complex biological systems can optimise the effect of drugs and minimise drug side effects(20). The current systems pharmacology approach integrates a variety of computational tools and biological databases to discover molecular targets, analyze pharmacological mechanisms, and forecast therapeutic effects based on genomics, transcriptomics, proteomics, metabolomics, network pharmacology, pathway analysis, molecular docking and artificial intelligence as detailed herein in Table 1(21). Modulation of biological pathways by the phytochemicals is one of the most important part of systems pharmacology which includes several pathways such as PI3K/Akt, MAPK, NF- κ B, JAK/STAT, Wnt/ β -catenin, AMPK, TGF- β and apoptosis pathways that all play a role in inflammation, oxidative stress, immune responses, metabolism, cell proliferation and programmed cell death(22). These molecular effects are transduced via complicated signal transduction networks, in which extracellular signal leads to intracellular signal cascades, which ultimately affects gene expression and cellular function through a receptor, kinases, transcription factors, and regulatory proteins. By analysing the signalling networks at the system level, key regulatory nodes and hub proteins can be identified that play a role in disease progression and therapy. Moreover, systems pharmacology enables the study of pharmacodynamic mechanisms, as it allows the study of the molecular interactions with physiological responses, laying the ground for understanding dose–response relationships, synergistic effects between different phytochemicals, therapeutic selectivity, and inter-individual biological variability(23). The integration of AI, machine learning, and computational models based on networks further facilitates systems-level therapeutic prediction, helping researchers to predict drug efficacy, discover novel drug targets, predict adverse effects, optimise herbal formulations, and prioritise lead phytochemicals for experimental validation. Thus, systems pharmacology has emerged as an essential tool for elucidating the multi-level mechanisms of medicinal plants, for expediting the evidence-based development of phytopharmaceuticals, for precision medicine and for the discovery of safe, multitarget drugs for prevention and treatment of complex human diseases(24).

Table 1. Major Systems Biology Approaches, Computational Tools, and Applications in Medicinal Plant Research

Approach	Major Tools/Databases	Primary Application
Genomics	NCBI, Ensembl	Gene identification and genetic variation analysis
Transcriptomics	GEO, RNA-Seq	Differential gene expression profiling
Proteomics	UniProt, STRING	Protein identification and protein–protein interaction analysis
Metabolomics	HMDB, METLIN	Metabolite profiling and biomarker discovery

Network Pharmacology	Cytoscape, STRING, TCMSP	Compound–target network construction and mechanism prediction
Pathway Analysis	KEGG, Reactome, Gene Ontology	Biological pathway enrichment and functional annotation
Molecular Docking	AutoDock, Schrödinger, AutoDock Vina	Target validation and binding affinity prediction
Artificial Intelligence	Machine Learning, Deep Learning, TensorFlow, PyTorch	Target prediction, biomarker discovery, drug repurposing, and therapeutic prediction

5. ARTIFICIAL INTELLIGENCE AND SYSTEMS BIOLOGY INTEGRATION

Artificial intelligence (AI) is now indispensable in systems biology, as it enables analysis, integration and interpretation of massive biological information being generated from genomics, transcriptomics, proteomics, metabolomics, epigenomics and microbiomics. AI integration with systems biology opens a new realm of possibilities for understanding the intricate therapeutic mechanisms of medicinal plants at a systems level and for rapid drug discovery and precision medicine(24). In recent years, the use of machine learning (ML) algorithms has become common to process high dimensional omics data, uncover hidden biological patterns, classify disease phenotypes, prioritize therapeutic targets, and predict functional relationships among genes, proteins, metabolites and signaling pathways. From complex biological data, supervised and unsupervised learning approaches enable the selection of features, the identification of biomarkers, disease classification and prediction of therapeutic response. At the same time, deep learning (DL) has been widely used to boost biomarker discovery, through auto-extraction of the hierarchical features from multi-omics data without manual feature engineering. The use of advanced neural network architectures, such as convolutional neural networks (CNNs), recurrent neural networks (RNNs), graph neural networks (GNNs), and transformer-based models, enhances the ability to detect disease-related biomarkers, molecular signatures, and regulatory networks, helping to facilitate early diagnosis and targeted therapeutic interventions(25). AI also plays a crucial role in AI-assisted target prediction, where computational models integrate chemical structures, molecular descriptors, protein sequences, biological pathways, and interaction networks to accurately predict potential molecular targets of medicinal plant phytochemicals. This capability can significantly lower experimentation costs and speed up identification and optimization of leads. In addition, by integrating AI with network pharmacology, molecular docking, pharmacokinetic modeling, and systems biology, predictive systems pharmacology facilitates the simulation of drug–target interactions, prediction of therapeutic efficacy, estimation of toxicity, forecasting ADRs, and optimization of multi-component herbal formulations for complex diseases. An increasing focus has been also directed towards Explainable Artificial Intelligence (XAI), a paradigm that enhances transparency, interpretability, and reliability of AI predictions by elucidating the biological features, molecular pathways, and computational reasoning that underlie model outputs(26). Explainable AI offers a way to increase scientific trust, gain regulatory approval, and aid in clinical decision-making by delivering more meaningful and biological explanations than black box predictions. The combination of AI and systems biology is thus a paradigm shift in medicinal plant research which can be used to conduct in-depth multi-omics analysis, gain systems-level understanding of the mechanisms, develop precision phytomedicine and rationally create safe, effective and evidence-based plant-based therapeutics for complex human diseases(13).

6. COMPUTATIONAL MODELING OF BIOLOGICAL SYSTEMS

The increasing importance of systems biology in the study of medicinal plants and how they can be used in medicine has made computational modelling a valuable tool. They are multi-omics models, complex computational algorithms, and provide a systems-level perspective on disease mechanisms and phytochemical effects(18). The first step in computational modeling is the construction of gene regulatory networks (GRNs) that represent relationships among genes, transcription factors, and regulatory RNAs, and the next step is to identify important genes in the development of disease and their role in therapeutic response (as illustrated in Figure 2)(12). Protein interaction networks (PINs) also offer clues to functional relationships among proteins and serve to identify proteins that are “hubs”, and important signaling molecules that may be potential targets for drug development. Moreover, metabolic pathway modelling reconstructs the connected metabolic pathways and provides insights

on the function of plant bioactive compounds in regulating metabolic processes, metabolic balance, and metabolic changes associated with disease(27). These integrated datasets can be utilized for dynamic biological simulations, such as the prediction of temporal changes in biological systems, the simulation of drug responses, pathway perturbations, and the estimation of therapeutic efficacy in different physiological states, using mathematical and computational modeling. These are enhanced by the new technologies of digital twins, which incorporate omics, clinical, and physiological data to create virtual models of biological systems or even individual patients. Using these digital models, prognosis of treatment results is individualized, phytotherapeutic interventions optimized and real-time monitoring of the disease course. So, computational modelling can bridge experimental biology and artificial intelligence and systems pharmacology for the identification of targets, elucidation of mechanisms, discovery of biomarkers and development of precision medicinal plant-based drug development earlier, and offer a solid foundation for the use of computational predictions for the transition to clinically relevant therapeutic strategies, as summarized in Figure 2.

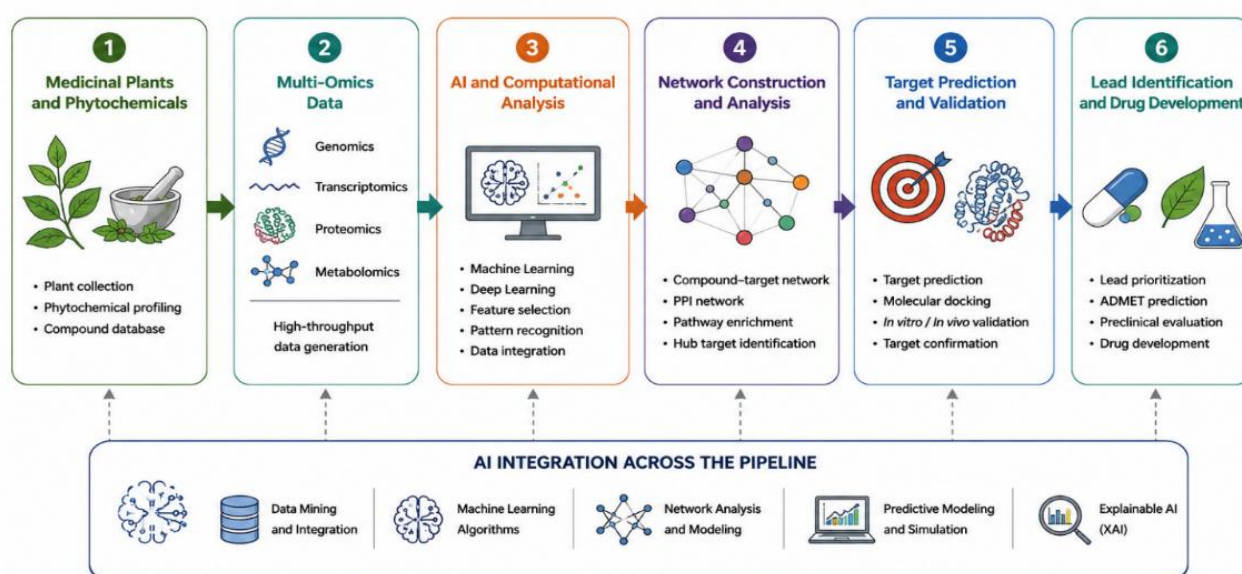


Figure 2. AI-Integrated Systems Biology Pipeline for Medicinal Plant-Based Drug Discovery

7. APPLICATIONS IN DISEASE-SPECIFIC THERAPEUTICS

With the advent of systems biology, there has been a dramatic increase in the number of medicinal plants used in the development of new therapeutic strategies, especially in understanding the molecular mechanisms of different diseases and designing multiple target drug strategies. The holistic approach of systems biology has greatly extended the applications of medicinal plants, particularly with regard to understanding the molecular mechanisms of different diseases for the development of multiple target drugs(18). In cancer, systems biology combines multi-omics technologies, network pharmacology and artificial intelligence to detect phytochemicals capable of modulating cell proliferation, apoptosis, angiogenesis, metastasis, immune evasion, and oxidative stress through the signaling pathways involved, including PI3K/Akt, MAPK, NF- κ B, and p53. Medicinal plants contain bioactive compounds that are known to exert modulation of lipid metabolism, endothelial function, oxidative stress, inflammation, thrombosis and vascular remodeling which plays a significant role in prevention and management of cardiovascular diseases such as hypertension, atherosclerosis, myocardial infarction, and heart failure. In the context of neurodegenerative diseases, systems pharmacology has demonstrated that phytochemicals could act on several pathogenic mechanisms, such as the protein aggregation, neuroinflammation, mitochondrial dysfunction, oxidative stress and synaptic impairment, that are involved in neurological diseases including Alzheimer's, Parkinson's and Huntington's disease(24). Medicinal plants modulate the AMPK, PI3K/Akt, PPAR and insulin receptor signaling networks in an integrated manner, which plays a key role in the management of type 2 diabetes, obesity, metabolic syndrome and its associated complications in diabetes and metabolic diseases. In addition, systems biology is also contributing to the fight against infectious diseases by helping to identify antiviral, antibacterial, anti-fungal and anti-microbial compounds from plants that can disrupt the replication

of infectious agents in hosts, host–pathogen interactions, immune regulation and pathogen resistance mechanisms. Moreover, phytochemicals from medicinal plants have been found to have therapeutic potential in inflammatory diseases by reducing the production of cytokines, activation of inflammasomes, oxidative stress, cyclooxygenase pathways and transcription factors like NF- κ B and STAT3 in rheumatoid arthritis, inflammatory bowel disease, psoriasis, asthma and other chronic inflammatory diseases(12). The application of multi-omics technologies, computational modeling, network pharmacology, molecular docking, and artificial intelligence has significantly improved the potential for identification of disease associated targets, therapeutic biomarkers, and personalized treatment strategies. As a result, systems biology has provided a solid scientific basis for developing safe, effective and evidence-based phytotherapeutics for various complex human diseases, and the study of the multitarget pharmacological activities of medicinal plants has been propelled.

8. CHALLENGES, LIMITATIONS, AND FUTURE PERSPECTIVES

Although great progress has been made, there are still some issues that hinder the application of systems biology in medicinal plant research. The integration of heterogeneous multi-omics datasets is technically challenging due to the different formats, scales and complexity of the various datasets including genomic, transcriptomic, proteomic, metabolomic and microbiome. Incomplete biological databases, lack of data quality and standardisation further diminish reproducibility and cross-study comparisons, while variability in experimental protocols further diminishes that(23). Despite strong information provided by computational prediction based on artificial intelligence and network pharmacology, experimental validation based on in vitro, in vivo and clinical studies is still needed to ensure the accuracy of the predictions made. Explainable Artificial Intelligence (XAI) is crucial in enhancing the transparency, interpretability, and trust in AI predictions. Developing precision phytomedicine will rely on the successful merging of patient-specific genomic and clinical data with the pharmacology of medicinal plants to facilitate personalised therapeutic action. In addition, standardized herbal formulations are essential for successful clinical translation, as are strong regulations, detailed safety evaluations, and properly designed clinical trials to demonstrate efficacy, safety, and clinical reliability of plant-based medicines(13).

9. CONCLUSION

Medicinal plant research has been revolutionized by systems biology, which combines multi-omics technologies, computational modeling, network pharmacology, and artificial intelligence to understand the intricate molecular mechanisms responsible for the effectiveness of phytotherapy. These are multidisciplinary approaches that have greatly facilitated identification of bioactive compounds, molecular targets, biological pathways and disease associated biomarkers, as well as the development of multitarget therapeutic strategies. The use of sophisticated computational tools coupled with experimental validation has enhanced the scientific basis of evidence-based phytomedicine and broadened its scope of application for precision medicine. Future developments in the field of systems biology supported research on medicinal plants are likely to be accelerated by the further development of artificial intelligence, explainable computational modelling, digital twin and personalized healthcare. These innovations will enable the identification of safer, more effective and clinically translatable phytopharmaceuticals, which will in turn help prevent and treat complex human diseases using a precision, data-driven and systems-based therapeutic strategy.

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Ethical Approval: Not applicable, as this study is based solely on published literature.

REFERENCES

- [1] Tavassoly I, Goldfarb J, Iyengar R. Systems biology primer: The basic methods and approaches. *Essays in Biochemistry*. 2018;62(4):487–500.
- [2] Mukherjee A, Abraham S, Singh A, Balaji S, Mukunthan K. From data to cure: A comprehensive exploration of multi-omics data analysis for targeted therapies. *Molecular Biotechnology*. 2025;67(4):1269–1289.

- [3] Del Sol A, Balling R, Hood L, Galas D. Diseases as network perturbations. *Current Opinion in Biotechnology*. 2010;21(4):566–571.
- [4] Ogunjobi TT, Ohaeri PN, Akintola OT, Atanda DO, Orji FP, Adebayo JO, et al. Bioinformatics applications in chronic diseases: A comprehensive review of genomic, transcriptomics, proteomic, metabolomics, and machine learning approaches. *Medinformatics*. 2026;3(2):110–127.
- [5] Tanaka M, Szabó Á, Vécsei L. Redefining roles: A paradigm shift in tryptophan–kynurenine metabolism for innovative clinical applications. *International Journal of Molecular Sciences*. 2024;25(23):12767.
- [6] Graham DB, Xavier RJ. Pathway paradigms revealed from the genetics of inflammatory bowel disease. *Nature*. 2020;578(7796):527–539.
- [7] Sindelar RD. Genomics, other “OMIC” technologies, precision medicine, and additional biotechnology-related techniques. In: *Pharmaceutical Biotechnology: Fundamentals and Applications*. Springer; 2024. p. 209–254.
- [8] Martínez-Esteso MJ, Morante-Cariel J, Samper-Herrero A, Martínez-Márquez A, Sellés-Marchart S, Nájera H, et al. Proteomics: An essential tool to study plant-specialized metabolism. *Biomolecules*. 2024;14(12):1539.
- [9] Hashiguchi A, Tian J, Komatsu S. Proteomic contributions to medicinal plant research: From plant metabolism to pharmacological action. *Proteomes*. 2017;5(4):35.
- [10] Lao Y, Wang X, Xu N, Zhang H, Xu H. Application of proteomics to determine the mechanism of action of traditional Chinese medicine remedies. *Journal of Ethnopharmacology*. 2014;155(1):1–8.
- [11] Aghaei K, Komatsu S. Crop and medicinal plants proteomics in response to salt stress. *Frontiers in Plant Science*. 2013;4:8.
- [12] Satrio RD, Fendiyoanto MH, Miftahudin M. Tools and techniques used at global scale through genomics, transcriptomics, proteomics, and metabolomics to investigate plant stress responses at the molecular level. In: *Molecular Dynamics of Plant Stress and Its Management*. Springer; 2024. p. 555–607.
- [13] Ma X, Meng Y, Wang P, Tang Z, Wang H, Xie T. Bioinformatics-assisted, integrated omics studies on medicinal plants. *Briefings in Bioinformatics*. 2020;21(6):1857–1874.
- [14] Sonbol HS. Nutritional proteomics: A pathway to understanding and optimizing human health. *Journal of Medical Science Interdisciplinary Research*. 2023;3(2):45–64.
- [15] Debnath M, Pandey M, Bisen P. An omics approach to understand plant abiotic stress. *OMICS: A Journal of Integrative Biology*. 2011;15(11):739–762.
- [16] Latif R, Nawaz T. Medicinal plants and human health: A comprehensive review of bioactive compounds, therapeutic effects, and applications. *Phytochemistry Reviews*. 2025:1–44.
- [17] Jean Beltran PM, Federspiel JD, Sheng X, Cristea IM. Proteomics and integrative omic approaches for understanding host–pathogen interactions and infectious diseases. *Molecular Systems Biology*. 2017;13(3):MSB167062.
- [18] Noor F, Tahir ul Qamar M, Ashfaq UA, Albutti A, Alwashmi AS, Aljasir MA. Network pharmacology approach for medicinal plants: Review and assessment. *Pharmaceutics*. 2022;15(5):572.
- [19] Hakeem KR, Chandna R, Ahmad P, Iqbal M, Ozturk M. Relevance of proteomic investigations in plant abiotic stress physiology. *OMICS: A Journal of Integrative Biology*. 2012;16(11):621–635.
- [20] Efferth T, Koch E. Complex interactions between phytochemicals: The multi-target therapeutic concept of phytotherapy. *Current Drug Targets*. 2011;12(1):122–132.
- [21] Mukherjee PK, Banerjee S, Kar A. Molecular combination networks in medicinal plants: Understanding synergy by network pharmacology in Indian traditional medicine. *Phytochemistry Reviews*. 2021;20(4):693–703.
- [22] Rana N, Gupta P, Singh H, Nagarajan K. Role of bioactive compounds, novel drug delivery systems, and polyherbal formulations in the management of rheumatoid arthritis. *Combinatorial Chemistry & High Throughput Screening*. 2024;27(3):353–385.
- [23] Kumar A, Patil C. *Network Pharmacology: Principles, Processes, and Applications*. CRC Press; 2025.
- [24] Özenver N, Efferth T. Integration of phytochemicals and phytotherapy into cancer precision medicine. In: *Approaching Complex Diseases: Network-Based Pharmacology and Systems Approach in Bio-Medicine*. Springer; 2020. p. 355–392.
- [25] Patil S, Asutkar S. Cutting-edge pharmacological innovations for enhanced post-surgical wound healing: Integrating nanomedicine, targeted drug delivery, and natural therapeutics. *Journal of Pharmacology and Pharmacotherapeutics*. 2025:0976500X251367992.
- [26] Pellosi DS, Paiva GS, Vital VG, Mendes AL, Santos NG, Kuriki FK, et al. Harnessing copper nanoparticles for antimicrobial applications: Advances and challenges. *Antibiotics*. 2025;14(11):1170.

- [27] Kumar D, Gupta V, Tanwar R, Jaiswal NK. Revolutionizing diabetic macular edema treatment: FDA approval of Susvimo. *SN Comprehensive Clinical Medicine*. 2025;7(1):194.