was derived from a patient with no prior CAZ-AVI exposure. Whole genome sequencing will be performed to identify other genes or mutations that may confer resistance.

Disclosures. All authors: No reported disclosures.

622. The Accessory Genome in Enterococcal Bacteria: Results from the Vancomycin-Resistant Enterococcal Bacteremia Outcomes Study (VENOUS) Shelby Simar, MPH; Blake Hanson, PhD; German Contreras, MD; Katherine Reyes, MD, MPH; Pranoti V. Saharbhogue, MD; Helina Musik, MPH; Catherine Liu, MD; Yohesi Dou, MD, PhD; Fernanda Barberis, MD; Lilian Albo, MD, FIDSA; An Q. Dinh, BS; Maria Spencer, BSc, MS, PhD; Marcus Zervos, MD; Samuel L. Aitken, PharmD; Samuel L. Aitken, PharmD; David van Duijn, MD, PhD; Samuel A. Sheldurn, MD, PhD; Samuel A. Sheldurn, MD, PhD; Truc T. Tran, PharmD; Jose M. Munta, MD; Cesar A. Arias, MD, MSc, PhD, FIDSA; Maria de los Angeles Spencer, Program Coordinator; 1School of Public Health, University of Texas Health Science Center at Houston, Houston, Texas; 2McGovern Medical School, University of Texas Health Science Center, Houston, Texas; 3Tenet Ford Health System, Detroit, Michigan; 4The University of Texas MD Anderson Cancer Center, Houston, Texas; 5Fred Hutchinson Cancer Research Center, Seattle, Washington; 6School of Medicine, University of Pittsburgh, Pittsburgh, Pennsylvania; 7SADIL, Buenos Aires, Ciudad Autonoma de Buenos Aires, Argentina; 8Miller School of Medicine, University of Miami, Miami, Florida; 9Center for Antimicrobial Resistance and Microbial Genomics, University of Texas Health, Houston, Texas; 10Genomics and Resistant Microbes (GeRM), Instituto de Ciencias e Innovacion en Medicina, Facultad de Medicina Clinica Alemana, Universidad del Desarrollo, Chile; 11Millennium Initiative for Collaborative Research on Bacterial Resistance (MICROB-IR), Santiago, Region Metropolitana, Chile; 12School of Medicine, University of North Carolina, Chapel Hill, North Carolina; 13Genomics and Resistance Microbes (GeRM) Group, Millennium Initiative for Collaborative Research On Bacterial Resistance (MICROB-IR), Santiago, Region Metropolitana, Chile, 14CARMIC, University of Texas Health and Science Center at Houston, Houston, Texas; 15Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bog, COL, Houston, Texas

Session: 66. Molecular and Genomic Epidemiology of Resistant Pathogens Thursday, October 3, 2019: 12:15 PM

Background. Vancomycin-resistant enterococci (VRE) are a major cause of nosocomial bloodstream infections. Enterococci exhibit remarkable genomic plasticity and can recombine through the acquisition of genetic material via mobile genetic elements (MGEs), including resistance genes. The accessory genome plays a major role in the evolution of enterococci within the human host. Thus, dissecting the entire genome (pan-genome) is of paramount importance to characterize the population structure of enterococci causing disease.

Methods. VENOUS is an ongoing prospective, observational study of adults with enterococcal bacteremia. From September 2016 to March 2018, E. faecalis (Efm) and E. faecium (Efm) were collected in 14 hospitals of a single hospital system and a major cancer center in Houston, TX, and a general hospital in Detroit, MI. Short- and long-read genomic sequencing were performed with Illumina MiSeq and Oxford Nanopore Technologies GridION X5, respectively. A proprietary bioinformatics pipeline was utilized for genome assembly and further analyses.

Results. 156 Efm and 98 Efm isolates from single patients were analyzed. The average proportion of core genes in each genome was 64.6% (53.0-74.1) and 49.1% (45.2-51.0) for Efm and Efm, respectively. The vanA gene cluster was identified in 5.1% (8/157) of Efm and 57.1% (56/98) of Efm. The plasmid-encoded aac(6’)-Ie-aph(2’)-Ie gene conferring high-level resistance to aminoglycosides was found in 37.6% (59/157) Efm, seven of which also possessed vanA. Long-read sequencing of vanA harboring plasmids from a subset of VRE revealed that the vanA cluster was carried in plasmids ranging from 31.2 to 132.3 kb. Although the vanA operon was fairly conserved, insertions of MGE were identified in the intergenic regions of vanA/vanH and vanX/vanY. Furthermore, a variety of MGE insertions mediated integration of the vanA operon, including IS2126 and IS256 (figure).

Conclusion. Accessory genes, including AMR genes, comprise a significant proportion of the enterococcal pan-genome, indicating major genetic plasticity within these organisms. Acquired resistance genes seem to have a high degree of recombination and play a substantial role in the expansion of the genomic repertoire in clinical isolates.

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

623. Antimicrobial Resistance in Non-Typhoidal Salmonella from Retail Poultry Meat by Antibiotic Usage-related Production Claims—Pennsylvania, 2008–2017 Xin Yin, MPH; Nkuchia M. Mikantha, PhD, MPH; Lisa Dettinger, Medical Technologist; Melinda Johnston; William Eckroth; Brigitte Husband; James Tait; Epphania Nyiraruhazi, PhD; Heather Tate, PhD; 1Penn State College of Medicine, Hershey, Pennsylvania; 2Pennsylvania Department of Health, Harrisburg, Pennsylvania; 3Food and Drug Administration, Laurel, Maryland; 4US Food and Drug Administration, Laurel, Maryland

Session: 66. Molecular and Genomic Epidemiology of Resistant Pathogens Thursday, October 3, 2019: 12:15 PM

Background. Antimicrobial-resistant (AMR) nontyphoidal Salmonella infections are a public health concern. Injudicious use of antimicrobials fuels emergence of resistance. The National Antimicrobial Resistance Monitoring System (NARMS) tracks AMR in Salmonella from humans, animals and foods. There is limited evidence regarding antimicrobial use in food animals and AMR bacteria in retail meat.

Methods. We reviewed antimicrobial susceptibility and whole-genome sequencing data from 320 Salmonella isolated from poultry meat in Pennsylvania as part of NARMS activities. Salmonella strains were isolated from 3,481 samples purchased from randomly selected retail outlets during 2008–2017. Antibiotic usage claims on meat packages were used to compare AMR Salmonella from conventional and antibiotic-free (Abx-free) samples. Genetic mechanisms for AMR were investigated in a subset of isolates.

Results. The prevalence of Salmonella in conventional poultry meat 10.2% (280/2,733) was significantly higher than the prevalence in poultry meat labeled as Abx-free (5.3%, 40/748; P < 0.0001). Salmonella from conventional poultry meat was more likely to be resistant to 3 or more drugs (55.6%, 154/280) compared with poultry meat labeled as Abx-free (27.5%, 11/40; P = 0.0011). Salmonella from conventional poultry exhibited significantly higher resistance to 4 drug classes including β-lactams (P = 0.060) (figure). One hundred isolates from conventional poultry meat and 8 isolates from antibiotic-free organic samples harbored a gene conferring resistance to the β-lactam class: 24.3% (68/280) of isolates from conventional and 7.5% (3/40) of isolates from Abx-free samples (P = 0.0145) contained the extended-spectrum β-lactamase (ESBL) gene blaCMY-2.

Conclusion. Meat samples from conventionally-raised poultry were more likely to be associated with AMR Salmonella strains and have genes that reduce the effectiveness of antimicrobial drugs recommended for treatment of severe infections. Contamination of poultry with Salmonella strains is concerning as is the presence of genes that decrease the power of critical antibiotics such as β-lactams. These findings highlight the importance of judicious use of antibiotics in food-producing animals.

Disclosures. No reported disclosures.

624. Molecular Characterization of Baseline Enterobacteriaceae and Pseudomonas aeruginosa from a Phase 3 Nosocomial Pneumonia (ASPECT-NP) Clinical Trial Mariana Castanheira, PhD; Matthew G. Johnson, MD; Brian Yu, PharmD; Jennifer A. Huntington, PharmD; Samuel Carmelitano, MS; Christopher Bruno, MD; Elizabeth G. Rhee, MD; Mary Motyl, PhD; 13IM Laboratory, North Liberty, Iowa; 3Merck & Co., Inc., Kenilworth, New Jersey

Session: 66. Molecular and Genomic Epidemiology of Resistant Pathogens Thursday, October 3, 2019: 12:15 PM

ASPECT-NP, a phase 3, randomized, double-blind, multicenter trial, evaluated ceftolozane/tazobactam (C/T) 3 g q8h vs. meropenem 1 g q8h for...