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DIETARY PATTERNS, GUT MICROBIOTA, AND HEALTHY AGEING: A NARRATIVE LITERATURE REVIEW

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Abstract. Healthy ageing is increasingly understood not merely as prolonged survival but as the preservation of functional capacity, resilience, and autonomy in later life. In this context, the gut microbiota has attracted growing attention as a potential biological interface linking diet to ageing trajectories. This narrative review evaluates what can reasonably be concluded from the recent literature regarding the role of dietary patterns in shaping gut microbiota-related pathways relevant to healthy ageing. To enhance transparency, selected elements of systematic review methodology were incorporated, including an explicit search strategy, clearly stated eligibility criteria, and a structured approach to source selection**.** The synthesis prioritised recent narrative and systematic reviews and examined evidence on frailty, physical function, inflammaging, and microbiota-derived metabolites in older adults. Its added value lies in distinguishing between clinically meaningful dimensions of ageing while also considering relevant mechanistic evidence, rather than treating healthy ageing as a single undifferentiated outcome. The available literature suggests that plant-forward, fibre-rich, and polyphenol-rich dietary patterns, particularly the Mediterranean diet, are frequently associated with microbiota features generally regarded as favourable, including a greater abundance of short-chain fatty acid-producing taxa and potentially beneficial metabolite profiles. However, the evidence does not support the existence of a single, uniform, and reproducible "healthy ageing microbiota". Diet may shape ageing-related microbial pathways, but the reported effects remain heterogeneous and vary according to dietary assessment, participant characteristics, microbiota assessment methods, and the operationalisation of healthy ageing outcomes. More robust longitudinal and interventional studies in humans are therefore required before microbiome-informed dietary recommendations for older adults can be made with confidence.
Keywords: gut microbiota, healthy ageing, dietary patterns, inflammaging, review

Introduction

Healthy ageing is increasingly understood not simply as the extension of lifespan, but as the preservation of functional capacity, resilience, and autonomy in later life. Within this broader perspective, the gut microbiota has emerged as a potentially important interface between cumulative environmental exposures and ageing-related biological processes. Dietary patterns may influence microbial composition, diversity, and metabolic activity, while age-associated alterations in the gut ecosystem may, in turn, be linked to frailty, chronic low-grade inflammation, impaired physical performance, and other adverse ageing outcomes (Bradley & Haran, 2024; Gyriki et al., 2025; Ramasinghe et al., 2025). The relevance of the gut microbiota to healthy ageing therefore lies not only in taxonomic composition, but also in its functional capacity to generate metabolites, interact with the intestinal barrier, and influence immune and metabolic regulation.

The available evidence, however, remains methodologically and conceptually heterogeneous. This is particularly apparent in systematic reviews of the Mediterranean diet. Khavandegar et al. (2024) reported broadly favourable associations between adherence to the Mediterranean diet and gut microbiota diversity, composition, function, and selected clinical outcomes. By contrast, Kimble et al. (2023) found no clear and consistent effect of the Mediterranean diet on gut microbiota composition or metabolism across randomised and observational studies. These conclusions are not necessarily mutually exclusive. Rather, they illustrate how differences in study populations, dietary characterisation, adherence assessment, intervention duration, microbiota methods, and outcome selection can produce divergent interpretations of the same general relationship (Khavandegar et al., 2024; Kimble et al., 2023). The central problem is therefore not simply whether diet affects the gut microbiota, but under which conditions such effects are detectable, reproducible, and clinically meaningful.

A further conceptual challenge concerns the definition of healthy ageing itself. Bradley and Haran (2024) associate healthier ageing, particularly in later life, with a diverse microbiome containing organisms capable of producing potentially anti-inflammatory metabolites such as short-chain fatty acids. Simbirtseva and O'Toole (2025), however, emphasise that age-related health decline is not uniform and may depend partly on the differential loss of gut commensals and the increased abundance of pathobionts. Their analysis shifts attention away from chronological age alone and towards the distinction between healthy and unhealthy ageing trajectories. Individuals of a similar chronological age may therefore exhibit substantially different functional, inflammatory, and microbial profiles.

This distinction has important implications for the interpretation of the literature. Frailty, physical function, inflammaging, and exceptional longevity are related to ageing, but they represent distinct biological and

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clinical dimensions rather than interchangeable indicators of a single state. Treating them as equivalent manifestations of healthy or unhealthy ageing may obscure meaningful differences in both microbial patterns and clinical relevance. Similarly, mechanistic evidence concerning microbial metabolites, intestinal barrier function, and immune regulation should be distinguished from evidence demonstrating associations with clinically observable outcomes. A central premise of this review is therefore that heterogeneity in the definition and measurement of ageing outcomes is as important as heterogeneity in microbiota methods when interpreting diet–microbiota relationships.

Against this background, the present article aims to synthesise and critically interpret recent literature on dietary patterns, gut microbiota, and healthy ageing. Rather than seeking to identify a single microbial profile of healthy ageing, the review examines how current evidence varies across clinically meaningful ageing dimensions and mechanistic pathways. It addresses the following question: what can reasonably be concluded from the recent literature regarding the role of dietary patterns in shaping gut microbiota-related pathways relevant to healthy ageing?

Research methods and conditions

This narrative review adopted a critical and interpretive analytical approach. Its methodological design drew on recommendations for strengthening narrative reviews through selected elements of systematic review methodology, including a transparent search strategy, clearly stated eligibility criteria, and a structured approach to the selection and synthesis of sources (Ferrari, 2015; Green et al., 2006).

The literature search was conducted in PubMed in April 2026. PubMed was selected as the principal database because the review addressed a biomedical topic at the intersection of dietary patterns, gut microbiota, ageing, and clinically relevant outcomes in older adults. Given the focused scope and narrative design of the article, PubMed was considered an appropriate database for identifying recent peer-reviewed biomedical literature. To broaden coverage and reduce the risk of omitting conceptually important publications, the reference lists of key review articles were also screened manually.

The search was iterative rather than based on a single fixed search string. It used combinations of keywords related to gut microbiota, ageing, dietary patterns, frailty, inflammaging, muscle mass, and physical function. The Boolean operator OR was used to combine synonyms and spelling variants within each concept group, while AND was used to link different concepts. The search logic can be illustrated by the following representative combination: (“gut microbiota” OR “gut microbiome”) AND (“healthy ageing” OR “healthy aging” OR ageing OR aging) AND (“dietary pattern” OR “dietary patterns” OR “Mediterranean diet” OR fibre OR fiber OR polyphenol OR polyphenols). Additional searches combined microbiota- and ageing-related terms with frailty, inflammaging, muscle mass, and physical function. British and American spelling variants were used where relevant.

Titles and abstracts were screened for relevance, after which potentially eligible full texts were assessed against the eligibility criteria. Uncertainties regarding inclusion were discussed by the authors before the final source corpus was agreed.

Sources were eligible if they addressed at least two of the three central domains of the review: dietary exposure, gut microbiota, and outcomes relevant to healthy ageing. Topic-specific narrative and systematic reviews published from 2020 onwards were prioritised to establish the conceptual and evidential basis of the analysis. Publications were excluded if they were not peer-reviewed, were not written in English, or were not directly relevant to the review question. Topic-specific publications published before 2020 were excluded, whereas older methodological publications were retained when they informed the review approach. The final thematic corpus comprised 11 topic-specific review articles, while two additional publications were used solely to inform the methodological approach. The methodological publications were not included in the thematic synthesis.

The selected literature was synthesised thematically and comparatively. The analysis considered the type and scope of each source, the populations examined, the characterisation of dietary exposure, the methods used to assess gut microbiota, the ageing-related outcomes reported, and the principal limitations identified in the included sources. Four questions guided the synthesis: which dietary patterns were most consistently associated with gut microbiota modulation in later life; how the gut microbiota was interpreted in relation to healthy and unhealthy ageing; which microbiota-related pathways were considered relevant to ageing outcomes; and which methodological limitations constrained the interpretation of the available evidence.

Research results and their discussion

Diet as a modulator of the ageing gut microbiota

Current reviews identify diet as an important modifiable influence on gut microbiota composition and function throughout the life course, including later life. Ageing-associated changes include reduced microbial diversity, shifts in the abundance of specific taxa, loss of some beneficial commensals, and increased representation of potentially pathogenic or pro-inflammatory microorganisms. These changes are not uniform and are influenced by dietary habits, physical activity, medication use, disease, and physiological changes in the gastrointestinal tract (Bradley & Haran, 2024; Gyriki et al., 2025; Ramasinghe et al., 2025).

Ramasinghe et al. (2025) describe diet and gut microbiota as interconnected modulators of ageing-related biology. Their review indicates that Mediterranean and plant-based dietary patterns may increase the abundance of potentially beneficial microbial taxa and support related metabolic functions. By contrast, Western-style diets, particularly those rich in saturated fats and processed foods, are associated with dysbiosis and processes linked to accelerated ageing. The authors nevertheless emphasise the need for long-term, age-specific studies and standardised microbiome protocols before targeted dietary strategies for healthy ageing can be supported with confidence.

The Mediterranean diet: suggestive evidence but inconsistent findings

Among named dietary patterns, the Mediterranean diet occupies a prominent position in the recent literature. In a systematic review of 37 studies, Khavandegar et al. (2024) found that adherence to the Mediterranean diet was associated in many of the included studies with favourable changes in gut microbiota diversity, composition, and function. Faecalibacterium and Prevotella were the genera most frequently reported to increase in abundance. Reported clinical outcomes included improved glycaemic control, lower fat mass, improved bowel movements, reduced bloating and inflammation, and a lower risk of hospitalisation in some populations (Khavandegar et al., 2024).

Kimble et al. (2023), however, reached a more cautious conclusion in their systematic review of randomised controlled trials and observational studies. They found no clear evidence of a consistent effect of the Mediterranean diet on gut microbiota composition or metabolism. The authors attributed this inconsistency to heterogeneity in study populations, analytical methods, intervention duration, and dietary characterisation. They further argued that future research would benefit from a clearer conceptualisation of the "healthy gut microbiome", greater standardisation of Mediterranean diet interventions, and more consistent approaches to assessing dietary adherence and microbiota-related outcomes (Kimble et al., 2023).

Taken together, these reviews support a cautious conclusion. The Mediterranean diet remains highly relevant to research on gut microbiota and ageing, but the current evidence does not demonstrate a single, stable, and reproducible gut microbiota profile attributable to this dietary pattern across populations (Khavandegar et al., 2024; Kimble et al., 2023).

Fibre, polyphenols, and microbial metabolites

Evidence synthesised by Meiners et al. (2025) suggests that fibre- and polyphenol-rich dietary interventions can modify gut microbiota composition and microbial metabolite profiles. In their narrative review of human dietary intervention trials, the authors reported that such interventions were frequently associated with increased abundance of short-chain fatty acid-producing bacteria, including Faecalibacterium, Eubacterium, Roseburia, and Blautia, together with changes in plasma and faecal metabolites. They also suggested that relatively simple dietary modifications may produce meaningful microbiota and metabolite changes, particularly in older and metabolically compromised populations, while acknowledging that this conclusion was based on synthesis across studies rather than direct comparisons between population groups (Meiners et al., 2025).

The review also outlines the mechanistic relevance of microbial metabolites generated from dietary fibre. Acetate, propionate, and butyrate are major products of microbial fibre fermentation and have recognised roles in metabolic regulation, immune function, and maintenance of the intestinal barrier. Butyrate, in particular, contributes to colonocyte energy supply, tight-junction assembly, epithelial repair, mucus production, and anti-inflammatory immune regulation (Meiners et al., 2025). Taken together, the evidence reviewed by Meiners et al. supports the biological relevance of fibre- and polyphenol-rich dietary interventions, while the magnitude and consistency of their effects remain dependent on intervention design, baseline microbiota composition, and population characteristics.

Healthy ageing, unhealthy ageing, and the problem of definition

Recent reviews indicate that chronological age alone does not define a single gut microbiota profile. Bradley and Haran (2024) report that, particularly in later life, a diverse microbiome containing organisms capable of producing anti-inflammatory metabolites such as short-chain fatty acids is associated with healthy ageing. Simbirtseva and O'Toole (2025), however, emphasise that age-related health loss is not uniform and

may depend partly on the differential loss of gut commensals and the increased abundance of pathobionts. Their analysis therefore shifts the focus from chronological age alone to the distinction between healthy and unhealthy ageing states (Bradley & Haran, 2024; Simbirtseva & O'Toole, 2025).

Across the literature reviewed here, healthy ageing is operationalised through several distinct outcomes, including frailty, physical function, inflammatory status, cognition, and exceptional longevity. These outcomes reflect different biological and clinical trajectories and should not be treated as interchangeable indicators of a single ageing state (Barry et al., 2025; Caldarelli et al., 2024; Wen et al., 2024; Xiao et al., 2025). Accordingly, this review treats heterogeneity in the definition of healthy ageing as a central interpretive problem alongside heterogeneity in microbiota assessment. Distinguishing between these outcomes provides a more coherent basis for interpreting associations between gut microbiota and ageing.

Frailty as a clinically relevant ageing phenotype

Frailty provides a clinically meaningful phenotype through which to examine associations between gut microbiota and adverse ageing outcomes. Wen et al. (2024) synthesised 11 observational studies involving 912 older adults and identified differences in gut microbiota diversity and composition between frail and non-frail participants. Significantly lower α-diversity and greater β-diversity in frail older adults were each reported in two of the seven studies assessing these outcomes. At the genus level, a lower abundance of Prevotella was reported in three studies, while Faecalibacterium and Roseburia were lower in two studies each. The authors interpreted the overall pattern as suggesting a reduction in potentially beneficial taxa and an increased representation of potentially pathogenic taxa, while acknowledging substantial variation across the included studies and the need for further confirmation (Wen et al., 2024).

Interpretation of these findings requires caution. Most of the included studies were cross-sectional, sample sizes were generally small, and both frailty assessment and microbiota analysis varied considerably. Diet, medication use, physical activity, comorbidities, and other host and environmental factors may also have influenced the observed microbial profiles. The review therefore supports an association between frailty and altered gut microbiota, but it does not establish a causal relationship or a consistent frailty-specific microbial signature (Wen et al., 2024).

Physical function and the gut–muscle axis

Physical function and muscle-related outcomes provide a further clinically relevant perspective on the relationship between gut microbiota and ageing. In a systematic review of 20 studies involving 4,071 older participants, Barry et al. (2025) identified associations between gut microbiota diversity and composition and outcomes related to muscle mass, strength, and physical performance. The review included 14 observational and six interventional studies and reported substantial heterogeneity in study populations, interventions, microbiota methods, and outcome measures. Some interventional studies reported improvements in muscle strength, body composition, or physical function, whereas others found no significant benefit.

These findings support the biological plausibility and potential clinical relevance of the microbiota–gut–muscle axis, but they do not establish a consistent intervention effect. Interpretation is further limited by the use of multi-ingredient interventions in some trials, inadequate control of diet and physical activity, and the absence of microbiota assessment in four of the six interventional studies. The available evidence therefore suggests that gut microbiota may be associated with muscle health in older adults, while the effectiveness and mechanisms of microbiota-targeted dietary interventions remain uncertain (Barry et al., 2025).

Inflammaging and microbiota-related mechanisms

The relationship between gut microbiota and inflammaging is a recurring theme in recent literature. Caldarelli et al. (2024) describe ageing-associated changes in the gut microbiota as including reduced microbial diversity, loss of beneficial bacteria, and increased representation of pro-inflammatory microorganisms, thereby contributing to persistent low-grade inflammation. Gyriki et al. (2025) likewise describe a close association between dysbiosis and inflammaging, noting that age-related alterations in the gut microbiota may increase intestinal permeability and activate immune responses, thereby contributing to chronic inflammation, frailty, and morbidity. Together, these reviews position inflammaging as a key interpretive framework for understanding diet–microbiota interactions in later life.

Xiao et al. (2025) identify the gut microbiota as a potential target for interventions aimed at promoting healthy ageing. Their review examines ageing-associated microbial features, the gut microbiota of centenarians, microbial biomarkers, host mechanisms, and dietary approaches directed at age-related microbial imbalance. However, the authors emphasise that the effectiveness of microbiota-targeted interventions may depend on factors such as strain specificity, dosage, treatment duration, and individual variation, and they call for larger and longer longitudinal studies. Ramasinghe et al. (2025) reach a similarly cautious conclusion, highlighting the need for long-term, age-specific research, standardised microbiome protocols, and integrated omics approaches before targeted dietary strategies for healthy ageing can be supported with confidence.

Methodological limitations of the current evidence

Several limitations recur across the literature reviewed here. First, the evidence base is highly heterogeneous in dietary assessment, gut microbiota analysis, participant characteristics, intervention design, and outcome definition. This is particularly evident in the differing conclusions reached by Khavandegar et al. (2024) and Kimble et al. (2023), but similar concerns are also reported in reviews of frailty, physical function, and ageing-related dietary interventions (Barry et al., 2025; Ramasinghe et al., 2025; Wen et al., 2024). Second, healthy ageing is operationalised through distinct clinical and biological outcomes, including frailty, muscle mass and physical function, inflammatory status, and longevity-related features, while some studies focus instead on mechanistic indicators such as microbial metabolites. These outcomes reflect different biological and clinical dimensions and cannot be treated as interchangeable indicators of a single ageing state. Third, evidence relating to frailty and muscle-related outcomes is dominated by observational studies, while interventional studies remain heterogeneous in design, duration, participant characteristics, and outcome measurement. These limitations substantially restrict causal interpretation and comparison across studies.

The present review also has limitations. It was based on a search of a single biomedical database and followed an iterative narrative search process rather than an exhaustive systematic search. Although reference lists of key reviews were screened manually and the source-selection logic was made explicit, relevant publications indexed elsewhere may have been missed. Narrative synthesis also remains vulnerable to selection bias and interpretive subjectivity, even when transparent search and eligibility criteria are applied (Ferrari, 2015; Green et al., 2006).

Taken together, these limitations indicate that the current literature supports the relevance of diet–microbiota interactions to ageing, but does not yet permit firm conclusions about the direction, consistency, magnitude, or clinical significance of these relationships across older populations.

Conclusions

The current literature identifies diet as an important modifiable influence on gut microbiota composition and function in later life. Plant-forward, fibre-rich, and polyphenol-rich dietary patterns, particularly the Mediterranean diet, are frequently associated with potentially favourable microbial taxa, metabolic functions, and metabolite profiles. However, the magnitude and consistency of these associations vary across studies.

The available evidence does not support the existence of a single, stable, and reproducible gut microbiota profile that can be attributed to a particular dietary pattern or regarded as universally characteristic of healthy ageing. A more defensible conclusion is that diet may modulate microbial pathways relevant to ageing, while the observed associations remain dependent on population characteristics, dietary assessment, microbiota methods, intervention design, and the definition of ageing-related outcomes.

The findings are more interpretable when healthy ageing is examined through distinct clinical and biological dimensions, including frailty, physical function, inflammaging, and longevity-related features, rather than chronological age alone. Reviews of frailty and muscle-related outcomes support associations between altered gut microbiota and adverse ageing phenotypes, but the available human evidence remains predominantly observational, heterogeneous, and insufficient to establish causal relationships or consistent phenotype-specific microbial signatures.

Future research should apply clearer and more consistent definitions of healthy ageing, standardise dietary and microbiota assessment, and prioritise well-designed longitudinal and interventional studies in older populations. Microbiome-informed dietary strategies for healthy ageing therefore remain a promising area of investigation rather than an established basis for clinical dietary recommendations.

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