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BLOODSTREAM INFECTIONS IN ICU PATIENTS FROM TERTIARY CARE HOSPITAL ON AUTOMATED BLOOD CULTURE BD BACTEC AND VITEK 2 COMPACT SYSTEM

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Abstract

***Background:** Bloodstream infections are a leading cause of morbidity and mortality, especially in ICUpatients. This prospective observational study analyzed 750 ICU cases from May 1, 2022, to May 31, 2023, using automated BACTEC™ blood culture methods. These methods showed higher sensitivity, specificity, and faster results compared to traditional cooked meat enrichment broth methods.*

***Aim:** The study employed the VITEK 2 system, an advanced iteration of the original 1970s VITEK system,to identify organisms and conduct antimicrobial susceptibility testing (AST).*

***Methods**: A standardized method was employed using the 750 samples subjected to the BD BACTEC™ bloodculture system. Extended microbiological culture for two weeks is unnecessary with BACTEC™ methods, as most clinically significant organisms are detected within three days. The VITEK2 system, an automated platform for organism identification and antimicrobial susceptibility testing (AST) monitors reactions in every 15 minutes during incubation.*

***Results:** This prospective observational study included 750 samples, admitted to the ICU. Samples were cultured and assessed for antimicrobial susceptibility patterns: out of 132 positive samples, 84 (63.63%) blood cultures showed microbial growth with mono-microbial presence. Gram-negative bacilli were identified in 45 cases (53.57%), with E. coli being the most common, while Gram-positive organisms accounted for 39 cases (47.42%), predominantly S.haemolyticus.*

***Conclusions:** Gram-negative isolates exhibited sensitivity to only a limited number of drugs. Blood culture isolates from critically ill patients in the intensive care unit were multidrug-resistant, including MRSA, highlighting a significant concern regarding the rise of severe antibiotic resistance.*

***Keywords:** BD BACTEC™, VITEK 2 COMPACT, ICU, GNB*

Introduction:

Bloodstream infection (BSI) continues to be a major contributor to morbidity and mortality worldwide [1]. BSI is defined by the presence of a positive blood culture in a patient exhibiting systemic signs of infection, and it can either be secondary to a known source or primary with no identifiable origin.[2]

A wide range of organisms has been identified as causes of BSI, with variations influenced by geographical differences.[3] BSI remains one of the most challenging issues for clinicians treating ICU patients. The inappropriate use of antibiotics in managing BSI not only raises patient mortality but also heightens the risk of drug-resistant strains emerging. These infections lead to prolonged hospital stays, increased healthcare costs, and higher morbidity and mortality rates.[4] In India, where the burden of infectious diseases is among the highest in the world, the misuse and overuse of antimicrobials have contributed to the growing problem of antimicrobial resistance (AMR). Additionally, poor financial conditions, inadequate infrastructure, a high disease burden, and unregulated over-the-counter sales of inexpensive antibiotics have exacerbated the AMR crisis in India.[5,6] Routine laboratories are now utilizing instrumented blood culture systems like BD BACTEC™ for incubating various sterile site specimens. This continuous detection system eliminates the need for daily inspections and terminal subculturing.[7] The automated system for identification and antimicrobial susceptibility testing (AST) has evolved into the VITEK 2 system, which automatically completes all necessary steps for organism identification.[8]

Technological advancements enabling rapid bacterial identification and antimicrobial susceptibility testing (AST) are now acknowledged for their clinical and financial advantages.[9] This system performs kinetic analysis by reading each test every 15 minutes. It uses an optical system that integrates multichannel fluorimeter and photometer readings to capture fluorescence, turbidity, and colorimetric signals. Given the rising incidence of infections caused by these microorganisms and the growing resistance to various antimicrobial agents, these innovations have become increasingly important.[10-14]

The rising prevalence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) bacterial pathogens is a significant public health issue, placing a substantial economic strain on healthcare systems due to extended hospital stays and increased morbidity and mortality.[15] Tigecycline, a tetracycline-class antibacterial agent, has been developed to treat polymicrobial MDR infections.[16]

Further studies have demonstrated that tigecycline is effective against severe infections caused by resistant pathogens.[17,18] However, there is limited data available specifically for ICU patients with bacteraemia.[19] These analyses have concentrated on approved indications,[20,21] global microbiological results[22] and safety concerns.[23]

Therefore, this study aims to identify gram-negative organisms causing BSI in our hospital, especially in the ICU section using the original 1970s VITEK system and conduct its antimicrobial susceptibility testing (AST) of the isolated strains.

Materials and methods

This prospective observational study was carried out over a one-year period, from May 2022 to May 2023, at a tertiary care teaching hospital. It focused on consecutive cases of ICU patients who were treated with antibiotics. During the study, the Department of Clinical Microbiology processed a total of 750 clinical specimens.

Exclusion/inclusion criteria:

- The inclusion criterion was the effectiveness of tigecycline in treating bloodstream infections. The study was independently designed and involved a thorough review of all data related to bacterial infections. Only blood samples were included.
- Excluded other samples such as pus, sputum and endotracheal aspirates were excluded.

Out of 150 clinical specimens, 150 yielded microbial growth, with 132 consisting of Gram-negative bacilli and Gram-positive cocci. Among these, 84 samples (63.63%) were positive for mono-microbial growth. Gram-negative bacilli made up 53.57% of the cases, with *E. coli* being the most common, while Gram-positive cocci constituted 46.42%, with *Staphylococcus haemolyticus* being predominant. The BD BACTEC™ instrumented blood culture system and the VITEK 2 COMPACT system were used for identification and antimicrobial susceptibility testing (AST). All clinical specimens were plated on CLED, MacConkey, and Blood agar, and incubated at 37°C for 48 hours before being reported as sterile if no growth was observed.[24] Isolates that showed non-lactose fermenting colonies on MacConkey agar were further identified using a standard protocol, with gram staining morphology being one of the assessed characteristics.

Results

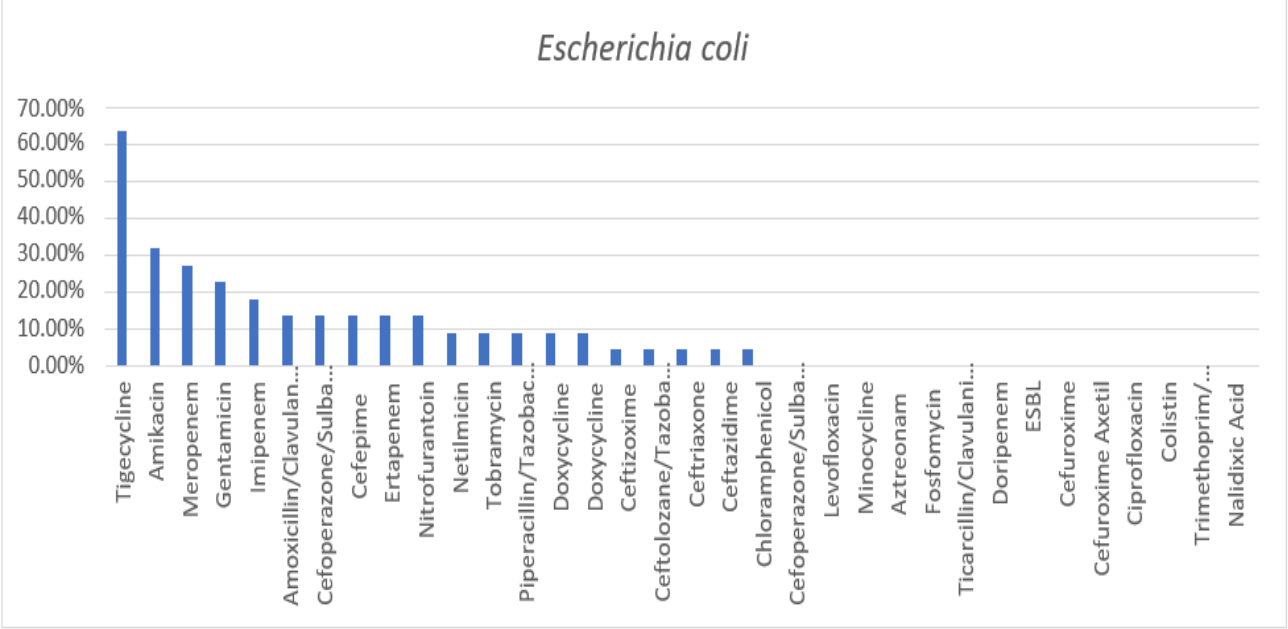
During the study period, out of 132 samples, 84 blood cultures tested positive, with the majority of isolates being Gram-negative bacilli (GNB) from bloodstream infections

STRAIN	TOTAL	BLOOD SAMPLE
GNB	90 (68.18%)	45 (53.57%)
GPC	42 (31.81%)	39 (46.42%)
TOTAL	132 (100%)	84 (63.63%)

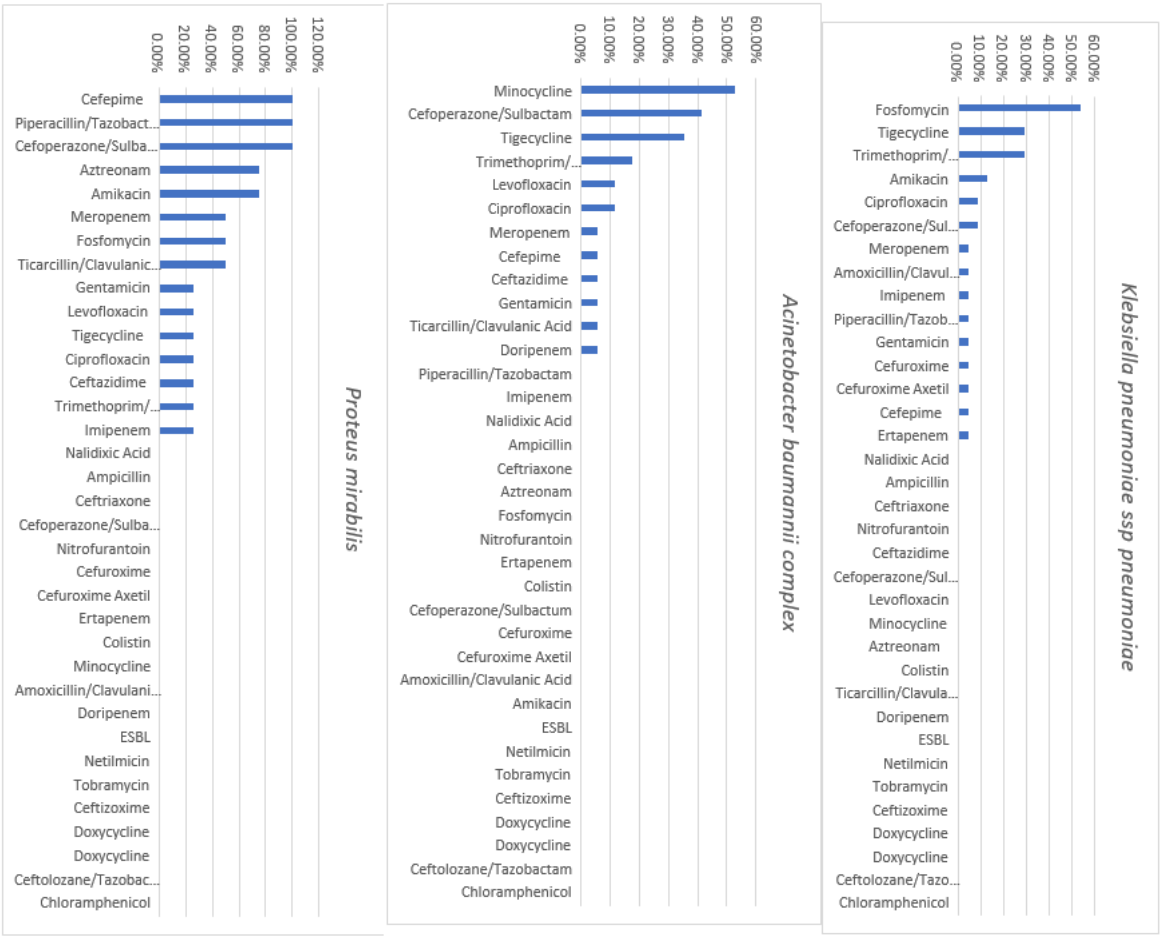
In this study, tigecycline demonstrated greater sensitivity compared to other drugs, particularly against Gram- negative bacilli (GNB), with success rates similar to those observed in clinical studies of severe infections.
Unlike its use in other countries, tigecycline here is primarily utilized in combination with agents specifically targeting Gram-negative microorganisms.

ISOLATED STRAINS OF GNB	PERCENT AGE	T. ISOLATES
Escherichia coli	24.44	22
Klebsiella pneumoniae ssp pneumoniae	26.67	24
Acinetobacter baumannii complex	18.89	17
Proteus mirabilis	4.44	4
Pseudomonas aeruginosa	3.33	3
Enterobacter cloacae complex	2.22	2
Achromobacter denitrificans	1.11	1
Achromobacter xylosoxidan	2.22	2
Acinetobacter lwoffii	1.11	1
Brevundimonas diminuta/vesicularis	1.11	1
Citrobacter amalonaticus	1.11	1
Morganella morganii ssp morganii	1.11	1
Ochrobactrum anthropic	2.22	2
Pandoraea spp	2.22	2
Salmonella enterica ssp diarizonae	1.11	1
Sphingomonas paucimobilis	2.22	2
Stenotrophomonas maltophilia	4.44	4

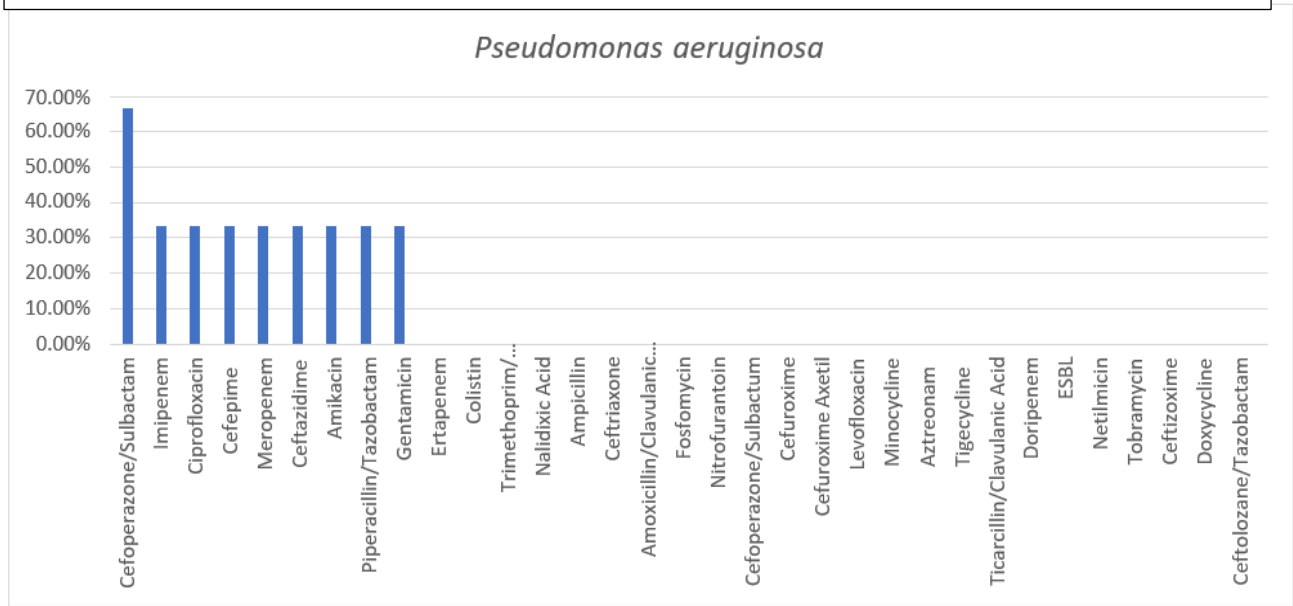
Graph1: Dsitribution of *Escherichia coli* strains based on the Antimicrobial Suscepticility Testing



Graph 2: Distribution of *Proteus mirabilis, Acinetobacter baumannii complex and Klebsiella pneumoniae spp pneumoniae* based on Antimicrobial Susceptibility Testing



Graph 2: Distribution of *Psuedomonas aeruginosa* based on Antimicrobial Susceptibility Testing



Discussion

We used the BD BACTEC™ instrumented blood culture system as a convenient, easy-to-use, and rapid diagnostic method. Our results demonstrated that it reliably detects slow-growing organisms, such as *Propionibacterium* species, without the need for prolonged culture periods. These findings can support earlier decisions on final antimicrobial prescribing.[25]

Using the VITEK 2 COMPACT system, 35 different antibiotics were tested for susceptibility against all Gram-negative

bacilli (GNB) strains. The most prevalent organisms identified in ICU patients with GNB infections were *E. coli*, *Klebsiella pneumoniae* spp., *Acinetobacter baumannii* complex, *Proteus mirabilis*, and *Pseudomonas aeruginosa*.[6]
The most frequently isolated Gram-negative bacilli were *E. coli* (24.44%) and *Klebsiella* spp. (26.67%), followed by *Acinetobacter* spp. (18.89%) and *P. aeruginosa* (3.33%). *E. coli* was the most common organism isolated from the bloodstream (17.6%). In contrast, *A. baumannii* and *K. pneumoniae* were the predominant organisms isolated from bloodstream infections in other studies.[26] *E. coli* is primarily associated with urinary tract infections, bloodstream infections, intra-abdominal infections, and wound infections, with fewer cases of respiratory tract infections, consistent with its distribution in the Asia-Pacific region, Latin America, and Southern Africa. Notably, while *E. coli* had the highest isolation rate,this rate has shown a fluctuating downward trend over the past 10 years. In contrast, the isolation rates of *K. pneumoniae* and *A. baumannii* have generally increased, except for a decline in 2021, likely due to the more severe antimicrobial resistance of *A. baumannii* and *K. pneumoniae* compared to *E. coli*.[27]
E. coli emerged as the leading pathogen responsible for septicemia, with tigecycline being the most effective drug against Gram-negative bacteria. Regular, unit-based microbiological surveillance, along with timely and repeated investigations of bloodstream infections (BSI) bacterial flora, is crucial. Fortunately, *E. coli* exhibited the lowest resistance rates to imipenem and meropenem,which have remained stable over the past 10 years, aligning with similar findings in Europe, Asia, and Latin America. Notably, despite both being third- generation cephalosporins, ceftazidime showed greater activity against *E. coli* and *K. pneumoniae* compared to ceftriaxone, likely due to ceftriaxone's higher susceptibility to hydrolysis.[28]
ICU patients are particularly vulnerable due to severe underlying conditions, impaired host defenses, and weakened immunity.[29] Additionally, multiple surgeries and the use of invasive devices—such as mechanical ventilation, tracheal tubes, arterial catheters, and central venous catheters—increase the risk of infection and colonization by multidrug-resistant (MDR) organisms.[30] Infections caused by MDR pathogens have become more prevalent in ICUs, making the selection of effective antimicrobial agents challenging. This contributes directly to higher morbidity, mortality, and increased hospitalization costs.[31]

Conclusion

750 samples from ICU patients were taken for our study.132 positive isolates, Blood C/S had the highest frequency of isolated ICU samples. *E.coli*, *Klebsiella* spp., *Acinetobacter* spp., and *P. aeruginosa* were the most frequently isolated gram-negative bacilli. *Klebsiella* spp was the top one organism isolated from bloodstream, Tigecycline show the highest sensitivity rates. The antimicrobial susceptibility results were interpreted by CLSI. Rates of MDR and XDR in *Klebsiellapneumoniae*, *Acinetobacterbaumannii*,and *Pseudomonas aeruginosa* were investigated.

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