

RESEARCH ARTICLE

Editorial Process: Submission:07/10/2025 Acceptance:13/10/2026 Published:24/10/2026

The Unusual Outbreak of Sepsis in a Cancer Hospital Caused by Intrinsically Contaminated Heparin Injection Vials

Vijeta Bajpai^{1*}, Akhil Kapoor², Anwita Mishra³, Bipinesh Sansar², Anuj Gupta², Rahul Sarode³, Jyotirmay Kirtaniya⁴, Archana Angrup⁵, Manisha Biswal⁵, Bal Krishna Mishra²

Abstract

Background: The outbreaks in oncology settings result in dreaded complications, especially in cancer patients who are already immunocompromised. Here, we describe the identification and response to an unusual hospital-acquired outbreak of bloodstream infections (BSIs) in cancer patients due to intrinsic contamination of a heparin injection vial with New Delhi metallo-beta-lactamase (blaNDM)-positive *Klebsiella pneumoniae*. **Methods:** An increased cluster of sepsis cases in cancer patients with chemoports was noted in the medical oncology department of a cancer center in North India in July 2024. These case clusters were identified by reviewing microbiological reports, and blood cultures were tested by automated identification and susceptibility testing, the Carba-R test, and molecular testing. Outbreak investigations were performed; causality assessment was also done. The clinical and demographic details of the case patients, along with other relevant histories, were collected from electronic medical records. Environmental samples were collected from high-touch surfaces, intravenous medications, saline, and heparin. **Results:** A cluster of 10 sepsis cases with culture-confirmed bloodstream infections (BSIs) was identified in the medical oncology department. Out of the 10 patients, 5 (50%) were admitted to the ward after visiting the central venous access device (CVAD) clinic, and 5 (50%) presented to the emergency department after recent chemotherapy. All cases had *Klebsiella pneumoniae* isolated from blood cultures, which alerted the oncology team to a possible outbreak. All isolates were multidrug-resistant strains sensitive to ceftazidime-avibactam and tigecycline. The multidrug resistance gene detected in all isolates was blaNDM. The heparin injection vial was found to be the primary cause and single source of the outbreak. All isolates from heparin and patients' clinical samples were confirmed by molecular typing using Enterobacterial Repetitive Intergenic Consensus Polymerase Chain Reaction (ERIC-PCR). Interestingly, the contamination was found to be intrinsic to a new batch of heparin manufactured by the company. **Conclusion:** This study highlights the importance of an infection surveillance system as part of pharmacovigilance, which helped detect the source of infection within a few days of the outbreak alert. Implementing standardized healthcare-associated infection (HAI) surveillance in a low-resource setting detected an ongoing heparin-associated outbreak. The outbreak investigation and the use of a multimodal approach reduced incident cases and informed changes in infection prevention and control (IPC) practices. The regulatory authorities (CDSCO and the Indian Pharmacopoeia Commission) were also notified, which helped them enforce strict quality control and regulatory oversight in drug manufacturing.

Keywords: Pharmacovigilance, Quality Care, Infection control, cancer

Asian Pac J Cancer Prev, 27 (10), 3629-3635

Introduction

Healthcare-associated infection (HAI) outbreaks remain a significant threat to patient care and safety in hospital settings. In addition to increasing morbidity and mortality, such outbreaks impose substantial financial burdens and can adversely affect the reputation of healthcare institutions. Although outbreaks are

frequently reported, they are not always systematically investigated. The absence of standardized policies and guidelines for the timely detection and response to HAI outbreaks contributes to delayed recognition and increased severity of complications, particularly among vulnerable populations such as cancer patients [1].

HAI outbreaks are typically identified by clustering of infection cases linked by time, place, and person.

¹Department of Microbiology, MPMCC, Varanasi (HBNI Mumbai), India. ²Department of Medical oncology, MPMCC/HBCH, Varanasi (HBNI Mumbai), India. ³Department of Microbiology, MPMCC/HBCH, Varanasi (HBNI Mumbai), India. ⁴Department of Critical Care, MPMCC/HBCH, Varanasi. (HBNI Mumbai), India. ⁵Department of Medical Microbiology, PGI, Chandigarh, India. *For Correspondence: vijetabajpaikgm@gmail.com

However, the true burden is likely underestimated, as many outbreaks remain unrecognized due to inadequate surveillance and underreporting. This issue is particularly critical in oncology settings, where patients are inherently immunocompromised and thus more susceptible to severe infectious complications [2].

Patients with cancer represent a high-risk group with increased incidence of hospital-acquired infections, especially central line-associated bloodstream infections (CLABSI), compared to the general hospital population. This heightened risk is largely attributed to the use of long-term vascular access devices such as chemo ports and peripherally inserted central catheters (PICCs), which are essential for administering chemotherapy and supportive care. These devices are inserted using strict aseptic protocols, including surgical aseptic non-touch technique (SANTT), typically in operation theatre settings by trained personnel [3, 4].

To maintain catheter patency and prevent thrombosis, heparin is routinely used for catheter flushing. Despite adherence to aseptic insertion techniques, bloodstream infections may still occur, commonly due to breaches in sterile technique during insertion or lapses in catheter maintenance practices. Additionally, contamination of intravenous (IV) fluids and medications is a well-recognized but often underdiagnosed source of hospital-acquired bacteraemia, as routine culturing of infuses is not commonly performed [5–7].

In India, the development of HAI surveillance networks supported by agencies such as ICMR, NCDC, and CDC has demonstrated the feasibility and importance of standardized surveillance systems in detecting bloodstream infections and improving infection control practices across healthcare facilities [7–9].

In this study, we describe an unusual outbreak of sepsis in cancer patients with chemo ports and PICCs, caused by multidrug-resistant *Klebsiella pneumoniae* harboring the New Delhi metallo- β -lactamase (blaNDM) gene. To the best of our knowledge, this represents a rare and previously unreported occurrence of an HAI outbreak linked to intrinsically contaminated heparin vials containing blaNDM-producing *K. pneumoniae*.

Materials and Methods

Hospital setting and patients

The study was conducted at the in 350 bedded Mahamana Pandit Madan Mohan Malviya Cancer Center of the Tata memorial Cancer Centre in Varanasi, India. Our center is a 350-bed, state of art tertiary care oncology center and teaching hospital in North India. As a regional referral cancer center, approximately one third of annual admissions of cancer patients transferred from other nearby or tertiary care hospital. The microbiology department along with Nursing department supervise the hospital's infection prevention control program. The infection prevention and control program participates in active ongoing Hospital acquired infection surveillance mainly CLABSI and CAUTI in collaboration to AIIMS, New Delhi and CDC Atlanta [10]. Under this collaboration, surveillance protocol of healthcare-associated infections

is adapted from protocols published by the US Centers for Disease Control and Prevention National Healthcare Safety Network. As per the baseline data retrieved from the HAI surveillance, the prevalence of carbapenem resistance among *K. pneumoniae* isolated from blood specimens is more than 70% comparable to recent national estimates [11]. The Hospital infection prevention control program also manages containment efforts for multidrug-resistant organisms (MDROs); these efforts involve implementation of standard contact precautions and isolation of patients, increased sensitization of hand hygiene, increased environmental cleaning of affected wards and communication among the staff working in the affected wards.

Study population, case definitions: The study population included all the sepsis patients in the medical oncology department and cases were defined as patients from whom multidrug-resistant *K. pneumoniae* in paired blood culture were isolated. Isolates were classified as multidrug-resistant (MDR) if they were non susceptible to 3 or more antibiotic classes as per the reference [12]. The patients enrolled under case definition were reviewed for their clinical details in their medical charts, demographic information, antibiotic prescription details, type of admission, collection of the blood culture and outcome.

Detection and confirmation of the outbreak: A routine review of laboratory reports of medical oncology department by clinicians and by Infection control team in July 2024 was done. This has found a high rate of BSIs caused by *Klebsiella pneumoniae* in medical oncology department. The clinical team also suspected the increasing number of cases of chemo port associated blood stream infections especially from CVAD and medical oncology wards. This review of HAI data also showed that these cases were associated with sepsis. Microbiology team investigated bacteriology laboratory records and the automated bacterial identification system (VITEK-2 Compact) master registers for *Klebsiella pneumoniae* cases starting on July 2024. Identification of Pathogen and antimicrobial susceptibility testing data from outbreak cases was collected from microbiology laboratory. Descriptive epidemiology data were collected from patient records using a standardized investigation form adapted from the CDC healthcare-associated-outbreak investigation tool kit [13]. The form captured sociodemographic data; clinical history; and exposure to intravenous medications, oral medications, fluids, procedures, and antibiotics. The data were stored and analyzed using Epi Info version 7.2 software.

Investigation of Outbreak and Infection control assessment: A multidisciplinary team consisting medical oncologists, microbiologists, ICNs, CVAD, nursing in charges were prepared. ICNs and other staff of team observed medication and intravenous fluid preparation and administration and adherence to hand hygiene and standard and transmission-based precautions in the CVAD, IR OT and medical oncology wards.

Outbreak Interventions and laboratory investigation

Blood cultures of the patients were sent to microbiology laboratory for the identification of cause of the sepsis.

Outbreak cases were identified by reviewing laboratory records and patient medical record forms. Bacterial identification and antimicrobial susceptibility testing data from outbreak cases was collected from microbiology laboratory. Blood specimens were collected and incubated as per standard laboratory protocols. Isolates were tested on Vitek 2 (bioMérieux, Marcy l'Etoile, France); identification was performed using the Vitek 2 GN card (bioMérieux); and antimicrobial susceptibility testing was performed using the Vitek 2 AST-N406 card (bioMérieux). All minimum inhibitory concentrations (MICs) were interpreted according to CLSI break points [14], except for colistin and tigecycline, which were interpreted according to EUCAST guidance [15]. Isolates that were determined to be resistant to colistin by Vitek 2 were also tested by BMD for confirmation. Antimicrobial susceptibility of the isolates was performed by the VITEK 2 system against amoxycillin clavulanic acid, cefuroxime, cefotaxime, ceftriaxone, cefepime, ertapenem, imipenem, meropenem, piperacillin-tazobactam, ciprofloxacin, levofloxacin, amikacin, gentamicin, tigecycline and trimethoprim-sulfamethoxazole. *Escherichia coli* ATCC 25922 was used as quality control strain for antibiotic susceptibility tests. Results were interpreted following Clinical and Laboratory Standards Institute (CLSI) guidelines (M-100, Ed 2024) [14]. Strains not susceptible to at least one agent in three or more antimicrobial classes were defined as multidrug-resistant and were used in the study [12]. Bacterial identification and antibiotic susceptibility were performed by automated identification system (Vitek-2 system, Biomeriux Germany and the results were evaluated according to CLSI 2024 criteria [12]. In antimicrobial sensitivity testing it was Multidrug-Resistant (MDR) strain resistant to third generation of cephalosporins, beta-lactam and beta-lactamase-inhibitor combinations, resistant to carbapenems, fluoroquinolones, aminoglycosides and sensitive to tigecycline, Ceftriaxone-Sulbactam-EDTA (CSDE) and Ceftazadime-avibactam (CZA). Carbapenem resistant gene was detected by performing molecular assay Carba R test (Xpert® Carba-R, Cepheid). Molecular analysis was done to check clonal similarity between the isolates. ERIC-PCR technique was carried out in thermocycler (Thermo ABI Veriti™ Biosystems) using ERIC primers-forward: 5'-ATG TAA GCT CCT GGG GAT TCAC-3' and reverse: 5'-AAG TAA GTG ACT GGG GTG AGC G3'. The PCR protocol consisted of an initial denaturation cycle at 95°C for 5 min, followed by 30 cycles of denaturation at 94°C for 1 min, annealing at 48°C for 1 min, extension at 72°C for 1 min, and a final cycle of amplification at 72°C for 10 min. PCR products were loaded on 1.5% agarose gel at constant voltage of 70V for one hour, and the banding patterns were visualized under ultraviolet radiation (Figure S1) [16]. Ethical approval for this study was provided Institutional ethical committee with IEC no. OIEC/11000947/2026/00002.

Environmental samples were collected from high-touch surfaces, air, water, and medication preparation areas using Hi Culture swabs (HI Media, India) (Table 1). Samples were enriched in thioglycolate broth and incubated at 37°C for 18 hours. Samples of intravenous

medications, saline IV Heparin fluid were collected. The enriched broth was then inoculated on tryptic soy agar supplemented with 5% sheep blood and MacConkey agar. Water samples were test kits (HI Media, India), incubated at 37°C for 12 hours, and then sub cultured on Mac Conkey agar. Identification and antimicrobial susceptibility testing (AST) of environmental isolates was performed on Vitek 2 system.

Results

In total, 10 patients met the outbreak case definition whose paired blood culture (one from chemo port and other from PICC) flashed positive for Gram Negative Bacteria (GNB) and differential time positivity between central line and peripheral blood was found approximately 2 hours and central line blood flashed positive before the peripheral line. All GNB grew hyper mucoid colonies of *Klebsiella pneumoniae* Figure 1.

Detailed clinical characteristics and demographic details of the patients are provided in the Table 2. All patients infected with *K. pneumoniae* cases began to increase in June 2024 and peaked in July 2024 (Figure 1). The median age was 33 years (range, 3 months–78 years). Although 2 (20%) of the case patients died (Table 2), these deaths could not be solely attributed to the *K. Pneumoniae* related infection or complications. Among them, 5 (50 %) of these cases were visited to emergency department and then admitted to medical oncology wards at the time of the infection. Medical records were available to review for all cases showed history of recent chemotherapy. As part of the investigation, efforts were made to identify MDR *K. pneumoniae* BSIs that occurred before the outbreak period. Between January and April 2024, there are zero cases of MDR blaNDM *K. pneumoniae* were reported from the medical oncology department. Figure shows the epidemic curve and onset and peak of the outbreak cases.

Almost all outbreak cases were having chemo port and underwent a documented chemotherapy cycle before *K. pneumoniae* BSIs detection. Among these cases, 7 (71%) had a chemo port insertion inside the hospital and in 3 of which 30% were inserted in the outside the hospital. The median number of days from chemotherapy cycle to positive *K. pneumoniae* blood culture collection for these cases was 2 (range, 1–4).

Table 1. Environmental Sampling Sites and Sample Numbers (68)

S. No.	Sample Source	Number of Samples
1	IR OT Water	5
2	Water – CVAD supply	2
3	Air sampling (settle plate method) IR OT	5
4	Ultrasound machine ports and transducers	6
5	Air sampling (settle plate method) CVAD	5
7	Dialysate water	10
8	IV normal saline	10
9	IV Heparin (Used and New Open)	5
10	Disinfectants – alcohol solution, glutaraldehyde	10

Table 2. Clinical and Epidemiological Characteristics of the Case Patients (n=10)

Variable	No.=10 (%)
Age, median y (range)	33 (3 month-72 year)
Male: Female	1:01
Diagnosis of the patients	
Ca Breast	5 (50%)
Ca pancreas	1 (10%)
Hematolymphoid malignancy	1 (10%)
Colorectal Adenocarcinoma	1 (10%)
Ewing sarcoma Right Distal Leg	1 (10%)
Gastro Esophageal Junction Cancer	1 (10%)
Location of Chemo port Insertion	
OT of the hospital	7 (70%)
Outside hospital	3 (30%)
Origin of admission	
Direct admission from emergency	5 (50%)
Transferred from CVAD	5 (50%)
Location on date of collection of first positive specimen	
CVAD follow-up	1 (10%)
Intensive care unit	1 (10%)
Medical Oncology OPD	8 (80%)
Deceased	2 (20%)

All (100%) were MDR and antimicrobial sensitivity interpretation is described in Table 3. All isolates were resistant to carbapenems, extended-spectrum cephalosporins, and penicillin/ β -lactamase inhibitors. The isolates were most commonly susceptible to tigecycline (100%), and CSDE. The most common carbapenemase genes among isolates were bla_{NDM}. The patients were prescribed intravenous CZA and AT in slow infusion. After starting of the antibiotic patients' symptoms resolved and patients recovered from sepsis. ERIC PCR revealed all isolates clonally related *K. pneumoniae* clusters comprising 10 case-patients

The GNB were isolated from 5 (8.6 %) of 58 environmental samples. Samples from total 3 used and 2 open batch of heparin vial (Biotech) were identified as *K. pneumoniae* which was tested for resistance gene and found to carbapenemase bla_{NDM} positive strain.

Table 3. Antibigram of All the Outbreak-Associated bla_{NDM} Positive *Klebsiella Pneumoniae* Isolates (N=10)

S. no.	Antibiotics	Interpretation
1	Amoxycillin –Clavulanic acid	Resistant
2	Cefuroxime	Resistant
3	Cefotaxime	Resistant
4	Ceftriaxone	Resistant
5	Cefepime	Resistant
6	Ciprofloxacin	Resistant
7	Levofloxacin	Resistant
8	Piperacillin-tazobactam	Resistant
9	Cefepirazole sulbactam	Resistant
10	Imipenem	Resistant
11	Meropenem	Resistant
12	Tigecycline	Sensitive
13	Amikacin	Resistant
14	Gentamicin	Resistant
15	Trimethoprim- Sulfamethoxazole	Resistant
16	Ceftazadime-avibactam	Susceptible
17	Ceftriaxone-sulbactam EDTA	Susceptible
18	Colistin (BMD)	Susceptible
19	Synergy testing between Ceftazadime-Avibactam & Aztreonam (Tested by Broth disc elution)	Synergy present

All isolates from 10 clinical samples of patients and contaminated heparin medications had the same antimicrobial susceptibility as mentioned above for the patients. All isolates were confirmed by molecular typing by Enterobacterial Repetitive Intergenic Consensus Polymerase Chain Reaction followed by pulsed-field gel electrophoresis which showed the similar bands of same base pair both from patients' sample and from intrinsically contaminated heparin medicine (Figure 2).

Outbreak response

In response to the ongoing chemo port sepsis outbreak, removal of chemo port done in patients with *K. pneumoniae* BSI as soon as blood culture positive flashes. All new and old batch of heparin injection vials was withdrawal from all wards, OT, CVAD clinic and IPDs by pharmacy team. Causality assessment of the adverse

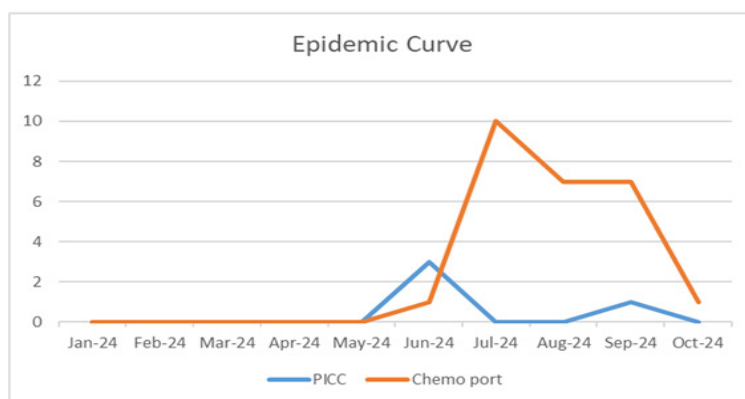


Figure 1. Epidemic Curve of outbreak showing the Chemoport Blood stream Infections (BSIs) cases represented by orange line, while Blue lines representing the PICC related BSIs.

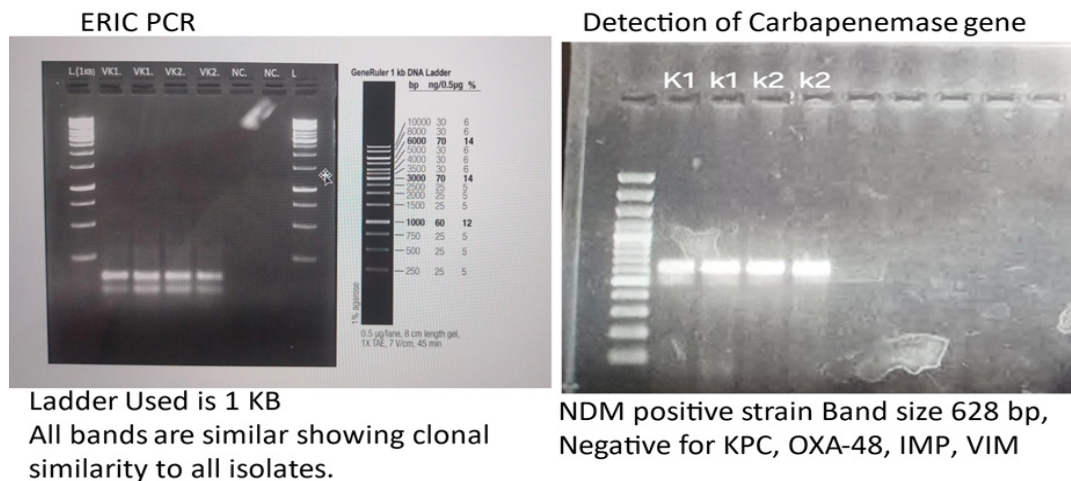


Figure 2. Molecular Analysis of Klebsiella Pneumoniae Isolates of Heparin Vial Blood Stream Infections associated Outbreak

event from heparin injection vial and the sepsis was undertaken by the Causality Assessment Committee of the Institute. The Adverse Drug Reaction Monitoring Cell (AMC) notified the adverse drug event with the causality assessment report to the Pharmacovigilance Commission of India and to the Central Drugs Standard Control Organization (CDSCO) with details of the brand name, formulation, batch number of the heparin injection vials for their independent inquiry and causality assessment, and subsequent regulatory actions. The Hospital Pharmacy procured single-use prefilled heparin lock flush syringes for use in patients with chemo ports and PICC. The use of multi-dose heparin vials was stopped in all over hospital. All patients were treated for sepsis and no mortality reported among these patients.

Discussion

To our knowledge, this is the first reported outbreak of bloodstream infections linked to intrinsically contaminated heparin injection vials containing blaNDM-producing *Klebsiella pneumoniae* in a tertiary oncology centre. Previous studies have described outbreaks and adverse events associated with heparin; however, these have largely focused on hypersensitivity reactions, including anaphylaxis leading to hypotension and mortality [17-24]. In contrast, our study highlights a microbiologically driven outbreak due to intrinsic contamination of a pharmaceutical product.

The high prevalence of multidrug-resistant (MDR) and carbapenem-resistant *Klebsiella pneumoniae* in tertiary care settings poses a significant challenge for outbreak investigations, often obscuring the identification of uncommon sources of infection. [25, 26] In this context, the detection of a contaminated heparin vial as the source of infection underscores the importance of considering non-conventional reservoirs during outbreak investigations. Notably, heparin plays a critical role in maintaining the patency of chemo ports and peripherally inserted central catheters (PICCs), and is routinely used in oncology practice. Therefore, outbreaks related to contaminated infusions or injectable medications caused

by MDR Gram-negative bacilli such as *K. pneumoniae* and *Escherichia coli* may remain underrecognized and be misclassified as routine healthcare-associated infections [27].

In the present study, a standardized, multidisciplinary approach involving clinicians, microbiologists, infection control teams, and pharmacovigilance units enabled early detection and effective containment of the outbreak. Real-time HAI surveillance and systematic data monitoring facilitated identification of case clustering and tracking of outbreak progression in response to infection prevention and control (IPC) interventions.

Several key factors contributed to the successful containment of chemo port-associated sepsis. First, the implementation of robust HAI surveillance protocols, including continuous training of healthcare workers and strengthening of microbiology laboratory capacity, enabled timely identification and reporting of bloodstream infections, including those caused by blaNDM-producing *K. pneumoniae*. Second, close coordination between clinical teams and infection control units allowed real-time analysis of surveillance data and exclusion of alternative sources of infection. The use of digital platforms for data reporting, analysis, and visualization further enhanced outbreak detection.

The short interval between chemotherapy administration and onset of sepsis suggested a potential role of central venous access devices. However, retrospective analysis revealed that a subset of patients had chemo ports or PICCs inserted at external healthcare facilities, thereby reducing the likelihood of a common breach in insertion practices within the study centre [28]. Subsequent evaluation of injectable medications identified heparin as the only common exposure among affected patients. Microbiological testing confirmed contamination of heparin vials, establishing it as the primary source of the outbreak. Withdrawal of the implicated heparin batches from all hospital areas resulted in a rapid decline in incident cases (Figure 1), further supporting causality.

This study has several limitations. First, incomplete medical records for patients referred from other institutions limited comprehensive data analysis. Second, the absence

of dedicated infection control personnel across all units constrained the collection of detailed data on multimodal IPC interventions. Third, although molecular typing demonstrated clonal relatedness among isolates, advanced genomic characterization (e.g., whole genome sequencing or subtype analysis) was not performed, limiting deeper epidemiological insights.

Our findings confirm that the heparin contamination was intrinsic, i.e., present at the time of manufacture. Intrinsic contamination represents a significant public health concern, as such products are widely distributed and may affect multiple patients across different healthcare facilities. This contrasts with extrinsic contamination, which is usually localized and easier to control.

These findings emphasize the urgent need for robust infection surveillance systems, strengthened microbiology services with rapid turnaround times, and close integration between infection control teams and pharmacovigilance programs such as the Indian Pharmacopoeia Commission and regulatory authorities like the Central Drugs Standard Control Organization. Strengthening these systems is essential to ensure early detection of outbreaks, improve patient safety, and maintain public trust in healthcare systems.

In conclusion, this outbreak confirmed intrinsically contaminated heparin injection vials as the single source of blaNDM K. pneumoniae bloodstream infections in cancer patients with chemo ports and PICCs. Rapid detection through surveillance, microbiological confirmation, causality assessment, and regulatory notification enabled timely containment and prevented mortality. Strengthening hospital infection control systems, pharmacovigilance linkages, and regulatory oversight of drug manufacturing is essential to prevent similar events.

Author Contribution Statement

All authors contributed equally in this study.

Acknowledgements

None.

References

1. National Centre for Disease Control. National guidelines for infection prevention and control in healthcare facilities, India. New Delhi: NCDC; 2024.
2. Centers for Disease Control and Prevention. International Infection Control Branch: HAI prevention and surveillance. Atlanta: CDC; 2024.
3. World Health Organization. Surveillance of healthcare-associated infections: a practical guide. Geneva: WHO; 2024.
4. National Centre for Disease Control. Healthcare-associated infections and their surveillance in India. New Delhi: NCDC; 2024.
5. Sharma V, Pandey A. A spectrum of chemoport-associated complications and their management in cancer patients. *Cureus*. 2024;16(4):e58052. <https://doi.org/10.7759/cureus.58052>.
6. Vescia S, Baumgärtner AK, Jacobs VR, Kiechle-Bahat M, Rody A, Loibl S, et al. Management of venous port systems in oncology: A review of current evidence. *Ann Oncol*. 2008;19(1):9-15. <https://doi.org/10.1093/annonc/mdm272>.
7. Haddadin Y, Annamaraju P, Regunath H. Central line-associated bloodstream infections. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2025.
8. Mathur P. Need for national-level surveillance of HAIs in India. *Journal of Clinical Infectious Disease Society*. 2023;1(2):137-9. https://doi.org/10.4103/cids.cids_52_23.
9. Vedachalam SK, Siromany VA, VanderEnde D, Malpiedi P, Vasquez A, Dikid T, et al. Implementing a healthcare-associated bloodstream infection surveillance network in India: a mixed-methods study on the best practices, challenges and opportunities, 2022. *Antimicrobial Resistance & Infection Control*. 2024 Dec;13(1):144.
10. Healthcare Associated Infections Surveillance India. Surveillance of CLABSI and CAUTI. Available from: <https://haisindia.com>
11. Indian Council of Medical Research. Annual report: AMR surveillance network. New Delhi: ICMR; 2023.
12. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. *Clin Microbiol Infect*. 2012;18(3):268-81. <https://doi.org/10.1111/j.1469-0691.2011.03570.x>.
13. Centers for Disease Control and Prevention. HAI outbreak investigation user's guide for completing the abstraction form. Atlanta: CDC; 2024.
14. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. 34th ed. CLSI supplement M100. Wayne (PA): CLSI; 2024.
15. European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters. Version 14.0. Växjö (Sweden): EUCAST; 2024.
16. Kundu J, Kansal S, Rathore S, Kaundal M, Angrup A, Biswal M, et al. Evaluation of ERIC-PCR and MALDI-TOF as typing tools for multidrug resistant klebsiella pneumoniae clinical isolates from a tertiary care center in India. *PLoS One*. 2022;17(11):e0271652. <https://doi.org/10.1371/journal.pone.0271652>.
17. Nyandwaro J, Hyland P, Ravinetto R, Jacobs J. Healthcare-associated bloodstream infections caused by bacterial and fungal contamination of intravenous fluids and medicines in healthcare facilities in low- and middle-income countries: A scoping review. *Antimicrob Resist Infect Control*. 2025;14(1):24. <https://doi.org/10.1186/s13756-025-01536-3>.
18. Macias AE, Huertas M, de Leon SP, Munoz JM, Chavez AR, Sifuentes-Osornio J, et al. Contamination of intravenous fluids: A continuing cause of hospital bacteremia. *Am J Infect Control*. 2010;38(3):217-21. <https://doi.org/10.1016/j.ajic.2009.08.015>.
19. Blossom DB, Kallen AJ, Patel PR, Elward A, Robinson L, Gao G, et al. Outbreak of adverse reactions associated with contaminated heparin. *N Engl J Med*. 2008;359(25):2674-84. <https://doi.org/10.1056/NEJMoa0806450>.
20. Liu H, Zhang Z, Linhardt RJ. Lessons learned from the contamination of heparin. *Nat Prod Rep*. 2009;26(3):313-21. <https://doi.org/10.1039/b819896a>.
21. Kaiser HA, Ben Abdallah A, Lin N, Tellor BR, Helwani M, Smith JR, et al. Contaminated heparin and outcomes after cardiac surgery: A retrospective propensity-matched cohort study. *PLoS One*. 2014;9(8):e106096. <https://doi.org/10.1371/journal.pone.0106096>.
22. Warkentin TE, Greinacher A. Heparin-induced anaphylactic

- and anaphylactoid reactions: Two distinct but overlapping syndromes. *Expert Opin Drug Saf.* 2009;8(2):129-44. <https://doi.org/10.1517/14740330902778180>.
23. Mohamed A, Abdelrahman A, Fadul KY, Elgassim M. Heparin-induced anaphylaxis shock. *Qatar Med J.* 2023;2023(2):17. <https://doi.org/10.5339/qmj.2023.sqac.17>.
24. Apondi OE, Oduor OC, Gye BK, Kipkoech MK. High prevalence of multi-drug resistant *Klebsiella pneumoniae* in a tertiary teaching hospital in western Kenya. *Afr J Infect Dis.* 2016;10(2):89-95. <https://doi.org/10.21010/ajid.v10i2.3>.
25. Ferreira RL, da Silva BCM, Rezende GS, Nakamura-Silva R, Pitondo-Silva A, Campanini EB, et al. High prevalence of multidrug-resistant *klebsiella pneumoniae* harboring several virulence and β -lactamase encoding genes in a Brazilian intensive care unit. *Front Microbiol.* 2018;9:3198. <https://doi.org/10.3389/fmicb.2018.03198>.
26. Farhadi M, Ahanjan M, Goli HR, Haghshenas MR, Gholami M. High frequency of multidrug-resistant (mdr) *klebsiella pneumoniae* harboring several β -lactamase and integron genes collected from several hospitals in the north of Iran. *Ann Clin Microbiol Antimicrob.* 2021;20(1):70. <https://doi.org/10.1186/s12941-021-00476-1>.
27. Goetz AM, Rihs JD, Chow JW, Singh N, Muder RR. An outbreak of infusion-related *Klebsiella pneumoniae* bacteremia in a liver transplantation unit. *Clin Infect Dis.* 1995;21(6):1501-3. <https://doi.org/10.1093/clinids/21.6.1501>.
28. O'Grady NP, Alexander M, Burns LA, Dellinger EP, Garland J, Heard SO, et al. Guidelines for the prevention of intravascular catheter-related infections. *Clin Infect Dis.* 2011;52(9):e162-93. <https://doi.org/10.1093/cid/cir257>.



This work is licensed under a Creative Commons Attribution-Non Commercial 4.0 International License.