

of whom were confirmed positive. Of the other 26 patients not tested, none developed measles infection. Exposures were minimized, and there were no secondary measles transmissions among patients. **Conclusions:** Using the ICS and development of tools and resources to prevent measles transmission, including a patient triage algorithm, the JHH team successfully identified, isolated, and evaluated patients with high suspicion for measles while minimizing exposures and secondary transmission. These strategies may be useful to other institutions and locales in the event of an emerging or reemerging infectious disease outbreak.

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**Presentation Type:**

Poster Presentation

**Use of Next-Generation Sequencing to Rule Out Cluster of *Pseudomonas aeruginosa* in a Cardiac Critical Care Unit**

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**Background:** In spring of 2019, 2 positive sputum cases of *Pseudomonas aeruginosa* in the cardiac critical care unit (CCU) were reported to the UFHJ infection prevention (IP) department. The initial 2 cases, detected within 3 days of each other, were followed shortly by a third case. Epidemiological evidence was initially consistent with a hospital-acquired infection (HAI): 2 of

the 3 patients roomed next to each other, and all 3 patients were ventilated, 2 of whom shared the same respiratory therapist. However, no other changes in routine or equipment were noted. The samples were cultured and processed using Illumina NGS technology, generating 1–2 million short (ie, 250-bp) reads across the *P. aeruginosa* genome. As an additional positive control, 8 *P. aeruginosa* NGS data sets, previously shown to be from a single outbreak in a UK facility, were included. Reads were mapped back to a reference sequence, and single-nucleotide polymorphisms (SNPs) between each sample and the reference were extracted. Genetic distances (ie, the number of unshared SNPs) between all UFHJ and UK samples were calculated. Genetic linkage was determined using hierarchical clustering, based on a commonly used threshold of 40 SNPs. All UFHJ patient samples were separated by >18,000 SNPs, indicating genetically distinct samples from separate sources. In contrast, UK samples were separated from each other by <16 SNPs, consistent with genetic linkage and a single outbreak. Furthermore, the UFHJ samples were separated from the UK samples by >17,000 SNPs, indicating a lack of geographical distinction of the UFHJ samples (Fig. 1). These results demonstrated that while the initial epidemiological evidence pointed towards a single HAI, the high-precision and relatively inexpensive (<US\$1500) NGS analysis conclusively demonstrated that all 3 CCU *P. aeruginosa* cases derived from separate origins. The hospital avoided costly and invasive infection prevention interventions in an attempt to track down a single nonexistent source on the CCU, and no further cases were found. This finding supports the conclusion reached from the NGS that this represented a pseudo-outbreak. Furthermore, these genomes serve as an ongoing record of *P. aeruginosa* infection, providing even higher resolution for future cases. Our study supports the use of NGS technology to develop rational and data-driven strategies. Furthermore, the ability of NGS to discriminate between single-

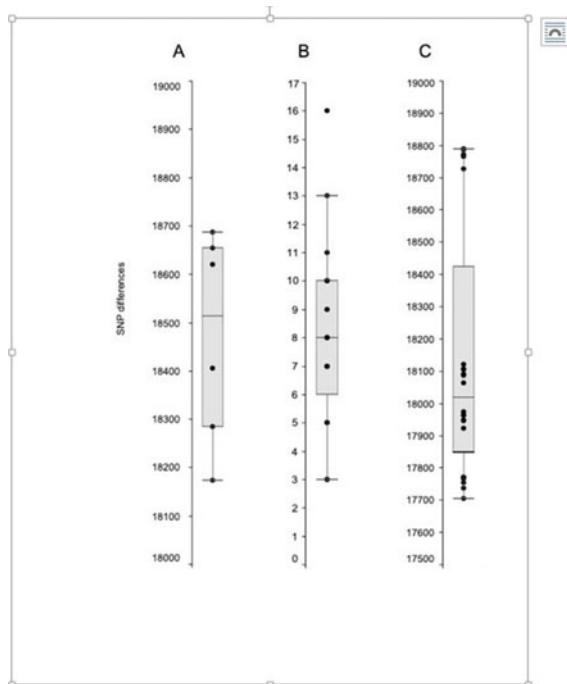


Figure 1. Boxplots of SNP differences among samples from A) UFHJ; B) UK; C) UFHJ vs. UK.

**Fig. 1.**

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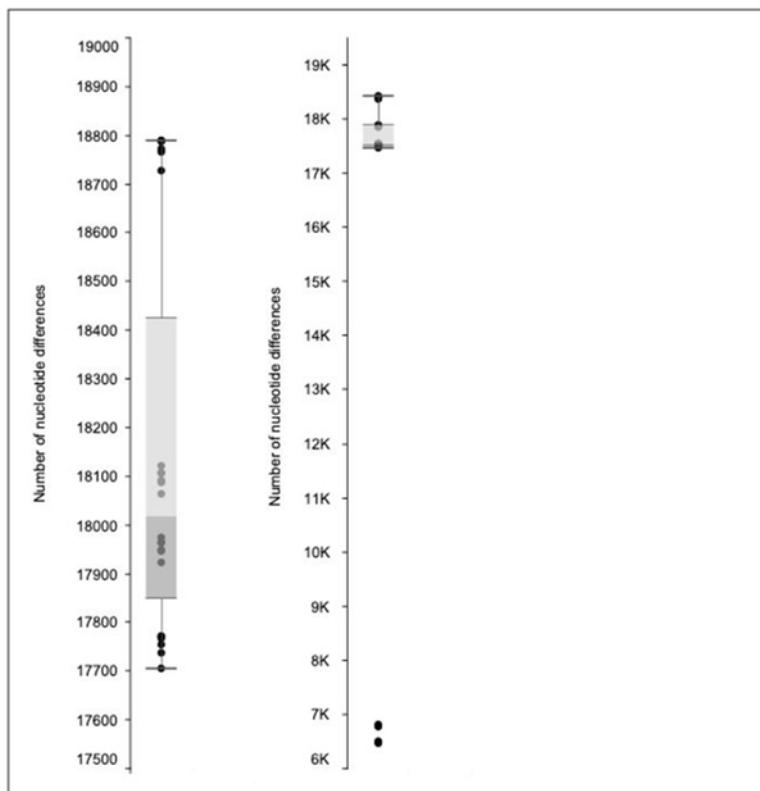


Figure 2. Boxplots of the number of nucleotide differences (y-axis) between UK samples and CCU samples using the PAO1 reference (left) and PAK reference (right)

Fig. 2

source and multiple-source outbreaks can prevent inaccurate classification and reporting of HAIs, avoiding unnecessary costs and damage to hospital reputations.

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#### Presentation Type:

Poster Presentation

#### Using Whole-Genome Sequencing to Improve Surveillance Measures: Case Study of Methicillin-Resistant *Staphylococcus aureus* (MRSA) in a Florida Hospital

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**Background:** The CDC considers methicillin-resistant *Staphylococcus aureus* (MRSA) one of the most important hospital-acquired infections (HAIs) in the United States. However, infection control departments (ICDs) often rely on subjective data to determine whether multiple MRSA cases are a true outbreak and whether the hospital is responsible (community- vs hospital-acquired). **Objective:** Our objective was to determine whether

whole-genome sequencing (WGS) of MRSA provided new insights into transmission dynamics at large, inner-city hospital in Jacksonville, Florida. **Methods:** Over a 4-month period, MRSA samples were obtained from 44 infected patients at 3 campuses within a single hospital system. Limited nonpatient identifying information was obtained, including date of collection, campus, unit, reason for admission, and days post admission (DPA) of MRSA diagnosis. Whole-genome sequences were generated using the Illumina platform. Raw reads were processed, and genetic distances were calculated and used to identify genetically linked bacterial infections using FoxSeq version 1.0 software. **Results:** Based on their length of stay, 10 patients were reported by the ICD as obtaining an HAI. Three distinct "episodes" were evident in which >5 MRSA cases were observed within a 3–5-day period. Genomic analysis identified 5 clusters of linked infections: 4 clusters contained 2 patients and another contained 3. Of these clusters, only 1 contained multiple cases that were reported as HAIs; however, because these cases were separated by 2 weeks, it is unlikely that they came from a source in the hospital. The results suggest that HAIs were overreported and that most MRSA present in the hospital likely came from community sources. **Conclusions:** WGS provided clear evidence that temporally clustered MRSA cases do not imply an outbreak is occurring. Furthermore, ongoing detection of the same community-acquired infections over several months is indicative of a shared source outside of the hospital, which could be uncovered through examination of clinical records. Considering the implications of HAIs, best approaches to combat them should include identifying their sources. As molecular surveillance approaches to infection control are rapidly becoming