Results: Of the 13 case-patients, 69% were male and the median age was 69 years (range: 30 to 77). All S. maltophilia infections were hospital-acquired (>3 days after admission) with 92% being respiratory and 46% resistant to more than one class of antibiotics. All case-patients were admitted to the ICU and had known risk factors associated with developing S. maltophilia infection, including intubation (100%) and receiving antibiotic therapy prior to infection (77%). Other major risk factors included invasive surgery (77%), co-infections (77%), chronic respiratory disease (62%), hypertension (54%), and renal failure (31%). All were severely immunocompromised. Forty-six percent of the case-patients died from complications associated with their illness. **Conclusion:** This is the first S. maltophilia outbreak reported in Alabama. The findings of this case series underscored the importance of employing strict infection prevention measures to reduce poor health outcomes and how strong antibiotic stewardship programs are needed to limit transmission among vulnerable patient populations in these settings. It is recommended that hospitals conduct routine environmental sampling and have a WMP that is effective in limiting S. maltophilia.

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Whole Genome Sequencing to Identify Multiple Clusters of Carbapenemase-Producing Enterobacterales Cases – Colorado, 2022-2023

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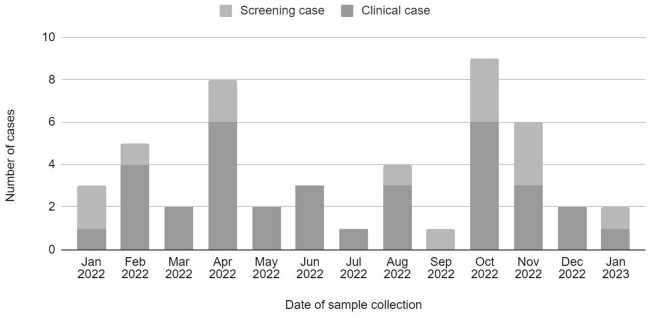
Background: The Colorado Department of Public Health and Environment (CDPHE) detected an increase in Klebsiella pneumoniae carbapenemase-producing carbapenem-resistant Enterobacterales (KPC-CRE) infections in October 2022. We investigated patient epidemiological links and isolate relatedness to characterize interfacility transmission of KPC-CRE in the Denver metro area and inform regional prevention strategies. **Methods:** We defined a case as polymerase chain reaction detection of KPC from clinical or screening specimens collected during January 2022 – January 2023. Cases were identified through statewide CRE surveillance and carbapenemase testing at the CDPHE laboratory and counted once within a 30-day period. Medical records were reviewed to identify healthcare facility admissions and patient facility overlap in the 12 months prior to sample collection. Whole genome sequencing (WGS) was performed for 34 patients with available KPC-CRE isolates using short- and long-read sequencing techniques. We performed multi-locus sequence typing, generated genome phylogenetic trees, and compared plasmid contig sequences to identify relatedness between KPC-CRE isolates. Clusters were defined as ≥2 genetically related isolates of the same organism or carbapenemase plasmid, from different patients. **Results:** We identified 48 cases (34 clinical and 14 screening) among 39 patients (figure). Patients had a mean age of 52 years (range 16-86) and median of three healthcare facility admissions (range 1-14). Twenty-eight patients (72%) were male. We identified 16 (41%) patients with epidemiological links to one acute care hospital (ACH), 11 (28.2%) patients to one long-term acute care hospital (LTACH), and four (10.2%) patients to each of two ventilator-capable skilled nursing facilities (vSNF). Five distinct clusters of

Klebsiella pneumoniae carbapenemase-producing carbapenem-resistant Enterobacterales -- Colorado, January 2022-January 2023



KPC-CRE were identified by WGS among 23 patients (E. hormaechei, two distinct E. cloacae clusters, K. pneumoniae, and K. oxytoca) with linkages to ten healthcare facilities, including two vSNFs, two LTACHs, and six ACHs. Three distinct KPC genes were identified among the clusters: KPC-2, KPC-3, and KPC-4. Genomes assembled from long reads identified identical or similar KPC-gene-containing plasmids across different species or sequence types, suggesting horizontal gene transfer of KPC. **Conclusions:** Multiple KPC-CRE strains co-circulated and were associated with patient movement between acute and post-acute care settings. WGS allowed us to identify multi-facility clusters. Time and location of carbapenemase acquisition were challenging to determine for genetically related isolates when epidemiologic links could not be determined from medical records. This could be due to undetected cases. We notified healthcare facilities of their shared transmission risk and advocated for improved attention to infection control, carbapenemase screening, and communication upon patient transfer.

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Evaluation of Practice Changes in Therapy for Stenotrophomonas maltophilia

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Background: Stenotrophomonas maltophilia (SM) is a non-fermenting, Gram-negative bacillus. Its intrinsic resistance to many beta-lactams makes for challenging treatment decisions. A preprint of the latest Infectious Diseases Society of America (IDSA) guidance on managing SM infections was published in December 2022 providing a recommendation for combination therapy including trimethoprim/sulfamethoxazole (TMP/SMX) and a second agent. An evaluation of the impact on SM treatment practices following this guidance was conducted at our institution. **Methods:** A list of 130 patients with non-urine SM cultures from December 2021-August 2023 was generated using a pharmacovigilance platform. Patients were excluded if on comfort measures or discharged to hospice prior to therapy completion, no directed antibiotics were given, or any history of prior SM infection. Twenty-five patients were randomly selected from the pre- and post-guidance periods (before and one month after December 1, 2022) for a total of 50 patients. Data was collected via manual chart review. The primary endpoint was frequency of combination antibiotic therapy in each time period. Secondary endpoints included treatment success (defined as resolution of infection symptoms and lack of infection recurrence), in-hospital mortality, 30-day mortality, and 30-day infection recurrence. **Results:** Overall, baseline characteristics were similar between groups, the median age was 65 years, 64% of patients were male, 20% were immunocompromised based on prespecified criteria, the

Figure 1. Primary and secondary outcomes

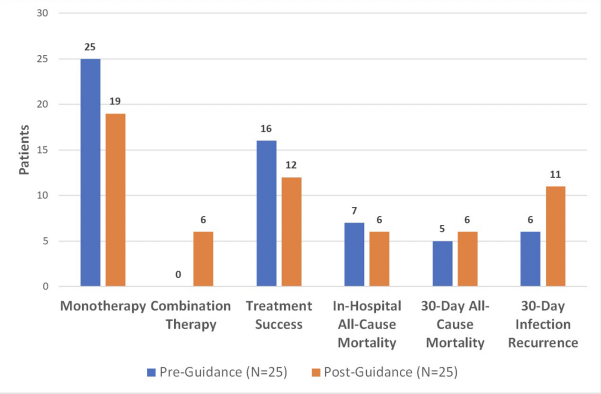

Table 1. Admission Prevalence and Model Prediction of CRE and Non-CRE MDRO Colonization at the Time of MICU Admission

Multidrug-Resistant Organism (MDRO) of Interest	Encounters with MDRO Detected at Admission n, % (N=1237)	Receiver Operator Curve C-statistic (95% CI)
Carbapenem-resistant Enterobacterales (CRE)	27 (2.2)	0.82 (0.72-0.91)
Carbapenem-resistant *Pseudomonas aeruginosa* (CRPA)	10 (0.8)	0.82 (0.66-0.97)
Composite carbapenem-resistant MDRO (including CRE and CRPA)	37 (3.0)	0.81 (0.74-0.90)
Vancomycin-resistant enterococcus (VRE)	160 (12.9)	0.76 (0.72-0.80)
Third-generation cephalosporin-resistant Enterobacterales (3GCR-E)	217 (17.5)	0.61 (0.57-0.65)
Methicillin-resistant *Staphylococcus aureus* (MRSA)	68 (5.5)	0.57 (0.50-0.64)

median Charlson comorbidity index was 5 (21% estimated 10-Year survival), and 76% of SM cultures were pulmonary isolates. Displayed in figure 1, combination therapy was given in 6 of 25 cases (24%) in the post-guidance group and zero patients in the pre-guidance group. Secondary endpoints of treatment success and all-cause mortality were similar between groups. Duration of therapy was similar between combination and non-combination therapy regimens (median 9 vs 10 days). Among patients who received combination therapy, all had ID consultation, 4 (66.7%) were admitted to the ICU, and 2 (33.3%) had treatment success. **Conclusions:** Patients treated for SM infection at our institution in the post-IDSA guidance period were more likely to receive combination therapy. A higher rate of treatment success was not observed in the post-IDSA guidance arm for SM infections. Limitations of this study include its small sample size and retrospective design, leading to inability to distinguish colonization from true infection. Additional studies are needed to evaluate the impact of combination antibiotic therapy on outcomes.

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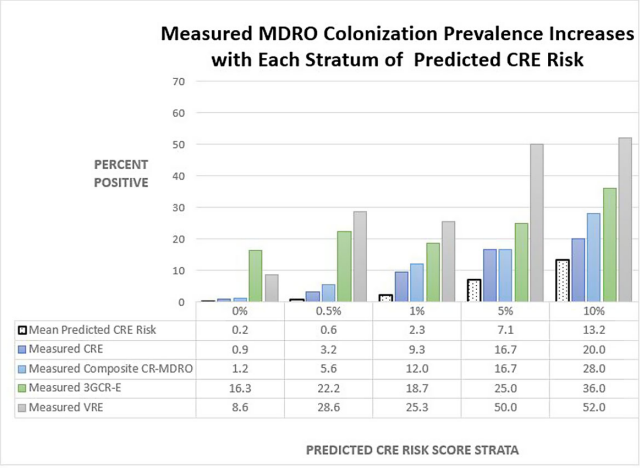

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Medical Informatics

Application of a Model Using Prior Healthcare Information to Predict Multidrug-Resistant Organism (MDRO) Carriage

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Background: Early identification of patients colonized with MDROs can help healthcare facilities improve infection control and treatment. We evaluated whether a model previously validated to predict carbapenem-resistant Enterobacterales (CRE) carriage on hospital admission (area under the curve [AUC]=0.86, Lin et al. OFID 2019) would generalize to predict a patient's likelihood of CRE and non-CRE MDRO colonization at the time of medical intensive care unit (MICU) admission. **Methods:** We analyzed data collected previously in a retrospective observational cohort study of patients admitted to Rush University Medical Center's MICU from 1/2017-1/2018 and screened within the first two days for rectal MDRO colonization. Organisms of interest included CRE, carbapenem-resistant Pseudomonas aeruginosa (CRPA), vancomycin-resistant enterococci (VRE), and third-generation cephalosporin-resistant Enterobacterales (3GCR-E). Methicillin-resistant Staphylococcus aureus (MRSA) nasal colonization at admission was determined by routine clinical screening. Each patient's first MICU admission during the study period was linked to Illinois' hospital discharge database and assigned a CRE colonization risk probability using the existing model. Model covariates were age, and during the prior 365 days, number of short-term acute care hospitalizations (STACH) and mean STACH length of stay, number of long-term acute care hospitalizations (LTACH) and mean LTACH length of stay, prior hospital admission with an ICD-10 diagnosis code indicating bacterial infection, and current admission to LTACH. Predictive value of the model was evaluated by receiver operating characteristic (ROC) curves. **Results:** We analyzed 1237 MICU admissions. MDRO admission prevalence is shown in the Table. The model performed well to predict carriage of healthcare-associated MDROs, including CRE, CRPA, composite CR-MDROs (CRE & CRPA), and VRE. However, the model performed poorly for MDROs with known community reservoirs, including 3GCR-E and MRSA (Table). In general, MDRO admission prevalence increased in parallel with predicted CRE colonization risk (Figure). The number needed to screen (NNS) to detect one healthcare-associated MDRO carrier was inversely related to the CRE colonization risk score. For example, NNS in the total cohort compared to those with CRE risk score of >0.5% was: CRE 111 vs 32 patients, CRPA 333 vs 42 patients, composite CR-MDRO 83 vs 18 patients, and VRE 12 vs 4 patients. However, higher CRE risk score cutoff was inversely related to screening sensitivity. **Conclusion:** A prediction model using prior healthcare exposure information successfully discriminated patients likely to harbor healthcare-associated MDROs upon MICU admission. Prediction scores generated by a public-health accessible database could be used to target screening/isolation or enact protective measures for high-risk patients.

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