RESEARCH ARTICLE

Detection of co-infections bacteria from respiratory tract in COVID-19 patients admitted to ICU

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ABSTRACT

This study was carried out to isolation of different type of co-infections bacteria from ICU patients with COVID-19 enter through the respiratory tract. The study was conducted in sputum samples were also obtained from treated patients in (Rozhawa hospital emergency - Erbil), in Department of Microbiology. Identify and antimicrobial sensitivity (AST) was done by Vitek 2 apparatus. Entire of sputum samples of Streptococcus pneumonia (41.6%), Acinetobacter baumanni (37.5%), Staphylococcus aureus (8.3%), Sphingomonas paucimobilis (4.2%), Pseudomonas aeruginosa (4.2%) and Klebsiella pneumonia (4.2%). Acinetobacter baumanni bacteria due to its universal antibiotic resistance and widespread proliferation among the study models' patients, the bacterial isolate displayed greater threat.

Key Word: Acinetobacter baumannii; Bacteria; COVID-19; Co-infection.

1-Introduction:

The corona virus pandemic is a current global health emergency and the greatest threat humanity has faced since the Second World War1. Not all of this pandemic's fatalities are attributable to the COVID-19 virus.   A common side effect of viral sickness is a subsequent a "super infection" is a bacterial infection that has been overlaid. These infections are to blame for the COVID-19 patients' comparatively high rates of severe infection and mortality according to the sparse published data2.

Approximately half of the COVID-19 mortality patients likely had super infection, according to credible theory. Super added infections by nosocomial bacteria are more likely to develop in patients with severe illnesses and those who have to remain in intensive care units (ICUs) for an extended period of time3. The most Urinary tract infections (UTIs), ventilator-associated pneumonia (VAP) and bacteremia with sepsis are the most common infection types (UTIs) among COVID-19 patients4. Because antibiotics are frequently prescribed to treat and prevent these illnesses, antibiotic resistance is being fueled (AMR). Super infections in COVID-19 patients can be the biggest treatment challenge in underdeveloped nations like India, where the prevalence of multidrug-resistant organisms in healthcare facilities is well-established to be significant and is known to increase mortality5.

On January 7, a patient's throat swab sample contained a new corona virus that the World Health Organization had previously identified as 2019-nCoV6. The WHO has named the condition corona virus disease 2019 (COVID-19)7. Later, the Corona virus study group altered the name of severe acute respiratory syndrome caused by this infection Coronavirus Type 2. In China, 7736 confirmed cases were reported as of January, 12,167 suspected cases and 82 confirmed cases had been found in 18 different countries8.

Despite the fact that COVID-19 has a high death rate and is only mildly infectious, the amount9. Assessing the prevalence of bacterial infections and antibiotic resistance in persons with corona virus disease was the main objective of this investigation (COVID-19).

2-Methods:

This study included 20 patients of both gender suffering from corona virus who were admitted to our ICUs   and were under treatment. Real-time polymerase chain reaction for reverse transcription was used to find COVID-19. To help the bacteria proliferate, sputum samples were also obtained from treated patients in (Rozhawa hospital emergency - Erbil) and cultured on various mediums. Gram staining and Vitek tests were used to identify formed colonies on the media after incubation and antimicrobial susceptibility testing was performed   by the standard microbiological methods to   MEM:Meropinim , IPM: Imipenim   ,   LEV:Levofloxaciliion, Azm:Azithromycin ,   CAZ:Ceftazdime , CIP:Ciprofloxacillin,   TE:Tetracycline, S:Streptomycin,   FOX:Cefoxitin, TMP-SXT: trimethoprim sulfamethoxazole,   PRL: piperacillin , APX: ampiclox, AK:Amikacin , Tob: Tobramycin and F:Nitrofurandantim 10.

3-Result and discussion:

Total of 40 sputum samples yielded a total of 24 positive cultures (60%). Streptococcus pneumonia 10 (41.6%), Acinetobacter Baumann 9 (37.5%), Staph. aureus 2 (8.3%), Sphingomonas paucimobilis 1 (4.2%), Pseudomonas aeruginosa 1(4.2%) and K. pneumonia 1(4.2%) isolates respectively were the most frequently isolated bacteria (Table 1).

Table (1): common isolated bacteria and their response to antibiotics

Isolated Bacteria	No. of isolate	Response to antibiotics.
Strep. pneumonia	10	S : (TPM,CN,TOB,TE,F,CIP,MEM). R: (KF,FEP, OX,AK,TMP,CAZ).
Acinetobacter baumannii	9	S: 0 R: (MEM , IPM, LEV, Azm, CAZ , CIP, TE, S, FOX, TMP-SXT, PRL, APX, AK, Tob and F)
Staphylococcus aureus	2	S :(S,F,CHL,RA,VA) R :(PRL,TMP,KF,AMC,TE)
Sphingomonas paucimobilis	1	S:(TIC,PIP,CTZ,CFP,AZM,TMP,AX,CN) R:(CIP,TMP)
Pseudomonus aeruginosa	1	S :(AK,LEV,IMP) R: PRL,TMP,KF,AMC
Klebsiella pneumonia	1	S :(CN,AK,LEV,IMP,CIP,PIP, AZM,) R :(TMP)

For all isolated strains, antibacterial susceptibility were tested as, result presented in the table (1) Acinetobacter baumannii a widespread nosocomial pathogen that causes infections in patients who are gravely unwell. It was the only isolate that showed both resistance and sensitivity to the tested antibiotics. This bacterium has gained the propensity to develop antibiotic resistance quickly. Colistin and Tobramycin were frequently the only treatment options at a number of Cape Town hospitals in South Africa. The clinical laboratory uses Vitek 2 automated susceptibility testing (AST) to identify specific susceptibility profiles.

In order to evaluate the effects of co-infections in COVID-19 patients, we set out to. Of these 40 COVID-19 patients, 24 developed bacterial infections later on. The majority of the bacteria found in the end tracheal aspirate were Klebsiella species, S. aureus, Enterobacter species, and P. aeruginosa. The risk of healthcare-associated infections and the development of multidrug-resistant pathogens are also increased by hospital admissions, both of which augment the demand for antibiotics. Even though only 54% of patients had a suspected or confirmed bacterial co-infection, intensive care units (ICU) in recent research found nations revealed that patients had taken at least one antibiotic, either as treatment or as antimicrobial prophylaxis. People took at least one dose of an antibiotic in another research11. While only 8% of patients with hospitalized COVID-19 were found to have bacterial supra-infections or fungal co-infections, according to two investigations, even though 72% of patients received antibiotics12, 13 .

The findings of this study, which aimed to evaluate the impact of co-infections in COVID-19 patients, highlight the potential for super infection of COVID-19 patients by Acinetobacter baumannii. Therefore, it is essential to watch out for bacterial co-infections in critically ill patients who have COVID-19 tested positive.

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