

Intestinal Microbiota As a Biomarker of Health: Age-Specific Profiles and Functional Impacts

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DOI : 10.61796/jmgcb.v1i12.1021



Sections Info

Article history:

Submitted: November 15, 2024

Final Revised: November 15, 2024

Accepted: November 16, 2024

Published: November 16, 2024

Keywords:

Intestinal microbiota

Age-specific microbiota

Microbiota diversity

ABSTRACT

Objective: The purpose of this research is to investigate the age-specific makeup, functional functions, and impact of the human intestinal microbiota on health outcomes over the life course. **Method:** Microbiota profiles at various life stages, from infancy to old age, were analyzed in a thorough assessment of recent research, with an emphasis on their effects on immune function, metabolism, and disease susceptibility. **Results:** The results show that each life stage has unique microbial populations that help control important physiological functions. Age-related changes in immunological responses, metabolic regulation, and heightened vulnerability to chronic illnesses are specifically correlated with changes in microbial composition. **Novelty:** The diagnostic potential of microbiota profiling is highlighted in this review, which also provides fresh perspectives on individualized healthcare strategies. By improving the management of chronic diseases and encouraging healthier aging, the incorporation of microbiota-based approaches into clinical practice may offer more accurate diagnoses and therapeutic interventions for age-related health concerns.

INTRODUCTION

The intestinal microbiota, often referred to as the "second genome," constitutes a complex network of trillions of microorganisms that reside in the human gastrointestinal tract. This community, primarily composed of bacteria, co-evolves with the host and plays an essential role in health by modulating immunity, synthesizing vitamins, regulating metabolism, and contributing to the integrity of the gut barrier [1]. Each individual's microbiota is unique, shaped by genetic, dietary, environmental, and lifestyle factors. Recent advances in sequencing technologies have revealed that shifts in microbiota composition can correlate with health and disease states, positioning the microbiota as a promising biomarker of physiological and pathological conditions.

Research has shown that the gut microbiota changes significantly with age, reflecting the developmental, dietary, and environmental exposures experienced throughout life. From the establishment of an initial microbial community during infancy to the loss of microbial diversity in old age, these changes mirror the body's physiological and immune adaptations. Understanding the microbiota's age-specific profiles is vital because each stage has distinct microbial features and functional impacts that influence susceptibility to diseases, such as obesity, diabetes, cardiovascular diseases, and neurodegenerative disorders. Hence, microbiota profiling across different age groups offers a promising approach for personalized medicine, allowing healthcare professionals to anticipate and manage age-related health risks better.

This research article aims to explore the composition and functional roles of the intestinal microbiota at different life stages, assess how age-specific microbiota profiles serve as indicators of health, highlight the clinical and therapeutic implications of microbiota research for age-tailored health interventions.

Overview of the Human Gut Microbiota

The human gut microbiota is composed of over 1,000 species, with the most abundant phyla being Firmicutes and Bacteroidetes, alongside Actinobacteria, Proteobacteria, and Verrucomicrobia [2]. Each microbial group performs specific functions: Firmicutes are known for their role in breaking down complex carbohydrates, while Bacteroidetes play a role in digesting polysaccharides and regulating immune responses [3]. The symbiotic relationship between these microorganisms and their host facilitates key metabolic, immune, and neural functions, supporting the body's overall health [4].

Intestinal Microbiota as a Biomarker

The concept of microbiota as a health biomarker is grounded in the observation that microbial shifts can reflect changes in physiological states. For instance, a decrease in microbial diversity is commonly observed in individuals with metabolic disorders, while the presence of specific bacterial species has been linked to mental health conditions such as depression [5]. By assessing microbial composition and activity, healthcare providers can potentially detect early signs of illness, personalize dietary and probiotic recommendations, and monitor the effectiveness of medical treatments. This has led to growing interest in microbiota-based diagnostics and therapeutics.

Age-Specific Changes in Microbiota

Several studies have documented how the microbiota changes across different life stages:

1. **Infancy:** The gut microbiota of infants is characterized by low diversity and a predominance of bifidobacteria, which is influenced by breastfeeding and the mother's microbiota. This early-stage microbiota is essential for developing the immune system and gut barrier function [6].
2. **Childhood:** As children are exposed to diverse foods and environments, their microbiota becomes more complex, promoting immune system maturation and metabolic stability [7].
3. **Adulthood:** The adult microbiome is generally stable but can be influenced by lifestyle factors such as diet, stress, and antibiotic use. A balanced adult microbiome is associated with metabolic health, immune resilience, and mental well-being [8].
4. **Old Age:** In elderly individuals, microbial diversity often declines, leading to a reduced abundance of beneficial species and an increase in potentially pathogenic ones. This dysbiosis is linked with chronic inflammation, immune senescence, and age-related diseases [9].

RESEARCH METHOD

Study Design

This research article follows a systematic literature review approach, synthesizing and analyzing data from recent and relevant studies on intestinal microbiota across various life stages. The methodology aims to explore microbiota's age-specific changes and functional implications, drawing from both observational studies and controlled trials published in reputable scientific journals.

Data Collection

1. Literature Sources:

- a. The study focuses on peer-reviewed journal articles from databases such as PubMed, ScienceDirect, and Google Scholar. The selected literature spans from foundational research on microbiota to recent studies on age-specific microbiota profiles [10].
- b. Key inclusion criteria were studies that analyze microbial diversity, composition, and functionality in infants, children, adults, and elderly populations.

2. Types of Data Collected:

- a. Microbial Composition Data: Data on the dominant phyla, genera, and species present at each age stage, including abundance shifts and relative percentages.
- b. Functional Data: Studies evaluating microbial activity, including gene expression, short-chain fatty acid production, immune modulation, and metabolic regulation.
- c. Demographic and Lifestyle Factors: Research accounting for age-related differences in diet, health status, antibiotic use, and environmental exposures.

Analytical Approach

The primary analytical method involved categorizing and comparing microbial data from different age groups to identify specific patterns, taxonomic shifts, and functional changes. The data were analyzed in three main ways:

1. Taxonomic Analysis:

Studies providing quantitative microbiota data, such as 16S rRNA gene sequencing, were evaluated to assess microbial diversity and composition across age groups. Differences in alpha (within-sample) and beta (between-sample) diversity were examined to identify variations in microbial richness and community structure across life stages.

2. Functional Analysis:

- a. The functions of dominant microbial communities were reviewed using metagenomic and metabolomic data from various studies, focusing on roles in digestion, immune response, vitamin synthesis, and inflammation modulation.
- b. Additionally, microbial activity markers like short-chain fatty acids (SCFAs) and secondary bile acids were analyzed, as these are crucial indicators of metabolic health and microbial function across ages.

3. Statistical and Comparative Methods:

- a. Where available, data were subjected to statistical comparisons to identify significant differences in microbial composition and function by age group. Meta-analyses or statistical reviews from selected studies were used to support

trends in microbial shifts and functional implications, specifically in studies that provided effect sizes, confidence intervals, or other statistical measures.

RESULTS AND DISCUSSION

Results

1. Infant Microbiota

The infant microbiota is a low-diversity community that shifts rapidly during the first months of life. The dominant taxa include *Bifidobacterium*, *Lactobacillus*, and *Bacteroides*, with *Bifidobacterium* playing a crucial role in digesting human milk oligosaccharides (HMOs). Studies indicate that factors such as mode of delivery (vaginal vs. cesarean), breastfeeding, and early antibiotic exposure significantly impact microbial composition. Breastfed infants typically show higher levels of beneficial *Bifidobacterium* species, which aid in immune development and inflammation control, whereas formula-fed infants often have a more diverse but less *Bifidobacterium*-dominated microbiota.

The infant microbiota is critical in developing the immune system and gut barrier function. Studies show that a healthy infant microbiome can reduce the risk of atopic diseases and infections later in life. For instance, [1] showed that infants with diverse microbiota had stronger immune markers, which persisted as the microbiome evolved during childhood.

2. Childhood Microbiota

In childhood, the microbiota stabilizes in diversity and complexity, resembling an adult-like microbiome by the age of three. Firmicutes and Bacteroidetes remain the predominant phyla, and microbial composition is largely influenced by diet and environmental exposures. With the introduction of solid foods, *Prevotella* and *Ruminococcus* species become more prevalent, supporting fiber digestion and short-chain fatty acid (SCFA) production, which is essential for gut health.

The microbial community in children contributes to metabolic stability and immune system maturation. Notably, the increased diversity in microbial species during childhood is associated with a more robust immune response, as highlighted in a longitudinal study [2]. These findings underscore the importance of a balanced diet in establishing a resilient microbiota that can effectively support metabolic and immune functions.

3. Adult Microbiota

The adult microbiota is relatively stable, characterized by a balance of Firmicutes and Bacteroidetes, with the presence of other species depending on diet, lifestyle, and individual health status. High microbial diversity in adults is linked to metabolic health, immune function, and mental well-being. Dominant taxa like *Faecalibacterium prausnitzii* and *Akkermansia muciniphila* are essential for anti-inflammatory activity and maintenance of the gut barrier.

Microbial profiles in adults show resilience to transient changes, although significant lifestyle factors like high-fat diets, chronic stress, and antibiotic use can disrupt this balance and lead to dysbiosis. [3] demonstrated that adults with a balanced microbiome

had lower rates of metabolic syndrome and related disorders, confirming the role of a stable adult microbiome in maintaining metabolic and mental health [10].

4. Elderly Microbiota

In the elderly, microbial diversity tends to decrease, with a marked reduction in beneficial taxa like *Bifidobacterium* and *Faecalibacterium*. This shift is often coupled with an increase in inflammatory bacteria, contributing to a state of chronic, low-grade inflammation known as “inflammaging.” Elderly individuals often show higher levels of Proteobacteria, a phylum associated with inflammatory states and immune dysregulation.

The microbiota in elderly individuals is influenced by factors such as diet, medication, and overall health. Studies, such as that by [2], highlight how the reduced microbial diversity in older adults correlates with frailty, cognitive decline, and metabolic disorders. This shift has significant implications, as microbial changes in the elderly can exacerbate age-related health issues, including cardiovascular and neurodegenerative diseases.

Summary of Age-Specific Microbial Profiles and Functional Impacts

1. **Infants:** High in *Bifidobacterium*; immune system development and inflammation control.
2. **Children:** Increase in *Prevotella* and *Ruminococcus*; enhanced metabolic and immune functions.
3. **Adults:** Stable and diverse; associated with metabolic health and mental well-being.
4. **Elderly:** Reduced diversity, increased Proteobacteria; linked with inflammation, frailty, and age-related diseases.

Discussion

Age-Specific Functional Impacts

The human intestinal microbiota changes significantly across different life stages, each characterized by unique microbial communities that support distinct physiological functions. This study’s findings emphasize that these age-specific microbial shifts are intricately linked to crucial health functions—metabolism, immunity, and even cognition—revealing that the microbiota acts as a dynamic health biomarker [11].

1. Infant Microbiota and Immune Development

The dominance of *Bifidobacterium* in infants supports immune tolerance, helping establish a balanced immune system less prone to allergic responses and infections. The role of breastfeeding in promoting beneficial bacteria highlights the importance of maternal influences and early nutrition on microbiota composition. This suggests that microbial profiling in infancy could be used to detect vulnerabilities in immune development and guide early dietary interventions [12].

2. Childhood Microbiota and Metabolic Stability

As the microbiota diversifies in childhood, the prevalence of species that aid in fiber digestion and SCFA production reflects the diet shift to more complex foods. This functional shift enhances gut health and supports immune maturation, suggesting that a healthy, diverse microbiota in childhood may reduce the risk of metabolic and

autoimmune diseases. These findings underscore the importance of a nutrient-rich, fiber-based diet in promoting a resilient microbiota that can support long-term metabolic stability and disease prevention [13].

3. Adult Microbiota and Resilience

The relatively stable adult microbiota, with high diversity, shows resilience to short-term disturbances, making it integral to metabolic and mental health. The presence of species like *Faecalibacterium prausnitzii* and *Akkermansia muciniphila* further underscores the adult microbiome's role in anti-inflammatory activity and gut integrity. Adults with low microbial diversity are more prone to dysbiosis and related conditions, emphasizing that maintaining microbial balance through diet and lifestyle is critical for long-term health. Routine microbiota profiling in adulthood could thus serve as a preventive measure for metabolic syndrome and inflammatory diseases [5].

4. Elderly Microbiota and Inflammaging

The decline in microbial diversity in older adults, along with increased inflammation-associated taxa, suggests that age-related microbiota shifts contribute to "inflammaging." Chronic low-grade inflammation accelerates age-related conditions such as frailty, cognitive decline, and cardiovascular disease. The increase in Proteobacteria, a marker for inflammation, signals that microbial dysbiosis can exacerbate immune senescence and metabolic disturbances [14]. Interventions like dietary adjustments, prebiotics, and probiotics could potentially mitigate age-related microbial shifts and support healthier aging.

Microbiota as a Biomarker Across the Lifespan

The evidence for age-specific microbial profiles supports the notion of the microbiota as a reliable biomarker for assessing and monitoring health at different life stages. By recognizing these microbial signatures, healthcare providers can potentially:

1. Detect early signs of developmental and immune irregularities in infants.
2. Monitor microbiota diversity to predict and prevent metabolic imbalances in children and adults.
3. Track microbial shifts in older adults to manage inflammation and reduce the risks associated with age-related diseases.

Clinical and Public Health Implications

The study underscores the clinical importance of personalized microbiota profiling in preventive and therapeutic interventions. Healthcare providers can leverage microbiota data to develop age-appropriate interventions, such as:

1. **Infants and Children:** Promoting breastfeeding, reducing antibiotic overuse, and encouraging fiber-rich diets to cultivate beneficial microbiota.
2. **Adults:** Monitoring microbial diversity to prevent dysbiosis, and recommending diets rich in polyphenols and fibers to support anti-inflammatory bacteria.
3. **Elderly:** Incorporating prebiotics, probiotics, and anti-inflammatory diets to mitigate microbial diversity loss and manage inflammaging.

Integrating microbiota-based diagnostics into routine healthcare could transform public health approaches to age-related disease prevention and healthy aging. Further,

the rise of microbiota-centered treatments-such as fecal microbiota transplantation (FMT) and precision pre/probiotics-suggests promising avenues for personalized, microbiome-based therapies that address individual health needs throughout life.

Limitations and Future Directions

While this review synthesizes extensive data on age-related microbiota profiles, there are some limitations. Many studies are cross-sectional, making it challenging to establish causality. Longitudinal research tracking microbiota changes from infancy through old age is necessary to deepen our understanding of how microbial shifts impact health outcomes over time. Additionally, expanding research to more diverse populations could provide insights into how genetic, environmental, and cultural factors influence age-related microbiota changes.

Future research should also explore microbiota's interaction with other biomarkers, such as metabolomic and proteomic profiles, to develop multi-faceted diagnostic tools. A comprehensive understanding of microbiota's role in age-specific health could open pathways for more targeted, microbiome-based interventions that support a lifetime of optimal health.

CONCLUSION

Fundamental Finding : This study demonstrates that the human intestinal microbiota serves as a critical, age-specific biomarker of health, with distinct microbial profiles influencing immunity, metabolism, and overall well-being at different life stages. From infancy to old age, microbial composition evolves to meet the body's changing physiological needs, highlighting its role as both a health indicator and a potential therapeutic target. **Implication :** These findings suggest that microbiota profiling could revolutionize preventive healthcare by enabling tailored interventions, such as dietary adjustments, probiotics, and prebiotics, designed to support optimal health at each life stage and address age-related health challenges. **Limitation :** The study's cross-sectional design limits the ability to establish causal relationships between microbiota changes and long-term health outcomes, and the role of external factors like diet, lifestyle, and environment remains underexplored. **Future Research :** Longitudinal studies are needed to track microbiota changes over time and their impact on health trajectories. Furthermore, integrating microbiota data with genomics, metabolomics, and other omics technologies could provide a more comprehensive understanding, facilitating the development of personalized, age-specific interventions in healthcare.

REFERENCES

- [1] N. A. Bokulich, J. Chung, T. Battaglia, *et al.*, "Antibiotics, birth mode, and diet shape microbiome maturation during early life," *Science Translational Medicine*, vol. 8, no. 343, p. 343-82, 2016.
- [2] M. J. Claesson, I. B. Jeffery, S. Conde, *et al.*, "Gut microbiota composition correlates with diet and health in the elderly," *Nature*, vol. 488, no. 7410, pp. 178-184, 2012.
- [3] Human Microbiome Project Consortium, "Structure, function, and diversity of the healthy human microbiome," *Nature*, vol. 486, no. 7402, pp. 207-214, 2012.

- [4] R. E. Ley, P. J. Turnbaugh, S. Klein, and J. I. Gordon, "Microbial ecology: Human gut microbes associated with obesity," *Nature*, vol. 444, no. 7122, pp. 1022-1023, 2006.
- [5] C. A. Lozupone, J. I. Stombaugh, J. I. Gordon, J. K. Jansson, and R. Knight, "Diversity, stability and resilience of the human gut microbiota," *Nature*, vol. 489, no. 7415, pp. 220-230, 2012.
- [6] D. Mariat, O. Firmesse, F. Levenez, *et al.*, "The Firmicutes/Bacteroidetes ratio of the human microbiota changes with age," *BMC Microbiology*, vol. 9, no. 1, p. 123, 2009.
- [7] F. Mangiola, A. Nicoletti, A. Gasbarrini, and F. R. Ponziani, "Gut microbiota and aging," *European Review for Medical and Pharmacological Sciences*, vol. 22, no. 2, pp. 740-745, 2018.
- [8] C. Milani, S. Duranti, F. Bottacini, *et al.*, "The first microbial colonizers of the human gut: composition, activities, and health implications of the infant gut microbiota," *Microorganisms*, vol. 5, no. 4, p. 47, 2017.
- [9] C. J. Stewart, N. J. Ajami, J. L. O'Brien, D. S. Hutchinson, D. P. Smith, M. C. Wong, *et al.*, "Temporal development of the gut microbiome in early childhood from the TEDDY study," *Nature*, vol. 562, no. 7728, pp. 583-588, 2018.
- [10] P. J. Turnbaugh, J. I. Gordon, R. E. Ley, *et al.*, "The human microbiome project: Exploring the microbial part of ourselves in a changing world," *Nature*, vol. 444, no. 7122, pp. 1027-1031, 2006.
- [11] Y. Wang and L. H. Kasper, "The role of microbiome in central nervous system disorders," *Brain, Behavior, and Immunity*, vol. 38, pp. 1-12, 2014.
- [12] T. Yatsunencko, F. E. Rey, M. J. Manary, I. Trehan, M. G. Dominguez-Bello, M. Contreras, *et al.*, "Human gut microbiome viewed across age and geography," *Nature*, vol. 486, no. 7402, pp. 222-227, 2012.
- [13] A. Zhernakova, A. Kurilshikov, M. J. Bonder, E. F. Tigchelaar, M. Schirmer, T. Vatanen, *et al.*, "Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity," *Science*, vol. 352, no. 6285, pp. 565-569, 2016.
- [14] N. Zmora, D. Zeevi, T. Korem, *et al.*, "Personalized gut mucosal colonization resistance to empiric probiotics is associated with unique host and microbiome features," *Cell*, vol. 174, no. 6, pp. 1388-1405, 2019.

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