may be facilitated by shared transferable genetic elements, nevertheless, analyses of the genetic MRG context in strains other than USA300-LV are lacking. In this study, we aimed to characterize possible mechanisms of acquisition and transfer of MRG in LA *S. aureus*.

Methods. We sequenced 6 MRSA and 2 MSSA clinical isolates harboring MRG from Colombia, Ecuador, Peru and Chile using short-read (Illumina) and long-read (ONT) sequencing. Hybrid assemblies were constructed using Flye and iterative polishing with Medaka and Racon. Identification of insertion sequences, rearrangements and assessment of the genomic context was investigated using ISfinder, MAUVE, PlasmidFinder and SnapGene.

Results. Highly contiguous genome assemblies allowed us to identify the localization and genetic background of MRG. For MRSA belonging to USA300-LV (SCC*mec*IVc/E) and Brazilian (SCC*mec*III) clones, we confirmed the presence of MRG within SCC*mec*. In contrast, for the 4 MRSA belonging to Chilean/Cordobes clone (SCC*mec*I), collected from Colombia, Chile and Peru, MRG were located on ~30kbp plasmids genetically related that also contained the blaZ beta-lactamase and cadmium/arsenic resistance genes. In MSSA strains, we observed both plasmidic and chromosomal localizations of MGR. Interestingly, in one of the MSSA, MRG were inserted downstream of *orfX*, along with *repA*, suggesting a plasmidic origin. In all these cases, MRG were flanked by IS6 family elements.

Conclusion. Genomic architecture of SCC*mec* types IVc/E and III might facilitate MRG transferability, whereas for the highly prevalent Chilean/Cordobes clone (SCC*mec*I) MRG acquisition occurs through plasmids. Our findings underscore the mechanisms of MRG transference in LA *S. aureus* likely related to antibiotic resistance co-selection.

Disclosures. **Cesar A. Arias, MD, MSc, PhD, FIDSA**, **Entasis Therapeutics** (Scientific Research Study Investigator)**MeMed** (Scientific Research Study Investigator)**Merck** (Grant/Research Support)

1443. Activity of Ceftazidime-Avibactam against Carbapemenase-negative Carbapenem-resistant Enterobacterales (CRE) Isolates from US Hospitals

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Session: P-66. Resistance Mechanisms

Background. Most CRE isolates in US hospitals produce KPC enzymes, but some do not carry carbapenemases. We investigated the prevalence, resistance mechanisms and activity of ceftazidime-avibactam and comparator agents against CRE that did not carry carbapenemase genes from US hospitals. Additionally, meropenem-resistant isolates were tested for meropenem-vaborbactam.

Methods. A total of 28,904 *Enterobacterales* isolates were collected in 70 US hospitals during 2016-2018, and susceptibility tested by reference broth microdilution. Meropenem-vaborbactam was tested using lyophilized panels following the manufacturer's instructions. CRE isolates were submitted to whole genome sequencing for the screening of b-lactamase genes, multilocus sequence typing, changes in outer membrane protein (OMP) genes and AmpC expression levels.

Results. A total of 304 (1.1%) CREs were observed in the study period and 45 (14.8%) isolates did not carry carbapenemases. These isolates were mainly *Klebsiella aerogenes*, *Enterobacter cloacae* and *Klebsiella pneumoniae* (11, 11 and 10 isolates, respectively), but also included 5 other species. Acquired b-lactamase genes were detected among 17 isolates and $bla_{\text{CTX-M-15}}$ was the most common (13 isolates). All *K. aerogenes* and 10 *E. cloacae* did not carry acquired b-lactamase genes. Ceftazidime-avibactam (100% susceptible) inhibited all isolates at the current breakpoint, followed by tigecycline and amikacin (> 80% susceptible). Other comparators were not active against non-carbapenemase-producing CRE. Nine of 35 meropenem-resistant isolates displayed meropenem-vaborbactam MIC values of ≥ 8 mg/L (nonsusceptible). Further analysis showed that 23 isolates had disruption of OmpC/OmpK36, 4 had disrupted OmpF/OmpK35 and 13 had both OMP genes disrupted. Additionally, 7 isolates had elevated AmpC expression among 17 isolates tested. Among 7 *E. coli*, 4 were ST131 and only 2 of 10 *K. pneumoniae* were clonal complex 11.

Conclusion. Therapy options for treatment of infections caused by CRE were very limited until recent approval of new agents with activity against these isolates. Ceftazidime-avibactam demonstrated full *in vitro* activity against all carbapenemase-negative CRE carrying multiple resistance mechanisms.

Disclosures. Mariana Castanheira, PhD, 1928 Diagnostics (Research Grant or Support)A. Menarini Industrie Farmaceutiche Riunite S.R.L. (Research Grant or Support)Allergan (Research Grant or Support)Allergan (Research Grant or Support) Amplyx Pharmaceuticals (Research Grant or Support)Cidara Therapeutics (Research Grant or Support)Cidara Therapeutics (Research Grant or Support)Cipla Ltd. (Research Grant or Support)Cipla Ltd. (Research Grant or Support)Fox Chase Chemical Diversity Center (Research Grant or Support)GlaxoSmithKline (Research Grant or Support)Melinta Therapeutics, Inc. (Research Grant or Support)Melinta Therapeutics, Inc. (Research Grant or Support)Melinta Therapeutics, Inc. (Research Grant or Support)Merck (Research Grant or Support)Merck (Research Grant or Support)Merck & Co, Inc. (Research Grant or Support)Merck & Co, Inc. (Research Grant or Support) Paratek Pharma, LLC (Research Grant or Support)Pfizer (Research Grant or Support) Qpex Biopharma (Research Grant or Support) Timothy B. Doyle, Allergan (Research Grant or Support)Allergan (Research Grant or Support)Cipla Ltd. (Research Grant or Support)Melinta Therapeutics, Inc. (Research Grant or Support)Pfizer (Research Grant or Support)Qpex Biopharma (Research Grant or Support) Cory Hubler, Allergan (Research Grant or Support) Rodrigo E. Mendes, PhD, A. Menarini Industrie Farmaceutiche Riunite S.R.L. (Research Grant or Support)Allergan (Research Grant or Support)Allergan (Research Grant or Support)Basilea Pharmaceutica International, Ltd (Research Grant or Support)Cipla Ltd. (Research Grant or Support)Department of Health and Human Services (Research Grant or Support)GlaxoSmithKline (Research Grant or Support)Melinta Therapeutics, Inc. (Research Grant or Support)Merck (Research Grant or Support)Merck (Research Grant or Support)Pfizer (Research Grant or Support) Helio S. Sader, MD, PhD, A. Menarini Industrie Farmaceutiche Riunite S.R.L. (Research Grant or Support)Allergan (Research Grant or Support)Allergan (Research Grant or Support)Allergan (Research Grant or Support)Cipla Ltd. (Research Grant or Support)Cipla Ltd. (Research Grant or Support)Melinta (Research Grant or Support)Merck (Research Grant or Support) Paratek Pharma, LLC (Research Grant or Support)Pfizer (Research Grant or Support)

1444. Characterization of a Novel Pathogen in Immunocompromised Patients: Elizabethkingia Anopheles

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Session: P-66. Resistance Mechanisms

Background. A 60-year-old woman with acute myeloid leukemia developed fever and cough post induction chemotherapy. Meropenem and vancomycin were administered as empiric therapy. A bloodstream infection due to resistant *E. meningoseptica* was initially identified. Ceftazidime-avibactam and aztreonam (ATM) were next administered. Minocycline and trimethoprim/sulfamethoxazole (TMP/SMX) were added as the patient deteriorated and died ten days later.

Methods. MIC testing /disc diffusion assays were done according to CLSI guidelines. Whole genome sequencing (WGS) was performed, assembled, and annotated using PATRIC.org and compared to Institute Pasteur cgMLST instance of the BIGSdb database tool. Resistant genes and plasmids were identified by the Center for Genomic epidemiology.

Results. Core genome MLST and average nucleotide identity of 99.46% revealed the organism as *E. anophelis,* not *E. meningoseptica*. The WGS assembly resulted in 118 contigs with a chromosome of 4,110,726 bp. Plasmids were not identified. Resistance genes bla_{B11}, $bla_{\text{GOB-13}}$ (a metallo beta-lactamase) and $bla_{\text{CME-1}}$ were detected. *E. anophelis* was resistant to multiple drug classes including aminoglycosides, vancomycin, cephalosporins, and carbapenems. Mechanism based susceptibility testing using double-disc diffusion assays demonstrated susceptibility to cefiderocol (MIC 1 µg/ml), minocycline, TMP/SMX, linezolid, and modestly wider zones of inhibition with the addition of ATM. Susceptibility results are shown in Table 1.

Antimicrobial susceptibility testing using various BLIs and combinations with Aztreonam

Table 1. Antimicrobial susceptibility testing using various BLIs and combinations with Aztreonam

Single Disk-Diffusion assays (in mm)

	MIN	TIG	MOX	CIP	RIF	LZD	VAN	TMP-SMX
E. anopheles	32	20	27	20	27	30	no zone	33

Beta lactam/BLI combinations (in mm)

	CAZ-AVI	PIP-AVI	IMI-AVI	MEM-VAB	MEM-NAC	FEP-ZID	IMI-REL	PIP-NAC
E. anopheles	11	22	no zone	no zone	no zone	22	no zone	24

Combinations with Aztreonam (in mm)

	CAZ-AVI+ATM	PIP-AVI + ATM	MEM-VAB + ATM	FEP-ZIDE+ATM	IMI-REL + ATM
E. anopheles	15	24	8	24	no zone

Abbreviations: PIP: piperacillin; CAZ: ceftazidime; IMI: Imipenem; TMP/SMX: trimethoprim/sulfamethoxazole; AVI: avibactam; MIN: minocycline MEM: meropenem; VAB: vaborbactam; REL: relebactam; NAC: nacubactam; FEP: cefepime; CIP: ciprofloxacin; MOX: moxifloxacin; RIF: rifampin VAN: vancomycin; LZD: linezolid; TIG: tigecycline; ATM: aztreonam

Conclusion. This is one of the first reports describing *E. anophelis* in immunocompromised hosts. More thorough testing methods are needed for distinguishing between species in the *Elizabethkingia* genus in hospital settings as there is concern that this may represent a novel opportunistic infection. Per CDC, *E. anophelis* outbreaks have occurred in three Midwestern states in 2016. Vigilance is warranted to the role of this pathogen in immunocompromised hosts.

Disclosures. Robert A. Bonomo, MD, Entasis, Merck, Venatorx (Research Grant or Support)

1445. Deciphering the Role of the Y221H Ω-loop Substitution in Pseudomonas-derived Cephalosporinase (PDC) in Cephalosporin Resistance

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Session: P-66. Resistance Mechanisms

Background. Antimicrobial resistance is a major global health threat. *Pseudomonas aeruginosa* is a leading cause of nosocomial infections and a key opportunistic pathogen in cystic fibrosis. Multidrug resistant strains are classified as a "serious threat" by the CDC. *Pseudomonas*-derived cephalosporinase (PDC) is largely