



Article

A study on Identification of Bacterial Isolated From ICU Induce Nosocomial Infections

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Abstract: The aim of this study was to identify bacterial isolates associated with nosocomial infections in Intensive Care Units (ICUs) in Basrah hospitals during the COVID-19 pandemic. The research involved the collection of 103 clinical and environmental specimens, including blood, urine, patient bed swabs, ICU instruments, and walls. Standard microbiological methods were used to identify the bacteria, followed by antibiotic sensitivity testing to determine resistance patterns. The results revealed 46 bacterial isolates, with Enterobacter species (42.55%), Staphylococcus species (34.04%), and Pseudomonas species (14.89%) being the most dominant. These findings highlight the significant level of contamination in ICU environments, which may contribute to the spread of nosocomial infections, particularly during public health crises like the pandemic. This study emphasizes the importance of implementing stringent infection control measures to prevent the spread of resistant pathogens in ICU settings, which is crucial for reducing healthcare-associated infection risks..

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1. Introduction

51% of patients were thought to have been infected while receiving intensive care unit care, The Extended Prevalence of Infection in Intensive Care (EPIC) II study supports this theory. infections connected to medical treatment HAI is the most common adverse event in healthcare in terms of patient safety[1.2.3]. Bacteria in the natural flora might originate from exogenous or endogenous sources. Opportunities presented by bacterial infections occur when the human immune system isn't functioning correctly. Negative for coagulase Common Gram-positive organisms include Enterococcus species (such as faecalis and faecium), Streptococcus species, and Staphylococci. C. Of all the bacteria linked to healthcare-associated infections (HAIs) in US hospitals, difficile is the most commonly reported, making up 15% of all infections with a recognised pathogen.[4]. An illness you get while hospitalised for a different cause is known as a nosocomial infection. It is also known as an illness linked to healthcare or an infection acquired in a hospital. Hospital surroundings are home to a variety of organisms that are linked to contaminations and HAI processes. Patients and healthcare staff carry germs into hospitals and spread them to one another [5]. The primary pathogens also comprise of the more recent emergent vancomycin-resistant Enterococcus sp. (VRE), oxacillin-resistant Staphylococcus aureus (ORSA), extended-spectrum beta-lactamases (ESBL), and carbapenem-resistant Acinetobacter baumannii.[6,7].

In terms of morbidity, death, and expense, they have a significant detrimental effect on people, families, and healthcare systems. The development of bacteria resistant to several medications is another problem with HAI. In the US and the EU/EEA, HAI affects 3.2% and 6.5% of hospitalised patients, respectively, and the prevalence is likely far higher worldwide. In 64% of instances, the illness had a respiratory origin. Despite the general prevalence of Gram-negative organisms as a group: 62.2 % (E. Coli, Enterobacter spp., Klebsiella spp., Pseudomonas spp., and Acinetobacter spp.), S aureus (20.5 %) was the most often isolated organism[8].

ICU clinical practice: research indicates that between 30% and 60% of antibiotic prescriptions are either inappropriate or inaccurate [9,22]. Due to these reasons, intensive care units (icus) experience a higher rate of nosocomial infections than other departments. Nosocomial infections are often caused by bacteria that are known to be resistant to medications [10,8, 11]. An international study including 13,793 critically ill patients discovered that MDR bacteria were responsible for 35% of infections that were reported. These bacteria are associated with a greater incidence of inappropriate first-time antibiotic treatments, increasing the risk of morbidity, mortality, and additional costs [23]. [12]

Employed Illumina shotgun metagenomics to analyse the relatedness and polymorphisms of pathogens in low-diversity newborn intensive care units. 16S rna sequencing, however, makes it impossible to do a thorough examination of resistomes, nosocomial strains, metabolic pathways, and pathogenome transmission.[13].

2. Materials and Methods

All isolated were cultivated on nutritional agar, macconkey agar, or manitol agar and incubated for 24 hours at 37 °C in order to guarantee purity and yield single colonies. Using the Vitek® 2 compact auto analyser equipment from AL Bayan lab, isolates were identified after bacterial colonies were isolated on culture media. This procedure was divided into various stages: To extract pure colonies from the culture medium, the microorganisms are suspended in approximately 3 millilitres of sterile saline (nacl 0.45%-0.50%, ph 7) using a sterile plastic stick applicator. Enough of the colonies are then transferred to a clear polystyrene test tube, measuring 12 by 75 mm. Before the sample was introduced to the analyser, the Using a densitometer (Densichek), the concentration of the bacterial suspension in saline was measured and adjusted to 0.50-0.63 Mcfarland. Using an internal suction mechanism, identification GN cards were loaded—that is, inoculated—with bacterial suspension. As the matching suspension tube is inserted into the transfer tube, the identification card is inserted into the slot next to it. Ten test tubes can fit on the cassette. The bacterial suspension-containing test tube is inserted into a specific rack (cassette). The loaded cassette was inserted into the vacuum chamber station of the Vitek® 2 compact machine. All of the test wells were filled with the bacterial suspension, which was driven down the transfer tube and into micro-channels once the hoover was released and air was once again delivered into the station. Before being loaded into the circular incubator, inoculated GN cards were run through a device that sealed the card and severed the transfer tube. A circular incubator could. Up to thirty cards may fit in a circular incubator, and all kinds of cards were nurtured at 35.5±1°C. Every fifteen minutes, each card was taken out of the incubator, brought to the optical system to record the response, and then put back in the incubator until the next read time. Throughout the incubation phase, data were gathered every 15 minutes.

3. Results

During the COVID-19 pandemic, 103 clinical and environmental specimens were gathered from Basrah hospitals in the ICUS between December 2020 and April 2021.

Blood (24), urine (20), and patient bed swabs (24), various ICU tools (15), and walls (20) were among the clinical specimens. This investigation yielded the identification of 46 distinct bacterial isolates. Table one (1)

Table (1). Number and percentage of isolates in various samples

Samples	NO.of Specimens	NO.of Isolates	%
Clinical specimens			
Blood	24	2	4.34%
Urine	20	1	2.17%
Environmental Specimens			
Patient bed	24	15	32.60%
Different instruments in ICU	15	15	32.60%
Walls	20	13	28.26%
Total	103	46	100

47 different bacterial species identified using biochemical Vitek2compact system confirmed reactions. Twenty isolates were identified as Enterobacter, sixteen isolates as Staphylococcus species, seven pseudomonas, two Klebsiella, one Pantoea, and one Escherichia coli spp., according to the results of the Vitek 2 compact. As seen below, Table (4–12) There were twenty (42.55%) Enterobacter spp. isolates, sixteen (34.04%) Staphylococcus spp. isolates, seven (14.89%) Pseudomonas spp. isolates, two (4.25%) Klebsiella spp. isolates, one (2.13%) Pantoea spp. isolate, and one (2.13%) Escherichia coli isolates revealed.

Table (2). Identification of 46 bacterial species by GN card in Vitek 2 Compact.

No	Vitek identification	Isolate number in Vitek2 compact	Bio number
1	<i>Enterobacter aerogenes</i>	41-1	0625634553507010
2	<i>Enterobacter cloacae ssp dissolvens</i>	26-1	4635734753533210
3	<i>Enterobacter cloacae ssp dissolvens</i>	36-1	0627634553543010
4	<i>Enterobacter cloacae ssp cloacae</i>	56-1	0627735553533210
5	<i>Enterobacter cloacae complex</i>	19	0625535753553010
6	<i>Enterobacter cloacae complex</i>	20	0627735553533050
7	<i>Enterobacter cloacae complex</i>	21	2625635553533010
8	<i>Enterobacter cloacae complex</i>	22	0625735553553050
9	<i>Enterobacter cloacae complex</i>	23	0627735553513010
10	<i>Enterobacter cloacae complex</i>	24	0627735553553010
11	<i>Enterobacter cloacae complex</i>	25	0627735553553010
12	<i>Enterobacter cloacae complex</i>	27	0607634153502010
13	<i>Enterobacter cloacae complex</i>	30	0627735553553052
14	<i>Enterobacter cloacae complex</i>	31	0627735553553052
15	<i>Enterobacter cloacae complex</i>	32	0627735553553010
16	<i>Enterobacter cloacae complex</i>	44	0627735553553010
17	<i>Enterobacter cloacae complex</i>	7	0607634153503010
18	<i>Enterobacter cloacae complex</i>	9	0627735553553010
19	<i>Enterobacter cloacae complex</i>	11	0625535553553010
20	<i>Enterobacter cloacae complex</i>	17	0627735553553010
21	<i>Staphylococcus Saprophyticus</i>	37-1	030002017270231
22	<i>Staphylococcus lentus</i>	24-1	470003547773631
23	<i>Staphylococcus lentus</i>	25-1	110002065763631

24	<i>Staphylococcus haemolyticus</i>	61-1	010002000720231
25	<i>Staphylococcus aureus</i>	33-1	030402063763231
26	<i>Staphylococcus xylosus</i>	32-1	430446035772031
27	<i>Staphylococcus haemolyticus</i>	62-1	010002003720271
28	<i>Staphylococcus saprophyticus</i>	11-1	030202017673631
29	<i>Staphylococcus xylosus</i>	34-1	430446035772231
30	<i>Staphylococcus vitulinus</i>	42-1	010000000041010
31	<i>Staphylococcus lentus</i>	65-1	500000401463431
32	<i>Staphylococcus saprophyticus</i>	12-1	030002017270231
33	<i>Staphylococcus saprophyticus</i>	36-1	030002417672631
34	<i>Staphylococcus epidermidis</i>	28-1	010000030620251
35	<i>Staphylococcus lentus</i>	28	172002613763531
36	<i>Staphylococcus lentus</i>	29	100000401243531
37	<i>Pseudomonas stutzeri</i>	37	0002001100200040
38	<i>Pseudomonas luteola</i>	14-1	5401600250100212
39	<i>Pseudomonas stutzeri</i>	30-1	0002001100200040
40	<i>Pseudomonas stutzeri</i>	9-1	0002001100200040
41	<i>Pseudomonas stutzeri</i>	10-1	0002001100200040
42	<i>Pseudomonas alcaligenes</i>	26	0000001100000042
43	<i>Pseudomonas stutzeri</i>	33	0001001100000042
44	<i>Klebsiella pneumoniae ssp pneumoniae</i>	35-1	6607734753164010
45	<i>Klebsiella pneumoniae ssp pneumoniae</i>	33-1	6607734753164010
46	<i>Pantoea spp</i>	58-1	0607730552522010
47	<i>Escherichia coli</i>	38-1	0405610550026610

4. Discussion

Intensive care units (icus) account for up to 30% of nosocomial infections in hospitals due to a combination of factors including multiple procedures, the use of invasive devices like urinary catheterisation, central venous cannulations, endotracheal intubation, and mechanical ventilation, as well as the extremely debilitated population with reduced host defence. Catheter-related blood stream infections, ventilator-associated pneumonia, and catheter-associated urinary tract infections are the most frequent hospital-acquired infections in the critical care unit. [14.15]. *Klebsiella* spp. were, according to Chidambaram et al. [16], the strain from MICU that was most frequently found. (49%) was followed by 13.3% from *E. Coli* and 15% from *Acinetobacter* spp. Of the 24 bacterial isolates from the SICU, *Klebsiella* spp. (50%) was the most prevalent organism, followed by *Pseudomonas aeruginosa* (8.33%) and *E. Coli* (8.33%). Of the 49, 14 were Gram-positive and 35 were Gram-negative cultures. The samples that were assessed were blood (44), urine (18), and sputum (11).[17] Gram-positive isolates outnumbered Gram-negative isolates in the 50 swab samples that were examined. Of the 85 isolates discovered, five (68.2%) were Gram-positive isolates; the remaining isolates were Gram-negative. *S. Epidermidis* comprised around 24% of all isolates of *Staphylococci*. *S. Aureus*, on the other hand, made up 20%. Thirteen (15%) *Bacillus* species were found. These results corroborated the findings made by. [18] *Streptococcus* species and *Staphylococcus saprophyticus*. were discovered in 4% and 6% of instances, respectively. These results validate the assertions made by. [19] Gram-positive bacteria were isolated at a very low rate, according to Naeem (2010) [20, 21]. More than half of the isolates that were Gram-negative had resistance to several tested antibiotics. Only weak resistance to imipenem (26.1%) and amikacin (21.3%) was seen. The bulk of Gram-negative isolates (over 60%) exhibited resistance to ceftriaxone, cefotaxime, and ceftazidime.

5. Conclusion

The present study concluded that *Staphylococcus* and *Enterobacter* are the most common bacterial isolates in ICU in Basrah city hospital. Vitek2 compact includes an extended identification database, which enables us to detect a large range of microorganisms during short time.

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