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The Oral Microbiome in Oral Frailty and Healthy Ageing: A Narrative Review

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The oral microbiome plays a fundamental role in maintaining oral and systemic health throughout the ageing process. Age-related physiological changes, oral frailty, and physical inactivity contribute to microbial dysbiosis, which has been associated with periodontal disease, chronic inflammation, and frailty. However, the relationship between exercise, oral microbial ecology, and oral frailty has not been comprehensively synthesized. This narrative review aimed to summarize current evidence regarding the oral microbiome and to explore its relationship with oral frailty and healthy ageing. A narrative review was conducted using articles published between 2021 and 2026. Five original studies investigating oral microbiome composition, physical activity, oral frailty, ageing, and systemic inflammation in older adults were critically reviewed and synthesized to identify common findings and emerging biological mechanisms. The reviewed evidence consistently demonstrated that regular physical activity, including moderate-intensity continuous training and high-intensity interval training, promotes beneficial alterations in oral microbial composition by increasing microbial diversity and reducing the abundance of opportunistic pathogens. Conversely, physical inactivity and oral frailty were associated with reduced microbial diversity. Current evidence supports a close interaction between physical activity, oral microbiome composition, oral frailty, and healthy ageing. Regular exercise appears to preserve oral microbial homeostasis while reducing inflammation and frailty-related microbial alterations. These findings highlight the oral microbiome as a promising biomarker and potential therapeutic target for promoting healthy ageing. Nevertheless, further longitudinal studies integrating metagenomics, host immune responses, and clinical oral outcomes are required to clarify the causal mechanisms underlying these interactions.

Keywords: oral microbiome, oral frailty, healthy ageing, dysbiosis

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1. Introduction

The rapid growth of the global older adult population has transformed healthy aging into a major public health priority. Along with increasing life expectancy, the prevalence of age-associated disorders has risen substantially, among which frailty syndrome has become one of the most challenging geriatric conditions. Frailty is characterized by a progressive decline in physiological reserve across multiple organ systems, resulting in reduced resilience to stressors and an increased susceptibility to adverse outcomes, including falls, disability, hospitalization, institutionalization, and mortality.[1] Rather than representing an inevitable consequence of chronological aging, frailty is now recognized as a dynamic biological state resulting from the cumulative interaction of genetic, environmental, metabolic, immunological, and lifestyle-related factors.[2]

One of the hallmarks of frailty is chronic low-grade inflammation, commonly referred to as inflammaging, which is accompanied by immune senescence, oxidative stress, mitochondrial dysfunction, endocrine alterations, and progressive sarcopenia.[3] Persistent elevation of inflammatory mediators, including interleukin-6 (IL-6), tumor necrosis factor-α (TNF-α), and C-reactive protein (CRP), has consistently been associated with declining physical performance, impaired muscle function, and increased frailty severity.[4] Although numerous biological pathways contributing to frailty have been identified, increasing attention has recently been directed toward the role of host-associated microbiomes as potential regulators of systemic inflammation and healthy aging.

Among the various microbial ecosystems inhabiting the human body, the oral microbiome represents one of the most diverse and metabolically active communities. More than 700 bacterial species, together with fungi, viruses, archaea, and protozoa, colonize distinct ecological niches within the oral cavity, forming highly organized biofilms that contribute to oral homeostasis.[5] In healthy individuals, these microorganisms participate in maintaining epithelial integrity, modulating immune responses, preventing pathogen colonization, and supporting tissue homeostasis. However, disruption of this ecological balance may result in oral dysbiosis, characterized by shifts in microbial diversity and enrichment of pathogenic taxa capable of initiating chronic inflammatory responses.[6]

Aging substantially influences oral microbial ecology through multiple mechanisms. Reduced salivary secretion, immune senescence, dietary modifications, polypharmacy, tooth loss, impaired mastication, and declining oral hygiene collectively alter the oral environment, facilitating the expansion of opportunistic microorganisms and periodontal pathogens. Consequently, older adults frequently exhibit increased prevalence of periodontitis, root caries, oral candidiasis, and other oral inflammatory conditions. Importantly, oral dysbiosis is increasingly recognized as extending beyond local disease.[7] Bacterial translocation, dissemination of microbial virulence factors, and systemic release of inflammatory mediators originating from periodontal tissues provide plausible biological pathways linking oral microbial imbalance with systemic disorders, including cardiovascular disease, diabetes mellitus, neurodegenerative disorders, respiratory diseases, and adverse pregnancy outcomes.[8]

The potential relationship between the oral microbiome and frailty has recently emerged as an area of growing scientific interest. Several epidemiological studies have demonstrated that frail older adults exhibit poorer oral health status, including severe periodontitis, tooth loss, reduced occlusal function, xerostomia, and impaired chewing efficiency.[9] In parallel, advances in next-generation sequencing technologies have revealed alterations in oral microbial composition associated with aging and frailty, suggesting that specific microbial signatures may reflect biological aging rather than chronological age alone.[10] These observations indicate that the oral microbiome may actively participate in frailty development through interconnected mechanisms involving chronic inflammation, immune dysregulation, nutritional impairment, and reduced functional capacity.

Despite these emerging findings, current knowledge remains fragmented. Existing reviews have predominantly focused on the gut microbiome, whereas evidence concerning the oral microbiome is dispersed across studies in dentistry, microbiology, gerontology, and immunology. Furthermore, the mechanistic pathways connecting oral dysbiosis with frailty have not been comprehensively synthesized, and the clinical implications of oral microbial profiling for frailty prevention, early diagnosis, and precision geriatric care remain insufficiently discussed. Given that the oral microbiome is a potentially modifiable ecosystem, understanding its contribution to frailty could provide new opportunities for preventive strategies, personalized oral healthcare, and microbiome-targeted interventions aimed at promoting healthy aging.

Therefore, this narrative review summarizes current evidence regarding the relationship between the oral microbiome and frailty syndrome. Specifically, this review discusses age-related alterations in oral microbial ecology, the biological mechanisms linking oral dysbiosis with frailty, evidence from clinical and molecular studies, potential salivary microbial biomarkers, and future perspectives for microbiome-based precision dentistry in geriatric populations. By integrating recent findings from oral microbiology, immunology, and geriatric medicine, this review aims to provide a comprehensive framework for understanding the role of the oral microbiome in the pathogenesis of frailty and to identify future research directions that may facilitate the development of targeted preventive and therapeutic strategies.

2. Method

This narrative review was conducted to summarize and critically discuss current evidence regarding the relationship between the oral microbiome and frailty syndrome. The review followed the general principles of transparent narrative reviews by clearly describing the literature search strategy, study selection, and narrative synthesis. Although this review was not designed as a systematic review, efforts were made to ensure that the included literature was comprehensive, relevant, and up to date. A literature search was performed using two electronic databases, PubMed and Google Scholar, to identify relevant publications. Articles published between January 2021 and March 2026 were considered to capture recent advances in oral microbiome research, aging, and frailty syndrome.

The search strategy combined Medical Subject Headings (MeSH) and free-text keywords using Boolean operators ("AND" and "OR"). The following search terms were used individually and in combination: "oral microbiome", "oral microbiota", "oral dysbiosis", "frailty", "frailty syndrome", "oral frailty", "older adults", "elderly", "aging", "periodontitis", "salivary microbiome", "inflammaging", "immunosenescence".

Studies were included if they met the following criteria written in English, investigated the oral microbiome, oral dysbiosis, periodontal microbiota, or salivary microbiome, evaluated frailty syndrome, oral frailty, biological aging, inflammaging, or immunosenescence, included original research articles, clinical studies, cohort studies, case-control studies, longitudinal studies, systematic reviews, meta-analyses, and high-quality narrative reviews relevant to the topic. The following publications were excluded conference abstracts, editorials, commentaries, letters to the editor, and unpublished manuscripts, studies without accessible full text, articles not written in English, studies focusing exclusively on the gut microbiome without discussing the oral microbiome.

The selected evidence was synthesized narratively and organized into the following thematic areas: (1) frailty syndrome and biological aging, (2) age-related changes in the oral microbiome, (3) oral dysbiosis and systemic inflammation, (4) mechanisms linking the oral microbiome to frailty, (5) clinical evidence, (6) salivary microbial biomarkers, and (7) future perspectives for microbiome-based interventions in precision geriatric dentistry.

3. Results And Discussion

Five studies published between 2021 and 2026 were included in this narrative review. Overall, the available evidence consistently demonstrated that oral microbiome composition is influenced by physical activity, frailty status, oral function, and systemic inflammation. Exercise interventions generally promoted microbial homeostasis, whereas physical inactivity and frailty were associated with oral dysbiosis and increased abundance of opportunistic microorganisms.

1. Physical Activity Promotes Oral Microbial Homeostasis

Moderate-intensity continuous training (MICT) and high-intensity interval training (hiit) significantly altered oral microbial communities after a 16-week intervention. MICT was associated with increased Shannon and Simpson diversity indices, reduced abundance of firmicutes, and increased bacteroidetes, whereas HIIT increased microbial richness but showed a slight reduction in overall diversity. both exercise modalities significantly reduced several pathogenic bacterial taxa.[11]

These findings suggest that exercise contributes to oral microbial homeostasis by improving ecological stability within the oral cavity. moderate exercise is thought to enhance salivary secretion, increase secretory immunoglobulin a (sIgA), improve antioxidant capacity, and strengthen mucosal immune surveillance. these physiological adaptations create an oral environment that favors commensal microorganisms while suppressing opportunistic pathogens, thereby reducing the risk of dysbiosis.[11]

2. Frailty Rather Than Chronological Age Drives Oral Dysbiosis

The reviewed evidence indicates that biological ageing is more strongly associated with oral dysbiosis than chronological ageing. Declercq et al. evaluated 1,357 Canadian adults and demonstrated that higher frailty scores were associated with significantly lower alpha diversity, including reduced richness, shannon diversity, and phylogenetic diversity. frailty was also associated with increased abundance of *Porphyromonas, Fusobacterium*, *Aggregatibacter, Neisseria*, *Corynebacterium,* and *Stomatobaculum,* while *Veillonella* abundance declined.[12]

These microbial shifts suggest that frailty reflects cumulative physiological decline affecting host–microbiome interactions more accurately than chronological age. increased abundance of periodontal-associated pathogens such as *Porphyromonas* and *Fusobacterium* may contribute to chronic oral inflammation and systemic diseases. consequently, oral dysbiosis may serve as a biological marker of ageing and frailty rather than ageing itself.[12]

3. Oral Frailty Facilitates Opportunistic Pathogen Colonization

Clinical evidence further supports the close relationship between oral frailty and oral dysbiosis. Chen et al. demonstrated that 53.4% of hospitalized older adults exhibited oral frailty, which independently increased the likelihood of enterobacterales colonization by more than three-fold. Poor articulatory oral motor performance represented the strongest predictor, increasing colonization risk by over five-fold.[13]

Reduced tongue mobility, impaired mastication, and swallowing dysfunction diminish natural oral clearance mechanisms, facilitating persistence of opportunistic microorganisms within the oral cavity. Such dysbiotic communities may subsequently increase susceptibility to aspiration pneumonia and other systemic infections frequently observed among frail older adults. These findings emphasize that preservation of oral function should be considered an essential component of healthy ageing strategies.[13]

4. Physical Inactivity Accelerates Microbial Dysbiosis and Frailty

The detrimental effects of physical inactivity were demonstrated using a head-down bedrest model that simulated prolonged immobilization. Alvaro-fuss et al. Found that only 14 days of inactivity induced significant alterations in both oral and gut microbial communities, accompanied by increasing frailty scores. Participants receiving multimodal exercise maintained higher abundance of beneficial taxa, including roseburia, and experienced less microbial disruption than inactive participants.[14]

These findings suggest that inactivity itself contributes to biological ageing through disruption of host-microbiome interactions. Reduced muscle activity, impaired circulation, diminished salivary secretion, and immune dysregulation may collectively promote microbial imbalance during prolonged immobilization. Exercise therefore appears capable of partially preventing inactivity-induced microbial dysbiosis and delaying early frailty development.[14]

5. Systemic Inflammation Links Exercise, Oral Microbiome, and Healthy Ageing

Another consistent finding among the reviewed studies is the role of chronic low-grade inflammation as a biological mechanism connecting physical activity, oral microbiota, and frailty. Memelink et al. demonstrated that a combined lifestyle intervention consisting of caloric restriction, resistance exercise, and HIIT significantly reduced circulating leptin and IL-1 receptor antagonist concentrations while improving insulin sensitivity and reducing adiposity. Protein supplementation did not provide additional anti-inflammatory effects.[15]

Exercise-induced reductions in systemic inflammation may indirectly stabilize the oral microbiome by improving mucosal immunity and reducing ecological conditions favorable to pathogenic anaerobic bacteria. Improved endothelial function, enhanced immune competence, increased salivary secretion, and reduced oxidative stress collectively contribute to preservation of oral microbial homeostasis. Conversely, chronic inflammation, immunosenescence, and impaired salivary function associated with frailty promote dysbiosis and periodontal tissue destruction.[16]

6. Clinical Implications and Future Perspectives

Collectively, the reviewed evidence indicates that the oral microbiome occupies a central position within the interaction between physical activity, oral function, systemic inflammation, and biological ageing. Regular exercise promotes microbial diversity, reduces pathogenic taxa, and supports oral immune homeostasis, whereas frailty and inactivity favor dysbiosis and opportunistic pathogen colonization.

From a clinical perspective, physical activity should be considered an adjunctive strategy for maintaining oral health in older adults. Routine assessment of oral frailty, including chewing efficiency, tongue pressure, articulatory performance, and swallowing function may facilitate early identification of individuals at risk for dysbiosis and related systemic complications.

However, interpretation of current evidence should consider several limitations. The reviewed studies differed substantially regarding study populations, exercise protocols, frailty assessment methods, and microbiome sequencing techniques. Most studies employed 16S rRNA sequencing, limiting functional characterization of microbial communities. Future longitudinal studies integrating metagenomics, metabolomics, transcriptomics, and host immune profiling are needed to clarify causal relationships between exercise, oral microbiome modulation, and healthy ageing.

4. Conclusion

Current evidence indicates that the oral microbiome plays a pivotal role in the complex interplay between physical activity, oral frailty, systemic inflammation, and healthy ageing. The studies reviewed consistently demonstrate that regular physical activity promotes a more balanced oral microbial ecosystem by enhancing microbial diversity and reducing the abundance of opportunistic pathogens. In contrast, physical inactivity and oral frailty are associated with oral dysbiosis, characterized by decreased microbial diversity and increased colonization by pathogenic bacteria, which may contribute to the progression of periodontal disease, aspiration pneumonia, and other age-related systemic disorders. Importantly, the reviewed literature suggests that biological ageing, as reflected by frailty status, exerts a greater influence on oral microbial composition than chronological age alone. These findings highlight the oral microbiome as a promising biomarker of biological ageing and a potential therapeutic target for maintaining oral and systemic health in older adults.

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