sulamethoxazole (TMP/SMX) the following day for pneumonia caused by TMP/SMX-susceptible S. maltophilia. BC finalized on day 29 to S. maltophilia resistant to TMP/SMX, regimen modified to ERV. Repeat BC on day 30 finalized to no growth and ERV was continued until day 42 with no recurrence of bacteremia; however, patient died on day 45. Patient 3 with renal failure and on day 11, CRO started for SRF prophylaxis. On day 13, patient was switched to daptomycin and cefepime (FEP) as patient was febrile and BC repeated. BC finalized to VRE faecium and was started on ERV on day 17 and completed a 7-day course with no recurrence of bacteremia; however, patient died on day 34. Patient 4 initially treated for bacterial superinfection with CRO and azithromycin; and subsequent treatment with Van and MEM (day 10-17). On day 19, patient was febrile and treated with Van and FEP until day 27. Repeat BC on day 29 finalized to VRE species and modified to ERV on day 32. ERV continued for a 7-day course and was discharged with no repeat BC obtained to confirm clearance. Patient in SS started on Van and MEM. On day 1, BC on admission finalized to VRE faecium and therapy switched to ERV. Repeat BC taken on day 3 after ERV initiation were negative. Discharged to complete two-week course of ERV.

**Conclusion.** ERV may be an option for bacteremia as demonstrated by clearance in four of five cases. More studies must be conducted as these reports show variable clinical outcomes.

**Disclosures.** Joshua R. Rosenberg, MD, Allergan/Abbvie (Consultant); La Jolla/Tetraphase (Consultant); Melinta (Consultant); Merck (Consultant); Paratek (Consultant); Sanofi (Consultant); Shionogi (Consultant)

**1244. In Vitro Activity of Ceftaroline-Avibactam and Comparator Agents Against MDR Enterobacteriales and *Pseudomonas aeruginosa* Collected in Latin America During the ATLAS Global Surveillance Program 2018-2019**

Sibylle Lob, PhD; Meredith Hackel, PhD MPH; Gregory Stone, PhD; Daniel F. Sahm, PhD

**Methods.** Non-duplicate clinical isolates were collected in 2018-2019 in 10 countries in Latin America. Susceptibility testing was performed using CLSI broth microdilution and interpreted using CLSI 2021 and FDA (tigecycline) breakpoints. MDR was defined as resistant (R) to ≥3 of 7 sentinel drugs: amikacin (AMK), aztreonam (ATM), cefepime (FEP), colistin (CST), levofloxacin (LVX), meropenem (MEM), and piperacillin-tazobactam (TZP).

**Results.** The activity of CAZ-AVI and comparators against all isolates and MDR subsets is shown in the table. MDR rates for the studied species ranged from 16.3% among E. cloacae to 35.7% among K. pneumoniae. CAZ-AVI was active against 98% of Enterobacteriales isolates and maintained activity against 74-98% of MDR isolates of the examined Enterobacteriales species. Only ticglycine showed higher activity. Among *P. aeruginosa*, CAZ-AVI was active against 87% of all isolates and 47% of MDR isolates; no other studied drug was more active. The three most common MDR phenotypes among Enterobacteriales were 1) R to ATM, FEP, LVX, and TZP (n=150, 12.4% of all MDR Enterobacteriales; 99.3% S to CAZ-AVI), and 3) R to all sentinel drugs except AMK and CST (n=115, 9.1% of all MDR isolates; 76.6% S to CAZ-AVI). The three most common MDR phenotypes among *P. aeruginosa* were 1) R to all sentinel drugs except CST (n=85, 19.7% of all MDR isolates; 24.7% S to CAZ-AVI), 2) R to all sentinel drugs except AMK and CST (n=42, 9.7% of all MDR isolates; 66.7% S to CAZ-AVI), and 3) R to AMK, LVX, and MEM (n=37, 8.6% of all MDR isolates; 24.3% S to CAZ-AVI).

**Conclusion.** These in vitro data suggest that CAZ-AVI can be an effective treatment option for infections caused by MDR Enterobacteriales and *P. aeruginosa* collected in Latin America.

**Disclosures.** Sibylle Lob, PhD, IHMA (Employee); Pfizer, Inc. (Independent Contractor); Meredith Hackel, PhD MPH, IHMA (Employee); Pfizer, Inc. (Independent Contractor) Gregory Stone, PhD, AztraZeneca (Shareholder, Former Employee); Pfizer, Inc. (Employee) Daniel F. Sahm, PhD, IHMA (Employee); Pfizer, Inc. (Independent Contractor)

**1245. In Vitro Activities of Ceftaroline and Comparator Agents Against Bacterial Pathogens Collected from Patients with Skin and Skin Structure Infections: Results of the 2018 ATLAS Program**

Meredith Hackel, PhD MPH; Gregory Stone, PhD; Daniel F. Sahm, PhD; IHMA, Inc.; Schaumburg, Illinois; Pfizer, Inc.; Groton, CT

**Session:** P-72. Resistance Mechanisms

**Background.** Ceftaroline fosamil is a parenteral cephalosporin that provides antibiotic coverage against clinically relevant pathogens associated with SSSIs.

**Methods.** From 2012 to 2019 the ATLAS program received 124,694 bacterial isolates from which were cultured 493 clinical laboratories in 71 countries from samples of patients diagnosed with SSSIs. All isolates were transported to IHMA. Clinical outcomes. More studies must be conducted as these reports show variable clinical outcomes.

**Conclusion.** Ceftaroline fosamil, the prodrug of ceftaroline, is a parenteral cephalosporin approved for the treatment of patients with skin and skin structure infections (SSSIs) caused by *Staphylococcus aureus* (both methicillin-susceptible [MSSA] and methicillin-resistant [MRSA] isolates), β-hemolytic streptococci (Streptococcus pyogenes, S. agalactiae, S. dysgalactiae); and select species of Enterobacteriales (Escherichia coli, Klebsiella pneumoniae, Klebsiella oxytoca). The current study is part of the ATLAS (Antimicrobial Testing Leadership and Surveillance) program and evaluated the current activities of ceftaroline and comparator agents against commonly encountered bacterial isolates associated with SSSIs.

**Results.** The in vitro activity of ceftaroline is summarized in the following table. Overall, >99.9% of MSSA and 92.8% of MRSA from SSSI were susceptible to ceftaroline (MIC ≤ 1 µg/mL); 7.1% of MRSA isolates were ceftaroline-susceptible dose-dependent (MIC 2-4 µg/mL) with greatest proportion being from Chile (53.3% of 392 isolates), South Korea (29.3% of 321 isolates), and China (24.7% of 652 isolates). Twelve ceftaroline-resistant MRSA were observed, consisting of 11 of 109 isolates from Thailand (10.1%) and 1 of 161 from China (0.6%). All *S. pyogenes* and 88.0% of ESBL-negative Enterobacteriales were susceptible to ceftaroline.

**Results Table**

**Disclosures.** Sibylle Lob, PhD, IHMA (Employee); Pfizer, Inc. (Independent Contractor) Gregory Stone, PhD, AztraZeneca (Shareholder, Former Employee); Pfizer, Inc. (Employee) Daniel F. Sahm, PhD, IHMA (Employee); Pfizer, Inc. (Independent Contractor)

**1246. Clinical isolates of *Pseudomonas aeruginosa* Harbor Preexisting Changes in Tobin-Dependent Receptors Associated with Decreased Susceptibility to Cefiderocol**

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inside the zone of inhibition. Breakthrough colonies were isolated on cetrimide agar, and DD studies were performed to determine FDC susceptibility.

**Results.** 6.1% of isolates (13/212) had preexisting mutations in the TBDR genes, including indels in *pir*R (n=2) and *pir*R (n=2), and a frameshift mutation resulting in premature stop codon in *pir*R (n=9). DD showed that isolates with predicted changes in TBDRs had a significantly smaller diameter of inhibition, as compared to controls (Fig 1). Of the PiuA or PirR mutants, 3 of 13 demonstrated breakthrough colonies (Fig 2); while none of the control specimens showed breakthrough colonies. Subcultures of isolated breakthrough colonies yielded more homogenous populations of PA with relatively lower DDs than the original strain (Fig 2).

**Figure 1** Cefiderocol disk diffusion (18 h) and Cefiderocol disk diffusion (48 h)

**Figure 2** Disk Diameter resistance phenotypes suggestive of heteroresistance among P. aeruginosa strains containing TBDR mutations (row 1) and their subsequent break through colony subculture resistance phenotypes (row 2) at 48 hour time points.

**Conclusion.** Mutations in genes encoding TBDR are present in clinical isolates of PA that predate the approval of FDC and are associated with the emergence of reduced susceptibility to FDC.

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**The tree is overlaid with predicted antimicrobial resistance genes and virulence factors for each isolate.**

**Conclusion.** The predominant carbapenemases among clinical Klebsiella species isolates in Qatar are NDM and OXA-48 like enzymes, disseminated through various plasmids. The detection of carbapenemase-producing isolate bearing *rmpA* and serotype K2 reflect the presence of both multidrug resistance and hypervirulence in *K. pneumoniae*.

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**1247. Molecular Epidemiology of Multi-drug Resistant Klebsiella pneumoniae and K. quasipneumoniae in Qatar**

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**Session:** P-72. Resistance Mechanisms

**Background.** The molecular epidemiology of carbapenem-resistant Klebsiella species is not well investigated in Qatar. The objective of this work was to characterize the genetic context of carbapenemase-producing Klebsiella isolates recovered from clinical specimens.

**Methods.** Klebsiella isolates (n=100) were collected at 7 tertiary hospitals from 2015–2017. Identification and susceptibility testing were performed using MALDI-TOF MS and BD Phoenix system, respectively. Whole Genome Sequencing was performed on the Illumina NextSeq platform. Phylogenomic analysis, screening of resistance and virulence genes, and comparison of genetic environment of carbapenemase were carried out.

**Results.** Klebsiella pneumoniae was common (80), followed by K. quasipneumoniae (16), K. aerogenes (3) and K. oxytoca (1). The most prevalent genes were encoding NDM-1 (38), OXA-48 (20), OXA-232 (10) and OXA-181 (12). KPC-2 (3) and KPC-3 (2) were also identified; no carbapenemase-encoding genes could be identified in 15 isolates. Plasmid locations of 24 carbapenemase-encoding genes were determined; blaNDM-1 was localized on IncFII replicon, while blaOXA-232 and blaOXA-48 were commonly associated with ColK3 plasmids. OXA-48-like plasmid was detected in 17/20 isolates harboring blaOXA-48, blaKPC-2, and K. pneumoniae was on a contig with ‘traditional’ Tn4401a mobile genetic element. Sequence types (STs) were diverse and the ‘traditional’ clonal group (CG) 258 was rare. K. pneumoniae ST147 was predominant (13), followed by ST231 (7) and ST11 (5). Nine K. quasipneumoniae isolates belonged to ST196 and were highly clonal. The virulence loci such as yersiniabactin (ybt) and rmpA were not detected within the study’s K. quasipneumoniae isolates. Amongst K. pneumoniae, there were 5 ybt+, 8 isolates had rmpA, and of these, 3 belonged to ST383. K. pneumoniae serotype K2, the capsular serotype associated with invasive liver abscess syndrome, was detected in 5 isolates. Genetic relationship of carbapenem-resistant Klebsiella pneumoniae and K. quasipneumoniae isolates in Qatar inferred from core genome SNPs.