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NETWORK PHARMACOLOGY IN AYURVEDA: A SYSTEMS BIOLOGY APPROACH TO UNDERSTANDING THE MULTI-TARGET ACTIONS OF HERBAL DRUGS

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Abstract: Ayurveda utilizes medicinal plants and polyherbal formulations for maintaining health and treating diseases through a holistic approach. Conventional pharmacology follows the "one drug–one target–one disease" paradigm, which often fails to explain the broad-spectrum actions of herbal medicines containing multiple bioactive constituents. Network pharmacology has emerged as a revolutionary discipline integrating systems biology, bioinformatics, pharmacology, and computational sciences to understand multi-component and multi-target therapeutic mechanisms. This approach is particularly relevant to Ayurveda, where therapeutic efficacy is attributed to synergistic interactions among phytoconstituents acting on various biological pathways simultaneously. Network pharmacology enables the identification of active compounds, molecular targets, signaling pathways, and disease networks associated with Ayurvedic drugs and formulations. Studies on Ashwagandha, Guduchi, Haridra, Guggulu, Triphala, and Chyawanprasha demonstrate that these medicines regulate inflammatory, metabolic, neuroendocrine, immune, and oxidative stress pathways through coordinated network interactions. Furthermore, integration with omics technologies, artificial intelligence, and Ayurgenomics offers new opportunities for precision Ayurveda and evidence-based herbal medicine research. This review discusses the principles, methodology, applications, correlation with Ayurvedic concepts, and future prospects of network pharmacology in understanding the mechanisms of Ayurvedic herbal drugs.

Keywords: Network Pharmacology, Systems Biology, Polyherbal Formulations, Rasayana, Precision Ayurveda

Introduction: Ayurveda is one of the oldest healthcare systems in the world and relies extensively on herbal medicines and polyherbal formulations. Unlike synthetic drugs that usually target a single molecule, Ayurvedic medicines contain numerous phytochemicals capable of acting on multiple biological targets simultaneously. This complexity presents challenges in explaining their mechanisms through conventional pharmacological models [1,2].

The concept of network pharmacology, introduced by Hopkins in 2007, shifted drug discovery from a reductionist approach toward a systems-level understanding of disease and therapeutics. Network pharmacology recognizes that diseases arise from disturbances in interconnected biological networks and that effective therapies often act on multiple targets and pathways [3,4].

The philosophy of network pharmacology closely aligns with Ayurveda, which views disease as a disturbance of *Dosha*, *Dhatu*, *Agni*, and *Srotas*, and treatment as restoration of systemic balance [5,6]. Consequently, network pharmacology has emerged as an ideal scientific framework for understanding Ayurvedic medicines [7,8].

Principles of Network Pharmacology: Network pharmacology integrates pharmacology, bioinformatics, systems biology, and computational modeling to study interactions among compounds, targets, pathways, and diseases [3,4].

Fundamental Concepts:

Conventional Pharmacology	**Network Pharmacology**
One drug – One target	Multi-component – Multi-target
Single mechanism	Multiple mechanisms
Linear pathways	Complex biological networks
Reductionist approach	Systems biology approach
Symptom-specific action	Network restoration

Network pharmacology is based on the understanding that biological systems function through interconnected molecular networks rather than isolated pathways [9,10].

Methodology of Network Pharmacology:

Flowchart:1 outlines the systematic computational and experimental pipeline used in network pharmacology to decode the complex mechanisms of herbal medicines. The process transitions sequentially from dry-lab computational predictions to wet-lab experimental validation [11,12].

Flowchart: 1. General Workflow of Network Pharmacology

Selection of Herb/ Formulation → Identification of Phytochemicals → ADME and Drug-Likeness Screening
↓
Protein–Protein Interaction Analysis←Network Construction←Disease Target Identification←Target Prediction
↓
Pathway Enrichment Analysis→Molecular Docking→ Experimental Validation

The workflow begins by selecting a specific herb or polyherbal formulation. Researchers mine specialized biomedical databases to catalog all known constituent phytochemicals. Because raw plants contain thousands of molecules, these compounds undergo ADME (Absorption, Distribution, Metabolism, and Excretion) and drug-likeness screening to filter out those with poor bioavailability [13].

Next, structural and machine-learning tools execute target prediction to identify human proteins these active molecules interact with, while disease target identification compiles genes associated with the condition being treated. Overlapping these datasets facilitates network construction and Protein-Protein Interaction (PPI) analysis, visualizing the physical web of compound-target intersections and isolating high-degree “hub genes” [14].

Downstream functional analysis relies on pathway enrichment (such as KEGG or Gene Ontology) to trace which cellular signaling networks are systematically modulated. Finally, the workflow transitions from theoretical to practical validation: molecular docking computationally tests binding affinities between the phytoconstituents and target proteins, setting a targeted foundation for definitive experimental validation using *in vitro*, *in vivo*, or multi-omics assays [15,16].

Important Databases Used for this Conceptual Study

Database	Application
IMPPAT	Indian medicinal plants and phytochemicals [17]
PubChem	Chemical information [18]
DrugBank	Drug-target relationships [19]
GeneCards	Disease-associated genes [20]
STRING	Protein-protein interaction networks [21]
UniProt	Protein information [22]
KEGG	Biological pathways [23]
SwissTargetPrediction	Target prediction [24]

Major Components of Network Pharmacology

1. Compound Identification: This foundational phase shifts the focus from a single synthetic molecule to the vast chemical treasury of a plant or formulation. Since herbal medicines contain hundreds of secondary metabolites, researchers utilize text mining, literature reviews, and specialized phytochemical databases—such as IMPPAT, TCMSP, and PubChem—to catalog every constituent [17,18]. For instance, Ashwagandha yields complex steroidal lactones like Withaferin A, while Haridra (Turmeric) yields curcuminoids [25,26]. Identifying these complex mixtures allows scientists to establish a comprehensive chemical profile, which is then filtered using ADME metrics to isolate the highly bioavailable, active compounds [13].

Examples:

Herb	Important Phytochemicals
Ashwagandha	Withaferin A, Withanolides [25]
Guduchi	Berberine, Magnoflorine [27]
Haridra	Curcumin, Demethoxycurcumin [26]
Guggulu	Guggulsterones [28]
Triphala	Gallic acid, Ellagic acid [29]

2. Target Prediction: Once the bioactive phytochemicals are mapped, target prediction determines which specific human proteins, receptors, or enzymes these molecules physically bind to. Unlike modern pharmaceuticals designed for a single receptor, a single phytoconstituent inherently possesses multi-target affinity. For example, Curcumin does not target just one structural defect; it simultaneously docks into and modulates major signaling nodes like TNF, IL6, COX-2, STAT3, and AKT1 [26,30]. Predicting these vast cross-reactive webs explains how a single Ayurvedic herb can concurrently exhibit anti-inflammatory, antioxidant, and anti-cancer properties, scientifically validating the classical concept of broad-spectrum therapeutic action [7,8].

3. Pathway Analysis: Pathway analysis elevates individual target proteins into an integrated, systemic view of human physiology. By cross-referencing identified target proteins with functional biological repositories like the Kyoto Encyclopedia of Genes and Genomes (KEGG) and Gene Ontology (GO) databases, researchers map out exactly which cellular pathways are being altered. Key survival cascades—such as NF-κB, PI3K-AKT, MAPK, JAK-STAT, and AGE-RAGE—are frequently revealed as therapeutic endpoints [23,31]. Tracking these interconnected pathways explains how complex formulations downregulate systemic inflammation, fine-tune the immune response, balance metabolic stress, and protect cellular integrity to ultimately restore holistic homeostasis [11,32].

Applications in Ayurvedic Herbal Drugs

Ashwagandha (Withania somnifera): Classified as an essential *Rasayana* drug in Ayurveda, Ashwagandha is traditionally utilized to manage stress disorders, neurodegenerative conditions, and immune dysfunction [25,33]. Network pharmacology analysis reveals that its major molecular targets include crucial signaling nodes such as AKT1, STAT3, MAPK1, TNF, and IL6 [34,35]. These targets govern pivotal cellular cascades, namely the PI3K-AKT signaling, NF-κB, and MAPK pathways. Rather than acting via a single channel, network studies show that Ashwagandha exerts its neuroprotective, immunomodulatory, anti-inflammatory, and adaptogenic effects through the coordinated, systems-level regulation of these multiple interconnected biological pathways [33,36].

Guduchi (Tinospora cordifolia): Traditionally revered as a potent *Rasayana* and therapeutic immunomodulator, Guduchi is widely applied to treat autoimmune, metabolic, and chronic inflammatory conditions [27,37]. Through network pharmacology, its multi-target mechanism has been mapped to key human proteins including TNF, IL6, AKT1, TP53, and VEGFA [38]. The systemic modulation of these target nodes translates into diverse biological activities, specifically immune regulation, robust anti-inflammatory responses, antioxidant action, and metabolic regulation. The network framework demonstrates that Guduchi achieves its therapeutic effects primarily through cytokine regulation and widespread immune network modulation [37,39].

Haridra (Curcuma longa): Haridra is heavily relied upon in Ayurveda for inflammatory disorders, skin conditions, and metabolic syndromes [26,40]. Curcumin, its principal constituent, stands out as one of the most extensively studied phytochemicals in systems pharmacology. Network analysis illustrates that Haridra maps to vital core targets, including TNF, IL1β, IL6, COX-2, and STAT3 [30,41]. This multi-target intersection drives its diverse anti-inflammatory, antioxidant, antidiabetic, and anticancer actions. Ultimately, Haridra's vast clinical versatility does not stem from a single mechanical block, but from its capacity to simultaneously modulate multiple molecular networks [26,40].

Guggulu (Commiphora mukul): In classical Ayurvedic medicine, Guggulu is a primary intervention for obesity, arthritis, and dyslipidemia [28,42]. Network pharmacology validates these applications by identifying its interactions with key metabolic and inflammatory targets, specifically PPARγ, APOE, FXR, and TNF [43]. The modulation of these specific nodes yields crucial therapeutic benefits, including systemic lipid regulation, targeted anti-inflammatory activity, and cardiovascular protection. By demonstrating how its active guggulsterones influence lipid regulation and suppress chronic inflammation, contemporary network studies successfully provide scientific validation for Guggulu's traditional *Medohara* (anti-obesity) and *Lekhana* (scraping) actions [28,42].

Triphala: Triphala is a renowned, classic polyherbal formulation composed of three medicinal fruits: Haritaki, Bibhitaki, and Amalaki. Network pharmacology models demonstrate that this formulation targets key biological nodes such as TNF, IL6, AKT1, and TP53 [29,44]. These molecular interactions translate into broad systemic actions, including antioxidant defense, anti-inflammatory responses, and deep tissue rejuvenation. Furthermore, recent systems biology studies indicate that Triphala's therapeutic efficacy operates through a dual-action mechanism, concurrently regulating the host's internal inflammatory signaling pathways while driving beneficial gut microbiome modulation to restore holistic metabolic balance [29,45].

Table: Network Pharmacology Profiles and Classical Ayurvedic Significance of Major Herbs and Formulations

Drug / Formulation	Major Phytochemicals	Core Molecular Targets	Primary Signaling Pathways	Therapeutic Actions & Ayurvedic Significance
Ashwagandha (*Withania somnifera*)	Withaferin A, Withanolide A, Withanoside IV, Withanoside V, Sitoindosides	AKT1, STAT3, MAPK1, TNF, IL6, VEGFA, HSP90AA1	PI3K-AKT signaling, NF-κB pathway, MAPK pathway, Apoptotic pathways	Neuroprotective, immunomodulatory, anti-inflammatory, and adaptogenic effects. Validates classical *Rasayana*, *Balya*, and *Medhya* properties [33,35].
Guduchi (*Tinospora cordifolia*)	Berberine, Magnoflorine, Palmatine, Tinosporaside, Cordifolioside	TNF, IL6, AKT1, TP53, VEGFA, CASP3, MAPK8	TNF signaling, NF-κB signaling, JAK-STAT signaling, Toll-Like Receptor signaling	Immune regulation, cytokine modulation, anti-inflammatory, antioxidant, and metabolic regulation. Validates its *Tridoshaghna* and *Vyadhikshamatva* actions [37,38].
Haridra (*Curcuma longa*)	Curcumin, Demethoxycurcumin, Bisdemethoxycurcumin, Turmerones	TNF, IL1β, IL6, COX-2 (PTGS2), STAT3, AKT1, VEGFA	NF-κB signaling, PI3K-AKT signaling, AGE-RAGE pathway, HIF-1 signaling	Potent anti-inflammatory, antioxidant, antidiabetic, and anticancer actions. Explains its traditional use in metabolic syndromes (*Prameha*) and skin disorders (*Kustha*) [26,41].
Guggulu (*Commiphora mukul*)	Guggulsterone E, Guggulsterone Z,	PPARγ, APOE,	Lipid metabolism pathways,	Lipid regulation, anti-inflammatory activity, and

	Myrrhanol, Commipherol	FXR, TNF, IL6, AKT1	PPAR signaling, Chronic inflammatory pathways	cardiovascular protection. Scientifically decodes classical *Medohara* (anti-obesity) and *Lekhana* (scraping) actions [28,43].
Triphala (Polyherbal Formulation)	Gallic acid, Ellagic acid, Chebulagic acid, Chebulinic acid, Quercetin	TNF, IL6, AKT1, TP53, CASP3, MAPK1	Oxidative stress regulation, Apoptosis regulation, Inflammatory signaling, Gut microbiota modulation	Antioxidant, anti-inflammatory, and tissue rejuvenation. Acts via a dual network involving host pathways and gut microbiome modulation to fulfill its *Rasayana* role [29,44].

Correlation of Network Pharmacology with Ayurvedic Principles: The primary strength of network pharmacology lies in its profound ability to translate ancient, qualitative Ayurvedic concepts into the quantifiable, molecular language of contemporary systems medicine. Rather than viewing health through a reductionist lens, both paradigms recognize that physiological well-being is the product of intricate, interconnected biological webs [7,34].

At the core of Ayurveda is the *Dosha* theory (*Vata*, *Pitta*, *Kapha*), which can be scientifically interpreted as global biological regulatory networks governing neuroendocrine, immune, and inflammatory functions [46,47]. Consequently, *Dosha Vaishamya* (imbalance) directly equates to a network perturbation, while *Dosha Samyata* (equilibrium) aligns with the preservation of network homeostasis [9,48]. When this homeostatic balance shifts, pathological networks expand. This process mirrors the concept of *Samprapti* (disease pathogenesis), which network medicine conceptualizes as disease-network development across structural tissue systems (*Dhatu*) [49].

Furthermore, central metabolic concepts like *Agni* and *Srotas* find precise modern equivalents. *Agni*, the determinant of metabolic digestion and transforming bioenergetics, operates as an intricate web of metabolic pathways and mitochondrial functions [50]. *Srotas*, the classical physiological channels, represent the body's cellular communication and transport networks, such as the circulatory, lymphatic, and neural signaling systems [51]. When these channels are blocked or networks are perturbed, multi-component therapeutic interventions are required to restore balance.

The strategy used to disrupt this disease network is known as *Samprapti Vighatana* (interruption of pathogenesis). In network pharmacology, this translates directly to network correction, achieved not by blocking a single target, but by simultaneously modulating multiple therapeutic nodes to collapse the disease web [11,49]. This systems-level approach is perfectly exemplified by *Rasayana* (rejuvenation) therapy. Instead of serving as a narrow remedy, *Rasayana* acts through systems-level regulation, universally fine-tuning antioxidant defense networks, immune responses, and cellular resilience [33,52]. Finally, the unique Ayurvedic concept of *Yogavahi*— substances that enhance the efficacy of co-administered formulations—is explained as pharmacokinetic enhancement. A prime example is piperine, which structurally improves absorption and downregulates metabolic enzymes to maximize bioactivity [53]. Ultimately, network pharmacology serves as a definitive scientific bridge, validating that Ayurveda's holistic principles are early understandings of network medicine [7,8,34].

Table: Correlation Between Ayurveda and Network Pharmacology

Ayurvedic Concept	Network Pharmacology Equivalent
Dosha	Biological regulatory networks
Dosha Vaishamya	Network perturbation
Dosha Samyata	Network homeostasis
Dhatu	Tissue systems
Agni	Metabolic pathways
Srotas	Communication and transport networks
Samprapti	Disease-network development
Samprapti Vighatana	Network correction

Rasayana	Systems-level regulation
Yogavahi	Pharmacokinetic enhancement

Samprapti and Disease Networks: The concepts of *Samprapti* in Ayurveda and disease-network evolution in modern systems biology share a profound conceptual synergy, both viewing pathogenesis as a dynamic, multi-staged progression rather than a sudden, isolated event [49,54].

The process initiates with *Nidana Sevana* (exposure to etiological or causative factors, such as faulty diet, stressful lifestyle, or environmental triggers). In systems medicine, this stage represents the prolonged exposure to cellular stressors, genetic vulnerabilities, or epigenetic triggers. This exposure leads directly to *Dosha Prakopa* (the aggravation and vitiation of the regulatory principles — *Vata*, *Pitta*, or *Kapha*). In the language of network pharmacology, this stage is equivalent to early-stage cellular stress or metabolic imbalance, where homeostatic biological networks experience initial disruptions or micro-perturbations [48]. As the imbalance intensifies, it transitions into *Dosha Sanchara* (the spreading or circulation of these vitiated factors throughout the body via the physiological channels). Systems biology views this as the systemic propagation of danger signals, where localized cellular stress begins to trigger broader systemic cascades, such as the circulating release of pro-inflammatory cytokines, altered signaling molecules, or metabolic intermediates. This circulation culminates in *Sthanasamshraya* (localization or nesting of the vitiated factors in a weakened tissue or organ system, known as *Dhatu Khavaigunya*). This is the critical stage where circulating pathological signals interact with vulnerable biological nodes, giving rise to localized protein-protein interaction abnormalities, tissue-specific oxidative stress, and structural cell damage [51].

Once these network disruptions fully consolidate, *Vyakti* (the full clinical manifestation of the disease) occurs. Systems biology conceptualizes this as the tipping point where individual pathway aberrations aggregate into an established, self-sustaining disease network — such as chronic inflammation, insulin resistance, or endothelial dysfunction — producing noticeable clinical symptoms. If left unmanaged, the disease web continuously expands, altering secondary downstream pathways to cause structural complications. By treating pathogenesis as a progressive evolution, both Ayurveda and systems biology show that chronic disorders are not single-point failures. Instead, they are complex systems-level failures that require comprehensive, multi-target network interventions (*Samprapti Vighatana*) to systematically dismantle the disease web and restore holistic homeostasis [49,54].

Flowchart: 2. Ayurvedic Disease Development and Network Dysfunction:
Nidana Sevana →Dosha Prakopa →Dosha Sanchara →Sthanasamshraya →Vyakti (Disease) →Complications

mechanism. Instead, they regulate multiple physiological systems simultaneously, producing broad-spectrum rejuvenative, immunomodulatory, and adaptogenic effects [33,52].

Major Biological Networks Influenced by Rasayana Drugs

Network	Examples
Antioxidant	Nrf2, SOD, Catalase
Immune	Cytokines, T-cells
Neuroprotective	BDNF, Neuroinflammatory pathways
Endocrine	Stress hormone regulation
Metabolic	PI3K-AKT, AMPK

This systems-level activity explains the rejuvenating and adaptogenic properties of *Rasayana* drugs such as Ashwagandha, Guduchi, Amalaki, and formulations like Chyawanprasha [33,52].

Omics Technologies and Precision Ayurveda

Genomics: Genomics investigates the complete DNA sequence of an organism, mapping out disease-associated genes and structural variations. In network pharmacology, it serves as the foundational blueprint for identifying genetic susceptibilities and specific disease-related targets. By discovering these genetic anchors, researchers can build precise disease networks. In the context of Ayurveda, genomics helps decode individual therapeutic variations, allowing scientists to understand why certain herbal compounds interact efficiently with specific genetic profiles. This structural mapping forms the bedrock of personalized medicine, tracing complex chronic illnesses down to their initial hereditary and genetic network components [51,55].

Transcriptomics: Transcriptomics evaluates the complete set of RNA transcripts, or gene expression changes, within a biological system following an intervention. In herbal research, analyzing the transcriptome before and after administering a formulation reveals exactly which genes are up- or down-regulated. This validation allows researchers to confirm network pharmacology predictions by proving that a specific Ayurvedic herb systematically influences predicted genetic cascades, validating that multi-component treatments effectively shift global gene expression patterns back toward homeostatic health [16,56].

Proteomics: Proteomics investigates protein-level alterations, examining the expression, structure, and functional interactions of the entire cellular protein complement. Since proteins are the actual functional units executing cellular signaling, proteomics provides crucial physical evidence that mirrors genomic and transcriptomic activity. In network pharmacology, high-throughput proteomics identifies changes in signaling proteins and maps out physical Protein-Protein Interaction (PPI) networks. This technology bridges the gap between computational predictions and actual biological outcomes, proving exactly how Ayurvedic phytoconstituents bind to, modulate, and regulate vital "hub proteins" within a living disease network [16,57].

Metabolomics: Metabolomics is the comprehensive analysis of small-molecule metabolites within biological fluids, cells, or tissues, offering a direct reflection of metabolic changes. This approach is uniquely relevant to Ayurveda because many classical therapeutics focus heavily on metabolic transformation. Metabolomics allows researchers to trace systemic changes in lipid, glucose, and amino acid networks following herbal therapy. By measuring end-stage metabolic readouts, this technology effectively serves as a modern scientific tool to track the functional status of *Agni*, illustrating how Ayurvedic drugs resolve toxic accumulation (*Aam*) and restore metabolic equilibrium [58,65].

Microbiomics: Microbiomics evaluates gut microbial interactions, studying the complex ecosystem of microorganisms residing in the digestive tract and their collective genome. Emerging systems biology research reveals a profound axis between herbal medicines and the gut microbiome. Many complex Ayurvedic formulations, such as Triphala, exert major therapeutic actions by enhancing beneficial gut microflora, improving intestinal barrier integrity, and regulating microbial metabolites. Microbiomics maps these intricate interactions, showing how traditional medicines manipulate the gut ecosystem to regulate systemic immunity, reduce chronic inflammation, and drive holistic rejuvenation [45,59].

Ayurgenomics: Ayurgenomics is an innovative, integrative field that merges the core Ayurvedic concept of *Prakriti* (constitutional phenotypes determined by *Vata*, *Pitta*, and

Kapha) with modern genetic variability. Research has demonstrated that distinct *Prakriti* types correlate with specific genetic polymorphisms, global gene expression patterns, immune responses, and metabolic characteristics. By validating that ancient constitutional classifications possess a verifiable biological and molecular basis, Ayurgenomics enables the development of network-based Precision Ayurveda. This integration ensures that multi-target herbal therapies can be customized to an individual's distinct genetic and physiological baseline [51,60].

Summary of Omics Technologies in Precision Ayurveda

Omics Technology	**Core Scientific Purpose**	**Specific Role in Network Pharmacology**	**Precision Ayurveda Integration**
Genomics	Studies DNA structure and disease-associated genes	Identifies baseline target genes and genetic susceptibility nodes	Explains heritable therapeutic variations and individual disease risks
Transcriptomics	Examines global gene-expression (mRNA) changes	Validates network pathway predictions through observed gene regulation	Tracks real-time, dynamic cellular responses to herbal formulations
Proteomics	Investigates protein-level expression and alterations	Maps out physical Protein-Protein Interaction (PPI) networks and hub genes	Confirms direct target binding and alterations in active cellular signaling
Metabolomics	Analyzes small-molecule metabolic profiles	Tracks functional end-stage biochemical changes across systemic pathways	Provides a quantifiable readout of metabolic networks (*Agni* regulation)
Microbiomics	Evaluates gut microbial populations and interactions	Maps how herbal compounds alter and interact with the intestinal flora	Explains the systemic therapeutic actions of digestive and *Rasayana* herbs
Ayurgenomics	Integrates *Prakriti* concepts with genomic variations	Customizes network models based on baseline constitutional phenotypes	Validates *Prakriti* types with distinct genetic and immune markers

Precision Ayurveda Framework: The framework initiates with *Prakriti* Assessment, the traditional Ayurvedic process of diagnosing an individual's unique constitutional phenotype based on the equilibrium of *Vata*, *Pitta*, and *Kapha*. To validate and enrich this phenotypic baseline with quantitative biological data, the patient next undergoes Genomic Analysis. This step leverages the field of Ayurgenomics to map individual genetic polymorphisms and baseline gene expression patterns that naturally correlate with specific *Prakriti* types. Following this, Microbiome Profiling evaluates the patient's unique gut microbial ecosystem. Once these comprehensive multi-omics data layers are gathered, the framework advances to Network Mapping. Advanced computational algorithms integrate the patient's genetic, microbial, and constitutional baseline to construct a personalized biological network map. This network map exposes specific perturbed pathways, metabolic blockages (*Srotorodha*), or tissue vulnerabilities unique to that individual.

Armed with this systems-level view, clinicians can prescribe Personalized Herbal Therapy. Rather than utilizing a standardized formula, multi-component Ayurvedic herbs or polyherbal mixtures are precisely selected to sync with the patient's personalized network map, simultaneously targeting multiple disease nodes while respecting their natural constitution. This targeted intervention systematically drives the final stage, a successful Clinical Outcome, characterized by restored network homeostasis (*Dosha Samyata*) and long-term systemic resilience [51,60].

Flowchart: 3. Precision Ayurveda Framework

Prakriti Assessment→Genomic Analysis→ Microbiome Profiling→Network Mapping
↓
Clinical Outcome ←Personalized Herbal Therapy

Artificial Intelligence in Network Pharmacology: Artificial intelligence (AI) has emerged as a transformative tool in herbal drug research and network pharmacology. By leveraging machine learning, deep learning, and big data analytics, AI significantly enhances the speed, accuracy, and predictive power of complex multi-component herbal studies [31,61,66].

Applications of AI

- **Compound screening**: Rapid identification of bioactive phytochemicals from large libraries.
- **Target prediction**: Accurate prediction of compound-target interactions using structural and network-based models.

- **Toxicity assessment**: Early prediction of potential adverse effects and herb-drug interactions.
- **Drug repurposing**: Identification of new therapeutic applications for traditional Ayurvedic herbs and formulations.
- **Personalized medicine**: Integration of patient-specific data (Prakriti, genomics, microbiome) for tailored herbal prescriptions.

AI excels at analyzing massive datasets generated through multi-omics technologies and facilitates the rapid identification of therapeutic networks, synergistic interactions, and key regulatory hubs within biological systems [31,62].

Challenges and Limitations: Despite its significant promise, network pharmacology applied to Ayurvedic medicine faces several important limitations that must be addressed for its full potential to be realized [63,64].

Major Challenges

1. Complexity of herbal medicines — A single herb or polyherbal formulation may contain hundreds to thousands of phytochemicals, making comprehensive network modeling extremely challenging.
2. Incomplete phytochemical databases — Many Ayurvedic compounds remain poorly characterized or absent from current databases.
3. Variability in herbal composition — Geographical, seasonal, and processing differences lead to inconsistency in phytochemical profiles.
4. Overreliance on computational predictions — Many studies lack sufficient wet-lab validation.
5. Limited experimental validation — Bridging *in silico* findings with robust *in vitro*, *in vivo*, and clinical evidence remains difficult.
6. Difficulty correlating molecular findings with classical Ayurvedic concepts — Abstract principles such as *Ojas*, *Prana*, and subtle *Dosha* dynamics are not easily translated into molecular networks.

Therefore, computational predictions must always be rigorously validated through laboratory experiments and well-designed clinical studies to ensure scientific credibility [12,63].

Conclusion: Network pharmacology has emerged as a powerful scientific approach for understanding the complex mechanisms of Ayurvedic herbal medicines and formulations. By embracing multi-component, multi-target, and multi-pathway interactions, it aligns closely with the holistic philosophy of Ayurveda. Studies on major Ayurvedic herbs such as Ashwagandha, Guduchi, Haridra, Guggulu, and Triphala demonstrate that their therapeutic actions arise from coordinated regulation of biological networks involved in inflammation, immunity, metabolism, oxidative stress, and tissue homeostasis. Integration with omics technologies, artificial intelligence, and Ayurgenomics further strengthens the potential of network pharmacology to bridge traditional Ayurvedic knowledge with modern biomedical science. Continued research and clinical validation will help establish network pharmacology as a key framework for evidence-based Ayurveda, personalized medicine, and future herbal drug discovery.

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