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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Poster Presentation

Where To From Here? Identifying and Prioritizing Future Directions for Addressing Drug-Resistant Infection in Australia

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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

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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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