

Decoding gut microbiome diversity through *Prakriti*: Insights from an Ayurgenomics perspective: A narrative review

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Ayurveda classifies individuals into three major *Prakriti* types *Vata*, *Pitta*, and *Kapha* based on *Dosha* dominance at the time of conception. Ayurgenomics aims to integrate this traditional concept with molecular biology, offering a novel lens to explore individual variations in gut microbiome diversity. This narrative review followed a systematic search strategy across PubMed, Research Gate, and Google Scholar. Six relevant studies published between 2018 and 2025 were selected. These studies employed cross-sectional designs using 16S rRNA sequencing, metagenomic profiling, and predictive functional analysis to explore microbial patterns across *Prakriti* types. Distinct gut microbial profiles were associated with each *Prakriti*. *Vata* types showed enrichment of microbes involved in carbohydrate metabolism, *Pitta* types with oxidative stress and toxin degradation pathways, and *Kapha* types with lipid metabolism and obesity-linked functions. Key taxa like *Bacteroides*, *Prevotella*, and *Faecalibacterium* varied in abundance among groups. Some studies extended findings to oral and skin microbiota. Functional similarities with Korean Sasang types supported the broader relevance of constitution-based biology. The reviewed evidence indicates a strong association between *Prakriti* and microbial diversity, supporting Ayurveda's personalized health concepts. By linking constitutional types with gut microbial signatures, Ayurgenomics can guide targeted health strategies that are preventive, inclusive, and culturally grounded. These insights contribute toward promoting individualized, evidence-based interventions that enhance well-being and disease prevention. Further longitudinal and multi-layered studies are needed to validate these associations and explore clinical applications.

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