ISSN: 3007-3545
Doi: 10.69788/jmsth/2025.02.01

Isolation and Diagnosis of Some Bacterial Species Responsible for Tooth Caries

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Abstract

Dental cavities, an infectious ailment, are characterized by mineral erosion within the teeth, resulting in the creation of holes. This condition, also known as tooth decay, is fundamentally triggered by a triangular relationship. This involves the presence of carbohydrates, the activity of bacteria that cause decay within plaque, and the natural vulnerability of the hard surfaces of teeth. mouths are home to a variety of bacteria, including some that can lead to tooth decay, often referred to as cariogenic bacteria. These are considered the primary factors in the occurrence of cariogenic bacteria. These are considered major determinants of tooth caries. We obtained 50 samples with a wooden stick and a margin of gum around the teeth. The other samples were derived from teeth removed in a dentist's office. The made sterile specimens were moved to a sterile cup made for this purpose with the help of the dentist. The samples were sent over to MacConkey agar, blood agar and mannitol by the microbiology lab for growth. salt agar. Each plate was incubated for 24 h at 37 °C. After this time of incubation, we observed some visible growth on the plated inoculate and recorded the utimption at 14 d. The colony morphology. The isolates were cultured in standard microbiological conditions (Gram technique, and then identified the colonies based on their appearance and with Gram staining. Microbiological analysis showed that the isolates identified, of the Gram-positive cocci, were mutans and lactobacilli. via culture methods, were largely made up of Streptococcus spp. This type of organism dominated, occurring in 50% (44 out of the full range of bacteria were the same type. samples). Next in order of frequency were Staphylococcus spp., which were detected in 29.5% (26 samples) and 20.5% (18 specimens) of Enterococcus faecalis, respectively. Conversely, the observed proportions were less compared to Gram-negative. positive counterparts. Among them, P. aeruginosa was the largest group with a total of 54.54% (12 isolates) of the positive samples. The minimum prevalence rate in the surveyed cases of dental caries was found in the case of E. coli, with a percentage of 45.45% (i.e., 10 samples).

Keywords: dental caries, gram-positive bacteria, Staphylococcus species, Escherichia coli, Escherichia coli isolates.

Article history: Received: *6 Apri. 2025*, ***Accepted:*** *21 Sep 2025*, ***Published:*** *1 Dec. 2025*

1. Introduction

The calcified tissues are destroyed by the acids produced during the metabolism of carbohydrates by acidic bacteria, leading to caries [1]. The oral cavity is a suitable environment for different bacteria due to the availability of nutrients, epithelial waste, and secretions. Oral bacteria include types such as streptococci, staphylococci, lactobacilli, and corynebacteria, as well as a large number of anaerobic bacteria [2]. Upon being born, the oral space presents as a germ-free environment. However, this condition is short-lived, as it is rapidly inhabited by microbes drawn from its surroundings. A key source of these initial colonizers is the mother, primarily during the infant's initial feedings. [3].

Tooth caries is considered among the most common illnesses globally [4], affecting between 60 and 90 percent of school-age children and a sizable percentage of adults. It is also one of the most common oral diseases in some countries in Asia and Latin America, while it seems to be less common and less severe in most African countries [5]. In many countries, geographical determinants include social variables in the rate of tooth caries. Even with advancements, dental deterioration remains a prevalent issue for the majority of youngsters, and in some instances, it's quite serious. Tooth caries is the most common oral disease among children and also contributes to tooth loss in adults [6]. Cavities are considered localized erosion of tooth tissues resulting from bacterial activity [7].

Dental plaque, which accumulates on the surfaces of teeth, is formed from the natural oral flora and is the main factor behind the occurrence of cavities [1], [8]. This plaque continuously forms on the teeth, and when exposed to fermentable carbohydrates, the bacteria within it produce acids. These acids lead to a decrease in the acidity level in the mouth, causing the demineralization of tooth enamel. Although the process of remineralization occurs naturally over time, if the rate of demineralization exceeds that of remineralization, it results in the formation of cavities in the teeth [9].

The basic mechanisms of clinical relevance and sex equivalence behind the beginning of urodynamic symptoms are difficult to clearly define, but they seem to be related to biomechanical factors, leading also to urge incontinence with arge ethanol consumption without development of the Equation 5 school admission dental cavities, can you digest when boiled down into the simplest components (0) -302 more terms saved aspects. Dental plaque is a further significant factor. harboring a substantial bacterial load. The composition of the same, the plaque is so crucial; more of an acid-ripsi forces jóvenes. generating bacteria contributes significantly. Moreover, the habitual intake of readily fermentable carbohydrates, and especially sugars, increases the risk. In addition, reduced saliva volume or decreased saliva's failure to buffer acid properly is contributory. Genetic factors that predispose to Test2 vulnerability to cavities are also important [10]. Specifically, the Streptococcus mutans and Streptococcus sobrinus bacteria have been identified as the leading cause of cavities, and other microorganisms, such as lactobacilli, could stimulate the process [11]. F Certain there is international acceptance that a) certain pathogens, including Staphylococcus species. And Candida spp., joint infections, should be regarded as potential extracellular defence mechanisms, for instance, people suffering from chronic pathogenic factors (4-6). diseases such as diabetes, neutropenia periodontal.; leukopenia, and AIDS [12].

Studies S tracheal colonization by have dont have burbs colonized strains of microorganisms also vary every year. bacteria may be found solely in the mouth transiently; they merely play a role in the initiation of several orofacial health problems, including tooth decay. example [13, 14]. The microbial environment in the behavioral modifications, and other similar disorders and the mouth are affected by everyday behaviors (hyper) starches-feeds-forces-the-population-explosion-of-and Other gram-negative and Gram-positive food-borne vibrio. acid-resistant and decay-causing bacteria, particularly mutans streptococci and lactobacillus bacteria. Scientific studies show that the risks among diabetic patients are significantly higher and other oral diseases, such as gum issues and salivary rash, rendering them Predisposed to infections 305 Salivary disorders more vulnerable to the same. recurrent tooth decay. However, the large proportions of elderly people are taking drugs they are taking can induce decreased salivary rats). secretion, which interferes with the homeostasis of bacteria in the mouth [15]. The prevalence of dental disease of the teeth is very evident on the part of people nowadays, and it is increasingly recognized by those who do not consistently take care of their dental health. Wei and Hemen said a lot of students don’t brush long enough or in the right direction. proper way, which does not allow deleting of the full plaque [16]. The first aim of this investigation was to purify S. aureus bacteria associated with dental caries and recognize the associated risk factors

2. Materials and Methods

The patients who were selected for the study vstackrelrelstud Patients seen at numerous dental clinics in the city of Baqubah during 1, 2024 October 1, 2024 December 1, 2024. A total of 50 samples had been taken, some samples were harvested a wooden spatula in which the local lesion or a counter. on the gums that are next to the teeth, and on the parts of the RTCT edges of theedTextBox 15 But котор он included teeth removed by dental extraction carried out in a clinical setting. Specimens were collected in strictly sterile situations, with the aid of a dentist. They were then immediately collected in the disinfected containers designed for biological samples. Each container was carefully marked with the full name of the patient, their age and the date on which the sample was taken. The prepared specimens were then sent to the microbiology laboratory for further screening. Upon time of arrival, the samples were subjected to culture on appropriate agar, manitol salt agar and blood agar) were used to measure the. MacConkey agar. This inoculated each of these plates was was then put in an incubator at a at 37 degrees Celsius for a total311 of three hours. duration of 24 hours.

After incubation, the plates were inspected for the presence of any visible growth. The attributes of any bacterial growth formed were carefully documented. To achieve precise Identification of the isolated bacteria, after biochemical identification, the isolated bacteria were subjected to a battery of standard microbiological methods. This comprised not only additional growth on the earlier 1.8% of gross domestic product crop acreage but also investment in areas like civil engineering, real estate development and schools. referred media (Mannitol, Blood, and MacConkey agar) and even some of the more sophisticated tests like API strep and an automated system for microbial identification. These techniques were integrated with comprehensive colonial characteristics and the use of complete identification of the isolates was performed for Gram staining isolates. 1 and as well as on mannitol salt broth in addition to the blood agar. agar, blood agar and MacConkey agar. All plates were cooled at room temperature for 10 minutes. 24 hours. Visible growth on. the plates were there was no growth of the inoculated, and colony sec. recorded. Identification of the bacterial isolates was carried out based on singly cultured the isolates on culture media (Mannitol, Blood, and macConky agar plate) and application of strep API. testing and the bioMgrieux Vitek or Vitek 2 (bioMirieux Inc., Marcy l'Etoile, France) automated microbial identification system.). rough as well as morphological appearance of the 2 types at the categories. colonies and Gram staining.

3. Result and Discussion

A collection of fifty samples was taken from patients with dental caries and plaque. This yielded a total of 110 bacterial isolates, which were subsequently categorized as either gram-positive or gram-negative. Identification to the genus level was achieved by cultivating the isolates on mannitol salt agar, blood agar, and MacConkey agar. Utilizing API 20 Strep tests alongside the Vitek 2 Compact system revealed that 88 of the isolates (equivalent to 80%) were gram-positive, while the remaining 22 isolates (20%) were gram-negative with a high statistical significance, this result agree with Diash and Abbas [17] study in Thi -Qar province who showed that G+ve bacteria in the oral cavity compared to G-ve bacteria appear significant differences ($p < 0.05$) [17]. This study is also in agreement with the study by Mahdi et al. [18], which was conducted in health centers in Baghdad City, showing that most of the obtained bacterial isolates (69.0%) were Gram-positive [18]. These results indicate that Gram-positive bacteria play a key role in tooth decay.

As shown in the Table, G+ve bacteria isolated through microbial cultivation were dominated by the type Streptococcus spp., accounting for 50% (44 samples) of the total bacteria isolated from teeth and Staphylococcus spp. at 29.5% (26 samples), and then Enterococcus faecalis at 20.5% (18 samples). This result is in Diash and Abbas's [17]. Analysis of the bacteriological cultures revealed that Gram-positive bacteria were common and Streptococcus species exhibited the highest incidence. Specifically, these bacteria were 51% of all. all teeth-sourced bacterial isolates. The second predominant species: the most prevalent bacterial organism was Staphylococcus species, with 11.67% was followed closely by Lactobacillus species at 11.11%

Table 1: G+ve bacteria Species

Number	G+ve **bacteria**	**number**	**%**
1	***Streptococcus Spp***	44	50
2	***Staphylococcus Spp***	26	29.5
3	*Enterococcus faecalis*	18	20.5

Enterococcus faecalis was identified at a rate of 8.33%, the same percentage as *Gemella morbillorum* [17]. This information indicates that the bacteria *Streptococcus* spp. are most responsible for the development of tooth decay.

Another study showed that Streptococcus bacteria were the most common among the bacterial species isolated from participating patients, with an isolation rate of 53.5%, followed by Staphylococcus aureus at 33.8% [19]. This result agrees with that of Mahdi et al. [18], who showed that Most of the obtained bacterial isolates (69.0%) were Gram-positive, represented by Streptococcus mutans and Staphylococcus aureus [18]. The presence of Staphylococcus bacteria, particularly Staphylococcus aureus, in the oral cavity aligns with what was indicated by Ali 2006, that the prevalence of these bacteria in that area may be due to their status as one of the main pathogenic factors capable of causing opportunistic infections [20], [21]. This is attributed to their ordinary existence in the carrier's skin, as well as in the upper part of the oral cavity, the nose, the digestive system and the system of reproduction [22]. They also possess numerous surface antigens and enzymes that facilitate their penetration into body tissues [23].

The percentage of G-ve bacteria was lower than that of G+ve (Table 2), where it constituted 54.54% (12 isolates) of Pseudomonas aeruginosa, and it reached 45.45% (10 isolates of E. coli). This result agrees with the study of Mahdi et al. [18], which showed that (30.9%) of the obtained isolates were Gram-negative, represented by Klebsiella pneumoniae (21.3%) and E. coli (9.5%) [18]. This result disagrees with the study of Diash and Abbas [17], who showed an equal percentage of P. aeruginosa and E. coli [17].

Variations in how frequently bacteria are found depend on how often infections occur. Sulaiman's research pointed out a link: the more cavities someone has, the more likely it is that bacteria will be isolated. Besides this, experts suggest that other influences exist. This includes the culture medium quality, how bacteria are extracted, and maybe even elements we don't fully understand. Additionally, how much people understand about health, how often they see a dentist, and the wider culture of the community all make a difference in the process [24].

Table 2. G-ve bacterial isolates

Number	G-ve bacteria	Number	%
1	Pseudomonas. Aeruginosa	12	54.54
2	E. coli	10	45.45

4. Conclusion

Oral disease is a serious public health issue. concern and one of the most common diseases globally. When analyzing samples from affected individuals, bacteria like Streptococcus spp. And Staphylococcus spp. consistently emerges as leading culprits. suffering from dental caries. The development of carious lesions is often associated with a mixture of elements. These include a neglect of oral habits, b current smoking, and diabetes. Caries incidence is generally increasing in those who ignore effective and regular toothbrushing, in particular if not the use of fluoride-containing toothpaste. Scientific association between: strong evidence has demonstrated the association of toothbrushing status, smoking and the content of DA subjected to: Products of oral hygiene, state of oral cleanness and the occurrence of dental cavities. The current study shows that two varieties of bacteria, namely the. first category is gram-positive bacteria, the amounts of which are masses, 80% of which are gram-negative. bacteria, which make up 20%. Furthermore, it is evident and that each kind is composed of several species and combinations, as previously mentioned. research could focus on the Str.ptococcus mutans and certain Patogenos. community.SP. Lactobacillus and other potentially cariogenic bacteria. Research directions: Availability of these compounds can be studied in bacteria in various population types, their virulence and other patient factors, and impact of various diagnostic and treatment strategies.

Acknowledgements:

The authors would like to acknowledge Bilad Alrafidain University (BAUC), Baqubah City staff, such as the employees and instructional staff at the clinic in the College of Dentistry, for which we are Now that this has been accomplished to a certain extent, it. their generous assistance during the study. **Financial support and sponsorship :**
Self-funded

Conflicts of interest :

The authors declare that they have **no conflicts of interest. Statement of Generative AI and AI-assisted technologies in the writing process:**
The authors note that in this work, we do not apply generative AI or AI-assisted technologies.

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Doi: 10.69788/jmsth/2025.02.01

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