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Early organism identification by Matrix Assisted Laser Desorption Ionization Time of Flight Mass Spectrometry (MALDI-TOF-MS) decreases the time to appropriate antibiotic modifications for common bacterial infections

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SUMMARY

Objective: MALDI-TOF-MS facilitates the identification of microorganisms from positive cultures in a timely and accurate manner. It eliminates the necessity for the application of biochemicals and operates on the principle of proteomics. It decreases the time required to report culture results. Prompt detection and notification of the pathogen, prior to the disclosure of antimicrobial susceptibilities, could potentially shorten the duration until the initial antibiotic adjustment is necessary, thereby influencing patients' clinical prognoses.
Methodology: Fifty patients in the conventional arm and one hundred patients in the interventional arm were compared in a pre and post quasi-experimental study conducted at a tertiary care centre in North India. Patients with positive cultures from medical wards and intensive care units were included. Comparing the time to first antibiotic modification after culture positivity, MALDI-TOF-MS-based identification, and clinical outcomes in both arms was the primary objective. Antibiotic modifications, escalation, and de-escalation were all recorded.
Results: The intervention arm exhibited a substantially shorter median time to first antibiotic modification (2010 mins vs 2905 mins, p=0.002) than the conventional arm. In the interventional group, a total of 44 out of 100 antibiotic modifications were implemented. Of these, 19 (43.3%) were determined solely by the MALDI report, without the anticipation of susceptibility assessments. De-escalation of antibiotics constituted the predominant form of modification (47.4%). The difference between the 27% and 32% mortality rates in the intervention arm and the conventional arm was not statistically significant (p=0.52).
Conclusion: MALDI-TOF-MS facilitates the modification of antibiotics early on. The primary benefit lies in the reduction of superfluous antibiotic usage. Early organism identification and reporting prior to the availability of susceptibility results did not result in any mortality benefit. This strategy, when combined with a strong antimicrobial stewardship programme, can aid in the reduction of antibiotic use.

Keywords: MALDI-TOF-MS, antibiotic modification, antimicrobial stewardship, MALDI TOF microbial identification, Clinical Outcome.

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INTRODUCTION

The discovery of antibiotics significantly extended human life by reducing infection-related deaths. However, misuse and overuse of antibiotics led to Multi-Drug Resistant (MDR) microorganisms, making infections harder to treat. Consequently, combating antimicrobial resistance is essential [1-6].

In the treatment of serious infections caused by multi-drug resistant organisms, early antibiotic therapy has been found to reduce mortality. When antibiotic therapy was started as soon as 3 hours after the onset of sepsis, patients' outcomes improved [7]. However, in the majority of these instances, the treatment is empirical at first because making an etiological diagnosis based solely on clinical symptoms is challenging. However, it is also true that using insufficient or incorrect antibiotics at the outset is linked to increased mortality [8]. This necessitates the development of novel microbiological techniques that can detect organisms early, allowing for the administration of targeted antibiotic therapy.

Clinical microbiology has been transformed by automation. Matrix-Assisted Laser Desorption Ionization Time of Flight Mass Spectrometry is one such automated method (MALDI-TOF-MS). It uses the principles of proteomics and mass spectrometry to aid in the early and precise identification of organisms directly from pure cultures, eliminating the requirement for traditional biochemical processing [9]. It rapidly decreases the turnaround time for identification and communication to the clinician. This technique has a lead time advantage over conventional processing of at least 24 hours, allowing targeted antibiotics to be administered earlier to patients with infections, thereby reducing morbidity and mortality [10].

The demand for pure culture and the inability to produce antibiotic sensitivity patterns are two major drawbacks of MALDI-TOF-MS, while platforms with these capabilities are being researched in the literature [11-13]. As a result, the benefit of knowing the organism sooner is outweighed by the fact that the physician would have to wait a further 24 hours for the sensitivity report anyhow. However, in healthcare settings with an effective Antibiotic Stewardship Program (ASP), MALDI-TOF-MS was a useful tool for reducing antibiotic use, making rational antibiotic choices, lowering healthcare costs, and improving clinical outcomes [14, 15].

Table 1 - Full antibiogram of Gram negative isolates.

Organism	*Amikacin*	*Cefotaxime*	*Ceftazidime*	*Cefoperazone /sulbactam*	*Ciprofloxacin*	*Imipenem*	*Meropenem*	*Piperacillin/ tazobactam*	*Nitrofurantoin (Urine)*	*Only Colistin*
E. coli (29)	15 (51.7%)	3 (10.3%)	3 (10.3%)	14 (48.3%)	1 (3.4%)	20 (69.0%)	12 (41.4%)	13 (44.8%)	15/18 (83.3%)	2 (6.9%)
Klebsiella pneumoniae (39)	6 (15.4%)	1 (2.6%)	1 (2.6%)	10 (25.6%)	3 (7.7%)	17 (43.6%)	13 (33.3%)	9 (23.1%)	7/11 (63.6%)	18 (46.2%)
Acinetobacter baumannii (40)	1 (2.5%)	1 (2.5%)	1 (2.5%)	23 (57.5%)	1 (2.5%)	6 (15.0%)	8 (20%)	1 (2.5%)	0	14 (35%)
Pseudomonas aeruginosa	8 (38.1%)	6 (28.6%)	7 (33.3%)	10 (47.6%)	8 (38.1%)	12 (57.1%)	9 (42.9%)	7 (33.3%)	0	6 (28.6%)

Table 2 - Full antibiogram of Gram-positive isolates.

Orgamism	*Amikacin*	*Amoxycillin-clavulanic acid*	*Cefoxitin*	*Penicillin*	*Ciprofloxacin*	*Erythromycin*	*Gentamycin*	*Linezolid*	*Vancomycin*	*Teicoplanin*	*Nitrofurantoin*
S. aureus (5)	–	1	2	1	2	1	2	5	5	5	–
S. haemolyticus (3)	2	0	1	0	0	-	0	3	3	3	
Enterococcus faecium (7)	–	–	–	1	0	–	1	7	5	5	2/3
Enterococcus faecalis (3)	–	–	–	0	1	–	1	3	3	3	1/2

MALDI-TOF-MS can swiftly identify organisms from culture isolates. However, while it is acknowledged for reducing identification time, whether this translates to early antibiotic modification in the absence of a sensitivity report has yet to be determined. The physician's readiness to make an antibiotic alteration solely based on the MALDI-TOF-MS report, as well as the type of modification performed, will be important to learn about. Furthermore, if it decreases the time it takes to modify antibiotics, it is prudent to observe if this correlates to better clinical outcomes. Thus, we postulate that early reporting of the organism, even prior to the availability of sensitivity data (Table 1 and 2), might, notwithstanding the drawback, shorten the time required for the first antibiotic modification. This early modification has the potential to affect the patients' clinical outcomes.

MATERIAL AND METHOD

This was a pre and post quasi-experimental study conducted at "All India Institute of Medical Sciences, New Delhi", India. A total of 150 patients from medical wards and ICU with positive blood cultures were recruited, with 50 in the conventional arm and 100 participants in the interventional arm. The study focused on evaluating the impact of a specific intervention on clinical outcomes and antibiotic stewardship. In the pre-intervention phase, we observed the conventional reporting system which included reporting the organism identified by MALDI TOF along with the sensitivity when it became available. In the intervention phase, the investigator directly reported MALDI-TOF results to the physician in charge without waiting for routine antibiotics susceptibility reports. This approach aimed to examine how this intervention influenced antibiotic modifications and clinical outcomes by knowing the organism earlier.

A total of 150 patients from medical wards and the ICU with positive blood cultures were recruited, with 50 in the conventional arm and 100 participants in the interventional arm. The study was conducted from 2016 to 2022. Included patients were over 14 years old, had single culture-positive biological samples, and were either on empirical antibiotics or not on antibiotics.

Patients under treatment for another infection, on specific medications (anti-tubercular, antifungal, antiviral), or with modifications based on new cultures were excluded. The primary objective was to compare the conventional and interventional arms with regard to the time to first antibiotic modification following culture positivity, which was the primary aim. Additionally, escalation, de-escalation, and any antibiotic modifications were documented. Furthermore, a comparison of clinical outcomes between these approaches was sought.

Recruitment spanned a six-year period, encompassing all positive cultures, without employing random or consecutive selection. The recruitment process was lab driven, in which when a culture was positive in the microbiology laboratory, investigator went bedside to assess if that was clinically relevant. We recruited only those patients whose clinical conditions matched the positive culture results. Since this was a lab driven recruitment process, the investigator was unaware of the clinical severity of the patients being recruited in either arms of the study.

In the interventional arm, organisms were identified using MALDI-TOF-MS on the same day as culture positivity without sensitivity pattern, with observed time delays in MALDI-TOF-MS reporting and immediate in-charge physician communication by the investigator. Analysis of modification patterns by physician, such as relying on MALDI-TOF-MS or conventional report with sensitivity pattern, was conducted. The conventional arm involved evaluating the conventional reporting practice (MALDI-TOF-MS report and antibiotic susceptibility pattern). All antibiotic susceptibility tests were performed using the disk diffusion method. Time delays in conventional reporting, post-report antibiotic modification delay noted from bedside nursing chart. Until death or discharge, all patients were monitored in order to document final clinical outcomes (Figure 1 for detail description).

Statistical analysis

SPSS version 26 was employed for all computations. Descriptive analysis was conducted, with categorical data expressed as frequencies and percentages, and continuous data presented as means with standard deviations or medians with Interquartile Ranges, as applicable. Significance tests, accounting for assumptions, were employed to compare variables between the conventional and

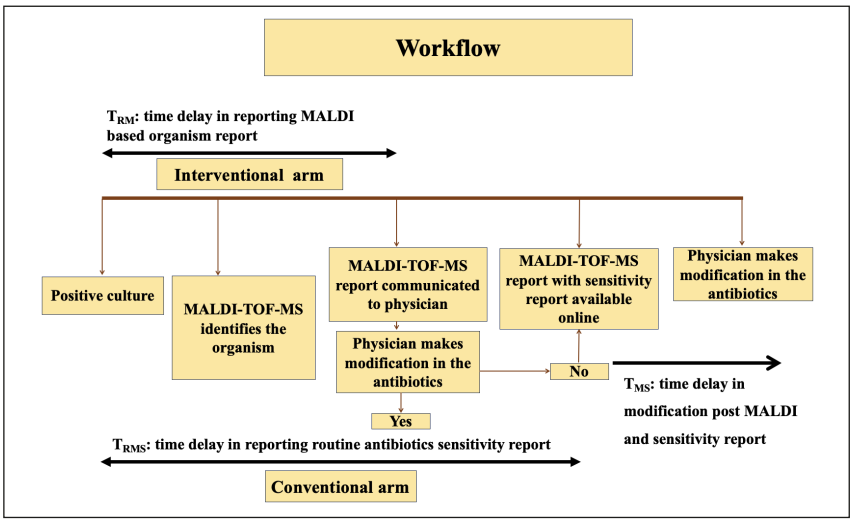

Figure 1
Timeline and workflow for interventional and conventional arm.

interventional arms. Statistical significance was set at a p-value of ≤0.05.

RESULTS

The median age of patients in conventional arm was 48 (28-57) years and 52% participants were male. In interventional arm was 43 (30-57) years with 52% male. Total respiratory samples in both arms were 82 (54.6%) which included sputum and endotracheal aspirate representing an infection profile including community acquired pneumonia, hospital acquired pneumonia and ventilator associated pneumonia. There were 38 (25.3%) urine samples representing urinary tract infections, including both community acquired and

Table 3 - Description of baseline characteristics, primary and secondary outcomes.

Variable		*Conventional arm (50) Median (IQR), n (%)*	*Intervention arm (100) Median (IQR), n (%)*	*p-value*
Age (in years) (CI)		48 (28-57)	43 (30-57)	0.68
Males		26 (52)	52 (52)	<0.001
Specimen	Sputum	22 (44)	60 (60)	0.006
	Urine	10 (20)	28 (28)	
	Blood	11 (22)	6 (6)	
	Pus	7 (14)	6 (6)	
T (RM) (mins)		1803 (1658-1849)	390 (360-420)	<0.001
Antibiotic modifications		32 (64)	44 (44)	0.02
Modification made based on MALDI report only		NA	19/44 (43.2)	
T (PCM) (mins)		NA	270 (110-1020)	
Modification made post sensitivity		32 (64)	29 (29)	<0.001
T (MS) (mins)		1088 (234-2624)	1233 (453-1567)	0.71
T PC (mins)		2905 (1995-4470)	2010 (1350-2939)	0.002
Mortality		16 (32)	27 (27)	0.52

Footnotes: T_{RM} – Time delay in reporting of MALDI-TOF-MS with antibiotic sensitivity was recorded from the online report. T_{MS} – Time delay in modification of antibiotics post availability of MALDI-TOF-MS and sensitivity report was noted from the bedside nursing chart. T_{PC} – Total time delay in modification post culture positivity will also be noted. T_{PCM} – Time delay in modification of antibiotics post availability of MALDI-TOF-MS report will be noted.

catheter-associated urinary tract infection (UTI). Organisms were isolated from 11 (11.3%) blood samples representing bloodstream infection. Pus samples were 13 (8.6%) representing cellulitis, empyema and pyopericardium.

In the conventional arm, the online availability of organism and sensitivity reports took a median of 1803 minutes (30 hours and 3 minutes), whereas in the interventional arm, the investigator communicated the MALDI-TOF-MS report within a median of 390 minutes (6 hours and 30 minutes) ($p<0.001$) to the in-charge physician in person. Antibiotic modifications were more prevalent in the conventional reporting approach, with rates of 64% (32/50) compared to 44% (44/100) in the MALDI-TOF-MS based reporting approach ($p=0.02$). In

Table 4 - Detailed showing the type of antibiotic therapy modifications.

Type of Modification	*Conventional arm n=32*	*Interventional arm n=19*
De-escalation	2 (6.3%)	3 (15.8%)
De-escalation + Modification	13 (40.6%)	6 (31.6%)
Total de-escalations [24/51(47%)]	15 (46.8%)	9(47.3%)
Initiation of new antibiotic therapy (no prior antibiotic use)	5 (15.6%)	4 (21.1%)
Escalation	12 (37.5%)	6 (31.6%)

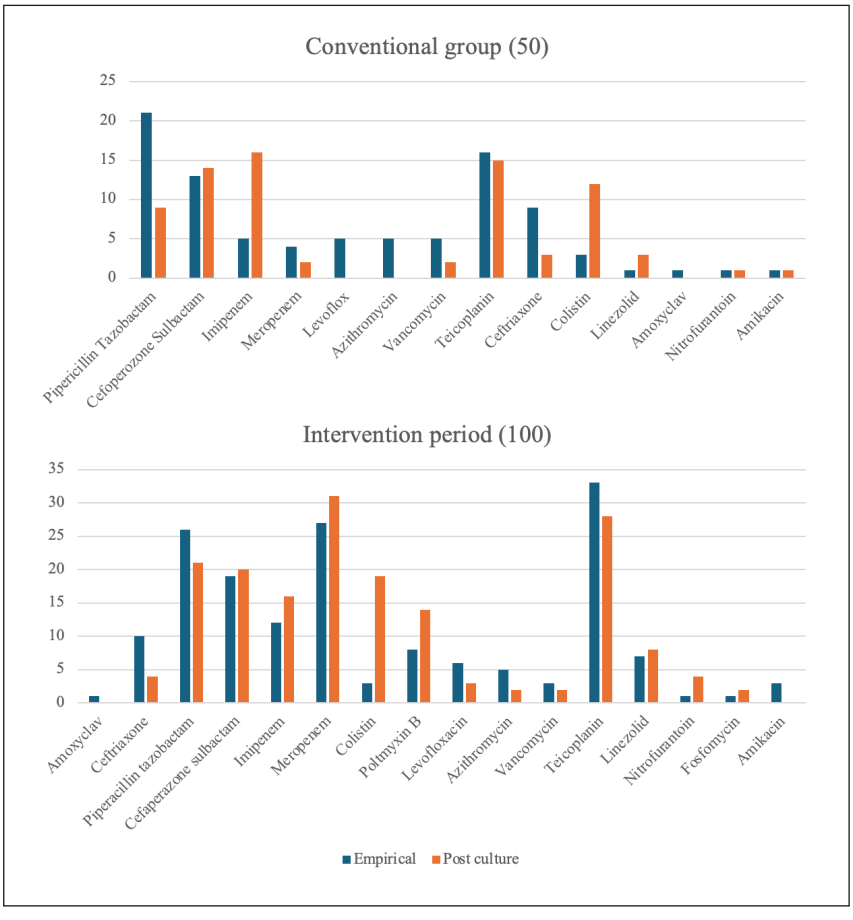

Figure 2
Antibiotics received by patients empirically and post culture sensitivity in the conventional and intervention groups.

Table 6 - Baseline characteristics and outcome description between groups making modification just based on MALDI TOF report and those making after sensitivity report.

Variable		*Modification post MALDI (8)*	*Modification post sensitivity (12)*	*p-value*
Age (years)		36 (18)	41 (14)	0.46
Males		5 (62.5)	7 (58.3)	1
Heart rate		96 (23)	106 (17)	0.26
Mean arterial pressure		81.8 (10.3)	75.8 (14.7)	0.34
Respiratory rate		21 (19-29)	22 (19-25)	0.88
Glasgow Coma Scale		11 (7-15)	15 (10-15)	0.27
Hematocrit		27.7 (7)	30 (4.4)	0.37
White blood cell		8305 (5260-12455)	11605 (9575-16660)	0.08
Creatinine		2.1 (1-4)	0.9 (0.5-4.4)	0.37
Sodium		140.5 (5.8)	137 (6.5)	0.25
Potassium		4.2 (0.6)	4.2 (0.6)	0.78
APACHE		15 (10-24)	12 (9-17)	0.21
Specimen	Sputum	6 (75)	7 (58.3)	0.8
	Urine	2 (25)	4 (33.3)	
	Pus	0	1 (8.3)	
T (RM) (mins)		396.3 (48.7)	432.7 (67.5)	0.23
T PC (mins)		1620 (540-2880)	2920 (2153-3660)	0.02
Mortality		2 (25%)	5 (41.7%)	0.59

Footnotes: T_{RM} – Time delay in reporting of MALDI TOF with antibiotic sensitivity was recorded from the online report. T_{MS} – Time delay in modification of antibiotics post availability of MALDI TOF and sensitivity report was noted from the bedside nursing chart. T_{PC} – Total time delay in modification post culture positivity will also be noted. T_{PCM} – Time delay in modification of antibiotics post availability of MALDI TOF report will be noted.

Table 5 - Comparison of baseline characteristics and outcomes between antibiotic modification groups.

Variable		*No Modification (30)*	*Modification (20)*	*p-value*
Age (years)		41.3 (17.8)	39.5 (15.6)	0.7
Males		12 (40)	12 (60)	0.17
Heart rate		90 (18)	101 (19)	0.04
Mean arterial pressure		77 (13.1)	78.2 (13)	0.75
Respiratory rate		19 (18-24)	22 (19-25)	0.26
Glasgow Coma Scale		15 (8-15)	15 (8-15)	0.75
Hematocrit		28.9(6.9)	29.1(5.6)	0.92
White blood cell		10650 (8580-14670)	9945 (7640-14790)	0.69
Creatinine		2.3 (0.8-4)	1.2(0.6-3.9)	0.37
Sodium		136 (8.1)	138.5(6.3)	0.25
Potassium		4.5 (0.9)	4.1(0.6)	0.11
APACHE		15 (7-23)	12 (10-18)	0.98
Specimen	Sputum	20 (66.7)	13 (65)	0.63
	Urine	10 (33.3)	6 (30)	
	Pus	0	1 (5)	
T (RM) (mins)		421.9 (75.2)	418.1 (62.04)	0.76
Mortality		7 (23.3)	7 (35)	0.81

Footnotes: T_{RM} – Time delay in reporting of MALDI TOF with antibiotic sensitivity was recorded from the online report. T_{MS} – Time delay in modification of antibiotics post availability of MALDI TOF and sensitivity report was noted from the bedside nursing chart. T_{PC} – Total time delay in modification post culture positivity will also be noted. T_{PCM} – Time delay in modification of antibiotics post availability of MALDI TOF report will be noted.

comparison to the conventional arm, the median time to first antibiotic modification was significantly reduced in the interventional arm (2010 min vs. 2905 min, p = 0.002) (Table 3).

Antibiotics modification was studied in both groups. Overall, in the interventional arm, major modification included de-escalation of antibiotics in 47.4% (9/19) of patients. In the conventional arm, major modification consisted of de-escalation with modification of antibiotics in 40.6% (13/32) and escalations in 37.5% (12/32), while new antibiotics were initiated in 15.6% (5/32) of cases. In the intervention arm, MALDI-TOF-MS driven modifications encompassed 31.6% (6/19) de-escalations, 31.6% (6/19) escalations, and 21.1% (4/19) initiation of new antibiotics (Table 4). Details of the antibiotics received by patients empirically and post culture sensitivity in the conventional and intervention groups are shown in Figure 2. The final patient outcome in both arms were compared. The interventional arm had a 27% mortality rate compared to the 32% mortality rate in the conventional arm; however, this difference was not statistically significant (p=0.52) (Table 3). A subgroup analysis of 50 patients in the interventional arm, with complete clinical and laboratory data was performed. Within this subgroup, we observed no difference in mortality rates between the modification and non-modification groups, or between modifications guided solely by MALDI and those performed after receiving sensitivity reports. This groups had similar clinical severity at baseline as assessed by APACHE score (Table 5 and 6).

DISCUSSION

The use of automation in diagnostic microbiology has revolutionized the field by providing rapid and accurate results, in contrast to the lengthy turnaround times associated with traditional approaches. In our study, we aimed to investigate the effectiveness of MALDI-TOF-MS, a proteomics-based tool that quickly identifies organisms, thereby eliminating the need for traditional biochemical tests. The usefulness of MALDI-TOF-MS for identifying organisms in various labs is frequently overlooked as the communication of results is usually delayed until antibiotic sensitivity patterns are accessible.

The objective of our study was to emphasize the clinical significance of direct organism reporting through MALDI-TOF-MS and its potential impact on both antibiotic stewardship and patient outcomes. When organism identification using MALDI-TOF-MS become accessible, clinicians could make use of the local antibiogram to guide their antibiotic choices. Our findings revealed that antibiotic adjustment in the intervention group took significantly less time (33 hours and 30 minutes) compared to the conventional group (48 hours and 25 minutes), which is consistent with the results of previous studies and meta-analyses [12, 14, 16].

In a recent meta-analysis by Chia Hung Yo et al. compared conventional reporting to reporting using MALDI-TOF-MS based organism identification. They assert that a combined analysis of 13 studies revealed a reduction of 5.07 hours in the time required for effective antibiotic therapy [17]. This further supports the notion that direct organism reporting through MALDI-TOF-MS can lead to faster antibiotic adjustments, ultimately improving patient outcomes.

According to studies, the utilization of MALDI-TOF-MS in conjunction with a robust antimicrobial stewardship program has been shown to reduce mortality rates, enhance early de-escalation rates, and shorten the time needed to administer appropriate antibiotic therapy [14, 17]. In our study, the prevalent form of antibiotic modification done was de-escalation. Overall, the rate of de-escalation in the interventional group was 47%. The MALDI-TOF-MS report resulted in a greater percentage (15.8%) of pure de-escalations compared to the conventional group (6.3%). Indicating that MALDI-TOF-MS was most useful in de-escalation of antibiotics, as soon as physician aware of the developing organism. The majority of patients in our study were from ICU and received empiric broad-spectrum antibiotics. MALDI-TOF has been shown to safely and effectively reduce hospitalization costs and antibiotic resistance in ICU patients [18-20]. Our results showed a decrease in time for appropriate antibiotic therapy, but no benefit in mortality was observed. Participants in both categories of our study had high APACHE scores at baseline. and multiple confounding factors for overall mortality, which could be a potential reason for the lack of mortality benefit. Although, modifying antibiotics early based on MALDI-TOF-MS reports may be beneficial, as indicated by data [14, 17].

Through our study we were able to generate an antibiogram and make the clinicians aware of the local susceptibility pattern (Table 7). This helped in choosing appropriate empirical antibiotics. In terms of baseline characteristics and clinical severity, the two groups were comparable. The fact that an organism had grown on culture made the physician to actively trace the susceptibility report. Through the application of MALDI-TOF-MS technology, we were able to demonstrate a substantial increase in the frequency of de-escalations, as confirmed by the comprehensive organism identification report produced by this advanced diagnostic technique. This noteworthy achievement underscores the invaluable role of MALDI-TOF-MS in bolstering the effectiveness of the Antimicrobial Stewardship Program. We were able to highlight the importance of early organism identification by MALDI-TOF-MS and spread awareness about the utility of automation in microbiology laboratory. Most of the similar studies have focussed on one infection, i.e. bloodstream infections, but through our study we have explored the utility across different infection profiles.

However, the research is not devoid of limitations. Due to the absence of randomization, alterations in the standard of care during the study period might not have been accounted for in our study. We are unaware of any substantial alterations to the standard of care. Furthermore, changes in hospital ecology and patterns of resistance can happen gradually. Additionally, the duration until effective therapy and optimal therapy can be achieved is constrained due to the fact that antimicrobial administration periods were exclusively documented for inpatients. Prior to admission,

Table 7 - Detailed organism profile depending on the site of infection.

Sample/Site of infection	*Organism*	*Conventional arm*	*Intervention arm*
Respiratory (82)	*Acinetobacter baumanii* (42.7%)	11 (50%)	24 (40%)
	Klebsiella pneumoniae (29.3%)	5 (22.7%)	19 (31.7%)
	Pseudomonas aeruginosa (19.5%)	5 (22.7%)	11 (18.3%)
	Escherichia coli (8.5%)	1 (4.5%)	6 (10%)
Urine (38)	*Escherichia coli* (47.4%)	5 (50%)	13 (46.4%)
	Klebsiella pneumoniae (28.9%)	1 (10%)	10 (35.7%)
	Enterococcus faecium (7.9%)	1 (10%)	2 (7.1%)
	Enterococcus faecalis (5.3%)	2 (20%)	0
	Acinetobacter baumanii (2.6%)	0	1 (3.6%)
	Pseudomonas aeruginosa (2.6%)	0	1 (3.6%)
	Enterobacter hormaechi (2.6%)	1 (10%)	0
	Citrobacter freundii (2.6%)	0	1 (3.6%)
Blood (17)	*Enterococcus faecium* (23.5%)	3 (27.3%)	0
	S. haemolyticus (17.6%)	1 (9.1%)	2 (33.3%)
	Acinetobacter baumanii (17.6%)	2 (18.2%)	1 (16.7%)
	Klebsiella pneumoniae (11.8%)	1 (9.1%)	1 (16.7%)
	Staphylococcus aureus (11.8%)	1 (9.1%)	1 (16.7%)
	Salmonella typhi (5.9%)	1 (9.1%)	0
	Escherichia coli (5.9%)	1 (9.1%)	0
	Enterococcus faecalis (5.9%)	1 (9.1%)	1 (16.7%)
Pus (13)	*Pseudomonas aeruginosa* (30.8%)	3 (42.9%)	1 (16.7%)
	Escherichia coli (23.1%)	1 (14.3%)	2 (33.3%)
	Staphylococcus aureus (23.1%)	1 (14.3%)	2 (33.3%)
	Klebsiella pneumoniae (15.4%)	1 (14.3%)	1 (16.7%)
	Acinetobacter baumanii (7.7%)	1 (14.3%)	0

patients who received treatment outside of hospitals, in extended care facilities, clinics, or emergency departments did not have the duration of antimicrobial administration documented. As a result, it is possible that a higher proportion of patients received optimal or efficacious treatment before their admission. Additionally, prescribers were granted discretion in determining the number and scheduling of repeat cultures required to document microbiologic clearance, which may have contributed to variation between groups. We did not evaluate the effects of additional antibiotic adjustments in patients who underwent MALDI-TOF-MS-based modifications and received further antibiotic changes following sensitivity reports in the intervention arm. Although the numbers in the subgroups (clinical syndromes) are small and their impact on the outcome may be limited, it is crucial to consider this potential bias when interpreting the results, especially when comparing mortality benefits.

In summary, this study emphasises the potential benefits of MALDI-TOF-MS in guiding antimicrobial therapy. Further research in this area is needed to fully explore the impact of early organism identification on the patient outcomes. Time to antibiotic modification can be more effectively reduced by platforms which can directly identify micro-organisms from clinical samples without the need for pure culture and provide susceptibility results.

CONCLUSIONS

This study underscores the critical importance of timely and accurate identification of microbial pathogens which further helps in early modification of antibiotics. Despite the current limitation of not providing sensitivity patterns, MALDI-TOF-MS helps in the de-escalation of antibiotics. When integrated with an effective antimicrobial stewardship program, this approach has the potential to mitigate the unnecessary use of antibiotics. Readily available antibiogram may also help in choosing appropriate antibiotics when the organism is known. Whether this has any mortality benefit needs to be more systematically analyzed.

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Disclosure
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Conflict of interest
The authors declare no conflict of interest.

Ethical approval
We obtained approval from the Ethics Committee of the All India Institute of Medical Sciences, New Delhi (IECPG-380/28.09.2017, RT-7/16.10.2017) on October 27, 2017. An extension of the ethics approval (IECG-380/28.09.2017, RT-7/16.10.2017, OT-06/28.11.2019) was subsequently acquired on November 29, 2019.

Author's contribution
The study was conducted by a team from the Department of Medicine and Microbiology at AIIMS, New Delhi. Dr. Vishakh C Keri led data handling and manuscript preparation. Dr. Ankesh Gupta aided in manuscript preparation. Dr. Sarita Mohapatra provided lab analysis. Dr. Manish Soneja reviewed clinical aspects. Drs. Arti Kapil, Immaculata Xess, and Naveet Wig offered critical feedback. Dr. Bimal Kumar Das contributed to design and analysis. All approved the final manuscript.

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