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Phenotypic Analysis and Antibiogram of Oral Infections-Causing Bacteria Isolated from Dental Patients

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ABSTRACT: Oral infections are commonly observed in individuals and frequently result in enduring inflammatory states that impact the teeth, such as caries, the gingival tissues surrounding the teeth, including gingivitis and endodontic lesions, as well as the structures that provide support to the teeth, such as periodontitis. A total of 100 clinical samples were collected from patients with various oral infections. The individuals in the study encompassed a wide range of ages, ranged from 9 to 70 years, over the timeframe between October 2023 and December 2023. Fifty pathogenic bacterial strains were obtained from specimens of clinical origin, with the genus Streptococcus accounting for 27 of these isolates, representing 54% of the total, the highest proportion observed among all specie. The specimens were identified through the examination of cultural and microscopic features, in addition to being confirmed using the Vitek2 system for species-level diagnosis. The multidrug-resistant isolates exhibited resistance to various antibiotics including Erythromycin (100%) classified under the Macrolide group, Cefotaxime (100%), Cefepime (100%), Ceftriaxone (100%), and Penicillin (96.29%) which falls under the βeta-Lactam category. Additionally, resistance was also observed against Clindamycin (92.59%) which is categorized as a Lincosamide antibiotic. In the susceptibility testing of antibiotics, Augmentin demonstrated the highest level of activity among the tested molecules, thereby affirming its overall efficacy against oral streptococci. Additionally, Trimethoprim-sulfamethoxazole and Ampicillin exhibited favorable activity, while Vancomycin also demonstrated effectiveness against oral streptococci.

Keywords: oral infections, oral streptococci spp., multidrug resistant strain.

1. INTRODUCTION

The oral cavity represents a distinctive and diverse bacterial environment characterized by unique ecological niches, these niches arise from the presence of various surfaces suitable for bacterial colonization, coupled with significant fluctuations in environmental factors such as pH, nutrient availability, temperature, and redox potential, these conditions in conjunction with human behavioral factors like dental hygiene, smoking, and dietary habits, as well as overall health status and genetic predisposition, collectively affect the native microbial communities composition [1]. The oral environmental conditions may undergo alterations under specific circumstances, potentially disrupting the usual commensal interaction between the host and the indigenous oral microflora, this can result in a shift in equilibrium towards a heightened susceptibility to oral diseases, notably an increased prevalence of dental caries and periodontal diseases [2]. The surfaces of the teeth that do not shed, along with the dorsal and lateral surfaces of the tongue, the periodontal pockets, and the rest of the epithelial surfaces of the oral mucosa, provide favorable conditions for the formation of specific microbial communities [3].

Among the various organisms found in the oral cavity, the genus Streptococcus is widely regarded as the most prominent [4], particularly during the initial phases of colonization [5]. Streptococci are characterized by their facultative anaerobic nature, with certain strains being strictly anaerobic, they are classified as Gram-positive, non-motile, non-

spore-forming, and catalase-negative cocci are typically observed in chains or pairs, some strains are commonly found as part of the normal flora in the oral and gastrointestinal tracts, whereas others possess pathogenic [6]. These cocci fall into six major clusters or species groups, specifically the salivarius, mitis, bovis, mutans, pyogenic, and anginosus groups [7]. On blood agar, the growth of these microorganisms is robust due to their hemolytic activity, Streptococci can be divided into three categories: Alpha hemolytic (produce a green zone of partial hemolysis), Beta hemolytic (produce translucent zone of complete hemolysis), Gamma hemolytic (produce no effect, non- hemolytic) [8]. These streptococci demonstrate the capacity to adhere to elements of the salivary pellicle and to other oral bacteria via adhesin proteins present on their cellular surface, consequently they along with numerous other oral microorganisms, participate in the formation of multispecies biofilms [4]. The development of dental plaque on the surfaces of the teeth that do not shed represents a well-documented phenomenon involving a diverse community of biofilm species; while dental plaque is a common occurrence in individuals with good oral health, it is also linked to the onset of various oral conditions such as dental caries, gingivitis, and periodontal diseases [9].

The synthesis of hydrogen peroxide by oral streptococci is believed to provide a competitive advantage against pathogenic microorganisms, thus promoting their colonization and survival in the oral cavity [10]. oral Streptococci demonstrate unique characteristics, including the ability to thrive in an acidic milieu (aciduricity), the generation of acids (acidogenicity), as well as the production of polysaccharides both extracellularly and intracellularly [11]. They capable of synthesizing and generating endodextranase, enabling their involvement in the formation of dental plaque. [12]. These bacteria are equipped with an enzyme termed Glucosyltransferase (GTF), which employs sugars like sucrose as a foundation for the production of extracellular polysaccharides, consequently Streptococci are able to accumulate and adhere to the surfaces of the teeth [12].

The current investigation was conducted with the aim of isolating and characterizing Streptococcus species from oral infections, as well as investigating the susceptibility of these isolates to various antibiotics such as penicillin G, ampicillin, tetracycline, vancomycin, erythromycin, cefotaxime, ceftriaxone, doxycycline, cefepime, meropenem, levofloxacin, amoxicillin-clavulanic acid, trimethoprim-sulfamethoxazole, and clindamycin.

2. MATERIALS AND METHODS

2.1. Collection of the sample

A total of 100 samples were obtained through the collection of swabs from the oral cavity of patients presenting with various oral infections. These specimens were collected using sterile swabs and placed in aseptic containers with transport media, followed by cultured on blood agar and then subcultured on streptococcus selection agar. This process took place over the time period spanning from October 2023 to December 2023. The individuals from whom the samples were taken sought treatment at the Dental Specialist Center, a specialized medical facility in Al-Kut city, for the purpose of identifying and isolating Streptococcus, which was further examined under a microscope. Information pertaining to these cases, including patient names, ages, diabetic status, and clinical symptoms, was recorded by the attending physician on a survey document.

2.2. Bacterial isolation and identification

2.2.1. Isolation of *Streptococcus spp.*

Samples from the oral cavity were streaked onto blood agar and then incubated in a candle jar under anaerobic conditions for 48 hours at 37 °C. After growing on blood agar, bacterial isolates were streaked onto streptococcus selection agar. This medium limit the growth of other bacterial species while promoting the growth of streptococci because it contains Sodium azide, sodium sulphite inhibits gram-negative rods and the crystal violet suppresses Staphylococci. Growth of coliforms, proteus, pseudomonas and bacillus species is markedly suppressed in this medium [13].

2.2.2. Identification of Streptococcus isolates

Based on their cultural traits, biochemical testing, and VITIK-II system, bacterial isolates were identified.

2.2.2.1. Gram stain

A small amount of bacteria colony was spread with drop of normal saline on clean slide, fixed by heat and stained with crystal violet, treated with Iodine, decolorized with alcohol and stained with safranine then examined under oil immersion lens (100X) [14].

2.2.2.2. Biochemical tests

2.2.2.2.1. Catalase test

Using a wooden stick applicator, a clump of growth from a pure culture of each bacterial isolate was placed onto a microscopical slide, then two drops of a 3% hydrogen peroxide solution were added to the bacterial cells. A positive result (catalase production) is indicated by the presence of gaseous bubbles [15].

2.2.2.2.2. Blood hemolysis test

This test was used to detect the ability of bacterial isolates to produce hemolysin and determine the type of hemolysis, and was achieved by streaking each bacterial isolate on blood agar medium, then incubated under anaerobic conditions for 48 hours at 37 °C [16].

2.2.2.2.3. VITEK-II identifying system identification

The VITEK-II microbial identification system, renowned for its innovation, boasts an extensive identification database, the most automated platform available, swift outcomes, enhanced reliability, and requires only a short period of training. Utilizing the VITEK-II identification system, bacterial isolates believed to be *Streptococcus spp*. were accurately identified.

2.3. Antibiotic susceptibility test

This test is performed by Kirby-Bauer procedure on Muller Hinton agar [17]. An inoculums isolates were prepared by emulsifying colonies from an overnight culture in sterile normal saline until a turbidity equivalent to 0.5 McFarland solution standards. The bacterial suspension was uniformly spreaded on Muller Hinton agar using sterile swab and left to dry. With sterile forceps selected antibiotic disks (Penicillin G (10 IU), Ampicillin (10 µg), Tetracycline (30 µg), Vancomycin (30 µg), Erythromycin (15 µg), Cefotaxime (30 µg), Ceftriaxone (30 µg), Doxycycline (30 µg), Cefepime (30 µg), Meropenem (10 µg), Levofloxacin (5 µg), Amoxicillin-clavulanic acid (30 µg), Trimethoprim-sulfamethoxazole (25 µg), Clindamycin (2 µg)) were placed on the inoculated plates and incubated at 37°C for 48 hrs in an inverted position. After this period of incubation, the diameters of inhibition zones were noted and measured by a ruler in (mm), results were determined according to CLSI (2023).

2.3.1. Determination of Multiple Antibiotic-Resistant Index

Multiple antibiotic resistance index (MARI) was determined to ascertain the number of antibiotics the isolates are resistant to according to the formula described by Akinjogunla and Enabule [18]

MARI = a/b.

Where;

a = number of antibiotics to which the isolate was resistant to;

b = total number of antibiotics to which the isolates was subjected to;

3. RESULTS

3.1. Collection of samples

One hundred samples were collected from the oral cavity of patients with various oral infections to isolate *Streptococcus spp*. These samples were taken by sterile clean swabs with transport media in a sterile container to keep them fresh and then streaked on blood agar. The bacterial isolates that grew on blood agar were subsequently subcultured on Streptococcus selection agar and incubated in a candle jar under anaerobic conditions for 48 hours at 37 °C. This medium limit the growth of other bacterial species while promoting the growth of streptococci because it contains Sodium azide, sodium sulphite inhibits gram-negative rods and the crystal violet suppresses Staphylococci. Growth of coliforms, Proteus, Pseudomonas and Bacillus species is markedly suppressed in this medium.

3.2. Identification of isolated bacteria

Identification of bacterial isolates suspected to be *Streptococcus spp*. was based on their morphological and cultural characteristics, as well as biochemical tests.

3.3. Morphological and cultural characteristics

Bacterial isolates grown on blood agar and Streptococcus selection agar medium were initially distinguished based on their morphological and cultural characteristics. The findings indicated that these isolates exhibit gram-positive characteristics, appearing as spherical or ovoid cells. The microbial colonies displayed features such as translucency or

opacity, ranging in color from white to gray on Streptococcus selection agar, whereas on blood agar, they were observed as small, pin-shaped, mucoid or smooth, glossy, and translucent with areas displaying non hemolysis as shown in (Fig. 1 and 2). Isolated bacteria that may be Streptococcus spp. were staining with Gram stain, Streptococcus bacteria were observed under the microscope exhibiting a Gram-positive reaction, with a cocci morphology, and arranged in both long and short chains (Figure 3).

FIGURE 1. ***Streptococcus spp.*** **on blood agar during 48 hours anaerobic incubation period at 37 °C**

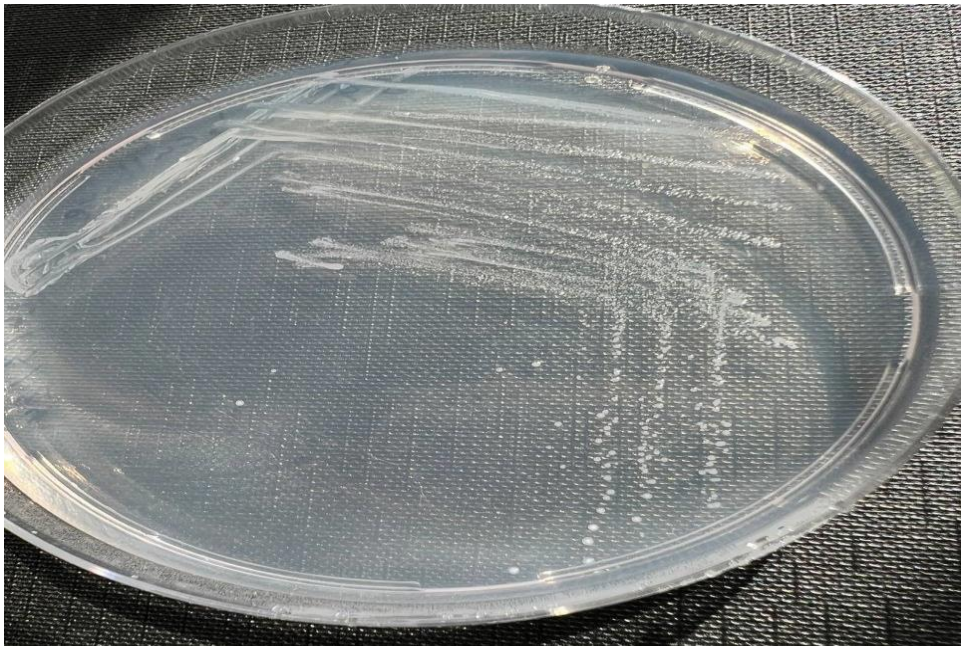

FIGURE 2. ***Streptococcus spp.*** **on streptococcal selection agar after incubation at 37c for 48h under anaerobic condition**

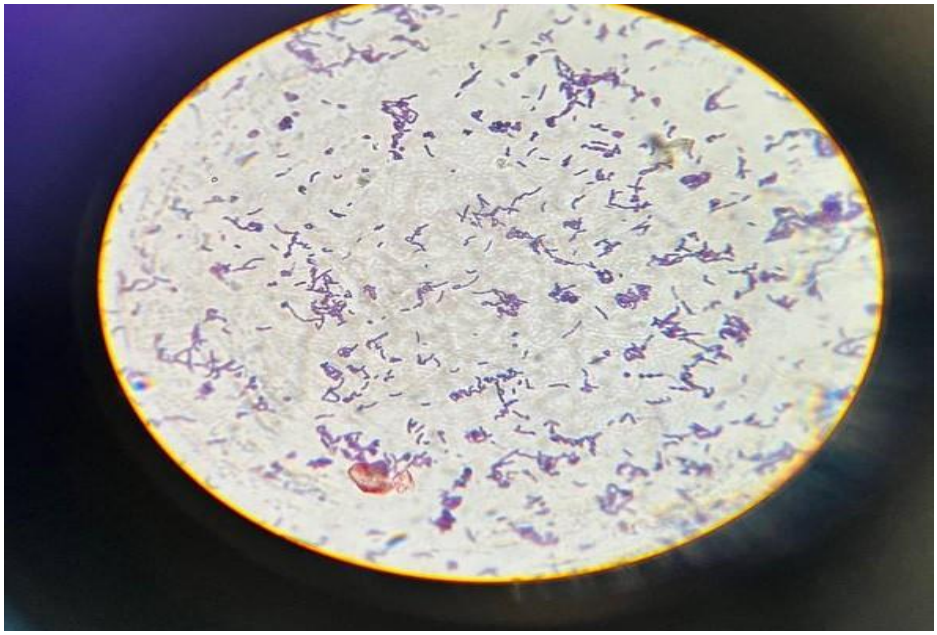

FIGURE 3. Gram staining results of *streptococcus spp.* isolates

3.4. Biochemical identification

The findings presented in (Figure 4) indicated that the Streptococcus bacteria were negative for catalase activity, as evidenced by the absence of oxygen gas bubbles, incapable of generating hemolysin and displaying gamma hemolysis on blood agar (Figure 5). Based on these results, these specimens were classified as *Streptococcus spp.*

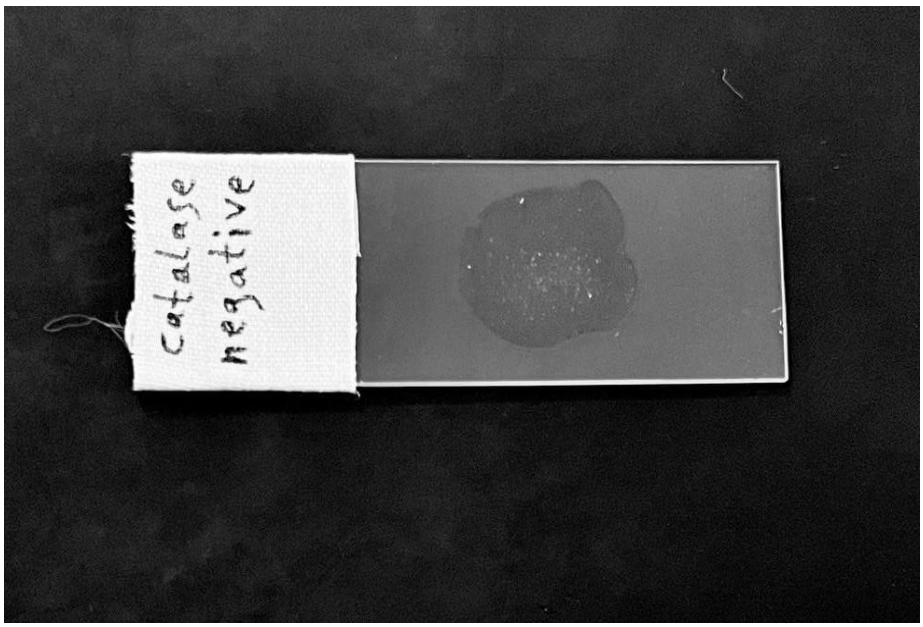

FIGURE 4. Negative catalase test of *streptococcus spp.* isolates

FIGURE 5. ***Streptococcus spp.*** **on blood agar**

To confirm the identification of bacterial isolates identified as *Streptococcus spp.*, an analysis of the biochemical traits of these isolates was conducted by utilizing the VITEK-Π system. Out of a total of 100 bacterial isolates, half were classified as gram-positive while the other half were categorized as gram-negative. Within the gram-positive isolates, 27 were identified as belonging to the Streptococcus spp. category (table 1).

Table 1. Vitek 2 device analysis for Streptococcus spp. Recognition

Total number	Total number of isolated	Number & type of Streptococci	
50	27	6 (22.22%)	*S. sanguinis*
		2 (7.40%)	*S. mitis*
		2 (7.40%)	*S. oralis*
		3 (11.11%)	*S. salivarius*
		4 (14.81%)	*S. pluranimalium*
		5 (18.51%)	*S. pseudoporcinus*
		4 (14.81%)	*S. alactolyticus*
		1 (3.70%)	*S. parasanguinis*

Out of a total of 50 gram-positive isolates, 27 were from *Streptococcus spp.* (54%), *Enterococcus faecalis* 4(8%), *Kocuria rosea* 2(4%), *Kocuria kristinae 1(2%)*, *Kytococcus sedentarius* 1(2%), *Staphylococcus aureus* 9(18%) and *Bacillus subtilis* 6(12%) (table 2).

Table 2. Opportunistic and pathogenic bacteria strains isolated from oral cavities

Gram-positive bacteria strains	Result [No. (%)]
Streptococcus spp.	27 (54%)
Enterococcus faecalis	4 (8%)
Kocuria rosea	2 (4%)
Kocuria kristinae	1 (2%)
Kytococcus sedentarius	1 (2%)
Staphylococcus aureus	9(18%)
Bacillus subtilis	6(12%)
Total	50

Table 3. sites distribution of *Streptococcus spp.* isolates from patients with oral infections

Infections sites	Result [No. (%)]
Gums	6 (22.22%)
Subgingival dental plaque	3 (11.11%)
Lower gingival dental plaque	2 (7.40%)
Inside lips	2 (7.40%)
inside cheeks	1 (3.70%)
Tongue	1 (3.70%)
Plaque	12 (44.44%)
Total	27

3.5. Antibiotic susceptibility of *Streptococcus spp.* isolates

The antibiotic susceptibility test for fourteen antibiotics was determined through the agar disc diffusion test (Kirby-Bauer method) in accordance with the guidelines set by the Clinical Laboratory Standards Institute (CLSI) in 2023. The isolates showed a variable level of resistance to antibiotics used in this study; the overall susceptibility patterns of isolates are displayed in (table 4).

Table 4. Antibiotic susceptibility of *Streptococcus spp.*

Antibiotics	*s. sanguinis*	*s. mitis*	*s. oralis*	*s. parasanguinis*	*s. salivarius*	*s. pluranimalium*	*s. pseudoporcinus*	*s. alactolyticus*
Penicillin/								
S	1	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0
R	5	2	2	1	3	4	5	4
Ampicillin/								
S	6	2	2	1	3	4	5	4
I	0	0	0	0	0	0	0	0
R	0	0	0	0	0	0	0	0
Tetracycline/								
S	2	1	2	0	0	2	1	1
I	4	0	0	0	1	2	1	0
R	0	1	0	1	2	0	3	3
Vancomycin/								
S	6	2	2	1	3	4	5	4
I	0	0	0	0	0	0	0	0
R	0	0	0	0	0	0	0	0
Erythromycin/								
S	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0
R	6	2	2	1	3	4	5	4
Cefotaxime/								
S	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0
R	6	2	2	1	3	4	5	4
Ceftriaxone/								
S	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0
R	6	2	2	1	3	4	5	4
Cefepime/								
S	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0
R	6	2	2	1	3	4	5	4
Doxycycline/								
S	4	1	0	0	0	1	0	0
I	2	0	0	0	0	0	1	0
R	0	1	2	1	3	3	4	4

Meropenem/								
S	2	0	2	0	1	0	1	1
I	0	0	0	1	0	0	0	0
R	4	2	0	0	2	4	4	3
Levofloxacin/								
S	3	2	2	0	0	0	1	1
I	1	0	0	0	0	1	0	0
R	2	0	0	1	3	3	4	3
Amoxicillin-clavulanic acid/								
S	6	2	2	1	3	4	5	4
I	0	0	0	0	0	0	0	0
R	0	0	0	0	0	0	0	0
Trimethoprim-sulfamethoxazole								
S	6	2	2	1	3	4	5	4
I	0	0	0	0	0	0	0	0
R	0	0	0	0	0	0	0	0
Clindamycin/								
S	0	0	0	0	0	1	0	0
I	0	0	1	0	0	0	0	0
R	6	2	1	1	3	3	5	4

*S: sensitive, I: intermediate, R: resistant

Finally, the table-5 displays the multiple antibiotic-resistant index (MARI) of the oral *Streptococcus* isolates, showing a range of 0.3-0.7. Any values exceeding 0.2 are deemed to possess clinical significance.

Table 5. The Multiple Antibiotic-Resistant Index of the oral *Streptococcus* isolates

Type of streptococci	No. of sample	Antibiotic resistance (a)	The total number of antibiotics to which the isolate was exposed to (b)	MARI (a/b)
S. oralis	1	P, E, CTX, CRO, FEP, DXT, CD.		0.5
	2	P, E, CTX, CRO, FEP, DXT.		0.42
S. mitis	3	P, TE, E, CTX, CRO, FEP, DXT, MRP, CD.		0.64
	4	P, E, CTX, CRO, FEP, MRP, CD.		0.5
S. sanguinis	5	E, CTX, CRO, FEP, CD.		0.35
	6	P, E, CTX, CRO, FEP, MRP, CD.		0.5
	7	P, E, CTX, CRO, FEP, LEV, CD.		0.5
	8	P, E, CTX, CRO, FEP, MRP, CD.		0.5
	9	P, E, CTX, CRO, FEP, MRP, LEV, CD.		0.57
	10	P, E, CTX, CRO, FEP, MRP, CD.		0.5
S. parasanguinis	11	P, TE, E, CTX, CRO, FEP, DXT, LEV, CD.		0.64
S. salivarius	12	P, E, CTX, CRO, FEP, DXT.		0.42
	13	P, TE, E, CTX, CRO, FEP, DXT.		0.5
	14	P, TE, E, CTX, CRO, FEP, DXT.		0.5

S. pluranimalium	15	P, CTX, CRO, FEP, DXT, MRP, LEV, CD.		0.57
	16	P, CTX, CRO, FEP, DXT, MRP, LEV, CD.		0.57
	17	P, CTX, CRO, FEP, MRP.		0.35
	18	P, CTX, CRO, FEP, DXT, MRP, LEV, CD.	14	0.57
S. pseudoporcinus	19	P, TE, E, CTX, CRO, FEP, DXT, MRP, LEV, CD.		0.71
	20	P, TE, E, CTX, CRO, FEP, DXT, MRP, LEV, CD.		0.71
	21	P, E, CTX, CRO, FEP, LEV, CD.		0.5
	22	P, TE, E, CTX, CRO, FEP, DXT, MRP, LEV, CD.		0.71
	23	P, E, CTX, CRO, FEP, DXT, MRP, CD.		0.57
S. alactolyticus	24	P, E, CTX, CRO, FEP, DXT, LEV, CD.		0.57
	25	P, TE, E, CTX, CRO, FEP, DXT, MRP, CD.		0.64
	26	P, TE, E, CTX, CRO, FEP, DXT, MRP, LEV, CD.		0.71
	27	P, TE, E, CTX, CRO, FEP, DXT, MRP, LEV, CD.		0.71

4. DISCUSSION

All figures should be the oral cavity of humans represents a miniature ecosystem consisting of various niches such as the dorsal and ventral sides of the tongue, buccal epithelium, hard palate, soft palate, and supra-gingival plaque on tooth surfaces, all of which are inhabited by a vast array of microorganisms, including fungi, various types of viruses, and a diverse bacterial population. Approximately 1100 distinct taxa have been identified within the oral cavity and documented in the Human Oral Microbiome Database [19]. During our study it was revealed that the majority of cultural outcomes 27 (54%) result in the growth of the *Streptococcus spp.*, followed by *Enterococcus faecalis* 4 (8%), *Kocuria rosea* 2(4%), *Kocuria kristinae 1(2%), Kytococcus sedentarius* 1(2%), *Staphylococcus aureus* 9(18%) and *Bacillus subtilis* 6(12%). These results are consistent with previous studies (Mohammed & Al Niaame, 2022) [20] that support the idea that *Streptococcus spp.* is primarily responsible for oral infections.

The oral bacterial profile identified in this present investigation exhibits some similarities with those from previous research. For example, Saleem et al., [21] documented nine distinct bacterial species: *Streptococcus species* (21.7%), *Staphylococcus aureus* (19.6%), *Pseudomonas species* (19.6%), *Klebsiella species* (2.2%), *Corynebacterium species* (6.5%), *Citrobacter species* (10.9%), *Enterococcus faecium* (10.9%), *Enterococcus avium* (2.2%), and *Neisseria species* (6.5%), which were not recorded in the current study. Similarly, Yadav et al., [22] also recognized nine bacterial species: *S. mitis* (9.84%), *S. mutans* (40%), *S. vestibularis* (5.23%), *S. albus* (7.38%), *Enterobacter spp.* (1%), *S. aureus* (28.92%), *K. pneumoniae* (2.76%), *Pseudomonas spp.* (3.38%), and *P. vulgaris* (1.52%), which were not recorded in the current study.

The aforementioned comparisons have contributed to the reinforcement of the idea that the human oral cavity serves as a conducive environment for the proliferation of a varied, plentiful, and intricate microbial population, this is attributed to its elevated temperature, abundance of nutrients, constant presence of saliva, and a pH level approaching neutrality. Consequently, it emerges as an optimal habitat for the development of a wide spectrum of bacteria, encompassing both pathogenic and nonpathogenic strains [23].

In relation to the antibiotic susceptibility profile of the oral isolates obtained from dental patients, the present study agrees with Maripandi et al., [24] who investigated the efficacy of seven antibiotics (Clindamycin, Vancomycin, Bacitracin, Tetracycline, Penicillin, Chloroamphenicol, and Streptomycin) against dental caries strains. Their findings revealed that Streptococcus strains exhibited resistance to penicillin, while being susceptible to tetracycline.

The findings of this research demonstrate that Augmentin, Trimethoprim-sulfamethoxazole, Ampicillin, and Vancomycin exhibit significant potency and have the potential to be utilized in the efficient management of oral infections owing to their bacteriostatic/bactericidal properties against the strains, considering the notable degree of susceptibility observed. The insensitivity displayed by certain oral strains to specific antibiotics employed indicates the rise of antimicrobial resistance in these microorganisms, primarily attributed to the indiscriminate utilization and misuse of these medications. In our investigation, elevated levels of resistance were observed. The findings revealed that all the isolates exhibited resistance towards Erythromycin, Ceftriaxone, Cefepime, and Cefotaxime. With respect to Penicillin, the results indicated that 96.29% of the isolates displayed resistance, while 92.59% showed resistance to Clindamycin. Hence, it is imperative to discourage the act of self-medicating among individuals. Concurrently, it is essential to conduct antibiotic susceptibility testing following established protocols in order to determine the optimal medications for guiding empirical treatment [25][26].

This discussion would be incomplete without note on the multiple antibiotic resistance index (MARI) of the isolates. The calculation of MARI involves dividing the number of antibiotics to which the isolates demonstrated resistance by the total number of antibiotics to which the isolates were exposed, as outlined by Apun et al., [27]. Mishra et al., [28] have suggested that a MAR index of 0.2 or higher signifies potential high-risk sources of contamination, whereas a MAR index of 0.4 or above is indicative of contamination originating from human faecal sources. Furthermore, Thenmozhi et al., [29] asserts that MAR index values exceeding 0.2 imply the presence of isolates from sources at high risk of contamination with a history of frequent antibiotic usage, while values less than or equal to 0.2 indicate bacteria originating from sources with lower antibiotic usage. It is crucial to note that elevated MAR indices necessitate vigilant pharmacosurveillance and the implementation of appropriate remedial actions. In the present investigation, the greatest degree of multidrug resistance (MDR) was identified in the configuration (3, 9, 11, 15, 16, 18, 19, 20, 22, 23, 24, 25, 26, 27), wherein these strains exhibited the capability to resist approximately (8→10) antimicrobial agents. Conversely, the lowest level of MDR was observed in the arrangement (5, 2, 12, 17), with a mere 5, 6 antibiotics being resisted in total. The emergence of MDR *Streptococcus spp.* is considered to possible reasons is the presence of specific resistance genes or genetic mutations can contribute to higher MDR. Some bacteria have acquired genes through horizontal gene transfer that provide resistance to multiple antibiotics, Mechanisms such as efflux pumps, enzyme production (like beta-lactamases), or altered target sites can lead to resistance against several drugs. The isolates with pattern (3, 9, 11, 15, 16, 18, 19, 20, 22, 23, 24, 25, 26, 27) may possess more of these mechanisms compared to those with pattern (5, 2, 12, 17), Overuse or misuse of antibiotics in healthcare settings can lead to the selection and proliferation of resistant strains. The high MDR pattern could reflect areas or conditions with poor antibiotic stewardship. The conclusions presented in my study are consistent with those of Patnool et al., (2024) [30] in their review which supports the notion that inappropriate use of antibiotics contributes significantly to multidrug resistance in *Streptococcus species*. Masood et al., (2013) [31] agree with my observations regarding the prevalence of multidrug resistance in oral streptococci. Their research corroborates the high rates of antibiotic resistance seen in various species of the Viridans group, including *S. sanguis*, *S. mitis*, *S. oralis*, and *S. salivarius*, as well as other related species. This agreement reinforces the significance of multidrug resistance among oral streptococci, highlighting a consistent trend across different studies. In contrast to the findings of Enitan et al., (2023) [32] whichh reported a Multidrug Antibiotic Resistance Index (MARI) of zero for Streptococcus, our study observed significant multidrug resistance among oral streptococci. The high rate of multidrug resistance in oral streptococci observed in our study, involving resistance to 8 to 10 antibiotics, indicates a notable difference from the absence of such resistance in the bacterial strains reported by Enitan et al. (2023) [32]. This discrepancy suggests that oral streptococci may exhibit different resistance pattern or that the antibiotic panels used in each study may contribute to differing results. Hence, it is imperative that empirical therapy be informed by meticulous laboratory analyses, specifically antibiotic susceptibility testing [33][34].

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