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Frequency of Fascial Space Involvement and Microbial Flora in Patients with Odontogenic Infections: A Cross-Sectional Study

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Name of Author:
Nida Khalid[1], Muslim Khan[2], Omer Ali[3]

Affiliation: *[1] Department of Oral and Maxillofacial Surgery, Khyber College of Dentistry, Peshawar, Khyber Pakhtunkhwa, Pakistan.*
[2] Department of Oral and Maxillofacial Surgery, Khyber College of Dentistry, Peshawar, Khyber Pakhtunkhwa, Pakistan.
[3] Department of Pediatric Dentistry, Bacha Khan College of Dentistry, Mardan, Khyber Pakhtunkhwa, Pakistan.

Corresponding Author:
Professor Dr. Muslim Khan
Email: nidakhalid475@yahoo.com

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Abstract: **Background:** Odontogenic infections may spread into the facial fascial spaces and are associated with diverse microbial flora. Understanding the distribution of involved spaces and the organisms isolated from clinical specimens is important for clinical assessment and appropriate management. **Objective:** To determine the frequency and distribution of fascial space involvement and characterize the microbial flora isolated from patients with odontogenic infections. **Methods:** This observational study, conducted cross-sectionally, encompassed 97 individuals suffering from odontogenic infections between May 2025 and Aug 2025. Demographic and clinical attributes, anatomical distribution of fascial space involvement, and microbiological culture findings were documented and analysed descriptively. The relationships between multi-space engagement and specific clinical factors were also evaluated. **Results:** The average age of participants was 33.36 ± 14.19 years, with 65 individuals (67.0%) being male. Mandibular infections represented 59 cases, constituting 60.8%. The submandibular region was the most commonly affected primary area (37/97; 38.1%), succeeded by the buccal space (27/97; 27.8%). Involvement of secondary fascial spaces was recorded in 28 individuals, representing 28.9%. Out of 96 specimens submitted for culture, 88 (91.7%) demonstrated microbial proliferation. Mixed growth was seen in 49 (55.7%) culture-positive samples. Of the 147 documented isolates, viridans group streptococci were the most prevalent (50/147; 34.0%), succeeded by Staphylococcus aureus (27/147; 18.4%) and the Streptococcus anginosus group (23/147; 15.6%). Multiple-space involvement was not significantly associated with sex, jaw origin, or fever (all $p > 0.05$). **Conclusion:** Odontogenic infections predominantly involved the submandibular and buccal spaces, with mandibular infections being more common. Culture results demonstrated a high frequency of microbial growth and a diverse isolate profile. These findings highlight the value of assessing anatomical spread and investigating microbial flora in patients with odontogenic infections.

Keywords: Odontogenic infections; fascial spaces; microbiology; microbial flora; bacterial culture; cross-sectional study.

INTRODUCTION

Odontogenic infections are a considerable source of morbidity in oral and maxillofacial surgical procedures, encompassing localised dentoalveolar abscesses as well as infections affecting the face and cervical fascial compartments (1). They typically arise from pulpal, periapical, or periodontal ailments and can disseminate beyond the original location via anatomically delineated tissue pathways. The trajectory and magnitude of dispersion are influenced in part by the interrelation among the teeth, adjacent muscle, and fascial connections (2). While numerous infections stay confined, their progression into deeper fascial areas can lead to trismus, dysphagia, systemic

disease, and, in extreme instances, airway obstruction or other critical problems. Precise evaluation of the anatomical scope of infection and recognition of the odontogenic origin are thus crucial for prompt intervention and suitable therapeutic therapy (3).
The distribution of odontogenic infections throughout fascial compartments reflects the origin location and the anatomical routes accessible for propagation. Frequently engaged main regions include the submandibular, buccal, canine, submental, sublingual, and infratemporal areas. Secondary compartments, such as the masseteric, pterygomandibular, and both superficial and deep temporal spaces, might be affected when an infection spreads beyond its original anatomical confines (4).

Recognising the impacted areas is therapeutically significant as the degree of involvement may affect disease severity, functional limitations, and the strategy for drainage and source management. Nonetheless, the documented prevalence of specific areas differs with clinical groups. Bahl et al. determined that the submandibular space was the most commonly affected area in a clinical study of 100 patients (5). In a research conducted in Lahore, Pakistan, Rahim et al. found that 47.1% of patients exhibited involvement of the submandibular area (6). These results underscore the significance of submandibular involvement in the analysed populations; nevertheless, variations in patient selection, referral practices, and clinical manifestations may hinder direct comparisons between institutions.

The microbiological properties of odontogenic diseases are significant as these infections can encompass several bacterial factions derived from the oral microbiota (7). Oral streptococci and several facultatively anaerobic microorganisms can thrive alongside obligate anaerobes, such as Prevotella and Fusobacterium species (8). In the study conducted by Bahl et al., a combination of aerobic and anaerobic growth was observed in 60 out of 100 patients, whereas growth exclusively aerobic and exclusively anaerobic was noted in 25 and 15 patients, respectively. These results demonstrate the potentially varied microbial makeup of odontogenic diseases. Staphylococci, enterococci, and various other bacterial classifications have been documented, but with varying prevalence across different investigations (9). This variation may indicate discrepancies in specimen collection and transit, culture methodologies, organism identification protocols, prior antibiotic exposure, and the traits of the studied populations. Thus, microbiological results from a single institution should not be indiscriminately deemed indicative of other clinical environments (10). Culture-oriented analyses can identify the organisms isolated from clinical samples and offer insights that may enhance clinical evaluation. Antimicrobial susceptibility testing can enhance the characterisation of bacterial isolates' in-vitro reactions to antimicrobial drugs when conducted and analysed using suitable methodologies and standards (11). A comprehensive scoping review conducted by Ardila and Bedoya-García, encompassing 21 prospective observational studies and randomised clinical trials with a total of 1,506 patients, recorded antimicrobial resistance across various bacterial groups linked to odontogenic infections and underscored the variability in the existing evidence. These results highlight the significance of analysing microbiological data within their clinical and geographical frameworks. Nevertheless, culture data alone do not ascertain the pathogenic role of each isolated organism or dictate the optimal treatment for a certain patient. Microbiological analysis should thus be regarded in conjunction with the severity of infection, clinical manifestations, and suitable treatment of the underlying dental origin (12).

Despite evidence describing the anatomical distribution and microbial characteristics of odontogenic infections, comparisons across studies remain challenging because of differences in study populations, specimen types, and microbiological methods (13). Research conducted by Rahim et al. in Pakistan detailed the prevalence of impacted teeth and fascial gaps within a Lahore demographic (14). The reviewed in this study fails to delineate the associated distribution of fascial space involvement and culture results among patients at Khyber College of Dentistry, Peshawar. Data specific to an institution can serve as a valuable descriptive foundation for comparison with other demographics, although conclusions drawn from a single-centre investigation should not be presumed to reflect the broader area (15).

Accordingly, this study aimed to determine the frequency and distribution of primary and secondary fascial space involvement and to characterize the microbial flora recovered from clinical specimens of patients with odontogenic infections at Khyber College of Dentistry, Peshawar, Pakistan. By examining anatomical involvement alongside culture findings, the study provides a local description of the clinical and microbiological patterns observed in this patient population. The findings are intended to contribute to the available descriptive evidence while recognizing the limitations of a cross-sectional design and avoiding causal or treatment-effect conclusions.

MATERIALS AND METHODS

Study Design and Setting

This cross-sectional observational study was conducted at Khyber College of Dentistry, Peshawar, Pakistan, from May 2025 and Aug 2025. The study

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assessed the distribution of fascial space involvement and the microbial flora recovered from patients with odontogenic infections.

Study Population and Sampling

A total of 97 patients with clinically identified odontogenic infection were enrolled by consecutive sampling. Individuals of any gender and age group were qualified. Patients of either sex and all ages were eligible, patients using antibiotics prior to specimen collection were omitted based on the study's eligibility requirements. Demographic and clinical data were documented for every participant.

Clinical Assessment and Fascial Space Classification

Documented characteristics encompassed age, gender, living environment, presumed jaw origin, symptom duration, impacted side, fever, trismus, dysphagia, and diabetes mellitus. The presumed odontogenic source was categorised as either mandibular or maxillary through clinical and radiographic evaluation. Imaging data was documented when accessible. Infections were categorised based on the principal fascial compartment affected. The documented principal areas included submandibular, buccal, canine, infratemporal, submental, and sublingual. Secondary participation was recorded for the superficial temporal, deep temporal, pterygomandibular, and masseteric regions. Involvement of other spaces was noted when the illness spread beyond the initial area.

Specimen Collection and Microbiological Analysis

Pus samples were collected by aspiration with a sterile 18- or 22-gauge needle and syringe or using a sterile swab, depending on the clinical context. Samples were swiftly conveyed to the microbiological laboratory utilising the appropriate transport medium, including thioglycollate broth when necessary.

The microbiological assessment comprised Gramme staining and culturing. Blood agar, MacConkey agar, and chocolate agar were employed for the isolation of bacteria. Anaerobic cultivation was conducted with thioglycollate broth and anaerobic blood agar within an anaerobic jar equipped with a gas-generating apparatus. Cultures were maintained at 37°C, while anaerobic cultures were sustained for a duration of 72 hours.

Bacterial isolates were identified using colony morphology, Gram-staining results, and biochemical assays. The VITEK automatic identification system was utilised for the identification of microorganisms. The microbiological examination detailed in this research concentrated on culture positive, the prevalence of mixed or solitary organism proliferation, and the allocation of discovered isolates. Antimicrobial susceptibility data were unavailable for examination and are hence not disclosed.

Statistical Analysis

The analysis of data was conducted utilising IBM SPSS Statistics version 22. Categorical variables were presented as frequencies and percentages. Continuous variables were characterised by means and standard deviations or medians and ranges, depending on their distributions. Relationships between multi-space engagement and specific demographic and clinical factors, such as gender, origin jaw, and fever condition, were evaluated utilising Pearson's chi-square test. Statistical significance was set at $p < 0.05$.

Ethical Considerations

Ethical approval was obtained from the Research Review Board of MTI–Khyber College of Dentistry, Peshawar (Certificate No. 192/ADR/KCD; 14 October 2024). Informed consent and confidentiality procedures were implemented in accordance with the approved study protocol.

RESULT

Demographic and Clinical Characteristics

A cumulative total of 97 patients were incorporated into the analysis. The mean age was 33.36 ± 14.19 years (with a range of 5–73 years), while the median age was 32 years. Among the participants, 65 (67.0%) were male, while 32 (33.0%) were female. The infection originated in the mandible for 59 individuals (60.8%) and in the maxilla for 38 patients (39.2%). Fever was recorded in 36 patients (37.1%), trismus in 20 (20.6%), dysphagia in 12 (12.4%), and diabetes mellitus in 6 (6.2%). The mean duration of symptoms was 4.39 ± 2.86 days. Supplementary demographic and clinical attributes are displayed in Table 1.

Table 1. Demographic and clinical characteristics of the study population (N = 97)

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Characteristic	Value	Denominator	Percentage (%)
Age, years, mean ± SD	33.36 ± 14.19	97	—
Age, years, median (range)	32 (5–73)	97	—
Male sex	65	97	67.0
Female sex	32	97	33.0
Mandibular origin	59	97	60.8
Maxillary origin	38	97	39.2
Rural residence	49	97	50.5
Urban residence	48	97	49.5
Fever	36	97	37.1
Trismus	20	97	20.6
Dysphagia	12	97	12.4
Diabetes mellitus	6	97	6.2
Duration of symptoms, days, mean ± SD	4.39 ± 2.86	97*	—
Right-sided involvement	48	97	49.5
Left-sided involvement	47	97	48.5
Bilateral involvement	2	97	2.1
Intraoral/OPG radiograph recorded	71	97	73.2
CT recorded	11	97	11.3
Imaging information missing	15	97	15.5
Specimen submitted	96	97	99.0

Values are presented as n (%) unless otherwise indicated. SD, standard deviation; OPG, orthopantomogram; CT, computed tomography. Percentages are calculated using all 97 patient records.

Fascial Space Involvement

The submandibular space was the most frequently recorded primary fascial space, accounting for 37 of 97 cases (38.1%), followed by the buccal space (27/97, 27.8%), canine space (12/97, 12.4%), infratemporal space (9/97, 9.3%), submental space (8/97, 8.2%), and sublingual space (4/97, 4.1%). Secondary fascial space involvement was recorded in 28 patients (28.9%). The superficial temporal and deep temporal spaces were each recorded in eight patients, followed by the pterygomandibular space in seven and the masseteric space in five. The distribution of primary and secondary fascial spaces is summarized in Table 2.

Table 2. Distribution of primary and secondary fascial spaces

Fascial space	Patients (n)	Denominator	Percentage (%)
Primary spaces			
Submandibular	37	97	38.1
Buccal	27	97	27.8
Canine	12	97	12.4
Infratemporal	9	97	9.3
Submental	8	97	8.2
Sublingual	4	97	4.1
All primary-space records	97	97	100.0
Secondary spaces			
Superficial temporal	8	97	8.2
Deep temporal	8	97	8.2
Pterygomandibular	7	97	7.2
Masseteric	5	97	5.2
Any secondary space recorded	28	97	28.9
No secondary space recorded	69	97	71.1

Percentages for individual secondary spaces use the full cohort (N = 97).

Microbiological Findings

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Out of the 96 specimens documented, 88 (91.7%) were identified as culture-positive, whereas eight (8.3%) exhibited no microbial growth. Out of the 88 culture-positive samples, 49 (55.7%) exhibited mixed growth, whereas 39 (44.3%) demonstrated the presence of a single organism. The dataset at the isolate level had 147 distinct isolate identifiers. The Viridans group streptococci were the most commonly identified species (50/147, 34.0%), succeeded by Staphylococcus aureus (27/147, 18.4%) and the Streptococcus anginosus group (23/147, 15.6%). The recorded organism distribution is summarized in Table 3.

Table 3. Specimen findings and distribution of recorded organisms

Measure/category	n	Denominator	Percentage (%)
Specimen findings			
Pus aspirate	68	96	70.8
Pus swab	28	96	29.2
Culture growth	88	96	91.7
No growth reported	8	96	8.3
Mixed growth among growth-positive specimens	49	88	55.7
Single-organism growth among growth-positive specimens	39	88	44.3
Organism distribution (unique isolates)			
Viridans group streptococci	50	147	34.0
Staphylococcus aureus	27	147	18.4
Streptococcus anginosus group	23	147	15.6
Enterococcus spp.	13	147	8.8
Coagulase-negative staphylococci	9	147	6.1
Bacteroides spp.	8	147	5.4
Prevotella spp.	7	147	4.8
Peptostreptococcus/Peptostreptococcaceae	7	147	4.8
Fusobacterium spp.	3	147	2.0

Exploratory Inferential Analysis

Pearson's chi-square tests were used to examine associations between multiple-space involvement and selected demographic and clinical characteristics. No statistically significant associations were identified between multiple-space involvement and sex ($\chi^2 = 1.137$, df = 1, $p = 0.286$), jaw of origin ($\chi^2 = 0.817$, df = 1, $p = 0.366$), or fever status ($\chi^2 = 0.033$, df = 1, $p = 0.856$).

DISCUSSION

This cross-sectional study describes the demographic, clinical, anatomical, and microbiological attributes of 97 individuals suffering from odontogenic fascial-space infections who were treated at Khyber College of Dentistry, Peshawar. Males represented 67.0% of the group, with an average age of 33.36 ± 14.19 years. Mandibular engagement was noted in 60.8% of patients, with the submandibular and buccal regions being the most commonly affected main areas. These results offer a localised account of the clinical and microbiological characteristics of odontogenic infections within a tertiary dental care environment.

The male dominance noted in this group contrasts with the results of a previous investigation by Ishfaq et al. at the same facility, which indicated a female majority among 155 patients. Nonetheless, the average age in that research (33.77 ± 13.45 years) was similar to that of the current group (16). Rahim et al. similarly noted that mandibular teeth and the submandibular region were often affected in individuals receiving treatment in Lahore (17). Variations in sex distribution among studies may indicate discrepancies in patient selection, referral trends, and healthcare-seeking behaviours; yet, these elements were not explicitly assessed in the current investigation and cannot be confirmed as reasons for the noted disparities.

The submandibular space was the most commonly documented primary space (38.1%), succeeded by the buccal space (27.8%). This distribution aligns with the previous Khyber College of Dentistry research, which indicated submandibular and buccal involvement in 46.5% and 30.3% of instances, respectively. Rahim et al. also recognised the submandibular space as the most commonly affected area, comprising 47.1% of their sample. The anatomical connection between the apices of mandibular molar roots and the mylohyoid muscle offers a credible rationale for the common dissemination of infections into the submandibular region (18). Infection originating from mandibular teeth may propagate into the submandibular or sublingual area, contingent upon the connection between the root apices and muscle attachment. However, the results provided do not quantify tooth-

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specific origins, hence the prevalence of mandibular involvement should not be construed as definitive proof that mandibular molars were the primary cause. Secondary-space involvement was observed in 28.9% of patients, suggesting that the infection spread beyond the primary space in a significant fraction of the group. No statistically meaningful correlations were seen between multiple-space involvement and sex, origin of the jaw, or fever status. These results must be viewed with caution due to the potentially smaller sample size affecting the detection of correlations. The lack of statistical significance does not confirm that these traits are disconnected from the anatomical severity of infection (19).

Culture growth was reported in 91.7% of the specimens presented. Of the culture-positive samples, 55.7% were identified as exhibiting mixed growth. The Viridans group streptococci constituted the most commonly documented organisms at 34.0%, succeeded by Staphylococcus aureus at 18.4% and the Streptococcus anginosus group at 15.6%. These results delineate a microbial range encompassing organisms typically linked to oral illnesses alongside many other bacterial categories (20). Comparisons with earlier research must consider variations in specimen collection, culture environments, identification methodologies, and the denominators employed for calculating organism prevalence. This study involved both pus aspirates and swabs, potentially affecting the microbes isolated. The documented mixed-growth outcomes align with the existence of several organisms in certain specimens, although they do not independently confirm microbial synergism or the pathogenic role of each isolate (21).

Nevertheless, the current study did not clarity the reasons for the isolation of these organisms, whether their existence correlates with prior antibiotic exposure, or if they exhibited antimicrobial resistance. Such analyses necessitate authenticated laboratory findings and pertinent clinical data (22) (23). Thus, the microbiological results underscore the necessity of proper specimen collection and precise organism identification, although they should not just be utilised to deduce local resistance trends or the efficacy of a specific antibiotic treatment. Clinical management should remain guided by the severity and extent of infection, appropriate dental source control, established clinical recommendations, and verified microbiological findings when available (24). Several limitations must be acknowledged while analysing these results. The single-center design and consecutive sampling can limit the applicability to different clinical environments. The cross-sectional design facilitates the depiction of anatomical and microbiological patterns, although it fails to determine causal linkages. The use of pus aspirates and swabs may have affected microbial retrieval, whereas the lack of accessible antibiotic susceptibility results hindered the evaluation of the antimicrobial resistance characteristics of the isolated organisms. Future multicenter studies employing standardised specimen collection, validated microbiological identification, and recorded antimicrobial susceptibility testing are necessary to enhance comprehension of the regional distribution and resistance trends of odontogenic infections (25).

CONCLUSION

This study demonstrates that odontogenic infections commonly involve the submandibular and buccal fascial spaces, with mandibular infections accounting for the majority of cases. Secondary fascial space involvement occurred in approximately one-third of patients, highlighting the potential for infection to extend beyond the primary anatomical site. Microbiological analysis revealed a high culture positivity rate, with mixed growth observed in more than half of culture-positive specimens. Viridans group streptococci, Staphylococcus aureus, and the Streptococcus anginosus group were the most frequently identified organisms, emphasizing the diverse microbial profile of odontogenic infections.

These results underscore the significance of prompt clinical evaluation, meticulous assessment of fascial space involvement, and suitable microbiological analysis to inform patient care. Nonetheless, the lack of statistically significant correlations between multi-space involvement and sex, jaw origin, or fever should be approached with caution and does not rule out clinically pertinent linkages. Due to the single-centre design and the constraints of cross-sectional data, additional multicentre studies with larger cohorts, standardised specimen collection, and confirmed antimicrobial susceptibility testing are necessary to strengthen the evidence for the clinical management of odontogenic infections.

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