

Genomic Surveillance of Carbapenemase-Producing *Klebsiella pneumoniae* in Hospital Wastewater Across Sub-Saharan Africa: A Systematic Review

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ABSTRACT

Background: Carbapenemase-producing *Klebsiella pneumoniae* (CPKP) is a major antimicrobial resistance threat, while hospital wastewater represents an important reservoir and potential pathway for environmental dissemination. Genomic surveillance can reveal resistance determinants, genetic lineages, and transmission patterns, but evidence from Sub-Saharan Africa remains fragmented.

Objective: This systematic review evaluated genomic evidence on CPKP in hospital wastewater across Sub-Saharan Africa, focusing on carbapenemase determinants, genomic lineages, mobile genetic elements, and surveillance approaches.

Methods: Major electronic databases were systematically searched using predefined eligibility criteria and the PRISMA 2020 framework. Eligible studies investigated CPKP recovered from hospital wastewater or associated effluents in Sub-Saharan African countries. Data on detection methods, carbapenemase genes, resistance determinants, sequence types, plasmids, genomic approaches, and epidemiological findings were extracted and narratively evaluated.

Results: Hospital wastewater harboured genetically diverse CPKP carrying clinically important carbapenemase determinants

and mobile genetic elements. Reported isolates exhibited diverse sequence types and plasmid-associated resistance profiles, indicating both clonal and potentially horizontal dissemination. However, genomic evidence was geographically uneven and concentrated in relatively few countries. Targeted molecular methods predominated, whereas whole-genome and metagenomic approaches were less frequently applied, limiting resolution of genomic relatedness and transmission pathways. **Conclusion:** Hospital wastewater represents an important but underutilized genomic surveillance interface for CPKP in Sub-Saharan Africa. Standardized wastewater surveillance, expanded genomic sequencing and bioinformatics capacity, and integration of environmental and clinical genomic data are needed to strengthen early detection, track resistance dissemination, and support coordinated One Health antimicrobial-resistance control.

Keywords: *Klebsiella pneumoniae*, Carbapenemase, Hospital wastewater, Genomic surveillance, Antimicrobial resistance and Sub-Saharan Africa.

Introduction

Antimicrobial resistance (AMR) is a major global health threat, with resistant bacterial infections responsible for substantial morbidity and mortality worldwide [1]. Carbapenem resistance is particularly concerning because carbapenems remain important therapeutic options for severe infections caused by multidrug-resistant Gram-negative bacteria. Among these pathogens, *Klebsiella pneumoniae* is a prominent healthcare-associated organism with a remarkable capacity to acquire and

disseminate antimicrobial-resistance determinants [2]. Carbapenemase production, mediated predominantly by enzymes such as KPC, NDM, VIM, IMP, and OXA-48-like carbapenemases, can confer resistance to most β -lactam antibiotics and substantially restrict treatment options. The African context is especially challenging because surveillance and laboratory capacities remain uneven, potentially limiting accurate characterization of the regional AMR burden.

A recent systematic review and meta-analysis reported substantial occurrence of carbapenem-resistance genes among *K. pneumoniae* from clinical samples across Africa, confirming the importance of this pathogen in the continent's carbapenem-resistance landscape [3].

Hospital wastewater has increasingly been recognised as an important environmental interface in the epidemiology of AMR because it receives continuous inputs of resistant bacteria, resistance genes, antimicrobial residues, and other biological contaminants from healthcare facilities [4, 5]. The high microbial density and diverse biological composition of wastewater can facilitate persistence, interaction, and horizontal transfer of antimicrobial-resistance determinants. Consequently, wastewater surveillance can complement conventional clinical surveillance by providing an integrated picture of resistant organisms circulating within healthcare environments. Evidence from Burkina Faso demonstrated that wastewater from healthcare centres contained ESBL-, AmpC- β -lactamase-, and carbapenemase-producing *Escherichia coli* and *K. pneumoniae*, confirming its potential role as a reservoir of clinically important resistance [6, 7]. At the broader continental level, a recent systematic review and meta-analysis identified carbapenemase genes in hospital wastewater across Africa, but also revealed substantial geographical and methodological heterogeneity in the available evidence [8]. These findings highlight the need for more systematic investigation of wastewater-associated carbapenem-resistant *K. pneumoniae* within Sub-Saharan Africa.

The epidemiological value of wastewater surveillance is strengthened when conventional microbiological detection is combined with genomic characterization. Whole-genome sequencing (WGS) can simultaneously resolve antimicrobial-resistance determinants, sequence types, virulence-associated characteristics, plasmids, and other mobile genetic elements, thereby providing greater discriminatory power than phenotypic testing or single-target molecular assays [9, 10]. Genomic surveillance is particularly valuable for *K. pneumoniae* because resistance can spread through both clonal expansion and horizontal transfer of mobile genetic elements. Environmental investigations have demonstrated this genomic diversity; Ekwanzala et al. [5], for example, characterized carbapenem-resistant *K. pneumoniae* isolates recovered from the environment and identified a novel sequence type associated with carbapenem resistance [11]. Such findings demonstrate that environmental reservoirs can harbour genetically distinctive resistant lineages with potential epidemiological relevance. Integrating genomic analysis with wastewater surveillance can therefore provide insights into the identity, diversity, and potential dissemination of carbapenemase-producing *K. pneumoniae* that cannot be obtained from resistance-gene detection alone.

Despite growing recognition of environmental AMR reservoirs, genomic surveillance of carbapenemase-producing *K. pneumoniae* in hospital wastewater remains insufficiently characterized across Sub-Saharan Africa. Earlier evidence documented the emergence and spread of carbapenemase-producing bacteria across African countries, establishing the continent as an important setting for carbapenem-resistance surveillance [12]. However, substantial gaps remain in determining how specific *K. pneumoniae* lineages, resistance determinants, and mobile genetic elements are distributed within hospital wastewater systems.

The recent evidence base remains geographically uneven, and many investigations rely on targeted molecular methods that identify resistance genes without providing sufficient resolution to establish genomic relatedness or distinguish clonal from plasmid-mediated dissemination [13,14]. At the same time, clinical surveillance alone cannot adequately capture environmental reservoirs or potential routes of dissemination beyond healthcare facilities. These limitations underscore the need to consolidate available genomic evidence and evaluate how wastewater-based surveillance can contribute to a more integrated understanding of carbapenem-resistant *K. pneumoniae* in the region.

This systematic review focuses specifically on genomic surveillance of carbapenemase-producing *K. pneumoniae* in hospital wastewater across Sub-Saharan Africa. It synthesizes evidence on the occurrence of these organisms, carbapenemase genes and associated resistance determinants, genomic lineages and sequence types, plasmid-associated features, and genomic approaches used for their detection and characterization. The review further examines evidence concerning potential dissemination pathways and identifies geographical, methodological, and genomic surveillance gaps across the region. By consolidating these findings, the review aims to define the current genomic landscape of carbapenemase-producing *K. pneumoniae* in hospital wastewater and identify priorities for standardized environmental surveillance, integration with clinical AMR monitoring, and strengthened One Health approaches to carbapenem-resistance control.

Methods

Search Strategy and Information Sources

A systematic literature search was conducted in PubMed, Google Scholar, CORE and Europe PMC to identify published evidence on carbapenem-resistant and carbapenemase-producing *Klebsiella pneumoniae* associated with wastewater and related aquatic environments. The search strategy combined terms for the organism, carbapenem resistance and carbapenemases, and wastewater using the Boolean operators AND and OR. The principal search structure was: “*Klebsiella pneumoniae*” AND (carbapenemase OR “carbapenem-resistant” OR “carbapenem resistant”) AND (wastewater OR “waste water” OR sewage OR effluent OR “hospital wastewater” OR “hospital effluent”). Retrieved records were consolidated, duplicates removed, and remaining records screened by title and abstract before full-text assessment against predefined eligibility criteria. The study-selection process followed the PRISMA 2020 framework and is presented in Figure 1.

Eligibility Criteria

Original research studies were eligible if they investigated *K. pneumoniae* recovered from wastewater, hospital wastewater, sewage, effluent, or related aquatic environments and reported findings relevant to carbapenem resistance, carbapenemase production, carbapenemase genes, resistance determinants, genomic characteristics, sequence types, plasmids, or epidemiological dissemination. Studies were excluded if they did not focus on *K. pneumoniae*, lacked a relevant wastewater or aquatic-environmental component, did not provide information relevant to carbapenem resistance, or were reviews, editorials, commentaries, conference abstracts, or other non-original publications. No geographical restriction was applied.

Study Selection and Data Extraction

After duplicate removal, records were screened by title and abstract, followed by full-text assessment of potentially eligible studies. Data were extracted using a standardized framework covering publication characteristics, study location, wastewater source, sampling context, *K. pneumoniae* occurrence, carbapenem resistance phenotype, carbapenemase genes, other resistance determinants, sequence types and genomic lineages, plasmid-associated determinants, and genomic or molecular surveillance approaches. Relevant findings were organized according to the specific resistance and epidemiological characteristics reported in each study.

Data Synthesis

Extracted data were organized according to the objectives of the review and synthesized across four principal domains: occurrence of carbapenemase-producing *K. pneumoniae* in hospital wastewater; carbapenemase genes and resistance determinants; genomic lineages, sequence types and plasmid-associated dissemination; and genomic surveillance methods and epidemiological insights. Particular attention was given to patterns of carbapenemase distribution, genetic diversity, mobile genetic elements, and evidence of dissemination in wastewater-associated settings.

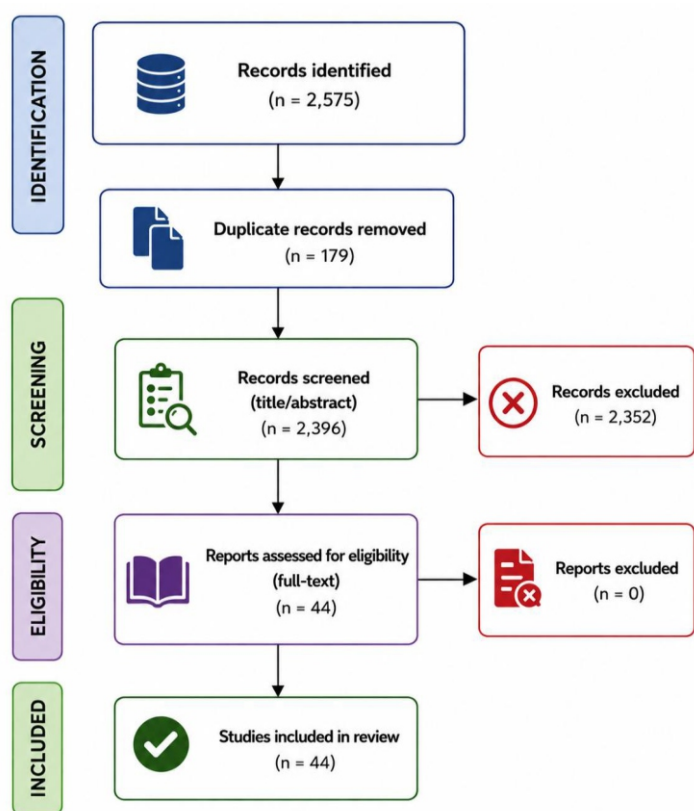


Figure 1. PRISMA flow diagram of the study selection process

Results

Occurrence of Carbapenemase-Producing *K. pneumoniae* in Hospital Wastewater

The reviewed studies consistently identified carbapenem-resistant or carbapenemase-producing *Klebsiella pneumoniae* in hospital wastewater and associated wastewater systems, although reported occurrence varied with sampling location, wastewater characteristics and detection methods.

In Burkina Faso, carbapenemase-producing *K. pneumoniae* was recovered from hospital effluents together with carbapenemase-producing *Escherichia coli*, demonstrating the presence of clinically important carbapenemase producers at the hospital–wastewater interface [15]. Similar findings were reported in hospital wastewater in China, where recovered *K. pneumoniae* isolates exhibited extensive antimicrobial resistance and diverse genomic characteristics [16]. Detection has also extended beyond untreated hospital effluent to wastewater treatment systems and receiving environments. Carbapenem-resistant *K. pneumoniae* was identified in hospital-associated wastewater treatment systems in Southern Romania, with wastewater isolates showing considerable carbapenemase diversity [17]. Environmental sampling in South Africa likewise recovered antibiotic-resistant *Klebsiella* spp. from hospital effluents and wastewater treatment plants [18]. More recently, Werner et al. [24] recovered 297 *K. pneumoniae* isolates from wastewater-associated samples, including 253 confirmed carbapenemase-producing isolates, demonstrating the capacity of systematic wastewater surveillance to detect substantial populations of clinically relevant resistant organisms [19]. Evidence of downstream dissemination is further supported by studies detecting KPC-producing *K. pneumoniae* along pathways extending from hospital effluent through municipal sewage to receiving streams [20]. Taken together, the findings indicate that hospital wastewater represents an important reservoir and potential dissemination pathway for carbapenemase-producing *K. pneumoniae*, although differences in sampling and detection strategies limit direct comparison of occurrence between studies.

Carbapenemase Genes and Resistance Determinants

The resistance determinants identified across wastewater-associated *Klebsiella pneumoniae* were genetically diverse, with bla_{KPC} , bla_{NDM} and $bla_{OXA-48-like}$ representing recurrent carbapenemase families. In Southern Romania, bla_{NDM-1} , bla_{OXA-48} and bla_{KPC-2} predominated, while $bla_{OXA-162}$ was detected among water isolates, illustrating diversity in the carbapenemase repertoire [21]. Hospital effluents in Burkina Faso similarly contained isolates carrying bla_{KPC} , bla_{NDM} , bla_{IMP} , bla_{VIM} and bla_{OXA-48} -related determinants [22]. Recent genomic surveillance has expanded the range of detected determinants. Werner et al. [24] identified bla_{KPC-2} , bla_{NDM-1} , bla_{NDM-5} , bla_{OXA-48} , $bla_{OXA-181}$ and $bla_{OXA-427}$ among wastewater-associated isolates [23]. This diversity frequently occurred within broader multidrug-resistant backgrounds. Wastewater-derived genomes from Southern Romania carried additional ESBL-associated bla_{SHV} , bla_{CTX-M} , bla_{TEM} and bla_{OXA} determinants, together with resistance genes affecting aminoglycosides, quinolones and other antimicrobial classes [24]. Plasmid-mediated resistance further increases the epidemiological significance of these determinants. In hospital wastewater in China, *K. pneumoniae* isolates carried multiple resistance genes and plasmid replicons, while transfer experiments demonstrated mobility of bla_{KPC-2} from wastewater isolates [25]. Thus, wastewater-associated carbapenem resistance reflects not only the presence of individual carbapenemase genes but also their integration within multidrug-resistant and potentially mobile genetic backgrounds.

Table 1: Carbapenemase and genomic characteristics of wastewater-associated Klebsiella pneumoniae

Study	Wastewater context	Carbapenemase determinants	Major sequence type	Principal genomic finding
Kagambèga et al. [11]	Hospital effluent	bla_{KPC}, bla_{NDM}, bla_{IMP}, bla_{VIM}, bla_{OXA-48}	Not reported	Multiple carbapenemase families occurred within hospital effluent
Surleac et al. [22]	Hospital and WWTP wastewater	bla_{KPC-2}, bla_{NDM-1}, bla_{OXA-48}-like	ST11, ST17, ST35, ST101, ST307, ST395, ST485	Diverse resistance determinants, plasmid profiles and genomic lineages
Xie et al. [26]	Hospital wastewater	bla_{KPC-2} and other resistance determinants	ST11, ST15, ST824, ST2433, ST3184	Diverse plasmid replicons and experimentally demonstrated bla_{KPC-2} transfer
Zagui et al. [28]	Hospital effluent, municipal sewage and urban stream	KPC	Not reported	Evidence of dissemination along the hospital sewage receiving-water pathway
Werner et al. [24]	Wastewater treatment plants	bla_{KPC}, bla_{NDM}, bla_{OXA-48}-like	ST147, ST273, ST258, ST35, ST15, ST37, ST307, ST485	WGS revealed diverse lineages, resistance profiles and phylogenetic relationships

Abbreviations: WWTP_wastewater treatment plant; WGS_ whole-genome sequencing; KPC_Klebsiella pneumoniae carbapenemase; NDM_New Delhi metallo-β-lactamase; OXA-48_oxacillinase-48; IMP_imipenemase; VIM_Verona integron-encoded metallo-β-lactamase.

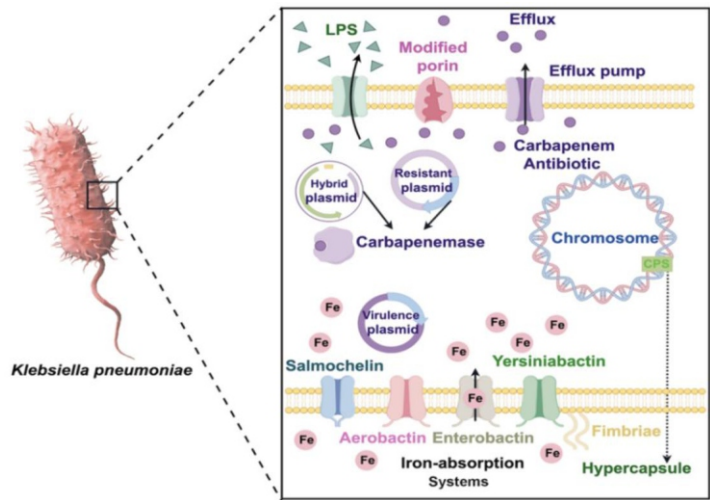


Figure 2. Carbapenem-resistance mechanisms and virulence features of carbapenem-resistant *Klebsiella pneumoniae*. Schematic representation of the major molecular mechanisms underlying carbapenem resistance in CRKP and their relationship with virulence-associated characteristics. **Source:** Zhu et al. [29]

Genomic Lineages, Sequence Types and Plasmid-Associated Dissemination

Genomic investigations revealed substantial lineage diversity among wastewater-associated carbapenem-resistant *K. pneumoniae*. Surleac et al. [22] identified 14 sequence types among clinical and wastewater-associated isolates, including ST11, ST17, ST35, ST101, ST219, ST258, ST307, ST395 and ST485. Several of these lineages are also recognized in clinical carbapenem-resistant *K. pneumoniae* populations, indicating that wastewater may capture both environmental populations and clinically important lineages. More recent WGS analysis identified eight sequence types among wastewater carbapenemase-producing isolates, including ST147, ST273, ST258, ST35, ST15, ST37, ST307 and ST485 Werner et al. [24]. Closely related isolates belonging to the same sequence type were recovered from different wastewater treatment plants, providing evidence of genetically related populations across geographically separated sampling points. Conversely, the coexistence of different STs carrying distinct carbapenemase genes demonstrates that dissemination is not attributable to a single dominant clone. Plasmid-associated dissemination provides an additional mechanism for resistance spread. Wastewater-derived *K. pneumoniae* have carried diverse plasmid replicons, while bla_{KPC-2} has been associated with mobile genetic structures capable of horizontal transfer [26].

The complete genome characterization of an ST11 *K. pneumoniae* carrying bla_{KPC-2} from sewage-associated water further demonstrated the environmental presence of a clinically important lineage and a carbapenemase-bearing plasmid [22-25]. These findings indicate that both clonal expansion and horizontal gene transfer contribute to the persistence and dissemination of carbapenem resistance in wastewater environments.

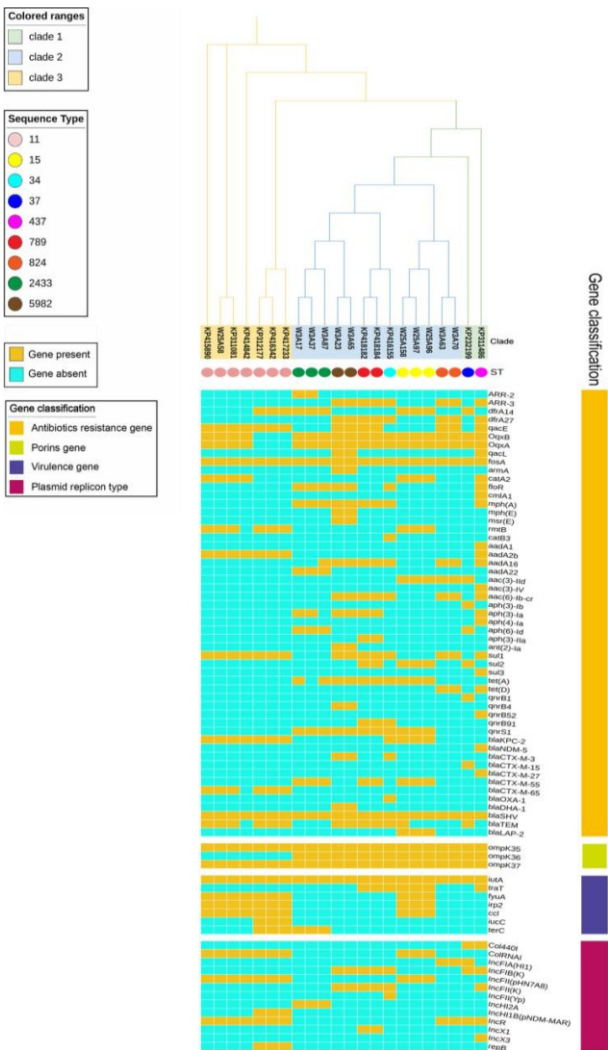


Figure 3. Genomic characteristics of carbapenem-resistant *Klebsiella pneumoniae* from hospital wastewater: Phylogenetic relationships among 22 CRKP genomes are integrated with sequence types, virulence factors, plasmid replicon types, and antimicrobial-resistance genes, illustrating substantial genomic diversity and the coexistence of multiple resistance and mobile genetic determinants within wastewater-associated CRKP populations **Source:** Xie et al. [26]

Genomic Surveillance Methods and Epidemiological Insights

The reviewed evidence demonstrates increasing use of integrated culture, antimicrobial susceptibility testing, PCR and whole-genome sequencing for wastewater surveillance. Conventional culture and susceptibility testing establish phenotypic resistance, while PCR enables targeted detection of major carbapenemase genes. WGS provides broader characterization of resistance determinants, sequence types, plasmid replicons and phylogenetic relationships within a single analytical framework [22, 24]. The epidemiological value of WGS is particularly evident where environmental isolates can be compared with clinical or publicly available genomes. In hospital wastewater, genomic analysis has linked resistance determinants with specific lineages and demonstrated the transferability of bla_{KPC-2} [23, 26]. Similarly, comparative genomic analysis of wastewater isolates has enabled identification of closely related populations across wastewater treatment systems and improved resolution of potential dissemination pathways [24]. Overall, the evidence supports wastewater genomic surveillance as a complementary approach for monitoring clinically important *K. pneumoniae*. Its greatest value lies in integrating carbapenemase detection, resistance profiling, sequence typing, plasmid characterization and phylogenomic analysis, thereby providing information that cannot be obtained reliably from phenotypic surveillance alone. The findings also indicate that wastewater surveillance can complement clinical surveillance by identifying resistance determinants and lineages circulating outside conventional healthcare sampling frameworks.

Table 2: Integrated genomic epidemiological evidence for carbapenemase-producing *Klebsiella pneumoniae* in hospital wastewater

Genomic features	Evidence	Epidemiological significance
Carbapenemase genes	KPC, NDM, OXA and other determinants	Major molecular basis of carbapenem resistance
Sequence types	Clinically important and environmentally detected lineages	Indicates circulation of high-risk clones
Plasmids/mobile elements	Resistance-associated plasmid and integron structures	Supports horizontal dissemination
Resistance virulence convergence	Co-occurrence of resistance and virulence determinants	Potentially increases clinical and environmental risk
Genomic relatedness	Related isolates across clinical, wastewater and environmental settings	Supports possible epidemiological linkage
Environmental persistence	Resistant organisms detected following wastewater treatment	Indicates incomplete removal and persistence
Downstream dissemination	Detection in treated effluent and receiving waters	Demonstrates potential environmental spread

Adapted from Heljanko et al. [9]; Surleac et al. [22]; Xie et al. [26]

Transmission and Dissemination Pathways

The evidence supports hospital wastewater as an important interface through which resistant *K. pneumoniae* can move from healthcare environments into broader wastewater networks. Genomic investigations have demonstrated related resistant populations across hospital and wastewater-associated settings, while longitudinal analysis of an ST101 clone showed persistence from inpatients to hospital effluent despite chlorine treatment [23, 24]. This persistence indicates that conventional treatment processes may reduce bacterial loads without completely eliminating epidemiologically important resistant organisms. Dissemination can extend beyond hospital boundaries into municipal wastewater and receiving waters. Carbapenemase-producing organisms have been detected across hospital wastewater, wastewater treatment plants and

Discussion
Genomic Epidemiology of Wastewater-Associated *K. pneumoniae*

The reviewed evidence demonstrates substantial genomic diversity among wastewater-associated carbapenem-resistant *K. pneumoniae*, encompassing multiple sequence types, resistance determinants, plasmid replicons and virulence-associated genes. Whole-genome analyses have identified clinically important lineages and complex resistance profiles in isolates recovered from hospitals and connected wastewater systems, indicating that wastewater can capture clinically relevant genomic diversity beyond routine phenotypic surveillance [22, 26]. The detection of clinically relevant carbapenemase-producing sequence types in Finnish wastewater further supports its value as a population-level source of genomic surveillance [9]. The genetic context of resistance is particularly important because carbapenemase genes may occur alongside additional resistance determinants and mobile genetic elements. Hospital wastewater has been shown to contain diverse carbapenemase-associated genetic structures, including integron-associated determinants, highlighting the potential for environmental maintenance and redistribution of resistance genes [28]. However, wastewater populations should not automatically be considered direct representations of clinical populations. Differences between patient and effluent isolates indicate that environmental populations may undergo independent selection and ecological adaptation, making wastewater surveillance complementary rather than interchangeable with clinical surveillance [15].

surface waters, while KPC-producing *K. pneumoniae* has been traced along a pathway from hospital effluent through municipal sewage to an urban stream [20]. Resistant *K. pneumoniae* has also been detected in treated wastewater, emphasizing that treatment systems may represent control points but not absolute barriers to environmental dissemination [12]. Dissemination may occur through both bacterial persistence and horizontal movement of resistance determinants. The detection of carbapenemase-producing *K. pneumoniae* in hospital wastewater and the identification of diverse mobile resistance structures support the importance of environmental genetic reservoirs in maintaining resistance [28, 29]. Therefore, genomic surveillance should distinguish clonal transmission from the wider environmental circulation of transferable resistance determinants.

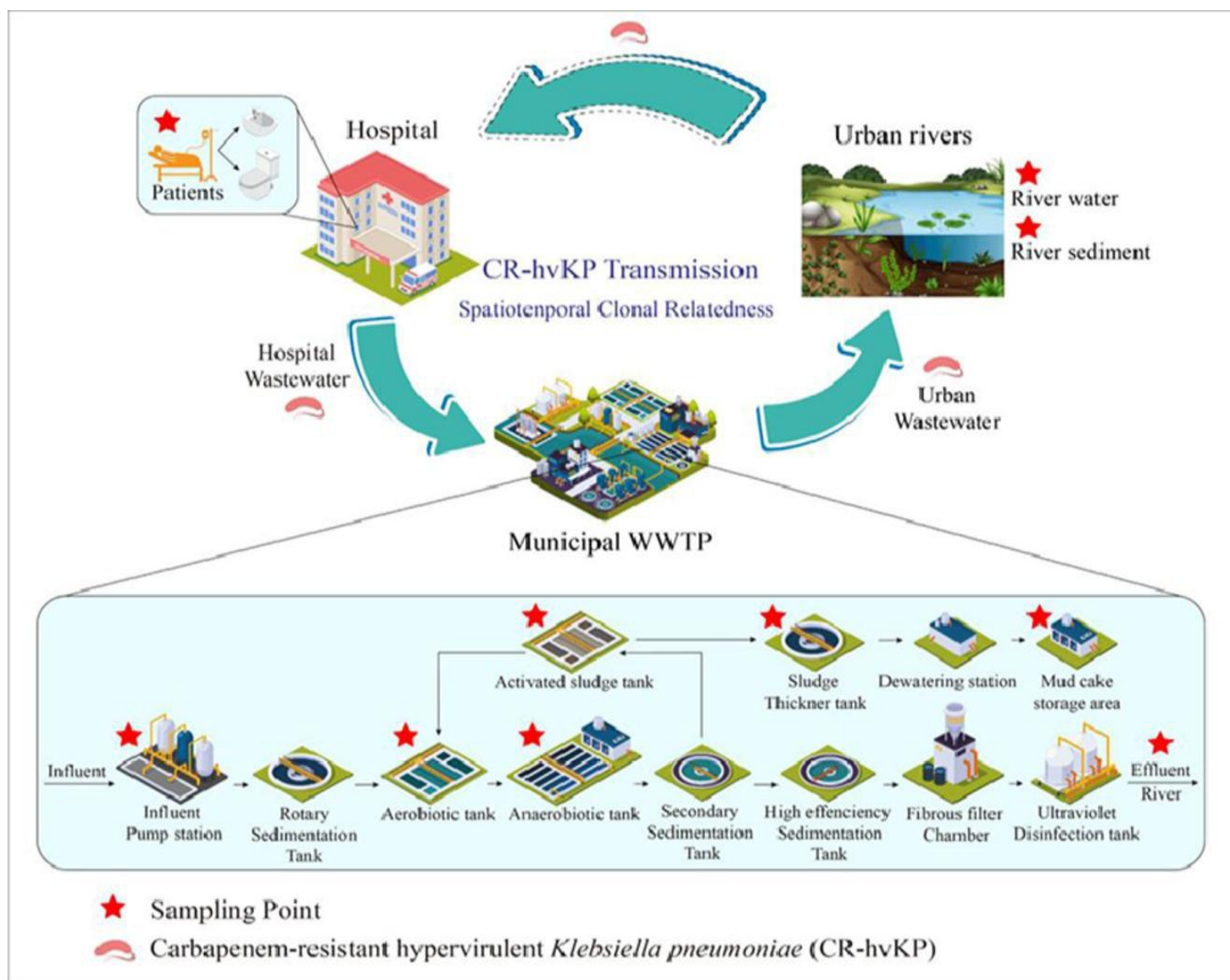


Figure 4. Potential transmission and environmental dissemination pathways of carbapenem-resistant *Klebsiella pneumoniae*. Potential movement of carbapenem-resistant *K. pneumoniae* from hospitals through wastewater treatment to downstream aquatic environments, highlighting persistence and environmental dissemination.
Source: Zou et al. [30]

Implications for Hospital and One Health Surveillance

Wastewater surveillance can complement hospital-based AMR monitoring by providing population-level information on circulating resistance determinants and clinically important bacterial lineages. Routine hospital wastewater monitoring has successfully detected carbapenem-resistance genes associated with healthcare-associated pathogens, demonstrating its potential for continuous environmental surveillance [25]. Detection of clinically relevant carbapenemase-producing *Klebsiella pneumoniae* sequence types in wastewater further supports its application as an early-warning component of AMR surveillance [26]. Nevertheless, wastewater findings require contextual interpretation. Factors such as patient shedding, hospital characteristics, antimicrobial exposure, wastewater dilution and sampling strategy can influence environmental signals. The absence of a consistent genomic correlation between patient and effluent isolates in some settings demonstrates that wastewater cannot invariably be used as a direct proxy for clinical prevalence [30]. Conversely, the identification of persistent clones across clinical and wastewater compartments demonstrates that strong epidemiological links can be established when longitudinal sampling and genomic characterization are combined [18].

Within a One Health framework, the significance of wastewater surveillance extends from hospital infection control to environmental protection. The detection of resistant organisms across treated effluent and receiving waters demonstrates interconnectedness between human healthcare, wastewater management and environmental exposure [10, 16]. Integrated surveillance combining clinical microbiology, wastewater monitoring and environmental sampling would therefore provide a more comprehensive assessment of carbapenem resistance dissemination.

Evidence Gaps and Surveillance Limitations

Interpretation of the available evidence is constrained by substantial methodological heterogeneity. Differences in sampling locations, sampling frequency, culture methods, susceptibility testing, carbapenemase detection and genomic workflows limit direct comparison between studies. Environmental and clinical isolates may also exhibit distinct resistance mechanisms, reinforcing the need to consider ecological context when interpreting wastewater-derived genomic data [16]. A further limitation is that detection and genomic similarity do not necessarily establish transmission direction.

Although genomic evidence can demonstrate relatedness between clinical and environmental isolates, differences between patient and effluent populations may reflect selective pressures and environmental adaptation rather than absence of connection [17]. Consequently, longitudinal, multicentre sampling combined with comparative whole-genome analysis is required to strengthen causal epidemiological interpretation. Geographical representation also remains uneven, particularly across Sub-Saharan Africa. Existing African studies demonstrate the feasibility and value of genomic tracking but remain insufficient to characterize regional diversity, transmission patterns and environmental persistence comprehensively [6]. Future surveillance should prioritize standardized longitudinal sampling, coordinated clinical–wastewater investigations and genomic characterization of sequence types, resistance genes, plasmids and other mobile genetic elements. Such integration would improve the ability to distinguish persistent clones from transferable resistance determinants and strengthen the role of wastewater surveillance within hospital and One Health AMR programmes [19, 23, 30].

Table 3: Major evidence gaps and priorities for genomic surveillance of carbapenem-resistant *K. pneumoniae* in hospital wastewater

Evidence gap	Limitation	Priority for future research
Geographic coverage	Limited genomic evidence from Sub-Saharan Africa	Multicentre, geographically representative surveillance
Sampling approaches	Variation in sampling sites, frequency and sample types	Standardized longitudinal sampling protocols
Clinical wastewater linkage	Limited paired sampling of patients and wastewater	Integrated clinical wastewater genomic surveillance
Genomic resolution	Inconsistent characterization of plasmids and mobile genetic elements	Routine WGS with resistome and mobilome analysis
Wastewater treatment	Limited before-and-after treatment genomic assessment	Systematic monitoring of treatment performance
Epidemiological integration	Limited linkage between genomic, clinical and environmental data	Integrated One Health surveillance systems

Adapted from Heljanko et al. [9]; Majlander et al. [14]; Masalane et al. [15].

Conclusion

Genomic surveillance of carbapenemase-producing *Klebsiella pneumoniae* in hospital wastewater provides an important means of characterizing the occurrence, diversity and environmental dissemination of clinically relevant resistance. The evidence indicates that hospital wastewater can contain high-risk *K. pneumoniae* lineages, diverse carbapenemase determinants and mobile genetic elements, while resistant organisms may persist through wastewater-treatment systems and reach downstream environments. Integrating genomic information with clinical and environmental surveillance can improve early detection, strengthen epidemiological investigation and support targeted infection-control and environmental interventions. Future surveillance should emphasize standardized longitudinal sampling, broader geographical coverage, integrated clinical–wastewater investigations and higher-resolution genomic characterization to clarify transmission pathways and strengthen One Health antimicrobial-resistance preparedness.

Authors' Contributions

The authors of this research have significantly contributed to the study's conception, data collection, and manuscript development. All authors were involved in writing the manuscript or critically reviewing it for its intellectual value. They have reviewed and approved the final version for submission and publication and accepted full responsibility for the content and integrity of the work.

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Conflict of Interest

The authors declared that there are no conflicts of interest.

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