



ISOLATION AND IDENTIFICATION OF ORAL BACTERIA FROM IRAQI PATIENTS WITH ORAL INFECTION AND DETERMINING THE RESISTANCE OF PATHOGENIC ISOLATES TO ANTIBIOTIC

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ABSTRACT

A complex and diversified microbial community vital to both health and disease is found in the mouth cavity. Periodontal disease, dental cavities, and severe oral infections. The variety of oral microbiota, which includes certain opportunistic, potentially harmful bacterial and fungal strains that were found in comparatively high prevalence among the individuals under analysis, may raise the possibility of infections spreading from the mouth to nearby tissues and other organs. The main roles that oral pathogenic bacteria can play in infection are outlined in current research. A total of 100 oral swabs clinical samples were specifically obtained from 100 patients, both male and female, aged 2 to 70 years, who had various types of oral infections. Of these, 40 samples from healthy individuals were selected as control samples, 60 samples were patients with oral infection (dental caries, Periodontal disease and tooth decay) without taking any treatment at the time the samples were being collected. Using the Vitek-2 technique, the distribution of harmful bacteria among the presumed isolates revealed that 82,3% of the isolates were pathogenic and 17,6% were normal flora. Antibiotic susceptibility tests utilizing the Vitek-2 method have produced the following results. All isolate were 50% resistant to Amoxicillin, Gentamicin, Cephalothin, Tetracycline, Ceftriaxone, Amoxicillin, Erythromycin, Cefixime, Ciprofloxacin, Azithromycin. Isolates exhibit remarkable sensitivity to numerous antibiotics, such as (Clarithromycin, Cephalothin, Cefixime, and Ciprofloxacin). The results of this retrospective investigation showed how urgently pretreatment assessment of oral microbiota components has to be prioritized. Particularly those strains that are very harmful to senior citizens and are recognized as human opportunistic infection etiological agents.

Key words: Microbial community, Oral infection, Periodontal disease, oral swabs, Microbiota., Antimicrobial resistance

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عزل وتشخيص بكتيريا الفم من المرضى عراقيين مصابين بالتهابات الفم وتحديد مقاومة العزلات المرضية للمضادات الحيوية

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الخلاصة

يحتضن تجويف الفم مجتمعاً ميكروبياً معقداً ومتنوعاً يلعب دوراً هاماً في الصحة والمرض. تشمل العدوى الفموية الرئيسية تسوس الأسنان ومرض اللثة والتهابات الفم الشديدة. تنوع الاحياء المجهرية في الفم، بما في ذلك انتشارات مرتفعة نسبياً لبعض سلالات البكتيريا الانتهازية والممرضة بشكل محتمل، والفطريات التي تم اكتشافها في المرضى الذين تم اجراء فحص لهم، قد يؤدي إلى زيادة مخاطر الإصابة بالعدوى المنتشرة من التجويف الفموي إلى التراكيب المجاورة والأعضاء الأخرى. في الدراسة الحالية تم تلخيص الأكثر أهمية من الميكروبيوم الممرض للفم الذي يمكن أن يلعب دوراً في العدوى. تم جمع مجموعة من 100 عينة سريرية من الفم خصيصاً من 100 مريض يتراوح أعمارهم بين 2 و 70 عاماً، من الذكور والإناث، مع أنواع مختلفة من العدوى الفموية، وتم اختيار 40 عينة من أشخاص أصحاء كعينات سيطرة و 60 عينة من المرضى مصابين بالعدوى الفموية بما في ذلك تسوس الأسنان ومرض اللثة دون تلقي أي دواء خلال فترة جمع العينات. أظهر توزيع البكتيريا الممرضة بين العزلات المشكوك بها المفترض باستخدام نظام Vitek-2 أن 82.3% من العزلات كانت ممرضة و 17.6% من العزلات كانت *normal flora*. تمت دراسة نتائج الحساسية للمضادات الحيوية باستخدام نظام Vitek-2 كانت جميع العزلات مقاومة بنسبة 50% للأموكسيسيلين والجنتاميسين والسيفالوتين والتتراسيكلين والسيفترياكسون والأموكسيسيلين والإريثروميسين والسيفيكسيم وسيبروفلوكساسين وأزيتروميسين. وكانت العزلات حساسة بشكل كبير إلى العديد من المضادات الحيوية بما في ذلك الكلاريثروميسين والسيفالوتين والسيفيكسيم وسيبروفلوكساسين. أظهرت نتائج هذه الدراسة الحاجة الملحة لإيلاء المزيد من الاهتمام لفحص مرحلة ما قبل العلاج لمكونات *microbiome* الفموي، خصوصاً السلالات التي تعتبر عوامل مسببة للعدوى لدى الإنسان والتي تشكل خطراً خاصاً على كبار السن.

الكلمات المفتاحية: المجتمع الميكروبي، العدوى الفموية، أمراض اللثة، المسحات الفموية، الكائنات الحية الدقيقة، مقاومة المضادات الحيوية.

INTRODUCTION

After the intestine, the human mouth cavity is home to the second-most varied microbial community. More than 700 different types of bacteria, fungus, viruses, and archaea, make up the oral microbiome (Lamont et al., 2018). This microbial population contributes in several of ways to the preservation of both systemic and dental health. Oral cancer, periodontitis, gingivitis, and dental caries are all linked to microbiota dysbiosis (Jiang et al., 2019; Yang et al., 2018). Furthermore, there is a connection between oral microbial dysbiosis and atherosclerosis, rheumatoid arthritis, diabetes, and inflammatory bowel disease (Chen et al., 2018). Because these different diseases are linked to the oral microbiome, who it is composed can offer non-invasive indicators of illness. To identify oral microbiome biomarkers that are differently abundant across states of health and sickness, it is essential to first collect samples of the oral microbiome from individuals who are in good health and characterise their composition. Indeed, several of studies have looked at oral microbiomes that are in good health (Nearing et al., 2020) and have documented associations between the oral microbiome and particular characteristics that may affect the composition of the oral microbiome, like smoking (Wu et al., 2016), alcohol intake (Fan et al., 2018), vegan diet (Hansen et al., 2018), and ethnicity (Huang et al., 2011).



The mouth cavity of humans is invaded by more than 700 different types of microbes (**Hajishengallis et al., 2021**). The human microbiome project has identified the oral microbiome as one of its five study priorities, along with the nasal cavity, vagina, intestine, and skin. One of the most important and intricate microbial communities in the human body is the oral microbiome (HMP). The human microbiome project's completion has led to a deeper understanding of oral microbes, which goes beyond just knowing how oral germs contribute to periodontal disease, caries, and other oral illnesses (**Zuza et al., 2020**). More and more evidence points to Miller's oral lesion theory being correct. Loss of bones and connective tissues is the result of periodontal inflammation (**Willis & Gabaldón, 2020**). There is a notable influx of inflammatory cells in the connective tissue near the periodontal pocket epithelium (**Peng et al., 2022**). The majority of people believe that this low-grade inflammation will worsen other systemic conditions or have a detrimental effect on general health (**Al-Ghalebi & El-Samarrai, 2011**). Consequently, persistent periodontitis may be a significant contributor to imperceptible peripheral inflammation in the general population. Because it affects many other systemic disorders, periodontitis is frequently referred to as a "low-grade systemic disease." Many diseases that are common in human populations can impact the mouth, such as dental caries, periodontitis, and gingivitis. These diseases have all been linked to changes in the oral microbiome. However, due to its high vascularization and role as an entrance point for the digestive and respiratory systems, the mouth may have consequences for various systemic disorders related to the oral microbiota. An increasing body of research has demonstrated links between modifications in the oral microbiome and various illnesses. According to this, oral microbiota may offer prospective biomarkers for the detection of several systemic illnesses (**Willis & Gabaldón, 2020**). Dental caries and periodontal disorders are directly impacted by oral microorganisms. Through bidirectional contact between the oral cavity and systemic organs, the dynamic oral microbiota collaborates with the host to reflect immune and metabolic conditions. One of the most significant places of contact between the human body and its surroundings is the oral cavity. Through bidirectional contact between the oral cavity and systemic organs, the dynamic oral microbiota collaborates with the host to reflect immune and metabolic condition. One of the most significant places of contact between the human body and its surroundings is the oral cavity. The microbial makeup of the microenvironment varies at different regions within the oral cavity, and its regulation is influenced by complicated signals, hosts, and external environmental factors. Because systemic diseases are linked to the destruction of the microbial population and some health states appear to be related to the makeup of mouth bacteria, these processes may have an impact on or reflect human health (**Peng et al., 2022**). A few earlier research conducted in Iraq examined the prevalence of gingivitis and its connection to nutritional condition. In the Governorate of Al Nassiyria, Al-Galebi (2012) found a greater percentage for the moderate level of plaque (**Al-Ghalebi & El-Samarrai, 2012**). According to Al-2016 Awadi's report, in the Al-Dewaniya Governorate, a greater proportion of youngsters (79.5%) showed plaque scores between 1.1-2. (**Al Rawi & Khafaji, 2019**) Nevertheless, other Iraqi research (Al-Galebi, El-Samarrai, Hassan, and Droosh) did not discover a statistically significant difference between boys' and girls' plaque indices. **Al-Galebi and El-Samarrai, (2012)** noted that nine to ten-year-olds in Al-Nassiyria City had a moderate form of gingivitis (**Al-Ghalebi & El-Samarrai, 2011**). The majority of



the sample, according to the study, had normal gingival health conditions. Regarding gender, there was no discernible variation in the gingival index.

MATERIALS AND METHODS

Isolation and Identification of Bacterial Isolates

A total of 100 oral swabs clinical samples were especially collected from 100 patients from 2 to 70 years old male and female with different types of oral infection from different Iraqi hospitals and Private medical centers for dentistry, 40 samples were selected as control (apparently healthy people) and 60 samples patients with oral infection include (dental caries, tooth decay and periodontal disease) without receiving any medication during the period of sample collection. The information and clinical signs of any other disease were recorded according to the patient's history. Oral swabs were gathered (keeping samples free of external contaminants, such as before a meal or dental procedure) samples were transported to the laboratory by using sterile transport swabs and collected from healthy and from patients with different type of oral infection. The swabs were stored at 4 °C until reached to laboratory and culture. then sample culture on different culture media (blood agar, MacConky agar and chocolate agar) for 24 hours at 37 °C, overnight sample were tested for any isolate and different isolate with biochemical test and the hemolysis on blood and chocolate agar. The isolates were subculture on mannitol salt agar, mitis salivarius agar and Sabouraud dextrose agar for 24 hours at 37 °C. Different type of isolates appeared after the incubation period then its identified by microscopic examination and biochemical test and the results were confirmed by the Vitek system (Alghamdi, 2022).

Antibiotics Susceptibility Test (AST)

Vitek-2 was used to screen for antibiotic resistance in all of the verified isolates. Among the antibiotics that have been studied are (Clarithromycin, gentamycin, cephalothin, tetracycline, ceftriaxone, amoxicillin, erythromycin, cefixime, ciprofloxacin, azithromycin, nystatin, Itraconazole, ketoconazole, miconazole, fluconazole and amphotericin).

RESULTS AND DISCUSSION

Isolation and Identification of Bacterial Isolates

Table (1) lists 188 isolates from patient samples that were examined for the presence of various bacteria within the clinical sample between 18 and 24 hours. Upon 37°C incubation and microscopic analysis, pathogenic gram-positive and negative bacteria are visible, and after 18 to 24 hours, 58 isolates from control samples show normal flora .

After 18 to 24 hours at 37°C, different types of bacteria with hemolytic properties (α -, β -, and even non-hemolytic) can be seen on blood and chocolate agar, while colonies of white and pink form on MacConky agar after the same amount of time at 37°C. By microscopic analysis, biochemical testing, and subculturing on the particular medium that exhibits distinct types of pathogenic and normal flora, all of the isolates were identified. These include, *Staphylococcus haemolyticus*, *Granulicodella adiacens*, *Streptococcus pnemoniae*, *Escherichia coli* , *Klebsiella pneumonia spp. Pneumonia*, *Pseudomonase aeruginosa*, *Enterobacter cloacae*, *Streptococcus*



alatalyticus, *Staphylococcus xylosus*, *Staphylococcus carprae*, *Kocuria kristinae*, *Pontoea spp.*, *Staphylococcus aureus*, *Streptococcus mutans*. Table (1)

Table (1): Different type of bacteria microbial isolates from oral swabs from between the patients and control.

Sample	Isolate	Gram stain	No.(%)
Patients (No. of sample =60 sample)	<i>Staphylococcus haemolyticus</i>	+ ve	10 (5,3%)
	<i>Granulicodella adiacens</i>	+ve	1(0,53%)
	<i>Streptococcus pnemoniae</i>	+ ve	32(17,02%)
	<i>Escherichia coli</i>	-ve	20(10,6%)
	<i>k.pneumonia spp. pneumonia</i>	-ve	35(18,6%)
	<i>Pseudomonase aeruginosa</i>	-ve	5(2,65%)
	<i>Enterobacter cloacae</i>	-ve	3 (1,59%)
	<i>Streptococcus alatolyticus</i>	+ ve	10(5,3%)
	<i>Staphylococcus xylosus</i>	+ ve	2 (1,06%)
	<i>Staphylococcus carprae</i>	+ ve	1 (0,53%)
	<i>Kocuria kristinae</i>	+ve	2 (1,06%)
	<i>Pontoea spp.</i>	- ve	5(2,65%)
	<i>Staphylococcus aureus</i>	+ ve	25(13,29%)
	<i>Streptococcus mutans</i>	+ ve	27 (14,36%)
	<i>Streptococcus pyogenes</i>	+ ve	10 (5,3%)
Total isolates			188(100%)
Control (No. of sample =40 sample)	<i>Streptococcus mitis</i>	+ ve	15 (26%)
	<i>Streptococcus salivarius</i>	+ ve	32 (55%)
	<i>Candida albicans</i>	\	11 (19%)
Total isolates			58 (100%)

Table (1) indicates that the most common isolates from patients with oral infections that Saad Alghamdi found were *S.treptococcus pneumonia* (17.02 %percent), *Escherichia coli* (10.6 %percent), and *K.lebsiella pneumonia* (18.6 %percent). Fifteen distinct bacterial strains were identified for the study, eight of which were gram-positive and seven of which were gram-negative. *S.treptococcus pneumoniae* (n = 26) was the species most frequently seen in the gram-positive strains. Conversely, among the gram-negative strains, *Escherichia coli* (n = 26) was the most common species. Enterobacteriaceae accounted for 19.36% of the total abundance, while *Streptococcaceae* came in second with 13.83 percent. Additionally, one of *Klebsiella pneumoniae*'s most cariogenic strains (n = 14) was identified.

In addition to these noteworthy discoveries, *Streptococcaceae*, among which *Streptococcus pneumonia* and *Streptococcus pyogenes* were the most common species in both healthy and unhealthy oral cavities. *Streptococcaceae* may result in a number of illnesses, such as necrotizing fasciitis, endocarditis, bacterial pneumonia, meningitis, and erysipelas. Nonetheless, a large number of streptococcal species that are found in the mouth, skin, intestine, and upper respiratory tract are not harmful. *Streptococcus salivarius* isolate from both healthy and non-healthy oral cavities (Lee & Baek, 2022). Olson et. al, (2019) found S.



salivarius, a rarely reported cause of infection originating from the oral mucosa, following a dental cleaning.

S. aureus, *S. pneumoniae*, *H. influenzae*, *K. pneumoniae*, *P. aeruginosa*, *E. coli*, and *Candida* species are among the potentially dangerous bacteria that colonize the oral microbiome and exhibit microbiological indicators of aspiration pneumonia in elderly individuals, according to S. Khadka *et al.* (Khadka *et al.*, (2021), especially in residential care. The current study presents *P. aeruginosa* as five isolates from non-healthy oral cavities. An interesting finding was the identification of *E.coli*, *K. pneumoniae*, and *P. aeruginosa* in the lips of elderly patients suffering from aspiration pneumonia. *Klebsiella* species and *Escherichia coli* are typical GI tract microbiota. Their oral presence might be connected to the gastro-esophageal reflux disease that many elderly persons, particularly those who have dysphagia, suffer from. This implies that to reduce the risk of aspiration pneumonia and provide appropriate therapeutic therapy, dental professionals treating elderly patients' dental health issues should be aware of the telltale signs and symptoms of reflux. According to Zawadzki *et al.* (Zawadzki *et al.*, 2017), *Escherichia coli* strains were found among Gram-negative bacteria in all patient groups, exhibiting varying prevalence. Patients in Group I and Group II had oral cavities from which *Pseudomonas aeruginosa* was isolated. Only patients in Group I had certain strains of *Klebsiella oxytoca*, *K. pneumonia*, and *Acinetobacter baumannii* identified, while patients in Group II were the only ones with *Pantoea agglomerans*. There were no discernible statistically significant variations in the frequency of specific bacteria between individuals who were male and female. *Pseudomonas aeruginosa* and *Escherichia coli* are two of the Gram-negative bacteria that are most renowned for their epidemiological roles. These bacteria are especially harmful to those with impaired immune systems and have also been found in the mouths of those suffering from systemic illnesses (Zawadzki *et al.*, 2016). Sepsis and nosocomial infections may be caused by enteropathogenic, enterotoxic, and enterohemorrhagic strains of *E.coli* rods. Notably, *P. aeruginosa* bacteria are most likely to cause oral (Zawadzki *et al.*, 2017).

The detection of *S. aureus*, *S. hominis*, *S. xylosus*, and *S. haemolyticus* isolate only from non-healthy oral cavities, Garbacz *et al.* (Garbacz *et al.*, (2021) reported that *S. warneri*, *S. haemolyticus*, *S. saprophyticus*, *S. pasteurii*, *S. epidermidis*, *S. hominis*, *S. xylosus*, *S. equorum*, *S. kloosii*, *S. succinus*, *S. cohnii*, and *S. simulans* are from the 103 species that make up the group known as coagulase-negative staphylococci (CoNS). These CoNS are considered to be a source of multidrug resistance and methicillin resistance. In particular, *S. haemolyticus* and *S. saprophyticus* appear to be more prevalent in the oral cavity. Significant challenges may arise from *Staphylococcus aureus* strains that also aid in the formation of biofilms; these bacteria are typically accountable for biomaterial-associated diseases (Khoshnood *et al.*, 2019; Stańkowska *et al.*, 2019). Pathogens, especially MRSA methicillin-resistant forms, can spread to far-off locations and cause illnesses that are challenging to treat, like endocarditis, pneumonia, and surgical-associated infections (Stańkowska *et al.*, 2019; Blomqvist *et al.*, 2015).

This study's main objective was to clarify how Iraqi people's perceptions toward bacteria changed from being nonpathogenic in healthy samples to pathogenic in patient samples, mostly those with chronic illnesses. Gram-positive bacteria known as *Kocuria spp.*



were identified as oral flora in healthy individuals. Mohammed (**Mohammed, (2021)**) shows that *K. rosea* lacks virulence enzymes like catalase and urease, which are potential virulence factors in many pathogenic bacteria. Contrary to all of these findings, however, this bacterium is an infectious agent that contributes to nosocomial infections through its adherence to surfaces such as catheters and prosthetic devices. Catheter removal is therefore one of the initial procedures in the therapeutic protocol.

The most common causes of intravascular infections caused by *Granulicodella adiacens* one isolate are infections in nutrient-rich tissues such as the endocardium or the eye, which can result in endocarditis or endophthalmitis. An infection in this area can lead to endovascular infections, infections of the central nervous system, infections of the eyes, jawbones, joints, and urinary tract. According to Achmad *et al.* (**Achmad et al., (2020)**) nineteen out of the eighteen isolated samples from individuals with chronic periodontitis and those with periodontal pockets deeper than seven millimetres contained *Granulicodella adiacens*.

Candida albicans isolated 11 (19%) from healthy people as oral flora, Nouraei *et al* (**Nouraei et al., (2021)**) From the oral cavities of diabetic patients, 108 species of *Candida* were found, comprising 33 non-*Candida albicans* and 75 *Candida albicans*. Commonly found in the human environment are yeast-like fungi from the *Candida* genus, primarily belonging to the *Candida albicans* group, which were isolated and identified from the oral cavities of all age groups examined. The fungi infiltrate humans early in the ontogenetic growth phase; later, they may also spread through the epidermis to infect other host tissues and organs. damaged mucous membranes, ingestion, or inhalation. Several factors contribute to the development of candidosis and fungal infections in the oral cavity. These include dental prostheses made of acrylic that stick to the mucosal membrane and alter its surface, foreign items present, improper oral hygiene, and microdamage. It has recently been thought that yeast-like fungi are especially likely to form biofilms (**Lima et al., 2017; Knop et al., 2018**), and that this propensity is a key component of these diseases' pathogenicity. *Candida spp.* strains have been detected in oral cavities in up to 70% of human populations.

Antibiotics Susceptibility Test (AST)

Antibiotic susceptibility tests by the Vitek-2 System have produced the following results. Clarithromycin, Gentamicin, Cephalothin, Tetracycline, Ceftriaxone, Amoxicillin, Erythromycin, Cefixime, Ciprofloxacin, Azithromycin for bacterial isolate and Nystatin Itraconazole, Ketoconazole, Miconazole, Fluconazole, Amphotericin for fungal isolate. All isolates were 50% resistant to Amoxicillin, Gentamicin, Cephalothin, Tetracycline, Ceftriaxone, Amoxicillin, Erythromycin, Cefixime, Ciprofloxacin, Azithromycin. Isolates exhibit remarkable sensitivity to numerous antibiotics, such as (Clarithromycin, Cephalothin, Cefixime, and Ciprofloxacin). Table (2)

**Table (2):** Antibiotic susceptibility Result.

Antibiotic		Resistance (50% of isolate)	Intermediate (25% of isolate)	Sensitive (50% of isolate)
semisynthetic macrolide	Clarithromycin	-	-	S
aminoglycoside	Gentamicin	R	-	-
cephalosporin	Cephalothin	R	-	-
Tetracycline	Tetracycline	R	-	-
third-generation cephalosporin	Ceftriaxone	-	-	S
third generation cephalosporin	Cefixime	-	-	S
penicillin G	Amoxicillin	R	-	-
macrolide	Erythromycin	R	-	-
macrolide	Azithromycin	R	-	-
second generation fluoroquinolone	Ciprofloxacin	-	-	S
Amphotericin B	Amphotericin B	-	I	-
triazole	Fluconazole	-	I	-
Azole	Miconazole	-	I	-
Ketoconazole	Ketoconazole	-	I	-
triazole	Itraconazole	-	I	-
polyene ionophore	Nystatin	-	I	-

Antimicrobial resistance (AMR) poses an increasing hazard to public health with regarding the effective treatment of bacterial infections. Most current analyses by **Murray et al., (2022)** indicate that AMR is responsible for an estimated 1.2 million deaths annually worldwide. The estimated yearly cost of these illnesses in terms of health care and lost productivity in the EU alone is EUR 1.5 billion (**World Health Organization, 2022**). Determining the site of AMR development and elucidating the reservoirs of antimicrobial resistance genes (ARGs), also present in the human microbiome, are critical steps in combating the disease. AMR has been found to spread through a several of different channels, including medical settings, animal and human reservoirs, and the environment. At their core, the food chain connects each of these reservoirs (**Berendonk et al., 2015; Isticato and Ricca, 2016**). One example of such a varied microscale ecology is the oral microbiome. The oral cavity can be colonized by about 1,000 different microbial species, some of which are incomplete colonies found in specific oral habitats, such as dental plaque (**Lamont et al., 2018**). The microbial cells in this instance are arranged into a biofilm, whose properties—such as their close proximity and polymicrobial makeup—allow for interactions like horizontal gene transfer (**Roberts & Mullany, 2010; Sultan et al., 2018**). Stable oral microbiota homeostasis benefits both the host and its bacteria in a healthy state. Environmental variables, on the other hand, have the power to tip the scales in favour of a dysbiotic shift, which can exacerbate oral conditions like periodontitis and caries (**Costalonga & Herzberg, 2014**). These are distinguished by specific microbiota variations in relation to health and bacterial taxa with the capacity to cause disease (**Anderson et al., 2023**) demonstrate the high prevalence of phenotypic resistance to beta-lactams (cefuroxime and penicillin), fluoroquinolones (ciprofloxacin), and macrolides lacosamide (azithromycin, erythromycin, and clindamycin). With genotypic analysis, tetracycline resistance was revealed to be the most common resistance; however, phenotypic



resistance did not support this finding. This might be because the isolates chosen for phenotypic testing had lower levels of this resistance gene's phenotypic expression. According to **Köhler et al., (2019)**, Of the multidrug-resistant *Acinetobacter*, *Pseudomonas*, and *Klebsiella* strains, *P. aeruginosa* strains showed the lowest susceptibility, whereas most *A. baumannii* strains were BZK-sensitive.

CONCLUSIONS

In conclusion, this study highlights the urgent need for pretreatment assessments of oral microbiota, particularly in patients with oral infections such as dental caries, periodontal disease, and tooth decay. Our findings indicate that a significant portion (82.3%) of the bacterial isolates obtained from untreated patients were pathogenic. Additionally, there was a concerning resistance rate of 50% to multiple antibiotics, including Amoxicillin and Ciprofloxacin, despite notable sensitivity to others like Clarithromycin. These results underscore the importance of understanding the microbial landscape in the oral cavity, especially among vulnerable populations such as senior citizens, to inform treatment strategies and improve patient outcomes.

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