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Review

Multidrug-Resistant *Acinetobacter* spp. and Lytic Bacteriophages in Hospital Wastewater—A Five-Year Narrative Review

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Abstract

In recent decades, antibiotic-resistant bacteria have become an increasingly urgent public health concern. The uncontrolled use of antibiotics, along with inadequate implementation of prevention and control measures, is the primary factor contributing to this issue. The hospital environment is a major source of multidrug-resistant bacteria, and in recent years, there has been growing concern about hospital wastewater, which acts as a significant reservoir for these bacteria and their resistance genes. This situation leads to the spread of multidrug-resistant bacteria in the environment. One particular concern is *Acinetobacter*, especially *Acinetobacter baumannii*, which has emerged as a pathogenic threat in healthcare-associated infections. This bacterium is found in high densities in hospital wastewater. Most strains of *A. baumannii* express resistance not only to carbapenems but also to several other classes of antibiotics, including tetracyclines, fluoroquinolones, and aminoglycosides. These strains must be combated through effective measures. Bacteriophages represent a potential mitigation strategy for antibiotic-resistant *Acinetobacter* spp. originating from hospital wastewater. This review summarizes studies from online databases regarding the identification and characterization of *Acinetobacter* strains in hospital wastewater worldwide, and presents progress in isolating and characterizing bacteriophages against *A. baumannii* found in hospital wastewater.

Keywords: *Acinetobacter*; hospital wastewater; multidrug-resistant

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1. Introduction

The genus *Acinetobacter* comprises non-motile, Gram-negative coccobacilli that form smooth, mucoid colonies on solid media. Biochemically, the organisms exhibit catalase activity, lack oxidase activity, and do not ferment carbohydrates. According to a genome-based study, the genus *Acinetobacter* comprises 144 species, including 68 formally named species and 76 unnamed taxa [1]. The main virulence factors of *Acinetobacter baumannii* include lipopolysaccharides (LPSs), capsular polysaccharides (CPSs), and various outer membrane proteins (such as OmpA, CarO, Omp33, OprD, and OmpW). Additionally, outer membrane vesicles (OMVs), phospholipase, pili, and biofilm formation contribute to its

pathogenicity. Among these, OmpA is one of the most significant virulence factors. It plays a crucial role in cell adhesion, invasiveness, and apoptosis in the respiratory tract, as well as in biofilm formation. LPSs can trigger an exaggerated inflammatory response, leading to the release of pro-inflammatory cytokines such as IL-6, IL-8, and TNF-alpha. This response is a key factor in the clinical manifestations of infections caused by this organism. The CPS antigen is vital for protecting against the complement system, phagocytic cells, antimicrobial factors, and disinfectants. Furthermore, capsular polysaccharides are responsible for the development of a mucoid phenotype, which creates a protective barrier around the microorganism, helping to prevent the effects of antibiotics [2,3].

A. baumannii can form biofilms on both living tissues and inert surfaces, such as various types of hospital equipment, like endotracheal tubes. A central role in biofilm formation is played by the polysaccharide capsule. The mechanisms involved in biofilm formation differ between biotic (living) and abiotic (non-living) surfaces. For instance, on abiotic surfaces, the chaperone-usher pilus system known as Csu pili is crucial for biofilm formation, whereas on biotic surfaces it is not. *A. baumannii* forms mature biofilms by utilizing large surface proteins such as BapAb and Bap-like proteins, which are secreted via the type I secretion system. These proteins facilitate cell-to-cell adhesion and help establish the biofilm structure on medical materials. Additionally, other factors such as RTX-like proteins, PNAG, capsular polysaccharides, and autotransporters contribute to biofilm development and could serve as potential therapeutic or vaccine targets [4].

About one-third of the species within the genus *Acinetobacter* are involved in hospital-associated infections [5]. Among the clinically relevant species of *Acinetobacter*, *A. baumannii* is the most commonly associated with infections, followed by *A. calcoaceticus* and *A. lwoffii*. Other species, such as *A. haemolyticus*, *A. johnsonii*, *A. junii*, *A. nosocomialis*, *A. pittii*, *A. schindleri*, and *A. ursingii*, have been reported as occasional opportunistic pathogens. Additionally, *A. seifertii* has recently emerged as a clinically significant pathogen in Asia. *A. baumannii* primarily affects immunosuppressed individuals and is known to colonize the skin, as well as oropharyngeal and respiratory secretions, although it is less commonly found in urine. Gastrointestinal colonization is rare. This species can cause a wide range of infections, including pneumonia, skin infections, endocarditis, meningitis, and urinary tract infections. The main modes of transmission for this microorganism are through contaminated surfaces, as it can survive in the external environment, and via transient colonization on the hands of healthcare personnel. Its transmission may also occur through aerosols from infected or colonized patients [6,7].

A. baumannii infections account for 4% of healthcare-associated infections in Asia, compared to about 2% in Europe and the United States. A significant issue with this organism is that nearly half of the isolated strains are multidrug-resistant, with the percentage reaching up to 70% in Latin American countries [4]. This bacterium is highly resilient in the external environment and can survive exposure to various disinfectant solutions [8].

A. baumannii exhibits intrinsic resistance to several antibiotic classes, including aminopenicillins and first- and second-generation cephalosporins. It also has an extraordinary ability to acquire resistance to other antibiotics, leading to multidrug-resistant or extensively drug-resistant strains. This extensive antimicrobial resistance is facilitated by multiple mechanisms, including enzymatic inactivation or modification of antibiotics, mutations in target genes, reduced permeability of the external membrane, and overexpression of multidrug efflux systems [5]. In 2019, the CDC classified carbapenem-resistant *A. baumannii* infection as an "urgent threat" in the United States [9]. A consistent increase in the number of cases has been observed in recent years. A study conducted in China between 2020 and 2021 among ICU patients found an increase in infections in 2021 compared to 2020. Most of these infections were caused by multidrug-resistant strains, primarily

isolated from the lower respiratory tract. Additionally, the study found a higher prevalence of strains resistant to tobramycin, gentamicin, and trimethoprim-sulfamethoxazole in 2021 compared to the previous year [10].

It has been demonstrated that strains of *A. baumannii* responsible for hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP) exhibit an average multidrug-resistance of 80%. In reported cases from Central America and Croatia, this resistance reaches 100%. The mortality rate in these cases exceeds 50% [11]. Traditionally, carbapenems have been the preferred treatment for multidrug-resistant *A. baumannii* strains. However, in recent years, resistance to these antibiotics has become increasingly common, creating significant challenges in patient management. Extensively drug-resistant (XDR) *A. baumannii* refers to isolates that are resistant to three or more major classes of antimicrobials, including penicillins and cephalosporins (with or without β-lactamase inhibitors), fluoroquinolones, and aminoglycosides, and often also to carbapenems. Pandrug-resistant (PDR) *A. baumannii* refers to XDR strains that additionally exhibit resistance to last-resort agents, specifically polymyxins and tigecycline [11].

This review summarizes studies from online databases regarding the identification and characterization of *Acinetobacter* strains in hospital wastewater worldwide, and presents progress in isolating and characterizing bacteriophages that infect *A. baumannii* in hospital wastewater. We conducted a narrative review of studies published in the last 5 years (2021–2025) across databases such as PubMed and Google Scholar. We chose the period 2021–2025 to provide a recent analysis of the data on this topic. We used the keywords "acinetobacter" AND "hospital wastewater". We included original articles, written in English, and excluded reviews, clinical cases, articles that analyzed *Acinetobacter* spp. from sources other than hospital wastewater, and articles that analyzed *Acinetobacter* spp. from veterinary hospital wastewater (Figure 1). The items were imported into Zotero, and duplicates were removed with the Duplicate function.

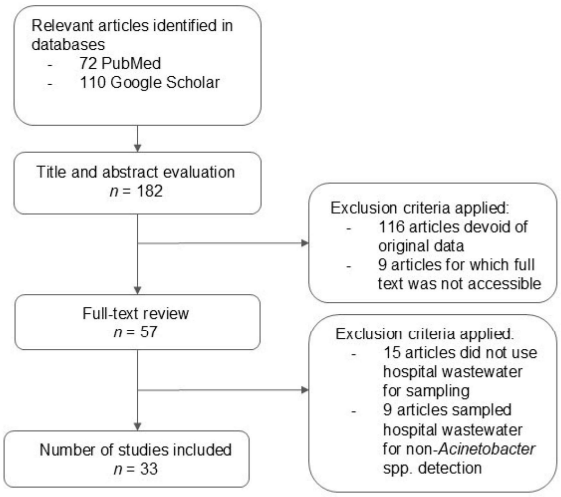


Figure 1. Flowchart describing the selection method for the articles included in this review.

2. Hospital Wastewater as a Reservoir for Multidrug-Resistant *A. baumannii*

A. baumannii is a microorganism capable of surviving in a wide range of environmental conditions and can persist on surfaces for extended periods. In aquatic environments, it can survive for up to 50 days and thrives in saline conditions, being commonly found in seawater [12]. Environmental reservoirs of *A. baumannii* can harbor various clinically relevant β-lactam resistance determinants, including the ADC-5 cephalosporinase and OXA enzymes. The detection of these enzymes in sequences from non-clinical environments

highlights the ecological scope of resistance mechanisms and underscores the importance of monitoring environmental sources for emerging resistance-associated genotypes [13]. According to a report by the European Centre for Disease Prevention and Control (ECDC), data on antibiotic use in hospitals are concerning. The report indicates that at least one in three hospitalized patients and one in two patients undergoing surgery receive antibiotic treatment. It is crucial to recognize that hospital effluents contain numerous bacteria that may pass through treatment plants and enter the environment. Despite dilution, this can lead to water contamination. Additionally, even if these microorganisms do not reach the natural environment, the presence of antibiotics is a major factor in the development of antibiotic resistance [14].

Hospital wastewater harbors a wide variety of bacteria, fungi, parasites, and viruses, making it a significant reservoir for pathogenic microorganisms [15]. Recent advances in medicine have enabled the successful identification of more pathogens in hospital wastewater. The most common bacterial phyla included Proteobacteria (51%), Bacteroidetes (34%), Firmicutes (11%), and Actinobacteria (1%) [16]. Hospital wastewater is a significant source of pollution to soil and aquatic environments and serves as a pathway for the transmission of infectious diseases, often involving highly resistant germs [13].

Hospital wastewater generation is higher in developed countries than in developing ones. Hospital wastewater contains an accumulation of various drugs, many of which remain active, along with microorganisms exhibiting different degrees of resistance, resistance genes, and toxic substances, including disinfectants, detergents, and heavy metals such as cadmium, copper, nickel, mercury (Hg), and tin (Sn) [17]. The main sources of heavy metals are medical devices, pharmaceuticals, imaging contrast agents, etc. [18]. The most commonly detected antibiotics in hospital wastewater are ciprofloxacin, sulfamethoxazole, trimethoprim, and norfloxacin [17]. Thus, sublethal amounts of antibiotics found in hospital wastewater allow bacteria to develop resistance [19,20].

A recent meta-analysis showed that carbapenem, sulfonamide, and tetracycline resistance genes, along with mobile genetic elements, were detected at high relative levels ($>10^{-4}$ gene copies per 16S rRNA gene copy) in hospital wastewater. From 2014 to 2018, the prevalence of genes conferring resistance to extended-spectrum β-lactams, carbapenems, sulfonamides, and glycopeptides declined significantly, whereas the abundance of tetracycline resistance genes increased. ARG levels varied significantly among countries but showed no significant seasonal variation. On-site hospital wastewater treatment processes were unable to fully eliminate ARGs, and their removal efficiencies differed depending on the specific resistance genes involved [21]. The main resistance genes identified in hospital wastewater include extended-spectrum β-lactamase (ESBL) genes, carbapenemases (*blaKPC*, *blaNDM*, and *blaOXA* variants), as well as colistin resistance determinants (mcr-1 and related variants). It also encompasses vancomycin resistance genes (vanA and vanB) [22].

The following sections summarize data on the presence of *Acinetobacter* spp. in hospital wastewater from studies conducted in the last five years, categorized by region.

2.1. Europe

Carbapenem resistance is the most common form of antibiotic resistance among isolates in Europe. Resistance to aminoglycosides, tetracyclines, and fluoroquinolones has also been reported [23–25]. There is significant variation in strains. For instance, in Finland, where antibiotic use is lower, the presence of *Acinetobacter* in hospital wastewater is less frequent than in countries with excessive antibiotic use [22]. In Romania, several strains of *A. baumannii* carrying multiple resistance genes have been identified [24,26–28] (Table 1).

Table 1. Summary of the studies that identified *A. baumannii* in hospital wastewater in Europe.

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Type of Wastewater	Conclusions
Silvester et al. [29]	United Kingdom (Wales)	2025	*A. baumannii*	bla_{OXA-23}, bla_{ADC-73}	Shotgun metagenomics; ARG* profiling	Untreated hospital wastewater discharged to municipal WWTPs*	This study concludes that metagenomics is a useful and comprehensive method for surveillance of ARGs* in wastewater epidemiology, and it supports the implementation of improved wastewater treatment technologies and policies.
Gheorghe-Barbu et al. [26]	Romania	2024	*A. baumannii*: 183 (from both aquatic and clinical samples)	- Târgoviște—hospital sewages: blaOXA-23, blaADC-73, blaADC-30; resistance genes for phenicols, sulphonamides, tetracyclines, macrolides, and streptogramin B - Surface water: blaOXA-121, blaOXA-378, blaOXA-710; blaADC-165 and blaADC-117 in 2021, blaADC-163 in 2022 - Râmnicu Vâlcea—hospital sewages: a broad spectrum of β-lactam, aminoglycosides, phenicols, sulphonamides, and tetracyclines resistance genes - Surface water: blaOXA-23, blaOXA-12, blaADC-156, blaADC-73, and a suite of genes for AMEs*, phenicols, sulphonamides, macrolides, and streptogramin B resistance	Culture-based isolation; MALDI-TOF MS*; WGS*; conjugation assays	Mixed hospital + urban wastewater treated in municipal WWTPs*	This study demonstrates that *A. baumannii* isolated during 2019–2022 from clinical infections and environmental sources in Târgoviște and Râmnicu Vâlcea, including hospital sewage and downstream aquatic environments, share a complex network of resistance and virulence determinants carried on mobile genetic elements. Hospital wastewater serves as a significant reservoir of antibiotic resistance genes, which can disseminate through wastewater treatment systems into the natural environment.

Table 1. *Cont.*

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Type of Wastewater	Conclusions
Gheorghe-Barbu et al. [24]	Romania	2024	33 *A. baumannii* (isolates recovered from Glina, Bucharest's WWTP*)	bla_{OXA-23}, bla_{OXA-72}, bla_{TEM-1}—Bucharest $bla_{OXA-121}$—Târgoviște	Culture on selective chromogenic media; MALDI-TOF MS*; PCR*; WGS*; 16S metagenomics	Urban municipal WWTPs* (mixed hospital + urban wastewater)	This study demonstrates that multidrug-resistant *A. baumannii* is present in hospital wastewater and associated aquatic environments, with a high microbial load and diverse resistance profiles. The frequent detection of the bla_{OXA-23} ARG and distinct sequence types (the ST2 cluster found in isolates from Bucharest and the ST10 cluster associated with isolates from Târgoviște) suggests ongoing dissemination between clinical and environmental reservoirs.
Savin et al. [25]	Germany	2024	*A. baumannii* *A. pittii*	$bla_{OXA-500}$ $bla_{OXA-132}$ $bla_{OXA-506}$ bla_{OXA-98}	Culture-based isolation; MALDI-TOF MS*; WGS*; cgMLST*	Municipal and hospital wastewater (influent/effluent)	Only one *A. baumannii* isolate from wastewater was carbapenem-resistant. No wastewater isolates carried plasmids. In contrast, the clinical isolates showed the highest levels of antimicrobial resistance and carried the most plasmids.
Ramos et al. [30]	Portugal	2024	*Acinetobacter* spp.	bla_{OXA} bla_{AmpC}	Shotgun metagenomics; resistome analysis	Raw urban and hospital wastewater	Wastewater metagenomics reveals hospital-specific microbiota and a diverse array of antibiotic resistance genes, with *Acinetobacter* spp. and *Aeromonas* spp. hosting the highest abundance of ARGs* against beta-lactams. Surveillance of wastewater offers valuable, community-representative insights for AMR and pathogen monitoring.

Table 1. *Cont.*

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Type of Wastewater	Conclusions
Gheorghe-Barbu et al. [27]	Romania	2023	*A. baumannii*	bla_{OXA-23} bla_{OXA-24} bla_{OXA-51} bla_{PER} bla_{TEM}	Culture-based isolation; MALDI-TOF MS*; PCR*	Hospital wastewater and polluted surface waters	The study concludes that Ag NPs* are an effective alternative treatment against MDR *A. baumannii* strains.
Dželalija et al. [31]	Croatia	2023	*Acinetobacter* spp.	Not available	16S rRNA amplicon sequencing; microbiome profiling; resistome prediction	Untreated municipal sewage and treated municipal/hospital wastewater	Using 16S rDNA sequencing, taxonomic profiling of the microbiomes from beach waters, a water treatment plant, and sewage was performed. *Acinetobacter* was among the most frequently identified genera and featured multiple ARGs. The study concludes that treated wastewater still poses a significant hazard to natural waters.
Gheorghe-Barbu et al. [28]	Romania	2022	*A. baumannii* Total isolates: 220 (clinical + sewage + wastewater treatment plants) Wastewater isolates: 194	bla_{OXA-23} bla_{OXA-24} bla_{OXA-72}	Culture-based isolation; MALDI-TOF MS*; PCR*; WGS*; MLST*; conjugation assays	Hospital wastewater discharged into municipal WWTPs*	The study reported the clonal spread of clinical *A. baumannii* ST2 strains into wastewater and the detection of carbapenem-resistant *A. baumannii* at the examined sampling sites (hospitals, their sewage systems, and WWTPs). The study emphasizes the importance of screening for antimicrobial resistance genes in the environment and may provide crucial information for tracking the spread of ARGs from hospitals into water bodies.
Teban-Man et al. [32]	Romania	2022	*Acinetobacter* spp.	bla_{NDM} bla_{VIM} bla_{KPC} bla_{OXA-48}	16S rRNA amplicon sequencing; qPCR	Municipal wastewater (with and without hospital input)	Municipal wastewater harbors clinically important carbapenemase genes and a diverse microbial community, with *Acinetobacter* as a prominent genus. These resistance genes are abundant regardless of whether hospital sewage is included in the influent, suggesting that municipal wastewater can reflect broader community and clinical resistance profiles.

Table 1. *Cont.*

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Type of Wastewater	Conclusions
Majlander et al. [33]	Finland	2021	*A. baumannii*	Not available	High-throughput qPCR (216 targets); 16S rRNA	Untreated hospital wastewater (separate sewer lines)	*A. baumannii* was more frequently detected in Finnish hospitals' wastewater than *P. aeruginosa* and *K. pneumoniae*; the overall bacterial abundance in the water samples was low. The study claims that the low prevalence of *A. baumannii* in wastewater is due to reduced antibiotic use in Finland.

A. baumannii—*Acinetobacter baumannii*; *A. pitii*—*Acinetobacter pitii*; ARG—antibiotic resistance gene; AME—aminoglycoside-modifying enzyme; AMR—antimicrobial resistance; Ag NP—silver nanoparticle; MDR—multidrug-resistant; *P. aeruginosa*—*Pseudomonas aeruginosa*; *K. pneumoniae*—*Klebsiella pneumoniae*; MALDI-TOF—Matrix-Assisted Laser Desorption/Ionization Time-of-Flight; WGS—Whole-Genome Sequencing; WWTP—wastewater treatment plant; PCR—Polymerase Chain Reaction; MLST—Multilocus Sequence Typing.

Across Europe, *Acinetobacter baumannii* is a critical sentinel germ for the dissemination of antimicrobial resistance (AMR) from clinical settings into the broader environment. Methodologically, these studies employ a combination of culture-based techniques (isolating specific strains from hospital sewage and WWTPs) and culture-independent metagenomic profiling, the latter of which reveals that *Acinetobacter* spp. often hosts a high abundance and diversity of carbapenemase-encoding genes. Results consistently demonstrate a "spillover" effect: phylogenetic analyses in Romania and Germany show that high-risk clinical clones (notably the ST2 cluster) migrate from hospitals into municipal wastewater and survive treatment, appearing in downstream surface waters. While geographical variations exist—such as Finland's lower prevalence, attributed to stricter antibiotic stewardship—the overarching trend indicates that hospital effluents serve as primary "hotspots" where high antibiotic concentrations (such as ciprofloxacin and β-lactams) exert selective pressure. Furthermore, recent longitudinal data suggest that the COVID-19 pandemic may have exacerbated resistance levels, underscoring the dynamic nature of the *A. baumannii* resistome and the necessity of integrating wastewater-based epidemiology into national public health surveillance. Metagenomic results need to be carefully analyzed, as they seem to show the presence of ARGs from Enterobacterales associated with *Acinetobacter* spp.

2.2. Asia

In 2025, Mallonga et al. reported the first strain of *Acinetobacter towneri* carrying both the NDM-1 and tet(x7) resistance genes [34]. An interesting finding comes from the study of Wang et al. They analyzed bacteria in hospital wastewater aerosols and found higher concentrations during the summer. They concluded that bioaerosols from hospital sewage in summer pose a significant pathogenic risk [35]. Conversely, Zhao et al. examined the COVID-19 pandemic and noted that the amount of *Acinetobacter* in hospital wastewater decreased in winter. However, they emphasized that COVID-19 may have influenced the expression of resistance genes. During the COVID-19 pandemic, antibiotics were frequently used in patients infected with the SARS-CoV-2 virus, often in an irrational manner. Additionally, bacterial infections caused by microorganisms such as *E. coli*, *Klebsiella*, and *Acinetobacter*, carrying resistance genes such as blaOXA, blaKPC, and blaNDM, were more frequently identified among hospitalized COVID-19 patients. These findings support the conclusions drawn in the study by Zhao et al. [36].

A. baumannii, found in hospital wastewater in Asia, exhibits various resistance mechanisms, with mutations in the genes responsible for carbapenem resistance being the most frequently identified. Other species, such as *A. pittii*, *A. nosocomialis*, and *A. towneri*, have also been detected and show antibiotic resistance. Notably, resistance to carbapenems and the latest generation of tetracyclines has been observed among these species [37] (Table 2).

In this context, monitoring hospital wastewater is crucial, and metagenomics plays a vital role by providing valuable information. Researchers warn of the imminent spread of this multidrug-resistant microorganism from the hospital environment into the broader ecosystem, with serious implications for public health [38].

Table 2. Summary of the studies that identified *A. baumannii* in hospital wastewater in Asia.

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Type of Wastewater	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Conclusions
Mallonga et al. [34]	Philippines	2025	*A. towneri*	bla_{NDM-1} *tet*(X7) *tet*(39) *sul*1 *sul*2 *qac*EΔ1 *aac*(6′)-Ib *arr*-3 *dfr*A19 *msr*(E) *mph*(E)	Untreated hospital wastewater (aeration tank sludge)	Culture; hybrid WGS* (Illumina + ONT); plasmid reconstruction	This study reports the first isolation of an *A. towneri* strain carrying both bla_{NDM-1} and *tet*(X7). This study highlights the potential for the spread of such clinically significant resistance genes in the environment, underscoring the need for ongoing surveillance and intervention.
Chaudhury et al. [39]	Thailand	2025	*A. baumannii*	bla_{TEM} bla_{NDM} bla_{OXA-23} bla_{OX51} bla_{OXA-69}	Hospital wastewater	Culture; PCR*; WGS*; cgMLST*	This study showed that untreated wastewater from a tertiary hospital with a high incidence of nosocomial infections harbored high levels of multidrug-resistant ESKAPE pathogens. AST* phenotypes, AMR* genes, and WGS* have shown high concordance and, in some cases, no allelic differences between hospital and wastewater isolates.
Mannan et al. [40]	Bangladesh	2024	*A. baumannii*	bla_{NDM} bla_{KPC}	Untreated hospital wastewater	Culture; PCR*	This study found B-lactamase-producing bacteria in hospital wastewater. All isolates harbored bla_{NDM} and were resistant to Meropenem, and a high proportion were resistant to Ampicillin, Ceftriaxone, and Cefuroxime. bla_{KPC} was found only in *A. baumannii*.

Table 2. *Cont.*

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Type of Wastewater	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Conclusions
Gu et al. [37]	China	2024	*A. baumannii:* 32 *A. nosocomialis:* 14 *A. gerneri:* 7 *A. sichuanensis:* 6 *A. pittii:* 4 *A. rudis:* 3 *A. soli:* 2 *A. johnsonii:* 1 *A. seifertii:* 1	*A. baumannii*: *aac*(3′)-Ib *aph*(6′)-Id $bla_{TEM-181}$ bla_{OXA-23} bla_{OXA-66} $bla_{OXA-217}$ bla_{OXA-68} $bla_{OXA-909}$ $bla_{OXA-510}$ *amr*A *msr*E *mph*E *A. gerneri*: *aac*(3′)-IIb *aac*(6′)-Ib *aph*(3′)-VI bla_{OXA-23} $bla_{OXA-308}$ bla_{PER-1} *qnr*VC6 *tet*(39) *msr*E *mph*E *A. sichuanensis*: *mph*E *msr*E *mph*F *A. pittii*: $bla_{OXA-421}$ *msr*E *mph*E *A. rudis*: *msr*E *mph*E *A. soli*: *aph*(3′)-VI bla_{NDM-1} *A. johnsonii*: *mph*E *msr*E $bla_{OXA-421}$ *amr*A	Untreated hospital wastewater	Culture; WGS*; MLST*; SNP* phylogeny	Untreated hospital wastewater serves as a reservoir for multidrug-resistant pathogens, of which *A. baumannii* was the most prevalent. The dissemination of ST2-type *A. baumannii* is responsible for the high prevalence of carbapenem resistance in hospital wastewater isolates.

Table 2. *Cont.*

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Type of Wastewater	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Conclusions
Wang et al. [35]	China	2024	*Acinetobacter* spp.	Not available	Hospital wastewater	16S sequencing	This study compared the microbial composition of bioaerosols from hospital sewage versus municipal sewage and evaluated the pathogenic risk of these aerosols. It was reported that bacterial concentrations in hospital wastewater aerosols were higher than in municipal aerosols. Additionally, *Pseudomonas* spp. and *Acinetobacter* spp. aerosols were more abundant in autumn. The pathogenic risk of these bioaerosols increased during the summer season.
Zhao et al. [36]	China	2023	*Acinetobacter* spp.	During COVID-19, the abundance of bla_{OXA} increased significantly and was more than 2 times higher than in the pre-COVID-19 phase	Treated hospital wastewater	Shotgun metagenomics; resistome analysis	Given the severe bacterial co-infections in SARS-CoV-2 patients, this study evaluated the evolution in pathogenic composition of hospital wastewater during the COVID-19 pandemic. *Acinetobacter* spp. detection declined from 17% to 7%.
Wang et al. [41]	China	2023	*Acinetobacter* spp.	bla_{NDM-1}	Untreated hospital wastewater	Shotgun metagenomics; conjugation assay	Using metagenome next-generation sequencing, this study evaluated the effects of silver and silver nanoparticles (AgNPs*) on the hospital wastewater microbiome. The study found that hospital wastewater was abundant in antimicrobial resistance genes (ARGs*) and in clinically relevant bacteria, including *Acinetobacter*, *Pseudomonas*, *Escherichia*, and *Klebsiella*. Bacteria belonging to the orders Pseudomonadales, Enterobacterales, and Bacteroidales were the main ARG* hosts. The authors found that 20 nm AgNPs* reduced microbiome diversity and increased the relative abundance of *Acinetobacter*. AgNPs increased the abundance of ARGs and favored the conjugation of plasmids carrying bla_{NDM-1}.
Talat et al. [42]	India	2023	*A. baumannii*	bla_{NDM-1}	Untreated hospital wastewater	Shotgun metagenomics; MAGs*	In this study, shotgun metagenomics was used to examine ARGs in wastewater from six Indian hospitals. The study demonstrated the preponderance of ARGs for aminoglycosides, macrolides, carbapenems, trimethoprim, and sulfonamides in each sample. Four of the six samples contained bla_{NDM-1}, which was carried by *Pseudomonas aeruginosa* in HWW*-2, *Klebsiella pneumoniae* in HWW-4 and HWW*-6, and *A. baumannii* in HWW*-5. The absence of appropriate wastewater treatment that meets international standards is a critical factor in the dissemination of plasmid-mediated ARGs*.

Table 2. *Cont.*

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Type of Wastewater	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Conclusions
Ma et al. [43]	China	2022	*Acinetobacter* spp. (16.65%) *Acinetobacter johnsonii* (9.30%)	*acr*B *ade*J *mdt*B *mex*T *aac*(3)-II *aph*(3″)-I *aph*(6)-I *opr*M *cat*	Hospital wastewater	Shotgun metagenomics	Wastewaters from a general hospital and an eye specialty hospital were evaluated for microbial composition and the presence of ARGs* using metagenomic sequencing. The main bacteria from the wastewater of the general hospital were *Aeromonas* and *Acinetobacter*, and the most frequent ARG* was *tet*39. *Acinetobacter* was the main host of ARGs* in the general hospital water.
Wang et al. [44]	China	2022	*A. baumannii*	Not available	Hospital wastewater	Air sampler; culture; 16S sequencing	The study showed that bioaerosols containing pathogenic bacteria had a higher bacterial concentration at the hospital treatment station than at the municipal treatment station. Additionally, it highlights the need for better protective measures for the plant personnel exposed to these aerosols.
Yao et al. [45]	China	2021	*Acinetobacter* spp. (3.59%)	Not available	Untreated and treated hospital wastewater	LC–MS/MS; qPCR; 16S sequencing; culture counts	A significant amount of viable bacteria remained in the treated hospital effluent. The treated wastewater contained high concentrations of opportunistic or pathogenic bacteria, including *Acinetobacter*, *Klebsiella*, *Aeromonas*, and *Pseudomonas*. While wastewater from a tertiary hospital contained newer antibiotics (such as meropenem and cefepime), wastewater from a primary hospital typically contained conventional antibiotics (such as cefradine and ofloxacin). Based on the increased ARG* levels in treated wastewater, this study showed that hospital wastewater treatment plants are ineffective at eliminating all ARGs*.

A.—*Acinetobacter*; AST—antibiotic susceptibility testing; AMR—antimicrobial resistance; ARG—antibiotic resistance gene; HWW—hospital wastewater; MALDI-TOF—Matrix-Assisted Laser Desorption/Ionization Time-of-Flight; WGS—Whole-Genome Sequencing, WWTP—wastewater treatment plant; PCR—Polymerase Chain Reaction; MLST—Multilocus Sequence Typing; SNP—single-nucleotide polymorphism; MAGs—Metagenome-assembled genomes.

Research from Asia (including the Philippines, Thailand, Bangladesh, China, and India) identifies hospital wastewater as a volatile reservoir for multidrug-resistant (MDR) *Acinetobacter* species, characterized by a unique preponderance of blaNDM-1. Methodologically, these studies utilize Whole-Genome Sequencing (WGS) and shotgun metagenomics to reveal that *Acinetobacter* is often the primary host for antimicrobial resistance genes (ARGs) in general hospital effluents, frequently carrying clinically significant markers such as blaKPC, tet(X7) and tet(39). A critical observation across the region is the role of non-baumannii species, such as *A. towneri*, in harboring these high-threat carbapenemases. Furthermore, studies show that existing wastewater treatment infrastructures are often ineffective, as viable pathogenic *Acinetobacter* and plasmid-mediated ARGs persist in treated effluents and even disseminate via bioaerosols. Notably, experimental evidence suggests that interventions like silver nanoparticles (AgNPs) may inadvertently favor the conjugation of plasmids carrying blaNDM-1, potentially exacerbating the resistance profile of the wastewater microbiome.

2.3. Africa

In Africa, pandrug-resistant and extensively resistant bacterial strains have drawn significant attention to the urgent need for methods to control and prevent antibiotic resistance across the continent. Most studies analyzing hospital wastewater in Africa report a high prevalence of *Acinetobacter* strains with considerable antibiotic resistance, including MDR and XDR strains. Analyses of isolated strains reveal that many carry the carbapenemase genes, particularly NDM-1 and OXA-23, as well as genes associated with resistance to antibiotics such as tetracyclines, aminoglycosides, sulfonamides, and even colistin [46–48]. These findings suggest that hospital wastewater serves as a significant reservoir for multidrug-resistant bacteria that survive despite existing preventive measures. In this context, recent studies have also explored the use of nano-adsorbent materials and artificial intelligence to help control the spread of these bacteria [49] (Table 3).

The collective findings from research in Africa (including Egypt, Nigeria, and South Africa) characterize hospital wastewater as a critical reservoir for pandrug-resistant and extensively drug-resistant (XDR) *Acinetobacter baumannii*. Similarly to findings in Asia, African isolates show an increasing prevalence of the blaNDM-1 carbapenemase, often co-occurring with blaOXA-23 in high-risk clones such as ST-231. Methodologically, African studies place a unique emphasis on advanced remediation and monitoring; for instance, nano-adsorbents such as nano-zero-valent iron (nZVI) and nano-copper (CuONPs) have shown high efficiency in removing both antibiotics and ARGs, while smart artificial intelligent systems (SAISs) like XGB and Cubist models are proposed to reduce the turnaround time for evaluating bacterial density in water. Unlike the phenotypic resistance without detectable genes observed in some Mexican isolates, African strains frequently harbor high-frequency markers such as ampC (92%) and tetA (70%). Furthermore, these studies conclude that the robust biofilm-forming capacity of *A. baumannii* allows it to withstand treatment procedures, leading to the discharge of viable, resistant pathogens into the environment, which poses a severe risk to surrounding communities.

Table 3. Summary of the studies that identified *A. baumannii* in hospital wastewater in Africa.

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Type of Wastewater	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Conclusions
Hamad et al. [50]	Egypt	2023	*A. baumannii*	The study focuses more on the presence of ARGs and their removal than on characterizing specific resistance mechanisms in *Acinetobacter* or linking resistance genes to individual taxa.	Untreated + treated hospital wastewater	HPLC*; culture; qPCR* (37 ARGs); metagenomics	The main focus is on nano-adsorbent removal of levofloxacin and ARGs* from hospital wastewater. Nano-zero-valent iron (nZVI) and nano-copper (CuONPs) demonstrated high adsorption efficiencies for both levofloxacin and antibiotic resistance genes in hospital wastewater, suggesting their potential utility in advanced wastewater treatment applications.
Odih et al. [51]	Nigeria	2023	*A. baumannii*: 77 *A. pittii*: 5	bla_{NDM-1} bla_{OXA-23} bla_{OXA-58}	Untreated + treated hospital wastewater	Culture; WGS*; MLST*; SNP* phylogeny	The study supports the rising bla_{NDM-1} prevalence among *A. baumannii* isolates described in previous research, mainly in the Middle East and Africa. The distribution of bla_{NDM-1} and bla_{OXA-23} among isolates in different phylogenetic clusters indicates that the main cause of the rising carbapenem resistance in *A. baumannii* is the clonal growth of carbapenem-resistant strains. Various strains of *A. baumannii* that are resistant to carbapenems can withstand the hospital wastewater treatment procedure and be discharged into the environment.
Ekundayo et al. [49]	South Africa	2023	*Acinetobacter* spp.	Not available	Receiving waterbodies impacted by hospital and municipal wastewater effluents	CHROMagar; PCR* confirmation; ML regression models; physicochemical analysis	This study showed that using smart artificial intelligent systems (SAISs) is an evidence-based method for reducing the turnaround time in evaluating *Acinetobacter* density in water. The two best models were XGB and Cubist, and they could be developed into standalone SAISs* or integrated into current instruments.
Cherak et al. [52]	Algeria	2022	*A. baumannii*	*blaNDM-1*, *blaVIM-4*, *blaOXA-48*	Untreated hospital wastewater	Culture; MALDI-TOF*; CarbaNP; PCR*; MLST*	The identification of carbapenemases in multiple Gram-negative bacteria, including *A. baumannii*, from hospital wastewater demonstrates the potential role of this wastewater discharge in the dissemination of carbapenem resistance.

Table 3. *Cont.*

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Type of Wastewater	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Conclusions
Mapipa et al. [53]	South Africa	2022	*A. baumannii*: 53	*tet*A *amp*C	Untreated hospital wastewater	CHROMagar; PCR*;	The *tet*A and *amp*C genes were detected in 70% and 92% of isolates, respectively, indicating high tetracycline and beta-lactam resistance. The isolates exhibited high levels of antibiotic resistance, suggesting that hospital wastewater effluents pose a potential public health concern.
Eze et al. [47]	South Africa	2022	*A. baumannii*: 3	$bla_{ADC\text{-}25\text{-}like}$, $bla_{OXA\text{-}23}$, $bla_{OXA\text{-}51}$, $bla_{OXA\text{-}69}$, $bla_{NDM\text{-}1}$ *ant*(2′′)-Ia-like, *aph*(3′)-VIa, *aad*A1, *aph*(3′′)-Ib-like, *arm*A, *aph*(6)-Id, *aac*(3)-I-like *tet*(B)-like *sul*1, *sul*2 *mph*(E), *msr*(E) *cml*A1-like *dfr*A1 *arr*-2 *Lpx*A, *Lpx*C	Untreated hospital wastewater	Culture; WGS*; MLST*; cgMLST; resistome and plasmid analysis	One pandrug-resistant and two extensively drug-resistant *A. baumannii* strains isolated from hospital effluents in South Africa emphasize that untreated hospital wastewater poses a serious risk to surrounding communities and the environment.
Eze et al. [48]	South Africa	2022	*A. baumannii*: 1	$bla_{ADC\text{-}25\text{-}like}$, $bla_{NDM\text{-}1}$, $bla_{OXA\text{-}23}$, $bla_{OXA\text{-}69}$ *aac*(3)-I-like, *aad*A1, *aph*(3′)Ic, *arm*A, *str*A-like, *str*B-like *tet*(B) *mph*(E) *msr*(E) *cm*lA1-like ARR-2 *sul*1, *sul*2 *dfr*A1	Untreated hospital effluent wastewater	Culture; VITEK2; WGS*; MLST*; ResFinder; phylogenomics	This study reports the identification of an ST-231 *A. baumannii* strain in hospital wastewater that carries both $bla_{OXA\text{-}23}$ and $bla_{NDM\text{-}1}$, underscoring the concern that carbapenem resistance may be mediated by environmental pollution.

Table 3. *Cont.*

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Type of Wastewater	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Conclusions
Eze et al. [46]	South Africa	2021	*A. baumannii*: 71 - 36 (50.7%) from final effluent - 19 (26.8%)s from the pathology laboratory - 16 (22.5%) from the main hospital ward	Not available	Untreated hospital wastewater	VITEK2; plasmid typing; biofilm assays	Hospital effluent serves as a reservoir for multidrug-resistant *A. baumannii* capable of robust biofilm formation (which is not determined by the level of antibiotic resistance). These phenotypes enhance persistence in wastewater environments and pose a potential public health threat if released without adequate treatment.

A. baumannii—*Acinetobacter baumannii*; ARG—antibiotic resistance gene; nZVI—Nano-zero-valent iron; CuONP—CuO nanoparticles; SAIS—smart artificial intelligent system; MDR—multidrug-resistant; XDR—extensively drug-resistant; PDR—pandrug-resistant; MALDI-TOF—Matrix-Assisted Laser Desorption/Ionization Time-of-Flight; WGS—Whole-Genome Sequencing; WWTP—wastewater treatment plant; PCR—Polymerase Chain Reaction; MLST—Multilocus Sequence Typing; SNP—single-nucleotide polymorphism.

2.4. America

There are a few studies analyzing *Acinetobacter* in hospital wastewater in America. Among the studies conducted, *A. baumannii* was identified most frequently, whereas other species, such as *A. haemolyticus* and *A. johnsonii*, were rarely observed [54] (Table 4).

Table 4. Summary of the studies that identified *A. baumannii* in hospital wastewater in America.

Authors	Country	Year	*Acinetobacter* Species	Resistance Mechanism	Type of Wastewater	Detection Method (Bacteria and Resistance Genes in Hospital Wastewater)	Conclusions
Krul et al. [55]	Brazil	2025	*A. baumannii*	The isolates of the *A. baumannii* complex did not show resistance to carbapenems	Treated hospital wastewater (chlorination)	Culture-based isolation; MALDI-TOF MS*; carbapenemase PCR*; WGS* (subset)	Hospital wastewater acts as a direct extension of the clinical reservoir of antimicrobial resistance.
Martins-Gonçalves et al. [56]	Brazil	2025	*A. baumannii*	bla_{OXA-23}	River impacted by treated hospital effluent	Culture-based isolation; MALDI-TOF MS*; Whole-Genome Sequencing; phylogenomic analysis	This study showed that a high-risk nosocomial OXA-23-producing *A. baumannii* ST79 clone has adapted to an urban river.
Galarde-López et al. [54]	Mexico	2022	*A. haemolyticus* *A. modestus*	Phenotypic resistance (ARGs not detected in *Acinetobacter* spp.)	Raw and treated hospital WWTP* effluent	Culture-based isolation; MALDI-TOF MS* identification; targeted PCR*	The four *A. haemolyticus* clones found in treated wastewater demonstrated an ability to persist during the hospital water treatment process. This study shows that monitoring hospital wastewater is an important method for detecting clonal clusters of potentially pathogenic bacteria and identifying the risk of dissemination.
Murphy et al. [57]	USA	2021	*A. baumannii* *A. johnsonii*	*Cfx*A6 oxa-280 *tet*(39) *aad*A4 *msr*E *mph*E	Municipal WWTP effluent (hospital included in catchment, no separate hospital wastewater)	Shotgun metagenomics (Illumina)	Effluent from a rural wastewater treatment plant, including hospital wastewater, substantially elevates the abundance of antibiotic resistance genes, including those linked to *A. baumannii*, in downstream river water. The four principal *A. baumannii* ARGs account for 37% of the total ARG hits found, which are enriched near discharge points relative to upstream sites, and this enrichment persists multiple kilometers downstream.

A. baumannii—*Acinetobacter baumannii*; *A.*—*Acinetobacter*; MIC—minimum inhibitory concentration; ARG—antibiotic resistance gene; MALDI-TOF—Matrix-Assisted Laser Desorption/Ionization Time-of-Flight; WGS—Whole-Genome Sequencing; WWTP—wastewater treatment plant; PCR—Polymerase Chain Reaction; MLST—Multilocus Sequence Typing.

The findings from the Americas (encompassing the USA, Brazil, and Mexico) reinforce the concept that hospital wastewater is not merely a waste stream but a direct, functional extension of the clinical reservoir of antimicrobial resistance. Methodologically, these studies utilize shotgun metagenomics and culture-dependent clonal tracking to demonstrate how high-risk lineages, such as the OXA-23-producing ST79 clone, transition from clinical environments to urban rivers. A critical observation from South American and Mexican settings is the high environmental fitness of these strains; for instance, ST79 has successfully adapted to aquatic ecosystems, while diverse *A. haemolyticus* clones exhibit the capacity to persist through the hospital water treatment process, maintaining viability even in treated effluents. Furthermore, longitudinal analysis in North America shows that hospital-linked *A. baumannii* ARGs are significantly enriched at discharge points, accounting for 37% of the total ARG burden and persisting for multiple kilometers downstream in rural river systems. This regional data underscores that current treatment protocols are insufficient to contain the dissemination of these pathogens, necessitating more robust surveillance of hospital effluents to mitigate the public health risk posed by environmental "hotspots."

3. Hospital Wastewater as a Source of Bacteriophages

Bacteriophage therapy appears to be a promising alternative for treating patients with multidrug-resistant bacterial infections. Bacteriophages are widely distributed in nature, and sewage represents the main reservoir, particularly in hospital settings [58]. Compared with antibiotic therapy, the use of bacteriophages has the advantage of their specific action against bacteria, without altering the normal microbial flora. Another significant advantage of bacteriophage therapy is its safety compared to antibiotics, which often have numerous side effects [52]. However, it is important to note that bacteriophage cocktails can affect the intestinal barrier and potentially lead to conditions such as leaky gut. Studies on laboratory animals have demonstrated that oral administration of bacteriophages can trigger an inflammatory response, resulting in increased levels of circulating pro-inflammatory cytokines and changes in intestinal mucosal permeability [59]. Furthermore, using a single bacteriophage over an extended period can lead to the development of resistant bacterial strains through natural selection. Other disadvantages are immunogenicity issues, regulatory approval, and phage delivery systems [60].

In recent years, significant progress has been made in the discovery and characterization of bacteriophages in hospital wastewater (Table 5). Recently, in Benin, three new phages (fBenAci001, fBenAci002, and fBenAci003) associated with the genus *Friunavirus* were isolated from hospital wastewater and evaluated against 57 clinical *Acinetobacter* spp. The phages met the criteria established for phage therapy. However, they had a small host range [52]. Also, in Dakar (Senegal), two novel *Friunavirus* bacteriophages, vAbBal23 and vAbAbd25, active against XDR-resistant *A. baumannii,* were characterized and shown to significantly disrupt biofilm formation, highlighting the potential of phage therapy as an alternative or adjunctive strategy [53]. The same authors described a novel lytic bacteriophage, vAbaIN10, belonging to the genus *Friunavirus*, active against carbapenem-resistant *A. baumannii*. The phage exhibited robust lytic activity and broad environmental stability, and lacked identifiable antibiotic resistance or virulence genes, indicating its potential suitability as a biocontrol agent against carbapenem-resistant *A. baumannii* infections [61]. Furthermore, Essam et al. isolated and characterized two phages that could be useful against carbapenem-resistant *A. baumannii*. The two phages showed lytic activity against 24.3% and 31.7% of the clinical isolates, respectively. The phages demonstrated promising stability in different tested conditions, including pH, temperature, and UV exposure. The study concluded that phage ΦZC3 could be a potentially effective therapy for pneumonia caused by MDR *A. baumannii* [62]. In line with this, a study by Zhang et al. identifies and characterizes MRABP9, a novel lytic bacteriophage in the genus *Friunavirus*, effective MDR *A. baumannii* clinical isolates, demonstrating its potential as a therapeutic agent for challenging MDR infections. The genomic and phenotypic properties of MRABP9 support its broad lytic ability and suitability for further preclinical investigation as an alternative or adjunct to conventional antibiotics [63]. In Iran, the bacteriophage vB_AbaS_SA1, isolated from hospital sewage, exhibits potent lytic activity against MDR *A. baumannii* clinical isolates. Its combination with conventional antibiotics enhances antibacterial efficacy, demonstrating significant phage–antibiotic synergy. These findings underscore the therapeutic potential of bacteriophages sourced from clinical wastewater environments to mitigate MDR *A. baumannii* infections [58]. Another study from Iran, conducted by Ghaznavi-Rad et al., investigated bacteriophages isolated from hospital wastewater against 19 strains of *Acinetobacter baumannii*, which were classified as XDR and exhibited the following resistance genes: *ade*A, *ade*B, *ade*C, *ade*R, *ade*S, bla_{OXA-23}, and bla_{OXA-24}. In this study, a novel lytic bacteriophage, vB-AbauM-Arak1, belonging to the Myoviridae family, targeting extensively drug-resistant *A. baumannii* clinical isolates, was isolated and shown to possess favorable lytic properties and in vitro stability, as well as therapeutic effectiveness in a rat

burn infection model. These findings support the potential of phage therapy to combat XDR *A. baumannii* infections, particularly when conventional antibiotics fail [64].

Numerous studies have highlighted *A. baumannii*'s ability to form biofilms, a significant virulence factor that contributes to increased antibiotic resistance. Biofilms can significantly reduce the effectiveness of antibiotic treatments, making biofilm-producing strains a considerable threat. In response, various methods have been developed and implemented to inhibit biofilm formation or eliminate biofilms. One promising approach is the use of bacteriophages [65]. Bacteriophages can disrupt the biofilm matrix, thereby exposing bacterial receptors. This exposure enables specific binding between the bacteriophage and the bacterium, facilitating penetration of the bacteriophage and initiating its replication cycle [65]. Wang et al., in a recent study, used a clinical isolate of *A. baumannii* (AB48) as a host to isolate phage HZY2308 from hospital wastewater. After 24, 48, and 72 h, the phage drastically lowered the overall biofilm mass of the *A. baumannii* strain. The phage exhibited considerable antibiofilm activity and enhanced antibacterial activity when combined with antibiotics, suggesting that it could be used as an antibacterial agent to manage *A. baumannii* infections. Furthermore, a study conducted in Iran characterized a new lytic bacteriophage specific to *A. baumannii*, named vB-AbaMfThrA, which was isolated from hospital wastewater. The phage has demonstrated the ability to block biofilm formation or destroy existing biofilms, positioning it as a potential candidate for phage therapy. In another study, Lin et al. isolated an *A. baumannii* phage, P425, from medical wastewater and showed that it increased the survival rate of mice infected with a multidrug-resistant strain of *A. baumannii*. Similarly, Zheng et al. isolated phage P1068, which exhibits lytic activity against *A. baumannii* strains resistant to carbapenems, as well as those capable of producing biofilms [66].

Table 5. Summary of the phages isolated from hospital wastewater.

Authors	Phage Source	Phage Designation	Phylogenetic Classification
Arazi et al., 2025 [67]	Raw hospital sewage (Tehran, Iran)	vB-AbaM-fThrA	Class: *Caudoviricetes*; Genus: *Obolenskvirus* (Myovirus morphotype)
Essam et al., 2025 [62]	Hospital wastewater (Egypt)	vB_AbaP_ZC2 (ΦZC2)	Class: *Caudoviricetes*; Family: *Autographiviridae*; Genus: *Friunavirus*
		vB_AbaM_ZC3 (ΦZC3)	Class: *Caudoviricetes*; Genus: *Obolenskvirus*
Ndiaye et al., 2025 [61]	Hospital wastewater (Senegal)	vAbaIN10	Class: *Caudoviricetes*; Family: *Autographiviridae*; Genus: *Friunavirus*
Lin et al., 2025 [66]	Medical wastewater (China)	P425	Class: *Caudoviricetes*; Family: *Podoviridae*; Genus: *Friunavirus*
Rastegar et al., 2024 [58]	Hospital sewage (Iran)	vB_AbaS_SA1	Class: *Caudoviricetes*; Genus: *Vieuvirus* (Siphovirus morphotype)

Table 5. *Cont.*

Authors	Phage Source	Phage Designation	Phylogenetic Classification
Zhang et al., 2024 [63]	Hospital sewage (China)	MRABP9e	Class: *Caudoviricetes*; Family: *Autographiviridae*; Genus: *Friunavirus*
Zheng et al., 2024 [68]	Medical wastewater (China)	P1068	Class: *Caudoviricetes*; Genus: *Obolenskvirus* (T4-like Myovirus)
Kolsi et al., 2023 [69]	Hospital wastewater (Benin)	fBenAci001; fBenAci002; fBenAci003	Class: *Caudoviricetes*; Family: *Autographiviridae*; Genus: *Friunavirus*
Bagińska et al., 2023 [70]	Municipal and hospital wastewater (Poland)	Acba_1, Acba_3, Acba_4, Acba_6, Aclw_8, Aclw_9, Acba_11, Acba_13, Acba_14, Acba_15, Acba_16, Acba_18	Class: *Caudoviricetes*; Subfamilies: *Junivirinae* (*Vieuvirus*, *Shemyakinvirus*); *Beijerinckvirinae* (*Friunavirus*)
Zhu et al., 2022 [71]	Hospital wastewater (China)	BUCT628	Class: *Caudoviricetes*; Family: *Myoviridae*
Ghaznavi-Rad et al., 2022 [64]	Urban wastewater (Iran)	vB-AbauM-Arak1	Class: *Caudoviricetes*; Family: *Myoviridae*
Yang et al., 2019 [72]	Hospital sewage management center (China)	φAbp2	Class: *Caudoviricetes*; Family: *Myoviridae*; Subfamily: *Peduovirinae*

4. Conclusions

This review emphasizes that hospital wastewater represents a significant reservoir for *Acinetobacter* species. It is important to note that many of the isolated strains meet the criteria for multidrug-resistant, extensively drug-resistant, or even pandrug-resistant strains. The rise of blaNDM (New Delhi metallo-beta-lactamase) in *Acinetobacter baumannii* represents a significant evolution in the species' resistance profile, shifting the threat from serine-carbapenemases (Class D OXA enzymes) to metallo-beta-lactamases that render most current beta-lactamase inhibitors ineffective. The isolation of *A. baumannii* strains from hospital effluents highlights the serious risks posed by hospital wastewater to surrounding communities and the environment. The integration of culture-based isolation with high-resolution metagenomic sequencing is transitioning from specialized research into routine environmental surveillance, providing a standardized, real-time "radar" for tracking the persistence and dissemination of multidrug-resistant *Acinetobacter* across global water systems. These findings underscore the necessity for hospital wastewater surveillance and the implementation of effective treatment measures. Hospital wastewater serves as a reservoir for bacteriophages that lyse multidrug-resistant strains of *A. baumannii*, making it a valuable option for treating patients infected with these resistant strains.

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Abbreviations

The following abbreviations are used in this manuscript:

A. baumannii	*Acinetobacter baumannii*
MRSA	Methicillin-resistant *Staphylococcus aureus*
ICU	Intensive Care Unit
CDC	Centers for Disease Control and Prevention
HAP	Hospital-acquired pneumonia
VAP	Ventilator-associated pneumonia
XDR	Extensively drug-resistant
PDR	Pandrug-resistant
ECDC	European Centre for Disease Prevention and Control
Cd	Cadmium
Cu	Copper
Ni	Nickel
Hg	Mercury
Sn	Tin
ARG	Antibiotic resistance gene
AME	Aminoglycoside-modifying enzyme
WWTP	Wastewater treatment plant
AMR	Antimicrobial resistance
Ag NP	Silver nanoparticle
MDR	Multidrug-resistant
P. aeruginosa	*Pseudomonas aeruginosa*
K. pneumoniae	*Klebsiella pneumoniae*
AST	Antibiotic susceptibility testing
WGS	Whole-Genome Sequencing
nZVI	Nano-zero-valent iron
CuONP	Nano-copper
SAIS	Smart artificial intelligent system
MIC	Minimum inhibitory concentration
UV	Ultraviolet

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