JGK-Vol.18, No.1 Januari 2026

Gut Microbiota on the Incidence of Hypertension in Elderly Aged 60-89 Years : Scoping Review

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ABSTRACT

Hypertension is a growing global health problem. Identification of the causes of hypertension is highly variable and challenging, but in reality, it is multifactorial, both internal and external, including genetic, environmental, hormonal, and inflammatory factors. Hypertensive patients have decreased gut microbiota diversity, which is strongly correlated with the presence of gram-negative bacteria, such as *Klebsiella, Streptococcus, Parabacteria, Desulfovibrio, Prevotella*. This article aims to review the results of previous research related to the influence of gut microbiota on the incidence of hypertension in the elderly, as well as the mechanisms that link gut microbiota to the occurrence of hypertension in the elderly. The method used is a scoping review with the PICOS approach (Population, Intervention, Comparison, Outcome, Study Design) in compiling questions as a reference to identify keyword concepts that are appropriate to the objectives and questions reviewed and to determine inclusion and exclusion criteria. The elderly tend to have more Enterobacteriaceae and Oscillospira associated with inflammation, whereas younger people have more Bifidobacteria and SCFA-producing bacteria. The elderly with hypertension exhibit significant differences in gut microbiota composition. Longer-lived individuals have a higher proportion of short-chain fatty acid (SCFA)-producing bacteria such as Bacteroides, Faecalibacterium, and Alistipes, which play a role in stabilizing blood pressure through acetate production. The gut microbiota is a key component in the pathophysiology of hypertension in the elderly, with dysbiosis contributing to inflammation, metabolic disturbances, and decreased therapeutic efficacy. The reviewed studies suggest that SCFA-producing microbiota have protective effects and may be a potential target in hypertension management strategies.

Keywords: Gut, Microbiota, Hypertension, Elderly

INTRODUCTION

Hypertension is a growing global health problem. Hypertension is a risk factor for heart disease and stroke, the leading cause of death worldwide after kidney disease (Raymond & Morrow, 2021). The prevalence of hypertension among adults in Brazil is 30%, 5% among children and adolescents, and 50% among the elderly. Data from the 2023 Indonesian Health Survey (SKI) recorded a hypertension prevalence of 10.7% in the 18–24 age group and 17.4% in the 25–34 age group (Ministry of Health of the Republic of Indonesia, 2023) . The prevalence of hypertension in Indonesia is 11.8% in those aged 45 years and elderly (Ministry of Health of the Republic of Indonesia, 2023). The identification of the causes of hypertension is varied and challenging, but in reality, the causes of hypertension are multifactorial, encompassing both internal and external factors, including genetic, environmental, hormonal, and inflammatory factors (Silveira-Nunes et al., 2020).

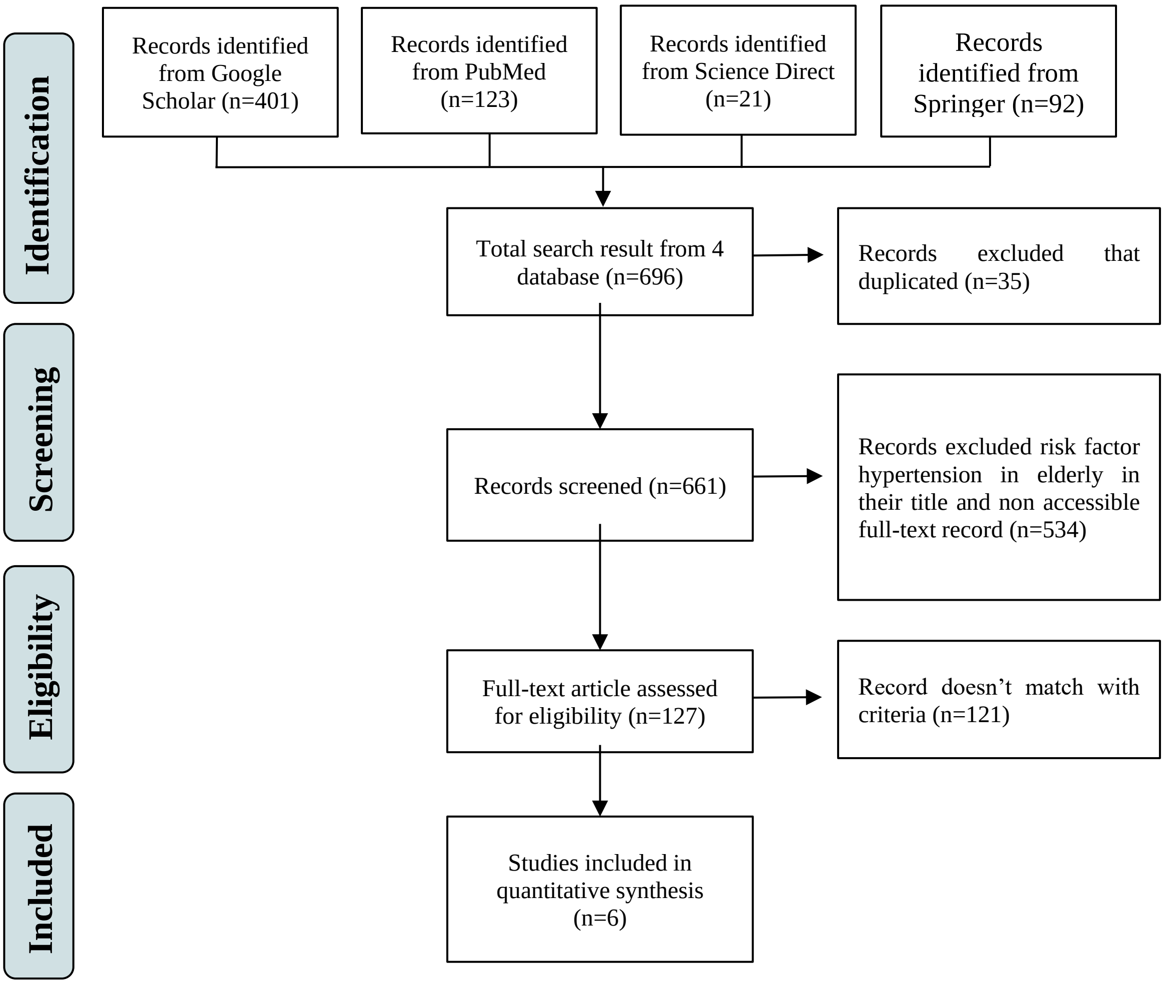
According to research, age plays a major role in increasing the incidence of hypertension, which affects up to 65% of the elderly worldwide. There is a notable decline in the diversity and abundance of the gut microbiome after the age of 60 (Haran & McCormick, 2021). Currently, specific populations are being studied and more comprehensively explored in regards to the gut microbiome of the elderly (Valdez-palomares et al., 2025). Studies in physiological mouse models of hypertension have shown that hypertension develops and worsens with age (Tukhovskaya et al., 2024).

The gastrointestinal tract is the largest immune surface environment in the human body. The relationship between hypertension and gut microbiota has been found in both human and animal models (Avery et al., 2021). Gut microbes are bacteria or microbes that can live in the gastrointestinal tract (intestines), which function to ferment unabsorbed food waste (fiber) (Raymond & Morrow, 2021). Numerous studies have demonstrated that gut microbiota plays a crucial role in the development and pathogenesis of hypertension (Zhang et al., 2023). Hypertensive patients have decreased gut microbiota diversity, which is strongly correlated with an increase in gram-negative microbes like *Klebsiella*, *Streptococcus*, *Parabacterium, Desulfovibrio*, and *Prevotella*. However, *Faecalibacterium* and *Roseburia spp*., which produce short-chain fatty acids, decrease (Verhaar et al., 2020). Hypertension is correlated with gut dysbiosis in a rat model of spontaneous hypertension. A mouse model of hypertension, intervened with human fecal bacteria, showed gut microbiota outcomes similar to (Li et al., 2017).

Changes in gut microbiota can lead to changes in microbial-derived metabolites, such as SCFAs (short-chain fatty acids), a product of bacterial fermentation of dietary fiber, which are beneficial for health (Zhang et al., 2023). Previous research has shown that efficient absorption in the large intestine can lower blood pressure in experimental animals with higher SCFA levels compared to a group of experimental animals with hypertension (Kaye et al., 2020). Previous studies have shown that SCFA-producing bacteria, such as fiber-fermenting bacteria—*Ruminococcus* UCG-002, DTU 089, and members of the *Lachnospiraceae* family—for hypertension control (Valdez-palomares et al., 2025). Gut microbiota is currently popularly associated with improving hypertension, especially in the elderly. Several studies on gut microbiota that are beneficial for improving hypertension still have varying and inconsistent results regarding the type, dosage, and research subjects.

METHOD

A scoping review was developed by Arskey and O’Malley with the aim of harmonizing and defining differences of opinion from several theories (Levac et al., 2010). Researchers used the PICOS (Population, Intervention, Comparison, Outcome, Study Design) approach in compiling questions as a reference to identify keyword concepts that are in accordance with the objectives and questions reviewed and to determine inclusion and exclusion criteria. The inclusion criteria in this scoping review include: (1) the study population is patients with hypertension; (2) Population age >60 years; (3) Discusses risk factors related to diet; (4) One of the variables is gut microbiota; (5) published in the last 5 years. Meanwhile, the research exclusion criteria include: (1) cannot be accessed in full text. Researchers identified several relevant studies using Google Scholar, PubMed, Science Direct, and Springer databases related to the influence of gut microbiota on elderly people with hypertension. The first keywords used in the search were “Hypertension” AND “Gut Microbiota” AND “Elderly”. A search for articles using these three keywords identified 696 articles. After filtering based on year, duplication, title relevance, full-text availability, and research design, six articles were identified. The literature search process is explained below.



Articles discussed the relationship between gut microbiota, age, and hypertension in the elderly, including studies conducted in Brazil, Mexico, Europe, and China in the 60-100 age range. The articles used are based on research articles on individuals with normotensive, controlled, and uncontrolled hypertension. The following is a comparison of each article used.

No	Author, Year	Study Title	Outside (points discussed in the journal)	Subject	Study Design	Conclusion
1	Nunes G. et al, 2020	Hypertension Is Associated With Intestinal Microbiota Dysbiosis and Inflammation in a Brazilian Population	hypertension, elderly, gut microbiota, dysbiosis, immune profile	48 hypertensive individuals and 38 normotensive individuals (normal blood pressure) in Brazil based on next generation sequencing of the 16S rRNA gene.	Research study	Gut microbiota dysbiosis in hypertension is characterized by a reduced diversity of different bacterial signatures. Hypertensive individuals experience a decrease in bacteroidetes, an increase in the proportion of lactobacillus and akkermansia, and a decrease in roseburia and faecalibacterium (butyrate producers). Hypertensive individuals have an inflammatory immune profile with an increased TNF/IFN-γ ratio and TNF and IL-6 production. Hypertensive individuals are susceptible to inflammation-related disorders.
2	Hung, et al (2025)	Association between the gut microbiotic composition and dietary patterns in hypertensive elderly patients: a cross sectional study	Hypertension, Diet, Nutrient Intake, Microbiotic Composition, Elderly	20 hypertensive patients and 21 normotensive individuals (normal blood pressure) aged 65-80 years	Case-control study	This study found that beneficial microbiota species, such as Bacteroides caccae, were found to be lower in abundance and negatively associated with unhealthy dietary habits, including high

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						consumption of saturated fat, sodium, and staple foods. Diet and nutrient intake may influence gut microbiota and could improve blood pressure in elderly people by affecting gut microbiota..
3	Valdez-palomares et al, 2025	Changes in the gut microbiome of elderly according to hypertension control	Elderly, hypertension, gut microbiome, systolic and diastolic blood pressure	240 individuals aged >60 years (men and women) diagnosed with hypertension and undergoing antihypertensive treatment for at least 4 years.	Research study	This study found no significant differences in microbiota composition based on hypertensive control for systolic and diastolic blood pressure. Bacterial abundance analysis identified a core microbiome in hypertensive elderly, with increased abundance of *Escherichia Shigella* and decreased alpha diversity with age. Ruminococcus UCG-002, DTU 089, and members of the *Lachnospiraceae* family were typically abundant in hypertensive individuals, as these bacteria ferment fiber and produce short-

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						chain fatty acids (SCFAs), and their different abundances based on hypertensive control suggest complex interactions among SCFA producers.
4	Zhang et al, 2023	Protection effect of gut microbiota composition and acetate absorption against hypertension-induced damages on the longevity population in Guangxi, China	Hypertension, gut microbiota, elderly, short-chain fatty acids, urinary metabolites, diet	32 individuals, subjects were divided into 2 groups based on age, namely elderly hypertensive (HTE, age 70.5 ± 8.59, n = 19) and long-term hypertensive (HTL, age 100 ± 5.72, n = 13).	Cross sectional study	Elderly people with hypertension have significantly higher levels of hypertension-associated bacteria, namely Klebsiella and Streptococcus, while elderly people with long-lived hypertension have higher levels of short-chain fatty acid-producing bacteria (Bacteroides, Faecalibacterium, Alistipes).

DISCUSSION

The relationship between microbiota and hypertension

Hypertension is a chronic condition characterized by persistently elevated blood pressure, likely caused by a complex interaction between endogenous (genetic) factors, such as family history, and environmental factors, such as an unhealthy lifestyle. Gut microbes play a crucial role in blood pressure regulation through microbial metabolites and microbial diversity. Individuals with hypertension exhibit characteristic microbial changes, including decreased *Bacteroides caccae* and *Barnesiella* levels and increased *Enterobacteriaceae, Enterobacter, Acidaminococcus,* and *Bacteroides plebeius* counts. These compositional changes are mechanistically relevant, as they affect the production of short-chain fatty acids (SCFAs), trimethylamine-N-oxide (TMAO), and lipopolysaccharide, which are involved in vascular tone, sympathetic activity, and inflammatory signaling. Importantly, *Bacteroides caccae*, a butyrate-producing species, has been negatively associated with dietary sodium and saturated fat intake, supporting dietary modulation of the gut microbiota as a key determinant in hypertension pathophysiology (Hung et al., 2025).

The pathogenesis of hypertension involves various factors, including genetic, environmental, hormonal, hemodynamic, and inflammatory factors. The gastrointestinal tract houses the largest immune cell compartment in the body (Jiang et al., 2025). A study of the microbial composition of feces from 48 hypertensive individuals and 32 normal individuals in Brazil found that gut microbiota dysbiosis in people with hypertension had a higher biodiversity and bacterial characteristics compared to individuals with normal blood pressure. Dysbiosis is an imbalance of bacteria in the digestive tract, and an imbalance in the gut microbiota is closely related to the occurrence of hypertension (Yang et al., 2023). People with hypertension have a lower diversity than people with normal blood pressure, as well as a decrease in SCFA-producing bacteria such as Roseburia and Faecalibacterium compared to those with normal blood pressure. Additionally, certain bacteria like Lactobacillus and Akkermansia, which can trigger inflammation, have increased in prevalence (Silveira-Nunes et al., 2020).

The gut microbiota plays a crucial role in regulating various bodily functions, such as metabolism, the immune system, and blood pressure. Imbalances in gut microbial balance are associated with an increased risk of hypertension through several mechanisms, including increased inflammation throughout the body, impaired microbial metabolism (particularly decreased production of short-chain fatty acids (SCFAs), and activation of the sympathetic nervous system and the renin-angiotensin system. SCFA-producing bacteria, such as Bacteroides, Faecalibacterium, and Alistipes, are known to help lower blood pressure by regulating the immune response and maintaining a healthy gut wall. Conversely, increased numbers of harmful bacteria, such as Klebsiella and Streptococcus, are associated with increased blood pressure and blood vessel damage. Therefore, the gut microbiota is a potential target for preventing and treating hypertension (Zhang et al., 2023).

The relationship between microbiota and elderly patients

The aging process is accompanied by physiological and metabolic changes that increase the risk of changes in the gut microbiota ecology in individuals. In the elderly, decreased microbiota diversity and increased pro-inflammatory taxa are often observed, contributing to age-related comorbidities. The body mass index (BMI) and waist circumference of hypertensive participants were higher than those of normotensive controls in a cohort of elderly participants 65–80 years old, consistent with metabolic risk profiles known to be associated with the elderly. Furthermore, the relative abundance of Enterobacteriaceae, a microbial family associated with inflammatory and oxidative pathways, was increased in elderly hypertensive subjects. These findings suggest that gut dysbiosis in the elderly may interact synergistically with aging-related metabolic disturbances, thereby exacerbating susceptibility to chronic disease (Hung et al., 2025).

There is a change in the composition of our microbiota as we age. Elderly tend to have more *Enterobacteriaceae* and *Oscillospira*, which are associated with inflammation, while younger adults have more Bifidobacteria and SCFA-producing bacteria, which are protective. However, the hallmarks of dysbiosis in hypertension can still be found in all age groups. The provision of probiotics can reduce inflammation and hypertension risk by improving the balance of the microbiota (Silveira-Nunes et al., 2020).

Elderly individuals with hypertension exhibit significant differences in gut microbiota composition. Longevity individuals have a higher proportion of short-chain fatty acid (SCFA)-producing bacteria such as Bacteroides, Faecalibacterium, and Alistipes, which play a role in stabilizing blood pressure through acetate production. In contrast, hypertensive elderly individuals without longevity tend to be dominated by pathogenic bacteria such as Klebsiella and Streptococcus, which can potentially worsen hypertension. The more efficient absorption of acetate in the colon in the long-lived group suggests that SCFA-producing bacteria may be a potential target for future hypertension therapy (Zhang et al., 2023).

The relationship between microbiota, hypertension, and elderly patients

The interaction between gut microbiota, hypertension, and aging is a complex and reciprocal relationship, in which microbiota dysbiosis both contributes to and is affected by patients' physiological decline. Elderly individuals with hypertension in this study showed a characteristic loss of butyrate-producing taxa, such as *Bacteroides caccae*, along with an expansion of potentially pathogenic taxa, including *Enterobacteriaceae* and *Acidaminococcus*. These microbiota changes are functionally relevant, as they promote systemic inflammation, disrupt endothelial function, and disrupt metabolic regulation, collectively contributing to elevated blood pressure. Dietary exposures, particularly excessive sodium and saturated fat intake, further modulate these microbiota patterns, suggesting a diet–microbiota–hypertension axis that is amplified in the elderly population. Overall, these findings highlight the gut microbiota as a modifiable target for additional strategies in the prevention and management of hypertension in the elderly (Hung et al., 2025).

A study conducted by Zhang *et al*. in 2023 involved elderly hypertensive patients divided into two groups: the Hypertension Elderly (HTE) group with an average age of approximately 70.5 years and the Hypertension Longevity (HTL) group with an average age of approximately 100 years. The HTE group had a higher proportion of hypertension-associated bacteria, such as *Klebsiella* and *Streptococcus*, compared to the long-lived hypertensive group. Conversely, the HTL group showed an increase in short-chain fatty acid (SCFA)-producing bacteria such as *Bacteroides*, *Faecalibacterium*, and *Alistipes*. Long-lived hypertensive patients had higher systolic blood pressure, and their microbiota composition and ability to efficiently absorb acetate appeared to help mitigate the damaging effects that typically arise from hypertension. Therefore, the microbiota producing SCFAs and their metabolites (acetate) plays a protective role in the elderly and are a potential therapeutic target for improving hypertension management in the elderly population (Zhang et al., 2023).

The difference between elderly people with controlled and uncontrolled hypertension lies in their microbiota. Controlled hypertension is associated with an increase in SCFA-producing bacteria such as Ruminocaccaeae UCG-002 and DTU-089. SCFAs themselves play a role in blood pressure regulation, which can improve blood pressure control. Meanwhile, elderly people with uncontrolled hypertension have a higher tendency for bacteria associated with inflammation or drug metabolism, which can affect the effectiveness of antihypertensive drugs and body metabolism. Elderly people with uncontrolled hypertension have a decrease in beneficial bacteria such as Eubacterium halli, Dorea, and Prevotella 7 and an increase in genes related to free oxygen radical (ROS) production, which can potentially reduce the effectiveness of hypertension therapy. This study shows that modulating the gut microbiota, for example, with a high-fiber diet and probiotics, can have potential in managing hypertension in the elderly (Valdez-palomares et al., 2025).

CONCLUSION

The gut microbiota is a key component in the pathophysiology of hypertension in the elderly, with dysbiosis contributing to inflammation, metabolic disturbances, and decreased therapeutic efficacy. The reviewed studies suggest that SCFA-producing microbiota have protective effects and may be potential targets in hypertension management strategies. Probiotics and dietary interventions offer promising approaches to improving the quality of life of the elderly with hypertension, although further research is needed to strengthen the clinical evidence and expand generalizability.

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