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Carbapenamase-producing carbapenem-resistant Enterobacterales (CP-CRE) is an urgent public health threat for healthcare facilities. Solid organ transplant (SOT) recipients carry an increased risk for CRE infection and colonization due to prolonged exposures to antimicrobials, healthcare facilities and immunosuppression. CRE infection in SOT patients is associated with an increase in morbidity and mortality. Here, we describe a hospital outbreak investigation of three cases of New Delhi metallo-beta-lactamase (NDM) - CRE that led to novel findings with implications for further interdisciplinary investigations. An NDM-CRE infection in a critically-ill patient was identified during passive surveillance and prompted an investigation. Previous CP-CRE passive surveillance cases were reviewed. Rectal screening was performed for potentially exposed patients. 403 rectal swabs were tested for carbapenemase genes in active surveillance. Patients identified to have a new NDM-CRE isolate on active or passive surveillance were considered cases and underwent in-depth chart review including possible patient-to-patient exposures, hospital locations, procedures, devices, and consultations. NDM-CRE isolates were sent to the Minnesota Department of Health (MDH) for whole genome sequencing (WGS) to assess relatedness. Five NDM-CRE cases were identified, with all isolates harboring blaNDM including three NDM-Klebsiella pneumoniae (NDM-KP) cases (Figure 1). The first NDM-KP case, patient 1, developed mediastinal infection following lung transplantation. Review of United Network for Organ Sharing revealed that respiratory specimens from patient 1's donor grew NDM-KP and a bronchial wash at the time of transplant yielded NDM-KP. The second NDM-KP case (patient 3) developed ventilator-associated pneumonia and was found to have used sequentially the same ventilator as patient 1. The third NDM-KP case (patient 4) was detected via rectal swab in active surveillance and shared wound care personnel in common with patients 1 and 3 (Figure 2). WGS demonstrated two single nucleotide polymorphisms (SNP) among all three isolates, strongly suggesting relatedness (Figure 3). Best practices for infection prevention were reviewed with wound care personnel. To date, no further NDM-KP isolates have been identified. Investigation was facilitated by in-depth chart review and WGS via the Central Region Antimicrobial Resistance Laboratory Network at MDH. Detection of the NDM-KP from a lung donor specimen appears genetically linked to clinical isolates in other patients, raising the possibility of a donor-derived hospital outbreak. This investigation is the first to describe a donor-derived NDM outbreak in a healthcare facility. Communication between organ procurement agencies, transplant centers, and infection prevention must be optimized to prevent CRE-associated morbidity in SOT receipts and CRE hospital outbreaks.

Figure 1: NDM-CRE Case Identifications

Patient	Source of Isolate	Date of Isolate	Active or Passive Surveillance	Organism	Resistance genes	Collection Location
1	Mediastinal aspirate	July 7 2023	Passive	*Klebsiella pneumoniae*	*bla*NDM	Medical critical care unit
2	Urine	Aug 6 2023	Passive	*Escherichia coli*	*bla*NDM	Medical critical care unit
3	Sputum, Blood	Aug 20 2023	Passive	*Klebsiella pneumoniae*	*bla*NDM	Cardiac critical care unit
4	Rectal swab	Aug 31 2023	Active	*Klebsiella pneumoniae*	*bla*NDM	Step-down unit
5	Rectal swab	Sept 1 2023	Active	*Citrobacter freundii*	*bla*NDM	Medical critical care unit

Figure 2: NDM-KP case timeline

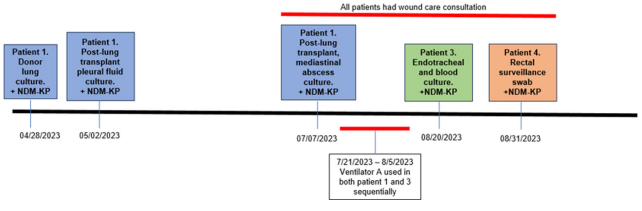

Figure 3: Single nucleotide polymorphism (SNP) heat map of NDM-KP cases. All NDM-KP isolates are multilocus sequence type (MLST) 111. Low SNP numbers suggest genetic relatedness.

	Reference*	Patient 1 **	Patient 3	Patient 4
Reference*		1197	1196	1199
Patient 1**	1197		2	2
Patient 3	1196	2		2
Patient 4	1199	2	2	

*Outlier control reference *K. pneumoniae* isolate that is MLST 111 containing a different carbapenemase gene (*bla*$_{KPC-4}$)
**Pre-transplant donor lung isolate used

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Containment of a KPC-CRE Outbreak Associated with Premise Plumbing in a Long-Term Care Facility— Minnesota, 2022-2023

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Background: On March 23, 2022, the Minnesota Department of Health (MDH) was notified of Klebsiella pneumoniae carbapenemase (KPC)-producing Klebsiella oxytoca isolated from a resident's urine in long-term care facility A (LTCF-A). Carbapenem-resistant Enterobacterales (CRE) are reportable statewide with required isolate submission to MDH Public Health Laboratory (MDH-PHL), where carbapenemase production and mechanism identification is confirmed. **Methods:** MDH partnered with LTCF-A on a containment response, including infection prevention and control (IPC) measures, KPC-CRE education, and colonization screening. Rectal swabs were screened for carbapenemase genes by real-time PCR (Cepheid Xpert Carba-R), with positive specimens undergoing culture, isolation, and whole genome sequencing (WGS). MDH-PHL conducted WGS including multilocus sequence typing (MLST) and single nucleotide polymorphism (SNP) analysis to describe genetic relationships among isolates. When screening indicated a potential environmental source, due to species diversity and ongoing resident transmission, an environmental screening plan was developed including collection of premise plumbing samples from room faucets, aerators, sinks, toilets, and shared shower drains. **Results:** KPC-CRE was detected in 23 residents (urine, n=2; rectal swab, n=21) during March 2022–November 2023. 21 isolates comprising 10 Enterobacterales species were cultured from KPC-positive screening specimens. SNP analysis performed on bacteria of the same species demonstrated 5 distinct clusters of relatedness comprising 2-3 residents per cluster (Cluster 1: Klebsiella oxytoca, n=3; Cluster 2: Klebsiella oxytoca, n=3; Cluster 3: Escherichia coli, n=2; Cluster 4: Klebsiella pneumoniae, n=2; Cluster 5: Raoultella planticola, n=2). 7 KPC-positive resident specimens did not yield a culturable organism. KPC-CRE was detected throughout the premise plumbing including 8 of 9 shared shower room

drains and 6 of 75 resident room sink drains. WGS and SNP analysis suggest relatedness among resident and environmental KPC-CRE isolates. Gaps in IPC measures including hand hygiene, use of personal protective equipment (PPE), environmental cleaning and disinfection, and sink hygiene practices were observed during onsite assessments. Use of an EPA-registered biofilm disinfectant in facility drains and repeated environmental sampling has demonstrated a decrease in KPC-harboring bacteria within the premise plumbing, but not complete elimination. **Conclusion:** Containing the spread of KPC-CRE within LTCF-A has been challenging due to environmental reservoirs of KPC-CRE along with insufficient implementation of IPC practices. Continued colonization screening has been necessary to detect newly colonized residents and reinforce efforts to increase IPC compliance. Strict implementation and adherence to IPC measures, including those that minimize the spread of KPC-CRE from facility premise plumbing, are needed to fully halt KPC-CRE transmission within LTCF-A.

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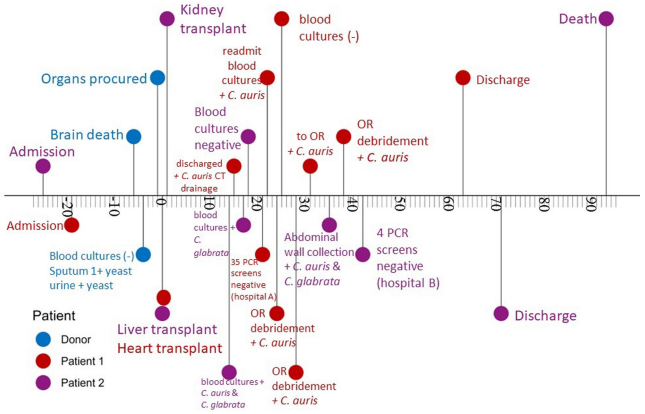

Figure: Timeline of *C. auris* cluster at the Medical University of South Carolina hospitals A & B in September – December 2023. Axis depicts days relative to the heart and liver transplant date (day 0). PCR screens refer to axilla-groin screening PCR tests for patients co-located in inpatient units with patients 1 & 2.

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Poster Presentation - Poster Presentation
Subject Category: Outbreaks
Candida auris cluster in a center with no previous infections associated with a single organ donor

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Background: Candida auris is an opportunistic pathogen reported in the US since 2016. C. auris infections (CAI) are frequently healthcare-associated, but only one case of donor-derived CAI in a lung transplant recipient has been reported (PMID 28520901). We describe a cluster of two CAIs at a single center in South Carolina occurring in 2 different recipients from the same solid organ transplant donor. **Methods:** We describe two cases of invasive CAIs occurring in an academic medical center without prior CAI in Charleston, SC in October 2023. C. auris was identified using Bruker MALDI-TOF and confirmed by the state health department. **Results:** Patient 1: 40-49 year-old male underwent heart transplantation on day 19 from admission complicated by growth of C. auris on post-op day #15 from a drain. He was readmitted post-op days 22-63 with positive blood cultures for C. auris and underwent re-operation with debridement and hardware removal. C. auris pericarditis required multiple returns to the OR (Figure). He was discharged on micafungin/posaconazole with plans for long-term antifungal therapy. Patient 2: 50-59 year-old male underwent liver and kidney transplantation on day 25 from admission from the same donor as Patient 1 in a separate hospital complex. His course was complicated by possible infected biloma not amendable to drainage and C. auris/C. glabrata fungemia, which was further complicated by abdominal wall collection cultures growing C. auris on post-operative day 35 on washout. He was managed with dual micafungin/posaconazole however, he died of unrelated causes at 93 days after transplant (Figure). Investigation: The donor for both recipients was a 10-19 year-old male who suffered brain death after trauma and was hospitalized for 56 days prior to procurement in Atlanta, GA without known CAI. Airway cultures at the time of organ procurement were positive for rare Pseudomonas and light unidentified yeast of multiple morphologies; urine cultures also grew 40,000 cfu/ml un-identified yeast. Screening of 35 and 4 inpatients in units exposed to patients 1 & 2, respectively, with axilla/groin PCR was negative (Figure). A third organ recipient for this donor (kidney) at our center was identified and had negative urine fungus cultures. **Conclusions:** Despite no definitive link to a known donor infection, this cluster of CAI occurring simultaneously in 2 patients in separate hospitals/units at a single center with no known prior cases represents likely donor-derived CAI. Our experience suggests that organ procurement organizations should consider improved screening techniques for C. auris in donor cultures.

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Multi-year Epidemiology of Nontuberculous Mycobacteria Across a Diverse Healthcare System

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Background: Nontuberculous mycobacteria (NTM) are ubiquitous potential pathogens implicated in healthcare-associated outbreaks. There is a paucity of studies describing transmission risk in the healthcare setting. To estimate the potential healthcare-associated transmission of NTM, we characterized the frequency of NTM clinical isolates across our multi-facility healthcare system. **Method:** We performed a retrospective review of all clinical NTM isolates at 21 healthcare facilities in a large health system between January 2019 through June 2023 (inclusion criteria: all first unique species). We analyzed the quarterly frequency of isolates for each species, by facility. We identified higher-than-expected species frequencies, which was defined as a quarterly frequency ≥50% higher than the average quarterly frequency for that facility, for the entire study period (analysis omitted for any hospital with an average quarterly frequency 10 unique patient isolates in any 12-month period or >2 in a single month except for M. abscessus at Hospital A. The quarterly frequency of the three most common species among hospitals with ≥2 unique isolates per 12-month period are displayed in figure 2. An increase of 50% from the average