

Quality Improvement Study to Evaluate the Effects of Implementation of a Rapid Identification Diagnostic Test on Multidrug-Resistant Bloodstream Infections at a Large Academic Institution.

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Quality Improvement Study to Evaluate the Effects of Implementation of a Rapid Identification Diagnostic Test on Multidrug-Resistant Bloodstream Infections at a Large Academic Institution

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BACKGROUND / INTRODUCTION

Bloodstream infections (BSI) are severe infections with a high associated patient mortality. Studies show that gram negative bacteria contribute to approximately 25% of BSI and have become increasingly resistant to antibiotic therapy and exhibit extended-spectrum beta-lactamases (ESBL) and carbapenem-resistance genes. Vancomycin-resistant Enterococcus (VRE) BSI also appear to be becoming more prevalent. The introduction of a rapid nucleic acid identification test (NAT) for BSI that identifies the bacteria and its resistance markers promises results with a turnaround time of 2 hours. This allows for prompt modification of the patient's antibiotic therapy. This test was introduced to the Lehigh Valley Health Network Cedar Crest and Muhlenberg campuses on April 13th, 2015.

OBJECTIVES

This retrospective study sought to analyze the effect of the NAT compared to traditional multidrug-resistance (MDR) identification methods in the following areas:

- Time to result
- Time to appropriate antibiotics
- Impact on 30-day mortality rates

METHODS

69 patients qualified for retrospective study

Pre-NAT Intervention
(April 13th, 2014 – April 12th, 2015)
n=24

Post-NAT Intervention
(April 13th, 2015 – April 12th, 2016)
n=45

- NAT data was received from the Health Network Laboratories
- Results were analyzed for appropriate antibiotic escalation from time for the following:
 - Antibiotic initiation
 - Blood culture result
 - Blood culture collection
- Basic statistical measures were implemented to assist in interpreting results

RESULTS

Table 1: Results of MDR Organism Identification and Appropriate Escalation of Antibiotics before and after Introduction of NAT

	Pre- intervention N = 22	Post- intervention N = 45	P Value
Mean time to identification of MDR organism (±SD), hours	68.4 (10)	27.6 (18)	<0.001
Mean time to appropriate antibiotics from antibiotic initiation (±SD), hours	76.3 (81)	92.9 (130)	0.529
Mean time to appropriate antibiotics from MDR organism identification (±SD), hours	-26.7 (33)	6.8 (29)	<0.001
Mean time to appropriate antibiotics from blood culture collection (±SD), hours	41.8 (30)	34.3 (32)	0.364
Mean time to appropriate antibiotics from MDR identification with Infectious Diseases (ID) consultation (±SD), hours	-32.6 (29)	-5.2 (26)	0.006

**Excludes patients with death prior to availability of blood culture results

Figure 1: Time to Appropriate Antibiotic Escalation from Blood Culture Collection Period

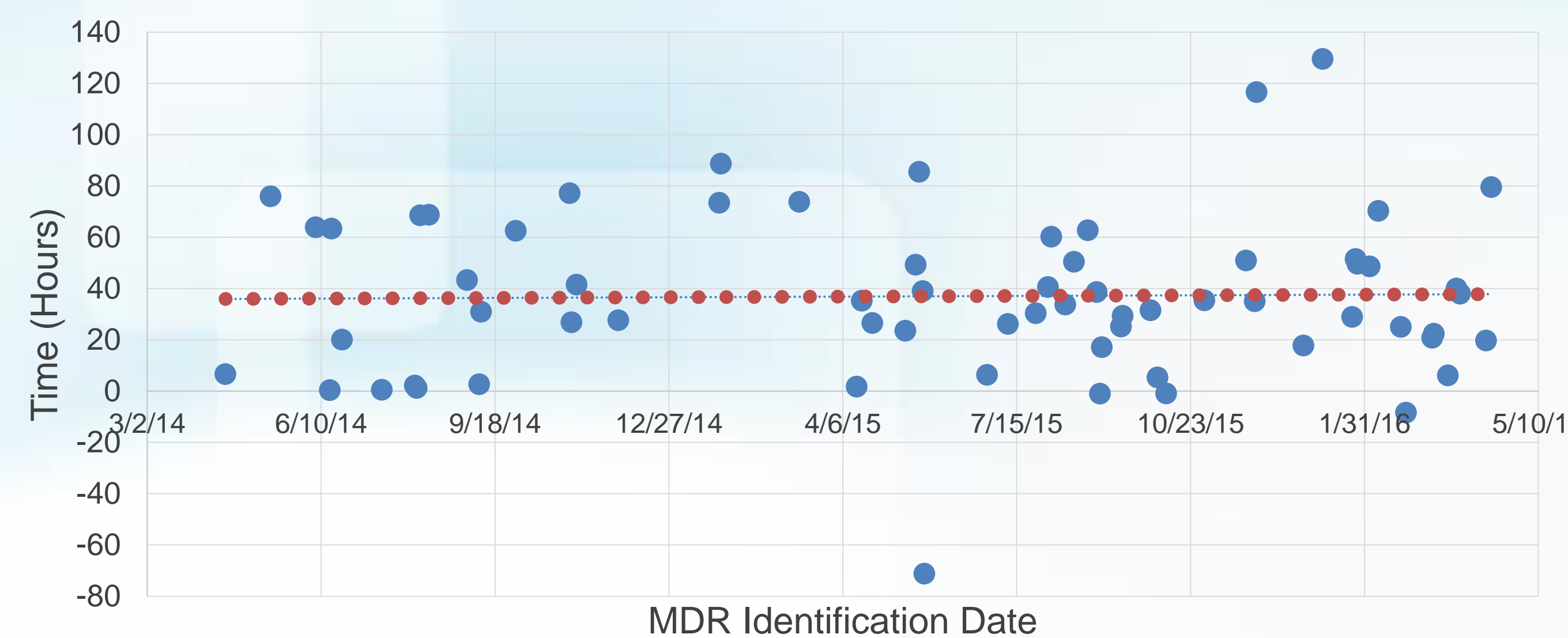
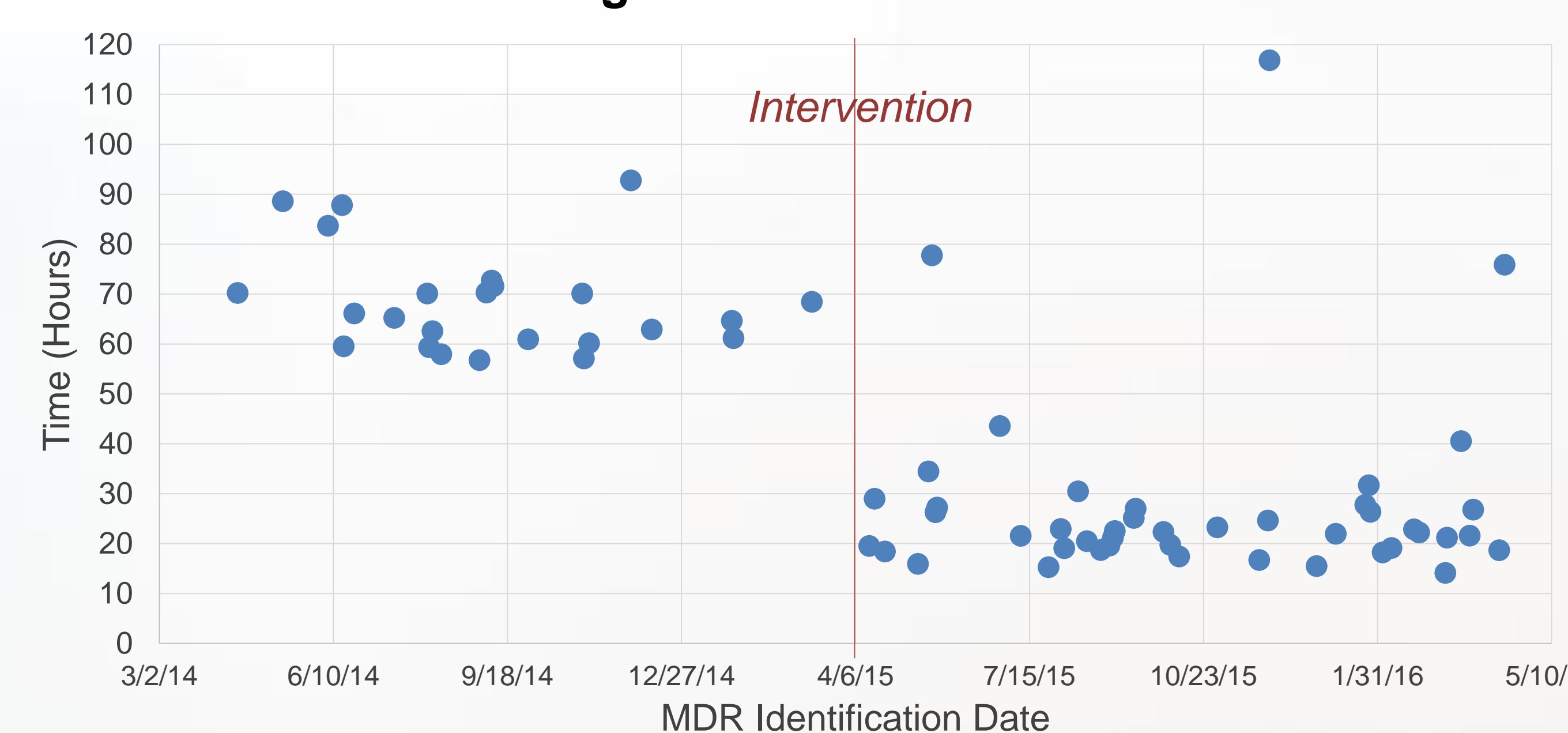


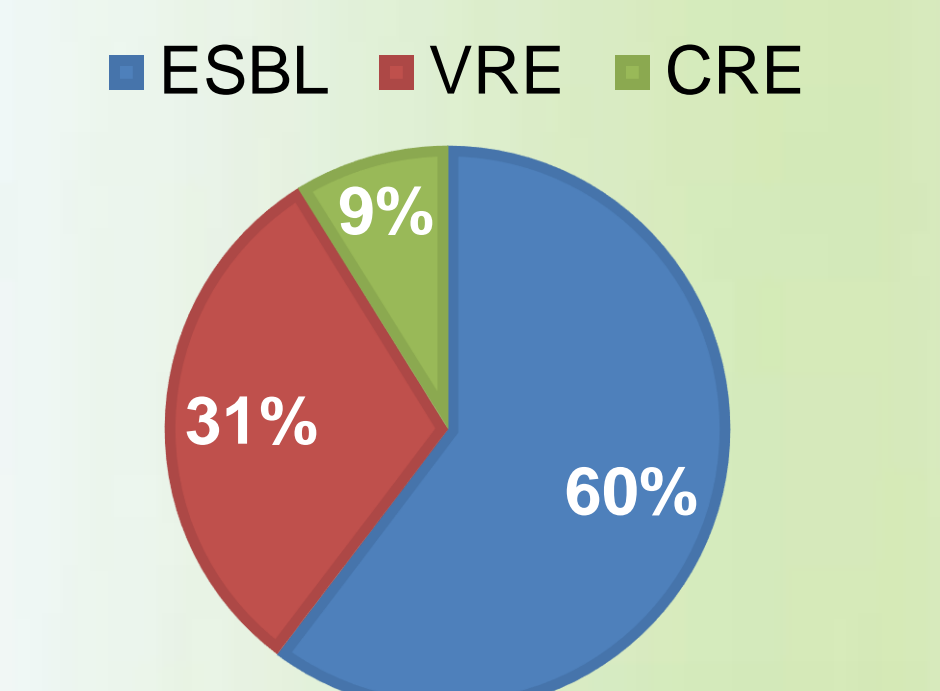
Figure 2: Time to Blood Culture Result for MDR Organism Identification



DISCUSSION

- Time to identify the MDR organism from collection of the blood sample was significantly lower using the NAT
- Average time to appropriate antibiotics from blood culture collection date showed a trend toward improvement
- Time to appropriate antibiotics after identification of a MDR organism did not improve significantly in the post-intervention cohort
 - Providers may not be familiar with NAT and more education may be necessary
 - More patients in the pre-intervention cohort had an ID consult or an antecedent culture revealing a MDR organism
- Of the MDR organisms identified in this study, ESBL seemed the most prevalent
- 30-day patient mortality did not significantly change after NAT implementation
 - Larger studies with more data is needed to address this topic

TOTAL MDR ORGANISMS IDENTIFIED



*Abbreviations: Extended-spectrum beta-lactamase (ESBL), Vancomycin-resistant Enterococcal (VRE), and Carbapenem-resistant Enterobacteriaceae (CRE)

CONCLUSIONS

The study shows that the NAT for BSI provides rapid results compared to traditional identification methods. This study in particular was limited by a small sample size (n=69) with a disproportionate number of participants per cohort. Therefore, support from larger studies is required to confirm results.

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