Background: In hospitals, Verona integron-encoded metallo-β-lactamase (VIM)–positive *Pseudomonas aeruginosa* (VPPA) frequently colonize sink drains. Sink use has been shown to disperse VPPA to other surfaces surrounding sinks, creating a potential transmission source. **Objective:** Because VPPA have been isolated from sinks and patients within our hospital, we analyzed colonization dynamics in 2 sinks identified as VPPA hot spots between 2012 and 2018. **Methods:** One sink was in an intensive care unit (ICU) patient room and the other was in a gastrointestinal surgery (GIS) patient room. ICU patients were screened for VPPA on admission, at discharge, and weekly during hospitalization. GIS patients were screened for VPPA only on clinical indication. In this study, patient and sink isolates were typed at 8 loci using multiple-locus variable-number tandem repeat (VNTR) analysis (MLVA). **Results:** Overall, 19 sink isolates from the ICU room were included. In 2013, VPPA isolates with identical VNTR genotypes ("clone *B*," VNTR nos. 2-4-8-4-4-5-10-[-2]) were found in the wash basin, aerator, drain, and siphon. The drain plug was replaced in August 2013, but *B* was isolated from the drain 1 month later. Every year between 2014 and 2018, clone *B* and other closely related genotypes were recovered from this drain. In 2018, clone *B* was also found on the wash basin and counter. No positive patients were identified in this room until 2016, when a patient acquired clone *B* 6 days after admission. From the GIS room, 6 sink isolates and 4 patients' isolates were included. In 2012, clone *B* was found on the wash basin and sink drain plug. Also, 3 VPPA-positive patients stayed in this room in 2012: at discharge, 1 patient was colonized by "clone *A*," VNTR numbers 6-7-8-5-9-8-6-1. Furthermore, 2 other patients screened positive for clone *B* prior to admission in 2012, so they likely acquired VPPA elsewhere. The drain plug was replaced in 2013, and no VPPA was found again until 2017, when 2 VPPA-positive patients stayed in this room: 1 was already a carrier of clone *B*, and the other was a carrier of clone *B* 1 day after admission. No positive sink cultures were found until January 2018, when closely related *B* isolates were recovered from the wash basin, drain, and drain plug. **Conclusions:** Between 2013 and 2018, clone *B* persisted in the ICU room sink. In the GIS room sink, clone *B* may have disappeared after 2012, but it was reintroduced by known carriers. However, few patients became colonized after being admitted to these rooms, even when VPPA were discovered on surfaces outside the sink drain (ie, the wash basin and counter).

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Poster Presentation

What's in a Handshake? Exploring the Best Form of Greeting to Prevent Hand to Hand Spread of Viruses

Lucas Jones, Northeast Ohio VA Healthcare System; Wilson Ha, Northeast Ohio VA Healthcare System; Jennifer Cadnum, Cleveland VA Medical Center; Thriveen Sankar; Chittoor Mana; Annette Jencson; Curtis Donskey, Cleveland VA Medical Center

Background: Respiratory and enteric viruses are highly contagious pathogens that can be spread by contaminated hands and surfaces. We hypothesized that alternatives to handshake greetings that reduce the time and surface area of hand contact would be associated with decreased transfer of viral particles. **Methods:** In a simulation of hand-contact greetings, volunteers (N = 22) used a keyboard contaminated with the benign bacteriophage MS2 and then performed a handshake and fist bump with additional volunteers. To assess viral transfer, hands were cultured for MS2, and plaque-forming units (PFU) were compared for the different types of hand contact. Additional simulations (N = 10) were conducted to compare viral transfer with the fist bump versus a cruise tap greeting (ie, a modified fist bump involving single knuckle contact). **Results:** The handshake greeting resulted in significantly greater transfer of MS2 than the fist bump (1.31 vs 0.54 $\log_{10}$ PFUs, $P < .001$) (Fig. 1A), but the frequency of transfer of virus was high for both greetings (91% transfer by handshake vs 59% by fist bump). The cruise-tap greeting did not result in reduced transfer of viral particles in comparison to the fist bump (Fig. 1B), and the frequency of transfer remained high (70%). **Conclusions:** The fist-bump and cruise-tap greetings could potentially reduce transmission of viruses in comparison to the handshake, but transfer occurred frequently, even with these

Figure. Comparison of bacteriophage MS2 transfer by different greeting methods.

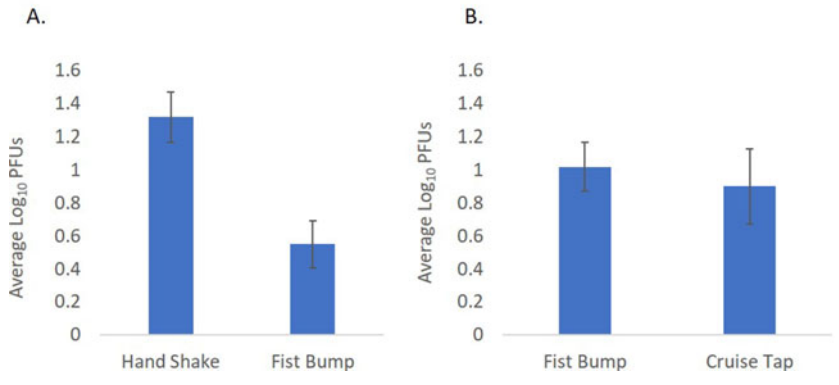

Fig. 1.

greeting methods. To eliminate hand-to-hand transmission of respiratory and enteric viruses, alternative greeting methods that do not involve physical contact are needed.
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Where To From Here? Identifying and Prioritizing Future Directions for Addressing Drug-Resistant Infection in Australia

Lisa Hall, The University of Queensland; Greg Merlo, Primary Care Clinical Unit, Faculty of Medicine, University of Queensland; Minyon Avent, Queensland Statewide Antimicrobial Stewardship Program; Trent Yarwood, Queensland Statewide Antimicrobial Stewardship Program; Bonnie Smith, Queensland Statewide Antimicrobial Stewardship Program; Mieke van Driel, Primary Care Clinical Unit, Faculty of Medicine, University of Queensland

Background: The Australian Government released a national strategy for antimicrobial resistance in 2015 that calls for a collaborative effort to change practices that have contributed to the development of drug-resistant infection and for the implementation of new initiatives to reduce antibiotic use. Although many achievements have been made in antimicrobial stewardship (AMS), particularly in the acute-care hospital setting, progress more broadly has been slow, and novel solutions are now required to improve clinical practice and community awareness. A facilitated workshop was undertaken at the 2019 National Australian Antimicrobial Resistance Forum to explore the complexity of AMS implementation in Australia and to prioritize future action. **Methods:** Participants engaged in rotating rounds of discussion using a world café format. The participants sat face-to-face at tables of 7 or fewer. At each table were 2 facilitators: one was a note taker and the other was the discussion leader. Each of the 6 facilitator pairs had a topic for discussion related to implementing antimicrobial stewardship in different contexts, with a focus on experience with strategies that have worked, major implementation barriers, and prioritizing the next steps. The topics for discussion included (1) engaging with hospital staff; (2) implementation in resource-poor settings; (3) implementation in primary care and aged care; (4) engaging and empowering the public; (5) linking data with implementation strategies; and (6) leadership. The facilitators moved between tables at 15-minute intervals to encourage evolving rounds of conversation. Once all tables had discussed all of the themes, the discussion concluded and notes were summarized. A qualitative analysis using an interpretive description approach was conducted using the discussion summaries. The documents were independently openly coded by 2 researchers to identify elements relating to the implementation of antimicrobial stewardship. An iterative approach was used to identify themes and reach a consensus on overarching emergent themes from the workshop. **Results:** In total, 39 experts (ie, pharmacists, infectious disease physicians, infection prevention nurses, researchers, journalists and consumers) participated in the facilitated discussions. Strategies were discussed relating to engaging with clinicians, consumers, and politicians; adapting to funding, governance, and accreditation limitations; and models for outreach of antimicrobial services. Other themes included the role of clinical champions and mentors as leaders and improving use of audit and feedback through focusing on monitoring appropriateness rather than usage. **Conclusions:** Recommendations from the workshop will be used to prioritize novel ideas to improve the implementation of AMS initiatives across Australia.
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Whole-Genome Sequencing for Bacterial Strain Typing Using the iSeq100 Platform

Grant Vestal, Tampa General Hospital; Steven Bruzek, Tampa General Hospital; Amanda Lasher, Tampa General Hospital; Amorce Lima, Tampa General Hospital; Suzane Silbert, Tampa General Hospital

Background: Hospital-acquired infections pose a significant threat to patient health. Laboratories are starting to consider whole-genome sequencing (WGS) as a molecular method for outbreak detection and epidemiological surveillance. The objective of this study was to assess the use of the iSeq100 platform (Illumina, San Diego, CA) for accurate sequencing and WGS-based outbreak detection using the bioMérieux EPISEQ CS, a novel cloud-based software for sequence assembly and data analysis. **Methods:** In total, 25 isolates, including 19 MRSA isolates and 6 ATCC strains were evaluated in this study: *A. baumannii* ATCC 19606, *B. cepacia* ATCC 25416, *E. faecalis* ATCC 29212, *E. coli* ATCC 25922, *P. aeruginosa* ATCC 27853 and *S. aureus* ATCC 25923. DNA extraction of all isolates was performed on the QIAcube (Qiagen, Hilden, Germany) using the DNEasy Ultra Clean Microbial kit extraction protocol. DNA libraries were prepared for WGS using the Nextera DNA Flex Library Prep Kit (Illumina) and sequenced at 2×150-bp on the iSeq100 according to the manufacturer's instructions. The 19 MRSA isolates were previously characterized by the DiversiLab system (bioMérieux, France). Upon validation of the iSeq100 platform, a new outbreak analysis was performed using WGS analysis using EPISEQ CS. ATCC sequences were compared to assembled reference genomes from the NCBI GenBank to assess the accuracy of the iSeq100 platform. The FASTQ files were aligned via BowTie2 version 2.2.6 software, using default parameters, and FreeBayes version 1.1.0.46-0 was used to call homozygous single-nucleotide polymorphisms (SNPs) with a minimum coverage of 5 and an allele frequency of 0.87 using default parameters. ATCC sequences were analyzed using ResFinder version 3.2 and were compared in silico to the reference genome. **Results:** EPISEQ CS classified 8 MRSA isolates as unrelated and grouped 11 isolates into 2 separate clusters: cluster A (5 isolates) and cluster B (6 isolates) with similarity scores of ≥99.63% and ≥99.50%, respectively. This finding contrasted with the previous characterization by DiversiLab, which identified 3 clusters of 2, 8, and 11 isolates, respectively. The EPISEQ CS resistome data detected the *mecA* gene in 18 of 19 MRSA isolates. Comparative analysis of the ATCCsequences to the reference genomes showed 99.9986% concordance of SNPs and 100.00% concordance between the resistance genes present. **Conclusions:** The iSeq100 platform accurately sequenced the bacterial isolates and could be an affordable alternative in conjunction with EPISEQ CS for epidemiological surveillance analysis and infection prevention.
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