Type of Solid Tumor

Disclosures: Roy F. Chemaly, MD, MPH, FACP, FIDSA, Chimerix: Advisory Board; Research Grant; Clistigen: Advisory Board; Merck: Advisory Board, Consultant, Grant/Research Support, Research Grant, Speaker’s Bureau; Oxford immuno; Consultant Grant/Research Support; Shire: Research Grant, Speaker’s Bureau; Viracor: Grant/Research Support.

2682. Prophylaxis-Driven Molecular Epidemiology of Pseudomonas aeruginosa Bloodstream Infections in Adults With Leukemia
Bradley T. Endres, PhD1; Michael J. Burge, PharmD2; Kayleigh Marx, PharmD1; Pranoti V. Sahasrabudhe, MS1; Jessica Galloway-Peña, PhD2; Kevin W. Garey, PharmD, MS, FASHP2, Jiwon Kim, MS3; David E. Greenberg, MD4; Xiaowei Zhan, PhD5; Samuel A. Shelburne, MD, PhD6; Samuel A. Shelburne, MD, PhD7; Samuel L. Aitken, PharmD7; Samuel L. Aitken, PharmD7; University of Houston College of Pharmacy, Houston, Texas; Memorial Sloan Kettering Cancer Center, New York, New York; The University of Texas MD Anderson Cancer Center, Houston, Texas; University of Texas Southwestern Medical Center, Dallas, Texas

Session: 275. Transplant ID: Malignancy and Neutropenia
Saturday, October 5, 2019: 12:15 PM

Background: Fluoroquinolones (FQs) are routinely used as antimicrobial prophylaxis in leukemia patients receiving chemotherapy to prevent Pseudomonas aeruginosa infections. Patients who are intolerant to FQs may receive cephalosporine (CPD) or another agent. How FQ use affects the resistance profile and epidemiology of bloodstream P. aeruginosa infections is unknown. To determine this, we performed a whole-genome sequencing (WGS)-driven epidemiologic study of leukemia patients with P. aeruginosa bloodstream infections.

Methods: All adult (age > 17 years) inpatients with leukemia and a first episode of monomicrobial P. aeruginosa bloodstream infection were included. Clinical data were extracted from the electronic medical record. Isolates were sequenced using an Illumina NextSeq and phylogenomics was performed using an in-house analysis pipeline consisting of Bowtie2, SAMtools and bcftools.

Results: 110 patients were included and most had a diagnosis of acute myeloid leukemia (n = 66). Twenty (18%) patients received FQ prophylaxis, 56 (54%) received CPID, and the remaining 34 (31%) received other agents. 9 (8%) isolates were multidrug-resistant (MDR). MDR was more common in those receiving FQ prophylaxis (20% vs 6%, P = 0.06). 76 sequence types (STs) were represented with ST235 (n = 3) being most common followed by ST244 (n = 7). ST235 strain was genetically distinct, but closely related (≥10 but < 250 SNPs) in comparison to other STs. 2 ST244 strains were genetically identical despite being isolated 4 months apart, suggesting horizontal transmission. MDR was more common among ST235 isolates compared with other STs (38% vs 6%, P = 0.02). ST235 strains were more common in patients receiving FQ vs other prophylaxis (20% vs 4%, P = 0.04). 1 ST244 isolate harbored a VIM-2 β-lactamase. In 20 FQ-resistant isolates, 80% had mutations in either parC (SOFT) or gyrA (T81H) and 50% had both. FQ-resistance mutations were more common in FQ recipients (50% vs 8%, P = 0.01).

Conclusion: Most P. aeruginosa infections occurred in non-FQ recipients, while MDR P. aeruginosa infections were more common in FQ recipients. These data suggest that decisions on empiric treatment of patients with P. aeruginosa bacteremia must take antimicrobial prophylaxis history into account.

Disclosures: Samuel L. Aitken, PharmD, Melinta Therapeutics: Grant/Research Support, Research Grant; Merck, Sharp, and Dohme: Advisory Board; Shionogi: Advisory Board.

2683. Evaluation of the Negative Predictive Value (NPV) of Methicillin-Resistant Staphylococcus aureus (MRSA) Nasal Swab Screening in Acute Myeloid Leukemia Patients
Bailee Binks, PharmD; Dayna McMahan, PharmD, BCPS; Sarah Perreault, PharmD, BCPS, BCO; Jeffrey E. Topal, MD; Yale New Haven Hospital, New Haven, Connecticut

Session: 275. Transplant ID: Malignancy and Neutropenia
Saturday, October 5, 2019: 12:15 PM

Background: Methicillin-Resistant Staphylococcus aureus (MRSA) nasal swabs are utilized to guide discontinuation of empiric MRSA therapy. In multiple studies, MRSA nasal swabs have been shown to have a negative predictive value (NPV) of ~99% in non-oncology patients with pneumonia and other infections. At Yale New Haven Hospital (YNHH), a negative MRSA nasal swab is utilized in acute myeloid leukemia (AML) patients to de-escalate empiric MRSA antibiotic therapy. The primary endpoint was to assess the percentage of patients with a negative MRSA nasal swab who developed culture documented (CD) MRSA infection during their admission. Secondary endpoints included the number of MRSA nasal swabs that were initially negative but oped a culture documented (CD) MRSA infection during their admission. Secondary endpoints were extracted from the electronic medical record. Isolates were sequenced using an Illumina NextSeq and phylogenomics was performed using an in-house analysis pipeline consisting of Bowtie2, SAMtools and bcftools.

Methods: This was a retrospective chart review of AML patients with a suspected MRSA nasal swab within the past year.

Results: 110 patients were included and most had a diagnosis of acute myeloid leukemia (n = 66). Twenty (18%) patients received FQ prophylaxis, 56 (54%) received CPID, and the remaining 34 (31%) received other agents. 9 (8%) isolates were multidrug-resistant (MDR). MDR was more common in those receiving FQ prophylaxis (20% vs 6%, P = 0.06). 76 sequence types (STs) were represented with ST235 (n = 3) being most common followed by ST244 (n = 7). ST235 strain was genetically distinct, but closely related (≥10 but < 250 SNPs) in comparison to other STs. 2 ST244 strains were genetically identical despite being isolated 4 months apart, suggesting horizontal transmission. MDR was more common among ST235 isolates compared with other STs (38% vs 6%, P = 0.02). ST235 strains were more common in patients receiving FQ vs other prophylaxis (20% vs 4%, P = 0.04). 1 ST244 isolate harbored a VIM-2 β-lactamase. In 20 FQ-resistant isolates, 80% had mutations in either parC (SOFT) or gyrA (T81H) and 50% had both. FQ-resistance mutations were more common in FQ recipients (50% vs 8%, P = 0.01).

Conclusion: Most P. aeruginosa infections occurred in non-FQ recipients, while MDR P. aeruginosa infections were more common in FQ recipients. These data suggest that decisions on empiric treatment of patients with P. aeruginosa bacteremia must take antimicrobial prophylaxis history into account.

Disclosures: Samuel L. Aitken, PharmD, Melinta Therapeutics: Grant/Research Support, Research Grant; Merck, Sharp, and Dohme: Advisory Board; Shionogi: Advisory Board.
2684. The Prospective Pilot Study of Infectious Complication Surveillance in Active Systemic Lupus Erythematosus Patients with Intense Immunosuppressive Therapy: Cellular Response and Clinical Outcomes

Purpose: To implement and evaluate the feasibility of an infectious complication surveillance registry in active SLE patients at the University of California, San Francisco (UCSF).

Methods: Between December 2012 and June 2018, 173 of 520 patients screened were included; 76 of 173 (44%) were high-risk (≥20% risk of infection at any specific site). A total of 23 patients with ≥20% risk of infection at any specific site were enrolled; 91.3% were female with a median age of 43 years (range 17–79). Fluoroquinolone prophylaxis was used in 64 (71%) of patients.

Results: Of 520 patients screened, 173 (33.3%) were included in the study; 76 of 173 (44%) were high-risk (≥20% risk of infection at any specific site). A total of 23 patients with ≥20% risk of infection at any specific site were enrolled; 91.3% were female with a median age of 43 years (range 17–79). Fluoroquinolone prophylaxis was used in 64 (71%) of patients.

Conclusion: The use of infectious complication surveillance programs in active SLE patients to identify high-risk individuals and personalize prophylaxis regimens is needed.

Disclosures. All authors: No reported disclosures.