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Ayurveda-Based Gut Microbiome Modulation and AI-Guided Ayurvedic Pharmacomicrobiomics: An Integrative Review and Translational Framework

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Abstract

Background: The gut microbiome influences digestion, immune regulation, metabolism, intestinal barrier function, and the biotransformation of orally administered medicines. Pharmacomicrobiomics examines how interindividual variations in microbial composition and function affect drug metabolism, efficacy, and toxicity. Ayurveda offers a constitution-based framework involving *Prakriti*, *Agni*, *Koshtha*, *Satmya*, diet, lifestyle, and individualized pharmaceutical administration. These features provide a potential basis for integrating Ayurveda with microbiome science and artificial intelligence.

Objective: To review evidence concerning Ayurveda-based gut microbiome modulation and to propose an artificial intelligence-guided framework for Ayurvedic pharmacomicrobiomics.

Methods: A narrative review was conducted using classical Ayurvedic literature and contemporary publications concerning the human gut microbiome, pharmacomicrobiomics, Ayurvedic constitutional phenotyping, *Triphala*, dietary modulation, machine learning, microbiome research standards, and artificial intelligence governance.

Results: Diet can rapidly alter gut microbial composition, while microbial enzymes can activate, inactivate, or transform orally administered compounds. Human studies have identified associations between Ayurvedic *Prakriti* phenotypes and microbial signatures. A randomized pilot trial found that *Triphala* and *Manjistha* supplementation modified selected gut microbial features, while experimental studies indicate that *Triphala* constituents undergo microbial transformation and may influence microbial metabolites. However, available Ayurveda-specific evidence remains limited by small samples, heterogeneous interventions, short follow-up, and inadequate standardization. Artificial intelligence may support integration of constitutional data, dietary exposure, microbiome profiles, formulation chemistry, clinical response, and safety signals. Potential applications include response prediction, microbial metabolite mapping, formulation selection, adverse-effect surveillance, and personalized dietary co-interventions.

Conclusion: Ayurveda-based gut microbiome modulation is a promising but emerging research domain. AI-guided Ayurvedic pharmacomicrobiomics could provide a translational platform for studying how individualized host characteristics and gut microbial functions influence Ayurvedic medicines. Clinical implementation requires standardized formulations, high-quality multicentric datasets, prospective validation, transparent algorithms, ethical governance, and continued physician oversight.

Keywords: Ayurveda, Gut Microbiome, Pharmacomicrobiomics, Artificial Intelligence, Triphala, Prakriti, Agni, Personalized Medicine

Introduction

The human gastrointestinal tract contains a complex ecological community of bacteria, archaea, fungi, viruses, and their collective genetic and metabolic products. This microbial ecosystem contributes to nutrient metabolism, bile-acid transformation, vitamin production, immune development, intestinal barrier maintenance, and communication with distant organs. Diet, age, geography, medication, environment, disease, and host physiology shape microbiome composition and function. Dietary change can alter the gut microbiome within a short period, demonstrating that the microbial ecosystem is biologically dynamic rather than fixed.[2]

The gut microbiome also interacts with orally administered medicines. Microbial enzymes may activate prodrugs, deactivate therapeutic compounds, generate toxic metabolites, alter enterohepatic circulation, or compete with host metabolic pathways. The classical example of microbial drug inactivation involving digoxin and *Eggerthella lenta* demonstrated that the abundance and functional capacity of a particular intestinal organism can affect drug exposure.[3] Larger experimental studies have subsequently shown that many oral medicines can be chemically modified by gut bacteria and that microbial drug metabolism varies between individuals.[4–7]

The study of these interactions is termed **pharmacomicrobiomics**. It examines how variations in the microbiome influence drug pharmacokinetics, pharmacodynamics, efficacy, and toxicity, as well as how medicines reshape the microbiome.[4–7] This field extends personalized medicine beyond host genetics and recognizes the microbiome as an important determinant of therapeutic variability.

Ayurvedic treatment is intrinsically individualized. Selection of diet, formulation, dose, vehicle, timing, pharmaceutical processing, and purification procedures may depend on *Prakriti*, *Vikriti*, *Agni*, *Koshtha*, *Satmya*, *Bala*, age, season, locality, disease stage, and concurrent diet.[1] These variables are clinically relevant to digestion, intestinal transit, exposure of medicines to the gastrointestinal environment, and individual response.

This convergence creates a new research opportunity: **Ayurvedic pharmacomicrobiomics**, defined in this review as the study of how the gut microbiome modifies the disposition and effects of Ayurvedic medicines and how Ayurvedic medicines, diets, and procedures modify microbial composition and function. The addition of artificial intelligence may enable simultaneous analysis of complex host, microbial, pharmaceutical, dietary, and clinical datasets.

However, the field remains exploratory. Ayurvedic concepts must not be simplistically equated with individual microbial taxa or biomarkers. *Agni* is not synonymous with the microbiome, and *Ama* is not identical to dysbiosis or endotoxemia. These concepts arise from different epistemological systems. Their relationship should be investigated through carefully designed translational research rather than assumed equivalence.

Aim

To review the evidence concerning Ayurveda-based modulation of the gut microbiome and to propose an artificial intelligence-guided translational framework for Ayurvedic pharmacomicrobiomics.

Objectives

1. To examine the relationship between the gut microbiome and the metabolism of orally administered medicines.
2. To discuss Ayurvedic concepts relevant to digestion, individual variation, diet, and pharmaceutical response.
3. To review available evidence concerning *Prakriti*, Ayurvedic interventions, and gut microbiome modulation.
4. To describe potential applications of artificial intelligence in Ayurvedic pharmacomicrobiomics.
5. To identify methodological, ethical, pharmaceutical, and clinical requirements for future research.

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Materials and Methods

A narrative review methodology was adopted. Classical concepts related to digestion, diet, constitutional assessment, gastrointestinal function, and therapeutic individualization were examined from the *Charaka Samhita*. Contemporary literature was reviewed for evidence related to gut microbiome modulation, pharmacomicrobiomics, microbial drug metabolism, Ayurvedic constitutional phenotyping, *Triphala*, dietary intervention, machine learning, and research reporting standards.

Evidence was organized under five domains:

1. microbiome-mediated drug metabolism;
2. Ayurvedic concepts relevant to gastrointestinal individuality;
3. evidence concerning Ayurveda and microbiome modulation;
4. artificial intelligence applications;
5. research, safety, and governance requirements.

Because Ayurveda-specific microbiome studies remain limited and heterogeneous, the review presents a translational framework rather than a clinical guideline.

The Gut Microbiome as a Determinant of Therapeutic Response

Oral medicines encounter intestinal microorganisms before or during absorption. Gut bacteria may directly transform medicines through reduction, hydrolysis, decarboxylation, dehydroxylation, demethylation, and other enzymatic reactions. They may also influence treatment indirectly by altering bile acids, short-chain fatty acids, intestinal permeability, immune signalling, and host gene expression.[4–8]

The interaction is bidirectional. A medicine may alter microbial abundance or function, while the altered microbial community may subsequently change the medicine's metabolism. This creates a feedback loop between host, microbiome, and treatment.

Experimental mapping of 271 orally administered drugs against 76 gut bacterial strains demonstrated widespread microbial drug-transforming capacity.[5] Personalized ex vivo screening of human microbiome samples also showed substantial interindividual differences in the metabolism of therapeutic compounds.[6] These findings support the view that patients receiving identical doses may experience different exposure, efficacy, or toxicity because of differences in microbial function.

Herbal medicines present additional complexity. They contain multiple phytochemicals, many of which are poorly absorbed in their original form. Gut microorganisms can transform polyphenols, glycosides, tannins, alkaloids, and other compounds into metabolites with altered bioavailability or biological activity.[8] An Ayurvedic formulation may therefore function not only through its original ingredients but also through metabolites generated by microbial biotransformation.

The microbiome may also affect the activity of pharmaceutical excipients, fermentation products, lipid vehicles, and dietary co-administration. Consequently, evaluation of Ayurvedic medicines should consider the complete exposure context, including formulation, processing, dose, *Anupana*, meal timing, dietary pattern, bowel transit, prior antibiotics, and concurrent medication.

Ayurvedic Concepts Relevant to Microbiome Research

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Agni

Agni is a central Ayurvedic concept governing digestion, transformation, assimilation, and tissue metabolism. Balanced *Agni* supports appropriate digestion and nourishment, whereas impaired *Agni* contributes to abnormal processing and disease development.[1]

The microbiome participates in digestion and metabolism, but it represents only one component of the wider biological processes that may be examined under the broad Ayurvedic understanding of transformation. Therefore, the microbiome should not be presented as the sole biomedical equivalent of *Agni*.

Future research may investigate whether clinically assessed *Agni* states are associated with measurable differences in microbial diversity, functional pathways, stool metabolites, bowel transit, inflammatory markers, or treatment response.

Ama

Ama refers to improperly processed or incompletely transformed material arising in the context of impaired digestion and metabolism. It is described as heavy, obstructive, and pathogenic.[1]

Dysbiosis, increased intestinal permeability, endotoxin exposure, abnormal fermentation, and accumulation of microbial metabolites may provide relevant biomedical research domains, but none should be equated directly with *Ama*. The appropriate research question is whether clinical features attributed to *Ama* correlate with reproducible microbial and metabolic patterns.

Grahani and Gastrointestinal Regulation

Grahani is functionally associated with the retention, digestion, and appropriate release of ingested food. Disturbed gastrointestinal function is closely linked with impaired *Agni*.[1] Microbiome research may provide tools to examine intestinal transit, fermentation, barrier integrity, and microbial metabolism in patients with Ayurvedic patterns of gastrointestinal dysfunction.

Prakriti

Prakriti represents constitutional individuality and influences physiological tendencies, digestion, tolerance, disease susceptibility, and therapeutic planning.[1] Studies examining healthy individuals have identified differences in gut, oral, and skin microbial features across major *Prakriti* groups.[9,10]

These studies do not establish that individual microbial taxa define *Prakriti*. Microbiome composition is affected by diet, geography, age, and environment. Nevertheless, the findings support the possibility that constitution-based stratification may reduce biological heterogeneity in microbiome research.

Koshtha and Bowel Phenotype

Koshtha reflects the functional nature of the gastrointestinal tract, including bowel tendency and responsiveness to elimination therapies. Clinical categories such as *Mridu*, *Madhyama*, and *Krura Koshtha* may be relevant to intestinal transit time, stool consistency, microbial substrate exposure, and drug residence time.

A combined assessment of *Koshtha*, stool form, transit time, dietary fibre, microbial profile, and pharmacokinetic outcomes could generate a clinically meaningful research model.

Satmya, Ahara and Anupana

Satmya describes suitability or adaptation to substances and dietary practices. *Ahara* influences the gastrointestinal environment, and *Anupana* affects administration and therapeutic response.[1] Diet is one of the strongest modifiable determinants of microbial composition and function.[2]

The Ayurvedic practice of selecting food and vehicles according to constitution, digestion, disease, and season may therefore be investigated as a personalized microbiome-modulation strategy. Such studies should distinguish traditional rationale from experimentally demonstrated microbial effects.

Evidence Linking Prakriti and the Human Microbiome

An exploratory study of healthy individuals reported differential abundance of selected bacterial genera across Vata-, Pitta-, and Kapha-predominant participants in gut, oral, and skin samples.[9] The study was limited by its small sample size but provided early evidence that Ayurvedic phenotyping could be examined using microbiome methods.

A larger study involving 272 healthy individuals evaluated gut and oral microbiomes across predominant *Prakriti* groups. Although a core microbiome was shared, the investigators reported constitution-associated microbial signatures, including preferential representation of selected taxa in particular groups.[10]

These findings are biologically interesting but require cautious interpretation. *Prakriti* classification may be affected by observer variation, while microbial findings may reflect region, diet, household, socioeconomic status, or cultural habits. Cross-sectional associations cannot establish causality.

The scientific value of these studies lies in demonstrating that Ayurveda-based phenotyping can be incorporated into modern population research. Future work should use standardized *Prakriti* instruments, blinded assessment, multicentric recruitment, repeated sampling, dietary recording, metagenomics, metabolomics, and external replication.

Genomic and machine-learning studies have independently shown that extreme *Prakriti* phenotypes may be associated with biological and phenotypic patterns.[18,19] Integrating these data with microbiome profiles could support more comprehensive constitutional systems biology.

Evidence for Ayurveda-Based Gut Microbiome Modulation

Triphala

Triphala is a classical formulation comprising the fruits of *Amalaki* (*Phyllanthus emblica*), *Haritaki* (*Terminalia chebula*), and *Bibhitaki* (*Terminalia bellirica*). It contains tannins, polyphenols, gallic acid derivatives, and other compounds that may interact with intestinal microorganisms.[14]

A four-week, randomized, double-blind, placebo-controlled pilot trial evaluated supplementation with *Triphala*, *Manjistha*, or placebo in healthy adults. The study identified changes in selected microbial taxa and suggested that these formulations may modulate the human gut microbiota.[11] The trial was exploratory and was not designed to establish disease-specific clinical efficacy.

An experimental human faecal fermentation model evaluated *Triphala* extracts using microbiota from adults with obesity. The intervention produced detectable changes in the faecal metabolome, particularly pathways involving aromatic amino-acid metabolism, although major microbial compositional differences were not consistently

significant.[12] This illustrates an important principle: functional metabolic changes may occur even when taxonomic composition changes only modestly.

The effects of *Triphala* may depend on botanical identity, fruit ratio, extraction method, dose, formulation, host diet, baseline microbiome, and duration. Therefore, the generic term "*Triphala*" is insufficient for pharmacomicrobiomic research unless the tested product is pharmaceutically standardized.

Manjistha

Manjistha (*Rubia cordifolia*) was examined alongside *Triphala* in the randomized pilot trial.[11] Changes in selected microbial features were observed, but the limited sample and short duration prevent definitive conclusions. Its microbiome-related effects require further investigation with standardized extracts and clinical endpoints.

Ayurvedic Diet

Ayurvedic dietary practice emphasizes individual suitability, digestive capacity, meal timing, preparation, season, and disease state. Modern microbiome research confirms that diet can rapidly alter microbial structure and metabolism.[2]

Different individuals may respond differently to the same fibre or dietary substrate. Resistant-starch supplementation studies have demonstrated substantial person-to-person variability in microbial and metabolic response.[15] Structurally distinct fibres can also direct different short-chain fatty-acid outputs.[16] These findings support the need for personalized dietary intervention rather than universal assumptions about "microbiome-friendly" foods.

Ayurvedic constitution and digestive phenotype could potentially assist the stratification of such responses, but this hypothesis requires prospective testing.

Panchakarma Procedures

Reviews have discussed the potential microbiome effects of *Virechana*, *Basti*, diet restriction, oleation, and other Ayurvedic procedures.[13] However, high-quality clinical evidence is presently insufficient. These procedures combine dietary change, medicines, altered bowel transit, fasting, lipid exposure, and elimination. Any observed microbial change may therefore arise from multiple components.

Future studies should standardize the procedure, document all medicines and foods, collect pre-treatment and repeated post-treatment samples, monitor hydration and safety, and evaluate whether microbial changes correlate with clinical outcomes.

Dinacharya and Lifestyle

Sleep, physical activity, stress, meal timing, oral hygiene, and bowel habits may influence microbial ecology. Ayurvedic daily-regimen practices could be examined using longitudinal microbiome and metabolomic methods. Such research should avoid attributing benefits to tradition alone and should use appropriate comparison groups.

Proposed Definition of Ayurvedic Pharmacomicrobiomics

Ayurvedic pharmacomicrobiomics may be defined as:

> The study of bidirectional interactions among Ayurvedic medicines, diet, pharmaceutical processing, individual Ayurvedic phenotype, host biology, and the human microbiome, with the objective of

understanding variability in therapeutic response, safety, metabolism, and microbiome modulation.

This proposed field includes four major relationships:

1. microbial transformation of Ayurvedic ingredients;
2. modification of microbial ecology by Ayurvedic interventions;
3. influence of host phenotype and diet on these interactions;
4. prediction of therapeutic response and adverse effects.

It should be distinguished from general microbiome research because it explicitly includes Ayurvedic pharmaceutical and clinical variables such as *Prakriti*, *Agni*, *Koshtha*, *Satmya*, *Anupana*, *Kala*, and formulation processing.

Why Artificial Intelligence Is Relevant

Microbiome datasets are high-dimensional, sparse, compositional, and influenced by numerous confounders. Ayurvedic clinical datasets are similarly multidimensional and include qualitative, ordinal, narrative, and temporal variables. Conventional statistical methods remain essential, but machine learning may assist in identifying nonlinear interactions and complex response patterns.[20,21]

AI may integrate:

- demographic and clinical characteristics;
- *Prakriti* and *Vikriti* assessment;
- *Agni*, *Koshtha*, *Satmya*, and dietary history;
- metagenomic and metabolomic data;
- botanical and phytochemical profiles;
- formulation-processing parameters;
- dose, timing, and *Anupana*;
- concurrent medicines;
- clinical outcomes and adverse effects.

The output should support research and clinical interpretation rather than autonomous prescribing.

Potential AI Applications

Microbial Metabolite Prediction

Machine-learning models may link herbal phytochemicals with microbial genes, enzymes, and predicted metabolites. This could help identify which compounds require microbial transformation and which organisms are associated with activation or inactivation.

Predictions must be confirmed through culture systems, faecal incubation, metabolomics, and pharmacokinetic studies.

Response Stratification

Patients may be grouped according to baseline microbial function, constitution, diet, and clinical phenotype. Models could then estimate the probability of response to a standardized Ayurvedic formulation.

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Such models require external validation and must not be used clinically solely on the basis of retrospective associations.

Formulation Selection

AI may compare the phytochemical composition of formulations with microbial metabolic capacity and host characteristics. It could identify candidate formulations for further laboratory or clinical testing.

This approach may be especially useful when multiple formulations are traditionally indicated for the same disease but differ in ingredients, dose form, or pharmaceutical processing.

Dose and Timing Research

Microbial metabolism may vary according to dose, meal timing, bowel transit, and substrate availability. AI-assisted longitudinal models could examine how *Aushadha Sevana Kala*, *Anupana*, and food co-administration affect microbial transformation and clinical response.

Adverse-Effect and Herb–Drug Interaction Surveillance

Microbial metabolites may contribute to adverse effects or interactions between Ayurvedic and conventional medicines. AI can assist pharmacovigilance by analysing clinical records, laboratory trends, medication combinations, and microbiome-linked metabolic pathways.

Predicted interactions must be evaluated experimentally and should not replace established safety assessment.

Longitudinal Monitoring

Repeated stool samples, symptoms, diet logs, wearable data, and medication adherence can be integrated to assess temporal response. This is preferable to a single pre- and post-intervention sample because microbiomes fluctuate over time.

Knowledge Graph Development

A knowledge graph could connect:

- Ayurvedic drugs and formulations;
- botanical species and plant parts;
- phytochemicals;
- microbial enzymes;
- metabolites;
- host targets;
- *Dosha*, *Dhatu*, and *Srotas* indications;
- clinical outcomes;
- adverse reactions.

Every relationship should remain linked to an authenticated classical, pharmacopoeial, chemical, experimental, or clinical source.

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Proposed Translational Research Framework

Phase 1: Standardized Phenotyping

Participants should undergo standardized assessment of:

- *Prakriti*;
- *Vikriti*;
- *Agni*;
- *Koshtha*;
- *Satmya*;
- diet and meal timing;
- bowel habit;
- medication and antibiotic history;
- demographic and clinical variables.

Ayurvedic assessments should be performed by trained physicians using validated or consensus-based tools.

Phase 2: Pharmaceutical Characterization

The intervention should be documented for:

- authenticated botanical identity;
- plant part;
- ingredient ratio;
- manufacturing process;
- extraction method;
- dose form;
- chemical fingerprint;
- microbial contamination;
- stability;
- dose, *Anupana*, and administration time.

Without pharmaceutical standardization, microbiome findings cannot be reliably attributed to the tested formulation.

Phase 3: Baseline Microbiome and Metabolome

Baseline sampling should include stool collection using standardized methods. Depending on the study question, analysis may include:

- 16S rRNA gene sequencing;
- shotgun metagenomics;
- metatranscriptomics;
- targeted or untargeted metabolomics;
- short-chain fatty acids;
- bile acids;
- intestinal inflammatory markers.

Repeated baseline sampling may be necessary to estimate normal intraindividual variability.

Phase 4: Controlled Intervention

Randomized controlled trials should standardize diet where feasible or accurately record dietary intake. Concomitant medicines, probiotics, prebiotics, and antibiotics must be documented. Clinical outcomes should be prespecified.

Phase 5: AI Model Development

Data should be divided into training, validation, and independent testing sets. Feature selection must occur within the training process to avoid information leakage. Models should be compared with conventional statistical approaches.[20]

Phase 6: Explainability and Clinical Interpretation

Models should identify the variables contributing to predictions. Clinicians and microbiome scientists should assess whether the identified patterns are biologically and clinically plausible.

Phase 7: External and Prospective Validation

A model developed in one centre or region should be tested in independent populations. Prospective validation is essential before any clinical use.

Phase 8: Implementation Monitoring

If a validated tool is introduced, its effect on decisions, patient outcomes, equity, safety, and clinician workload should be monitored.

Methodological Requirements

Avoiding Taxonomic Overinterpretation

The presence or abundance of one bacterial genus should not be labelled universally beneficial or harmful. Microbial effects depend on strain, gene content, ecological context, substrate availability, and host status.

Functional Analysis

Functional pathways and microbial metabolites may be more informative than taxonomic abundance alone. Ayurvedic medicines may alter microbial metabolism without producing large compositional shifts.[12]

Controlling Confounders

Age, geography, diet, sex, household, socioeconomic conditions, stool consistency, transit time, medication, antibiotics, and sample handling can influence findings. Environmental factors may exert a substantial influence on microbiome composition.[28]

Compositional Data Analysis

Microbiome data are compositional and require appropriate statistical methods. Naive application of standard tests can generate misleading associations.

Avoiding Overfitting

Microbiome studies often contain many variables but relatively few participants. Complex AI models may memorize the training data rather than learn generalizable patterns. Transparent validation, calibration, and error analysis are essential.[20],[21]

Reporting Standards

Human microbiome studies should follow the STORMS reporting checklist.[23] Prediction models should follow TRIPOD+AI where applicable.[24] Detailed reporting of sampling, sequencing, preprocessing, missing data, model selection, and validation is necessary for reproducibility.

Pharmaceutical and Clinical Safety

Ayurvedic microbiome research must not assume that a microbiome-modulating effect is automatically beneficial. A change in microbial diversity or abundance does not establish clinical efficacy. Outcomes must include symptoms, validated clinical measures, laboratory markers, adverse events, and follow-up.

Herbo-mineral preparations require additional toxicological and quality evaluation. Microbiome metabolism may theoretically alter the chemical form or absorption of ingredients, but such effects cannot be inferred without direct evidence.

Patients receiving immunosuppressive therapy, chemotherapy, anticoagulants, transplant medicines, or drugs with a narrow therapeutic index require particular caution. Microbiome-based predictions must never substitute for established pharmacological monitoring.

Ethical and Governance Considerations

AI-guided microbiome systems may process sensitive health, genomic, dietary, cultural, and traditional-knowledge data. Ethical use requires:

- informed consent;
- privacy protection;
- secure data storage;
- controlled access;
- transparent data-sharing policies;
- protection against commercial misuse;
- representation of diverse populations;
- human oversight;
- clear accountability.

WHO guidance emphasizes responsible AI governance, evidence-informed use, protection of traditional knowledge, and cultural sensitivity in traditional medicine applications.[25–27]

Microbiome databases developed from indigenous or community-based practices should include appropriate attribution, benefit-sharing principles, and protection against unauthorized commercialization.

Potential Clinical Domains

Metabolic Disorders

Diet, microbial metabolites, bile acids, inflammation, and energy regulation contribute to obesity and metabolic disorders. *Triphala* and dietary interventions are plausible research candidates, but current evidence is insufficient for microbiome-based prescribing.[11,12]

Functional Gastrointestinal Disorders

Irritable bowel syndrome, constipation, and functional dyspepsia involve heterogeneous mechanisms. Stratification by *Agni*, *Koshtha*, bowel phenotype, diet, and microbial function may generate testable subgroups.

Inflammatory Conditions

Microbiome–immune interactions are relevant to inflammatory disease. Ayurvedic interventions with anti-inflammatory and dietary components may be examined, but clinical benefit must be demonstrated independently of microbial change.

Supportive Oncology

The microbiome can influence anticancer therapy response and toxicity. Any Ayurvedic intervention in oncology must be evaluated within supervised integrative care and should not interfere with established treatment.

Geriatric and Preventive Care

Aging is associated with changes in diet, medication burden, bowel function, and microbial ecology. Constitution-based diet and gentle Rasayana interventions may be investigated for effects on resilience and healthspan.

Discussion

Ayurveda-based microbiome research offers a valuable opportunity to connect individualized traditional medicine with contemporary systems biology. Ayurvedic assessment already considers digestive capacity, bowel phenotype, dietary suitability, constitutional variation, and pharmaceutical context. These variables are also relevant to microbial ecology and drug response.

The strongest direct evidence presently concerns exploratory associations between *Prakriti* and microbial profiles and limited studies of *Triphala* and *Manjistha*.[9–12] These findings support further research but do not establish routine microbiome-guided Ayurvedic treatment.

Pharmacomicrobiomics provides a scientifically appropriate framework because it focuses on therapeutic variability rather than merely identifying microbiome differences. Ayurvedic formulations contain numerous compounds that may be transformed by microbial enzymes. Conversely, the formulations may reshape microbial metabolism. The relationship is therefore bidirectional and potentially patient-specific.

Artificial intelligence may help manage the complexity of these interactions. It can combine clinical phenotype, microbial function, formulation chemistry, dietary exposure, and response data. However, AI cannot correct poor study design, unstandardized medicines, inaccurate phenotyping, or biased data. A sophisticated algorithm trained on unreliable data will produce unreliable conclusions.

The most responsible path is progressive translational research: standardized observational studies, mechanistic experiments, controlled clinical trials, validated prediction models, and supervised implementation. Ayurvedic physicians, microbiologists, pharmacologists, data scientists, statisticians, and ethicists should collaborate from the beginning.

Limitations

This is a narrative review and does not provide a quantitative meta-analysis. Ayurveda-specific microbiome evidence remains limited, and several proposed applications are conceptual. Associations between *Prakriti* and microbial profiles require independent replication. The long-term clinical significance of microbiome changes following Ayurvedic interventions is uncertain. AI-guided Ayurvedic pharmacomicrobiomics should therefore be regarded as a research framework rather than an established clinical service.

Conclusion

The gut microbiome influences the metabolism, bioavailability, efficacy, and toxicity of orally administered medicines. Ayurveda offers an individualized framework involving *Prakriti*, *Agni*, *Koshtha*, *Satmya*, diet, formulation, timing, and *Anupana*, all of which may be relevant to microbiome-mediated therapeutic variability.

Preliminary studies suggest associations between Ayurvedic constitutional phenotypes and microbiome patterns, while *Triphala* and *Manjistha* have demonstrated microbiome-related effects in early human and experimental research. The evidence is promising but insufficient for definitive clinical recommendations.

AI-guided Ayurvedic pharmacomicrobiomics may enable integration of constitutional assessment, microbial function, formulation chemistry, diet, and clinical outcomes. Its development requires standardized products, rigorous phenotyping, functional multi-omics, transparent algorithms, external validation, ethical governance, and physician supervision.

This emerging field should aim not merely to demonstrate that Ayurvedic interventions change the microbiome, but to determine whether specific microbial functions explain treatment response, improve safety, and support evidence-based personalization.

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