Medica Hospitalia
Journal of Clinical Medicine
Med Hosp 2023; vol 10 (1) : 38–43

Original Article

Comparison of Bacterial Pattern in Trachea and Tracheal Stoma with the Incidence of Tracheal Stoma Infection at Mohammad Hoesin Central Hospital Palembang

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p-ISSN: 2301-4369 e-ISSN: 2685-7898
https://doi.org/10.36408/mhjcm.v10i1.825

Accepted: September 17th, 2022
Approved: January 12th, 2023

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Abstract

Background : Tracheostomy is a procedure to incise or make a hole in the trachea. The use of tracheal cannula leads to direct exposure of pathogens to the respiratory tract. It is necessary to identify bacterial pattern in an attempt to overcome tracheal stoma infections in order to prevent further complications. The aims of this study was to compare bacterial pattern in trachea and tracheal stoma on the incidence of tracheal stoma infection.
Methods : Observational research with a cross–sectional design. Medical record data on 60 subjects who underwent tracheal and tracheal stoma swabs and culture examination from November 2020 to October 2021 were collected. Bivariate analysis using Fischer exact test and Chi-square categorical comparative test.
Results : Sixty subjects obtained 13 species of bacteria, all identified as gram-negative bacteria. Most of the bacterial sequences and analysis of bacterial pattern were *Pseudomonas aeruginosa* (p>0.05), *Klebsiela pneumonia* (p>0.05), *Escherichia coli* (p>0.05) and *Serratia marcescen*(p>0.05) on the incidence of tracheal stoma infection**.**
Conclusion : There is no difference in the bacterial pattern of the trachea and tracheal stoma on the incidence of tracheal stoma infection.

Keywords : tracheostomy, bacterial pattern, tracheal stoma infection

INTRODUCTION

A normal trachea is protected from bacterial colonization. The trachea of healthy individuals does not contain pathogenic bacteria, or few normal bacteria/flora present. The use of tracheal cannula in tracheostomy leads to direct exposure of pathogens to the respiratory tract, and also causes a local inflammatory reaction that increases risk of infection. Infection of the tracheal stoma can be local and mild, or as extensive as to be life-threatening. Incidence of infection in tracheal stoma varies from 4% to 63% after tracheostomy. Others report the proportion of infection in tracheal stoma as much as 36% of all tracheostomy cases. Exposure to contaminated oral secretions, contaminated sputum, colonization of respiratories, and trauma from repeated manipulation of the trachea contributes to infection of tracheal stoma. Previous studies have reported 88% no bacterial growth in tracheal aspiration cultures immediately after tracheostomy, a number of 72% positive cultures on day 7 after tracheostomy. Patients with immunodeficiency such as malignancy, diabetes, malnutrition, and undergoing radiotherapy or chemotherapy, tend to be more susceptible to infection.[1–4]

Tracheal stoma infection occurs due to the presence of bacteria, which could be identified using culture examination. Tracheal stoma swab can be use to identify bacterial pattern of patients using tracheal cannula. The type of organism found is useful to determine the type of antibiotic or for administering antibiotics after the patient has an infection, in order to reduce the use of broad-spectrum antibiotics which increases the risk of resistancy. Prevention of infection is accomplished by aggressive wound care and frequent dressing changes, regular tracheal cannula replacement, and humidified air during inspiration. Knowledge and competence in handling daily care of tracheal cannula is needed to prevent further infection.[5–8] The purpose of this study is to compare bacterial pattern in trachea and tracheal stoma against the incidence of tracheal stoma infection in order to choose empiric antibiotics for patients with infections.

METHODS

This research is an observational study with a cross sectional design. The subjects of the study were all patients who underwent tracheal cannula replacement (1 to 6 months) after tracheostomy and subsequently tracheal and tracheal stoma swab in the ENT-Laryngology Division. The swab is carried out just before the new tracheal cannula is inserted using a sterile cotton swab on the mucose of the tracheal stoma, then with a different cotton swab, a swab is taken in the trachea by inserting a sterile cotton swab through the tracheal stoma and continuing it up to the trachea without touching the area around the stoma. Swabs were performed on all subjects with or without signs of infection. Tracheal stoma infection is assessed clinically in the form of swelling, redness of the skin around the tracheal stoma, thick secretions, yellow-greenish color, distinctive odor, with or without granulation tissue. Culture examination were done at the Central Laboratory Installation of RSUP Dr. Mohammad Hoesin Palembang during November 2020 to October 2021 period. The inclusion criteria includes results of swab cultures on the trachea and tracheal stoma that showed bacteria growing and complete medical record data. The minimum sample determined is 52 subjects. Univariate analysis was done using basic data characteristics of the study subjects, namely age, comorbidities, nutritional status, use of dressings, tracheal cannula replacement intervals, bacterial pattern in trachea and tracheal stoma. In this study, the comorbidities analyzed were diabetes mellitus (DM), hypertension, head and neck malignancy, history of chemotherapy, and history of radiotherapy. Analysis of bivariate data with the incidence of infection in tracheal stoma are done using the Chi-Square and Fisher tests.[8–11]

RESULTS

Results of this study showed 60 subjects met the inclusion criteria, among them, 32 subjects had tracheal stoma infections whereas 28 subjects did not have tracheal stoma infections. In tracheal and tracheal stoma swab examination, it was found that 100% were gram-negative bacteria consisting of 13 bacterial species.

a. Characteristics of subjects

Demographic characteristics in this study were age, nutritional status, comorbidities, use of dressings and interval of cannula replacement. The data is presented in a table of distribution of frequencies and percentages, based on 2 infected and uninfected groups in tracheal stoma (Table 1). Bacterial pattern with the names of bacteria described in the infected and non-infected groups in tracheal stoma. (Table 2).

In this study, 13 species of bacteria were identified, Pseudomonas aeruginosa being the microorganism mostly found, a total of 54 specimens (45%) of 120 specimens that were cultured. Pseudomonas aeruginosa was found more in tracheal stoma as much as 32 out of 120 specimens.

b. Results of Bivariate Analysis

Bivariate analysis in this study uses a comparative categorical hypothesis test using Chi-Square and Fisher. From this study, 13 species of Gram-negative bacteria were found, however due to the frequency and distribution of 9 bacterial species found were small (less

TABLE 1
Subjects' Characteristics

Variable		Tracheal Stoma Infection		Total N(%) N = 60
		Yes N (%)	No N (%)	
Age	0–5 years	0	1 (1.7%)	1 (1.7%)
	6–11 years	2 (3.3%)	0	2 (3.3%)
	12–25 years	1 (1.7%)	6 (10%)	7 (11.7%)
	26–45 years	5 (8.3%)	6 (10%)	11 (18.3%)
	46–65 years	18 (30%)	10 (16.7%)	28 (46.7%)
	>65 years	6 (10%)	5 (8.3%)	11 (18.3%)
Nutritional Status	Undernutrition	10 (16.7%)	12 (20%)	22 (36.7%)
	Good Nutrition	14 (23.3%)	13 (21.7%)	27 (45%)
	Overnutrition	8 (13.3%)	3 (5%)	11 (18.3%)
Comorbid	Yes	25 (41.7%)	16 (26.7%)	41 (68.3%)
	No	7 (11.7)	12 (20%)	19 (31.7%)
Use of dressing	*Moist dressing*	3 (5%)	3 (5%)	6 (10%)
	Sterile gauze	19 (31.7%)	21 (35%)	40 (66.7%)
	Without *dressing*	10 (16.7%)	4 (6.7%)	14 (23.3%)
Interval of cannula replacement	>30 days	28 (46.7%)	25 (41.7%)	53 (88.3%)
	<30 days	4 (6.7%)	3 (5%)	7 (11.7%)

TABLE 2
Distribution of Bacterial Pattern in Trachea and Tracheal Stoma

No	Bacterial Pattern	Trachea N (%)	Tracheal Stoma N (%)	Total N (%) N = 120
1	*Pseudomonas Aeruginosa*	22 (36.7%)	32 (53.3%)	54 (45%)
2	*Klebsiela pneumonia*	13 (21.7%)	5 (8.3%)	18 (15%)
3	*Escherichia coli*	7 (11.7%)	3 (6%)	10 (8.3%)
4	*Serratia marcescens*	3 (5%)	7 (11.7%)	10 (8.3%)
5	*Proteus mirabilis*	4 (6.7%)	2 (3.3%)	6 (5%)
6	*Acinetobacter baumannnii*	4 (6.7%)	2 (3.3%)	6 (5%)
7	*Salmonela sp*	3 (5%)	1 (1.7%)	4 (3.3%)
8	*Providencia situarti*	3 (5%)	1 (1.7%)	4 (3.3%)
9	*Enterobacter cloacae*	0	3 (5%)	3 (2.5%)
10	*Enterobakter asburiae*	1 (1.7%)	1 (1.7%)	2 (1.7%)
11	*Citrobacter koseri*	1 (1.7%)	0	1 (0.8%)
12	*Sphingomonas paucimobilis*	1 (1.7%)	0	1 (0.8%)
13	*Providencia rettgeri*	0	1 (1.7%)	1 (0.8%)
	Total	60	60	120

TABLE 3
Comparison of Trachea and Tracheal Stoma Bacterial Pattern with Tracheal Stoma Infection

Bacterial Pattern		Tracheal Stoma Infection		Total (N (%))	P value
		Yes	No		
Pseudomonas aeruginosa	Trachea	12 (22.2%)	10 (18.5%)	22 (40.7%)	0.307[a]
	Tracheal Stoma	15 (27.8%)	17 (25.9%)	32 (59.2%)	
Klebsiela pneumonia	Trachea	4 (22.2%)	9 (50%)	13 (72.2%)	0.138[a]
	Tracheal Stoma	2 (11.1%)	3 (16.7%)	5 (27.8%)	
Escherichia coli	Trachea	5 (50%)	2 (20%)	7 (70%)	1.000[b]
	Tracheal Stoma	2 (20%)	1 (10%)	3 (30%)	
Serratia marcescens	Trachea	2 (20%)	1 (10%)	3 (30%)	1.000[b]
	Tracheal Stoma	5 (50%)	2 (20%)	7 (70%)	

[a]*Chi-square pearson,* [b]*Fischer exact test*

TABLE 4
Risk Factors Analysis of Tracheal Stoma Infection

Variable		Tracheal Stoma Infection		Total N (%)	p value
		Yes N (%)	No N (%)		
Age	0–5 years	0	1 (1.7%)	1 (1.7%)	0.179[b]
	6–11 years	2 (3.3%)	0	2 (3.3%)	
	12–25 years	1 (1.7%)	6 (10%)	7 (11.7%)	
	26–45 years	5 (8,3%)	6 (10%)	11 (18.3%)	
	46–65 years	18 (30%)	10 (16.7%)	28 (46.7%)	
	>65 years	6 (10%)	5 (8.3%)	11 (18.3%)	
Nutritional Status	Undernutrition	10 (16.7%)	12 (20%)	22 (36.7%)	2.235[a]
	Good Nutrition	14 (23.3%)	13 (21.7%)	27 (45%)	
	Overnutrition	8 (13.3%)	3 (5%)	11 (18.3%)	
Comorbid	Yes	25 (41.7%)	16 (26.7%)	41 (68.3%)	1.408[a]
	No	7 (11.7)	12 (20%)	19 (31.7%)	
Use of dressing	*Moist dressing*	3 (5%)	3 (5%)	6 (10%)	0.268[b]
	Sterile gauze	19 (31.7%)	21 (35%)	40 (66.7%)	
	Without *dressing*	10 (16.7%)	4 (6.7%)	14 (23.3%)	
Interval of cannula replacement	>30 days	28 (46.7%)	25 (41.7%)	53 (88.3%)	1.000[b]
	<30 days	4 (6.7%)	3 (5%)	7 (11.7%)	

[a]Chi-square pearson, [b]Fischer exact test

than 10), the bivariate analysis could not be carried out on these species. On the other hand, the bivariate analysis that could be carried out are *Pseudomonas aeruginosa, Klebsiella pneumonia, Escherichia coli* and *Serratia marcescens*.[7]

Risk factors of tracheal stoma infection in this study were age, nutritional status, comorbidities, use of dressings and interval of tracheal cannula replacement.

DISCUSSION

The use of tracheal cannula resulted in the growth of bacterial colonisation of the trachea, resulting in 72% positive cultures on the 7th day after tracheostomy. Gram-negative and gram-positive bacteria can be found from tracheal swab and tracheal stoma cultures although gram-negative bacteria are more dominant, in accordance with several previous studies. In this study, overall culture results of samples showed gram-negative bacteria. Gram-negative bacteria were found more allegedly due to the ability of these bacteria to form biofilms and colonise the trachea.[2,12–14]

In this study, 13 species of bacteria were found. The results of tracheal swab culture showed most bacteria that grew were *Pseudomonas aeruginosa, Klebsiella pneumonia*, and *Escherichia coli*, meanwhile the tracheal stoma swab culture, showed most bacteria that grew were *Pseudomonas aeruginosa, Serratia marcescens* and *Klebsiela pneumonia*.

Pseudomonas aeruginosa is an opportunistic pathogen which is quite difficult to eradicate once colonised. *Pseudomonas aeruginosa* can bind to tracheal cells much more strongly so that injury to the tracheal surface due to endotracheal intubation, tracheal cannula and suctioning can also create new binding sites for *Pseudomonas*. Although most *Pseudomonas aeruginosa* was found in both trachea and tracheal stoma in this study, when bivariate analysis were carried out, showed no significant difference between the 2 groups of bacteria in the occurrence of tracheal stoma infection. Antibiotic sensitivity of *Pseudomonas aeruginosa* was reported to be sensitive to meropenem (92.6%), amikacin (94.4%), ciprofloxacin (92.6%), piperacillin/tazobactam (90.7%), cefepime (92.6%), gentamicin (96.3%), ceftazidime (92.6%), aztreonam (81.5%) and resistant to cefazolin (98.1%) and tigecycline (92.6%).[1,6,15–17]

Risk factors such as age, nutritional status, comorbidities, interval of cannula replacement and use of dressings did not affect the occurrence of tracheal stoma infection. This could happen due to lack of detailed analysis carried out on these factors, which is related to the differences in the care of the cannula in each patient.

Escherichia coli, Klebsiella, Proteus, Enterobacter, Serratia, Citrobacter, Morganella, Providencia, Cronobacter, and *Edwardsiella* are gram-negative enteric bacilli (GNB) belonging to the *Enterobacteriaceae* family. Gram-negative enteric bacilli are a common organism causing nosocomial infections in patients with tracheal cannula. *Escherichia coli* can enter the human body through hands or appliances such as bottles, pacifiers, thermometers, and cutlery that are contaminated with faeces. *Serratia marcescens* are able to live in water, soil, leaf surfaces, in the bodies of insects, animals and humans.[1,2,10,12,16,18–20]

Limitations of this study is the usage of secondary data in the form of medical records of patients using tracheal cannula, the researcher were unable to assess the standard swab taking for each subject.

CONCLUSIONS AND SUGGESTIONS

There is no difference in bacterial pattern of the trachea and tracheal stoma on the incidence of tracheal stoma infection.

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