

Bacterial Profile And Sensitivity Test Overview From Endotracheal Tube Aspirate Specimens From Confirmed Positive For Covid-19 Patients In Special Isolation Room Dr. Soetomo Hospital Surabaya

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Abstract

Background: Patients with COVID-19 who are treated in the Special Isolation Room (RIK) 1 are patients who experience respiratory failure and therefore use mechanical ventilation. The use of mechanical ventilation has a very high risk of infection in the respiratory tract accompanied by increased morbidity, especially in Multidrug Resistant (MDR) microorganism infections. This study aims to determine the profile of bacteria and the description of their sensitivity to antibiotics from Endotracheal Tube (ETT) aspirate specimens in COVID-19 patients at RIK 1 RSUD Dr. Soetomo Surabaya.

Methods: This study is a descriptive study of secondary data on aerobic culture of ETT aspirate specimens of COVID-19 patients treated at RIK 1 RSUD Dr. Soetomo Surabaya for the period March 2020-December 2020.

Results: Collected as many as 107 data from bacterial culture and sensitivity test to antibiotics. Gram negative bacteria were the most common microorganisms, namely 71 (59.6%), while Gram positive bacteria were 32 (26.9%). *Acinetobacter baumannii* was the most common Gram negative bacteria, namely 27 (22.7%). Then 12 (10.1%) *Klebsiella pneumoniae* ESBL and 11 (9.2%) *Klebsiella pneumoniae*. From the group of Gram positive bacteria the most were *Streptococcus viridans* 8 (6.7%), *Corynebacterium striatum* and *Staphylococcus aureus* each with 3 (2.5%). MRSA bacteria were found as many as 2 (1.7%). The antibiotic that has the highest sensitivity to *Acinetobacter baumannii*, *Klebsiella pneumoniae* and *Klebsiella pneumoniae* ESBL is Amikacin. While the 2nd, MRSA found were still sensitive to Linezolid, Rifampicin, Quinupristin dalfopristin, Tetracyclin, Teicoplanin and Vancomycin.

Conclusion: *Acinetobacter baumannii* was the most common microorganism isolated from ETT aspirate specimens in RIK 1 COVID-19 patients at Dr. Soetomo Surabaya and has the highest sensitivity to Amikacin antibiotics.

Keywords: Bacterial profile, Antibiotic sensitivity, COVID-19, Endotracheal tube

1. Introduction

A new clinical syndrome caused by the never-before-known coronavirus, Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2), was first identified in Wuhan (China) in December 2019. Despite massive efforts to contain the spread of the virus, a worldwide pandemic has developed from this virus. The disease is now known as Coronavirus disease 2019 (COVID-19) (Whittle et al., 2020). More than 80% of confirmed cases reported mild fever, however, 14-17% of confirmed cases increased to severe COVID-19 with Acute Respiratory Distress Syndrome (ARDS) and 5% also progressed to septic shock and/or multi-organ dysfunction. Like other groups of patients with ARDS, patients with severe COVID-19 are likely to be considered for emergency endotracheal intubation and mechanical ventilation to support recovery from their disease. (Brewster, 2020).

Positive pathogenic cultures on tracheal aspiration were associated with an increased likelihood of death

and with longer ICU treatment (mean (SD) of 16.3 (4.4) days, compared to 9.9 (0.8) days for patients without growth; $p=0.006$). Interestingly, tracheal aspiration with positive culture results was more deadly ($p<0.05$) than positive blood cultures ($p=0.082$). Intubation is independently associated with infection, and this may partly explain the success of some institutions that use oxygenation strategies that avoid intubation, such as HFNC oxygen (Moolla et al., 2021).

2. Methods

This type of research is descriptive of secondary data which is carried out at Dr. Soetomo General Hospital Surabaya. The design of this research is cross sectional. The population in this study is data on bacterial isolates from ETT aspirate specimens of patients treated at RIK 1 Dr. Soetomo General Hospital Surabaya and registered at the Clinical Microbiology Laboratory of Dr. Soetomo General Hospital Surabaya in March – December 2020. Determination of this research sample using consecutive sampling on bacterial species according to the semi-automatic BD Phoenix™ Automated Microbiology System from ETT aspirate specimens of patients treated at RIK 1 Dr. Soetomo General Hospital Surabaya. The sample size in this study was the total culture data of the ETT aspirate samples of patients treated at RIK 1 Dr. Soetomo General Hospital Surabaya March 2020 - December 2020. Inclusion criteria: Data from the results of the microbiological examination of ETT aspirate samples from patients treated at RIK 1 Dr. Soetomo General Hospital Surabaya March 2020 – December 2020. Exclusion criteria: Patient room data is incomplete.

3. Result

The total number of samples included in the inclusion criteria was 107 samples. Of the total sample, 73 (61.3%) were men and 34 (28.6%) were women. The minimum age was 17 years and the maximum was 76 years with a mean of 50.70 years (SD = 12.353). Of the total of 107 samples, 59 (55.1%) were Gram negative bacteria and 27 (25.2%) were Gram positive. Then up to 16 (15%) did not find bacterial growth. There were only 5 (4.7%) that showed the growth of Gram positive and negative bacteria at the same time in one culture. A total of 4 (3.7%) samples were sterile. 64 (59.8%) found 1 type of germ. Then 36 (33.6%) grew two types of germs, either two species of bacteria or a combination of 1 species of bacteria and 1 species of fungus. And only 3 (2.8%) were found to grow 3 types of germs at once, namely 2 bacteria and 1 fungus. From 107 samples there were 119 germs that grew consisting of 32 species of bacteria and 9 species of fungi. The three most common bacteria are from the Gram-negative group of bacteria. *Acinetobacter baumannii* was the most common Gram negative bacteria, namely 27 (22.7%). Then 12 (10.1%) *Klebsiella pneumoniae* ESBL and 11 (9.2%) *Klebsiella pneumoniae*. Then followed by Gram positive bacteria, namely *Streptococcus viridans* as many as 8 (6.7%). From 107 samples, there are 42 (39%) samples that grow mushrooms with a total of 9 species of fungi. The most abundant were *Candida albicans* 18 (15.1%), *Candida tropicalis* 13 (10.9%), and *Cryptococcus laurentii* 3 (2.5%).

Table 1 Distribution of Gram negative and Gram positive bacterial species

Microorganisms	Frequency	Percent
Bacteria (-), Fungus (+)	12	10.1
STERILE	4	3.4
Gram negative		
<i>Acinetobacter baumannii</i>	27	22.7
<i>Klebsiella pneumoniae ESBL</i>	12	10.1
<i>Klebsiella pneumoniae</i>	11	9.2
<i>Enterobacter cloacae</i>	4	3.4
<i>Pseudomonas aeruginosa</i>	4	3.4
<i>Moraxella catarrhalis</i>	3	2.5
<i>Escherichia coli</i>	2	1.7
<i>Stenotrophomonas maltophilia</i>	2	1.7
<i>Klebsiella aerogenes</i>	1	0.8
<i>Klebsiella ozaenae</i>	1	0.8
<i>Pantoea agglomerans</i>	1	0.8
<i>Providencia stuartii</i>	1	0.8
<i>Pseudomonas stutzeri</i>	1	0.8
<i>Weeksella virus</i>	1	0.8
Total	71	59.6
Gram positive		
<i>Streptococcus viridans</i>	8	6.7
<i>Corynebacterium striatum</i>	3	2.5
<i>Staphylococcus aureus</i>	3	2.5
MRSA	2	1.7
<i>Streptococcus mitis</i>	2	1.7
<i>Streptococcus pseudoporcinus</i>	2	1.7
<i>Alcaligenes faecalis</i>	1	0.8
<i>Brevibacillus brevis</i>	1	0.8
<i>Citrobacter freundii</i>	1	0.8
<i>Corynebacterium pseudodiphtheriticum</i>	1	0.8
<i>Enterococcus faecium</i>	1	0.8
<i>Kocuria kristinae</i>	1	0.8
<i>Kocuria rosea</i>	1	0.8

Microorganisms	Frequency	Percent
<i>Pasteurella multocida</i>	1	0.8
<i>Rothia mucilaginosa</i>	1	0.8
<i>Staphylococcus haemolyticus</i>	1	0.8
<i>Staphylococcus schleiferi</i>	1	0.8
<i>Streptococcus epidermidis</i>	1	0.8
Total	32	26.9
Grand Total	119	100.0

Table 2 Distribution of fungal species

Mushroom Species	Frequency	Percent
No mold growth	77	64.7
<i>Candida albicans</i>	18	15.1
<i>Candida tropicalis</i>	13	10.9
<i>Cryptococcus laurentii</i>	3	2.5
<i>Candida dubliniensis</i>	2	1.7
<i>Candida glabrata</i>	2	1.7
<i>Candida ciferii</i>	1	0.8
<i>Candida krusei</i>	1	0.8
<i>Candida non albicans</i>	1	0.8
<i>Candida rugosa</i>	1	0.8
Total	119	100.0

4. Discussion

The sample in this study was dominated by male sex, up to 73 (61.3%). Approximately 34 (28.6%) of the female gender. The minimum age was 17 years and the maximum was 76 years with a mean of 50.7 years (SD = 12,353). In comparison, in a study conducted in the United States between February 28, 2020 and May 14, 2020 involving 10.131 patients with positive SARS-CoV2, the male sex reached 9221 (91.0%) while the female sex was only 910 (19, 6%). Meanwhile, the most of the age groups are from the age group 50-69 years (Ioannou et al., 2020).

Referring to Table 1, the three most common bacteria are from the Gram-negative group of bacteria. *Acinetobacter baumannii* was the most common Gram negative bacteria, namely 27 (22.7%). Among the *Acinetobacter* species, *Acinetobacter baumannii* is the most important species associated with hospital-acquired infections worldwide. This aerobic Gram-negative *Coccobacillus* is considered a low-grade pathogen, but it is the pathogen responsible for opportunistic infections of the skin, bloodstream, urinary tract, and other soft tissues. (Matar et al., 2017).

Then 12 (10.1%) *Klebsiella pneumoniae* ESBL and 11 (9.2%) *Klebsiella pneumoniae*. *Klebsiella pneumoniae*, which belongs to the Enterobacteriaceae family, is a normal flora of the digestive tract of healthy humans and animals. It is an opportunistic pathogen that frequently causes hospital-acquired infections, accounting for about one-third of all Gram-negative infections in general. These bacteria are involved in extraintestinal infections including urinary tract infections, cystitis, pneumonia, surgical wound infections, and life-threatening infections, such as endocarditis and septicemia. (Navon-Venezia et al., 2017).

Of the group of Gram-positive bacteria, namely *Streptococcus viridans*, the highest number is 8 (6.7%), which is the normal flora of the upper respiratory tract. Then *Corynebacterium striatum* and *Staphylococcus aureus* were 3 (2.5%). Also noteworthy is the discovery of MRSA bacteria as much as 2 (1.7%). In Table 2, it is stated that there are 42 (35.2%) samples that grow fungi. The most common are *Candida albicans* 18 (15.1%), *Candida tropicalis* 13 (10.9%), and *Cryptococcus laurentii* 3 (2.5%).

When compared with a study conducted in Jiangsu Province, China with a total sample of up to 257 patients confirmed positive for COVID-19, respiratory co-infections with bacteria in the order of 5 were *Streptococcus pneumoniae*, *Klebsiella pneumoniae*, *Haemophilus influenzae*, *Escherichia coli* and *Staphylococcus aureus*. From the group of fungi found the most are *Aspergillus*, *Mucor* and *Candida*. In this study, which was conducted on January 22 - February 2, 2020, it showed different results due to different microbiological examination methods, namely using RT-PCR from throat swab specimens as a method of bacterial identification. (Zhu et al., 2020).

In the London study, respiratory samples for microbiological culture were obtained from 112 (13.3%) of 836 SARS-CoV-2 patients, with 39 (34.8%) of 112 identifying bacterial pathogens. (Hughes et al., 2020). Results from a Brazilian study, among 35 patients who had pulmonary SARS-CoV-2 infection and concomitant positive bronchial aspiration, 28 (80%) were colonized by the fungus or *P. aeruginosa*. (Intra et al., 2020). Research in South Africa showed that from the culture results of tracheal aspirate samples obtained from Covid-19 patients, the most common bacteria found was *Acinetobacter baumannii*. Then followed by *Klebsiella* species and *Pseudomonas aeruginosa* (Moolla et al., 2021).

The weakness of this study is that it is not certain that all the bacteria mentioned above are bacteria associated with HAI or VAP and the same patient can be examined more than once.

5. Conclusions

Gram-negative bacteria species identified from ETT aspirate samples in confirmed Covid-19 patients at RIK 1 Dr. Soetomo General Hospital Surabaya up to 71 (59.6%), the most species being *Acinetobacter baumannii*, *Klebsiella pneumoniae* ESBL and *Klebsiella pneumoniae*. Although Gram positive bacteria isolates were 32 (26.9%), the majority of species are *Streptococcus viridans*, which is the normal flora of the upper respiratory tract. With the discovery of *Streptococcus viridans* as the most Gram-positive bacteria in this study, it is advisable to re-evaluate the ETT aspirate sampling procedure that has been carried out so that it is not contaminated by normal upper respiratory tract flora. More research is needed to determine the germs that cause HAI and VAP in COVID-19 patients at RIK1 dr. Soetomo General Hospital.

Conflict of interest

None.

Acknowledgement

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