

Presentation Type:

Poster Presentation

Whole-Genome Sequencing for Investigation of Possible Hospital Transmission of Tuberculosis

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Background: Whole-genome sequencing (WGS) is increasingly used in epidemiological investigations of infectious diseases. We describe the use of WGS to identify drug-resistance variants of tuberculosis (TB) and to determine potential transmission between patients at an academic medical center. **Methods:** Chart review and interviews of patients and healthcare workers along with WGS of *M. tuberculosis* isolates from the patients. **Clinical information:** In June 2019, patient A, a 20-year-old college student born in the United States was admitted with massive hemoptysis. The patient was identified as having active, cavitary TB that was acid-fast smear positive, and the mycobacterial culture grew *M. tuberculosis*. Patient B, a 40-year-old foreign-born patient with advanced lung cancer was acid-fast smear negative, but mycobacterial cultures were positive for *M. tuberculosis*. The 2 patients had overlapping stays in the medical intensive care unit. There was concern that patient B had acquired TB during her stay in the hospital from patient A, who was highly infectious. WGS showed that the mycobacterial isolates from the 2 patients were unrelated. Patient A was a student at a college campus where the state health department had previously issued a health advisory concerning active pulmonary TB in a student; and 7 additional TB cases were subsequently identified through contact investigation. Patient A denied any contact with other persons who were part of the outbreak and had not been included in the contact investigations of any of the cases. Of the 8 outbreak cases, 6 had been seen at our institution and had isolates available for testing. WGS showed that these 6 isolates matched patient A, establishing that she was part of the college

outbreak. **Conclusions:** WGS was useful in establishing the source of *M. tuberculosis* infection in a patient who did not have known exposure to TB and in demonstrating that transmission of TB did not occur in the hospital.

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You Cannot Manage What You Cannot Measure—Developing Central Sterilizing Performance Metrics

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Background: Metrics are critical to healthcare, particularly in areas that are highly process oriented. Our hospital's central sterilizing department functions on standardized processes that have almost no industry specific measurements. Furthermore, the department had no formal internal method for process performance evaluation. A multiphase 6 Sigma DMAIC project was initiated in February 2019 in the central sterilizing department, with 'phase 1' being the development of performance metrics to evaluate current state and track future improvement. **Methods:** A DMAIC team was formed and completed a data inventory that included identifying all existing data sources pertaining to central sterilizing. Sources identified as reliable included count of daily surgical cases, counts of defects based on surgical services communication logs, number of surgical trays processed in the central sterilizing department, and the number of unsterile trays in the department at the start of each 7:00 A.M. shift. **Results:** A multidisciplinary team including surgeons and senior leadership formed the DMAIC team. Using identified data sources and input from frontline staff

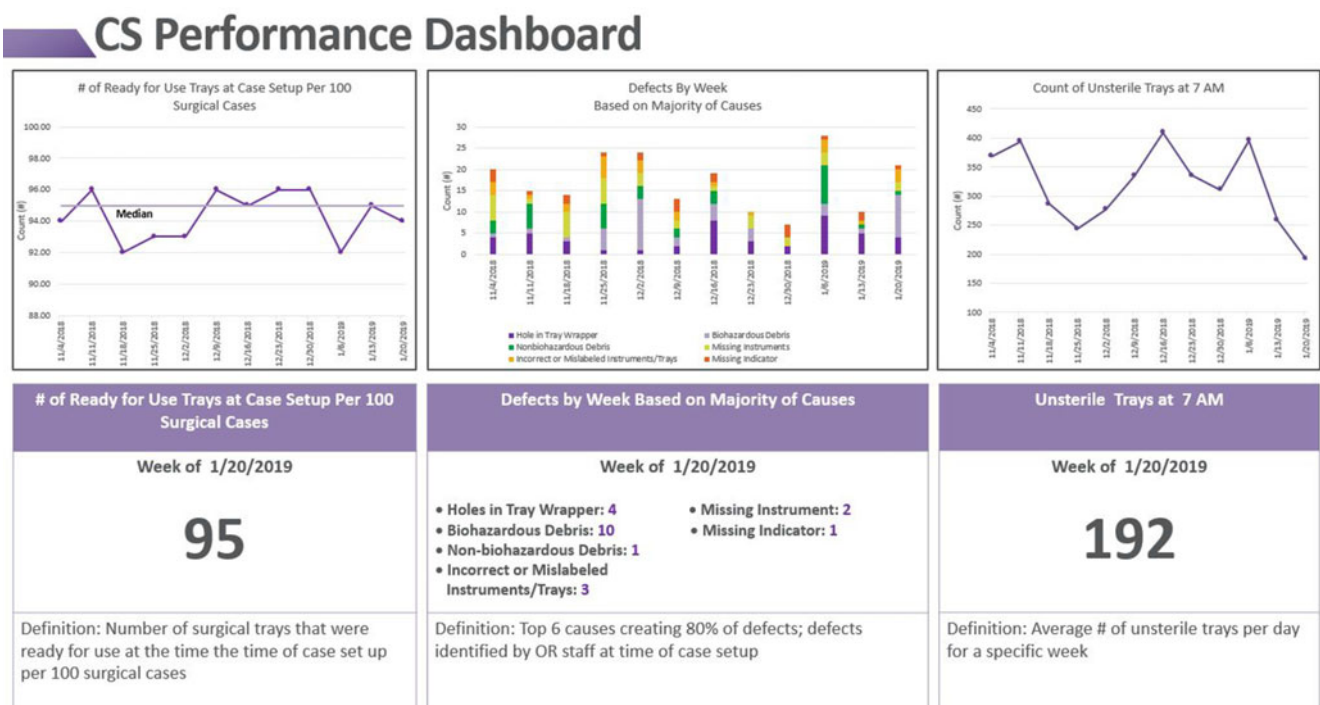


Fig. 1.