711. Molecular Epidemiology of Daptomycin Non-susceptibility in Methicillin-Resistant Staphylococcus aureus (MRSA) Bacteremia
Ayasha Sundaram, BS1; Mary Beth Perri, MT2; Katherine Gurdziel, PhD3; Hind Hadid, MD1; Erica Herc, MD4; and Marcus J Zervos, MD5; 1Wayne State University School of Medicine, Detroit, Michigan; 2Infectious Disease, Henry Ford Health System, Detroit, Michigan; 3Applied Genomics Technology Center, Detroit, Michigan

Session: 68. Resistance Mechanisms: Gram-Positive
Thursday, October 4, 2018: 12:30 PM

Background. While methicillin resistance in S. aureus strains is prevalent, non-susceptibility to vancomycin and daptomycin, first-line treatments for bacteremia, has emerged as well. Little is known about the molecular epidemiology of daptomycin resistance in S. aureus strains.

Methods. A retrospective study was conducted at an 800-bed hospital in Detroit, Michigan. Blood isolates of S. aureus were obtained over time in patients with persistent bacteremia. Isolates were initially classified as MRSA/ MSSA and MIC testing was performed. A total of 120 isolates from the microbiology laboratory were selected for molecular analysis. Isolates were reclassified into separate categories using Etest strips and microdilution broth testing. Non-susceptibility to daptomycin was defined as an MIC > 1 mg/mL. Isolates from each patient were also assessed for genomic similarity using pulse field gel electrophoresis (PFGE) and placed in the same strain group if they were ≥ 80% similar by Dice coefficient. Whole genome sequencing (WGS) on isolates and template strain ATCC29213 was done by the Applied Genomics Technology Center.

Results. There were 27 isolates from seven patients in the following distribution: six isolates each from Patients 1 and 2; three isolates each from Patients 3, 4, and 5; five isolates from Patient 6; and one isolate from Patient 7. All isolates from Patients 1 and 3 (n=9) were classified as MSSA strains and the remainder were MRSA strains. Daptomycin non-susceptible strains were found in the initial isolate on therapy in two patients; MIC increased from first to last isolates in the other five patients. A PFGE dendrogram revealed isolates within each patient and within established CDC lineages determined that (1) each patient’s first and last isolate remained within the same strain type and (2) the PFGE groups were USA100 (n=8), USA300 (n=7), USA900 (n=6), and USA1000 (n=3). WGS revealed the presence of vraSR, mprF, dleA, clx2, and gdpD, genes implicated in resistance to both vancomycin and daptomycin. However, gdpD was not detected in isolates classified as MSSA.

Conclusion. No genetic modification of strains from each patient was seen between the first isolate obtained and the last. The presence of cell wall regulation genes in both vancomycin susceptible and non-susceptible strains suggests gene upregulation.

Disclosures. M. J. Zervos, Merck: Consultant and Grant Investigator, Grant recipient.

712. Identification of a Novel Tedizolid Resistance Mutation in rpO8 of Methicillin-Resistant Staphylococcus aureus
Brian Worth, PharmD; Penewit M, MS1; Stephen Salapante, MD, PhD; Tianwei Shen, MS1; Libin Xu, PhD2 and Abhinav Nath, PhD3; 1Department of Pharmacy, University of Washington School of Pharmacy, Seattle (Washington), 2Washington, 3Department of Laboratory Medicine, University of Washington School of Medicine, Seattle (Washington), Washington, 4Department of Medicinal Chemistry, University of Washington School of Pharmacy, Seattle (Washington), Washington

Session: 68. Resistance Mechanisms: Gram-Positive
Thursday, October 4, 2018: 12:30 PM

Background. Tedizolid (TDZ) is an oxazolidinone antimicrobial with broad-spectrum activity against Gram-positive bacteria including methicillin-resistant S. aureus (MRSA). Resistance to TDZ is uncommon but mutations in the 23S rRNA target as well as in the transferrable RNA methyltransferase gene cfr, which also mediates resistance to linezolid and chloramphenicol have been implicated. The objective of this study was to determine whether other TDZ resistance pathways exist in MRSA.

Methods. Using a well-characterized MRSA strain, N315, we selected for TDZ resistance by serial passage in escalating concentrations of TDZ in Mueller Hinton broth (MH) starting with 0.5× the MIC. Once visible growth was achieved a sample of the broth was diluted 1:1,000 into fresh MH with twice the previous concentration of TDZ until an isolate with an MIC of ≥4 mg/L was recovered. This MIC was selected since it is 1 dilution above the breakpoint for resistance (≥2 mg/L). This isolate was subjected to whole genome sequencing (WGS) and MICS to other antimicrobials were assessed. Homology modeling was performed to evaluate the potential impact of the mutation on target protein function.

Results. After 10 days of serial passage we recovered a stable mutant with a TDZ MIC of 4 mg/L. WGS revealed a single nucleotide variant (A1345G) in the rpO8 gene corresponding to an amino acid substitution at D449N. The following table and figure summarize the changes in drug susceptibility between the parent and evolved strain and reveals the location of the amino acid substitution relative to the TDZ binding site.

| Drug          | N315 | N315-TDZ4 |
|---------------|------|-----------|
| Chloramphenicol| 8    | 128       |
| Doxycycline   | 0.125| 0.125     |
| Linezolid     | 8    |           |
| Minocycline   | 0.0625| 0.0625   |
| Rifampin      | 0.001| 0.001     |
| Teizolid      | 0.25 | 4         |
| Vancomycin    | 0.5  |           |

Conclusion. We have identified a novel mutation in the RNA polymerase gene, rpO8, that mediates oxazolidinone and chloramphenicol resistance. This variant lies outside of the rifampin resistance determinant clusters of rpO8 that span from 1,384 to 1,464 and 1,543 to 1,590, and as expected did not affect rifampin susceptibility. The underlying molecular mechanism by which this single nucleotide variant confers TDZ resistance remains unclear but may involve transcriptional modulation by altered sigma factor binding.

Disclosures. All authors: No reported disclosures.

713. Vancomycin Heteroresistance in Coagulase Negative Staphylococci (CoNS) Causing Central Line-Associated Bloodstream Infection (CLABSI) in Pediatric Patients with Leukemia
Tina Dao, BS1; Joshua Parsons, PhD2; Randall Hayden, MD3; Jeffrey Rubnitz, MD4; Thomas Wolf, MBBS FRACP5; and Jason Rosch, PhD1; Infectious Diseases, St. Jude Children’s Research Hospital, Memphis, Tennessee, 1St. Jude Children’s Research Hospital, Memphis, Tennessee

Session: 68. Resistance Mechanisms: Gram-Positive
Thursday, October 4, 2018: 12:30 PM

Background. Heteroresistance to vancomycin in Staphylococcus aureus may be associated with poor response to therapy. Although CoNS are the most important CLABSI pathogens in children with leukemia, and treatment failure is common, little is known about the frequency and clinical significance of heteroresistance. This is a retrospective study to evaluate frequency, risk factors and clinical impact of heteroresistance in CoNS CLABSI in immunocompromised children.

Methods. The study was approved by the Institutional Review Board. All patients undergoing treatment for leukemia at St. Jude Children’s Research Hospital with CoNS isolated from blood between 2010 and 2016 were eligible. The first available isolate from each blood culture episode was obtained from the clinical laboratory and tested for vancomycin heteroresistance by population analysis profiling in comparison to the hVISA strain Mu3. Clinical data were collected from the medical record for up to 9 months after the episode. Episodes with ≥2 positive cultures or a single positive culture from a single lumen CVC were classified as CLABSI. Outcomes of interest included treatment failure (death or relapse of infection) or poor response to vancomycin therapy (persistent of bacteremia ≥2 days after initiation of vancomycin or treatment failure). Logistic regression was used to test associations between heteroresistance and exposures, and cumulative incidence analyses were used to test the effect on outcomes.

Results. A total of 74 CoNS isolates were obtained from 65 participants, 39 with ALL and 26 with AML; 25/74 (33.8%) of isolates showed heteroresistance. The strongest identified risk factor for infection with a heteroresistant organism was number of days of vancomycin in the preceding 60 days (OR = 1.05/day; P = 0.035). In the 40 CLABSI episodes, heteroresistant isolates had a higher cumulative incidence of poor response and treatment failure compared with that of treatment failure associated with a heteroresistant organism was number of days of vancomycin in the preceding 60 days (OR = 1.05/day; P = 0.035). In the 40 CLABSI episodes, heteroresistant isolates had a higher cumulative incidence of poor response and treatment failure compared with that of treatment failure associated with a heteroresistant organism was number of days of vancomycin in the preceding 60 days (OR = 1.05/day; P = 0.035).

Conclusion. Vancomycin heteroresistance is common in CoNS causing CLABSI in children undergoing treatment for leukemia, and is associated with an increased risk of Treatment Failure. Further research should aim to validate this finding in an independent cohort and identify strategies to improve the diagnosis and treatment of these infections.

Disclosures. R. Hayden, Roche Molecular: Scientific Advisor, Consulting fee. Abbott Molecular: Scientific Advisor, Consulting fee. Quidel: Scientific Advisor, Consulting fee. J. Wolf, Karius Inc.: Investigator, Research support.

714. Predictors of Influenza-Associated Hospitalization and Pneumonia in a Pediatric Population in Bangkok, Thailand
Ali Sawani, BS1; Detchujit Suwanpakdee, MD2; Veerachat Wanataraveeja, MD3; Allen Weg, MD4; Damon Ellison, PhD5; Chonthicha Khlongthong, PhD1; Tiwiphat Phophonboksin, PhD2; Phrargkul Kerdpahn, MD3; Danabhaddh Phiboonbannakit, MD1; Robert Gibbons, MD2; Stefan Fernandez, PhD3; Louis Macareo, MD3, JD, MPH1; In Kyu Toon, MD3; Rick Jarman, PhD2; Sridook Simathisen, MD1; and Kathryn Anderson, MD, PhD, MSPH1; Oak Ridge Institute for Science and Education (ORISE), Oak Ridge, Tennessee, 1Phramongkutklao Hospital, Bangkok, Thailand, 2Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand, 3International Vaccine Institute, Seoul, Korea, Republic of (South), 4Walter Reed Army Institute of Research, Silver Spring, Maryland, 5University of Minnesota, Minneapolis, Minnesota

Session: 69. Respiratory Infections: Viral
Thursday, October 4, 2018: 12:30 PM

Disclosures. All authors: No reported disclosures.