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Types of bacteria isolated from the nasopharynx of Diabetics

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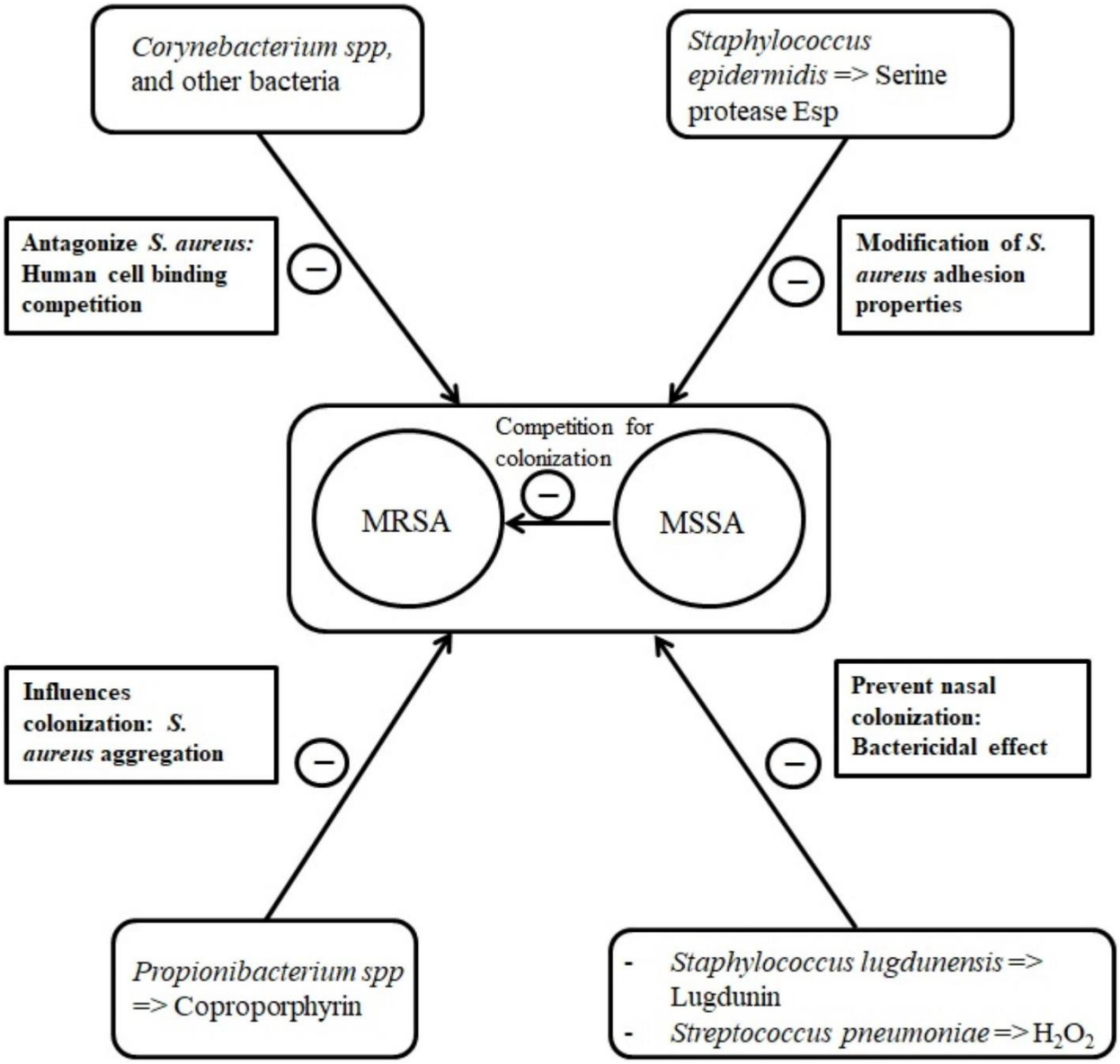
ABSTRACT

This review article examines the process of bacterial isolation and the most common bacteria from the nasal passages of diabetic patients between 2014 and 2024. It covers various studies analyzing the prevalence and characteristics of Staphylococcus aureus, the most commonly isolated bacteria in these patients. A comprehensive search was conducted in reputable databases including PubMed, Scopus, Google Scholar, Springer, and Elsevier. Studies that analyzed the isolation of S. aureus from the nasal passages of diabetic patients using valid microbiological methods, such as culture and PCR, were included. Only studies providing detailed information on the isolation process and methods used were selected. This study investigates the isolation of bacteria, particularly Staphylococcus aureus, from the nasopharynx of diabetic patients between 2014 and 2024. By conducting an extensive search of reputable databases, articles that analyzed the characteristics of this bacterium in diabetic patients using culture and PCR methods were selected. The results indicated that Staphylococcus aureus is commonly colonizing the nasopharynx of diabetic patients, and its colonization is associated with various factors, including antibiotic resistance and diabetic foot infections. This research highlights that nasal colonization can lead to severe infections, and identifying and managing it is crucial to reduce risks in diabetic patients

Introduction

Diabetes is a common metabolic disease that has become a global public health issue. According to the World Health Organization (WHO), nearly 1.6 million deaths worldwide are directly attributable to diabetes, making it one of the top 10 causes of death (Jafarvand et al, 2021). The International Diabetes Federation (IDF) estimated in 2019 that about 463 million adults between 20 and 79 had diabetes. This number is expected to rise to 700 million by 2045 (Standl et al, 2019). In addition, the IDF reported that one in five individuals aged over 65 has diabetes, representing 20% of the global prevalence. In Iran, it is estimated that 5.3 million adults, or 9.4% of the population, have diabetes. This number is predicted to increase to around 9.2 million by 2030 (Wild et al, 2004). Evidence shows that diabetes-related deaths in Iran increased from 8.7% in 2000 to 11.3% in 2015. Studies suggest the annual incidence rate of diabetes in Iran is about 1% of the total population, with an associated cost of approximately $843 per patient (Ala Maryam et al, 2019). Type 1 diabetes occurs when the pancreas is unable to produce insulin. It mainly affects children, adolescents, and people under 30. The exact cause remains unclear, but factors such as a genetic predisposition, viruses that damage the pancreas, and immune system disorders leading to the destruction of insulin-producing cells are involved (DiMeglio et al, 2018). Type 2 diabetes, the most common form, usually occurs in adults. Insulin is initially produced in sufficient amounts but becomes ineffective due to insulin resistance, leading to hyperglycemia (Chatterjee et al, 2017). The nasopharynx is often host to both commensal and pathogenic bacteria. Many pathogenic species, including *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Moraxella catarrhalis*, *Staphylococcus aureus*, and *Neisseria meningitidis*, are found in the nasopharynx of seemingly healthy individuals. *Staphylococcus aureus* is especially important in diabetic patients, who are prone to multiple infections. This bacterium often colonizes the nasopharynx and causes disease (Gunnarsson et al, 1998). In fact, some bacterial species are capable of secreting antistaphylococcal molecules modulating *S. aureus* abundance (Figure 1).

Figure 1: Main bacterial interactions with nasal S. aureus (Sakr, 2018)

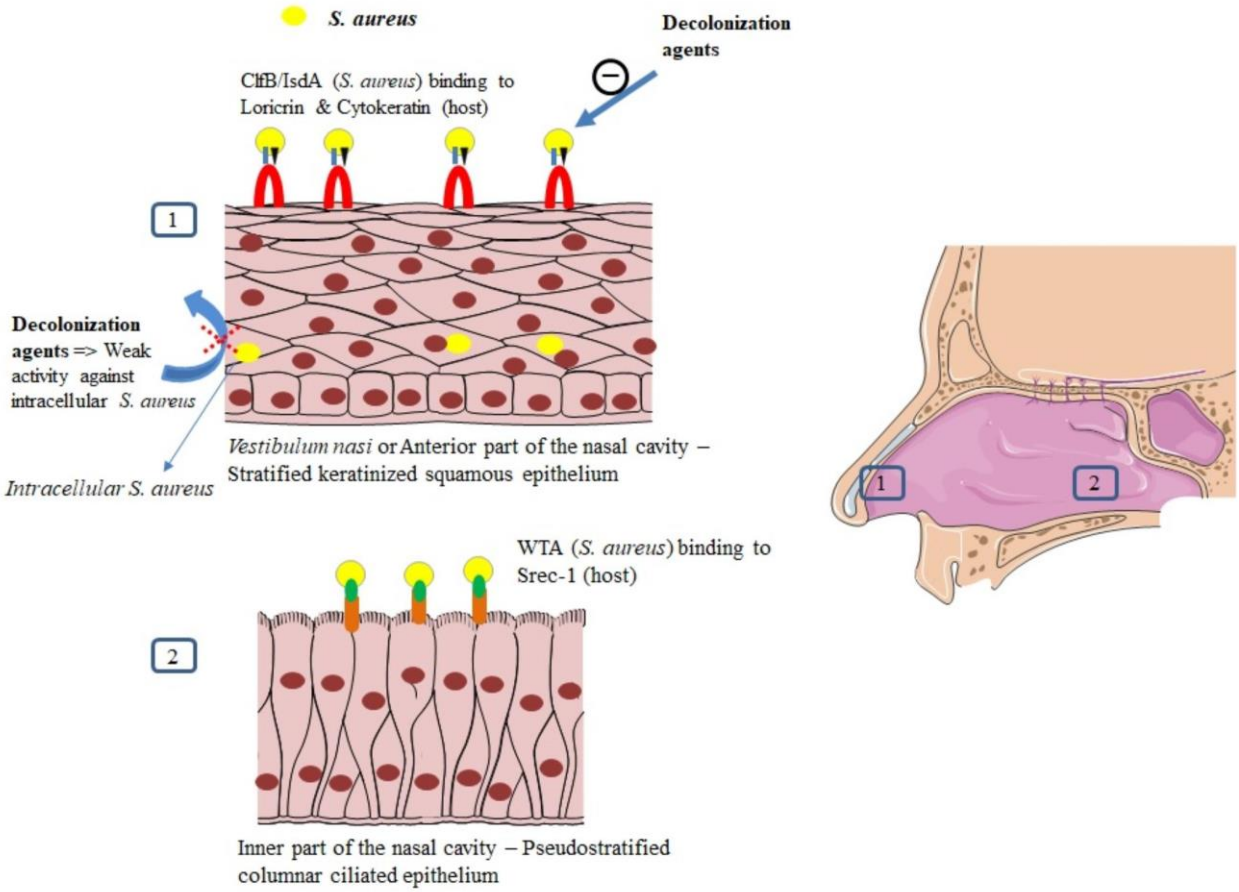


Staphylococcus aureus is a commensal bacterium of the human skin and mucosa that can lead to severe infections with high complications, mortality, and healthcare costs. The most common site of colonization is the nasal vestibule, which acts as a reservoir for this pathogen. Through surface proteins and components, it interacts strongly with nasal epithelial cells, forming a stable colony (8). Around 20%-80% of the human population carries *S. aureus* in the anterior nares. Studies have shown that nasal carriage of this bacterium plays a key role in the onset of *S. aureus*-related infections, especially in patients undergoing surgery, dialysis, or intensive care unit (ICU) patients. Carriers of *S. aureus* are at higher risk of infection, and previous studies have focused on either colonization or infections independently or in relation to certain conditions or surgeries (Price et al, 2017).

Intracellular Localization of *Staphylococcus aureus*:

Both epithelia have been described as habitats for S. aureus as it will be developed in this section. Intracellular localization in nasal tissue from healthy volunteers was also described. For a successful colonization, S. aureus expresses adhesive molecules, fundamental for the establishment of interactions with human cell surface components, as it was demonstrated in vitro and in vivo (Figure 2). *Staphylococcus aureus* can colonize epithelial, endothelial, and inflammatory nasal cells, especially mast cells. Studies using immunohistochemistry, hematoxylin-eosin staining, and animal models have shown that this bacterium can be found within epidermal layers, such as the stratum spinosum. Intracellular colonization can help protect *S. aureus* from the immune system and antibiotics. For instance, many antibiotics, such as mupirocin, have limited activity against this intracellular form, and even antibiotics like vancomycin may not fully control infections caused by intracellular bacteria (Ou et al, 2017).

Figure 2: Mechanisms of S. aureus nasal colonization (Sakr, 2018)



Immune System and Nasal Colonization by *S. aureus*:

Nasal colonization by *S. aureus* can activate both innate and adaptive immune systems. The bacterium, using proteins like staphylococcal protein A and staphylokinase, can escape the host's defense system and continue colonizing (Cole et al, 2016).

Diagnosis and Classification of Nasal Carriers:

Nasal carriers of *S. aureus* are diagnosed using sterile nasal swabs, followed by tests such as chromogenic agar

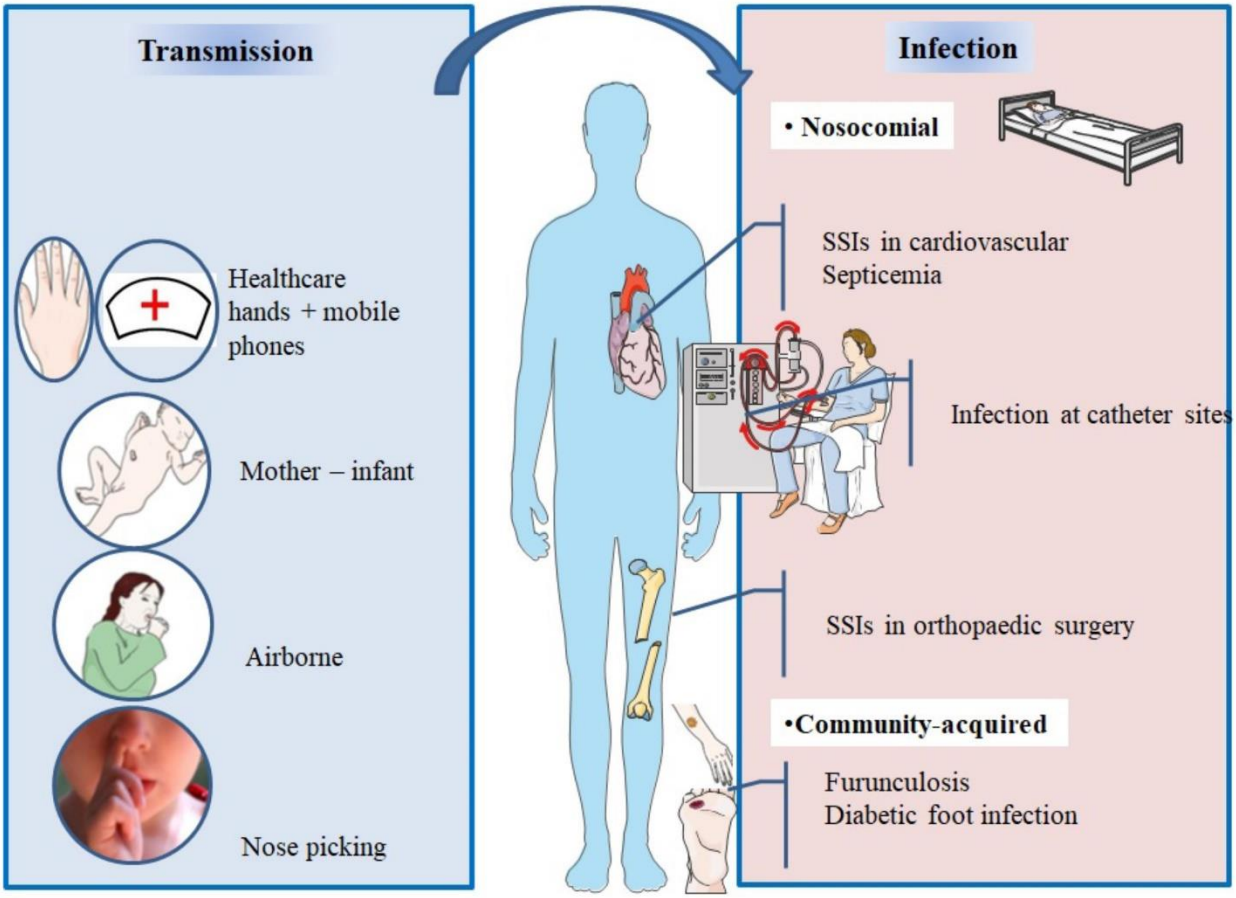
culture or PCR (the gold standard method) for identification. Epidemiological studies have identified three types of nasal carriers: persistent carriers, intermittent carriers, and non-carriers. Persistent carriers are more susceptible to infections and usually have a higher bacterial load in their samples (Warnke et al, 2016).

Role of Nasal Colonization in Infections:

Nasal colonization by *S. aureus* is a major risk factor for staphylococcal infections, increasing the risk by 2 to 10 times. These infections are commonly observed in patients undergoing surgery, dialysis, ICU patients, and individuals with HIV or recurrent wounds. In conditions such as furunculosis or impetigo, 60% of patients are nasal carriers of *S. aureus* (Walsh et al, 2013).

Some evidence suggests that nasal colonization with resistant bacteria can increase the risk of opportunistic and sometimes fatal infections in individuals with underlying conditions, such as diabetes. Another study found identical strains in 80% of infant–mother pairs. In 90% of these newborns, the source of *S. aureus* was the maternal nasal strain (figure 3).

Figure 3: Main spread and transmission mechanisms of S. aureus and impact of nasal carriage on subsequent infections. (Sakr, 2018)



Materials and Methods:

This systematic review follows the Preferred Reporting Items for Systematic Reviews and Meta-Analyses

(PRISMA) guidelines. The study protocol was registered in the PROSPERO database with the identification number PROSPERO: .... and reviewed by the Ethics Committee of the Medical University (Ethical code: IR.MUI.MED.REC.1400.358).

Search Strategy:

We conducted a comprehensive search in databases including Medline (PubMed), Web of Science, and Scopus using MeSH terms and relevant keywords.

Inclusion and Exclusion Criteria:

This systematic review included primary observational studies published in English that evaluated *Staphylococcus aureus* in the nasopharynx of diabetic individuals. Review articles, studies with insufficient or ambiguous results, and studies without statistical data for meta-analysis were excluded.

Data Extraction:

After removing duplicate articles, two independent evaluators (x and y) assessed the titles and abstracts of the retrieved articles and removed irrelevant ones. In cases of disagreement, a third evaluator (AT) was consulted. The full text of the remaining articles was then reviewed. Studies that met the inclusion criteria were considered eligible for analysis. After selection, general study characteristics, including the first author, year, country, study design, mean age, number of patients/groups, and wound classification, were extracted. Statistical data, including sample size, mean, and standard deviation for comparison groups, threshold values, and AUC, were also extracted. If the full text was not available, the authors were contacted.

Quality Assessment Tools:

The quality of the selected studies was evaluated using the NIH critical appraisal standards for cohort studies. Four aspects of each study were examined: (a) descriptive information, (b) study protocol, (c) statistical analysis, and (d) presentation of results. The NIH quality assessment details are available in the results section (supplementary files), and the studies were included in the systematic review if they scored 6 or higher.

Results:

Study Selection:

The initial search in electronic databases resulted in 50 articles. After removing 5 duplicate articles, 20 articles were excluded in the first stage of title and abstract screening. Three articles were contacted for full-text requests, but no responses were received. Upon full-text review, 5 more articles were excluded. In the end, 17 studies were included in this systematic review.

Discussion and Conclusion:

In 2014, Massartex examined the polymorphism of the vitamin D receptor gene (VDR) and nasal colonization with Staphylococcus aureus in patients with type 2 diabetes. Polymorphisms in the VDR gene are associated with susceptibility to various diseases, including type 1 diabetes (T1D), type 2 diabetes (T2D), and different infections. This study investigated whether VDR gene polymorphisms affect nasal colonization with Staphylococcus aureus in people with type 2 diabetes. A total of 173 patients with type 2 diabetes were genotyped for VDR gene polymorphisms including FokI (rs10735810), BsmI (rs1544410), ApaI (rs7975232), and TaqI (rs731236). Nasal swabs were taken to detect S. aureus colonization, and 162 of them underwent frequent sampling to estimate continuous colonization. The prevalence of S. aureus nasal colonization was 19.7%, and the prevalence of

persistent colonization was 8.6%. Nasal colonization with S. aureus was higher in people with the FokI f allele compared to those with the F allele (P = 0.05). People with the FokI ff genotype were more likely to be colonized than those with FokI FF and Ff genotypes (P = 0.03). Those with the FokI f allele were significantly more likely to have persistent colonization (P = 0.002). This study first showed a link between the FokI polymorphism in the VDR gene and nasal colonization with S. aureus in type 2 diabetic individuals (Messaritakis et al, 2014). In 2014, Halem investigated the role of nasal colonization with MRSA in increasing antibiotic resistance in diabetic foot ulcers (DFUs). Diabetic foot ulcers are often complicated by polymicrobial infections. Diabetic patients naturally have a weakened immune system and are more susceptible to infection if their skin is damaged. Microbiological culture studies have shown that Staphylococcus aureus (SA) is the most common bacterium found in DFUs. Nasal colonization with SA and its methicillin-resistant variant (MRSA) can worsen wound conditions. The study hypothesized that the presence of MRSA in the nasal cavity could be a risk factor for antibiotic resistance in diabetic foot ulcers. The study compared nasal and foot skin colonization in diabetic patients with diabetic foot ulcers (D+F+, n=50), diabetic patients without ulcers (D+F-, n=50), and healthy people (D-F-, n=40). (a) Nasal MRSA colonization was significantly higher in the D+F+ group compared to the D+F- and D-F- groups and was significantly associated with wound colonization in the D+F+ group (OR: 4.09; 95% CI: 1.12-15.05). (b) HbA1C levels in patients with MRSA-positive DFUs were significantly higher than those without MRSA (P < 0.02). (c) More than half of the MRSA strains (64%) isolated from DFU wounds were multidrug-resistant. These findings strongly suggest that nasal MRSA colonization can act as a risk factor for the development of antibiotic resistance in diabetic foot ulcers. Therefore, it is necessary for diabetic patients to be regularly screened for nasal and ulcers colonization (Haleem et al, 2014).

In 2015, Hart investigated the link between nasal colonization and infection in diabetic foot ulcers. Nasal colonization with Staphylococcus aureus (SA) is an important risk factor for surgical site infections. This study aimed at investigating the correlation between nasal colonization and diabetic foot ulcers (DFU) with SA, including MRSA. Seventy-nine diabetic foot ulcer patients were examined for nasal and DFU colonization with SA. Twenty-five patients (31.6%) had nasal SA, and 29 patients (36.7%) had SA in their DFU. Seven patients (8.8%) had MRSA in both the nasal cavity and ulcers. MRSA presence was associated with longer wound duration (P = 0.01). The sensitivity and characteristic the diagnosis of SA in DFUs based on nasal colonization were 41% and 74%, respectively. The findings show that there are significant differences between SA strains colonizing DFUs and the nasal cavity, indicating that nasal colonization is not always the source of infection in diabetic foot ulcers (Hart et al, 2015). In 2015, Kardak investigated the MRSA colonization rate in diabetic children. A study conducted at two time periods (2005 and 2013) found that MRSA colonization in diabetic children was low (0.7% in 2005 and 0.9% in 2013) (Karadag-Oncel et al, 2015).

In 2016, Lin studied the prevalence of MRSA in diabetic patients in a community. A cross-sectional study was conducted to determine the prevalence and factors associated with nasal colonization of S. aureus and MRSA in a diabetic population. A total of 956 people participated, including 529 diabetic patients. Among these, 46 were colonized with S. aureus, and 22 were colonized with MRSA. In non-diabetic individuals (427), 25 were colonized with S. aureus, and 12 with MRSA. Men were less likely to have nasal colonization with S. aureus (OR: 0.45), and those with better blood sugar control were more likely to be colonized (OR: 2.04). In the diabetic population, the rate of multidrug-resistant S. aureus strains (52.17%) was higher than in the non-diabetic population (28.00%). The most common MRSA strains were clonal complex 5 (CC5) and SCCmec IV. Furthermore, 17.65% of MRSA strains carried the Panton-Valentine leukocidin (PVL) gene (Lin et al, 2017).

In 2020, Lin investigated the prevalence of MRSA colonization in diabetic patients with diabetic foot ulcers (DFU) in Taiwan. This study aimed to investigate the prevalence of nasal MRSA colonization in diabetic patients

with DFUs and compare isolates from colonization and clinical strains. In total, 354 nasal samples were collected from 112 patients with DFU and 242 diabetic patients without DFU. Clinical MRSA isolates from DFUs were collected for comparison. The prevalence of nasal colonization with S. aureus and MRSA between DFU patients and those without DFU was similar (15.2% vs 16.9% for S. aureus and 5.4% vs 1.7% for MRSA). Nasal S. aureus colonization was an independent predictor of S. aureus wound infections (OR: 5.33). In addition, immunosuppressive drug use was associated with nasal S. aureus colonization, while the use of oral hypoglycemic agents was protective (Lin et al, 2020).

In 2021, Texera examined the epidemiology of MRSA in insulin-dependent diabetic patients. A study in Brazil found that 30.4% of insulin-dependent diabetic patients were colonized with S. aureus, and 4.8% with MRSA. Some identified strains, including ST398, were associated with multidrug resistance (Teixeira et al, 2021). In 2021, Anafo investigated MRSA prevalence in diabetic patients at Kerl Bo Hospital in Ghana. This cross-sectional study involved 300 diabetic patients and 106 non-diabetic individuals. Nasal swabs were taken and cultured bacteriologically. Identification and description of S. aureus and MRSA were carried out using standard bacteriological methods. The antibiotic susceptibility test was done using the Kirby-Bauer method. The prevalence of S. aureus was 31.0% in the diabetic group and 10.4% in the non-diabetic group. MRSA prevalence was 3.3% in the diabetic group, but it was not detected in the non-diabetic group. Diabetes was associated with an increased risk of S. aureus colonization but not with MRSA or coagulase-negative staphylococci (CoNS) colonization. CoNS colonization served as a protective agent against S. aureus and MRSA colonization in diabetic patients. The antibiotic resistance patterns showed high levels of multidrug resistance among diabetic patients (Anafo et al, 2021).

In 2021, Plataki studied the colonization of *Staphylococcus aureus* and the risk of hospitalization. The main objective of this study was to determine the prevalence and factors associated with nasal and axillary colonization of *Staphylococcus aureus* and MRSA in diabetic patients and to examine the association with hospitalization due to *S. aureus* infections. The cross-sectional study included 660 patients from the Fremantle Diabetes Study (Phase 2), with an average age of 65.1 years (SD 11.5) and 53.1% male. Nasal and axillary samples were collected during biannual check-ups. In Addition, serum 25(OH) D levels were measured in 358 patients. Of these, 258 patients (39.1%) were positive for *S. aureus* colonization, and 8 (3.1%) were carriers of MRSA. Colonization of *S. aureus* was independently associated with being married or having a partner and vice versa with older age and being born abroad ($P \leq 0.043$). Among 137 patients who were retested, 113 (82.5%) still had *S. aureus*. Of the 5 MRSA-positive patients retested, 4 remained positive. Independent predictors for hospitalization due to *S. aureus* infections after initial sampling included *S. aureus* colonization (hazard ratio: 5.42, 95% CI: 1.49–19.79), previous hospitalization due to *S. aureus* infections (hazard ratio: 4.84, 95% CI: 1.19–19.63), and being native-born (hazard ratio: 7.20, 95% CI: 1.91–27.17) ($P \leq 0.027$). No association was found between serum 25(OH) D levels and *S. aureus* colonization or hospitalization (Plataki et al, 2021). In 2021, Kang studied nasal colonization with methicillin-resistant *Staphylococcus aureus* (MRSA) in type 1 diabetic patients. MRSA nasal colonization is an important source of infection, especially in diabetic patients. However, there is limited information on MRSA colonization in type 1 diabetic patients. This prospective cohort study was conducted at Chang Gung Memorial Hospital in Taiwan from July 1 to December 31, 2020. Nasal samples were collected and MRSA was diagnosed. Molecular characteristics of MRSA strains were investigated, and factors associated with MRSA colonization were analyzed. A total of 245 type 1 diabetic patients entered the study. Nasal MRSA colonization was observed in 13 patients (5.3%). All isolates were community-associated MRSA strains. The most common strain was clonal complex 45 (53.8%), followed by the local strain ST59 (30.8%). MRSA colonization was positively correlated with age under 10 years, BMI under 18 kg/m², and a duration of diabetes under 10 years. In addition, this colonization was inversely correlated to serum LDL cholesterol levels of 100 mg/dL or more. No

independent factors were reported. The MRSA nasal colonization rate in type 1 diabetic patients in Taiwan is around 5%, with most of the colonized strains being community-associated, including clonal complex 45 and ST59 (Kang et al, 2021).

In 2022, Haak conducted a multicenter, prospective case-control study involving nasopharyngeal swabs from adult patients with community-acquired pneumonia (CAP) and healthy individuals without infection. Bacterial and viral profiles were determined using 16S ribosomal RNA sequencing and polymerase chain reaction (PCR), respectively. Bacterial, viral, and clinical data were used as inputs for random forest classification models to distinguish CAP patients from healthy controls. 117 cases and 48 healthy individuals were enrolled as control groups. CAP cases showed significant differences in beta diversity of nasopharyngeal microbiota compared to healthy controls (P = .016, R2 = .01). Random forest models could distinguish CAP caused by bacteria (AUC = .83), virus (AUC = .95), or mixed origins (AUC = .81) with accuracy from the healthy control group. This approach was validated with a dataset of 140 influenza patients and 38 controls, showing accurate separation (AUC = .93). Relative abundances of different bacteria and viruses in the nasopharynx could be used for detect CAP and identifying pathogens in adult patients. These data may help create a microbiota-based diagnostic panel using nasopharyngeal samples to identify CAP patients and causative pathogens, thereby improving diagnostic accuracy, efficiency, and antibiotic management (Haak et al, 2022).

In 2022, Luan analyzed the database of Chang Gung Memorial Hospital to gather information from 79 patients with non-severe abscess (NSA) who underwent incision and drainage surgery from 2004 to 2015. The patients were divided into two groups: those with diabetes (DM) and without diabetes (non-DM). By integrating the bacteria cultured from each patient, three most common bacterial species were identified and categorized into facultative anaerobes or aerobes and strict anaerobes. The microbiological cultures showed that in most cases, the infection was monomicrobial. The three most common facultative or aerobic bacteria in the NSA-DM group were:

1. *Klebsiella pneumoniae* (37.5%)
2. Methicillin-susceptible *Staphylococcus aureus* (MSSA) (25%)
3. Methicillin-resistant *Staphylococcus aureus* (MRSA) (12.5%) In the NSA-non-DM group, the three most common bacteria were:
4. MSSA (24%)
5. MRSA (20%)
6. *Pseudomonas aeruginosa* (16%) The three most common anaerobes associated with NSA in diabetic patients were:
7. *Prevotella intermedia* (25%)
8. *Peptostreptococcus* species (12.5%)
9. *Propionibacterium acnes* (12.5%) In non-DM patients, the three most common anaerobes were:
10. *Prevotella intermedia* (25%)
11. *Propionibacterium acnes* (16.7%)
12. *Fusobacterium nucleatum* (12.5%) In treating NSA in diabetic patients, physicians should consider *Klebsiella pneumoniae* and *Prevotella intermedia* when choosing empirical antibiotics. For NSA-non-DM patients, MSSA and *P. intermedia* should be prioritized (Luan et al, 2022).

In 2023, Wang conducted a study on foot infections in diabetes and nasal colonization with *Staphylococcus aureus*. Diabetic foot infections are one of the most common complication of diabetes. *Staphylococcus aureus* is

often isolated from diabetic foot infections and is normally colonized in the human nose. The study analyzed the nasal microbiome, showed a significant change in the nasal microbiome composition in diabetic patients with a reduction in diversity. Typically, fasting blood glucose (FBG) levels influenced the type and sequence of *S. aureus* strains in diabetic patients. They observed that highly virulent *S. aureus* ST7 strains were more common in patients with uncontrolled fasting glucose levels, while ST59 strains predominated in healthy individuals. The ST7 strain was more resistant to human antimicrobial peptides and formed stronger biofilms than ST59. Critically, ST7 strains were more virulent than ST59 in vivo. The predominance of ST7 in high glucose environments is due to increased activity of the SaeRS two-component system (TCS). ST7 strains outcompeted ST59 strains in both laboratory and diabetic mouse nasal colonization models, with this advantage disappearing when the SaeRS TCS was removed. These data show that highly virulent *S. aureus* strains prefer to colonize diabetic patients with uncontrolled blood sugar through the SaeRS TCS (Wang et al, 2023). In 2023, Taki studied the role of nasal MRSA colonization in diabetic foot infections, finding that many diabetic foot patients were colonized with MRSA in both their noses and wounds, indicating a link between nasal colonization and the wounds (Taki et al, 2023). In 2023, Koi conducted a meta-analysis study showing that nasal MRSA swabs have a high negative predictive value (over 90%) but a relatively low positive predictive value (less than 55%) (Coye et al, 2023). In 2023, Mizgala conducted a study involving 88 patients with type 2 diabetes, who were interviewed through a questionnaire. Patients with additional systemic diseases or those who had taken antibiotics in the past six weeks were excluded from the study. Microbiological tests involved collecting nasal and throat swabs from all enrolled patients. A total of 176 samples were analyzed from 88 type 2 diabetic patients. In total, 627 microbial species were identified, and 90 potential pathogenic strains were isolated from the nasal cavity and throat. Diabetic patients without infection symptoms often carried potentially pathogenic bacteria in the nasopharynx. Of these, 20.5% (18 patients) had 14 pathogenic microbial species in their throat swabs, with *Staphylococcus haemolyticus* MSCNS being the most common (3.3%). Other species found in 2.2% of patients included *Staphylococcus aureus* MSSA, *Escherichia coli* ESBL (-), *Enterobacter cloacae* ESBL (-), *Klebsiella oxytoca* ESBL (-), and *Klebsiella pneumoniae* ESBL (-). Other pathogenic species identified in 1.1% of patients were *Burkholderia cepacia* ESBL (-), *Citrobacter freundii* ESBL (-), *Enterobacter aerogenes* ESBL (-), *Proteus mirabilis* ESBL (-), *Stenotrophomonas maltophilia* ESBL (-), *Streptococcus* B-hemolyticus Group B, *Streptococcus* B-hemolyticus Group C, and *Streptococcus pneumoniae*. A significant difference was observed in the presence of *Staphylococcus aureus* MSSA (P=0.0001) and *Staphylococcus haemolyticus* MSCNS (P=0.006) in the nose and throat. No significant difference was observed for *Escherichia coli* ESBL (-) and *Proteus mirabilis* ESBL (-) in nasal and throat swabs of type 2 diabetic patients (Mizgala-Izworska et al, 2023). A cross-sectional study by Kanyiro in 2024 was conducted in the diabetes and eye clinics of MTRH Hospital. Participants were selected using systematic random sampling. Socio-demographic data and risk factors were collected through questionnaires completed by interviewers. Blood samples were taken to measure random blood sugar and HbA1c levels. Nasopharyngeal swabs were cultured, and antibiotic sensitivity was assessed within 24 hours. Data analysis was carried out using STATA software version 13. Associations were evaluated using Pearson's chi-square test, Fisher's exact test, independent t-test, and Wilcoxon test. A total of 124 participants with diabetes and 121 participants without diabetes were entered the study. Overall, 7.4% (95% CI: 4.4 to 11.4) of participants were carriers of Streptococcus pneumoniae. The carrier rate in diabetic patients was 12.1% (95% CI: 7.0 to 19.0), while in non-diabetic participants, it was 2.48% (95% CI: 1.0 to 7.0), which was statistically significant ($p = 0.004$). Diabetes was associated with a higher likelihood of being a carrier (adjusted OR 6.2, $p = 0.012$). No link was found with age, gender, cooking fuel type, presence of children under 5, or prior antibiotic use. Among diabetic patients, carriage of Streptococcus pneumoniae was only associated with insulin intake. The highest antibiotic resistance was observed against cotrimoxazole (94.44%), followed by amoxicillin (16.7%) and cefuroxime (11.1%). No resistance to macrolides was observed (Kanyoro et al, 2024). Nasopharyngeal carriage of Streptococcus pneumoniae was higher in diabetic patients, and significant resistance to common antibiotics

was found, although macrolides remained effective (Kanyoro et al, 2024).

Our research focused on the nasopharyngeal microbiota of individuals with type 2 diabetes who did not have active infection symptoms. In these patients, potentially pathogenic flora were found in the nasal cavity (over 80%, mainly Staphylococcus) and throat (over 20%). A total of 90 pathogenic strains were identified. Considering the multiple factors influencing microbiota composition, the relationship between bacterial carriage and anthropometric indices, duration of diabetes, glycemic control, and comorbidities was examined. The results showed no correlation between nasal and throat colonization by Gram-positive (+) or Gram-negative (-) strains and age, body mass index (BMI), HbA1c levels, or duration of diabetes. Other studies have also shown that nasal colonization by Staphylococcus aureus in diabetic patients does not correlate with blood glucose control, type of diabetes treatment, or disease duration.

1. Individuals with type 2 diabetes who do not have infection symptoms are often carriers of potentially pathogenic bacteria in the nasopharynx.
2. The species composition and microbial load of the nasal and throat microbiota in individuals with type 2 diabetes differ.
3. Nasal carriage of Staphylococcus aureus is not associated with long-term diabetes control or the presence of comorbidities leading to immune system dysfunction.

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