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Background. Local and systemic use of azole derivatives are common in the treatment of vulvovaginal candidiasis. However, there are cases unresponsive to these agents. Herein, we present treatment and follow-up of a patient with fluconazole–itraconazole and voriconazole-resistant recurrent vaginal candidiasis.

Methods. A 37-year-old woman with no comorbidity used topical and oral antifungal/antibacterial medications (including fluconazole and itraconazole) in the treatment of recurrent vulvovaginitis, was hospitalized due to continuous complaints. Intense, white-colored, odorless vaginal discharge was observed on physical examination. Urine and vaginal swab samples were taken for mycological and bacteriological culture. Metronidazole (500 mg 3x1 i.v.) and high dose fluconazole (600 mg/day i.v.) were initiated empirically for the possibility of dose-dependent resistant Candida infection, but there was no clinical response.

Results. Candida albicans was isolated in vaginal swab culture, but response to systemic fluconazole treatment for one week was inadequate. Antifungal susceptibility test was performed by microdilution method according to CLSI M27A3 guidelines and MIC values were reported respectively; fluconazole 4 μg/mL (SDD), itraconazole 1 μg/mL (R), posaconazole 0.06 μg/mL (WT), voriconazole 0.25 μg/mL (SDD), anidulafungin ≤ 0.015 μg/mL (S), amphotericin B 0.06 μg/mL (WT). For the resistance mechanism, point mutation in the ERG11 gene and MDR1 and MDR2 from efflux pumps were investigated and only the G464S mutation was detected in the ERG11 gene. Treatment was switched to IV anidulafungin (200 mg on day 1 followed by 100 mg/day). Clinical response was achieved in the patient whose complaints were reduced, and there was no Candida in the repeated vaginal swab culture taken on day 3 of treatment. The patient was discharged after 2 weeks of treatment. She had no recurrence after 2 years follow-up.

Conclusion. It should be kept in mind that resistant strains may be responsible for recurrent and unresponsive vulvovaginal candidiasis cases. Although there is no case report in which anidulafungin is used for treatment and it should be kept in mind that the anidulafungin is also in the treatment as it is summarized.

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619. High Multidrug-Resistant due to TEM and CTX-M-1 Types of Extended-Spectrum β-Lactamase and *bla*NDM-1 Type Carbapenemase Genes among Clinical Isolates of Gram-Negative Bacilli in Asella, Central Ethiopia

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Background. Acute infectious diseases and sepsis are among the leading causes of mortality in Ethiopia. The lack of local data concerning causative pathogens and resistance patterns results in suboptimal empirical treatment and unfavorable clinical outcome. The objective of this study was the characterization of bacterial pathogens in hospitalized patients with febrile infections in Central Ethiopia.

Methods. In total, 684 patients ≥1 year of age with fever admitted to the Asella Teaching Hospital from April 2016 to June 2018 were included. Blood and other appropriate clinical specimens were cultured. Susceptibility testing was performed using the Kirby–Bauer method and VITEK2. Confirmation of species identification and identification of resistance genes were conducted using MALDI-ToF and PCR at a microbiology laboratory in Düsseldorf, Germany.

Results. In total, 684 study participants were included; 54% were male and mean age was 26.7 years. Thus, the overall culture positivity rate was 7.5%. Of the 83 cultured organisms, 38(46%) were Gram-negative, 43(52%) Gram-positive, and 2(2%) Candida species. Among the 38 Gram-negative isolates, 16(42%) were *E. coli*, 15(39%) *K. pneumoniae*, and 4(11%) *P. aeruginosa*. Resistance against commonly used antibiotics for Gram-negative at the study site was: piperacillin/tazobactam 48%(13), ampicillin/sulbactam 93% (25), cefotaxime 89%(24), ceftazidime 74%(20), Cefipime 74%(20), meropenem 7%(2), amikacin 4% (1) and gentamicin 56%(15). Of 27 Gram-negative available for resistance-gene detection, blaNDM-1 was detected in one *K. pneumoniae* isolate and blaNDM-1 plus blaOXA-51 in *A. baumannii*. 81%(22/27) of the Gram-negative rods were confirmed to contain ESBL-genes as follows: TEM 17(77%), CTX-M-1-group 15(68%), SHV-6(27%) and CTX-M-9-group 2(9%). Among isolated *S.aureus,* 1(5%) was confirmed to be Methicillin-resistant *S. aureus*.

Conclusion. We found a high prevalence (81%) of ESBL-producing bacteria and 7.4% carbapenem resistance at the study site. More than half of Gram-negative isolates had two or more mobile resistance genes. These findings warrant the need for local national multidrug-resistant surveillance. Strengthening of antimicrobial stewardship programs is needed in order to face the threat of multidrug-resistant bacteria.

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

620. Sub-MIC Concentrations of Levofloxacin and Delafloxacin Enhance *Staphylococcus aureus* Biofilm Formation: Significance of Maximizing Exposure

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Background. Fluoroquinolones are utilized in Staphylococcal prosthetic joint infections due to their anti-biofilm activity. When antibiotic dosing is not optimized or antibiotics do not reach the site of infection, additional virulence factors may upregulate. We aimed to determine whether exposure to sub-MIC concentrations of levofloxacin and delafloxacin affect biofilm formation in *Staphylococcus aureus.*

Methods. This study utilized 50 diverse methicillin-susceptible *S. aureus* (MSSA) clinical isolates collected between 2004 and 2018. Sources included blood, skin/tissue, bone, and joint fluid. Minimum inhibitory concentrations and minimum bactericidal concentrations were identified according to CLSI. Biofilm assays were conducted as previously described by our program. Biofilm quantification was categorized as strong (OD570 ≥ 2), moderate (OD570 ≥ 1 and < 2), or weak (OD_{570} < 1). Prevention assays were conducted with the addition of increasing concentrations of delafloxacin or levofloxacin. We evaluated the amount of isolates that demonstrated increased biofilm formation in the presence of sub-MIC concentrations and extent of biofilm enhancement. Percent change was calculated between OD570 of the isolate growth control without antibiotic exposure and peak biofilm OD570 when exposed to the antibiotic.

Results. Of the 50 MSSA isolates, 14 (28%) exhibited moderate/strong formation and 36 (32%) exhibited weak biofilm formation. 52% and 58% of the isolates demonstrated a ≥50% increase in formation when exposed to sub-MIC concentrations of delafloxacin and levofloxacin, respectively. None of the strong biofilm formers demonstrated a ≥50% peak increase in formation when exposed to the antibiotics. Of the isolates that demonstrated a ≥50% peak increase, the average percent change was 267% (±29) with levofloxacin and 258% (±33) with delafloxacin.

Conclusion. Sub-MIC concentrations of delafloxacin and levofloxacin increased biofilm formation in *S. aureus* isolates that normally exhibit weak or moderate biofilm formation when not in the presence of antibiotics. Maintaining appropriate fluoroquinolone concentrations at the site of action is critical in preventing enhancement of biofilm formation. Further research is needed to identify the mechanism behind this increase.

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621. *In vitro* Ceftazidime: Avibactam Resistance in Carbapenem-Resistant Enterobacteriaceae Isolates

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Background. Ceftazidime–avibactam (CAZ-AVI) is a new antibiotic with activity against many Carbapenem-resistant Enterobacteriaceae (CRE). Although CAZ-AVI resistance in CRE has been reported, it is not consistently assessed. Our study aimed to assess the prevalence of CAZ-AVI resistance in CRE isolated from patients with and without prior exposure to CAZ-AVI.

Methods. We tested 116 CRE isolates for CAZ-AVI resistance by Kirby–Bauer (KB) disk diffusion susceptibility. Resistant isolates were verified by repeat KB and E-test performed by the Stony Brook Hospital laboratory. The bla_{KPC} gene of resistant strains was amplified by PCR and sequenced. Patient data were used to determine whether patients were colonized or infected, and whether they were exposed to CAZ-AVI.

Results. Of the 116 CRE isolates from 86 patients (96 encounters), 50% were *Klebsiella* species, 23.2% were *Enterobacter* species, 10.3% *Escherichia coli* and 16.5% other CRE. They were recovered from colonized (37%) and infected (63%) patients of which 18% were treated with CAZ-AVI during their hospitalizations (median duration of therapy, 6 days). Two CRE isolates (1.7%) were found to be resistant on repeated testing. One isolate was *K. pneumoniae* derived from the sputum of a patient diagnosed with ventilator-associated pneumonia who received 40 days of CAZ-AVI therapy prior to isolation of the resistant isolate (KB diameter 20 mm, MIC > 512 μg/mL by E-Test). Sequencing of the strain's bla_{KPC3} gene revealed a previously described Ambler-position D179Y mutation that has been shown to convey resistance. The second CAZ-AVI-resistant *K. pneumoniae* (KB diameter 19 mm, MIC 64 μg/mL by *E*-test) was isolated from the urine of a colonized patient naïve to CAZ-AVI therapy. The strain's bla_{KPC10} gene had no mutations.

Conclusion. In our strain collection, the rate of resistance to CAZ-AVI remains low <2%. Although we found one mutation (D179Y) previously linked to CAZ-AVI resistance we also discovered one *K. pneumoniae* isolate with *in vitro* resistance to CAZ-AVI that did not exhibit any bla_{KPC} mutations conveying CAZ-AVI resistance. Interestingly, this strain

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.

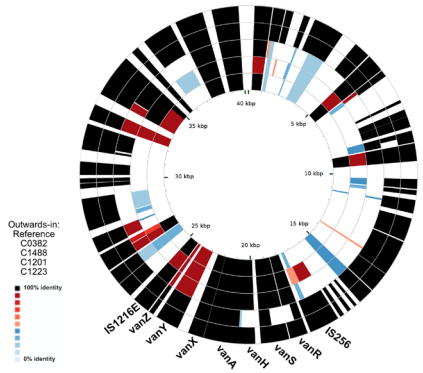

Figure. Composite view of homology within the coding sequences of plasmids containing the vanA operon obtained through long-read sequencing.
The outermost black ring denotes a reference plasmid containing a conventional vanA operon, and similarity to the reference decreases in an inwards direction.

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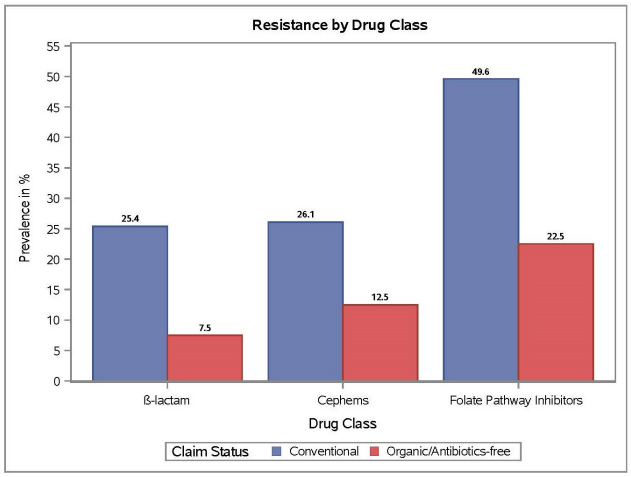
Background. Antimicrobial-resistant (AMR) nontyphoidal Salmonella infections are a public health concern. Injudicious use of antimicrobials fuels emergence of resistance. The National Antimicrobial Resistance Monitoring System (NARMS) tracks AMR in Salmonella from humans, animals and foods. There is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



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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 ceftolozane/tazobactam (C/T) 3 g q8h vs. meropenem 1 g q8h for