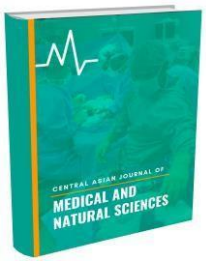

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*Article*

# 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..

**Keywords:** Genetics, Biology, Bacteria, ICU, Medical

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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 rrna 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 Klebsialla, 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 s by GN card in Vitek 2 Compact.

| No | Vitek identification | Isolate number in Vtek2 compact | Bio number |
|---|---|---|---|
| 1 | *Enterobacter aerogenes* | 41-1 | 0625634553507010 |
| 2 | *Enterobacter cloacae ssp dissolvens* | 26-1 | 4635734753533210 |
| 3 | *Enterobacter cloacae ssp dissolvens* | 36-1 | 0627634553543010 |
| 4 | *Enterobacter cloacae ssp cloacae* | 56-1 | 0627735553533210 |
| 5 | *Enterobacter cloacae complex* | 19 | 0625535753553010 |
| 6 | *Enterobacter cloacae complex* | 20 | 0627735553533050 |
| 7 | *Enterobacter cloacae complex* | 21 | 2625635553533010 |
| 8 | *Enterobacter cloacae complex* | 22 | 0625735553553050 |
| 9 | *Enterobacter cloacae complex* | 23 | 0627735553513010 |
| 10 | *Enterobacter cloacae complex* | 24 | 0627735553553010 |
| 11 | *Enterobacter cloacae complex* | 25 | 0627735553553010 |
| 12 | *Enterobacter cloacae complex* | 27 | 0607634153502010 |
| 13 | *Enterobacter cloacae complex* | 30 | 0627735553553052 |
| 14 | *Enterobacter cloacae complex* | 31 | 0627735553553052 |
| 15 | *Enterobacter cloacae complex* | 32 | 0627735553553010 |
| 16 | *Enterobacter cloacae complex* | 44 | 0627735553553010 |
| 17 | *Enterobacter cloacae complex* | 7 | 0607634153503010 |
| 18 | *Enterobacter cloacae complex* | 9 | 0627735553553010 |
| 19 | *Enterobacter cloacae complex* | 11 | 0625535553553010 |
| 20 | *Enterobacter cloacae complex* | 17 | 0627735553553010 |
| 21 | *Staphylococcus Saprophyticus* | 37-1 | 030002017270231 |
| 22 | *Staphylococcus lentus* | 24-1 | 470003547773631 |
| 23 | *Staphylococcus lentus* | 25-1 | 110002065763631 |

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

1. Allegranzi B, Bagheri Nejad S, Combescure C, Graafmans W, Attar H, Donaldson L, Pittet D. Burden of endemic health-care-associated infection in developing countries: systematic review and meta-analysis. Lancet. 2011 Jan 15;377(9761):228-41.
2. Atiyah M. Nurses' Knowledge Regarding Management of Hypovolemic Shock: A Cross-Sectional Study. Academia Open. 2024 May 12;9(2):10-21070.
3. Atiyah MA, Hsasn MF. Assessment of pharmacy staff Knowledge Towards prevention of osteoporosis in adolescent girls. Age.;20(6):30-9.
4. Brooks, B. Et al. Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. Nat. Commun. 2017.8, 1814.
5. Chaudhry, Dhruva, and Brijesh Prajapat "Intensive care unit bugs in India: how do they differ from the Westernworld?." The Journal of Association of Chest Physicians, Vol. 5, No. 1, 2017, p. .
6. Cieslinsk JM, Arend L, Tuon FF, Silva EP, Ekermann RG, Dalla-Costa LM, et al. (. Molecular epidemiology characterization of OXA-23 carbapenemase-producing Acinetobacter baumannii isolated from 8 Brazilian hospitals using repetitive sequence-based PCR. Diagn Microbiol Infect Dis.; 2013. 77(4):337-40.
7. Ekrami A. Isolation of common aerobic bacterial pathogensfrom the environment of seven hospitals, Ahvaz, Iran. JJM,2011;4:7582.
8. Jaillette E, Nseir S. Relationship between inhaled b2-agonists and ventilatorassociated pneumonia: a cohort study. Crit Care Med;2011.39:725e30.
9. Janda, J. M. & Abbott, S. L. 16S rrna gene sequencing for bacterial identification in the diagnostic laboratory: pluses, perils, and pitfalls. J. Clin. Microbiol. 2017.45, 2761–2764).
10. Jeon JH, Hong MK, Lee JH, Lee JJ, Park KS, Karim AM, et al. Structure of ADC-68, a novel carbapenem-hydrolyzing class C extended-spectrum β-lactamase isolated from Acinetobacter baumannii. Acta Cryst.; 2014.D70:2924-36.
11. Juayang C Alain. 1, Gemma B de Los Reyes 2, April Joy G de la Rama 2, Christine T Gallega Antibiotic Resistance Profiling of Staphylococcus aureus Isolated from Clinical Specimens in a Tertiary Hospital from 2010 to 20 Interdiscip Perspect Infect Dis.2014:2014:898457. Doi: 10.1155/2014/898457. Epub 2014 Sep 3.
12. Kaushal V Sheth1, Tejas K Patel2*, Saklainhaider S Malek1 and CB Tripathi1.)Antibiotic Sensitivity Pattern of Bacterial Isolatesfromthe Intensive Care Unit of a Tertiary Care Hospital inindia. Tropical Journal of Pharmaceutical Research December 2012; 11 (6): 991-999.
13. Luyt CE, Bréchot N, Trouillet JL, et al. Antibiotic stewardship in the intensive care unit. Crit Care; 2014.8:480.
14. Magill SS, Edwards JR, Bamberg W, Beldavs ZG, Dumyati G, Kainer MA, Lynfield R, Maloney M, mcallister-Hollod L, Nadle J, Ray SM, Thompson DL, Wilson LE, Fridkin SK., Emerging Infections Program Healthcare-Associated Infections and Antimicrobial Use Prevalence Survey Team. Multistate point-prevalence survey of health care-associated infections. N Engl J Med. 2014 Mar 27;370(13):1198-208.
15. Magill SS, O'Leary E, Janelle SJ, Thompson DL, Dumyati G, Nadle J, Wilson LE, Kainer MA, Lynfield R, Greissman S, Ray SM, Beldavs Z, Gross C, Bamberg W, Sievers M, Concannon C, Buhr N, Warnke L, Maloney

M, Ocampo V, Brooks J, Oyewumi T, Sharmin S, Richards K, Rainbow J, Samper M, Hancock EB, Leaptrot D, Scalise E, Badrun F, Phelps R, Edwards JR., Emerging Infections Program Hospital Prevalence Survey Team. Changes in Prevalence of Health Care-Associated Infections in U.S. Hospitals. N Engl J Med. 2018 Nov 01;379(18):1732-1744. [PMC free article] [pubmed]

16. Mohammed Kadhim M, Mahfoudh F H, Maher A A. Morphology of Medical Pathological Terms with the Prefix (Cardio). International Journal of Language Learning and Applied Linguistics. 2024;3(3):21-4.
17. Naeem, Akhtar. Hospital Acquired Infections in a Medical Intensive Care Unit. Journal of the College of Physicians and Surgeons Pakistan,2010; Vol. 20 (6): 386-390.
18. Of Association of Chest Physicians, Vol. 5, No. 1, 2017, p. .Chidambaram N., Ambujam G., Reena Rajan, Sasikala G. And Anandi V. Antimicrobial Profile of Clinical Isolates in Intensive Car e Unit at a Tertiary Care Hospital. International Journal of Medical Research & Health Sciences, , 2019;8(2): 160-166.
19. Shiferaw T. Bacterial contamination, bacterial profile and antimicrobial susceptibility pattern of isolates from stethoscopes at Jimma University Specialized Hospital. Annals Clin Microbiol Antimicrobials 2013;12:39-47.
20. Suetens C, Latour K, Kärki T, Ricchizzi E, Kinross P, Moro ML, Jans B, Hopkins S, Hansen S, Lyytikäinen O, Reilly J, Deptula A, Zingg W, Plachouras D, Monnet DL., Healthcare-Associated Infections Prevalence Study Group. Prevalence of healthcare-associated infections, estimated incidence and composite antimicrobial resistance index in acute care hospitals and long-term care facilities: results from two European point prevalence surveys, 2016 to 2017. Euro Surveill. 2018 Nov;23(46) [PMC free article] [pubmed]
21. Tiryag AM, Dawood SB, Jassim SK. Nurses' knowledge and attitudes about enteral feeding complications by nasogastric tube in intensive care units. Rawal Medical Journal. 2023 Jul;48(3):689-.
22. Varley, A. J., H. Williams, and S. Fletcher. "Antibiotic resistance in the intensive care unit." Continuing Educationin Anaesthesia, Critical Care and Pain, Vol. 9, No. 4, 2009, pp. 114-18.
23. Vincent J, Rello J, Marshall J, et al. International study of the prevalence and outcomes of infection in intensive care units. JAMA;2009.302:2323–9.
24. Vincent, J. L., Bihari, D. J., Suter, P. M., Bruining, H. A., White, J., Nicolas-Chanoin, M. H.et al. The prevalence of nosocomial infection in intensive care units in Europe. Results of the European Prevalence of Infection in Intensive Care (EPIC) Study. JAMA.1995. 274, 639–44.