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.

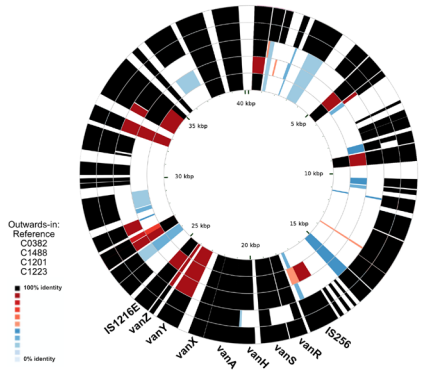

Figure. Composite view of homology within the coding sequences of plasmids containing the vanA operon obtained through long-read sequencing.
The outermost black ring denotes a reference plasmid containing a conventional vanA operon, and similarity to the reference decreases in an inwards direction.

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623. Antimicrobial Resistance in Non-Typhoidal Salmonella from Retail Poultry Meat by Antibiotic Usage-related Production Claims—Pennsylvania, 2008–2017

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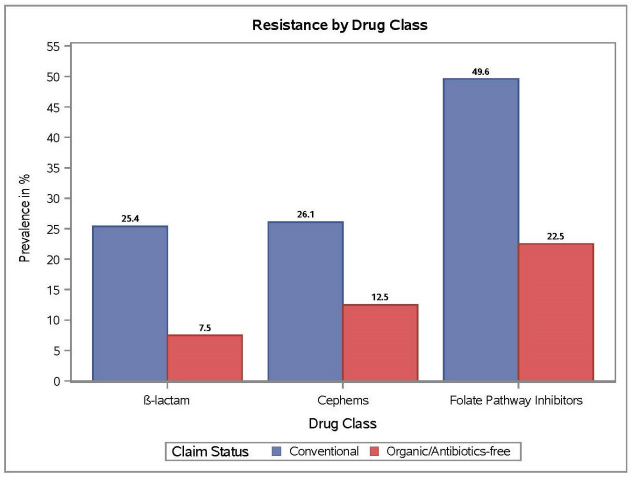
Background. Antimicrobial-resistant (AMR) nontyphoidal Salmonella infections are a public health concern. Injudicious use of antimicrobials fuels emergence of resistance. The National Antimicrobial Resistance Monitoring System (NARMS) tracks AMR in Salmonella from humans, animals and foods. There is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

8–14 days in adults for treatment of ventilated nosocomial pneumonia. Baseline Gram-negative (GN) isolates from patients were tested for mechanisms of resistance.

Methods. Lower respiratory tract (LRT) isolates were sent to a central laboratory for organism identification and susceptibility. Of 664 total Enterobacteriaceae (ENT) and *Pseudomonas aeruginosa* (PsA) isolates, 351 (53%) were nonsusceptible to broad-spectrum cephalosporins and/or carbapenems and underwent whole-genome sequencing, quantitative RT–PCR, and western blot analysis. ENT isolates were tested for the presence of acquired β-lactamase genes and AmpC levels (selected species). PsA isolates were tested for acquired β-lactamase genes, AmpC (PDC) levels, efflux pump expression, and OprD loss.

Results. Of 262 ENT isolates, 114 (44%) were susceptible to C/T (MIC ≤2 μg/mL). An extended-spectrum β-lactamase (ESBL) gene was carried by 89 (78%) of the C/T-susceptible isolates. Of 148 C/T-nonsusceptible (C/T-NS) isolates, 87 (59%) were carbapenemase negative, and the majority 135 (91%) also carried an ESBL gene. The most common ESBL was $bla_{\text{CTX-M15}}$ with $bla_{\text{OXA-1}}$ and $bla_{\text{OXA-30}}$. *Klebsiella pneumoniae* often displayed higher C/T MICs compared with other species carrying the same resistance genes. Among all C/T-NS isolates, 61 (41%) were carbapenemase positive, most commonly *K. pneumoniae* carrying $bla_{\text{OXA-48}}$, $bla_{\text{NDM-1}}$, and $bla_{\text{NDM-5}}$. Of 89 PsA isolates, 58 (65%) were susceptible to C/T (MIC ≤4 μg/mL), despite elevated AmpC expression, efflux pumps, or loss of OprD; only 5 isolates had an acquired β-lactamase. Of the 31 C/T-NS PsA isolates, only 12 (39%) were carbapenemase positive and carried bla_{VIM} or bla_{GES}; isolates carrying bla_{GES} had lower C/T MICs (8–32 μg/mL) compared with bla_{VIM} (MIC > 128 μg/mL). PDC alleles were similar in isolates with high and low C/T MICs.

Conclusion. In baseline GN LRT isolates from ASPECT-NP, the most common ESBL detected in ENT was $bla_{\text{CTX-M15}}$; carbapenemases were uncommon. There was no correlation of ESBL phenotype to C/T susceptibility among ENT, nor of PDC allele to C/T susceptibility among PsA.

Disclosures. **All authors:** No reported disclosures.

625. Genomic Epidemiology of Carbapenem-Resistant *Enterobacteriaceae* from Colombia: A Prospective Multicenter Study

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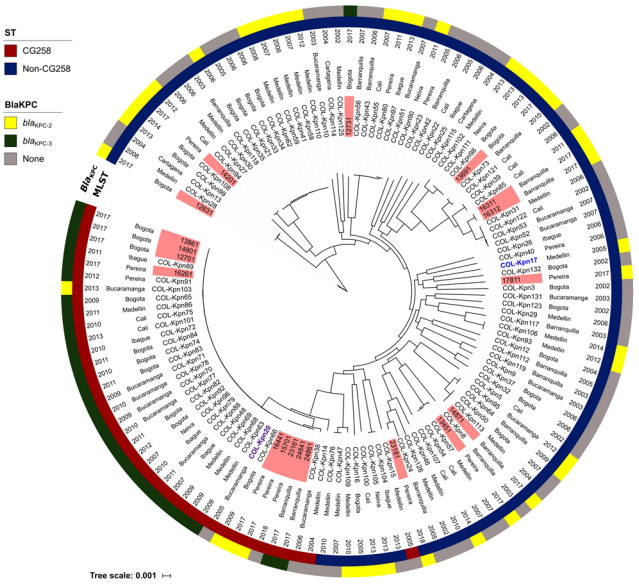
Background. Carbapenem-resistant *Enterobacteriaceae* (CRE) is a serious public health threat. A major epidemic of carbapenemase-producing *Klebsiella pneumoniae* has occurred in Colombia through complex mechanisms of bla_{KPC} dissemination. In the framework of a prospective, observational cohort study (CRACKLE-2), we aimed to characterize the genomic epidemiology of CRE circulating in Colombia.

Methods. We performed whole-genome sequencing of 52 isolates collected from the same number of patients (July 2017–April 2018) in 5 Colombian hospitals. Species confirmation and sequence type were determined using Strain Seeker and MLST database. Resistance genes were detected using ResFinder and CARD databases. Phylogenetic reconstruction included additional 108 isolates of carbapenem-resistant *K. pneumoniae* from a previous study.

Results. *K. pneumoniae* (36%), *Escherichia coli* (17%), and *Enterobacter cloacae* complex(17%) were the most frequent species. Genes conferring resistance to carbapenems were detected in 93% of isolates. $bla_{\text{KPC-2/3}}$, $bla_{\text{NDM-1}}$ and$bla_{\text{VIM-2/24}}$ were identified in 81%, 15%, and 5% of isolates, respectively. Phylogenetic reconstructions of *K. pneumoniae* showed that clonal group 258 (CG258) were the predominant genetic lineage (Figure 1). Among CG258, ST11 was the most common comprising ca. 26% of isolates. Of note, ST11 had been extremely rare in previous surveillance studies in Colombia. The non-CG258 were from 9 different STs and exhibited high genomic diversity. Among *E. coli* isolates 33% belonged to the high-risk clone ST131 harboring $bla_{\text{KPC-2}}$ and we detected both $bla_{\text{KPC-2}}$ and $bla_{\text{VIM-24}}$ in 1 *E. coli* ST131 isolate. ST510 *E. cloacae* complex harboring $bla_{\text{KPC-2}}$ was the most common (44%) lineage.

Conclusion. *K. pneumoniae* and *E. coli* are the most frequent CRE isolated from patients in Colombian hospitals. Dissemination of bla_{KPC} through horizontal gene transfer to several species of *Enterobacteriaceae* continues to be a common mechanism of spread. Although KPC continues to be the most common carbapenemase, a rise in high-risk clonal lineages harboring metallo-carbapenemases, in particular NDM-1 is worrisome. Our results indicate emergence of virulent genetic lineages of *K. pneumoniae* ST11 and *E. coli* ST131 carrying carbapenemases in Colombia.



Disclosures. **All authors:** No reported disclosures.

626. Mobile Genetic Element Dynamics of Co-Circulating *Klebsiella pneumoniae* Sequence Types Carrying *bla*KPC in Houston, Texas

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Background. Carbapenem-resistant *Klebsiella pneumoniae* (CR-Kpn) are a significant cause of hospital-associated infections. Class A β-lactamases, e.g., *Klebsiella pneumoniae carbapenemases* (KPCs), are major contributors to carbapenem resistance. Sequence type 258 (ST258) is the most common genetic lineage of CR-Kpn associated with bla_{KPC} carriage. Recently, a newly emergent lineage ST307 has been identified within the Houston metropolitan region. The transmission of bla_{KPC} and other antimicrobial resistance (AMR) genes is driven largely by exchange of mobile genetic elements (MGEs). We sought to describe the dynamics of horizontal gene transfer (HGT) in particular between co-circulating strains of ST307 and ST258.

Methods. Long-read sequencing technologies allow us to resolve plasmid sequences and their associated AMR genes as well as characterize a comprehensive range of MGEs enabling transmission of these clinically important resistance mechanisms. CR-Kpn isolates were collected as part of a study to describe CRE burden within a Houston metropolitan hospital system. The Oxford Nanopore Technology (ONT) GridION X5 was used for long-read sequencing with Illumina short-read data used to refine and generate high-quality, consensus assemblies. A custom bioinformatic pipeline was used to resolve plasmid structures and identify the genomic context of plasmids carrying bla_{KPC} variants.