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Klebsiella pneumoniae: Characteristics, Epidemiology, and Modern Diagnostic Methods

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Abstract *Klebsiella pneumoniae* causes both healthcare-associated and community-associated infections and combines extensive genomic diversity with a capacity to acquire antimicrobial-resistance and virulence determinants. This narrative review integrates its microbiological characteristics, global and molecular epidemiology, and contemporary diagnostic methods, with treatment discussed as a consequence of laboratory findings. Classical and hypervirulent *K. pneumoniae* are pathotype designations, whereas carbapenem resistance is a susceptibility phenotype and KPC production is a specific resistance mechanism. These categories overlap. Hypermucoviscosity cannot independently establish hypervirulence; clinical presentation, virulence-associated loci and their genomic context provide a more informative assessment. Recent surveillance demonstrates convergence through acquisition of resistance by established hypervirulent lineages and acquisition of virulence-associated elements by resistant hospital lineages. A modern laboratory pathway combines accurate species identification, phenotypic antimicrobial susceptibility testing, rapid carbapenemase detection and selective genomic investigation. Multiplex polymerase chain reaction and lateral-flow assays can accelerate actionable reporting, while whole-genome sequencing clarifies lineage, resistance, virulence and transmission relationships. Treatment of invasive KPC-producing infections now prioritizes active newer β-lactam/β-lactamase inhibitor combinations rather than historical polymyxin-based regimens. Regional differences in circulating clones, carbapenemases, diagnostic capacity and access to medicines require locally informed interpretation. Integrated clinical, laboratory and public-health surveillance is essential to recognize convergent strains and translate faster diagnosis into effective treatment and containment.

Keywords *Klebsiella pneumoniae*, Carbapenem resistance, Hypervirulence, Molecular epidemiology, Carbapenemase detection, Antimicrobial susceptibility testing

1. Introduction: Scope and Objectives

Klebsiella pneumoniae is an encapsulated, non-motile, facultatively anaerobic Gram-negative bacillus within the order Enterobacterales. It can colonize humans without causing disease, but also causes pneumonia, urinary tract infection, bloodstream infection and invasive abscess syndromes. Its clinical importance therefore extends beyond any single resistance enzyme. The 2024 World Health Organization (WHO) bacterial priority pathogen list places carbapenem-resistant Enterobacterales in the critical-priority category; this designation encompasses resistant *K. pneumoniae* rather than all members of the species indiscriminately [1].

The scope of this review is *K. pneumoniae* sensu stricto, with the wider species complex considered where it affects identification or interpretation. The objectives are to distinguish taxonomy, pathotype and resistance terminology; integrate regional epidemiology with circulating lineages and mobile genetic elements; explain convergence of resistance and hypervirulence; and provide a contemporary diagnostic framework linked to treatment and infection prevention. KPC-producing *K. pneumoniae* is addressed as one important subgroup within this broader framework. Table 1 defines the terms used throughout the review.

1.1. Evidence Selection and Limitations

This is a focused narrative review, not a systematic review or meta-analysis. Targeted web searches of biomedical journal pages, PubMed-indexed records and official WHO, ECDC, IDSA, CLSI and EUCAST resources were completed on 8 October 2026. Search combinations paired "*Klebsiella pneumoniae*" with hypervirulence, carbapenemase, convergence, genomic epidemiology, multiplex PCR, lateral flow, susceptibility testing and treatment. Publications from 2024–2026 were prioritized for changing epidemiology, diagnostics and guidance; older primary studies were retained for established methods and pivotal clinical evidence. Sources were selected for direct relevance and verifiable bibliographic information. No exhaustive database search, duplicate independent screening, pooled prevalence analysis or formal certainty grading was performed. Differences

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in specimen selection, hvKp definitions and sequencing coverage limit comparisons across studies. Publication year should not be confused with the years in which isolates were collected.

Table 1. Distinct levels of description used in this review

Level	Example	Meaning and limitation
Taxonomy	*K. pneumoniae* sensu stricto	Species identity; not a resistance or virulence designation.
Pathotype	cKp; hvKp	Clinical/biological behavior; operational hvKp criteria must be stated.
Phenotype	Carbapenem resistance; hypermucoviscosity	Measured trait; neither identifies a unique underlying gene.
Gene and enzyme	blaKPC; KPC	The gene encodes an enzyme; family membership does not establish every drug result.
Mechanism	Carbapenem hydrolysis; porin loss	Biological explanation of a phenotype; mechanisms may coexist.
Lineage	ST11; ST23; clonal group	Genetic relatedness; does not prove recent transmission.
Mobile element	Resistance or virulence plasmid	Genetic vehicle; presence of two loci does not establish same-plasmid location.

2. Biological Characteristics and Pathotype Definition

2.1. Species Identification and Clinical ecology

The *K. pneumoniae* species complex includes *K. pneumoniae* sensu stricto and related taxa such as *K. variicola* and *K. quasipneumoniae*. Routine identification can obscure this diversity. Genomic nomenclature provides a hierarchy for species and strain classification, but a species name, seven-locus sequence type (ST) and core-genome cluster answer different questions and should be reported separately. An ST is a lineage identifier, not a test of hypervirulence or antimicrobial susceptibility [2].

Intestinal carriage provides an important reservoir for subsequent infection. A prospective genomic study in an Australian hospital identified both diverse opportunistic infections and a smaller contribution from documented hospital transmission; resistance-associated lineages were disproportionately involved in the latter. Colonization and infection must therefore be distinguished when calculating frequency or evaluating interventions. A positive rectal screen identifies carriage, whereas infection requires compatible clinical and microbiological evidence. Community onset alone does.

2.2. Hypervirulence is not Equivalent to Hypermucoviscosity

Hypervirulent *K. pneumoniae* (hvKp) denotes strains with enhanced capacity to cause invasive disease, sometimes in otherwise healthy hosts, and to disseminate to distant sites. Liver abscess with metastatic ocular or central nervous system infection is a characteristic presentation, but neither that syndrome nor the absence of comorbidity is obligatory. Classical *K. pneumoniae* (cKp) usually behaves as an opportunistic pathogen, yet this distinction is not an absolute division between community and hospital disease [5].

Hypermucoviscosity is a colony phenotype commonly assessed by the string test. A positive result, conventionally involving a viscous string of approximately 5 mm or longer, is neither sufficient nor necessary to diagnose hvKp. Likewise, K1 or K2 capsule designation cannot independently establish hypervirulence. A foundational biomarker study found that iucA, iroB, peg-344 and plasmid-associated rmpA/rmpA2 discriminated enriched hvKp and cKp collections better than the string test. Performance estimates from those selected collections should not be transferred uncritically to unselected contemporary isolates [3].

The 2024 discussion by Stanton and Wyres emphasizes a further distinction: even carriage of a near-complete virulence plasmid does not invariably produce a hypervirulent phenotype in every genetic background. Accordingly, this review uses "putative hvKp" for isolates classified by molecular markers without adequate functional or clinical corroboration. Studies should state their operational definition, marker panel and supporting evidence. Genomic surveillance and clinical diagnosis can use related evidence without pretending that a universal binary definition has been established [6].

Experimental comparisons across several hvKp backgrounds identify the virulence plasmid as a major contributor, while illustrating the context dependence of individual determinants. Aerobactin-associated iuc, salmochelin-associated iro, capsule-regulatory rmp loci and other virulence-associated elements should therefore be interpreted collectively. Gene integrity and expression matter: detection of a disrupted regulator is not equivalent to demonstration of its biological activity. Animal models remain research tools rather than routine clinical confirmatory tests [7].

3. Resistance Mechanisms: Integrating ESBLs, AmpC and Carbapenemases

3.1. Extended-spectrum β-lactamases and Acquired AmpC

Extended-spectrum β-lactamases (ESBLs), including CTX-M and particular SHV or TEM variants, contribute to resistance to expanded-spectrum cephalosporins and aztreonam. Not every SHV or TEM allele is an ESBL. The laboratory should report a demonstrated allele or phenotype rather than

treating gene-family detection as a uniform functional result. ESBL carriage also frequently accompanies resistance determinants affecting other drug classes, complicating treatment even when the ESBL itself does not act on those drugs [8].

AmpC belongs in this resistance framework because it modifies the phenotype produced by other enzymes and permeability defects. *K. pneumoniae* does not characteristically possess the inducible intrinsic chromosomal ampC system found in organisms such as *Enterobacter cloacae* complex. It can acquire AmpC enzymes, including DHA and CMY families, commonly through plasmids. AmpC enzymes affect many penicillins, cephalosporins and cephamycins and are poorly inhibited by clavulanate. Reduced permeability combined with high enzyme activity can contribute to carbapenem nonsusceptibility without a carbapenemase. Thus, AmpC detection is relevant to both differential diagnosis and susceptibility interpretation, not a separate pathotype [9].

3.2. Carbapenemase Production and Non-Carbapenemase Resistance

Carbapenem resistance is a phenotype with more than one mechanistic explanation. Major acquired carbapenemases include class A KPC, class B metallo-β-lactamases such as NDM, VIM and IMP, and class D OXA-48-like enzymes. Their substrate profiles and inhibitor susceptibility differ. KPC enzymes have broad β-lactam activity, but many are inhibited by avibactam, vaborbactam and relebactam; variant-specific resistance and additional mechanisms can change the resulting susceptibility phenotype [10].

ESBL/AmpC activity combined with OmpK35/OmpK36 porin alterations can reduce carbapenem susceptibility. Genomic characterization complements phenotypic antimicrobial susceptibility testing (AST): a carbapenemase-negative result does not establish susceptibility, and gene detection does not quantify drug-specific resistance [11].

4. Global Epidemiology and Molecular Surveillance

4.1. Regional Patterns and Their Limits

Regional epidemiology is best described by combining sampling period, clinical setting, specimen, ST or clonal group, carbapenemase and virulence profile. A 2026 analysis of 22,569 human-associated genomes from 83 countries identified prominent global sublineages including SL258, SL147, SL17, SL15 and SL307. These rankings describe a deposited genome collection, not unbiased population prevalence. Hospital outbreaks and highly resistant isolates are more likely to be sequenced than susceptible carriage isolates. Country-level proportions from such datasets cannot be equated with national infection rates [12].

In East Asia, the Chinese multicentre study published in 2024 analyzed 1,017 carbapenem-resistant isolates collected during 2016–2020. It documented expansion of KL64 relative to KL47 and increasing representation of isolates classified as hypervirulent by the study. The findings show why capsule locus and virulence profile should accompany ST11 designation rather than assuming that all ST11 isolates share the same properties [13].

South and Southeast Asian surveillance must account for NDM and OXA-48-like enzymes as well as KPC. Genomic analysis has identified ST231 isolates combining resistance, frequently OXA-232, with aerobactin-associated loci in India and other countries. These observations illustrate regional combinations of lineage, enzyme and virulence content, while also showing that such combinations can cross national borders. The broad geographic distribution of hvKp ST23 reported by WHO further argues against restricting hvKp surveillance to a few Asian countries [11,14].

In Europe, an earlier multicountry genomic survey linked carbapenem-resistant *K. pneumoniae* dissemination strongly to hospital spread, including ST258/ST512. Contemporary ECDC assessment identifies continued expansion of high-risk lineages, transmission through healthcare networks and plasmid-mediated dissemination. Its 2025 assessment also highlights carbapenemase-bearing hvKp ST23. Europe therefore cannot be characterized solely by the historical KPC-associated clone, and surveillance should capture emerging enzyme–lineage combinations [15-16].

North American surveillance likewise needs to extend beyond KPC-associated ST258. The international analysis of KPC/NDM coproducers found distinct regional combinations, including KPC-3/NDM-1 among isolates from the United States. Co-production has direct diagnostic importance: identifying KPC does not exclude an additional metallo-β-lactamase. These deposited genomes demonstrate dissemination and diversity, but do not establish a national frequency of dual-carbapenemase infection [17].

Latin America contains substantial within-region heterogeneity. A prospective Colombian study of 335 isolates from 26 hospitals during 2020–2021 found numerous lineages, with ST11 and ST307 among important circulating types. A Peruvian investigation identified NDM-producing lineages including ST45, ST11 and ST147, contrasting with KPC-associated patterns in other South American datasets. Results from one country or referral hospital should not be generalized across the continent [18,19].

In Africa and the Middle East, surveillance from Kenya, Uganda and Jordan documented diverse resistant *K. pneumoniae* lineages, including internationally recognized high-risk clonal groups. The study also showed that the distribution of lineages differed between countries and sampling systems. These data support expanding laboratory and sequencing coverage rather than assuming that sparse reporting means a low burden. Central Asian and other incompletely represented settings require similarly cautious interpretation; the evidence synthesized here does not justify a numerical regional prevalence estimate [20].

For Oceania, the Australian hospital study demonstrates the coexistence of endogenous opportunistic infection, resistant

hospital transmission and community-onset virulence-associated isolates. These findings provide a useful counterpoint to surveillance restricted to carbapenem-resistant outbreaks. Together, the regional studies favor compatible sampling definitions and linked clinical metadata over a single purported worldwide resistance percentage [4].

4.2. From Sequence Types to Transmission Inference

Seven-locus multilocus sequence typing (MLST) supports comparison with historical datasets. Core-genome MLST and single-nucleotide polymorphism analysis provide greater discrimination within a lineage. Genome-based nomenclature can organize both broad sublineages and finer clusters, but matching STs alone does not demonstrate recent transmission. Interpretation must incorporate sampling dates, patient movements, ward overlap and unsampled intermediates. Genetic-distance thresholds depend on the organism, analytical pipeline and investigation context [2,15].

Whole-genome sequencing (WGS), interpreted with tools such as Kleborate, integrates species, lineage, resistance, virulence and antigen-locus information. Software/database versions and quality criteria should be documented. [11] Short-read assemblies may leave plasmid architecture unresolved. Long-read or hybrid assemblies can clarify linkage; detecting two loci in an isolate does not by itself demonstrate same-plasmid location or transferability [17].

4.3. Colonization, International Movement and Environmental Reservoirs

Transmission can involve colonized patients as well as clinically infected patients, particularly across interconnected hospitals and long-term care facilities. Infection-control assessment should therefore incorporate previous healthcare exposure and interfacility transfer, while avoiding assumptions based on ethnicity. ECDC emphasizes coordinated detection and response across healthcare networks because institutions do not operate as epidemiologically isolated units [16].

Environmental and animal reservoirs warrant One Health investigation, but shared genes or STs are not proof of direct spillover. A Norwegian study of 3,255 genomes from human, animal and marine sources found overlapping populations with relatively few recent cross-reservoir transmission events. That result supports a distinction between ecological overlap and demonstrated transmission. Environmental sampling is most informative when linked to a defined epidemiological question and sufficiently resolved genomes [21].

5. Convergence of Hypervirulence and Antimicrobial Resistance

Convergence can occur when an established hvKp lineage acquires resistance elements or when a resistant hospital lineage acquires virulence-associated material. Mobile genetic elements can also undergo rearrangement, yielding different architectures that combine these traits. The public-health concern is the resulting combination of invasive potential, restricted therapy and capacity for spread, rather than any single universal convergent clone. Figure 1 summarizes these routes conceptually [6,17].

The presence of iuc or rmp-associated loci in a resistant isolate should trigger closer characterization, but virulence gene carriage is not identical to proven hypervirulence. Surveillance reports should state whether “convergent” means coexistence of defined genetic markers, experimentally demonstrated virulence with resistance, or a compatible invasive clinical syndrome. Harmonizing these levels of evidence will improve comparisons and reduce inflated prevalence estimates [6,7].

Table 2. Selected internationally important *K. pneumoniae* lineages

Lineage	Epidemiological association	Interpretive point
ST258 / ST512	KPC-associated hospital spread, notably in Europe and the Americas. [15]	Historical high-risk group; other enzymes and variants require testing.
ST11	Prominent resistant lineage in China; also reported in the Americas. [13,18]	Capsule and virulence content vary within the ST.
ST15	Widely represented high-risk lineage in global genome collections. [12]	Geography and resistance profile must accompany the ST.
ST147	International resistant lineage; documented in Jordan and Peru. [19,20]	NDM-associated examples do not define all ST147 isolates.
ST307	International hospital-associated lineage, including Colombia. [18]	Expanded-spectrum cephalosporin resistance and carbapenemases are isolate-specific.
ST23	Major hvKp-associated lineage; carbapenemase-bearing isolates reported internationally. [14]	ST23 alone does not confirm hypervirulence or resistance.
ST65 / ST86	Additional established hvKp-associated backgrounds. [6]	Require virulence and susceptibility characterization.
ST231	Resistance–virulence convergence reported in South Asia and beyond. [11]	OXA-232 and iuc-associated examples warrant surveillance.

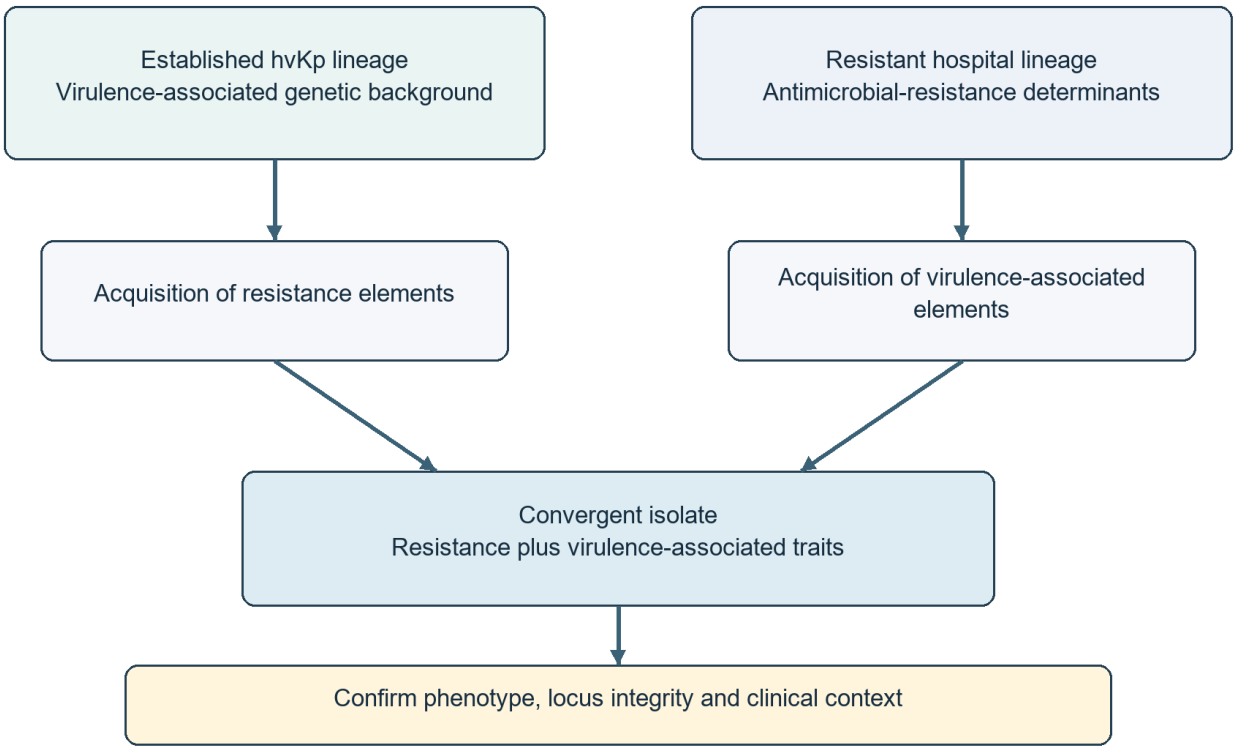

Figure 1. Conceptual routes to virulence–resistance convergence. Independent schematic; arrows describe acquisition pathways, not measured transfer frequencies. Genetic coexistence alone does not prove hypervirulence [6,17]

6. A Contemporary Diagnostic Framework

6.1. Establish the Organism and Retain an Isolate

Diagnostic testing begins with a clinically appropriate specimen and assessment of whether the finding represents infection or colonization. Culture remains important because it supplies an isolate for AST, additional characterization and epidemiological comparison. MALDI-TOF mass spectrometry can support rapid identification, but discrimination within the species complex depends on the validated database and workflow. A genomic or reference-laboratory method may be needed when a precise species assignment affects interpretation [22].

6.2. Rapid Molecular Detection and Multiplex Platforms

Targeted nucleic-acid assays rapidly identify common carbapenemase families, whereas syndromic multiplex panels can combine organism detection with selected resistance genes. These are different applications: a positive-blood -culture panel is not a direct-from-whole-blood test or a rectal screening assay. In the multicentre BIOFIRE BCID2 evaluation, testing provided results in approximately one hour after an eligible blood culture was positive. Its value lies in rapid actionable reporting, not replacement of culture or the entire susceptibility profile [23].

Panel coverage must be stated explicitly. A negative result excludes only detectable targets under the assay's validated conditions; it cannot exclude off-panel enzymes or non-carbapenemase resistance. In polymicrobial samples, attribution of a resistance gene to a particular organism may require isolate testing. Unexpected molecular–phenotypic discordance should be investigated rather than resolved by automatically privileging one test [10,23].

6.3. Protein Detection and Phenotypic Carbapenemase Tests

Lateral-flow immunochromatographic assays detect carbapenemase proteins and can differentiate major families within minutes from validated specimen preparations. Contemporary comparative studies support their operational usefulness, but weak expression and altered epitopes in enzyme variants can produce false-negative results. Performance depends on assay version, enzyme family and specimen type; claims of universal accuracy are inappropriate [24].

Phenotypic activity assays remain valuable, particularly when molecular panels are unavailable or do not explain resistance. The modified carbapenem inactivation method (mCIM) detects carbapenemase activity; it does not identify a precise gene. Its primary validation demonstrated a practical, relatively inexpensive approach. EDTA-modified testing can support metallo-β-lactamase differentiation in appropriate algorithms, with limitations for complex enzyme

combinations. The modified Hodge test should be treated as a historical method rather than the centerpiece of contemporary detection [10,25].

6.4. MALDI-TOF Applications Beyond Identification

Dedicated MALDI-TOF hydrolysis assays detect changes in a carbapenem substrate and can identify enzyme activity where locally validated. They are distinct from the routine organism-identification spectrum. A comparative study of commercial and in-house approaches illustrates this application, but detection of hydrolysis is not equivalent to identification of every carbapenemase allele. Likewise, a spectral classifier developed on one collection should not be presented as a universally validated hvKp diagnostic [26].

6.5. Susceptibility Testing and Current Interpretive Standards

Phenotypic AST establishes the drug-specific result required for treatment. Laboratories should use a validated method, appropriate quality controls and a consistent current interpretive system. At the review date, CLSI M100, 36th edition (2026), and EUCAST clinical breakpoint tables version 16.1 (2026) were current resources. CLSI methodology and interpretive categories should not be mixed selectively with EUCAST values. EUCAST "I" means susceptible with increased exposure, not an undefined intermediate category. Breakpoint edition, method and relevant exposure assumptions should be traceable in laboratory procedures [27,28].

For rapid AST directly from positive blood cultures, validated time-specific methods and interpretive criteria are necessary; conventional overnight disk-diffusion thresholds cannot simply be transferred to an early reading. EUCAST provides dedicated rapid AST guidance. The clinically useful endpoint is not merely a faster instrument result, but a verified report delivered to a team able to adjust treatment promptly [29].

6.6. Identifying Putative hvKp and Escalating to Genomics

For suspected hvKp, the laboratory should integrate the clinical syndrome with molecular characterization of a defined virulence-associated panel. The original biomarker evidence supports loci such as iucA, iroB, peg-344 and plasmid-associated rmpA/rmpA2; WGS adds lineage and locus-integrity information. The report should distinguish marker detection from a definitive statement about pathogenic behavior. Carbapenemase-bearing isolates with such markers warrant particular attention for clinical assessment and surveillance [3,7].

A practical pathway runs AST and rapid resistance characterization in parallel, escalates discordant or epidemiologically important isolates to a reference service, and uses WGS for convergence assessment and outbreak investigation. The complementary roles and limitations are summarized in Table 3 and Figure 2. No single test answers species identity, susceptibility, hypervirulence and transmission simultaneously.

Table 3. Complementary diagnostic methods and their limitations

Method	Primary contribution	Main limitation
Culture + species identification	Recover a viable isolate; identify organism. [22]	Species-complex resolution depends on method/database.
Multiplex PCR	Rapid organism/selected gene reporting from validated specimen types. [23]	Off-panel genes, mixed cultures and genotype–phenotype discordance.
Lateral-flow assay	Rapid detection of common carbapenemase proteins. [24]	Variant/low-expression false negatives; restricted family coverage.
mCIM / adjunct eCIM	Detect activity; support enzyme-class differentiation. [10,25]	Does not identify an allele; complex combinations can confound interpretation.
MALDI-TOF hydrolysis	Detect carbapenem breakdown in a dedicated workflow. [26]	Not identical to routine identification; needs local validation.
Phenotypic AST / rapid AST	Drug-specific susceptibility using validated criteria. [27,28,29]	Results depend on method, breakpoint version and exposure assumptions.
Virulence-marker PCR	Recognize a putative virulence-associated profile. [3]	Marker carriage is not definitive proof of hypervirulence.
WGS / hybrid sequencing	Lineage, loci and high-resolution comparison; improved plasmid resolution with long reads. [2,17]	Requires quality control and epidemiological context; not a substitute for AST.

Table 4. Current mechanism-informed options for invasive infections

Detected mechanism	Preferred options	Selected alternatives / qualification
KPC	Ceftazidime-avibactam; meropenem-vaborbactam; imipenem-cilastatin-relebactam.	Aztreonam-avibactam or cefiderocol.
NDM	Aztreonam-avibactam or cefiderocol.	Ceftazidime-avibactam plus aztreonam if aztreonam-avibactam unavailable.
OXA-48-like	Ceftazidime-avibactam.	Aztreonam-avibactam or cefiderocol.

Source: IDSA 2026, questions 3.4–3.6 [30]. Confirm susceptibility and consider infection site, exposure and local authorization.
This is not a dosing table; co-produced enzymes may alter the appropriate choice.

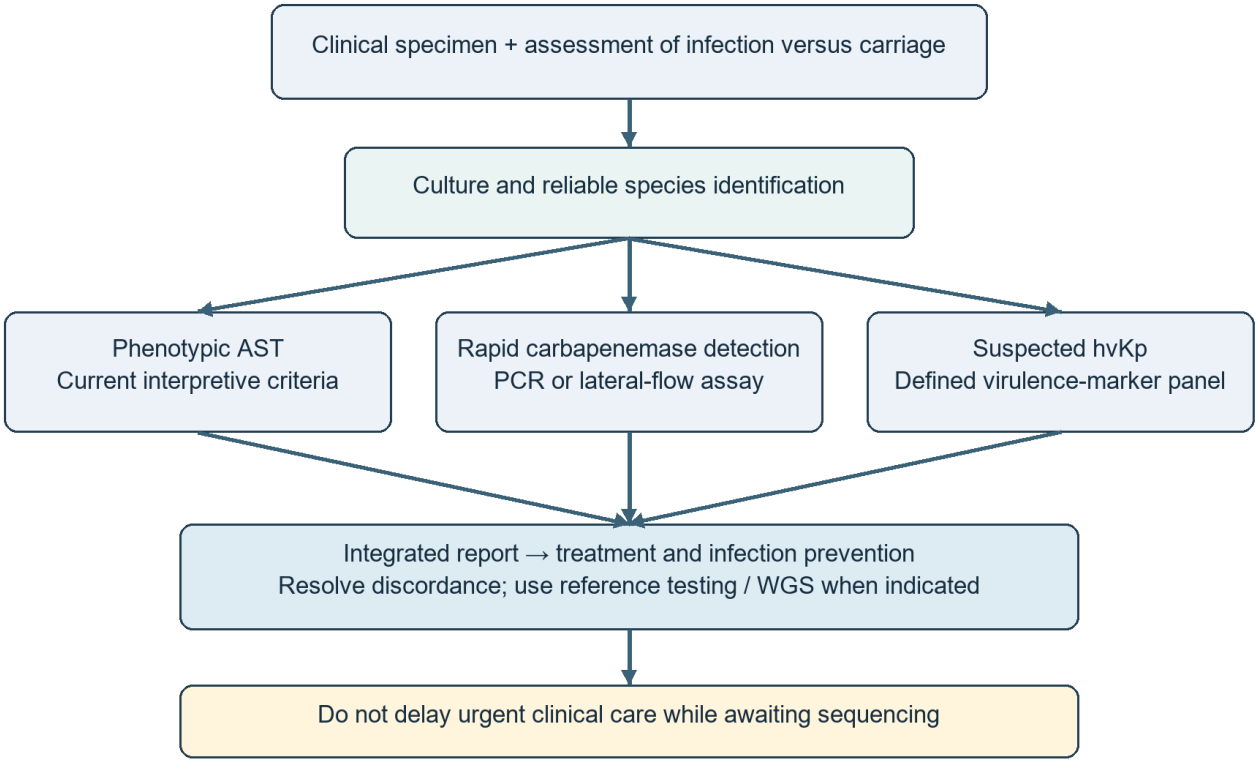

Figure 2. Integrated diagnostic pathway. Parallel testing provides complementary information; assay choice depends on specimen validation and resources. WGS supports selected characterization and surveillance. Independent schematic based on the framework in Section 6 [23,24,27]

Turnaround must distinguish assay time from specimen-to-result time. PCR, polymerase chain reaction; mCIM, modified carbapenem inactivation method; eCIM, EDTA-modified CIM; AST, antimicrobial susceptibility testing; WGS, whole-genome sequencing.

7. Antimicrobial Treatment: Translating Laboratory Findings into Care

7.1. Mechanism-Directed Therapy

Treatment selection requires a clinically established infection, an active drug and adequate exposure at the infected site. Table 4 summarizes the 2026 IDSA approach for invasive carbapenemase-producing Enterobacterales infections. The guidance is US-focused; availability, authorization and local epidemiology vary internationally. Carbapenemase identification narrows rational choices, while AST tests the actual isolate [30].

The shift away from historical regimens has clinical evidence behind it. In TANGO II, meropenem-vaborbactam improved clinical cure relative to best available therapy in a small randomized population with confirmed carbapenem -resistant Enterobacterales infection. The numerical mortality difference was imprecise, and the trial was not a head-to-head comparison of all newer agents. An observational comparison of ceftazidime-avibactam and colistin also favored the newer agent, although residual confounding remains possible. Together, these studies undermine the portrayal of colistin, tigecycline and aminoglycosides as the principal remaining options for invasive KPC infection [31,32].

Aztreonam-avibactam provides a newer option particularly relevant to metallo-β-lactamase producers. Its mechanism combines aztreonam stability to these enzymes with protection against accompanying susceptible serine β-lactamases. Regulatory scope must be distinguished from guideline recommendations: the initial US authorization in 2025 covered selected adults with complicated intra-abdominal infection, limited or no alternatives, and concomitant metronidazole. It should not be described as a universally licensed treatment for every resistant *K. pneumoniae* syndrome [33].

7.2. ESBL/AmpC, Restricted Roles of Older Agents and hvKp

For invasive ESBL-producing infections, carbapenems retain an established role when active. Acquired AmpC in *K. pneumoniae* requires interpretation of the complete resistance profile; recommendations for species with inducible intrinsic AmpC should not be transplanted automatically. Tigecycline and eravacycline have site-dependent alternative roles and are unsuitable for bloodstream or urinary tract infection. Aminoglycosides may be useful in selected susceptible urinary infections, but toxicity and exposure limit broader

reliance. Routine addition of an older agent to an active newer β-lactam is not supported as a default strategy [8,30].

Hypervirulence does not itself determine which antibiotic is active. Management combines susceptibility-directed therapy with source control and evaluation for clinically suspected metastatic disease. Ocular or neurological symptoms require urgent site-specific assessment. Duration depends on the focus, source control and response rather than the hvKp label alone. Uncontrolled abscesses, delayed effective therapy and poor penetration can cause failure even when the isolate is susceptible in vitro [5].

Treatment-emergent resistance also requires attention. A documented Argentine outbreak of ST11 carrying ceftazidime-avibactam-resistant KPC variants illustrates that newer agents are not immune to resistance and that such isolates can spread. Persistent or recurrent infection warrants renewed culture and AST; neither an earlier susceptible result nor carbapenemase-family detection guarantees continued activity [34].

8. Prevention, Evidence Gaps and Research Priorities

Current surveillance priorities include coordinated recognition of resistant lineages, detection of virulence–resistance convergence and communication across healthcare facilities. Laboratory capacity must be matched to the local setting: a reliable AST service with targeted rapid testing and reference-laboratory access can be more useful than advanced equipment without validated workflows or timely reporting. WHO and ECDC alerts support strengthening detection and containment of carbapenemase-bearing hvKp, alongside established infection-prevention measures [14,16].

The principal research gaps are a reproducible definition of hvKp, prospective validation of marker combinations in diverse lineages, representative sampling outside major referral hospitals and better linkage of genomes to clinical outcomes. Genomic collections should retain specimen type, colonization/infection status, healthcare exposure and collection date. Comparative treatment evidence specifically for convergent strains remains limited; recommendations generally derive from resistance mechanism and infection syndrome rather than trials confined to this subgroup. Regional genomic studies and experimental virulence studies address different components of that evidence gap [7,12].

9. Conclusions

K. pneumoniae should be understood through the interaction of species identity, lineage, virulence potential and resistance mechanisms. KPC production is one important component of that picture, while hypermucoviscosity is an imperfect phenotype rather than a definition of hypervirulence. The convergence of invasive potential and antimicrobial resistance connects previously separated clinical and epidemiological discussions. Modern diagnosis combines culture and standardized AST with rapid carbapenemase characterization and selective genomic analysis. Mechanism -informed use of newer agents has changed the treatment of invasive KPC-producing infections, but source control, resistance surveillance and access to effective care remain essential. Progress depends on comparable definitions and surveillance that links laboratory findings to clinical decisions and transmission prevention.

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