

# Impact of Implementing Matrix-Assisted Laser Desorption Ionization Time of Flight Mass Spectrometry (MALDI-TOF) at University of Texas Medical Branch (UTMB) – Galveston.



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## Introduction

- MALDI-TOF is a mass spectrometry method used to rapidly ID a microorganism based on its unique protein patterns and mass. By utilizing MALDI-TOF, the idea is that more rapid reporting of pathogen ID's can be achieved, thus allowing for a quicker time to effective treatment for optimal patient care outcome.
- In June 2014, the Division of Clinical Microbiology of the University of Texas Medical Branch at Galveston (UTMB) implemented MALDI – TOF, as part of routine clinical microbiology workflow as a means to reduce turnaround-time for microbial identification.
- The purpose of the study was to evaluate the impact of MALDI-TOF MS implementation in the UTMB Clinical Microbiology Laboratory.

## Aims

- Aim 1 analyzed the length of time it took for Clinical Microbiology Laboratory to identify an organism using MALDI-TOF.
- Aim 2 measured the impact of patients' hospital stays, based on the potential of a more rapid organism IDs.
- Aim 3 focused on cost-effective microbial identification for the Clinical Microbiology Laboratory.

## Methods

- A retrospective study using UTMB's electronic medical records (EPIC) and Clinical Microbiology Laboratory Information System (LIS) CERNER was used to gather the data for each respiratory isolate. Organism ID, turnaround times, patient length of stay and cost analysis were collected and were used when comparing the conventional biochemical workflow versus MALDI-TOF workflow.
- The data comparison timeframe for the study was eight months (pre- and post MALDI-TOF implementation); from June 2013 to January 2015.
- A t-test was used to compare the organism ID turnaround times of MALDI-TOF workflow vs. turnaround times of the conventional workflow to observe any difference in the results. The same statistical test was used to evaluate the two workflows for reduced length of hospital stay for patients due to rapid organism ID. A cost analysis was performed to determine the organism identification via MALDI-TOF is more cost effective versus previously utilized identification method, Vitek 2.

## Turnaround Time for organism ID

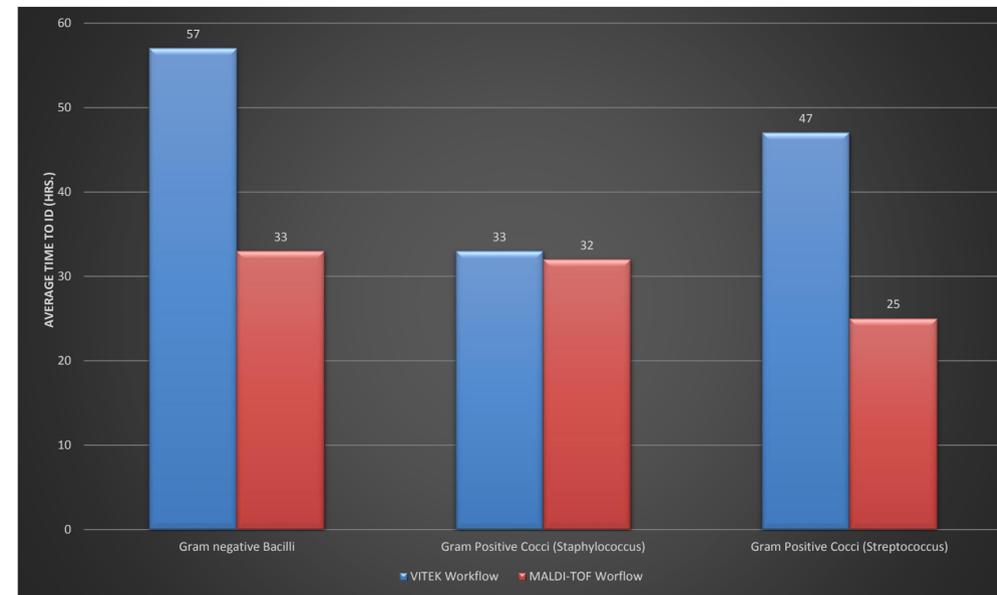


Fig. 1. Difference in time to ID isolates between conventional workflow and MALDI-TOF workflow.

## Cost analysis

Test	Cost of Individual Test	Estimated time for sample preparation (Hrs.)**	Employee hourly rate with benefits	Estimated cost in staff time per test	Total cost per test
<b>Conventional</b>					
PathoDx	\$ 7.13	0.02*	\$ 30.00	\$ 0.60	\$ 7.73
Rapid NH	\$ 5.71	0.12*	\$ 30.00	\$ 3.60	\$ 9.31
Latex Agglutination. VITEK	\$ 1.37	0.02*	\$ 30.00	\$ 0.60	\$ 1.97
	\$ 8.02	0.1	\$ 30.00	\$ 3.00	\$ 11.02
<b>MALDI-TOF</b>					
Latex Agglutination.	\$ 1.37	0.02*	\$ 30.00	\$ 0.60	\$ 1.97
MALDI-TOF	\$0.44	0.05	\$ 30.00	\$ 1.50	\$ 1.94

Fig. 2. Cost analysis comparison between conventional biochemical tests versus MALDI-TOF MS.

## Results

- Aim 1: The MALDI-TOF workflow showed a difference in average time to organism ID in comparison to the conventional biochemical workflow for both gram-negative bacilli and Streptococcus spp. groups ( $p < 0.05$ ). Average time to ID for both workflow were calculated in hours rather than days. Overall, the MALDI-TOF workflow reduced the time to ID organisms by ~ 24 hours for the group gram-negative bacilli and Streptococcus spp. For the group Staphylococcus spp., the MALDI-TOF workflow did not show a difference in time to ID organism when compared to the conventional biochemical workflow ( $p > 0.05$ ).
- Aim 2: The results from the study showed that there was not a significant difference in length of stay between the conventional biochemical workflow and MALDI-TOF workflow. There were several factors that contributed to this outcome. These factors include: short timeframe of the study (only 8 months), diverse patient population where respiratory infection is a comorbidity and finally removing respiratory samples from patients that were not admitted (office visits).
- Aim 3: Our study showed that when compared against the previous conventional biochemical workflow, MALDI-TOF workflow was a cost effective method for microorganism identification in two ways. First, price per test for organism identification in the MALDI-TOF workflow is less than \$2.00 while the price per test for the conventional biochemical workflow averaged at \$7.50. Second, there are fewer tests in the MALDI-TOF workflow than the conventional biochemical workflow (2 vs. 4).

## Conclusions

- The result of the study demonstrated that even during the implementation phase of MALDI-TOF MS, it can outperform the previously established conventional ID methods in terms of reduced turnaround time for organism identification, especially for gram-negative bacilli.
- Also, the study showed that by implementing MALDI-TOF in the clinical microbiology lab; decreased identification times for respiratory isolates can be achieved with reduced cost for both patients and clinical laboratory.
- Finally, new databases of protein spectra are becoming available through in-house testing and manufacturer updates. In this manner, there is the potential to reduce some of the limitations of MALDI-TOF MS, such as identification of organisms with identical protein patterns.