622. The Accessory Genome in Enterococcal Bacteria: 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 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 MinION XS, 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”)-Ia 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 31.7 to 132.3 kb. Although the vanA operon was fairly conserved, insertions of MGEs were identified in the intergenic regions of vanA/npnI and vanX/vanY. Furthermore, a variety of MGE insertions mediated integration of the vanA operon, including IS216 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.

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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) non-typhoidal 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 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%, 114/409; 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-lactam (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.

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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 cefluzoxane/tazobactam (C/T) 3 g q8h vs. meropenem 1 g q8h for the treatment of nosocomial pneumonia (NP) caused by aerobic gram-negative bacilli, specifically Pseudomonas aeruginosa (PAO1) and Enterobacteriaceae. Resistance to β-lactams (β-lactamase producers) is common among Enterobacteriaceae and PAO1. Resistance to β-lactams is driven by the expression of β-lactamase enzymes, which can be encoded by chromosomal or plasmid-borne resistance genes. C/T is a β-lactamase inhibitor/β-lactamase producing oral antibiotic combination. Figure 1. Composite view of homology within the coding sequences of plasmid containing β-lactamase enzyme from the Enterobacteriaceae and PAO1. The outward facing domain serves as the β-lactamase enzyme, enabling the internal β-lactamase enzyme to inhibit resistance to β-lactamase producing bacteria. The outward black ring denotes a reference plasmid containing a conventional vanA operon, and similarity to the reference decreased as an inward direction.

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