International Journal of Medical Science and Dental Research

Examination of the relationship between morphological differences in the human nose and bacterial colonization

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Abstract: *The airflow mechanism, influenced by structural differences, plays a crucial role in the localization of bacterial colonies in the human nose. The aim of this study is to evaluate the relationship between the internal and external anatomical structures of the nose and bacterial colonization in the nasal cavity. A total of 162 healthy volunteers (97 females and 65 males) aged 18-45 years, including hospital staff and medical students, participated in the study. Nasal morphometry was assessed using anthropometric instruments and acoustic rhinometry. Swab samples were collected from the nasal and nasopharyngeal regions of each participant for microbiological testing. Measurements revealed a very high correlation in the distance between the heights of the left and right nasal columellas (C-SN'(L)/C-SN'(R) = 0.903). Common pathogens isolated from the nasal cavity (35.6%) and nasopharynx (27.1%) includedStaphylococcus aureus, Streptococcus pneumoniae, Group A beta-hemolytic streptococcus, and Neisseria meningitidis. However, no statistically significant relationship was found between bacterial pathogens and the morphological structure of the nasal cavity or nasopharynx. Therefore, it has been revealed that the anatomical structure of the nose does not pose a potential risk factor for upper respiratory infections regarding pathogenic microorganisms, particularly among healthy individuals, healthcare professionals, and athletes.*

Keywords-*Acoustic rhinometry, Bacterial colonization, Nasal cavity, Nasal morphology,Upper respiratory infection*

I. INTRODUCTION

Identification of the nasal morphology of individuals plays a clinically important role in the selection of treatment modalities for regional bacterial colonization. This study aims to evaluate the relationship between the anthropometric measurements of the inner and outer anatomical structures of the nose and bacterial colonization in the nasal cavity. Nasal cavity morphology is a very important factor in determining the airflow and flow mechanics on the inner surface of the nose[1]. The mechanics of the airflow, influenced by structural differences, play a role in the localization of bacterial colonies[2]. Normal flora elements covering the mucosal surface are located in different parts of the body[3]. Many studies have been conducted on the bacteria in the nasal cavity. Staphylococcus aureus (S. aureus) colonizes the nasal vestibule in 40% of healthy adults, while most healthy individuals harbor Staphylococcus epidermidisin the nasal vestibule. The nasopharynx is commonly associated with opportunistic pathogens in children, including Streptococcus pneumoniae (S. pneumoniae), Streptococcus pyogenes (S. pyogenes), Haemophilus influenzae (H. influenzae), Moraxella catarrhalis (M. catarrhalis), and Staphylococcus aureus (S. aureus).The presence of these bacteria, along with Neisseria meningitidis, raises serious concerns about hospital-acquired infections. This is particularly worrying for those who work closely with patients in intensive care settings, as they are at a higher risk of spreading these harmful germs [4,5].

Acoustic rhinometry can be used to understand nasal space anatomy by calculating the volume of voids using the reflection of sound waves entering the nose at different distances[6].As a result of evaluating the relationship between differences in nasal morphology and the various bacterial colonies that may occur in this region, planning medical treatment may be beneficial in preventing complications during percutaneous and surgical procedures.

II. MATERIALS AND METHODS

2.1 Patient population

Individuals with no history of previous head trauma, nasal congenital anomalies, nasal septum deviation, nasal surgery, recurring upper respiratory tract infections, medication with nasal vasoconstriction effects, or metabolic diseases such as allergies, hypertension, diabetes mellitus, or hyperlipidemia were included in the study. A total of 162 healthy participants, comprising 97 females and 65 males aged between 18 and 45 years, including both hospital personnel and medical students, were enrolled in the study. Approval for this study was granted by the Ethics Committee of Akay Hospital, associated with protocol number 2015-1880-1.

2.2 Nasal anatomical measurements and rhinometrics

Nasal anthropometric measurements included:N-PRN (11-6) distance between nasion and pronasale; N-SN (11-3) distance between nasion and subnasale; AC-AC (4-5) distance between lateral nasal crus lateralis; AL-AL (1-2) maximum distance between ala nasi; PRN-SN (6-3) distance between pronasale and subnasale; SN'-SN' columella width; C-SN' (L) columella height of the left nostril; C-SN' (R) columella height of the right nostril; and MF-MF (9-10) nose root width in millimeters [7]. (Figure 1, 2) Measurements were performed using the Holter anthropometric set (code number: 98.601) and an Asimeto digital caliper (150mm 0.01mm).

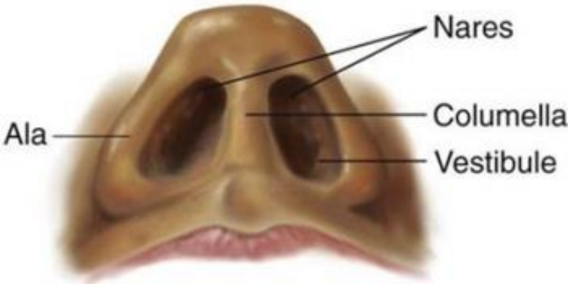


Figure 1: Nasal morphometric measurements.

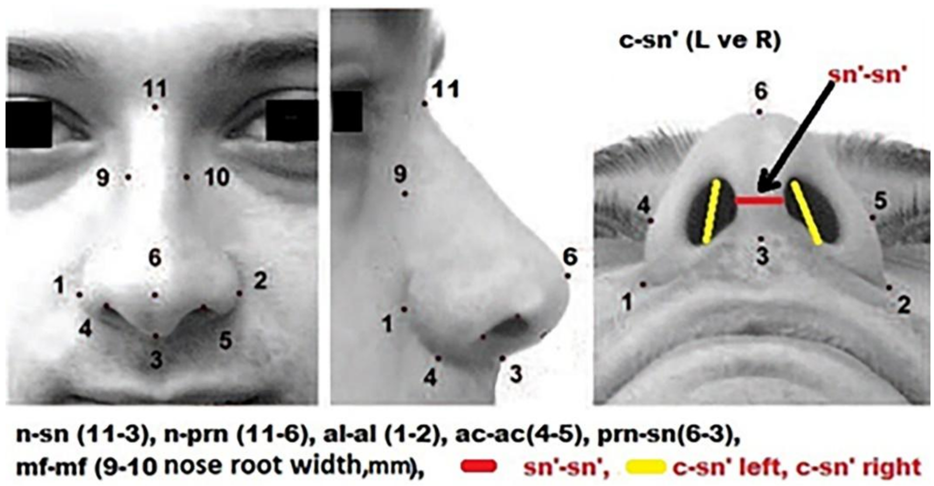


Figure 2: Nose anthropometric points (mm)

Additionally, anthropometric measurements of the nose were complemented with acoustic rhinometry measurements taken from the right and left nasal cavities. Acoustic rhinometry (ARhn) can be used to obtain information about the anatomy of the nasal cavity. ARhn evaluates the geometry of the nasal cavity through acoustic reflections and provides information about the cross-sectional areas and volumes of the nasal cavity at specific distances [8]. ARhn is an appropriate method for determining the pathogenesis causing nasal obstruction in clinical settings. Conditions such as allergic rhinitis, septal deviation, nasal polyposis, concha hypertrophy, and sleep apnea are evaluated to assess physiological nasal cycles [9-11]. It is also a valuable method for monitoring nasal cavity development in the pediatric age group [12]. In this study, measurements were taken using the Rhinometrics SRE 2000 Rhinoscan version 2.5 (Interacoustics A/S, Denmark) device, which produced an acoustic signal in the form of two impulses according to the criteria proposed by the Acoustic Rhinometry Standardization Committee. The smallest cross-sectional areas (A-Right (AR), A-Left (AL) / cm^2) within the first two centimeters from the right and left entrances of the nose, their distances from the entrances (D-Right (DR), D-Left (DL) / cm), and the volume of the nasal cavity (V-Right (VR), V-Left (VL) / cm^3) were obtained from the patients. A Pearson correlation test was conducted using Minitab17 Statistical Software to evaluate the relationship between nasal morphometric measurements, nasopharyngeal structures, and bacterial colonies isolated from nasal swabs. In the evaluation, correlations were observed between values ranging from 0.5 to 1.

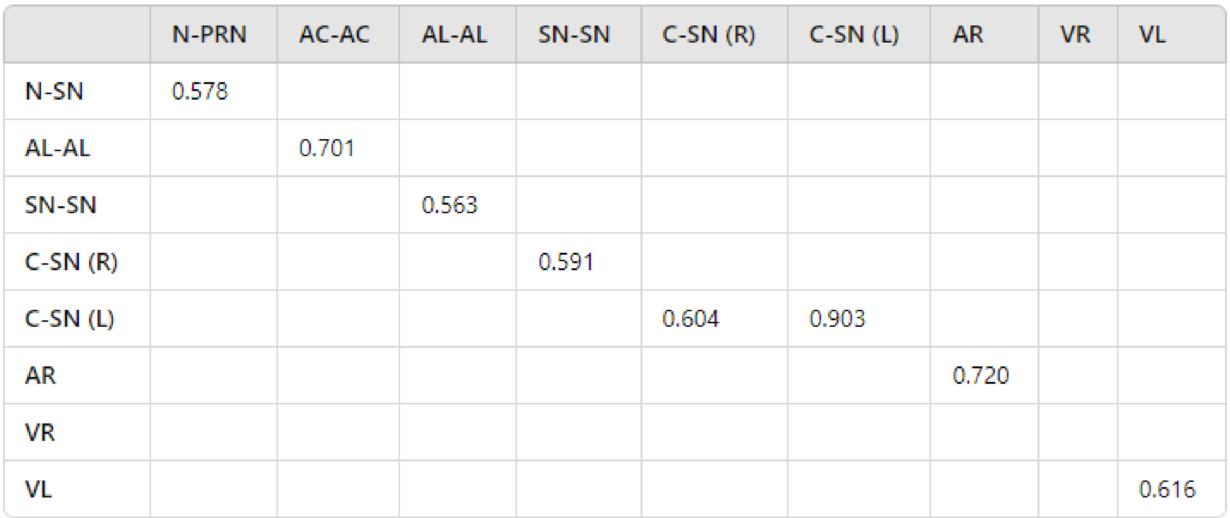
2.3 Microbiological examinations

Nasal and nasopharyngeal swab samples obtained from individuals in the study group were cultured in sheep blood and EMB agar at 37 °C overnight. At the end of the 24-hour incubation period,colonies compatible with S. aureus, S. pneumoniae, and M. catarrhalis were identified using conventional methods (Gram staining, catalase, coagulase, and oxidase tests).The results were confirmed as S. aureus, S. pneumoniae, Group A beta-hemolytic streptococcus (BETAH-N), and Neisseria meningitidis (N. meningitidis) through detailed identification studies. The antimicrobial susceptibility of the isolations was evaluated according to Clinical Laboratory Standards Institute (CLSI) recommendations. The following antibiotics were tested using the disc diffusion method: oxacillin, vancomycin, teicoplanin, azithromycin, tetracycline, ciprofloxacin, clindamycin, trimethoprim-sulfamethoxazole, chloramphenicol, rifampicin, linezolid, penicillin, amoxicillin-clavulanic acid, cefepime, and imipenem. The results were assessedaccording to CLSI standards.

III. RESULTS

In our study, the Pearson correlation test results related to nasal anthropometric points were found to be significant: N-SN / N-PRN (0.578), AL-AL / AC-AC (0.701), SN-SN / AC-AC (0.563), SN-SN / AL-AL (0.591), C-SN (R) / SN-SN (0.591), C-SN (L) / SN-SN (0.604), C-SN (L) / C-SN (R) (0.903), AR / VR (0.720), VL / AL (0.616) (Table 1).

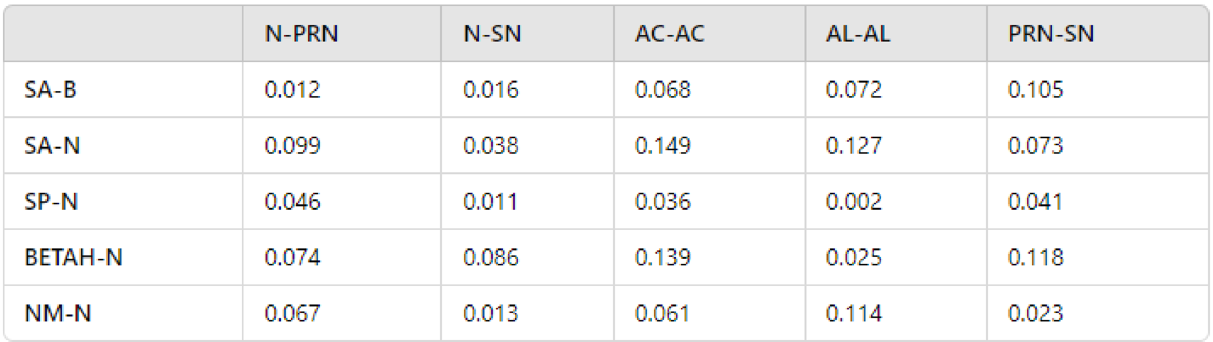
Table 1: The Pearson correlation test results between nasal anthropometric points. Correlations are significant (P Value: 0.5-1).



	N-PRN	AC-AC	AL-AL	SN-SN	C-SN (R)	C-SN (L)	AR	VR	VL
N-SN	0.578								
AL-AL		0.701							
SN-SN			0.563						
C-SN (R)				0.591					
C-SN (L)					0.604	0.903			
AR							0.720		
VR									
VL									0.616

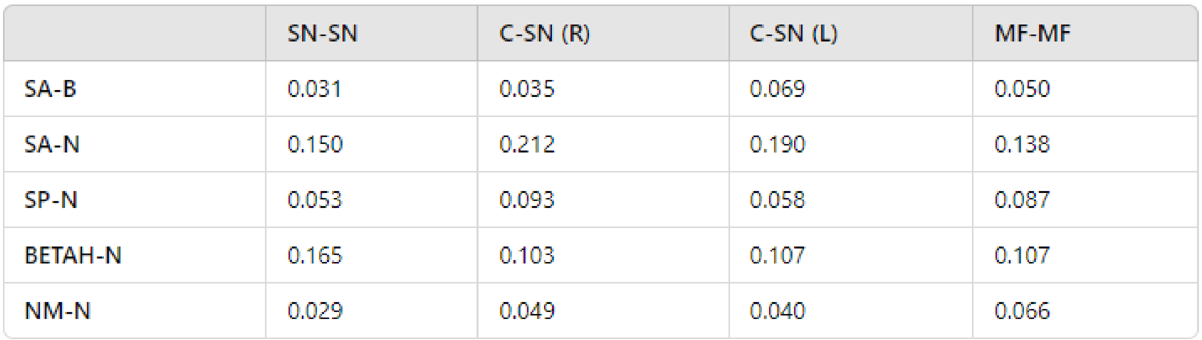
The bacterial flora of the nose and nasopharynx was examined in a total of 162 healthy individuals. Colonizations of S. aureus (SA-B) in nasal swabs, S. aureus (SA-N) in nasopharyngeal swabs, as well as S. pneumoniae **(**SP-N), BETAH-N, and N. meningitidis(NM-N) were observed. The findings indicated a diverse microbial population within the nasal and nasopharyngeal cavities, which plays a crucial role in maintaining overall respiratory health. The Pearson correlation test results showed that there was no significant correlation between nasal anthropometric measurements and bacteria (Table 2-4). This lack of correlation suggests that anatomical variations in nasal morphology may not significantly influence the colonization patterns of these bacterial species in healthy individuals.

Table 2: Correlation of Pearson test between morphometric measurements and bacterial colonization values are included (P Value: 0.5-1).



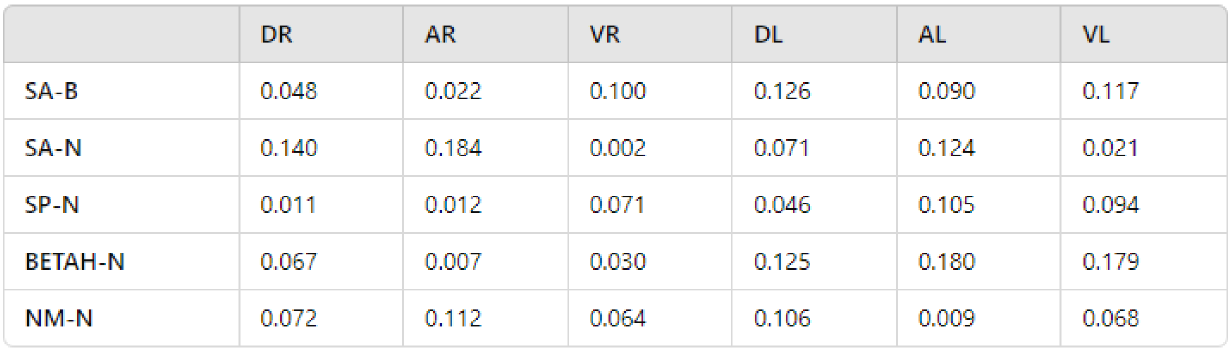
	N-PRN	N-SN	AC-AC	AL-AL	PRN-SN
SA-B	0.012	0.016	0.068	0.072	0.105
SA-N	0.099	0.038	0.149	0.127	0.073
SP-N	0.046	0.011	0.036	0.002	0.041
BETAH-N	0.074	0.086	0.139	0.025	0.118
NM-N	0.067	0.013	0.061	0.114	0.023

Table 3: Correlation of Pearson test between morphometric measurements and bacterial colonization values are included (P Value: 0.5-1).



	SN-SN	C-SN (R)	C-SN (L)	MF-MF
SA-B	0.031	0.035	0.069	0.050
SA-N	0.150	0.212	0.190	0.138
SP-N	0.053	0.093	0.058	0.087
BETAH-N	0.165	0.103	0.107	0.107
NM-N	0.029	0.049	0.040	0.066

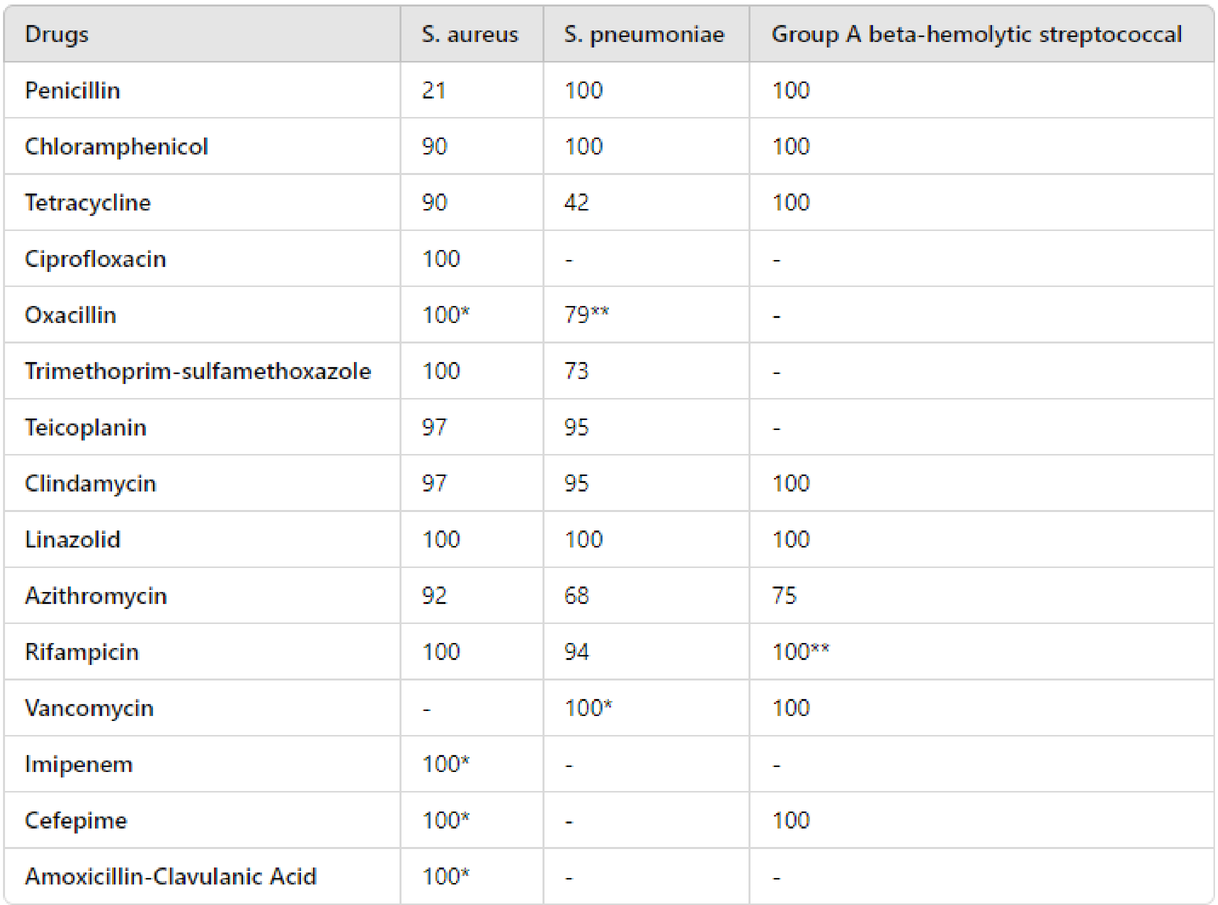
Table 4: Correlation of Pearson test between morphometric measurements and bacterial colonization values are included (P Value: 0.5-1).



	DR	AR	VR	DL	AL	VL
SA-B	0.048	0.022	0.100	0.126	0.090	0.117
SA-N	0.140	0.184	0.002	0.071	0.124	0.021
SP-N	0.011	0.012	0.071	0.046	0.105	0.094
BETAH-N	0.067	0.007	0.030	0.125	0.180	0.179
NM-N	0.072	0.112	0.064	0.106	0.009	0.068

Common pathogens (S. aureus, S. pneumoniae, BETAH-N, andN. meningitidis) were isolated from approximately 35.6% of nasal cavities in individuals included in the study. The same pathogens were isolated from 27.1% of nasopharyngeal samples. Notably, S. aureus was detected in both the nose and the nasopharynx, indicating its potential role as a significant pathogen in upper respiratory tract infections.According to this study, colonization rates were 20.3% for S. aureus (33 isolates) and 20.3% for S. pneumoniae (20 isolates) among healthy adult samples. The colonization rate of BETAH-N (4 isolates) was found to be 2.4%. Interestingly, N. meningitidis was detected only in one sample, resulting in a colonization rate of 0.6%, which highlights the rarity of this pathogen in healthy individuals within the studied population.The percentages ofS. aureus, S. pneumoniae, andBETAH-Nwith respect to the drugs included in the study (%) are indicated in Table 5 (*Evaluation based on CLSI 2012 standards [13], **Assessments made according to EUCAST 2017 [14] standards). N. meningitidis, isolated as a single isolate, was found to be susceptible to chloramphenicol, trimethoprim-sulfamethoxazole, rifampicin, and azithromycin according to CLSI standards (2016) [15]. These susceptibility patterns are crucial for guiding appropriate antibiotic therapy in cases of invasive meningococcal infections.

Table 5: Sensitivity percentages of bacteria against drugs (%). Remarks: * Evaluation based on CLSI 2012 standards, ** Assessments made according to EUCAST 2017 standards.



Drugs	S. aureus	S. pneumoniae	Group A beta-hemolytic streptococcal
Penicillin	21	100	100
Chloramphenicol	90	100	100
Tetracycline	90	42	100
Ciprofloxacin	100	-	-
Oxacillin	100*	79**	-
Trimethoprim-sulfamethoxazole	100	73	-
Teicoplanin	97	95	-
Clindamycin	97	95	100
Linazolid	100	100	100
Azithromycin	92	68	75
Rifampicin	100	94	100**
Vancomycin	-	100*	100
Imipenem	100*	-	-
Cefepime	100*	-	100
Amoxicillin-Clavulanic Acid	100*	-	-

IV. DISCUSSION

Recent studies examining the relationship between nasal morphology and nasal microbiology have gained significant interest in the scientific community. Nevertheless, very limited data are available regarding the potential relationship between nasal anatomy and its morphometric structure. In one study of nasal, nasopharyngeal, and sinonasal cavity masses in children, both developmental (e.g., congenital anomalies) and abnormal growths were considered, including congenital nasolacrimal duct mucocele, dermoid cyst (periorbita), cephalocele, and neuroglial heterotopia. The research also highlighted the importance of inflammatory and infectious processes, such as nasal mucocele, polyps, and pyogenic granuloma in altering bacterial colonization patterns[16]. Further studies on this relationship could help uncover critical details about how bacteria and other organisms colonize nasal passages.

Another significant difference was observed between healthy individuals and patients with upper respiratory infections (URIs)asthe study conducted by Fahim et al. reported no carriage of any of the three most common bacterial nasopharyngeal pathogens (S. pneumoniae, H.influenzae, or M. catarrhalis in the nasal cavity. Additionally,S. pneumoniae was identified from 31% of healthy subjects and only 15% of those patients. Microbiologically, the nasal cavity and nasopharynx are considered a reservoir for bacterial pathogens. The structure of the nose is believed to be linked anatomically with decreased mucociliary clearance [17].

The colonization of large numbers of microorganisms in the nasal cavity can lead to various complications following nasal surgery. The presence of microorganisms in the nasal cavity, along with postoperative buffering systems that promote this colonization, can increase the risk of infection. However, few studies have investigated the presence of bacteria in the middle meatus of normal, asymptomatic adults. In another study, samples were collected from the middle meatus under endoscopic vision in ten symptom-free adults, and a calcium alginate swab was placed adjacent to the maxillary sinus ostium. The swabs were left in place for 15 seconds before being cultured. It was found that 40% (4 out of 10 patients) of the samples were sterile, while 60% showed growth of various Staphylococcus species[18]. Using a similar endoscopic sampling method from the nasal cavity, a high prevalence of coagulase-negative Staphylococcus (50%), S. aureus(12%), and Corynebacteria (12%) was isolated. Only 22 of the samples (16%) could be cultured for anaerobes**;** in 2 of the 139 samples, S. pneumoniae and H. influenzae were cultured [19]. The isolation of Staphylococcus and Corynebacteria is believed to be due to contamination from the nasal vestibule. In both studies, the nasal vestibule was not sterilized prior to sampling. Thus, it was concluded that the nasal cavity is not normally contaminated with pathogenic bacteria found in the nasopharynx. The study further determined that morphological differences did not influence the formation of bacterial colonization. However, numerous other factors, such as nasopharyngeal oxygenation and moisture levels, may play a role in bacterial colonization. Moreover, structural differences, such as septal deviation, can increase the colonization rate of opportunistic pathogens, which is particularly relevant for healthcare workers. Opportunistic pathogens, which play a significant role in hospital-acquired infections, can cause serious infections when transmitted by healthcare personnel responsible for the treatment and care of immunocompromised patients. Thus, nasal and nasopharyngeal carriage is a critical factor in the spread of hospital infections. Nasal colonization in individuals outside the hospital can simultaneously contaminate the environment, water, and food through respiratory transmission or direct contact with infectious agents. The colonization of abundant microorganisms in the nasal cavity may not only increase the risk of infection in this region but also lead to complications following surgical interventions [20,21]. Studies have shown that the bacterial colonization of pathogenic bacteria colonies in the nasal cavity can lead to a significant reduction in overall diseases caused by these bacteria, especially in vulnerable groups and healthcare personel [22]. Specifically, after airflow changes due to morphological structure differences, various bacterial colonization may occur. Some of these colonies are beneficial for the organism, while others have a detrimental effect as pathogenic agents.

This effect is particularly significant in the case of certain opportunistic pathogens**.**S. aureus, S. pneumoniae, and N. meningitidis are opportunistic pathogens that can colonize the upper respiratory tract. They pose a significant risk of severe infections, particularly for vulnerable populations such as the elderly and children, especially in intensive care units. Additionally, when hospital staff carry these pathogens in their nasopharynx, it creates a notable risk factor for hospital infections [23].

In our study, the relationship between the anatomical structural differences of the nose and the colonization of the bacteria examined was not statistically significant. The rates of S. aureusand S. pneumoniae colonization were low, likely due to their community origin. Notably, some samples were collected from first-year medical students. Although the isolates were sensitive and the colonization rates were low, it is imperative to implement appropriate treatment and monitoring, as these students will interact with patients who have compromised immune systems in intensive care units. Infections acquired in hospitals due to health care workers pose a significant risk factor for inpatients in both developed and developing countries [24-27]. Furthermore, all health faculty students who will come into contact with patients should be screened for nasal and nasopharyngeal colonization, and necessary treatment should be administered prior to patient interaction.

V. CONCLUSION

This study, which examines the relationship between nasal morphology and bacterial colonization, found no statistically significant association between the morphological structures of the nasal cavity or nasopharynx and bacterial pathogens. Consequently, it is inferred that the anatomical structure of the nose does not represent a potential risk factor for upper respiratory tract infections caused by pathogenic microorganisms.

Limitations

Due to restricted access to healthy individuals, it was not possible to conduct the study on a larger sample size.

Conflict of interest and funding sources

The authors declare that they have no conflict of interest. This study was supported by funding from the Kırıkkale University Scientific Research Projects Coordination Unit, under project number 2015/139.

Ethics approval and consent to participate

This study was approved by the Ethic Committee of Akay Hospital under the protocol number 2015-1880-1.

Informed consent

Since the study had a prospective character, the patients were informed that their information could be used in the study on the condition of protecting their personal information, and consent was obtained, so no additional consent was obtained.

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