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Fixed Orthodontic Appliances and Periodontal Pathogen Colonisation: A Systematic Review and Meta-Analysis

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ADMINISTRATIVE INFORMATION

Support - 1.High-throughput sequencing of subgingival microbiota and study of osteoblast osteogenic differentiation-related lncRNAs in an inflammatory environment in adolescent orthodontic patients, Project No.: 2023AH052590; 2.Preparation of light-cured calcium fluoride hyaluronic acid composite hydrogel and its effect on the prevention of dental caries and leukoplakia in invisible orthodontic treatment, Project No.: AHWJ2022b035; 3. National Natural Science Foundation of China (22405008); 4. Natural Science Research Project of Anhui Educational Committee (2023AH052598); 5.High-level Talent Research Launch Fund Project of Anhui Medical College (2023RC011); 6. Research and Innovation Team Project of Anhui Medical College (WJH2023SMJK001); 7. Cooperative Project of Anhui Medical College with Anqing Zhu Xiaolong Dental Hospital (2023HXYF002).

Review Stage at time of this submission - Completed but not published.

Conflicts of interest - None declared.

INPLASY registration number: INPLASY202670059

Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 17 July 2026 and was last updated on 17 July 2026.

INTRODUCTION

Review question / Objective The objective of this systematic review and meta-analysis was to assess whether fixed orthodontic appliance therapy is associated with changes in periodontal pathogen colonisation and to determine whether quantitative pooling provides clinically meaningful inference in the presence of heterogeneous microbiological methods, time points and study designs.

Condition being studied Periodontal disease is a dysbiotic inflammatory condition involving disruption of host-microbe homeostasis and destruction of tooth-supporting tissues. The red complex organisms Porphyromonas gingivalis, Tannerella forsythia and Treponema denticola, along with other organisms such as Aggregatibacter actinomycetemcomitans, Prevotella intermedia and Fusobacterium nucleatum, have been repeatedly implicated in periodontal pathogenesis.

METHODS

Participant or population Human participants undergoing fixed orthodontic appliance therapy.

Intervention Fixed orthodontic appliance.

Comparator Studies were eligible when they enrolled human participants undergoing fixed orthodontic appliance therapy and reported microbiological outcomes for periodontal-associated taxa or bacterial complexes. Eligible designs included randomised or nonrandomised clinical trials, prospective cohort studies, self-controlled before-and-after studies, controlled cohort studies and cross-sectional comparisons when fixed appliance users were directly compared with removable appliance users or nonorthodontic controls.

Study designs to be included Randomised or nonrandomised clinical trials, prospective cohort studies, self-controlled before-and-after studies, controlled cohort studies and cross-sectional comparisons. No randomised trial contributed extractable quantitative data.

Eligibility criteria Studies were eligible when they enrolled human participants undergoing fixed orthodontic appliance therapy and reported microbiological outcomes for periodontal-associated taxa or bacterial complexes. Eligible designs included randomised or nonrandomised clinical trials, prospective cohort studies, self-controlled before-and-after studies, controlled cohort studies and cross-sectional comparisons when fixed appliance users were directly compared with removable appliance users or nonorthodontic controls. No randomised trial contributed extractable quantitative data. Studies were required to report periodontal pathogens or clearly defined periodontopathogen groups, including qualitative detection rates, relative abundance, counts, proportions or other extractable quantitative measures.

Information sources A comprehensive search was performed in PubMed/MEDLINE, Embase, Cochrane Central Register of Controlled Trials, Web of Science Core Collection, China National Knowledge Infrastructure (CNKI) and Wanfang Data for articles published between 1 January 2010 and 31 December 2025. The 2010 start date was selected because most contemporary molecular and sequencing-based investigations of orthodontic microbiology were published after this period, and prior systematic reviews had already summarised earlier culture- and PCR-dominant literature. Reference lists of included studies and relevant reviews were manually screened.

Main outcome(s) Studies were required to report periodontal pathogens or clearly defined periodontopathogen groups, including qualitative detection rates, relative abundance, counts, proportions or other extractable quantitative measures.

Quality assessment / Risk of bias analysis Risk of bias in individual studies was assessed independently by two reviewers using ROBINS-I.

Strategy of data synthesis The SMD with Hedges' g correction was used because the included studies reported pathogen positivity, relative abundance, proportions or counts on different scales. A positive SMD indicated higher periodontal pathogen levels after fixed appliance placement or in fixed appliance users compared with the comparator. Because SMD standardises statistical dispersion but does not make fundamentally different microbiological outcomes biologically equivalent, the overall pooled estimate was treated as exploratory and interpreted alongside subgroup, design and sensitivity analyses.

Random-effects meta-analysis was performed using the restricted maximum likelihood (REML) estimator with Hartung-Knapp-Sidik-Jonkman CIs. Heterogeneity was assessed using Cochran's Q, τ^2 and I^2, and a 95% prediction interval was calculated to represent the expected range of true effects in comparable future settings. Subgroup analyses examined detection method, sample type and study design. Sensitivity analyses excluded the cross-sectional study, omitted each study sequentially, excluded extreme outliers, varied the assumed pre-post correlation and compared REML with DerSimonian-Laird and Paule-Mandel estimators; corresponding robustness calculations are provided in Supplementary Table S5. Analyses were performed in R using the meta and metafor packages [18]. Funnel plots were considered exploratory only, and Egger's test was not performed because fewer than 10 quantitative studies were included and heterogeneity was extreme.

Subgroup analysis Subgroup analysis by detection method showed that 16S rRNA sequencing studies had a small, nonsignificant pooled estimate (SMD = 0.30, 95% CI: -1.03 to 1.63, I^2 = 58.3%) (Figure 4A); PCR-based studies showed opposing directions and extremely wide uncertainty (SMD = 2.23, 95% CI: -73.86 to 78.31, I^2 = 99.8%). The single checkerboard DNA-DNA hybridisation study reported an SMD of 1.38 (95% CI: 0.80-1.97), and the single qPCR study reported an SMD of 0.88 (95% CI: -0.45 to 2.21). The test for subgroup differences was not statistically significant (χ^2 = 6.38, df = 3, P = 0.0945), and subgroup interpretation was limited by the small number of studies per method.

Subgroup analysis by sample type also showed substantial instability (Figure 4B). Subgingival plaque studies had a nonsignificant pooled estimate with extreme heterogeneity (SMD = 1.56, 95% CI: -6.34 to 9.46, I^2 = 99.4%). The single plaque study showed an SMD of 0.63 (95% CI: 0.30-0.97), the saliva-only study showed an SMD of -0.42 (95% CI: -1.31 to 0.46) and the combined plaque and saliva study showed an SMD of 0.88 (95% CI: -0.45 to 2.21). The test for subgroup differences was not statistically significant (χ^2 = 5.22, df = 3, P = 0.1564).

Sensitivity analysis Sensitivity analyses excluded the cross-sectional study, omitted each study sequentially, excluded extreme outliers, varied the assumed pre-post correlation and compared REML with DerSimonian-Laird and Paule-Mandel estimators; corresponding robustness calculations are provided in Supplementary Table S5.

Country(ies) involved China.

Keywords Orthodontic appliances; fixed appliances; periodontal pathogens; oral microbiome; systematic review; meta-analysis.

Contributions of each author

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