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Comparative Efficacy Of Maldi-Tof Ms Versus Conventional Microbiological Methods In Identifying Bacterial Isolates From Puerperal Sepsis

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ABSTRACT

Background: Puerperal sepsis, a potentially fatal postpartum infection, continues to be an important cause of maternal morbidity and mortality. The prompt identification of the causal pathogens is vital for successful and timely treatment. While traditional microbiological techniques are the most used, they are limited by both speed and precision. In contrast, MALDI-TOF MS has a faster and more precise method for bacterial identification. This study will contrast these two approaches in the identification of puerperal sepsis patients' bacterial isolates.

Methods: his cross-sectional study was done from May 2023 to November 2024 in Lady Hardinge Medical College and Smt. Sucheta Kripalani Hospital, New Delhi. There were 96 puerperal sepsis patients enrolled, for whom blood and high vaginal swab samples were obtained for examination. Conventional microbiological methods as well as MALDI-TOF MS were used for identification of bacteria, and antibiotic resistance was evaluated with the VITEK 2 automated system.

Results: The comparison revealed that MALDI-TOF MS and the conventional techniques were in complete agreement in the case of routine pathogens like Escherichia coli and Klebsiella pneumoniae. MALDI-TOF MS, though, gave a more accurate species identification of pathogens like Pseudomonas stutzeri and Enterococcus faecalis, which was identified at the genus level using conventional techniques. High antibiotic resistance was noted, particularly among the gram-negative bacteria.

Conclusion: MALDI-TOF MS is a quicker and more accurate bacterial identification method compared to conventional methods, contributing to better management of puerperal sepsis.

Keywords: *MALDI-TOF MS, puerperal sepsis, bacterial identification, conventional microbiological methods, antibiotic resistance, diagnostic methods.*

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1. INTRODUCTION

Puerperal sepsis is a major global cause of maternal morbidity and mortality, usually due to bacterial infection following delivery. Rapid and precise identification of the causative microorganisms is crucial in order to direct antimicrobial therapy and improve patient outcomes. Conventionally, routine microbiological methods, including blood and vaginal cultures with subsequent biochemical analysis, have been the gold standard for the identification of pathogens. However, such methods take time and even in optimal circumstances, do not yield species-level identification of hard or uncommon organisms.

Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS) is becoming increasingly important technology in the field of clinical microbiology due to its ability to rapidly and accurately identify bacteria on the basis of their protein signatures. MALDI-TOF MS has been widely used in clinical labs and provided accurate species-level identification of pathogens, which often other technologies cannot provide. The benefits of MALDI-TOF MS, such as quicker results and better accuracy in the identification of a wider variety of microorganisms, make it a top choice for the diagnosis of puerperal sepsis. The purpose of this study was to evaluate the diagnostic performance of MALDI-TOF MS against conventional microbiological techniques for the identification of bacterial isolates of puerperal sepsis. In addition, we aimed to assess the antibiotic resistance patterns of these isolates and determine the risk factors for puerperal sepsis.

2. MATERIALS AND METHODS

Study Design:

This study was planned as a cross-sectional survey between May 2023 to November 2024 in Lady Hardinge Medical College and Smt. Sucheta Kripalani Hospital, New Delhi. Institutional review board approval and informed consent of all study patients were taken.

Study Population:

96 women with puerperal sepsis were enrolled in the study. The inclusion criteria were symptoms such as fever, pelvic tenderness, offensive discharge, and uterine complications within 42 days of delivery. Women with other infections not related to puerperal sepsis (e.g., respiratory or urinary tract infections) were excluded.

Sample Collection:

Blood samples and high vaginal swabs (HVS) were collected under sterile conditions. Blood cultures were done using the BacT/ALERT system, while HVS samples were cultured on blood and MacConkey agar.

Microbiological Identification:

1. **Traditional Methods:** Bacterial colonies were initially examined for their morphology, Gram staining, and biochemical characteristics, including catalase, coagulase, oxidase, and fermentation tests.
2. **MALDI-TOF MS:** Bacterial colonies were analyzed using the MALDI-TOF MS technique. A small sample of the bacterial colony was combined with a matrix and applied to a target plate. The Bruker Daltonics MALDI-TOF MS system was utilized to obtain the mass spectra, which were then compared with a reference database to accurately identify the bacterial species.

Antibiotic Susceptibility Testing:

Antibiotic resistance was tested using the VITEK 2 automated system following CLSI 2022 guidelines. The bacterial isolates were tested for their susceptibility to various antibiotics and categorized as susceptible, intermediate, or resistant.

Statistical Analysis:

Data were analyzed using SPSS software. Descriptive statistics were employed to summarize demographic and clinical information, while a comparative analysis was conducted to evaluate the bacterial detection rates between the two methods. Statistical significance was determined at a p-value of less than 0.05.

3. RESULTS

A total of 96 patients with puerperal sepsis were included. The mean age of the participants was 23.82 years (SD 2.82), with the majority (67.7%) of patients in the 20-30 years age group. The study showed that 62.1% of patients had normal vaginal delivery (NVD), while 37.9% had a cesarean section (LSCS). A significant proportion (75.8%) of patients were anemic.

Bacterial Isolates:

- From the 96 cases, 62 bacterial isolates were obtained from HVS samples and 6 isolates from blood cultures.
- The most common organisms identified were *Escherichia coli* (43.5%), *Klebsiella pneumoniae* (29.03%), and *Staphylococcus aureus* (6.4%).

Comparison of MALDI-TOF MS and Conventional Methods:

- **Conventional Methods:** 100% concordance was achieved for identifying *Escherichia coli* and *Klebsiella pneumoniae* between both methods. However, some organisms, such as *Pseudomonas stutzeri* and *Enterococcus faecalis*, were identified only to the genus level by conventional methods.
- **MALDI-TOF MS:** This method identified *Pseudomonas stutzeri*, *Enterococcus faecalis*, and several other species with greater accuracy, providing species-level identification for organisms that conventional methods could not identify precisely.

Antibiotic Resistance Patterns:

- **Gram-negative organisms** showed significant resistance to antibiotics, particularly *Klebsiella pneumoniae*, which exhibited resistance to multiple classes of antibiotics, including amoxycillin-clavulanic acid, ciprofloxacin, and ceftriaxone.
- **Gram-positive organisms** like *Staphylococcus aureus* exhibited 50% methicillin resistance (MRSA), with other resistances observed to penicillin, erythromycin, and clindamycin.

Table 1: Demographic and Clinical Characteristics of Participants

Characteristic	Value (%)
Age (mean ± SD)	23.82 ± 2.82 years
Socioeconomic Status	Low: 50%, Middle: 39.6%, High: 10.4%
Anemia	Yes: 75.8%, No: 24.2%
Mode of Delivery	NVD: 62.1%, LSCS: 37.9%
Parity	Primiparous: 43.8%, Multiparous: 56.2%

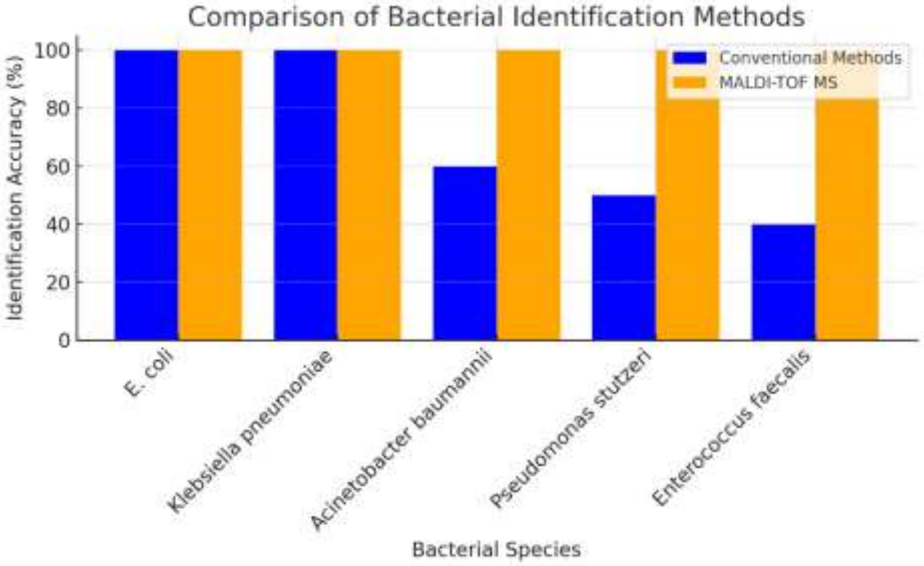
Table 2: Common Bacterial Isolates in HVS Samples

Organism	Conventional Method (%)	MALDI-TOF MS (%)
Escherichia coli	43.5	43.5
Klebsiella pneumoniae	29.03	29.03
Acinetobacter baumannii	3.9	7.06
Pseudomonas stutzeri	1.04	1.04
Enterococcus faecalis	0	3.9

Table 3: Antibiotic Resistance in Gram-negative Bacteria

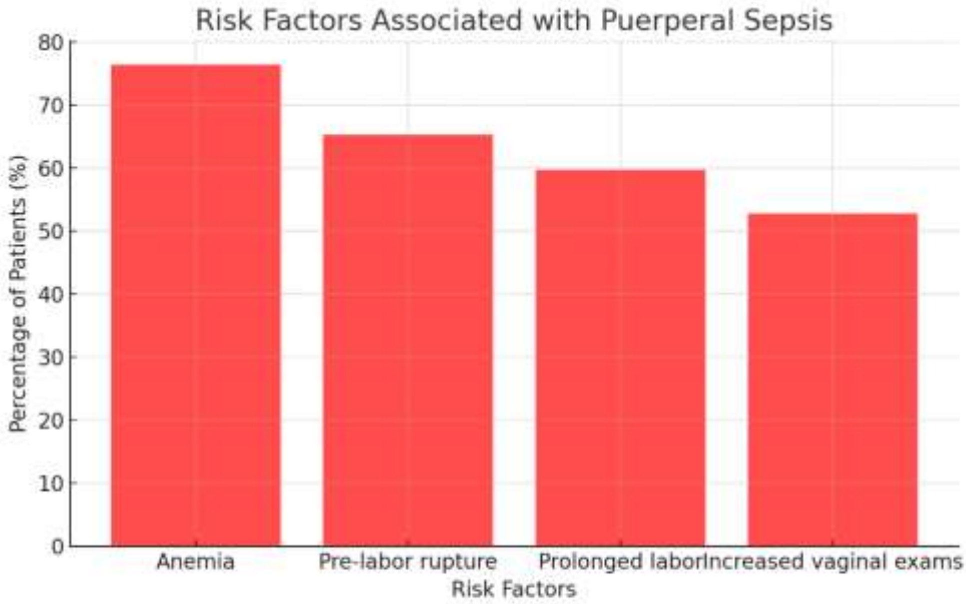
Organism	Amikacin	Ciprofloxacin	Ceftriaxone	Gentamicin	Meropenem
E. coli	18%	48%	30%	33.9%	14.8%
Klebsiella pneumoniae	40%	80%	60%	50%	11.1%
Acinetobacter baumannii	50%	100%	100%	50%	0%

Figure 1: Comparison of Bacterial Identification by Conventional Methods vs MALDI-TOF MS



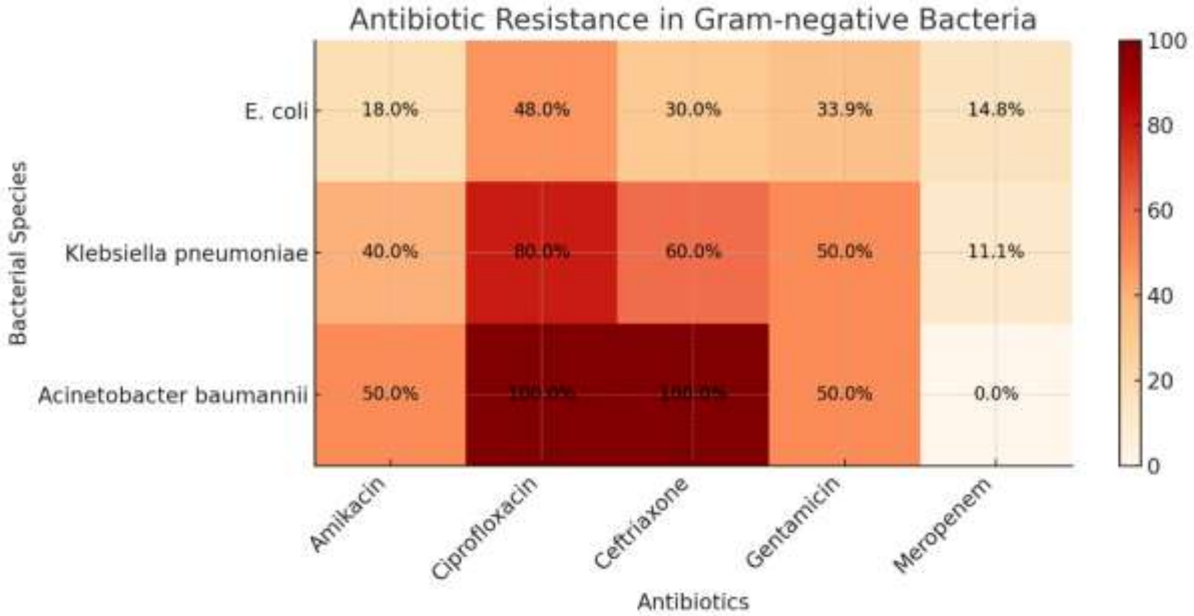
Graph showing higher detection rate of species-level identification by MALDI-TOF MS compared to conventional methods.

Figure 2: Risk Factors Associated with Puerperal Sepsis



Bar graph illustrating the prevalence of risk factors such as anemia, prolonged labor, and increased vaginal examinations.

Figure 3: Antibiotic Resistance in Gram-negative Bacteria



heatmap displaying the resistance percentages of *E. coli*, *Klebsiella pneumoniae*, and *Acinetobacter baumannii* against five major antibiotics.

4. DISCUSSION

This research assesses the efficacy of MALDI-TOF MS when compared to conventional microbiological techniques for characterizing bacterial isolates in puerperal sepsis. The results show that MALDI-TOF MS has several advantages over the conventional methods, including a faster turnaround time, higher precision of species identification, and the ability to identify a broader range of pathogens. These features are particularly important in sepsis treatment, where initiating the appropriate antibiotic therapy early is crucial.

The agreement rates as high as those found for frequent pathogens such as Escherichia coli and Klebsiella pneumoniae show The results show that MALDI-TOF MS would be a good diagnostic tool to use in clinical microbiology. Also, being able to detect species such as Pseudomonas stutzeri and Enterococcus faecalis that are not easily detected by standard methods also shows its strengths.

The resistance patterns identified in this study, especially in gram-negative bacteria, are cause for concern regarding antimicrobial resistance in hospital settings. The high rates of resistance in Klebsiella pneumoniae and Acinetobacter baumannii highlight the importance of rigorous infection control practices and antibiotic stewardship programs in obstetric practice.

5. CONCLUSION

MALDI-TOF MS is a fast and effective diagnostic tool for the identification of bacterial isolates in puerperal sepsis. It provides species-level identification, which facilitates timely treatment decisions. Its ability to identify a broader range of pathogens and its faster turnaround time make it a valuable tool in clinical microbiology, especially in sepsis management.

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