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 Bacteremia: Results from the Vancomycin-Resistant Enterococcal Bacteremia Outcomes Study (VENOUS)

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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* (*Efs*) 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 *Efs* 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 *Efs* and *Efm*, respectively. The *vanA* gene cluster was identified in 5.1% (8/157) of *Efs* and 57.1% (56/98) of *Efm*. The plasmid-encoded *aac(6´)-Ie-aph(2″)-Ia* gene conferring high-level resistance to aminoglycosides was found in 37.6% (59/157) *Efs*, 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 31.7 to 132.3 kb. Although the *vanA* operon was fairly conserved, insertions of MGE were identified in the intergenic regions of *vanS*/*vanH* and *vanX*/*vanY*. Furthermore, a variety of MGE insertions mediated integration of the *vanA* operon, including IS*1216* and IS*256* (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.

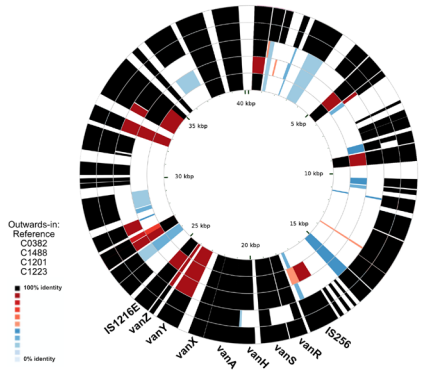

Figure. Composite view of homology within the coding sequences of plasmids containing the vanA operon obtained through long-read sequencing.
The outermost black ring denotes a reference plasmid containing a conventional vanA operon, and similarity to the reference decreases in an inwards direction.

Disclosures. Samuel L. Aitken, PharmD, Melinta 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

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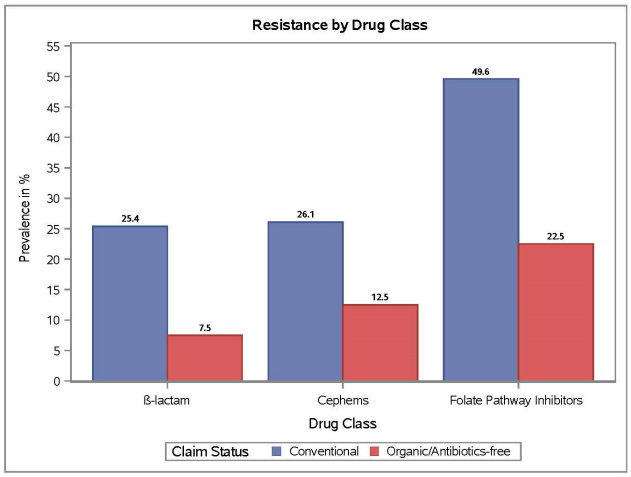
Background. Antimicrobial-resistant (AMR) nontyphoidal Salmonella infections are a public health concern. Injudicious use of antimicrobials fuels emergence of resistance. The National Antimicrobial Resistance Monitoring System (NARMS) tracks AMR in Salmonella from humans, animals and foods. There is 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/organic (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 (55.0%, 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 ($P = 0.006$) (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 contaminated with AMR Salmonella strains and have genes that reduce the effectiveness of antimicrobial drugs recommended for treatment of severe infections. Contamination of poultry with AMR 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. **All authors:** No reported disclosures.

624. Molecular Characterization of Baseline Enterobacteriaceae and *Pseudomonas aeruginosa* from a Phase 3 Nosocomial Pneumonia (ASPECT-NP) Clinical Trial

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