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AYURVEDA AND NEW BIOLOGY: INTEGRATING ANCIENT WISDOM AND MODERN SCIENCE

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Abstract

Ayurveda, with its emphasis on *Prakriti* (individual constitution), *Tridosha* (functional principles), *Rasayana* (rejuvenation), and lifestyle-based prevention, provides a time-tested framework for personalised and preventive healthcare. In parallel, New Biology, empowered by high-throughput omics technologies, epigenetics, systems biology and network pharmacology offer novel tools to decode biological complexity at multiple scales. This article examines how emerging research in new biology and Ayurveda, is integrating empirical traditions with molecular science by translating traditional views into quantifiable biological correlates. The promise of network pharmacology to reveal the synergistic mechanisms of polyherbal formulations, multi-omics techniques to examine *Prakriti* and systems modelling to predict health and disease dynamics are discussed. Together, Ayurveda and New Biology form the basis for predictive, preventive and personalised medicine. This approach suggests a scientifically coherent and sustainable model that advances Ayurveda into a data-driven, evidence-based discipline, bridging traditional principles with precision medicine.

Keywords: Ayurveda, New Biology, Systems biology, Ayurgenomics, Holistic health, Network pharmacology

1. Introduction

The evolving global burden of non-communicable chronic diseases (NCDs) has led to an increasing demand for complete, holistic, and patient-centric approaches in healthcare that integrate prevention, early diagnosis and individualised treatment[1,2]. Ayurveda, the ancient Indian traditional system of medicine, holds an important place in this regard. It provides a comprehensive, holistic approach that discerns health as a complex interaction of environmental, physical, mental and related aspects[3]. This integrated perspective, which has been practiced for millennia, represents an early form of systems thinking that is in line with the latest advancements in modern biology.

Concurrent with this resurgence of interest in traditional system, modern biology is undergoing a slow transition. For decades, reductionist molecular methods have dominated the life sciences. Despite providing important insights, these approaches frequently failed to account for the complexity of biological systems. To pass these constraints, biology is entering a new era called the New Biology, where complexity, integration, and system-level thinking are crucial[4]. New Biology integrates advanced molecular sciences, multi-omics technologies, network pharmacology and computational tools to generate a more comprehensive view of health and disease.

Efforts are underway to scientifically examine the Ayurvedic concepts, such as *Prakriti* (constitutional typing), *Dosha* (functional principles), *Rasayana* (rejuvenation and regenerative therapies), and *Swasthavritta* (preventive and promotive lifestyle practices), by employing omics technologies, including genomics, transcriptomics, proteomics and metabolomics, as well as by advanced imaging and systems-level computational approaches. This integration enables the development of predictive diagnostics through biomarker discovery, individualized therapeutic strategies tailored to both constitutional and molecular

profiles, and preventive frameworks that strengthen resilience and long-term wellness[5]. This review examines how classical Ayurvedic principles can be contextualised and validated within the framework of New Biology, highlighting areas of convergence ranging from personalised medicine and predictive health models to integrative therapeutics and systems-level prevention.

2. Basic Ayurveda doctrines

According to Ayurvedic doctrine, the five classical elements, known as the *Panchamahabhoota* (*Prithvi*, *Jala*, *Agni*, *Vayu* and *Akasha*), make up the human body, just as the cosmos[6]. The three proposed regulatory functional entities, known as the *Tridosha* (*Vata*, *Pitta* and *Kapha*), are composed of these basic elements[6,7]. The specific combination of *Doshas* formed at conception and established during *in utero* defines an individual's *Prakriti*, or constitutional type[4]. Throughout the lives, this *Prakriti* influences the mental, emotional, and physical traits of an individual[4]. Contemporary biological terminology compares *Prakriti* to a personal blueprint or genotype, suggesting that genes define and stabilise it[4].

An imbalance among *Doshas*, known as *Vikriti* (deviation from *Prakriti*), causes one of the main etiologic factors of disease. Therefore, through individualised treatments such as specific diets, lifestyle changes, and therapeutic techniques catered to each person's particular *Prakriti* and current *Vikriti*, Ayurvedic medicine seeks to preserve or restore the *Doshas* to their proper balance[8]. It forms the basis of Ayurvedic diagnostic and treatment framework. Thus, personalised health plans are directly influenced by the categorisation of individuals into distinct constitutional types, or *Prakritis*, according to the relative predominance of *Vata*, *Pitta*, and *Kapha doshas*[9].

3. Transition from Modern Biology to New Biology

3.1 The era of reductionism : From Cell theory to the Central dogma

For much of the twentieth century, modern biology was shaped by a reductionist philosophy; several foundational discoveries transformed our perception of life and established the basis of contemporary biology. Cell theory, the foundational scientific theory of biology, holds that cells are the fundamental structural and functional units of all living organisms and arise from pre-existing cells[10]. This hypothesis represented a significant conceptual advancement when it was first put forth in 1838 by German scientists Matthias Jakob Schleiden and Theodor Schwann. Essential discoveries made in the 1830s, such as Robert Brown's observation of the nucleus in 1833, solidified the concept that cells contained living substance rather than just empty pores. Rudolf Virchow later codified the vital principle that all cells only arise from pre-existing cells' (*Omnis cellula e cellula*). This was followed by key discoveries like Charles Darwin's theory of evolution through natural selection and Gregor Mendel's laws of inheritance, which laid the groundwork for genetics[11]. The concept of life as chemistry was firmed up with the identification of several biomolecules involved in various biological processes at the molecular level focussing on their structure and function and their role in cellular and organismal processes. Such molecular approaches also led to the identification of DNA as the genetic material carrying information from parent to offspring. Cells are alive and divide because they metabolize biochemicals and produce energy and precursor building block molecules for cell growth and division, respond to stimuli and communicate with one another. The molecularization of biology referred to the shift in biology toward understanding life processes at the molecular level. This field, known as molecular biology, emerged from the fields of biochemistry, genetics, and biophysics, focusing on the structure, function, and interactions of molecules like DNA, RNA and proteins. Key developments included the discovery of the double helix structure of DNA in 1953, which provided a new framework for understanding heredity and gene expression.

The Central Dogma, a fundamental tenet of molecular biology, initially articulated by Francis Crick (1957-1958), explains the flow of genetic information within a biological system[12,13]. DNA replication (copying DNA to DNA), transcription (DNA to messenger RNA, mRNA), and translation (mRNA to protein via transfer RNA, tRNA, and ribosomes) are all involved in this predetermined exchange of sequential information. Although there are certain exceptions, such as RNA replication and reverse transcription (RNA to DNA in retroviruses), the basic idea of information flow from nucleic acids to proteins remains fundamental.

DNA serves as the primary repository of hereditary information, which is copied and passed on during cell division. This information is transcribed into mRNA and translated into proteins which serves as action molecules by folding into precise structures to perform essential functions such as metabolism, signalling, structural integrity and enzymatic catalysis, thereby driving growth, development and homeostasis. Viewed through this lens, life can be understood as a coordinated expression of genetic information into functional proteins that maintain structure, function and continuity in every organism[14,15].

3.2. Limitations of a Molecular Mechanistic View of life

While enormously successful, this reductionist and mechanistic view of life has apparent limitations. The reductionist approach with increasing involvement of physicists and chemists has been largely responsible for astounding progress in elucidating biological principles, properties and functions of a given molecule or a structure in a cell or a specific phenomenon and underlying mechanisms. However, there is still the disconnect between individual discoveries and is necessary to integrate them to understand the phenomenon in a biological context. Molecular biology has given us a precise inventory of life's components, but the essence of human physiology cannot be reduced to its chemical building blocks. Despite providing a detailed parts list and enormous information at the molecular level, molecular biology does not offer much in the way of understanding how these parts integrate into a functioning whole. Although it has led to remarkable developments in the diagnosis and treatment of several disease conditions, the "single drug, single target, single disease" model falls short when confronted with the complexity of chronic, multifactorial illnesses.

3.3 The rise of New Biology : Complexity, Systems Thinking and Emergent Properties

Advances in technologies, development of new tools and techniques and high-throughput analysis led to generation of huge amount of biological data in recent decades. This has led to emergence of new approaches which transcend the traditional reductionist approach, to understand biological systems in all their complexity. This marks a shift from the molecular level study of biology to its study at a higher-level involving systems and networks. This interdisciplinary field combines knowledge from biology, physics, chemistry, mathematics, engineering and computer science to gain a deeper understanding of living systems. New Biology marks a shift in perspective—from studying life as a collection of isolated parts to understanding it as a web of dynamic, interconnected networks operating across multiple scales. At the heart of this approach is the idea of "downward causation" or the notion that higher-level systems can shape and guide the behaviour of their smaller components. This view moves beyond the purely mechanistic model, recognizing that living systems are layered hierarchies that display patterns of organization and function that repeat across scales from individual cells to entire organisms. The application of mathematical modelling and computer simulation to biology, a key feature of New Biology, is a direct response to the need to manage knowledge at multiple scales and explain emergent behaviours[16-18].

4.Ayurveda and New Biology

The intersection of New Biology and Ayurveda represents a significant conceptual synergy rather than a simple intellectual endeavour. New fields of study and research are emerging as a result of this convergence, aiming at an expanded and individualised understanding of health. Ayurveda thus transcends its role as a descriptive science, providing a process-oriented and contextual model that can develop reliable, predictive systems biology models.

Scientists regard the *Panchamahabhoota* concept of Ayurveda, like atomic and molecular composition, as the basic components of matter and energy. The "*Trisutra*" concept, which consists of the three interconnected aspects of *Hetu* (causes), *Linga* (characteristics) and *Aushadha* (therapeutics), provides an integrated systems approach to interpreting health and illness. Unlike modern medicine that focuses on symptom relief, Ayurveda places a higher priority on determining and treating the underlying root cause of an imbalance or disease[19]. It demands a careful assessment of external factors, such as place, time, and season, as well as internal factors, such as age, metabolic capacity, and mental state, to understand an individual's unique homeostatic state and any disruptions. Modern personalised genomic medicine approaches, which also seek to predict phenotypic outcomes by integrating cellular, multi- scalar genetic, physiological and environmental networks, are mirrored in this paradigm[5].

According to Ayurveda, the *Tridosha* are distinguishable physiological entities that are present in all systems, coordinate with one another, interact with the external environment and preserve equilibrium. Current research is actively investigating molecular correlates for these Doshas[5,8]. On the other hand, *Prakriti*, the Ayurvedic concept of an individual's unique constitution, is believed to have a genetic connotation and is often linked to the genotype, representing the innate, fixed genetic make-up[20]. Based on observable physical, mental and emotional traits, Ayurveda has classified people into different *Prakritis* (constitutional types). Ayurveda's seven *Prakriti* group classification and detailed phenotyping can provide "phenotype scaffolds", which can assist in identifying and assembling physiologically related variations[8]. To further support these conceptual alignments, the following sections present some of the studies aimed to provide scientific basis of Ayurveda's fundamental principles—covering evidence-based *Prakriti* classification, Ayurvedic physiology and systems mapping, pharmacology of Ayurvedic formulations, and epigenetic correlates.

4.1. Evidence Based *Prakriti* classification

Modern biological research is gradually providing scientific confirmation for the Ayurvedic idea of *Prakriti*, which is a fundamental component of personalised therapy. Current scientific studies have confirmed that the Ayurvedic idea of *Prakriti* has a genetic basis, although more evidence across different *Prakriti* is required. A specific *Prakriti* type is associated with genetic polymorphisms. For instance, scientists have found a link between *Pitta Prakriti* and the phosphoglucomutase 1 (PGM1) gene which codes for a key enzyme involved in the metabolism of carbohydrate[8,21,22]. Studies on the polymorphism of the human leukocyte antigen (HLA) gene have demonstrated plausible associations between Ayurvedic *Prakriti* types and specific HLA-DRB1 (major histocompatibility complex, class II, DR beta 1) alleles[23]. These discoveries offer molecular proof of the innate, stable genetic composition that determines a person's *Prakriti* [8,21,24]. An important oxygen sensor, the EGLN1 **(**Egl-9 Family Hypoxia-Inducible Factor 1) gene (also called PHD2), is a striking illustration of a biological correlate for *Prakriti*[25]. This gene is associated with high-altitude adaptation and varies among *Prakriti* types[5]. EGLN1 may be a molecular counterpart of *Tridosha* because of its ubiquitous roles, rhythmic nature, responsiveness to stimuli, and auto-feedback loop, which are traits associated with *Doshas* such as *Kapha*, that governs stability and structure[25]. The immunophenotyping of people categorised according to their dominant *Dosha Prakriti* were studied. Significant variations in the expression of CD markers, including CD14 (monocytes), CD25 (activated B cells), and CD56 (natural killer cells), were found in a pilot study assessing lymphocyte subset CD markers in healthy people classified into *Kapha*, *Pitta*, and *Vata Prakriti* groups[26]. In particular, *Kapha Prakriti* samples showed much higher expression of CD25 and CD56, which is consistent with Ayurvedic literature and may indicate a superiorimmunological response in people with this constitution[26]. According to studies on healthy subjects, individuals with *Vata-Pitta Prakriti* have the highest ADP-induced platelet aggregation potential compared to other types[19]. Additionally, these patients reacted better to lower aspirin dosages, indicating that determining *Prakriti* could aid in predicting illness proneness or customising treatment[19]. It also suggests a possible connection between physiological reactions related to cardiovascular health and constitutional type.

4.2 Ayurvedic concept of Physiology (*Kriya Sharira*)

The Ayurvedic concept of *Kriya Sharia* (physiology) describes the functional aspects of the body, mind, and senses, with the seven *Dhatus* (fundamental structural component of the body that support and nourish the entire body namely *Rasa*, *Rakta*, *Mamsa*, *Meda*, *Asthi*, *Majja*, and *Shukra*) considered the sustaining pillars that ensure vitality, nourishment, and structural integrity. Ayurveda presents intricate principles for the nourishment and rejuvenation of these tissues[27,28]. *Agni* (digestive process/transformative metabolism) modulates the metabolic input received by each *Dhatu* under the influence of *Tridoshas*. These models connect modern concepts in microcirculation and biochemistry with Ayurvedic tissue dynamics. The *Tridosha – Dhatu -Mala* interrelationship and *Dosha* equilibrium guarantees appropriate tissue (*Dhatu*) feeding and waste removal (*Mala*), which is comparable to systemic metabolic flux[29,30].

At the cellular and organ level, *Doshas* function as systemic and informational mediators[31]. Similar to mechanical and neurological signalling, *Vata* transmits motility (*Gati*) and impulses between the cells, tissues and organ systems serving as a physiological messenger (E.g. Gut- Brain axis)[31,32]. *Kapha* aids in barrier function, inter-tissue lubrication, and structural stability (*Sakthi*), thereby supporting

immunological signalling networks, ECM (extra cellular matrix) regulation and structural cohesiveness[29,33]. At the cellular and inter-organ level, through hormonal mediators and enzymatic cascades, *Pitta* mediates communication and metabolic transformation (*Parinama*)[29,33]. These modalities are in line with novel ideas of endocrine or paracrine signalling and metabolite mediated intercellular communications. Modern metabolomic analyses determine *Prakriti*-specific pathways such as oxidative stress and neurotransmitter pathways in *Vata* types, androgen/xenobiotic metabolism in *Pitta*, and sphingolipid, aromatic amino acid metabolism in *Kapha*[31,33]. *Tridosha* is viewed as a functional network, similar to systems biology, with nodes that indicate properties (*Guna*) such as temperature and viscosity connected both within and between *doshas* to control organismal dynamics[34]. These network characteristics offer a framework for matching emergent system- level physiological behaviour to traditional *dosha* descriptions.

Analysis of organ system and *Dosha* mapping from extensive Ayurvedic telemedicine datasets (including around 287K chronic patients) revealed a clear dosha preponderance by organ system[35,36]. In the neurological and skeletal systems, *Vata*-dominant diseases were most prevalent. *Pitta* dominated skin conditions. In respiratory and endocrine disorders, *Kapha* was highest. Mixed *Vata–Pitta* dominance was seen in digestive disorders[35,36]. Specific organ relationships are also described in classical Ayurvedic books. For instance, the liver, spleen, skin, and eyes are associated with *Pitta*, while joints, nerves, and bones are more frequently associated with *Vata*, and adipose tissue or the respiratory mucosa with *Kapha*. Pharmacometabolomic analyses, including NMR-based studies, identified several biochemical signatures linked to therapeutic benefit and safety profiles of Ayurvedic medicines[37]. Network pharmacology of thousands of phytochemicals demonstrated multi-target interactions aligned with dosha-related metabolic and signalling pathways, including CYP (Cytochrome P450) modulation, neurotransmission, and inflammation[38]. Herb action is further aligned with *dosha* domains through research on neuromodulatory phytochemicals that are connected with signalling pathways related to G protein, acetylcholine, and chemokines (E.g. *Pitta* transformation, *Vata* neuromodulation)[38].

4.3 Ayurveda Pharmacology

Ayurveda, with its pharmacological foundation in *Dravyaguna Vijnana*, has emphasised the systemic, multi-dimensional effects of natural substances and their formulations. The therapeutic potential of Ayurvedic drugs, is described through concepts such as *Rasa* (primary sensory perception linked to therapeutic action; reflects elemental composition influencing physiological effects), *Guna* (intrinsic physical attributes determining the mode and magnitude of action), *Veerya* (innate strength or energy responsible for the onset and intensity of action), *Vipaka* (transformation and effect of a substance after metabolism) and *Prabhava* (distinct, unexplainable effect beyond general attributes) and is not attributed to individual molecules. These principles determine how substances interact with *Doshas*, *Dhatus* and *Srotas* (microchannels)[30] and have an impact on dosage, therapeutic application and metabolic fate. Ayurvedic pharmacology applies these concepts to the understanding of absorption, distribution, metabolism and excretion (ADME) of drugs. Advances in omics and computational biology are clarifying these multitargeted actions, validating the holistic principles of Ayurveda in modern scientific terms.

Recent studies, aided by advanced analytical and computational methods, begin to unravel the mechanisms underlying Ayurvedic remedies. Studies have shown that polyherbal formulations and bioavailability-enhancing techniques can exert synergistic effects on multiple pathways simultaneously, thereby supporting healing, metabolic regulation, stress reduction and rejuvenation. Representative evidence from selected herbs and formulations is summarised in Table 1.

Table 1 Pharmacological evidence of certain Ayurvedic herbs and formulations

Ayurvedic medicines	Pharmacological effects	Key mechanisms/ Biomarkers
Brahmi - (*Bacopa monnieri*)	Neuroprotective, enhances cognition	Antioxidant activity, increased acetylcholine[39]

Tulsi [Ocimum Sanctum]	Cardioprotective, reduces stress, improves lipid profile, lowers blood pressure	Antioxidant activity, reduced cortisol levels[4]
Amalaki Rasayana	Cardioprotective, Reduces LVH (left ventricular hypertrophy), enhances exercise tolerance	Upregulated SERCA2, Myh11, CaM, autophagy markers, antioxidants, TCA cycle proteins, oxidative phosphorylation components in cardiac tissues, increased ADRB1/2, pCREB expression, decreased pAMPK and NF-κB[41].
Jasad Bhasma	Safe at therapeutic doses, immunomodulatory (TH1 response), no hepato-renal toxicity	Final Bhasma: zinc oxide; intermediate: zinc sulphide; affects platelet turnover, antioxidant status[42]
Abhraka Bhasma	Non-genotoxic, enhances DNA repair, antioxidant defence	Protects against EMS (Ethyl methanesulfonate)-induced chromosomal damage, increased DNA base excision repair repair[43].

These multitarget pharmacological actions resonate with the principles of New Biology, which conceptualises health and disease as emergent properties of dynamic and interconnected networks. By integrating Ayurvedic concepts with omics technologies—genomics, metabolomics and pharmacometabolomic, researchers are uncovering *Prakriti*-specific molecular signatures and drug responses[4,33,35].

4.5 Ayurveda and Epigenetics

Ayurvedic philosophy posits that harmful actions disrupt equilibrium (*Vikriti*) and lead to disease, while beneficial practices maintain the constitution (*Deha Prakriti*)[7,44]. This principle has a molecular parallel in epigenetics, where external influences, such as diet, stress and environment, induce chromatin modifications, including DNA methylation and histone modification, which ably alter expression and phenotype without altering the DNA sequence[9,45]. In this sense, the Ayurvedic notion of *Karma* (action) resonates with the idea that environmental inputs shape gene regulation and health outcomes[7].

A critical mediator linking environment, diet, and gene regulation is the gut microbiome. Contemporary research suggests that dietary components and microbial metabolites have a significant impact on the host's epigenetic state. Within this perspective, *Agni* (digestive fire) and *Ama* (metabolic toxins from impaired digestion) can be understood as macroscopic correlates of metabolic homeostasis or dysregulation, both of which are targets of microbiome – epigenome interactions[8].

Several recent landmark studies demonstrated these connections with the existing reductionist approach. By controlling DNA methylation and histone modifications, nutrients and bioactive food ingredients alter gene expression associated with ageing, cancer, metabolic disorders, and inflammation[46]. These findings established the field of Nutritional epigenetics. Direct evidence that early environmental exposures impact disease risk in later life was provided by the Dutch famine studies, which showed that prenatal starvation caused permanent epigenetic changes, including hypomethylation of the IGF2 gene, detectable in adult offspring decades later[47]. Further studies demonstrated that cellular metabolic fluxes, including glucose metabolism, influence epigenetic regulation, thereby linking the metabolic state to gene expression and disease risk[48]. Collectively, these studies illustrate the paradigm shift in biomedicine from a strictly genetic framework to one recognising dynamic, environment-sensitive epigenetic control—a perspective embedded in Ayurvedic theory of *Pathya-Apathya*.

Ayurvedic dietary prescriptions exemplify this convergence. Diets recommended for conditions such as Type 2 Diabetes emphasise fibres and polyphenols, which have been shown to enrich butyrate-producing bacterial populations and suppress lipopolysaccharide-producing species[49]. Such microbial remodelling generates metabolites that influence host epigenetic programming and metabolic pathways. Thus, personalised Ayurvedic diets not only support host physiology but also actively shape the microbial

ecosystem, which in turn modulates gene expression.

5. Ayurveda Biology: Scientific prospects

The new area of Ayurveda Biology, which has emerged in recent years, has prompted a fully integrated scientific framework that connects traditional Ayurvedic insights with contemporary biological technologies. It seeks to promote a scientific knowledge of Ayurvedic concepts and diagnostic and therapeutic claims[50]. This transdisciplinary approach serves as a link between the fundamental ideas of Ayurveda and the rapidly advancing modern sciences, aiming to reinterpret ancient principles through quantifiable parameters that promote individualised treatment techniques[51,52].

Experimental models have demonstrated the genotoxicity profile, immunomodulatory actions, DNA repair potential, pharmacodynamics, and safety of Ayurvedic drugs[53,54]. Meanwhile, computational tools such as molecular docking, molecular dynamics simulation and network pharmacology have mapped phytochemical–target interactions in formulations like *Medhya Rasayana*, *Triphala*, and *Guduchi*[55–57]. Clinical trials aligned with WHO protocols remain critical for validating efficacy in conditions such as diabetes, asthma, neurodegeneration, and ageing[52,58,59]. The recent integration of AI, machine learning, and omics technologies and big data analysis has enabled predictive diagnostics, *Prakriti*-based models, and clinical decision-support systems[45,60]. Genomic studies from the ASIIA (A Science Initiative in Ayurveda) program identified 52 markers differentiating *Vata*, *Pitta*, and *Kapha* constitutions, with corroborating evidence from DNA methylation patterns[52]. Functional studies have reinforced these findings—for instance, *Amalaki Rasayana* extended lifespan and improved stress resilience and neuroprotection in *Drosophila*[52,61], while personalised Ayurvedic therapy yielded significant clinical benefits in asthma, including improved lung function, and reduced IgE, eosinophils, and Th2 cytokines[52,61].

Integrative models such as the "Sandwich Model," which aligns *Satkriyakala* (six-stage pathogenesis) concept of Ayurveda with systems biology and epigenetic regulation, provide dynamic perspectives on health and disease progression[62,63]. Together, these convergent approaches—spanning physiology, genetics, epigenetics, and phenotype—establish a scientifically grounded basis for predictive, preventive, and personalised medicine within modern biomedical discourse[64].

5.1 Novel Instruments, Methods and Models

Rapid advances in high-throughput omics technologies—genomics, transcriptomics, proteomics, and metabolomics—have transformed the way biology is studied, shifting the focus from isolated molecules to comprehensive, system-wide analyses[65]. Instead of analysing individual genes, genomics and transcriptomics now record global expression patterns and whole-genome variation, while proteomics allows for the mapping of entire proteome, including post-translational modifications and networks of protein-protein interactions crucial to cellular function. Similarly, metabolomics does not target individual metabolites but instead profiles complete metabolic signatures, offering real-time insights into physiological states. This transition from a reductionist, "gene-centric" model to a holistic network-level exploration parallels Ayurveda's systems perspective, which views health as an emergent property of balanced interactions among the *Doshas*, *Agni*, *Dhatus*, and environmental influences. Recent research demonstrates this convergence: HLA alleles, DNA methylation patterns, and gene expression profiles linked to immune regulation and metabolic pathways have been found to differ across individuals categorised by Ayurvedic *Prakriti* types based on genomic and transcriptome profiling[23,66,67]. Similarly, the Ayurvedic categorisation of constitutional types with quantifiable molecular correlates has been supported by metabolomic examinations of the *Vata*, *Pitta*, and *Kapha* groups, which have shown unique biochemical signatures in energy metabolism, amino acid profiles, and lipid metabolism regulation. Proteomic investigations further highlight *Prakriti* differences in plasma protein abundance, which are linked to oxidative stress, antioxidant defences, and inflammatory responses[66,68]. Together, these findings provide mechanistic support for the phenotypic and pathological variability described in classical texts.

Parallel to this, the modern Physiome Project aims to develop a "complete virtual physiological human," integrating molecular, cellular, and organ-level data into a 3D computational model. This multiscale, systems-based approach resonates with Ayurveda's holistic perspective, and *Prakriti* could serve as a

stratification tool for developing personalised virtual physiological models[69].

Ayurgenomics has emerged as a discipline to formalise these links. Early studies reported associations between *Prakriti* and single-nucleotide polymorphisms (SNPs) in genes involved in immunity, metabolism, and inflammation[35,70]. Recent microbiome research shows that distinct gut microbial communities correlate with *Prakriti* types—*Vata* individuals harbour more carbohydrate-fermenting microbes, *Pitta* types show taxa associated with fat metabolism, and *Kapha* types are enriched with microbes linked to energy conservation. These results demonstrated *Prakriti* as a biologically relevant indicator for microbiome research and a viable tool for personalised nutrition, consistent with the physiological traits indicated in Ayurveda[71].

Epigenomics adds another dimension, as lifestyle, diet, and stress—core elements of Ayurveda—are known to induce heritable epigenetic changes, potentially explaining its strong emphasis on preventive and personalised healthcare[72]. In parallel, metabolomic studies are being applied to *Rasayana* therapies, providing quantifiable evidence for their immunomodulatory, rejuvenative, and anti-ageing effects. Future research must expand to longitudinal and population-scale studies that combine multi-omics data with Ayurvedic phenotyping. Integrating genomics, transcriptomics, proteomics, metabolomics, and epigenomics with digital health tools and AI-based analytics will enable comprehensive mapping of *Prakriti*. Linking these datasets with the network pharmacology of herbal formulations may reveal synergistic pathways and novel therapeutic targets[73-75]. Such approaches will transform Ayurveda into a data-rich, evidence-based discipline, validating traditional principles while generating new insights for precision medicine.

5.2 Systems biology, Network Pharmacology and Computational Approaches

The emergence of systems biology, which combines genetic, cellular, physiological, and environmental connections to predict phenotypic outcomes, is equally significant. Systems biology sees organisms as integrated networks rather than separate components[76,77]. This holistic perspective parallels Ayurveda's view of health as a dynamic balance of *Doshas*. Living organisms display a hierarchical organisation marked by Functional Self-Similarity (FSS), whereby essential processes—such as growth, metabolism, reproduction, and responsiveness—are preserved across scales from cells to entire organisms.

Expanding beyond traditional model organisms such as yeast or *Drosophila*, advances in genome sequencing, transcriptomics, and CRISPR-based gene editing now enable the use of diverse species to explore gene functions, regulatory networks, and protein interactions[78,79]. Such advances provide a foundation for an Ayurveda-inspired biology that can reframe classical concepts in terms of molecular and systems biology. Current projects, including the development of computational and mathematical biology platforms dedicated to Ayurveda, demonstrate how these technologies can mimic biological processes and predict the therapeutic outcomes of conventional therapies[80]. It is both clinically relevant and scientifically rigorous.

The polyherbal formulations, or *yogas*, which act through synergistic interactions among multiple ingredients to maximise efficacy, reduce side effects, and target multiple physiological pathways simultaneously, are the central norm in Ayurveda. This multi-target pharmacological approach is in line with the emerging field of network pharmacology, which aims to elucidate drug action by examining complex biological networks rather than the traditional "one drug– one target–one disease" model[81].

The network pharmacology framework can decode the therapeutic logic of Ayurveda by integrating data from genomics, proteomics, metabolomics, and interactomics. This model maps the relationship between bioactive compounds, molecular targets and disease pathways. It allows the construction of drug–target–pathway–disease networks that mirror the Ayurvedic understanding of health and disease. The multi-target modulation of pathways linked to oxidative stress, inflammation, immune regulation, and neuroprotection can thus be demonstrated computationally using network pharmacology. Similarly, pharmacogenomics and network-based stratification methods that explain individual differences in medication responses align with the Ayurvedic idea of *Prakriti*, which supports customised treatment plans[82].

Several studies illustrate this convergence. Active phytoconstituents (such as withanolides) that target signalling pathways linked to stress response, neuroprotection, and cancer regulation were identified through network pharmacology on the *Rasayana* drug *Withania somnifera* (*Ashwagandha*)[83,84]. According

to the docking data, *Tinospora cordifolia* (*Guduchi*) metabolites may interact with β-amyloid precursor protein cleaving enzyme 1 (BACE1) and Monoamine Oxidase B (MAO-B), two important targets for Alzheimer's disease, indicating a potential neuroprotective function[85]. Computational analyses of *Triphala* have demonstrated effects on gut microbiota, antioxidant defence, and anticancer pathways via modulation of the p53 (tumor suppressor protein encoded by the tumor protein 53 gene) and apoptosis signalling pathways[86,87]. More recently, network pharmacology studies on *Chandraprabha Vati* and *Chandanasava* identified bioactive molecules–target–pathway interactions underlying their therapeutic effects[88,89]. These results validate Ayurvedic principles such as synergistic action (*Samsarga*) multi-target effects of polyherbal formulations and the modulatory role of adjuvants (*Anupana*). Recent studies have also explored the potential of *Clitoria ternatea* (*Aparajita*) phytochemicals as inhibitors of snake venom phospholipase A_2 (PLA_2); in silico screening identified key bioactive compounds that can bind to the active sites of PLA_2[90]. This aligns with Ayurveda's comprehensive view of health, which emphasizes the use of natural substances for healing and protection.

Studies have been conducted to understand the antidiabetic and multitarget effects of formulations by analysing its components (*Gymnema sylvestre*, *Pterocarpus marsupium and Asphaltum punjabinum*) and their protein targets[91,92]. Similarly, molecular targets for well- known herbs such as *Curcuma longa* (*Haridra*) and *Withania somnifera* (*Ashwagandha*) have been linked to inflammatory cytokines, oxidative stress markers, and apoptotic regulators[93-95]. In addition, the mechanisms of action of Ayurvedic formulations, such as Ayush-64, and single herbs, such as *Glycyrrhiza glabra* (*Yastimadhu*), have been explored for complex diseases, notably during the COVID-19 pandemic, through their interactions with SARS-CoV-2 targets and associated host pathways[96,97]. Further, phytomolecules such as ginsenoside, glycyrrhizic acid, and hesperidin have been screened against viral proteins (main protease, spike-RBD) to identify potential lead compounds[98]. These findings underscore how Ayurveda's traditional pharmacopoeia can contribute to modern antiviral discovery when viewed through computational and systems biology frameworks. However experimental validation and clinical evaluation of these predictions are required.

Modern computational tools expand these insights by enabling molecular docking, molecular dynamics simulations, and ADMET (Absorption, Distribution, Metabolism, Excretion, and Toxicity) profiling. These approaches are now used to predict multi-target effects, optimise binding affinities, and assess pharmacokinetic/toxicity profiles, thereby accelerating the identification of safe, bioavailable lead compounds from Ayurvedic plants for clinical development. In parallel, bioinformatics-driven databases and Ayur-informatics platforms have emerged to systematically screen phytochemicals, assess multitargeting potential, and build computational pipelines specific to Ayurvedic formulations[99]. AI/ML (Artificial Intelligence/Machine Learning) approaches add another dimension: *Prakriti* classification has been objectively achieved using artificial neural networks (ANN), support vector machines (SVM), and CatBoost, with reported accuracies as high as 0.96 [100,101]. Such models also enable the large-scale screening of phytoconstituents, target prediction, and the construction of interaction networks, providing evidence for therapeutic effects and accelerating lead discovery[101].

Several computational studies provide concrete examples. Docking investigations targeting BACE1 revealed Somniferine from *Withania somnifera* as a promising inhibitor, while retinoic acid showed strong binding to acetylcholinesterase (AChE)[55,56,102]. The possibility of integrating data from transcriptomic and proteomics, network pharmacology and moleculardocking studies to examine the therapeutic potential of polyherbal Ayurvedic formulations has also been reported. Transcriptome analysis identified differentially expressed genes in glioblastoma cells resistant to anti-angiogenic therapy. Molecular docking of phytochemicals from multiple plants of *Medhya Rasayana* identified multiple molecules docking against multiple differentially expressed targets. Integrating these results with network pharmacological analysis revealed that phytochemicals from *Medhya Rasayana* herbs, such as *Celastrus paniculatus*, *Evolvulus alsinoides*, and *Glycyrrhiza glabra*, can target proteins expressed by hub genes associated with glioblastoma resistance to anti-VEGF therapy, indicating their potential as adjuvants[103,104]. Analogously, research on the synergistic interactions of *Triphala churna* phytochemicals with different angiogenesis-related signalling proteins showed that punicalagin inhibits phosphoinositide 3-kinase (PI3K)/protein kinase B (Akt) signalling[105], while chebulagic acid suppresses both glycogen synthase

kinase 3-beta (GSK3-beta)-β-catenin and protein kinase B (Akt) signalling[105] contributing to inhibition of neovessel formation, a potential approach to reduce tumor growth. Together, these findings demonstrate how systems biology, network pharmacology, and computational methods— including AI/ML and bioinformatics—transform Ayurveda from an empirical system into a data-driven, quantifiable, and globally relevant scientific discipline.

6.Conclusion

The convergence of Ayurveda and New Biology reframes health and disease as emergent properties of dynamic, interconnected biological networks. Though arising from different eras and traditions, both share a conceptual alliance that can redefine medical approach. New Biology provides the tools and models to validate and operationalise these age-old principles, while Ayurveda offers a time-tested framework for understanding health as a dynamic balance. The core principles of Ayurveda—such as *the Panchamahabhoota*, *Tridosha*, and the concept of *Prakriti* — can be seen as practical phenotypic scaffolds that guide the complex, multiscaleanalysis required by systems biology. There is growing empirical evidence that certain *Prakriti* types are associated with particular metabolic signatures, immunological profiles, and genetic variants. The multi-target actions of Ayurvedic formulations, once described qualitatively, can now be decoded through computational approaches that reveal their synergistic effects on complex networks. Comparably, the emphasis on lifestyle modifications in Ayurveda offers a strong, non-pharmacological method of regulating microbiome and epigenetic health, addressing the underlying causes of chronic, multiple diseases—a significant drawback of the reductionist model. Together, Ayurveda and New Biology represent a paradigm shift toward systems-based, personalised, and preventive medicine. New biology could develop more precise and predictive models of human health by utilising Ayurveda's extensive collection of clinical observations and complex diagnostic classifications.

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