

Table 1. Indicators of RVI Transmission Before and After Implementation of Universal Masking Policy on Malignant Hematology Units

Indicator	Before Implementation	After Implementation	P Value
Nosocomial RVI cases, no.	107	80	N/A
Nosocomial RVI ^a incidence (no. of cases per 1,000 patient days)	2.00	1.11	.033
RVI outbreaks, no.	3	2	N/A
RVI cases during outbreaks, no.	23	11	N/A

^aRVIs included influenza A/B, respiratory syncytial virus, metapneumovirus, and parainfluenza 1-4.

Funding: None

Disclosures: Susy Hota reports contract research for Finch Therapeutics.

Doi:10.1017/ice.2020.1182

Presentation Type:

Poster Presentation

Use of a Beta-Lactam Graded Challenge Process at an Academic Medical Center

Andrew Watkins, Nebraska Medicine; Lee Amaya, Beaumont Hospital - Royal Oak; Macey Wolfe, Nebraska Medicine; John Schoen, Nebraska Medicine; Erica Stohs, University of Nebraska Medical Center; Sara May, Nebraska Medicine; Mark Rupp, University of Nebraska Medical Center; Trevor Craig Van Schooneveld, University of Nebraska Medical Center; Bryan Alexander, Nebraska Medicine; Scott Bergman, Nebraska Medicine

Background: A penicillin allergy guidance document containing an algorithm for challenging penicillin allergic patients with β -lactams was developed by the antimicrobial stewardship program (ASP). As part of this algorithm, a “graded challenge” order set was created containing antimicrobial orders and safety medications along with monitoring instructions. The process is designed to challenge patients at low risk of reaction with infusions of 1% of the target dose, then 10%, and finally the full dose, each 30 minutes apart. We evaluated outcomes from the order set. **Methods:** Orders of the graded challenge over 17 months (March 2018 through July 2019) were reviewed retrospectively. Data were collected on ordering and outcomes of the challenges and allergy documentation. Use was evaluated based on ASP-recommended indications: history of IgE-mediated or unknown reaction plus (1) no previous β -lactam tolerance and the reaction occurred >10 years ago, or (2) previous β -lactam tolerance, now requiring a different β -lactam for treatment. Only administered challenges were included and descriptive statistics were utilized. **Results:** Of 67 orders, 57 graded challenges were administered to 56 patients. The most common allergies were penicillins (87.7%) and cephalosporins (38.6%), with the most common reactions being unknown (41.7%) or hives (22%). The most common antibiotics challenged were ceftriaxone (43.9%), cefepime (21.1%), and cefazolin (5.3%). Antibiotics given prior to challenge included vancomycin (48.2%), fluoroquinolones (35.7%), carbapenems (21.4%), aztreonam (19.6%), and clindamycin (12.5%). The median duration of challenged antibiotic was 6 days. The infectious diseases service was consulted on 59.6% of challenges and 75.4% of challenges were administered in non-

ICU settings. There was 1 reaction (1.8%) involving a rash with the second infusion, which was treated with oral diphenhydramine and had no lasting effects. Based on indications, 80.7% of challenges were aligned with ASP guidance criteria. The most common use outside of these criteria was in patients without IgE-mediated reactions (10.5%). Most of these had minor rashes and could have received a full dose of a cephalosporin. Allergy information was updated in the electronic health record after 91.2% of challenges. **Conclusions:** We demonstrated the utility of a graded challenge process at our academic medical center. It was well tolerated, ordered frequently by noninfectious diseases clinicians, administered primarily in non-ICU settings, and regularly resulted in updated allergy information in the medical record. With many patients initially receiving broad-spectrum antibiotics with high costs or increased rates of adverse effects, graded challenges can potentially prevent the use of suboptimal therapies with minimal time and resource investment.

Funding: None

Disclosures: Scott Bergman reports a research grant from Merck. Doi:10.1017/ice.2020.1183

Presentation Type:

Poster Presentation

Use of a Multidisciplinary Incident Command System in Response to Measles Outbreak in Maryland

Taylor McIlquham, Johns Hopkins Hospital; Anna Sick-Samuels, Johns Hopkins School of Medicine; Carrie Billman, The Johns Hopkins Hospital; Jennifer Andonian, The Johns Hopkins Hospital; Melissa Dudley, The Johns Hopkins Hospital; Amyna Husain, Johns Hopkins University; Robert Maloney, Johns Hopkins Medicine; Cagla Oruc, Johns Hopkins Medicine; Mary Brown, Johns Hopkins Medicine; Lisa Maragakis, Johns Hopkins University School of Medicine; Aaron Michael Milstone, Johns Hopkins University

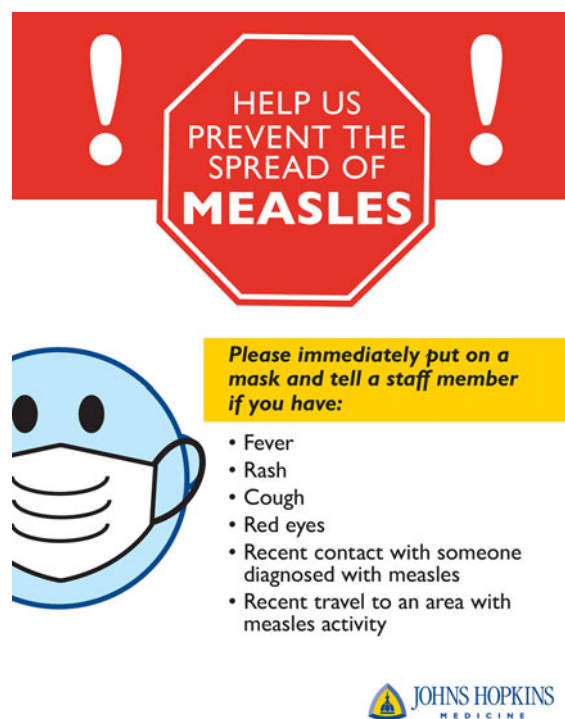
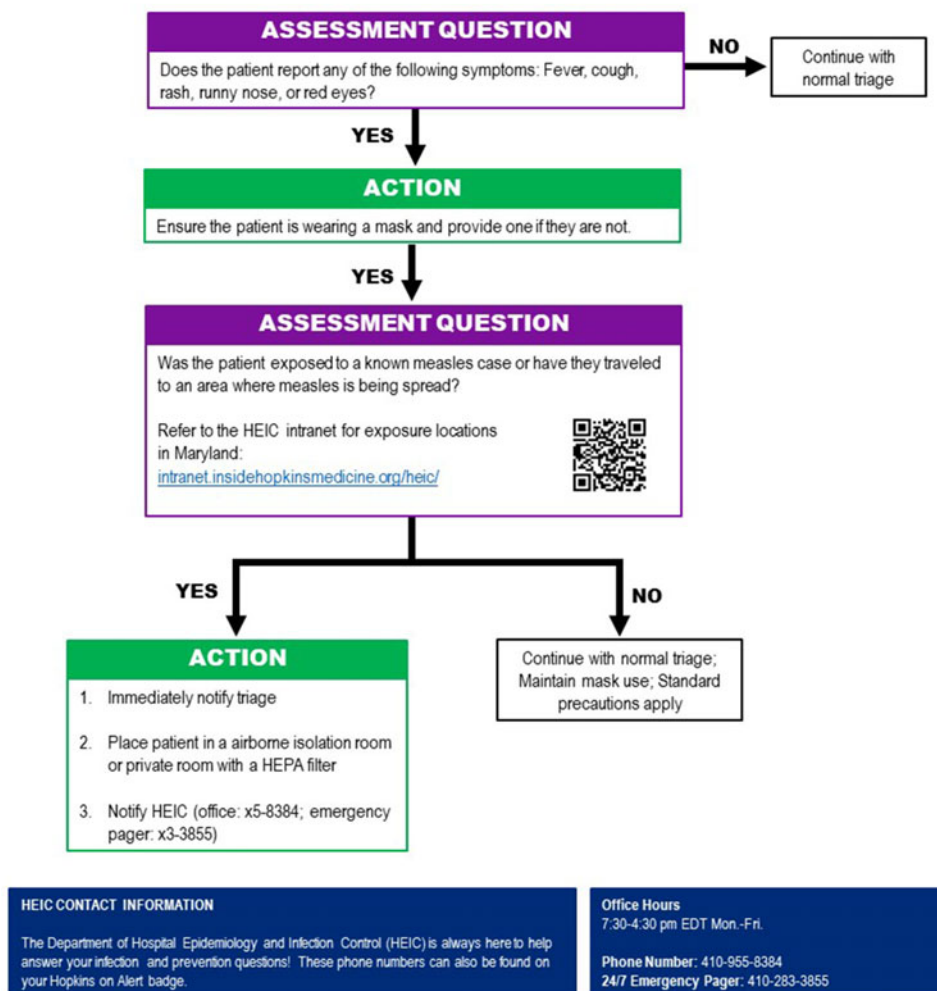


Fig. 1.

Background: Measles is a highly contagious virus that reemerged in 2019 with the highest number of reported cases in the United States since 1992. Beginning in March 2019, The Johns Hopkins Hospital (JHH) responded to an influx of patients with concern for measles as a result of outbreaks in Maryland and the surrounding states. We report the JHH Department of Infection Control and Hospital Epidemiology (HEIC) response to this measles outbreak using a multidisciplinary measles incident command system (ICS). **Methods:** The JHH HEIC and the Johns Hopkins Office of Emergency Management established the HEIC Clinical Incident Command Center and coordinated a multipronged response to the measles outbreak with partners from occupational health services, microbiology, the adult and pediatric emergency departments, marketing and communication and local and state public health departments. The multidisciplinary structure rapidly developed, approved, and disseminated tools to improve the ability of frontline providers to quickly identify, isolate, and determine

testing needs for patients suspected to have measles infection and reduce the risk of secondary transmission. The tools included a triage algorithm, visitor signage, staff and patient vaccination guidance and clinics, and standard operating procedures for measles evaluation and testing. The triage algorithms were developed for phone or in-person and assessed measles exposure history, immune status, and symptoms, and provided guidance regarding isolation and the need for testing. The algorithms were distributed to frontline providers in clinics and emergency rooms across the Johns Hopkins Health System. The incident command team also distributed resources to community providers to reduce patient influx to JHH and staged an outdoor measles evaluation and testing site in the event of a case influx that would exceed emergency department resources. **Results:** From March 2019 through June 2019, 37 patients presented with symptoms or concern for measles. Using the ICS tools and algorithms, JHH rapidly identified, isolated, and tested 11 patients with high suspicion for measles, 4

JHH Patient Measles Registration/Triage Algorithm



Updated April 23, 2019 – Internal Use Only
Department of Hospital Epidemiology and Infection Control
© The Johns Hopkins University, The Johns Hopkins Hospital, and Johns Hopkins Health System. All rights reserved.



Fig. 2

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.

Funding: None

Disclosures: Aaron Milstone reports consulting for Becton Dickinson.

Doi:10.1017/ice.2020.1184

Presentation Type:

Poster Presentation

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

Chad Neilsen, UF Health Jacksonville; Rebecca Rose, Bioinfoexperts, LLC; David Nolan, Bioinfoexperts, LLC; Yvette Simone McCarter, University of Florida College of Medicine-Jacksonville; Fabiana Rollini, University of Florida College of Medicine-Jacksonville; Susanna Lamers, BioInfoExperts LLC; Michael Lee Sands, University of Florida; Thuyvi Hoadley, UF Health Jacksonville

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-

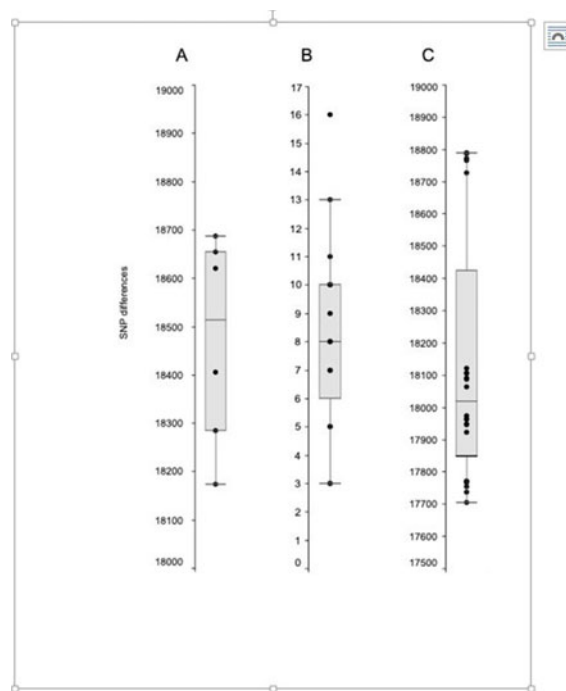


Figure 1. Boxplots of SNP differences among samples from A) UFHJ; B) UK; C) UFHJ vs. UK.

Fig. 1.