



Microbiological characterization and antibiotic resistance of nasopharyngeal microflora in patients with Type 2 diabetes mellitus

Elżbieta Mizgała-Izworska^{1,A-F}

¹ Department of Family Medicine, School of Medicine with Division of Dentistry in Zabrze, Medical University of Silesia, Katowice, Poland

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Abstract

Introduction and Objective. Patients with type 2 diabetes mellitus (T2DM) are predisposed to colonization of the nasopharynx by opportunistic and pathogenic bacteria due to impaired immune function. The aim of the study is to assess the prevalence and antibiotic resistance patterns of pathogenic microflora in the nasal cavity and throat of patients with T2DM.

Materials and Method. Nasal and throat swabs were collected from 88 T2DM patients. A total of 627 microbial isolates were analyzed, including 90 potentially pathogenic strains. Species identification was performed using standard culture techniques and VITEK 2. Antibiotic susceptibility was determined according to EUCAST guidelines.

Results. Pathogenic bacteria were detected in 88% of nasal samples. The most frequently isolated Gram-positive organisms were *Staphylococcus epidermidis* MSCNS (33.3%) and *Staphylococcus haemolyticus* MSCNS (3.2%). Predominant gram-negative isolates included *Proteus mirabilis*, *Escherichia coli*, and *Klebsiella pneumoniae*. Gram-positive bacteria showed highest susceptibility to cephalosporins, but exhibited significant resistance to quinolones and glycopeptides (50% each). For Gram-negative isolates, resistance to penicillins with inhibitors reached 67%.

Conclusions. The high prevalence and specific antibiotic resistance profiles of nasopharyngeal pathogens in T2DM patients underscore the importance of routine microbiological surveillance and tailored antibiotic stewardship.

Key words

antibiotic resistance, opportunistic pathogens, Type 2 diabetes mellitus, nasopharyngeal microflora, coagulase-negative staphylococci, Gram-negative bacilli

INTRODUCTION

Type 2 diabetes mellitus (T2DM) is one of the most common chronic metabolic diseases affecting millions of people worldwide. Patients with T2DM typically present with impaired immune function, dysbiosis, and increased susceptibility to infections, particularly of the respiratory tract [1, 2]. Colonization of the nasal cavity and throat with opportunistic and pathogenic microorganisms may predispose patients to recurrent infections and contribute to the spread of antimicrobial resistance [3]. Recent research has highlighted the role of hyperglycaemia in promoting bacterial growth and accelerating the development of antibiotic resistance, especially in *Staphylococcus aureus* [1]. Reviews of diabetic cohorts further indicate that coagulase-negative staphylococci (CoNS) and Enterobacteriaceae are frequently isolated from the upper respiratory tract of diabetic patients [2, 3]. The aim of the study is to determine the prevalence and antibiotic resistance of pathogenic microorganisms isolated from the nasopharynx of patients with T2DM.

MATERIALS AND METHODS

Study design. A cross-sectional study was undertaken which included 88 adult patients with confirmed T2DM.

- Sample collection – nasal and throat swabs were obtained from all participants under aseptic conditions.
- Microbiological procedures – swabs were cultured on standard media. Isolates were identified using conventional methods and VITEK 2 system.
- Antibiotic susceptibility testing – susceptibility to selected antibiotics was determined according to EUCAST guidelines, version 2024 [4].
- Analysis – descriptive statistics were used to summarize microbial distribution and resistance patterns.

Ethics approval was obtained from the Bioethics Committee of the Medical University of Silesia in Katowice (Resolution No. KNW/0022/KB1/117/14 of 14.10.2014).

RESULTS

Pathogenic bacteria were detected in 88% of nasal samples, while only 13% of patients showed purely physiological flora.

The distribution of Gram-positive isolates from nasal and throat swabs is presented in Table 1. These data are illustrated for nasal isolates in Figure 1 and for throat isolates

✉ Address for correspondence: Elżbieta Mizgała-Izworska, Department of Family Medicine, School of Medicine, Medical University of Silesia, Katowice, 41-800 Zabrze, Poland
E-mail: emizgla@o2.pl

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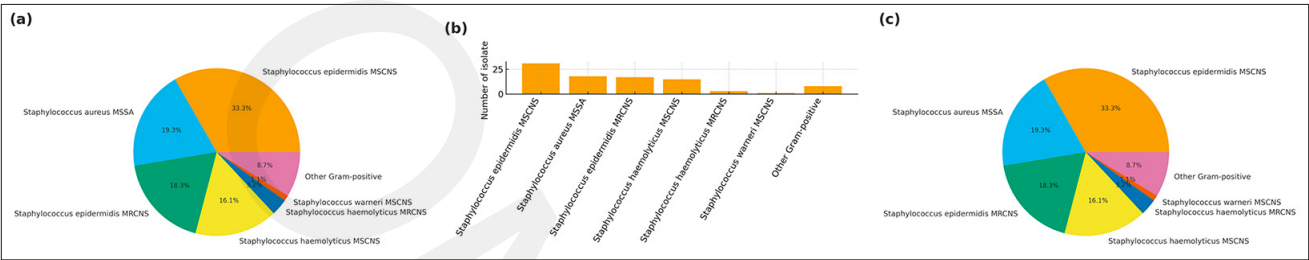


Figure 1. Nasal swab isolates from T2DM patients. (a) percentage distribution of pathogenic bacteria; (b) number of bacterial strains isolated; (c) percentage distribution of bacterial species

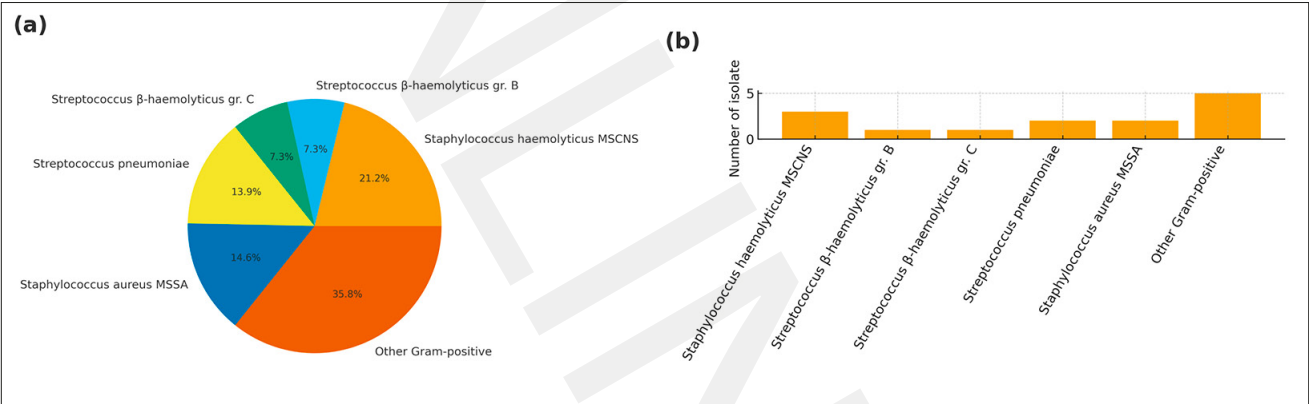


Figure 2. Throat swab isolates from T2DM patients. (a) percentage distribution of pathogenic bacteria; (b) number of bacterial strains isolated

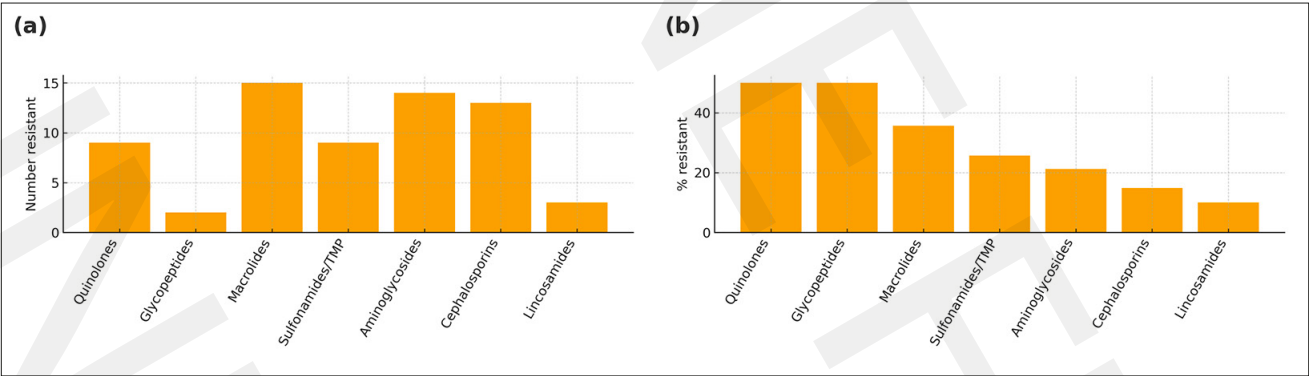


Figure 3. Antibiotic resistance among Gram-positive nasopharyngeal isolates. (a) number of isolates resistant to selected antibiotic groups; (b) percentage of isolates resistant to selected antibiotic groups

Table 1. Gram-positive bacterial strains isolated from the nasopharynx (nose and throat) of T2DM patients			
Bacterial species	Source	No. of isolates	% of isolates
Staphylococcus epidermidis MSCNS	Nasal	31	33.3%
Staphylococcus aureus MSSA	Nasal	18	19.3%
Staphylococcus epidermidis MRCNS	Nasal	17	18.3%
Staphylococcus haemolyticus MSCNS	Nasal	15	16.1%
Staphylococcus haemolyticus MRCNS	Nasal	3	3.2%
Staphylococcus warneri MSCNS	Nasal	1	1.1%
Other Gram-positive	Nasal	8	8.7%
Staphylococcus haemolyticus MSCNS	Throat	3	3.2%
Streptococcus β-haemolyticus gr. B	Throat	1	1.1%
Streptococcus β-haemolyticus gr. C	Throat	1	1.1%
Streptococcus pneumoniae	Throat	2	2.1%
Staphylococcus aureus MSSA	Throat	2	2.2%
Other Gram-positive	Throat	5	5.4%

Table 2. Antibiotic susceptibility of Gram-positive isolates (n=93)		
Antibiotic group	No. susceptible	% susceptible
Cephalosporins	79	85.0%
Aminoglycosides	73	78.5%
Macrolides	66	71.0%
Sulfonamides/TMP	58	62.4%
Lincosamides	52	55.9%
Quinolones	47	50.5%
Glycopeptides	47	50.5%

in Figure 2. Antibiotic susceptibility of Gram-positive isolates is summarized in Table 2, while resistance patterns are detailed in Table 3. Resistance profiles by antibiotic groups are visualized in Figure 3. The Gram-negative isolates are summarized in Table 4, and their resistance patterns are presented in Table 5.

Table 3. Antibiotic resistance of Gram-positive isolates (n=65)

Antibiotic group	No. resistant	% resistant
Quinolones	9	50.0%
Glycopeptides	2	50.0%
Macrolides	15	35.7%
Sulfonamides/TMP	9	25.7%
Aminoglycosides	14	21.2%
Cephalosporins	13	14.9%
Lincosamides	3	10.0%

Table 4. Gram-negative bacterial strains isolated from the nasopharynx (nose and throat) of T2DM patients

Bacterial species	No. of isolates	% of isolates
<i>Proteus mirabilis</i>	5	5.8%
<i>Escherichia coli</i>	4	11.8%
<i>Klebsiella pneumoniae</i>	4	11.8%
<i>Klebsiella oxytoca</i>	2	2.5%
<i>Enterobacter cloacae</i>	1	1.2%
<i>Enterobacter aerogenes</i>	1	1.2%
<i>Burkholderia cepacia</i>	1	1.2%
<i>Stenotrophomonas maltophilia</i>	1	1.2%
<i>Moraxella catarrhalis</i>	1	1.2%

Table 5. Antibiotic resistance of Gram-negative isolates (n=17)

Antibiotic group	% resistant	% susceptible
Penicillins + inhibitors	67.0%	33.0%
Quinolones	35.0%	65.0%
Sulfonamides/TMP	29.0%	71.0%
Aminoglycosides	24.0%	76.0%
Cephalosporins	12.0%	88.0%
Tetracyclines	10.0%	90.0%

DISCUSSION

The study demonstrated a high prevalence of pathogenic bacteria in the nasopharynx of patients with T2DM, with 88% of nasal swabs yielding potentially pathogenic microorganisms. This rate is considerably higher than colonization rates reported in general healthy populations where pathogenic isolates are found in approximately 30–40% of individuals [5, 6]. Although the absence of a control group in the study limited direct statistical comparisons, published data strongly suggest that diabetes predisposes to more frequent and persistent colonization. The predominance of coagulase-negative staphylococci (CoNS), particularly *Staphylococcus epidermidis* and *Staphylococcus haemolyticus* in this cohort, is in line with studies on diabetic patients [2, 3, 7]. In healthy populations, CoNS are usually considered commensals with lower clinical relevance [8]. Their high frequency in diabetics underlines the shift from commensal to opportunistic behaviour in the context of impaired immunity. Moreover, CoNS have been increasingly recognized as reservoirs of resistance genes, such as *mecA*, which can be transferred to *Staphylococcus aureus* [9]. The results of this study showed considerable

resistance among Gram-positive isolates, especially to quinolones and glycopeptides (50%). Similar resistance levels have been reported in diabetic cohorts from Asia and the Middle East [2, 7], whereas studies in non-diabetic populations demonstrate lower resistance rates, usually below 20–25% [5, 6, 10]. This highlights diabetes as a factor not only for colonization, but also for harbouring more resistant strains. Gram-negative bacteria, including *Proteus mirabilis*, *Escherichia coli*, and *Klebsiella pneumoniae*, were also frequently isolated in the current study. Their presence in the nasopharynx of diabetics has been documented previously [11, 12], although such isolates are far less common in healthy individual [5, 8]. It was found that 67% of Gram-negative isolates were resistant to penicillins with inhibitors, a rate higher than those reported in community-acquired respiratory flora [13]. These findings support the hypothesis that T2DM patients may serve as important reservoirs of antimicrobial resistance in the community. The influence of hyperglycaemia on microbial ecology is increasingly recognized. Conlon et al. [1] demonstrated that high glucose levels accelerate the development of antibiotic resistance in *S. aureus*. This biological mechanism may partly explain why diabetic patients are more likely to harbour resistant organisms, compared with healthy individuals. Additionally, studies using metagenomic sequencing have revealed reduced microbial diversity and enrichment of pathogenic taxa in the upper respiratory tract of diabetics, compared to healthy controls [11]. Limitations of the study. This study has several limitations. The main limitation is the absence of a healthy control group, which precludes direct comparison of colonization and resistance rates within the same population. Moreover, resistance was determined phenotypically without molecular confirmation of resistance genes. The sample size was relatively small, but adequate for descriptive purposes and limited to a single centre.

CONCLUSIONS

1. T2DM patients show high colonization of the nasopharyngeal mucosa by pathogenic bacteria.
2. Coagulase-negative staphylococci and Enterobacteriaceae are predominant.
3. High resistance to quinolones and beta-lactams necessitates surveillance and rational antibiotic use.
4. Improved glycemic control may contribute to reducing the emergence of resistance.

While the findings of this study confirm a high prevalence of pathogenic and resistant bacteria in the nasopharynx of T2DM patients, comparison with the available literature suggests that these patients are at significantly higher risk than the general population. These findings underscore the importance of targeted infection prevention and rational antibiotic use in this vulnerable group.

Future studies should include parallel analysis of diabetic and non-diabetic populations, employ genomic methods for resistance profiling, and assess the impact of glycaemic control on colonization dynamics. Longitudinal designs would also allow investigation of the persistence and temporal changes in colonization patterns.

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