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Impact of Dietary Supplementation with Haritaki - *Terminalia chebula Retz.* (Combretaceae) and Amalaki - *Phyllanthus emblica L.* (Phyllanthaceae) on Human Gut Microbiota: A Comparative Study

Research Article

Yogita Chaudhari[1], Smita Kadu[1], Manojkumar Chaudhari[2*]

1. Department of Kriya Sharir, Dr. D. Y. Patil College of Ayurveda and Research Centre, Pune, Maharashtra, India.
2. Department of Samhita Siddhanta, Ashtang Ayurved Mahavidyalaya, Pune, Maharashtra, India.

Abstract

The gastrointestinal (GI) system plays a crucial role in systemic health, with gut microbiota influencing immunity, digestion, and metabolic functions. Ayurveda emphasises digestive health through botanicals like *Haritaki - Terminalia chebula Retz.* (Combretaceae) and *Amalaki - Phyllanthus emblica L.* (Phyllanthaceae), traditionally used to promote gut balance. This study aimed to evaluate the impact of *Haritaki* and *Amalaki* supplementation on gut microbiota composition in healthy elderly volunteers over an 8-week period. A randomised, open-labelled, controlled experimental study was conducted at Dr. D.Y. Patil College of Ayurved and Research Centre, Pune, involving 30 participants aged ≥ 60 years. Participants were assigned to two groups: Haritaki (Group A, n=15) and Amalaki (Group B, n=15), receiving 2 grams of the respective herbal powder twice daily with lukewarm water. Stool samples were analysed pre- and post-intervention using 16S metagenomic sequencing to assess microbial diversity and composition. Results demonstrated distinct microbial shifts. Haritaki reduced Firmicutes and Bacteroidetes while increasing Actinobacteria, enhancing microbial stability and immune modulation. Conversely, Amalaki increased Bacteroidetes and fibre-fermenting genera while reducing Firmicutes, promoting microbial diversity and metabolic balance. Both interventions optimised short-chain fatty acid (SCFA) production without inducing dysbiosis. These findings support the Ayurveda's use of Haritaki and Amalaki in gut health, revealing their potential as microbiome modulators. Future studies should explore their long-term clinical applications and molecular mechanisms using functional metagenomics and metabolomics.

Keywords: *Ayurveda, Terminalia chebula, Emblica officinalis,* Microbiota, Gut microbiota, Prebiotic, *Haritaki, Amalaki.*

Introduction

Hippocrates said as early as 400 B.C. that "death sits within the bowels" and "bad digestion is the root of all evil" (1), demonstrating the longstanding importance of the gastrointestinal (GI) system in both health and illness. This demonstrates the long-standing understanding of the significance of gut health for general wellbeing. Understanding how intestinal microorganisms, such as gastrointestinal pathogens and the larger gut microbiota, affect systemic health and disease has become more important in recent years (2).

A different viewpoint on the importance of digestive health can be found in Ayurvedic teachings. In *Kalpa Sthana*, Dalhana explains the relationship between *Majjadhara Kala*, which is connected to marrow and immunity, and *Pittadhara Kala*, which is connected to bile and digestion (3). The *Grahani* (small intestine) is identified as the principal site of *Pittadhara Kala* according to the concepts of *Dhatuposhana Nyaya* (sequential nutrition of tissues), whereas the *Asthi* (bone tissue) is identified as the site of *Majjadhara Kala*. Furthermore, Ayurveda acknowledges that the liver, spleen, and tiny bones are the sites of *Rakta* (blood tissue) development, with Pitta emerging as a by-product. This suggests an integrated perspective of immunological and digestive processes (4).

Current studies support the complex relationship between immunity and intestinal health. Fermenting undigested food, generating nutrients, preserving immunological homeostasis, and avoiding pathogenic colonisation are all critical functions of the gut microbiota (5). But changes in microbial makeup brought on by aging, diarrhoea, or other conditions might affect systemic health and gut function (6).

A growing field of study is the gut-brain axis, a network of two-way communication that includes the immune system, neurotransmitters, short-chain fatty acids (SCFAs), vagus nerve, and others. This axis highlights the influence of gut bacteria on mental and neurological well-being (7).

Amalaki - Phyllanthus emblica L. (Phyllanthaceae) and *Haritaki - Terminalia chebula Retz.* (Combretaceae) are two Ayurvedic herbs that are well known for their restorative and digestive qualities. These herbs may improve gut barrier integrity, reduce

*** Corresponding Author:**
Manojkumar Chaudhari
Department of Samhita Siddhanta,
Ashtang Ayurved Mahavidyalaya, Pune,
Maharashtra, India.
Email Id: manojsamhita@gmail.com

inflammation, and restore microbial diversity, according to preliminary study (8,9). Systematic research on their impact on gut microbiota and the gut-brain axis is still lacking, despite their encouraging potential(10).

In light of aging-related alterations in gut microbial composition and GI function, this study examines the effects of Amalaki and Haritaki on faecal microbiota. Results may support their usage as dietary supplements to support general health and microbiological health.

Aim and Objectives

The study aimed to investigate the impact of *Haritaki - Terminalia chebula Retz.* (Combretaceae) and *Amalaki - Phyllanthus emblica L.* (Phyllanthaceae) on the gut microbiota of healthy volunteers, focusing on gut microbiome profiles during an 8-week supplementation period. It specifically sought to evaluate the effect of Haritaki and Amalaki on gut microbiota through stool analysis.

Materials and Methods

Study Design: The study was a randomised, open-labelled, controlled, experimental study that aimed to evaluate the effects of *Haritaki - Terminalia chebula Retz.* (Combretaceae) and *Amalaki - Phyllanthus emblica L.* (Phyllanthaceae) on gut microbiota in elderly volunteers.

Study Population

- **Location:** The study was conducted in the Pune Municipal Corporation and Pimpri-Chinchwad Municipal Corporation areas.
- **Study Site:** Dr. D.Y. Patil College of Ayurved and Research Centre, Pune
- **Source of Participants:** Participants were recruited from the Outpatient Department (OPD) and senior citizen groups who met the inclusion criteria.
- **Sample Size:** A total of 30 participants aged ≥ 60 years were enrolled and randomly allocated into two groups:
  - Group A: 15 participants received Haritaki churna.
  - Group B: 15 participants received Amalaki churna.
- **Sampling Technique:** Participants were selected using a random lottery method to ensure unbiased allocation.

Intervention

- Group A: Participants were administered *Survari Haritaki churna* (2 grams) orally twice daily with lukewarm water.
- Group B: Participants were administered *Amalaki churna* (2 grams) orally twice daily with lukewarm water.

Timing of Doses

- Morning dose: Administered on an empty stomach.
- Night dose: Administered at bedtime.

Duration

- The intervention lasted for 8 weeks.

Inclusion Criteria

Volunteers who were willing to comply with the protocol and had provided informed consent were included in the study. The participants were individuals' aged 60 years or older, irrespective of gender, caste, religion, or socio-economic background.

Exclusion Criteria

Individuals who had used prebiotic or probiotic drugs, antimicrobial or steroidal drugs in the previous three months, or had travelled internationally during this period were excluded from the study. Participants diagnosed with Alzheimer's disease, other neurodegenerative diseases such as Parkinson's disease, diabetes mellitus, or medical conditions affecting immune status, including rheumatoid arthritis and heart failure, were also not included. Additionally, individuals who were unwilling to provide consent or unable to comply with the protocol were excluded from participation.

Withdrawal Criteria

Participants were withdrawn from the study if they were unwilling to continue participation in the present study.

Criteria for Assessment

Participants were evaluated before and after the intervention using stool examinations to analyse gut microbiota.

Study Procedure

Participants provided informed consent and completed the case report form (CRF) before being randomly allocated into two groups (A and B). Stool samples and questionnaires were collected at baseline and after eight weeks. The collected data were then analysed, and statistical observations were drawn. Finally, conclusions were formulated based on the results.

Drug Authentication: The drugs were authenticated by a recognised affiliated laboratory.

Duration of Study:

- Total study duration: 2 years.
- Intervention period: 8 weeks.

Bioinformatic Analysis:

The analysis was carried out at a Government-recognised laboratory.

16S Metagenomics: This approach sequenced hypervariable regions of 16S rRNA (e.g., V3, V4, V3-V4) to identify microbial populations by comparing sequences to a reference genome database.

Analysis Pipeline (Figure 1)

Quality trimming was performed by removing low-quality reads (< Q30). Target amplicons for 16S rDNA detection were filtered using conserved regions. Dereplication and chimera removal were conducted by eliminating duplicate sequences and PCR-generated

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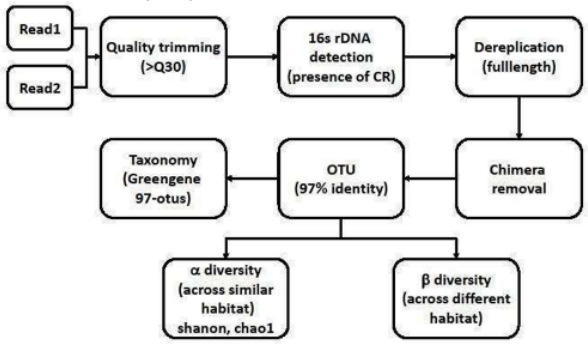
chimeras using the *uchime* algorithm. OTU picking was carried out by grouping sequences with ≥ 97% similarity while excluding artefacts. Taxonomy classification was performed by comparing OTUs against the Green Genes database at 97% similarity across taxonomic levels. Finally, α-diversity (Shannon, Chao1) and β-diversity (weighted/unweighted UniFrac) were measured to assess within-sample diversity and differences between habitats.

Figure 1. Bioinformatics Analysis Pipeline



Observations and Results

The study's results are summarised in the tables below, highlighting the effects of *Haritaki* - *Terminalia chebula Retz.* (Combretaceae) and *Amalaki* - *Phyllanthus emblica L.* (Phyllanthaceae) on gut microbiota profiles over the 8-week supplementation period.

***Haritaki*:**

Table 1: Comparative Analysis of Microbial Phyla Pre- and Post-Intervention

Phylum	Pre Test	Post Test
Firmicutes	106107	58263
Bacteriodetes	76306	37008
Actinobacteria	22772	28505
Unclassified from Bacteria	6294	1463
Proteobacteria	636	715
Aquificae	12	1
Streptophyta	8	1
Tenericutes	7	1
Cynobacteria	6	1
Fusobacteria	3	421

Comparative Analysis of Microbial Phyla Pre- and Post-Intervention - Haritaki reduced dominant phyla Firmicutes and Bacteroidetes while increasing beneficial Actinobacteria, promoting anti-inflammatory properties. A decline in unclassified bacteria improved stability, with minimal change in Proteobacteria indicating no inflammatory disruption. The rise in Fusobacteria requires further study for long-term implications.

Table 2: Comparative Analysis of Microbial of Microbial Classes Pre- and Post-Intervention

Class	Pre Test	Post Test
Bacteroidia	76021	36949
Clostridia	44850	14202
Negativicutes	31784	27478
Actinobacteria	22772	28505
Bacilli	18529	12626
Un from Bacteria	6294	1463
Erysipelotrichi	1637	231
Gammaproteobacteria	519	684
Flavobacteria	25	5
Betaproteobacteria	16	21
Aquificae	12	1
Epsinoproteobacteria	11	2

Haritaki reduced Bacteroidia, Clostridia, and Erysipelotrichi, indicating anti-inflammatory effects, while increasing Actinobacteria for gut integrity. Modest changes in Proteobacteria classes maintained balance, and unclassified taxa declined, enhancing microbial stability.

Table 3: Comparative Analysis of Microbial Orders Pre- and Post-Intervention

Order	Pre test	Post test
Bacteroidales	76201	36949
Clostridiales	44801	14175
Selenomonadales	31784	27478
Bifidobacterials	18272	21749
Lactobacillales	15223	9881
unclassified (derived from Bacteria)	6294	1463
Coriobacterials	2196	2244
Bacillales	1867	1567
Erysipelotrichales	1637	231
Actinomycetales	1068	3603
Enterobacteriales	427	236
Flavobacteriales	24	5
Pseudomonadales	18	417

Haritaki reduced orders like Bacteroidales and Clostridiales while increasing Actinomycetales and Bifidobacteriales, reflecting prebiotic-like effects. Minor taxa diversity declined, indicating stabilization, while Fusobacteriales increased, suggesting adaptive shifts.

Table 4: Comparative Analysis of Microbial Family Pre- and Post-Intervention

Family	Pre test	Post test
Prevotellaceae	40403	18681
Veillonellaceae	30609	27453
Bacteroidaceae	26446	14419
Bifidobacteriaceae	18272	21749
Lactobacillaceae	14036	7733
Unclassified (derived from Bacteria)	6294	1463
Ruminococcaceae	5100	467
Coriobacteriaceae	2196	2444
Clostridiaceae	1728	484

Erysipelotrichaceae	1637	231
Bacillaceae	1578	1311
Lachnospiraceae	1304	238
Micrococcaceae	601	2010
Eubacteriaceae	437	92
Enterobacteriaceae	427	236
Porphyromonadaceae	355	1564
Peptococcaceae	213	86
Enterococcaceae	179	226
Paenibacillaceae	82	53
Clostridiales Family XI. Incertae Sedis	61	30
Leuconostocaceae	58	252
Streptococcaceae	48	204
Streptomycetaceae	18	241
Pseudomonadaceae	17	417
Unclassified (derived from Bacillales)	4	150

Haritaki decreased Prevotellaceae, Veillonellaceae, and Lactobacillaceae, while increasing Bifidobacteriaceae (+19%) and Actinomycetaceae, enhancing immunity and balance. SCFA-producing families declined modestly, optimizing fermentation, while undetected minor families indicated streamlined stability.

Table 5: Comparative Analysis of Microbial Genus Pre- and Post-Intervention

Genus	Pre test	Post test
Prevotella	39951	18495
Bacteroides	26446	14419
Bifidobacterium	18155	21616
Megasphaera	16642	15036
Lactobacillus	13543	7507
unclassified (derived from Bacteria)	6294	1463
Clostridium	1486	410
Collinsella	959	1990
Bacillus	957	790
Dialister	938	918
Atopobium	709	309
Ruminococcus	609	45
Arthrobacter	514	106
Eubacterium	437	92
Faecalibacterium	430	35
Paraprevotella	420	180
Acidaminococcus	182	1
Enterococcus	177	226
Odoribacter	143	1
Selenomonas	124	82
Megamonas	75	20
unclassified (derived from Erysipelotrichaceae)	61	10
Parabacteroides	52	35
Cryptobacterium	45	29
Desulfitobacterium	45	42
Kocuria	42	42
Veillonella	42	481
Halobacillus	40	4
Paenibacillus	37	37
Streptococcus	37	198
Micrococcus	33	36
Brevibacillus	33	13
Weissella	18	246
Streptomyces	17	241
Pseudomonas	17	417
Enterorhabdus	15	26
Corynebacterium	12	52
Barnesiella	12	20
Escherichia	9	11
Unclassified (derived from Clostridiales Family XI. Incertae Sedis)	8	5
Capnocytophaga	7	4
Lactococcus	7	3
Porphyromonas	6	1499
Pantoea	6	93
Rothia	3	1761
Actinomyces	2	1018
Oribacterium	2	77
Leptotrichia	2	293

Haritaki reduced genera such as Prevotella and Lactobacillus, while increasing Bifidobacterium, Streptomyces, and Pseudomonas. SCFA-producers like Ruminococcus declined, optimizing fermentation, while minor genera loss indicated microbial stability.

***Amalaki*:**

Table 6: Comparative Analysis of Microbial Phyla Pre- and Post-Intervention

Phylum	Pre	Post
Firmicutes	73896	41662
Actinobacteria	44703	4841
Bacteroidates	30330	38745
Unclassified derived from bacteria	886	3705
Antrhopoda	10	6
Streptophyta	4	3
Chloroflexi	3	1
cynobacteria	3	1
Chlorphyta	3	1
cynobacteria	3	1

Amalaki reduced Firmicutes and Actinobacteria while increasing Bacteroidetes, enhancing diversity and metabolic balance. These shifts, driven by bioactive compounds, promoted energy metabolism and immune regulation.

Table 7: Comparative Analysis of Microbial Class Pre- and Post-Intervention

Class	Pre test	Post test
Bacilli	59803	12942
Actonobacteria	45703	4841
Bacteroidia	30202	38295
Clostridia	11619	20685
Negativicures	936	5283
Unclassified derived from bacteria	886	3705
Gammaproteobacteria	627	870
Erysipelotrichi	227	748
Alphaproteobacteria	21	9

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Flavobacteria	17	118
Insecta	10	6
Epsilonproteobacteria	9	482

Amalaki reduced Firmicutes and Actinobacteria, improving metabolic balance, while increasing Bacteroidetes for a leaner microbiota profile. Enhanced microbial diversity and stable minor phyla reflected ecosystem resilience.

Table 8: Comparative Analysis of Microbial Order Pre- and Post-Intervention

Order	Pre test	Post test
Lactobacillales	57330	11314
Bifidobacteriales	40413	2531
Bacteroidales	30202	38295
Clostridiales	11589	20665
Coriobacteriales	3408	369
Selenomonadales	936	5283
Unclass derived from bacteria	886	3205
Actinomycetales	649	1799
Enterobacteriales	538	666
Bacillales	367	535
Erysipalotrichales	227	748
Flavobacteriales	17	118

Amalaki decreased Lactobacillales and Bifidobacteriales while increasing Bacteroidales, Clostridiales, and Actinomycetales. These shifts fostered microbial diversity and gut health.

Table 9: Comparative Analysis of Microbial Family Pre- and Post-Intervention

Family	Pre test	Post test
Lactobacillaceae	47363	4639
Bifidobacteriaceae	40413	2531
Prevotellaceae	15772	32856
Coriobacteriaceae	3408	369
Lachnospiraceae	1592	1056
Veillonellaceae	928	5260
Unclassified from	886	3705
Clostridiaceae	869	2464
Enterobacteriacae	538	666
Enterococcaeceae	169	465
Eubacteriaceae	80	88
Micrococcaceae	68	190
Porphyromonadaceae	27	181
Paenibacilliaceae	21	25
Peptococcaceae	18	50
Listeriaceae	15	13
Pasteurellaceae	3	15
Mycobacteriaceae	1	12
Fusobacteriaceae	1	895

Amalaki intervention reduced Lactobacillaceae and Bifidobacteriaceae, enhancing diversity and SCFA-producer support, while increases in Prevotellaceae and Clostridiaceae improved fibre fermentation and anaerobic processes. Polyphenols and antioxidants drove these benefits.

Table 10: Comparative Analysis of Microbial Genus Pre- and Post-Intervention

Genus	Pre test	Post test
Lactobacillus	44542	4493
Bifidobacterium	40149	2521
Prevotella	15751	32841
Bacteroides	12531	2908
Collinsella	3174	260
Unclassified (derived	886	3705
Clostridium	834	2393
Megasphaera	181	1046
Enterococcus	168	453
Veillonella	165	2838
Bacillus	148	356
Weissella	83	26
Eubacterium	80	88
Ruminococcus	79	478
Faecalibacterium	78	123
Atopobium	50	78
Escherichia	41	37
Unclassified (derived from Erysipelotrichaceae)	40	73
Streptococcus	36	957
Dialister	33	48
Pediococcus	30	8
Kocuria	23	27
Arthrobacter	20	6
Micrococcus	20	3
Streptomyces	19	6
Paenibacillus	18	20
Paraprevotella	16	11
Pseudomonas	15	168
Corynebacterium	12	153
Selenomonas	11	208
Leuconostoc	8	15
Brochothrix	7	11
Desulfotomaculum	6	14
Odoribacter	5	12
Campylobacter	5	482
Actinomyces	3	569
Porphyromonas	3	90
Capnocytophaga	3	105
Megamonas	3	12
Microbacterium	2	9
Enterorhabdus	2	17
Parabacteroides	2	15

Amalaki reduced Lactobacillus and Bifidobacterium, favouring microbial diversity, while increasing fibre-utilisers like Prevotella and Veillonella. SCFA-producers such as Faecalibacterium and Ruminococcus supported gut health, and commensals like Escherichia bolstered mucosal resilience.

The comparative analysis of microbial composition pre- and post-intervention with Haritaki

(Terminalia chebula) and Amalaki *(Phyllanthus emblica)* demonstrates significant shifts in gut microbiota, aligning with their traditional use in Ayurveda for gut health and systemic balance.

Haritaki Intervention and Its Mechanism

Haritaki supplementation led to a notable reduction in the dominant phyla Firmicutes and Bacteroidetes, while increasing Actinobacteria, known for their anti-inflammatory properties. A decline in unclassified bacteria contributed to microbial stability, with minimal changes in Proteobacteria, indicating the absence of inflammatory disturbances. Interestingly, the rise in Fusobacteria suggests potential adaptive shifts, requiring further study to assess long-term implications.

At the class level, Haritaki reduced Bacteroidia, Clostridia, and Erysipelotrichi, which are often associated with inflammation, while boosting Actinobacteria, supporting gut integrity. At the order level, reductions in Bacteroidales and Clostridiales coupled with an increase in Actinomycetales and Bifidobacteriales suggest prebiotic-like effects. Similarly, family-level analysis showed decreased Prevotellaceae, Veillonellaceae, and Lactobacillaceae, with a significant increase in Bifidobacteriaceae (+19%) and Actinomycetaceae, enhancing immune modulation and microbial balance.

At the genus level, reductions in Prevotella and Lactobacillus and an increase in Bifidobacterium, Streptomyces, and Pseudomonas indicate a shift towards a more balanced microbiome. The decline in SCFA (short-chain fatty acid)-producers such as Ruminococcus suggests an optimised fermentation process, potentially enhancing metabolic efficiency. Compared to previous studies, Haritaki's effects align with its known role as a prebiotic and antimicrobial, similar to findings where Terminalia species modulated gut microbiota by increasing beneficial bacteria while reducing opportunistic pathogens. However, differences in specific microbial shifts highlight individual variations and dietary influences.

Amalaki Intervention and Its Mechanism

Amalaki supplementation exhibited a distinct pattern, reducing Firmicutes and Actinobacteria while increasing Bacteroidetes, contributing to enhanced microbial diversity and metabolic balance. These shifts, likely driven by Amalaki's rich polyphenol and antioxidant content, promoted energy metabolism and immune regulation.

At the class level, decreases in Firmicutes and Actinobacteria and an increase in Bacteroidetes indicated a shift towards a leaner microbiota profile, supporting metabolic health. The stability of minor phyla suggested ecosystem resilience, reinforcing its prebiotic potential. The order-level changes, particularly reductions in Lactobacillales and Bifidobacteriales alongside an increase in Bacteroidales, Clostridiales, and Actinomycetales, reflected improved microbial diversity and gut health.

At the family level, reductions in Lactobacillaceae and Bifidobacteriaceae and increases in Prevotellaceae and Clostridiaceae enhanced fibre fermentation and anaerobic processes, driven by Amalaki's bioactive compounds. These changes align with previous research on polyphenol-rich interventions that improve microbial diversity while supporting SCFA production. The genus-level alterations, including reductions in Lactobacillus and Bifidobacterium and increases in Prevotella and Veillonella, further emphasised Amalaki's role in fostering a diverse and resilient microbiome. Notably, the rise in Faecalibacterium and Ruminococcus supported SCFA production, while Escherichia played a role in mucosal resilience.

Compared to similar studies, Amalaki's effects resemble those of polyphenol-based dietary interventions, where increased Bacteroidetes and fibre-fermenting genera were linked to improved metabolic and immune functions. However, the degree of Firmicutes reduction differed across studies, suggesting potential influences from diet and baseline microbiota composition.

Discussion

The present study demonstrates the modulatory effects of *Haritaki - Terminalia chebula Retz.* (Combretaceae) and *Amalaki - Phyllanthus emblica L.* (Phyllanthaceae) on the gut microbiota composition of healthy individuals. The findings indicate that both interventions influenced microbial diversity and stability, albeit through distinct mechanisms.

Haritaki supplementation resulted in a significant reduction in the dominant phyla Firmicutes and Bacteroidetes, while increasing Actinobacteria, a phylum associated with anti-inflammatory properties and gut homeostasis. Notably, the minimal changes observed in Proteobacteria suggest that Haritaki did not induce an inflammatory response, further supporting its role as a gut-stabilizing agent. These shifts align with previous reports on *Terminalia* species, where increased Bifidobacteriaceae and Actinomycetaceae were linked to enhanced immune function and metabolic balance. However, the observed increase in Fusobacteria warrants further investigation, as its implications for long-term gut health remain unclear.

At the taxonomic class and order levels, Haritaki led to a decline in Bacteroidia, Clostridia, and Erysipelotrichi, all of which have been associated with pro-inflammatory states in various gut-related disorders. Simultaneously, an increase in Actinobacteria suggests improved gut barrier integrity and immune modulation. The enhancement of Bifidobacteriales and Actinomycetales further supports its prebiotic-like effects, contributing to microbial stability. Comparisons with previous studies reveal that while Haritaki shares similarities with other polyphenol-rich and tannin-containing botanicals in promoting beneficial microbiota, the extent of changes in minor taxa differs, highlighting potential interindividual variations and dietary influences.

Amalaki supplementation, in contrast, led to a reduction in Firmicutes and Actinobacteria, coupled with an increase in Bacteroidetes, a shift often

associated with improved metabolic efficiency and energy homeostasis. This microbiota composition aligns with previous findings on polyphenol-rich dietary interventions, where an increase in Bacteroidetes has been linked to enhanced microbial diversity and metabolic balance. The observed changes at the class and order levels, particularly the reduction in Lactobacillales and Bifidobacteriales and the increase in Bacteroidales and Clostridiales, suggest a transition toward a microbiome favouring fibre fermentation and SCFA production. These alterations, driven by the bioactive compounds present in Amalaki, indicate a potential role in promoting gut metabolic resilience.

At the family and genus levels, Amalaki intervention resulted in a decline in Lactobacillaceae and Bifidobacteriaceae, while increasing Prevotellaceae and Clostridiaceae, suggesting enhanced fibre fermentation and anaerobic metabolism. A notable increase in Faecalibacterium and Ruminococcus, key SCFA producers, further supports its role in maintaining gut homeostasis. Additionally, the increase in Escherichia, a commensal genus involved in mucosal resilience, aligns with findings from previous research on polyphenol-mediated microbial shifts. However, the extent of Firmicutes reduction observed in the present study differs from other studies, emphasising the need for further investigation into potential dietary and genetic factors influencing microbiota responses.

The differential microbial shifts induced by *Haritaki* and *Amalaki* highlight distinct but complementary mechanisms of action. While Haritaki predominantly stabilised microbial diversity and increased Actinobacteria, known for their immunomodulatory effects, Amalaki enhanced fibre-fermenting bacteria and promoted microbial diversity. These findings support the traditional use of these botanicals in Ayurveda for gut health and systemic balance. However, variations in microbial responses across studies suggest the need for longitudinal and multi-omics analyses to better understand their long-term effects and potential clinical applications.

Future studies should focus on functional metagenomics and metabolomics to elucidate the precise molecular pathways through which Haritaki and Amalaki exert their effects. Additionally, investigating their impact in individuals with dysbiosis or metabolic disorders could provide further insights into their therapeutic potential. The present study contributes to the growing body of evidence supporting the role of Ayurvedic botanicals in microbiome modulation, emphasizing their relevance in modern gut health interventions.

Conclusion

This study demonstrated that 8-week supplementation with *Haritaki - Terminalia chebula Retz.* (Combretaceae) and *Amalaki - Phyllanthus emblica L.* (Phyllanthaceae) induced distinct yet beneficial modulations in gut microbiota. Haritaki promoted microbial stability by reducing Firmicutes and Bacteroidetes while increasing Actinobacteria, supporting gut integrity and immune modulation. Amalaki enhanced Bacteroidetes, fostering microbial diversity and metabolic balance. Both interventions optimized SCFA production and fibre fermentation without inducing dysbiosis or inflammation. These findings support the traditional Ayurveda's use of Haritaki and Amalaki for gut health and highlight their potential for microbiome-based therapeutic applications. Further studies are needed to explore their long-term clinical implications.

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