Natural Resources for Human Health
eISSN: 2583-1194

Original Research

Received 21 May 2026
Revised 30 June 2026
Accepted 23 July 2026

Natural Resources for Human Health 2026, Vol. 6 (10s): 1253–1263

KEYWORDS:
chronic periodontitis; chronic tonsillitis; oral microbial continuum; probiotics; focal infection; interdisciplinary treatment

Chronic Tonsillitis Aggravates Chronic Periodontitis: Shared Pathogens and a Probiotic-Based Combined Sanation Protocol

Ferangiz Djurayeva[1]*, Firuza Turayeva[2], Tolibjon Tilavov[3]

[1]*Department of Dentistry, Asian International University, Bukhara, Republic of Uzbekistan; ORCID 0009-0002-0444-3434, djfera822@gmail.com
[2]Department of Pediatric Dentistry, Bukhara State Medical Institute named after Abu Ali ibn Sino, Bukhara, Republic of Uzbekistan; ORCID 0009-0006-6486-7633, turayeva.firuza@bsmi.uz
[3]Department of Histology, Cytology and Embryology, Bukhara State Medical Institute named after Abu Ali ibn Sino, Bukhara, Republic of Uzbekistan; ORCID 0009-0008-0781-9285, tilavov.tolibjon@bsmi.uz

ABSTRACT: Chronic periodontitis (CP) is a dysbiosis-driven inflammatory disease, yet the influence of a persistent oropharyngeal focus such as chronic tonsillitis (CT) on its clinical, microbiological and immunological phenotype remains poorly defined. This prospective, controlled study (2019–2024) enrolled 156 adults (18–60 years) in three groups: CP with CT (Group 1, n = 64), CP without CT (Group 2, n = 62), and periodontally healthy controls (Group 3, n = 30). Periodontal indices, quantitative culture of paired periodontal-pocket and tonsillar-crypt samples with 16S-rRNA genotyping, and serum and oral-fluid cytokines were assessed. Within Group 1, patients received a staged combined-sanation algorithm adding tonsillar lavage and natural biotherapeutics—probiotics (Lactobacillus rhamnosus, Bifidobacterium longum), topical hyaluronate and antioxidants (Subgroup 3.1, n = 31)- or standard periodontal therapy (Subgroup 3.3, n = 33), with follow-up to 6 months. Despite equivalent oral hygiene, Group 1 was more severe than Group 2 (probing depth 4.9 ± 0.8 vs 4.1 ± 0.7 mm; $p < 0.01$), carried a heavier, more mixed pathogen load, and showed periodontal–tonsillar species concordance in 64.1% of patients with genotype-level identity in up to 35.9%. Cytokines were higher and graded with tonsillitis form and severity (r=0.42–0.68). At 6 months, Subgroup 3.1 outperformed 3.3 for probing depth (3.1±0.5 vs 3.7±0.6 mm) and commensal-flora restoration (78.5% vs 62.8%; both $p<0.01$), with complete remission in 82% versus 63%. Chronic tonsillitis acts as an active modifier of periodontitis through shared pathogens; a combined protocol using natural biotherapeutics produced superior, durable improvement, supporting interdisciplinary care.

1. INTRODUCTION

Periodontitis is a chronic, multifactorial inflammatory disease of the tooth-supporting tissues and one of the most prevalent non-communicable conditions worldwide; severe periodontitis affects approximately 11% of adults and is a leading cause of tooth loss and impaired oral health–related quality of life (Kassebaum et al., 2014; Kinane et al., 2017). The 2017 World Workshop reframed the disease using a stage-and-grade system that captures severity, complexity, and rate of progression (Papapanou et al., 2018; Tonetti et al., 2018).

Periodontal destruction is initiated by a dysbiotic subgingival biofilm in which anaerobic consortia—classically the "red complex" of Porphyromonas gingivalis, Tannerella forsythia and Treponema denticola, together with Fusobacterium

nucleatum and Prevotella intermedia—shift the community toward pathogenicity (Socransky et al., 1998; Holt and Ebersole, 2005). Within this ecology, P. gingivalis acts as a low-abundance keystone pathogen that subverts host immunity to remodel a commensal microbiota into a dysbiotic one (Hajishengallis et al., 2012; Lamont and Hajishengallis, 2015), driving a host-mediated cascade of interleukin (IL)-1β, IL-6 and tumour necrosis factor-α (TNF-α) that culminates in connective-tissue breakdown and alveolar bone resorption (Hajishengallis, 2015). This local inflammation spills over systemically, and periodontitis is associated with elevated circulating C-reactive protein (CRP) (Paraskevas et al., 2008).

Chronic tonsillitis is a common latent oropharyngeal focus in which palatine-tonsil crypts sustain a persistent, biofilm-associated microbial reservoir. Molecular studies show that the tonsillar-crypt microbiota is more reminiscent of the periodontal than of the mucosal microbiota and harbours recognised periodontal pathogens, including P. gingivalis and T. forsythia (Jensen et al., 2013), while culture and sequencing of tonsils in acute and chronic tonsillitis recover overlapping anaerobes and Staphylococcus aureus (Khadilkar and Ankle, 2016; Yeoh et al., 2019). The historical concept of focal infection—whereby a chronic tonsillar focus seeds distant inflammation—has been revisited in recent clinical reports (Lakos, 2026). Because the periodontal pocket and the tonsillar crypt share an oropharyngeal habitat linked by continuous salivary transit, a persistent tonsillar focus could plausibly aggravate periodontitis through cross-focal recirculation of shared pathogens and sustained systemic inflammation. Direct, patient-level evidence that couples paired microbiology of both niches with genotype-level strain matching, however, is scarce.

Standard periodontal therapy—scaling and root planing with adjuncts (Sanz et al., 2020)—targets the dentition but not the tonsillar reservoir or the systemic inflammatory background, which may contribute to incomplete resolution and recolonisation. In this context, natural biotherapeutic resources have gained attention: adjunctive probiotics, chiefly Lactobacillus and Bifidobacterium species, help re-establish a commensal-dominated flora, lower periodontopathogen load and reduce bleeding after debridement (Teughels et al., 2013; Martin-Cabezas et al., 2016; de Mendonça et al., 2024; Baddouri and Hannig, 2024). Harnessing such living microbial resources—together with hyaluronate and antioxidants—aligns periodontal management with the wider goal of deploying natural resources for human health.

We therefore (i) characterised the periodontitis phenotype with versus without concomitant CT and quantified periodontal–tonsillar microbial concordance at the species and genotype level; (ii) tested the association of pathogen load and systemic mediators with severity and with tonsillitis form; and (iii) evaluated whether a staged algorithm combining tonsillar and periodontal sanation with natural biotherapeutics improves 6-month outcomes relative to standard therapy, using a purpose-built integral clinical–microbiological efficacy index. We hypothesised that CT aggravates periodontitis in a tonsillitis-form–graded manner and that combined sanation yields superior, durable clinical and microbiological resolution. The study is reported in accordance with the STROBE guidance (von Elm et al., 2007).

2. MATERIALS AND METHODS

2.1. Study design and participants

This prospective, controlled, comparative study with a nested two-arm interventional comparison was conducted between 2019 and 2024 at regional dental and otorhinolaryngology services. A total of 156 adults aged 18–60 years were enrolled in three groups: Group 1 (CP with concomitant CT, n = 64), Group 2 (CP without CT, n = 62), and Group 3 (periodontally healthy controls, n = 30). CP was diagnosed according to the 2017 World Workshop classification (Caton et al., 2018), and group assignment followed a joint dental and otorhinolaryngological assessment including pharyngoscopy.

Eligible patients had moderate-to-severe CP confirmed clinically and radiographically, with ≥ 20 teeth present; Group 1 additionally required compensated CT outside exacerbation confirmed by an otorhinolaryngologist, and Group 2 required the absence of chronic upper-airway inflammatory disease. Exclusion criteria were decompensated systemic disease influencing periodontal status, immunodeficiency or immunosuppressive therapy, acute infection or exacerbation, antibacterial or anti-inflammatory therapy within 4–6 weeks, specialised periodontal or tonsillar treatment within 6 months, and pregnancy or lactation. In Group 1, CT was classified as the simple (compensated) form or the toxic-allergic form of grade I (TAF-I) or grade II (TAF-II).

2.2. Clinical, imaging and microbiological assessment

Standardised periodontal charting by calibrated examiners recorded the papillary–marginal–alveolar (PMA) index, the Russell

periodontal index (PI), the simplified oral hygiene index (OHI-S), CPITN, probing pocket depth (PPD; six sites per tooth) with the proportion of sites ≥ 5 mm, bleeding on probing (BOP), the papillary bleeding index (PBI) and the sulcus bleeding index (SBI), Miller tooth mobility, and gingival recession; probing used a WHO probe under a controlled force of approximately 0.2 N. Panoramic radiography with targeted periapical views assessed alveolar bone, and pharyngoscopy graded tonsillar changes. Subgingival samples from the deepest pockets and, in Group 1, paired tonsillar-crypt contents were collected before treatment, transported in reduced medium, and cultured aerobically and anaerobically; isolates were identified by morphology, Gram staining and biochemical profiling, and burden was expressed as $\log_{10}$ colony-forming units (CFU)/mL. Paired periodontal and tonsillar isolates of the same species were compared by 16S-rRNA gene amplification and sequencing, with ≥ 95% sequence identity taken as indicative of a shared (identical) strain; because 16S typing does not achieve whole-genome resolution, genotype concordance is interpreted as suggestive rather than definitive of strain identity.

2.3. Inflammatory mediators

Serum and oral-fluid IL-1β, IL-6, TNF-α (pg/mL) and CRP (mg/L) were measured by enzyme-linked immunosorbent assay in duplicate, with the mean of the two readings used for analysis.

2.4. Staged combined-sanation algorithm and interventional comparison

Within Group 1, patients were allocated to the staged combined-sanation algorithm (Subgroup 3.1, n = 31) or standard periodontal therapy (Subgroup 3.3, n = 33); patients of Group 2 who were treated served as an additional non-tonsillitis reference. The algorithm comprised three sequential stages. Stage I (sanitising, jointly with the otorhinolaryngologist; 7–10 days): lacunar lavage of the tonsils with 0.02% miramistin and vacuum aspiration of caseous plugs, ultrasonic supra- and subgingival debridement, and periodontal-pocket irrigation with 0.05% chlorhexidine. Stage II (anti-inflammatory–antiseptic; 10–14 days): culture-guided systemic antibacterial therapy (amoxicillin–clavulanate 1 g twice daily for 10 days, or cefuroxime 500 mg twice daily; clarithromycin 500 mg twice daily in case of allergy) with local metronidazole–chlorhexidine gel and repeated pocket antisepsis. Stage III (restorative–supportive; 6–8 weeks): oral probiotics containing Lactobacillus rhamnosus and Bifidobacterium longum, topical sodium hyaluronate for epithelialisation, and B-group vitamins and antioxidants, with microflora re-assessment. Standard therapy comprised oral-hygiene instruction, scaling and root planing, and local antiseptics without tonsillar sanation or biotherapeutics. The algorithm was applied in three severity-matched variants (variant I for the simple form, II for TAF-I, III for TAF-II), and transition between variants was permitted when clinical response was insufficient.

2.5. Endpoints, integral efficacy index and statistical analysis

Assessments were made before treatment (T_0), at 14 ± 2 days (T_1), 6–8 weeks (T_2) and 6 months (T_3). The co-primary endpoints of the interventional comparison were the 6-month between-subgroup differences in PPD and in commensal-flora proportion; secondary endpoints included other clinical indices, pathogen load, mixed-association frequency, remission, and recurrence. Remission was defined a priori as PMA < 10%, BOP < 10%, and < 5% of sites with PPD ≥ 5 mm. To summarise overall response, a purpose-built integral clinical–microbiological efficacy index (IEI) was computed as the mean relative change from baseline to T_3 across seven parameters (PMA, Russell PI, mean PPD, BOP, P. gingivalis load, F. nucleatum load, and—inverted—the commensal-flora proportion), expressed as a percentage where 100% denotes full normalisation; IEI ≥ 90% was read as complete remission, 70–89% as marked improvement, 50–69% as partial, and < 50% as insufficient.

Analyses used SPSS 26 and Statistica 12 ($\alpha = 0.05$, two-sided). Normality was checked with the Shapiro–Wilk test. Three-group comparisons used one-way analysis of variance with Tukey post hoc tests, or the Kruskal–Wallis test with Dunn post hoc tests; categorical variables used the χ^2 or Fisher exact test. Two-group contrasts used the t or Mann–Whitney test with mean differences, 95% confidence intervals and Cohen's d. Ordered trends across tonsillitis forms used the Jonckheere–Terpstra test. Longitudinal changes used linear mixed-effects models with a random patient intercept and fixed effects for time, subgroup and their interaction; the primary 6-month contrast additionally used analysis of covariance adjusted for the baseline value and smoking, because smoking prevalence differed across groups. Associations used Spearman correlation. Multiplicity was controlled within analysis families by the Holm–Bonferroni procedure.

Natural Resources for Human Health
eISSN: 2583-1194

2.6. Ethics

The study followed the Declaration of Helsinki (2013 revision) and was approved by the Ethics Committee of the Bukhara State Medical Institute named after Abu Ali ibn Sino (Minutes No. 3, 30 June 2026). All participants gave written informed consent before enrolment, including consent to the use of anonymised data for scientific publication.

3. RESULTS AND DISCUSSION

3.1. Participants

Groups were comparable for age (38.6 ± 7.9, 39.4 ± 8.2 and 37.1 ± 7.4 years; p = 0.402), sex (χ^2 = 1.07, p = 0.585) and residence (χ^2 = 0.42, p = 0.810), and CP duration did not differ between the two disease groups (5.7 ± 2.6 vs 5.3 ± 2.9 years; p = 0.379). Current smoking differed (43.8%, 54.8% and 23.3%; χ^2 = 8.82, p = 0.012) and was carried as a covariate; somatic comorbidity showed only a non-significant trend (48.4%, 45.2% and 30.0%; χ^2 = 4.67, p = 0.097). In Group 1, CT was of the simple form in 38 patients (59.4%), TAF-I in 19 (29.7%) and TAF-II in 7 (10.9%) (Table 1).

Table 1. Baseline demographic and periodontal characteristics by group.

Variable	Group 1: CP+CT (n = 64)	Group 2: CP (n = 62)	Group 3: healthy (n = 30)	p
Age, y	38.6 ± 7.9	39.4 ± 8.2	37.1 ± 7.4	0.402
Male, n (%)	35 (54.7)	31 (50.0)	14 (46.7)	0.585
Current smokers, n (%)	28 (43.8)	34 (54.8)	7 (23.3)	0.012
CP duration, y	5.7 ± 2.6	5.3 ± 2.9	—	0.379
PMA, %	58.3 ± 11.4	46.7 ± 10.2	9.1 ± 2.8	<0.001
Russell PI	4.4 ± 0.6	3.7 ± 0.5	0.8 ± 0.2	<0.01
OHI-S	2.3 ± 0.4	2.2 ± 0.5	0.9 ± 0.3	0.462
SBI	3.6 ± 0.7	2.9 ± 0.5	0.7 ± 0.2	<0.001
PPD, mm	4.9 ± 0.8	4.1 ± 0.7	1.8 ± 0.4	<0.01
Sites ≥ 5 mm, %	37.5 ± 9.6	25.8 ± 8.3	—	<0.01
BOP, %	73.4 ± 12.2	60.6 ± 11.5	8.7 ± 3.1	<0.01
PBI	2.9 ± 0.6	2.2 ± 0.5	0.5 ± 0.1	<0.01
Miller mobility (0–III)	1.84 ± 0.42	1.36 ± 0.38	0.12 ± 0.06	<0.001
Recession, mm	2.3 ± 0.6	1.6 ± 0.5	0.3 ± 0.1	<0.001

Values are mean ± SD unless stated. The p column shows the Group 1 versus Group 2 contrast for periodontal indices (Holm–Bonferroni-adjusted) and the omnibus test for demographics; all periodontal indices also differed from Group 3 at p < 0.001. BOP, bleeding on probing; OHI-S, simplified oral hygiene index; PBI/SBI, papillary/sulcus bleeding index; PI, periodontal index; PMA, papillary–marginal–alveolar index; PPD, probing pocket depth.

3.2. Concomitant tonsillitis defines a more severe periodontal phenotype

Despite comparable oral hygiene (OHI-S 2.3 ± 0.4 vs 2.2 ± 0.5; p = 0.462), Group 1 was more severe than Group 2, with higher PMA (58.3 ± 11.4% vs 46.7 ± 10.2%), deeper pockets (PPD 4.9 ± 0.8 vs 4.1 ± 0.7 mm; Cohen's d = 1.06) and more

bleeding (BOP 73.4 ± 12.2% vs 60.6 ± 11.5%; all $p < 0.01$), together with greater tooth mobility and recession (Table 1). Severity increased monotonically with tonsillitis form: from the simple form to TAF-II, PMA rose from 51.2 ± 10.6% to 70.4 ± 8.7% and PPD from 4.5 ± 0.6 to 6.1 ± 0.9 mm (ANOVA $p < 0.001$; Jonckheere–Terpstra $p < 0.001$) (Table 2). Because the two periodontitis groups were matched for hygiene and disease duration, the excess severity is unlikely to reflect plaque control alone and instead points to the tonsillar focus as an active modifier of periodontitis rather than an incidental comorbidity (Jensen et al., 2013; Lakos, 2026).

Table 2. Periodontal severity by chronic-tonsillitis form within Group 1.

Index	Simple (n = 38)	TAF-I (n = 19)	TAF-II (n = 7)	p
PMA, %	51.2 ± 10.6	62.8 ± 9.8	70.4 ± 8.7	<0.001
Russell PI	4.1 ± 0.5	4.5 ± 0.6	4.9 ± 0.4	<0.01
PPD, mm	4.5 ± 0.6	5.2 ± 0.7	6.1 ± 0.9	<0.001
BOP, %	66.2 ± 10.8	77.5 ± 12.4	86.7 ± 9.3	<0.01
Miller mobility (0–III)	1.53 ± 0.38	1.86 ± 0.41	2.17 ± 0.36	<0.001

Values are mean ± SD; p from one-way ANOVA. A monotonic trend across ordered forms was confirmed by the Jonckheere–Terpstra test ($p < 0.001$). TAF-I/II, toxic-allergic form grade I/II.

3.3. A heavier subgingival community with periodontal–tonsillar strain overlap

Group 1 harboured a heavier, more complex community. Quantitative load exceeded that of Group 2 for every target species—P. gingivalis 5.93 ± 0.52 vs 5.11 ± 0.44 and S. aureus 4.83 ± 0.51 vs 4.12 ± 0.46 $\log_{10}$ CFU/mL (Table 3, Figure 1)—and mixed two- or three-species associations were nearly twice as frequent (69.5% vs 38.7%; $p < 0.01$), the commonest being P. gingivalis + F. nucleatum (41%) and P. gingivalis + S. aureus (27%). Total load correlated with PPD ($r = 0.64$), Russell PI ($r = 0.59$) and PMA ($r = 0.52$), and P. gingivalis load correlated most strongly with PPD ($r = 0.68$; all $p < 0.01$). Crucially, paired sampling of both niches showed species-level periodontal–tonsillar concordance in 41 of 64 patients (64.1%), and 16S-rRNA genotyping matched strains in up to 35.9% of cases, most often for S. aureus, F. nucleatum and P. gingivalis (Table 5). This genotype-level overlap is direct support for cross-focal recirculation: the tonsillar crypt sustains an anaerobic, periodontal-like microbiota that can reseed the dentition and perpetuate the dysbiotic biofilm orchestrated by the keystone pathogen P. gingivalis, providing a continuous source of re-infection that standard periodontal care does not address (Hajishengallis et al., 2012; Jensen et al., 2013).

Table 3. Quantitative subgingival microbial load by group ($\log_{10}$ CFU/mL).

Organism	Group 1	Group 2	Group 3	p (1v2)	p (1v3)
Porphyromonas gingivalis	5.93 ± 0.52	5.11 ± 0.44	2.37 ± 0.26	<0.001	<0.001
Fusobacterium nucleatum	5.71 ± 0.49	5.26 ± 0.46	2.64 ± 0.31	0.002	<0.001
Prevotella intermedia	5.52 ± 0.47	5.04 ± 0.43	2.23 ± 0.28	0.004	<0.001
Aggregatibacter actinomycetemcomitans	5.26 ± 0.45	4.91 ± 0.40	1.92 ± 0.24	0.016	<0.001
Staphylococcus aureus	4.83 ± 0.51	4.12 ± 0.46	1.58 ± 0.22	<0.001	<0.001

Values are mean ± SD; contrasts by Mann–Whitney U with Holm–Bonferroni adjustment. CFU, colony-forming units.

Natural Resources for Human Health
eISSN: 2583-1194

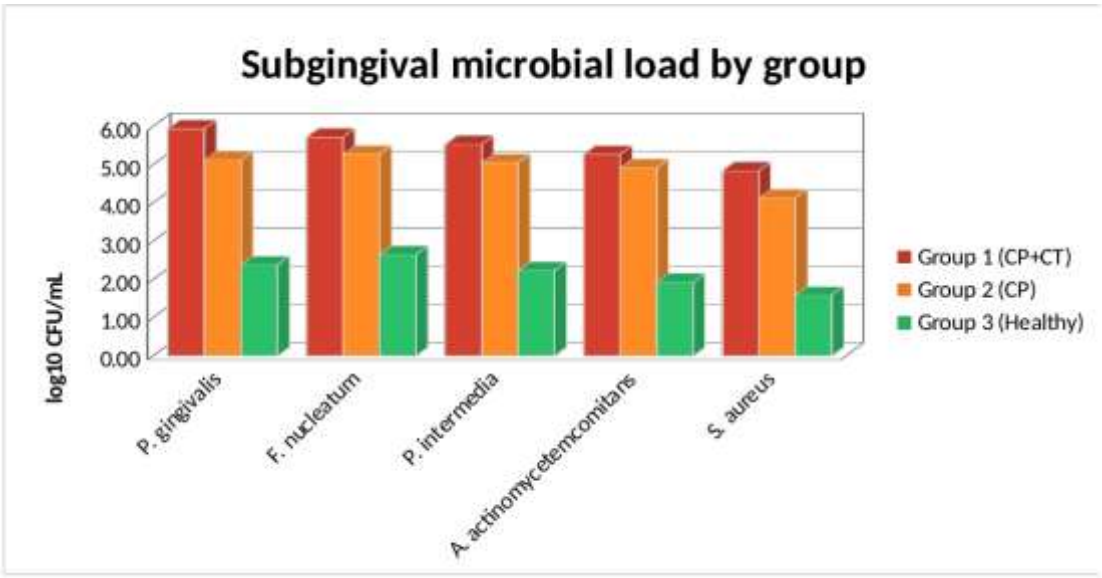

Figure 1. Mean subgingival microbial load (log_{10} CFU/mL) for five target organisms across the three groups (editable 3-D chart provided as a separate file).

Table 5. Periodontal–tonsillar microbial concordance in Group 1 (n = 64).

Organism	Species concordance, %	16S-rRNA genotype match, %
Staphylococcus aureus	43.8	35.9
Fusobacterium nucleatum	40.6	31.3
Porphyromonas gingivalis	37.5	29.7
Prevotella intermedia	32.8	26.6
Aggregatibacter actinomycetemcomitans	26.6	21.9

Concordance = proportion of Group 1 patients in whom the species was recovered from both the periodontal pocket and the tonsillar crypt; genotype match = paired isolates with ≥ 95% 16S-rRNA sequence identity (suggestive of a shared strain). Overall, 64.1% of patients shared ≥ 1 species across the two niches.

3.4. Systemic and local inflammatory amplification

Serum IL-1β (42.8 ± 6.7 vs 33.1 ± 5.4 pg/mL), IL-6 (26.3 ± 4.2 vs 18.5 ± 3.8 pg/mL) and CRP (8.7 ± 1.9 vs 6.1 ± 1.6 mg/L) were higher in Group 1 than Group 2 (all $p < 0.001$), with a smaller rise in TNF-α ($p = 0.012$); oral-fluid concentrations were concordant (Table 4, Figure 2). Mediators graded with tonsillitis form—serum IL-6 rose from 22.4 ± 3.9 (simple) to 33.5 ± 4.8 pg/mL (TAF-II; $p < 0.001$)—and correlated with severity (serum IL-1β with PPD, $r = 0.63$; CRP with Russell PI, $r = 0.57$; oral-fluid IL-6 with PMA, $r = 0.54$; all $p < 0.01$). This graded systemic response is congruent with the concept that a persistent tonsillar focus adds antigenic and inflammatory load, sustaining the low-grade systemic inflammation that characterises periodontitis and links it to systemic disease (Paraskevas et al., 2008; Hajishengallis, 2015).

Table 4. Inflammatory mediators in serum and oral fluid by group.

Marker	Biofluid	Group 1	Group 2	Group 3	p (1v2)
IL-1β, pg/mL	Serum	42.8 ± 6.7	33.1 ± 5.4	15.6 ± 3.2	<0.001
IL-6, pg/mL	Serum	26.3 ± 4.2	18.5 ± 3.8	8.9 ± 2.4	<0.001
TNF-α, pg/mL	Serum	17.2 ± 2.9	14.8 ± 2.6	9.1 ± 1.9	0.012
CRP, mg/L	Serum	8.7 ± 1.9	6.1 ± 1.6	2.4 ± 0.8	<0.001
IL-1β, pg/mL	Oral fluid	58.7 ± 8.9	42.3 ± 7.5	19.4 ± 4.1	<0.001
IL-6, pg/mL	Oral fluid	36.2 ± 6.1	26.7 ± 5.8	10.5 ± 3.3	<0.001
TNF-α, pg/mL	Oral fluid	22.4 ± 3.7	17.6 ± 3.2	8.7 ± 2.1	<0.001

Values are mean ± SD; contrasts by Mann–Whitney U with Holm–Bonferroni adjustment; all markers also differed from Group 3 at p < 0.001. CRP, C-reactive protein; IL, interleukin; TNF-a, tumour necrosis factor-a.

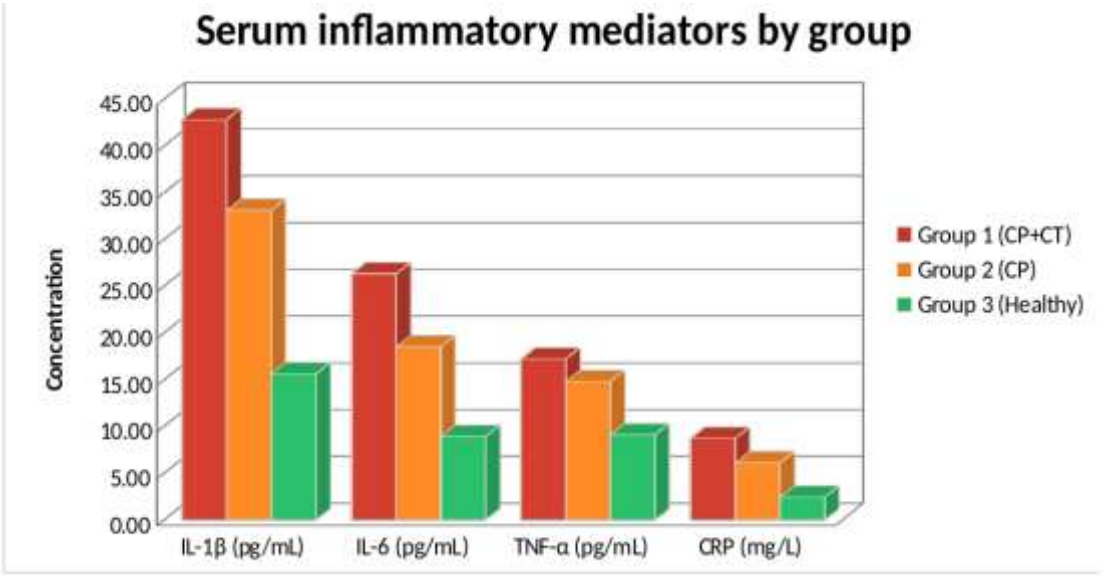

Figure 2. Serum inflammatory mediators (mean) across the three groups (editable 3-D chart provided as a separate file).

3.5. Combined sanation with natural biotherapeutics improves outcomes

Both subgroups improved, but the staged algorithm (Subgroup 3.1) produced greater and faster resolution than standard therapy (Subgroup 3.3). By 6 months (T_3), PMA fell by 47.6% versus 32.4%, PPD by 36.7% versus 22.9% (to 3.1 ± 0.5 vs 3.7 ± 0.6 mm; $p < 0.01$), BOP by 55.1% versus 41.2%, and tooth mobility by 49.5% versus 28.0%, with a significant time × subgroup interaction for each clinical outcome (Table 6, Figure 3). Microbiologically, mixed associations collapsed from 69.5% to 21.0% with the algorithm versus 67.7% to 37.8% with standard care, and the commensal-flora proportion—the study's co-primary endpoint—rose from 21.7% to 78.5% versus 23.4% to 62.8% ($p < 0.01$; Figure 4), approaching the physiological range in 79% of algorithm patients versus 58% under standard care. Complete clinical remission at T_3 reached 82% versus 63%, and the mean time to stable remission was shorter with the algorithm (47 ± 5 days). On the integral clinical–microbiological efficacy index, marked improvement (≥ 70%) was achieved by 79.4% of algorithm patients versus 56.3% ($p < 0.001$); stable remission was more frequent (64.5% vs 42.4%; $p < 0.05$) and recurrence rarer (3.2% vs 12.1%). Reduction of P. gingivalis and F. nucleatum load correlated with clinical improvement (Δ P. gingivalis with Δ PMA, $r = 0.68$;

p < 0.01), indicating that clinical benefit tracked microbiological resolution rather than occurring independently. No treatment-related adverse events occurred. Removing the tonsillar reservoir eliminates a niche that scaling and root planing leaves untouched, while the probiotic phase re-establishes a commensal-dominated flora—an effect consistent with contemporary evidence that Lactobacillus-based biotherapeutics lower periodontopathogen load and inflammation as adjuncts to non-surgical therapy (Teughels et al., 2013; de Mendonça et al., 2024; Baddouri and Hannig, 2024). These natural microbial resources thus complement mechanical debridement by restoring, rather than merely suppressing, the oral ecosystem.

Table 6. Six-month outcomes by treatment subgroup within Group 1.

Outcome	3.1 T_0	3.1 T_3	3.3 T_0	3.3 T_3	p (T_3)
PMA, %	57.4 ± 10.8	9.8 ± 3.7	56.8 ± 11.1	18.4 ± 5.8	<0.001
Russell PI	4.4 ± 0.6	1.9 ± 0.4	4.3 ± 0.6	2.4 ± 0.4	<0.01
PPD, mm	4.9 ± 0.8	3.1 ± 0.5	4.8 ± 0.8	3.7 ± 0.6	<0.01
BOP, %	73.4 ± 12.2	18.3 ± 6.4	70.9 ± 11.5	29.7 ± 8.5	<0.01
Mobility (Miller)	1.84 ± 0.42	0.93 ± 0.28	1.78 ± 0.39	1.28 ± 0.35	<0.05
Commensal flora, %	21.7 ± 6.5	78.5 ± 9.2	23.4 ± 6.9	62.8 ± 8.7	<0.01
Complete remission, %	—	82	—	63	—
IEI ≥ 70%, %	—	79.4	—	56.3	<0.001

Subgroup 3.1 = staged combined-sanation algorithm with natural biotherapeutics (n = 31); Subgroup 3.3 = standard therapy (n = 33). T_0, baseline; T_3, 6 months. p (T_3) is the between-subgroup comparison at 6 months (ANCOVA adjusted for the baseline value and smoking). IEI, integral clinical–microbiological efficacy index. Abbreviations as in Tables 1 and 4.

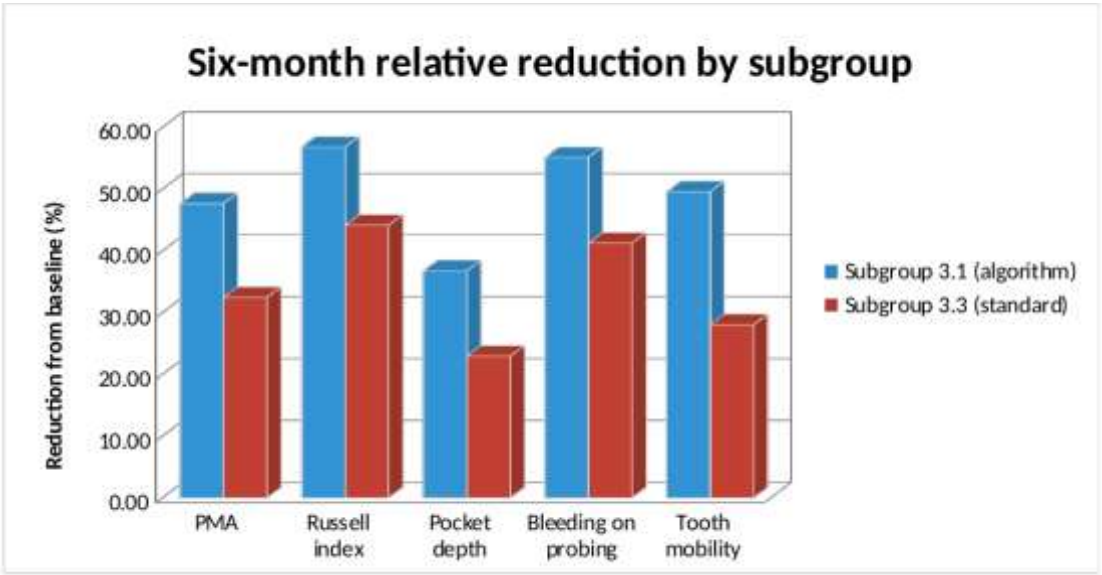

Figure 3. Six-month relative reduction (%) from baseline in key clinical outcomes by treatment subgroup (editable 3-D chart provided as a separate file).

Natural Resources for Human Health
eISSN: 2583-1194

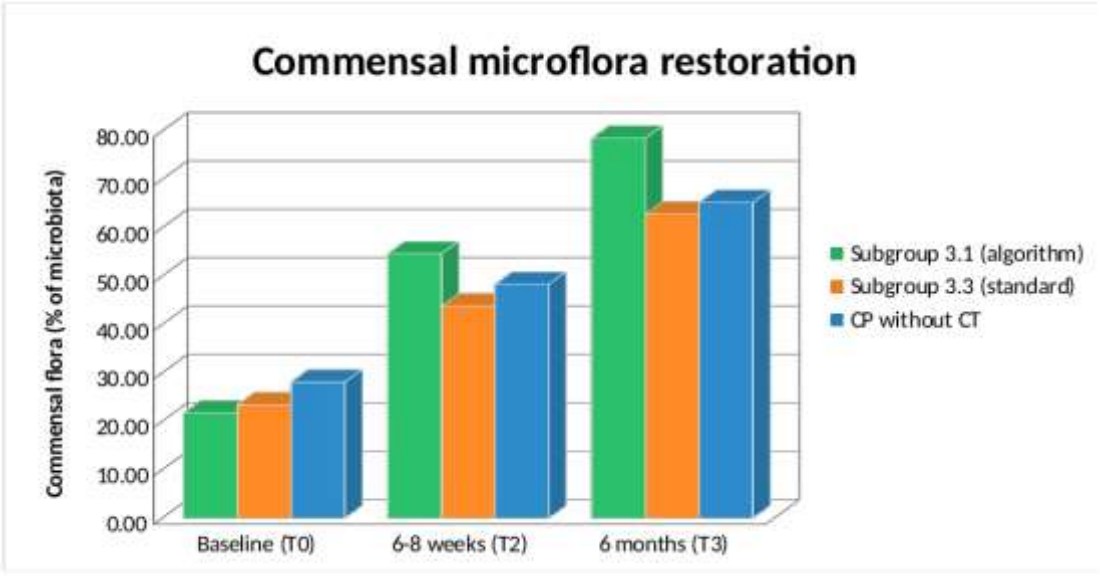

Figure 4. Restoration of the commensal microflora proportion (%) at baseline, 6–8 weeks and 6 months by subgroup, with the CP-without-CT reference (editable 3-D chart provided as a separate file).

3.6. Clinical implications, strengths and limitations

The algorithm proved adaptable in practice: residual gingival inflammation in seven simple-form patients resolved after a short antibacterial course; three TAF-I patients responded to added physiotherapy; and one TAF-II patient with persisting toxic-allergic features underwent tonsillectomy, after which serum IL-6 fell from 32.7 to 15.4 pg/mL and periodontal inflammation regressed—clinical corroboration that the tonsillar focus fed the periodontal process. Practically, a mismatch between high inflammatory indices and adequate hygiene should prompt oropharyngeal screening and otorhinolaryngological referral; in confirmed dual pathology, both niches should be treated simultaneously under culture guidance, with a biotherapeutic restorative phase and microbiological monitoring. Strengths include the integrated clinical–microbiological–immunological design, paired sampling of both foci with genotype-level matching, quantitative microbiology, 6-month follow-up, and analysis with effect sizes, adjusted models and multiplicity control. Limitations include the single-centre design and modest size; the interventional comparison was not a randomised, allocation-concealed, assessor-blinded trial, so residual confounding cannot be excluded, and 16S typing does not provide whole-genome strain resolution. These constraints define an agenda for a randomised multicentre trial with strain-resolved microbiology and longer follow-up.

4. CONCLUSIONS

Chronic tonsillitis acts as an active modifier that aggravates chronic periodontitis through shared pathogens, genotype-confirmed cross-focal recirculation, and amplified systemic and local cytokine responses, with severity graded by tonsillitis form. A staged algorithm combining tonsillar and periodontal sanation with natural biotherapeutics—probiotics, hyaluronate and antioxidants—produced greater and more durable clinical and microbiological improvement than standard therapy over 6 months, including near-physiological restoration of the commensal flora. Screening for, and co-managing, chronic tonsillitis should be integrated into the care of patients with periodontitis. Future work should confirm these findings in a randomised multicentre trial with strain-resolved microbiology and longer follow-up, and should define which natural biotherapeutic regimens best sustain a commensal-dominated oral ecosystem.

FUNDING

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

AUTHOR CONTRIBUTIONS

F.H.D.: conception and design; acquisition, analysis and interpretation of clinical, microbiological and immunological data; drafting of the manuscript. T.B.T.: acquisition and interpretation of morphological and laboratory data; critical revision; and

manuscript submission and correspondence. F.T.: study supervision; contribution to design and data interpretation; and critical revision. All authors approved the final version and agree to be accountable for all aspects of the work.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ETHICS STATEMENT

The study was conducted in accordance with the Declaration of Helsinki (2013 revision) and approved by the Ethics Committee of the Bukhara State Medical Institute named after Abu Ali ibn Sino (Minutes No. 3, 30 June 2026). Written informed consent was obtained from all participants.

ACKNOWLEDGEMENTS

The authors thank the staff of the affiliated dental and otorhinolaryngology services and the clinical-diagnostic laboratory for their assistance with data collection and analysis.

REFERENCES

[1] Baddouri, L., Hannig, M., 2024. Probiotics as an adjunctive therapy in periodontitis treatment—reality or illusion—a clinical perspective. npj Biofilms Microbiomes 10, 148. https://doi.org/10.1038/s41522-024-00614-5

[2] Caton, J.G., Armitage, G., Berglundh, T., et al., 2018. A new classification scheme for periodontal and peri-implant diseases and conditions. J. Clin. Periodontol. 45 (Suppl. 20), S1–S8. https://doi.org/10.1111/jcpe.12935

[3] de Mendonça, C.D., da Mata, A.D.S.P., Azevedo, L.F.R., Marques, J.F., Silveira, J.M.L., Marques, D.N.S., 2024. Probiotics in the non-surgical treatment of periodontitis: a systematic review and network meta-analysis. BMC Oral Health 24, 1224. https://doi.org/10.1186/s12903-024-05027-6

[4] Hajishengallis, G., 2015. Periodontitis: from microbial immune subversion to systemic inflammation. Nat. Rev. Immunol. 15, 30–44. https://doi.org/10.1038/nri3785

[5] Hajishengallis, G., Darveau, R.P., Curtis, M.A., 2012. The keystone-pathogen hypothesis. Nat. Rev. Microbiol. 10, 717–725. https://doi.org/10.1038/nrmicro2873

[6] Holt, S.C., Ebersole, J.L., 2005. Porphyromonas gingivalis, Treponema denticola, and Tannerella forsythia: the "red complex". Periodontol. 2000 38, 72–122. https://doi.org/10.1111/j.1600-0757.2005.00113.x

[7] Jensen, A., Fagö-Olsen, H., Sørensen, C.H., Kilian, M., 2013. Molecular mapping to species level of the tonsillar crypt microbiota associated with health and recurrent tonsillitis. PLoS One 8, e56418. https://doi.org/10.1371/journal.pone.0056418

[8] Kassebaum, N.J., Bernabé, E., Dahiya, M., Bhandari, B., Murray, C.J.L., Marcenes, W., 2014. Global burden of severe periodontitis in 1990–2010: a systematic review and meta-regression. J. Dent. Res. 93, 1045–1053. https://doi.org/10.1177/0022034514552491

[9] Khadilkar, M.N., Ankle, N.R., 2016. Anaerobic bacteriological microbiota in surface and core of tonsils in chronic tonsillitis. J. Clin. Diagn. Res. 10, MC01–MC03. https://doi.org/10.7860/JCDR/2016/20609.8578

[10] Kinane, D.F., Stathopoulou, P.G., Papapanou, P.N., 2017. Periodontal diseases. Nat. Rev. Dis. Primers 3, 17038. https://doi.org/10.1038/nrdp.2017.38

[11] Lakos, A., 2026. Chronic tonsillitis as a focal infection: a decade-long case involving severe systemic symptoms. Cureus 18, e100929. https://doi.org/10.7759/cureus.100929

[12] Lamont, R.J., Hajishengallis, G., 2015. Polymicrobial synergy and dysbiosis in inflammatory disease. Trends Mol. Med. 21, 172–183. https://doi.org/10.1016/j.molmed.2014.11.004

[13] Martin-Cabezas, R., Davideau, J.L., Tenenbaum, H., Huck, O., 2016. Clinical efficacy of probiotics as an adjunctive therapy to non-surgical periodontal treatment of chronic periodontitis: a systematic review and meta-analysis. J. Clin.

Periodontol. 43, 520–530. https://doi.org/10.1111/jcpe.12545

[14] Papapanou, P.N., Sanz, M., Buduneli, N., et al., 2018. Periodontitis: consensus report of Workgroup 2 of the 2017 World Workshop on the Classification of Periodontal and Peri-Implant Diseases and Conditions. J. Clin. Periodontol. 45 (Suppl. 20), S162–S170. https://doi.org/10.1111/jcpe.12946

[15] Paraskevas, S., Huizinga, J.D., Loos, B.G., 2008. A systematic review and meta-analyses on C-reactive protein in relation to periodontitis. J. Clin. Periodontol. 35, 277–290. https://doi.org/10.1111/j.1600-051X.2007.01173.x

[16] Sanz, M., Herrera, D., Kebschull, M., et al., 2020. Treatment of stage I–III periodontitis—the EFP S3 level clinical practice guideline. J. Clin. Periodontol. 47 (Suppl. 22), 4–60. https://doi.org/10.1111/jcpe.13290

[17] Socransky, S.S., Haffajee, A.D., Cugini, M.A., Smith, C., Kent, R.L. Jr., 1998. Microbial complexes in subgingival plaque. J. Clin. Periodontol. 25, 134–144. https://doi.org/10.1111/j.1600-051x.1998.tb02419.x

[18] Teughels, W., Durukan, A., Ozcelik, O., Pauwels, M., Quirynen, M., Haytac, M.C., 2013. Clinical and microbiological effects of Lactobacillus reuteri probiotics in the treatment of chronic periodontitis: a randomized placebo-controlled study. J. Clin. Periodontol. 40, 1025–1035. https://doi.org/10.1111/jcpe.12155

[19] Tonetti, M.S., Greenwell, H., Kornman, K.S., 2018. Staging and grading of periodontitis: framework and proposal of a new classification and case definition. J. Clin. Periodontol. 45 (Suppl. 20), S149–S161. https://doi.org/10.1111/jcpe.12945

[20] von Elm, E., Altman, D.G., Egger, M., Pocock, S.J., Gøtzsche, P.C., Vandenbroucke, J.P., 2007. The Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) statement: guidelines for reporting observational studies. Lancet 370, 1453–1457. https://doi.org/10.1016/S0140-6736(07)61602-X

[21] Yeoh, Y.K., Chan, M.H., Chen, Z., et al., 2019. The human oral cavity microbiota composition during acute tonsillitis: a cross-sectional survey. BMC Oral Health 19, 275. https://doi.org/10.1186/s12903-019-0956-5