AFMN BIOMEDICINE

ORIGINAL ARTICLE

FUSOBACTERIUM SPECIES IN ORAL AND MAXILLOFACIAL INFECTIONS: MICROBIAL ECOLOGY, COMMUNITY DYNAMICS, AND ANTIMICROBIAL SUSCEPTIBILITY

Kinga Markowska-Michalak[1] **Marta Kierzkowska**[2,3] **Edyta Podsiadły**[2,4]
Anna Majewska [1]

[1]Department of Medical Microbiology, Medical University of Warsaw, Warsaw, Poland [2]Laboratory of Microbiology, University Center of Laboratory Medicine, Medical University of Warsaw, Warsaw, Poland [3]Human Biome S.A., Gdansk, Poland [4]Department of Dental Microbiology, Medical University of Warsaw, Warsaw, Poland

Oral and maxillofacial infections (OMIs) are polymicrobial conditions in which obligate anaerobes, particularly *Fusobacterium* spp., play an important pathogenic role. Despite their relevance, the species distribution, ecological context, and antimicrobial susceptibility of *Fusobacterium* (F. -hereinafter) in OMIs remain incompletely understood. This study aimed to characterize their occurrence, co-isolation patterns, and resistance profiles to improve diagnostic accuracy and guide empirical therapy. Clinical specimens collected between October 2018 and August 2023 from 41 patients were cultured under aerobic and anaerobic conditions. *Fusobacterium* isolates were identified using MALDI-TOF MS, and susceptibility was reinterpreted according to EUCAST version 16 (2026). In total, 42 isolates were recovered, predominantly *F. nucleatum* (66.7%) and *F. necrophorum* (26.2%), with *F. periodonticum*, *F. gonidiaformans*, and *F. canifelinum* each representing 2.4%. Species distribution varied by specimen type: among 28 stomatognathic samples, *F. nucleatum* was found in 85.7%, *F. necrophorum* in 10.7%, and *F. periodonticum* in 3.6%. Peritonsillar abscesses were dominated by *F. necrophorum* (80%). All maxillary sinus samples exclusively contained *F. nucleatum*. Polymicrobial infections occurred in 85.4% of cases, frequently involving *Streptococcus* spp. (including the *S. anginosus* group) and members of the *Prevotellaceae* family, whereas peritonsillar abscesses more often exhibited monomicrobial growth. Isolates showed high susceptibility to β-lactam/β-lactamase inhibitor combinations and carbapenems, while metronidazole and clindamycin displayed broader MIC distributions. These findings highlight the importance of assessing the co-occurrence of *Fusobacterium* species with other members of the polymicrobial community within OMIs, as understanding these interspecies associations is crucial for selecting effective empirical therapy.

Keywords: anaerobic bacteria, antimicrobial susceptibility, biofilm, *Fusobacterium* spp., oral and maxillofacial infection, polymicrobial infections

Submitted: March 16, 2026 **Revised:** June 23, 2026
Accepted: June 24, 2026

Correspondence to:
Anna Majewska
Department of Medical Microbiology
Medical University of Warsaw
Warsaw, Poland
E-mail: anna.majewska@wum.edu.pl

INTRODUCTION

Oral and maxillofacial infections (OMIs) remain a frequent and clinically significant problem in dentistry and otolaryngology. Most OMIs originate from odontogenic foci; however, infections related to trauma, surgical procedures, diseases of the paranasal sinuses, and the upper respiratory tract are also commonly encountered. When inadequately treated or when source control is delayed, OMIs may lead to deep neck infections, mediastinitis, sepsis, cavernous sinus thrombosis, intracranial or orbital abscesses, and osteomyelitis (1). Because empiric antimicrobial therapy is often initiated before definitive microbiological results are available, a robust and accurate definition of the typical polymicrobial spectrum, including anaerobic contributors, is decisive for early therapeutic decision-making.

According to current knowledge, anaerobic bacteria are prominent contributors to OMIs, with *Prevotella* and *Porphyromonas* among the genera most frequently recovered from odontogenic and deep-space infections (2).

Species of the genus *Fusobacterium* are Gram-negative, obligate anaerobes that colonize the oral cavity and, to a lesser extent, the gastrointestinal tract. Their increasing recognition in clinical practice likely reflects both improvements in anaerobic diagnostic workflows and greater awareness of their pathogenic potential in polymicrobial infections (3). *F. nucleatum* is particularly prominent within the oral niche. It functions as a bridging organism within dental biofilms, mediating co-aggregation between early and late colonizers via multiple adhesins (RadD, Fap2, FadA, CmpA, FomA) and related virulence-associated factors (Figure 1). These ecological functions support the development and stability of complex microbial communities and have been linked to inflammatory and tissue-destructive processes in periodontal and deep-space infections (4, 5). Although *Fusobacterium* spp. are most commonly associated with periodontal and odontogenic infections, they have also been implicated in a spectrum of extraoral diseases, e.g., pleuropulmonary liver abscesses, intracranial infections, and intra-abdominal pathology (6-9).

Besides *F. nucleatum*, other clinically relevant species are *F. necrophorum, F. gonidiaformans, and F. periodonticum* (10-13). Notably, *F. necrophorum* is classically associated with Lemierre syndrome and is also recovered from severe head and neck infections in both pediatric and adult populations (10). Despite its considerable clinical significance, the local epidemiology, species distribution and antimicrobial susceptibility patterns of the *Fusobacterium* species involved in OMIs remain poorly understood. This is particularly evident in routine clinical settings, where the fastidious nature of anaerobic organisms continues to hinder reliable diagnostics. The need for optimal sampling further exacerbates this issue, including timely transport under anaerobic conditions, accurate species-level identification, and appropriate antimicrobial susceptibility testing. In addition, the interpretation of antibiotic susceptibility data over time is influenced by the evolution of antibiotic susceptibility testing (AST) methodologies and breakpoint criteria for anaerobes, which are systematically updated by the European Committee on Antimicrobial Susceptibility Testing (EUCAST) and the Clinical

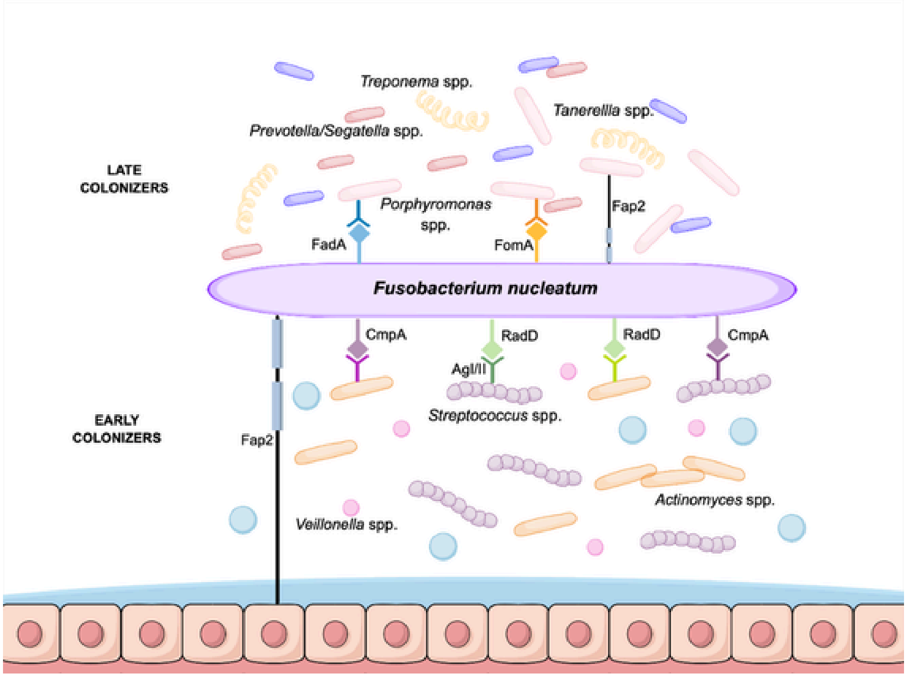


Figure 1. *F. nucleatum as a bridging organism linking early and late oral biofilm colonizers*
F. nucleatum mediates co-aggregation between early colonizers (e.g., *Streptococcus, Actinomyces, Veillonella)* and late colonizers (e.g., *Porphyromonas, Prevotella/Segatella, Treponema, Tannerella)* through multiple adhesins, including FadA, FomA, Fap2, RadD, CmpA.

and Laboratory Standards Institute (CLSI) to improve standardization and clinical relevance. Although these revisions strengthen the reliability of contemporary interpretations, they also limit direct comparability with historical datasets, as apparent temporal changes may reflect shifts in interpretive criteria rather than true epidemiological trends (14, 15).

This study aimed to investigate the prevalence and species distribution of *Fusobacterium* spp. in oral and maxillofacial infections and sinusitis, characterize their co-occurrence with other microorganisms, and to evaluate the antimicrobial susceptibility of *Fusobacterium* isolates with the aim of improving diagnostic and therapeutic decision-making in polymicrobial OMIs.

METHODS

A retrospective analysis of microbiological results was conducted using data obtained from clinical specimens collected from patients diagnosed with infections of the stomatognathic system and other maxillofacial tissues. Between October 2018 and August 2023, *Fusobacterium* spp. was identified in samples obtained from 41 hospitalized patients with OMIs. Patients were treated at the Department of Craniofacial and Maxillofacial Surgery (N = 33) and the Department of Pediatric Otolaryngology (N = 8), both located within a tertiary care hospital in Poland. Clinical specimens were collected by aspiration or surgical drainage, deep tissue biopsy from the affected sites, or deep wound swabbing. All samples were obtained in accordance with standard clinical procedures and transported under anaerobic conditions. Specimens were categorized according to anatomical site and patient age group (adult/pediatric) as follows: stomatognathic system infections (pus, biopsy tissue, deep wound swabs; 27/1), maxillary sinus infections (aspirates; 4/0), and peritonsillar abscesses (swabs; 2/7). Only microbiological results in which *Fusobacterium* spp. were identified, either as a sole pathogen or as part of a polymicrobial culture, were included in the analysis. All specimens were cultured under aerobic and anaerobic conditions using routine microbiological methods. Anaerobic cultures were performed on Schaedler agar supplemented with vitamin K1 and 5% sheep blood and incubated at 37°C for 48-72 h in an anaerobic chamber with a gas mixture of 85% N_2, 10% CO_2, and 5% H_2. Aerobic cultures were grown on Columbia blood agar with 5% sheep blood and on MacConkey agar, incubated at 37°C for at least 24 h. Fungal cultures were performed on Sabouraud agar, incubated aerobically at 30°C for 48 h. All culture media were supplied by bioMérieux, France. Species identification was performed using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS; Bruker, Germany). Antibiotic susceptibility testing was performed using the Epsilometer test (bioMérieux, France) and interpreted according to EUCAST recommendations applicable at the time of testing (versions 8.0–13.1). Periodic revisions of EUCAST guidelines, especially between 2018 and 2021, limit the direct comparability of antimicrobial susceptibility results across time. The minimum inhibitory concentration (MIC) values derived from routine diagnostic testing were available only for some *Fusobacterium* spp. isolates. Routine MIC testing was not consistently performed during the earlier study period, partly because interpretive criteria were not yet established. To ensure comparability, all available MIC results were reinterpreted according to the current EUCAST criteria (version 16.0, 2026).

Data distribution was assessed using the Shapiro-Wilk test. Categorical variables, including comparisons between age groups, were analyzed using Fisher’s exact test. Statistical significance was defined as $P < 0.05$. Statistical analyses and data visualization were performed using R software version 4.5.3 (R Foundation for Statistical Computing, Vienna, Austria).

RESULTS

Specimen characteristics

During the study period, 41 clinical specimens were analyzed. Most samples originated from the stomatognathic system (28/41; 68.3%), including pus aspirates (13; 31.7%), deep wound swabs (12; 29.3%), and biopsy tissue (3; 7.3%). Additional specimens comprised swabs from peritonsillar abscesses (9/41; 22.0%) and maxillary sinus biopsies (4/41; 9.8%).

Patient demographics

The adult cohort included 17 females (51.5%) and 16 males (48.5%). The pediatric cohort showed a similar sex distribution (50/50%). The median age of adult patients was 40.5 years (IQR: 36.8–66.8), and the median age of pediatric patients was 17 years (IQR: 9.5-17.25).

Fusobacterial infections were most frequently observed in the 30–39 years (24%) and 70–79 years (20%) age groups; however, age-group distribution did not differ significantly ($P = 0.7902$).

Patient characteristics varied by infection site, with marked differences in age distribution across stomatognathic infections, sinusitis, and peritonsillar abscess. Stomatognathic infections (N = 28): the mean age was 49.0 years, and the median age was 48.0 years (IQR 33.0–70.0); peritonsillar abscess (N = 9): the mean age was 17.56 years, and the median age was 17.0 years (IQR 9.0–25.5), sinusitis (N = 4): the mean age was 48.25 years, and the median age was 42.0 years (IQR 35.0–61.5).

Microbiological findings and species distribution

Overall, 25 microbial species were detected across the biological samples analyzed, including pathogens and commensal taxa, known to contribute to opportunistic infections.

In total, 42 *Fusobacterium* isolates were recovered from 41 specimens taken from 41 patients. The most frequently isolated species were *F. nucleatum* (66.7%) and *F. necrophorum* (26.2%), followed by *F. periodonticum, F. gonidiaformans*, and *F. canifelinum* (2.4%).

Species distribution varied by specimen type. Among stomatognathic samples (28), *F. nucleatum* was identified in 24 (85.7%), *F. necrophorum* in 3 (10.7%), and *F. periodonticum* in 1 (3.6%) sample. Isolates from peritonsillar abscesses included *F. necrophorum* (8/80%), *F. gonidiaformans* (1/10%), and *F. canifelinum* (1/10%). Two *Fusobacterium* species were isolated from a sample taken from one patient: *F. necrophorum* and *F. gonidiaformans*.

All maxillary sinus samples yielded *F. nucleatum* (4/100%).

Co-infection patterns

Polymicrobial growth was observed in 85.4% of specimens ($P < 0.001$). The majority of co-detected organisms were anaerobic bacteria. In stomatognathic infections, the most common co-isolated taxa were *Streptococcus* spp., particularly *Streptococcus anginosus* group (SAG: *S. anginosus, S. constellatus*) detected in 17 specimens (60.7%) from 16 patients. Other streptococci included *S. mitis/oralis* (N = 3), *S. parasanguinis* (N = 2), *S. gordonii* (N = 1), and *S. salivarius* (N = 1). Members of the *Prevotellaceae* family (*Prevotella* and *Segatella*) were detected in 15 specimens (53.6%). It is important to note that some species classified as *Prevotella* by MALDI-TOF MS have been renamed *Segatella*, including *Seg. buccae, Seg. maculosa, Seg. oris*, and *Seg. baroniae*. The most frequently cultured species was *P. nigrescens* (N = 6), followed by *Seg. buccae* (N = 3), *Seg. oris* (N = 3), *P. intermedia* (N = 2), *P. denticola* (N = 2), *Seg. baroniae* (N = 2), *Seg. maculosa* (N = 1), *P. jejuni* (N = 1), and one unidentified *Prevotella* sp. Other anaerobes detected in ≥3 cases included *Parvimonas micra, Actinomyces* spp. (*A. denticolens, A. graevenitzii*), *Dialister pneumosintes*, and *Gemella* spp. (*G. morbillorum, G. haemolysans*).

From clinical specimens of peritonsillar abscesses, *F. necrophorum* was isolated in both adult and pediatric patients, while monomicrobial *F. necrophorum* growth was detected in 55.6% of cases. In polymicrobial peritonsillar infections, isolates from clinical specimens of one adult patient included *F. necrophorum, F. gonidiaformans, S. anginosus,* and *Bulleidia extructa*. Among pediatric patients, isolates from peritonsillar abscesses included *F. necrophorum* in combination with *Klebsiella pneumoniae, Veillonella dispar*, or a mixed microbiota comprising *S. intermedius, Eikenella corrodens*, and *Aggregatibacter aphrophilus*.

From maxillary sinus specimens, *F. nucleatum* was isolated in all cases, with each specimen showing polymicrobial growth. Associated taxa included *S. anginosus* (50%), *Parvimonas micra* (50%), *Prevotella*/*Segatella* spp. (50%), and *Peptoniphilus* spp. (25%).

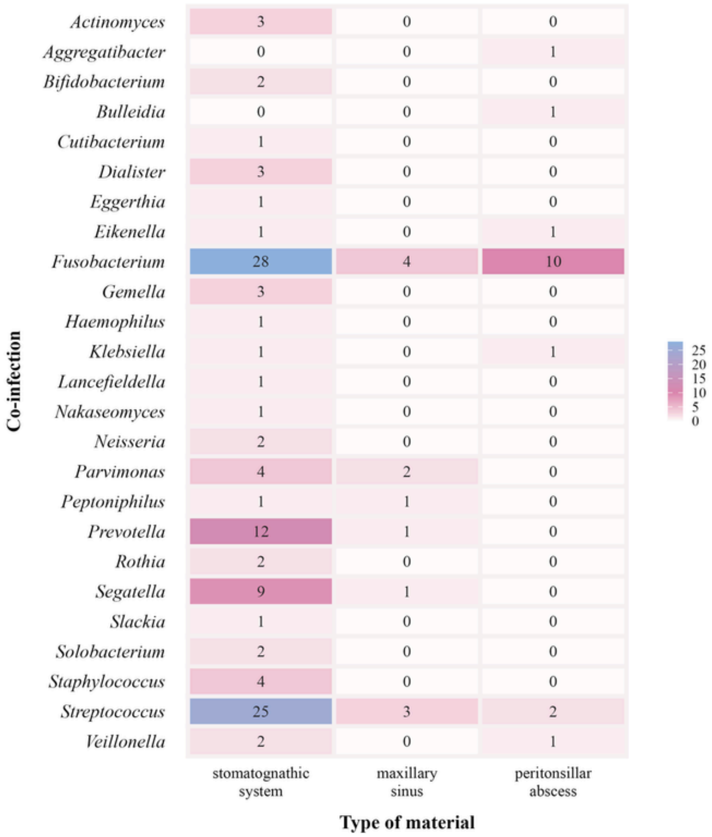
The overall distribution of taxa by specimen type is shown in Figure 2. Figure 3 illustrates the frequency of co-occurrence of individual microorganisms with *Fusobacterium* species.

Antimicrobial susceptibility testing

The AST was interpreted according to the latest EUCAST version (v16.0; 2026) based on MIC values. Overall, *Fusobacterium* isolates showed 100% susceptibility to β-lactam/β-lactamase inhibitor combinations and carbapenems. In contrast, susceptibility to metronidazole and clindamycin was lower, with broader MIC distributions. The MICs of the antimicrobial agents and their distributions by species are presented in Table 1.

DISCUSSION

The findings presented in this study, together with available literature, underscore the importance of laboratory-based identification of bacteria and antimicrobial susceptibility testing in oral and maxillofacial infections. In our cohort, *Fusobacterium* spp. were co-detected with other microorganisms in 85% of cases, most commonly alongside *Prevotella* spp. (including taxa reclassified to *Segatella*) and notably with members of the SAG. Further investigation of these co-infections should be a research priority because they directly affect the understanding of disease mechanisms and treatment management. The repeated co-infections observed in this study appear to reflect ecological cooperation within polymicrobial communities rather than incidental colonization.



Co-infection	stomatognathic system	maxillary sinus	peritonsillar abscess
Actinomyces	3	0	0
Aggregatibacter	0	0	1
Bifidobacterium	2	0	0
Bulleidia	0	0	1
Cutibacterium	1	0	0
Dialister	3	0	0
Eggerthia	1	0	0
Eikenella	1	0	1
Fusobacterium	28	4	10
Gemella	3	0	0
Haemophilus	1	0	0
Klebsiella	1	0	1
Lancefieldella	1	0	0
Nakaseomyces	1	0	0
Neisseria	2	0	0
Parvimonas	4	2	0
Peptoniphilus	1	1	0
Prevotella	12	1	0
Rothia	2	0	0
Segatella	9	1	0
Slackia	1	0	0
Solobacterium	2	0	0
Staphylococcus	4	0	0
Streptococcus	25	3	2
Veillonella	2	0	1

Figure 2. *Heatmap of co-infection species across different sample types. Species names are based on NCBI Taxonomy (16)*

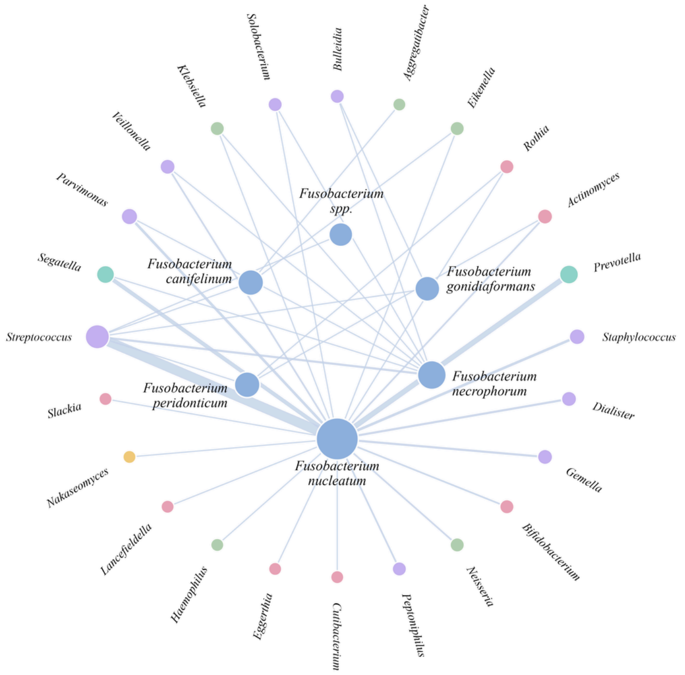


Figure 3. *Co-occurrence of Fusobacterium species with other taxa. Colors indicate bacterial phyla, and line thickness represents the frequency of co-isolation from clinical specimens*

Among fusobacteria, *F. nucleatum* warrants particular attention as a prevalent oral pathobiont repeatedly implicated in odontogenic and deep head-and-neck infections, including periodontal and peri-implant disease, dental abscesses, peritonsillar abscesses, and sinusitis (17). *F. nucleatum* has also been studied as an organism associated with extra-oral disease (including malignancy-associated dysbiosis); however, its relevance in the present context lies in its ability to persist in complex biofilms and to shape microbial community architecture at the mucosal surfaces (18, 19).

Mechanistically, *F. nucleatum* is a prototypical "bridging" organism: it co-aggregates with phylogenetically diverse taxa, promotes biofilm maturation, and modifies local physicochemical conditions (e.g., redox potential and pH) in ways that favor strict anaerobes (20). Single-species biofilms of *F. nucleatum* are typically less robust than multispecies communities, underscoring their reliance on metabolic complementarity. Quorum-sensing signals, such as autoinducer-2, further facilitate interspecies coaggregation with periodontal "red complex" organisms and can amplify inflammatory signaling (21, 22). Several surface adhesins (e.g., FadA, Fap2, RadD, FomA) contribute to attachment and-critically-co-aggregation with diverse oral taxa, thereby stabilizing multispecies biofilms (5, 20, 23). *Fusobacterium*-derived lipopolysaccharide and metabolic products can activate Toll-like receptor-linked pathways and induce the production of pro-inflammatory mediators (5, 24).

In vitro studies have shown that proteolytic activity in *F. nucleatum*, including autotransporter serine proteases such as fusolisin, can degrade host substrates and modulate host immune responses (25). Short-chain fatty acids are major metabolic products of supra- and subgingival bacteria, including *F. nucleatum*. Elevated butyrate levels have been detected in gingival crevicular fluid from patients with periodontitis, suggesting a potential role in the pathogenesis of oral infections (26). High concentrations of butyric acid have been shown to stimulate the production of reactive oxygen species in osteoblasts. This, in turn, stimulates the secretion

Table 1. *Antimicrobial susceptibility of Fusobacterium spp. MIC values determined by the Epsilometer test interpreted according to EUCAST recommendations (version 16; 2026)*

Antibiotic	***F. nucleatum***				***F. necrophorum***				***F. gonidiaformans***				***F. canifelinum***			
	N	N with MIC	S (%)	**MIC (µg/mL)**	N	N with MIC	S (%)	**MIC (µg/mL)**	N	N with MIC	S (%)	**MIC (µg/mL)**	N	N with MIC	S (%)	**MIC (µg/mL)**
AMC	30	10	100	0.016-0.19	9	9	100	0.016-0.25	1	1	100	0.016	1	1	100	0.016
PG	18	2	100	0.023-0.25	4	4	100	0.016-0.125	-	-	-	-	-	-	-	-
IMP	16	4	100	0.006-0.47	-	-	-	-	-	-	-	-	-	-	-	-
MEM	4	4	100	0.008-0.012	4	2	100	0.04-0.023	-	-	-	-	-	-	-	-
TZP	1	1	100	0.016	2	0	-	-	-	-	-	-	-	-	-	-
CM	26	10	80	0.016-256	9	5	80	0.016-0.5	1	1	100	0.032	1	1	100	0.064
MTR	23	7	100	0.016-1	10	7	86	0.016-0.75	1	1	100	0.047	-	-	-	-

Legend: AMC; amoxicillin/clavulanic acid, PG; benzylpenicillin, IMP; imipenem, MEM; meropenem, TZP; piperacillin/tazobactam, CM; clindamycin, MTR; metronidazole, N; number of tested isolates. N with MIC; the number of isolates for which the MIC was determined during routine testing; S; susceptible, MIC; minimum inhibitory concentration.

of 8-isoprostaglandin and matrix metalloproteinase-2, leading to bone destruction and affecting bone repair (27).

Prevotella spp. (including *Segatella*-reclassified species) are common oral commensals that frequently act as opportunistic pathogens in chronic periodontitis, pulpal infections, and odontogenic abscesses. Their pathogenic potential in polymicrobial infection may be enhanced by physical and metabolic integration into fusobacteria-centered biofilms. Both genera can modulate innate immune responses through Pathogen-Associated Molecular Patterns diversity and secreted factors, contributing to an inflammatory milieu that supports suppuration, tissue destruction, and clinical persistence (28-31).

Similarly, the co-detection of *Fusobacterium* spp. with SAG in our cases is likewise clinically meaningful. Although SAG members are often considered part of the commensal microbiota, they are well known for their propensity to form abscesses and cause invasive disease, including deep neck infections (32, 33). Experimental models suggest that co-inoculation of SAG with *F. nucleatum* yields greater virulence than monomicrobial infection, supporting synergistic pathogenicity (29, 34-36). The co-isolation of *Fusobacterium* spp. and SAG underscores the clinical relevance of their polymicrobial involvement, indicating that both taxa may participate in the infectious process rather than representing incidental co-occurrence.

Therapeutic management of OMIs should integrate prompt source control (drainage and debridement when indicated) with antimicrobials that cover the expected polymicrobial spectrum, including strict anaerobes. Commonly used options include β-lactams, β-lactam/β-lactamase inhibitor combinations, carbapenems in severe disease, and metronidazole as an anaerobic agent—typically as part of a regimen that also covers streptococci (30, 37). In our cohort, susceptibility profiles were generally favourable for β-lactam/β-lactamase inhibitor combinations and carbapenems, whereas reduced susceptibility was observed for clindamycin.

Advances in genomic methods have improved the detection of antimicrobial resistance, particularly in fastidious anaerobes, while providing a broader view of the resistome in polymicrobial infections. Resistance determinants have been reported in odontogenic abscess microbiomes and in collections of *Fusobacterium* and *Prevotella* isolates, including genes associated with resistance to tetracyclines (e.g., tet variants), β-lactams (β-lactamase production; *blaTEM, cfxA, cfxA2*), macrolides, lincosamides, and streptogramin B (MLS$_B$ phenotype; e.g., *erm* genes), and—more rarely—nitroimidazoles, such as metronidazole (*nim*) (2, 30, 38, 39). High sequence identity between resistance genes found in anaerobes and in oral streptococci supports the plausibility of horizontal gene transfer within multispecies biofilms, providing a mechanistic explanation for the emergence and dissemination of resistance in polymicrobial niches (39).

Our findings suggest that when *Fusobacterium* spp. is detected in a sample, a polymicrobial infection should be considered rather than an isolated pathogen, since it is frequently recovered together with *Prevotella*/*Segatella* and SAG. Clinically meaningful characterization of these consortia depends on appropriate sampling (preferably aspirates or tissue rather than superficial swabs), rapid transport under anaerobe-preserving conditions, species-level identification, and antibacterial susceptibility testing. The main advantage of this study is that it initiates the characterization of *Fusobacterium* species in multi-bacterial infections of the oral cavity, maxillofacial region, and sinuses, including clinically relevant co-infection patterns, which may form the basis for empirical and targeted treatment. Limitations include an insufficient sample size and the fact that it originated from a single hospital. Furthermore, the evolution of AST standards has made direct comparison of drug susceptibility with historical data sets difficult.

Acknowledgments

None.

Author contributions

Conceptualization: A.M.; Methodology: K.M-M. and M.K.; Formal analysis: K.M-M. and A.M.; Investigation: K.M-M. and M.K; Data curation: K.M-M., E.P. and M.K. Writing – Original Draft Preparation: K.M.-M.; Writing – Review and Editing: K.M-M., M.K., E.P. and A.M.; Supervision: A.M.

Statement of Ethics

This retrospective study was conducted using anonymized data extracted from medical records. According to local regulations, formal approval of the bioethics committee was not required. All procedures were performed in accordance with the ethical standards of the institutional research committee and with the 1964 Helsinki Declaration and its later amendments.

Statement of Competing Interest

The authors declare no relevant conflicts of interest.

Statement of Data Availability

The datasets analyzed during the current study are not publicly available due to institutional restrictions, but they are available from the corresponding author on reasonable request and subject to applicable regulations.

Statement of Generative AI Use

No generative AI was used.

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