IGRA tested. Five employee conversions were identified: one surgeon, one circulating OR nurse, two CSPD decontamination staff, and one respiratory therapist. At time of detection, none of the conversions had evidence of active tuberculosis. Additionally, 46 patients and visitors were tested with zero conversions. HCP compliance with IGRA testing was initially 15% before engagement from hospital and unit leadership and human resources. With intervention, employee compliance reached 100%. **Conclusion:** Despite standard use of surgical masks for OR and CSPD staff, aerosolization of infected bone graft material played an important role in tuberculosis transmission during surgery and instrument cleaning. Respiratory therapy practices in the ICU setting likely also increased risk for pulmonary tuberculosis transmission. Achieving 100% HCP compliance for baseline and follow-up IGRA testing is challenging and requires engagement of both unit and hospital leadership and human resources to ensure all HCP are tested.

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Subject Category: Outbreaks
Implementation of the WHO IPC Ring Approach During the 2022 Uganda Sudan Ebola Virus Disease (SUDV) Response at the Epicentre
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Background: At the onset of an outbreak, immediate infection, prevention and control (IPC) measures and strategies are critically important in stopping the transmission. During the 2022 Sudan Virus Disease (SUDV) outbreak in Uganda, the IPC technical working group (TWG) adopted the WHO ring approach for intensive and targeted IPC support to interrupt transmission in high-risk areas and healthcare facilities (HCFs). Objectives: a) Leverage surveillance and epidemiological activities to guide response efforts and implement targeted IPC interventions. b) To rapidly interrupt SUDV transmission at the source through multiple IPC interventions. **Methods:** The IPC TWG delineated outbreak perimeters (rings) to include health facilities and community sites within 500 meters in urban centres and 1 kilometer in rural areas around each confirmed case. A data base with this information was developed and updated daily with information provided by the surveillance team. To activate response within 12 hours, interventions included rapid needs and risk assessments , health educational materials, deployment of decontamination teams and district IPC mentors with hygiene supplies delivered within 24 hours and a 72-hour follow-up. Trained Village Task Forces (VTF) and IPC mentors conducted health education, set up screening points, holding units, and rapid notification channels. **Results:** 56 rings including HCFs (38) and community sites (78) were identified within the radius of confirmed cases. Using the IPC scorecard, health facility mean scores significantly increased from 18% to 61.7% at follow-up in three weeks. Community WASH baseline scores improved from 11.1% (inadequate) to 69% with a basic level in two weeks. There was marked reduction in the incidence of new cases in the epicentre within the first 32 days. **Conclusion:** The results suggest that the IPC ring approach is an instrumental strategy health ministries can adopt to rapidly provide targeted comprehensive support at the source to interrupt transmission. A collaborative effort across pillars and partners in the implementation of the ring approach is key through concerted efforts and information sharing across response pillars.

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Clearing the Air, Breathe Easy: Intensive Care Unit Remodeling Unveils Insights into Aspergillosis Prevention
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Background: Invasive aspergillosis (IA) poses a substantial threat to morbidity and mortality, particularly among immunocompromised individuals. In 2023, a New York City Intensive Care Unit (ICU) experienced an aspergillus outbreak following a structural water leak, resulting in two patients diagnosed with Invasive Aspergillus niger in their bronchial cultures. Immediate interventions, including patient relocation and ICU reconstruction were implemented to mitigate further impacts. This study aims to assess the impact of timely relocation of patients and renovation of the ICU, on the incidence of invasive aspergillosis. **Method:** A quasi-experimental study design of ICU patients over a nine month period included surveillance by the Infection Prevention department from March 1 to December 1, 2023. Surveillance included review of microbiology reports, environmental cultures, and patient chart reviews. The Pre-intervention spanned March 1 to May 1, and the post-intervention from May 4 to December 1. Indoor mold assessments of pre- and post-intervention involved testing wall surfaces for moisture, air sample collection for fungal spores, and surface swabs for direct fungal analysis. The intervention included relocating all seventeen patients from the impacted ICU and comprehensive reconstruction. Reconstruction involved the removal and replacement of all sheetrock within the unit extending four feet from the floor with moisture-resistant sheetrock. Additionally, moisture resistant single sheet welded vinyl flooring and cove-bases were installed. All heating, ventilation, and air-conditioning (HVAC) systems were inspected and cleaned. Construction activities strictly adhered to Infection Control Risk Assessment (ICRA) guidelines, with emphasis on maintaining negative pressure, to ensure a safe environment. **Result:** Environmental swab samples from 50% of ICU rooms indicated growth of Aspergillus/Penicillium, Chaetomium, and Stachybotrys/Memnoniella type spores during the pre-intervention phase. Environmental microbiology results strongly suggest the indoor environment as the fungal spore source, with the presence of fruiting structures indicating surface mold growth. Indoor air samples, when compared to outdoor samples collected during pre-intervention, showed rare (2-6 raw count) growth of Aspergillus in 55% of the sampled rooms and subequently no growth post-intervention. Prospective surveillance revealed no further aspergillus growth in the ICU population and environment. **Conclusion:** Our findings highlight a potential correlation between environmental modifications and reduced IA incidence. Swift mitigation and structural interventions are crucial in averting potentially fatal outcomes, marking a significant advancement of prevention strategies for inner-city hospital settings. Although promising, study limitations include the inability to speciate environmental aspergillus for comparison to patient bronchial cultures and the absence of baseline bronchial cultures for affected patients on admission.

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Investigation of a Donor-derived Carbapenamase-producing Carbapenem-resistant Enterobacterales Hospital Outbreak
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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

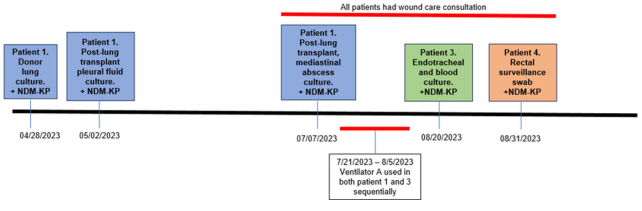

Figure 3: Single nucleotide polymorphism (SNP) heat map of NDM-KP cases. All NDM-KP isolates are multilocus sequence type (MLST) 111. Low SNP numbers suggest genetic relatedness.

	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