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Emergence and Molecular Epidemiology of Carbapenem-Resistant Enterobacterales in Tertiary Healthcare Facilities in Northwestern Nigeria

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ABSTRACT
Carbapenem-resistant Enterobacterales (CRE) have become an important threat to healthcare delivery because resistance to carbapenems can substantially limit treatment options for serious bacterial infections. The problem is particularly concerning in Nigeria, where laboratory capacity for routine antimicrobial resistance surveillance and molecular characterization remains uneven. This study proposes to investigate the emergence, phenotypic resistance patterns, carbapenemase genes, and molecular epidemiology of CRE in selected tertiary healthcare facilities in Northwestern Nigeria. A multicentre cross-sectional study is proposed across selected tertiary hospitals in Kano, Kaduna, Sokoto, Katsina, and Zamfara States. Clinical Enterobacterales isolates will be identified and subjected to antimicrobial susceptibility testing, followed by phenotypic and molecular detection of carbapenem resistance. Selected CRE isolates will undergo PCR screening for major carbapenemase genes, including blaNDM, blaKPC, blaVIM, blaIMP, and blaOXA-48-like. Whole-genome sequencing will be used for selected isolates to determine sequence types, resistance determinants, plasmid-associated elements, and genetic relatedness. The expected findings are a measurable burden of CRE, with Klebsiella pneumoniae and Escherichia coli likely to constitute a substantial proportion of resistant isolates. The study also expects blaNDM and blaOXA-48-like genes to be important molecular determinants, consistent with previous Nigerian findings. Molecular epidemiological analysis is expected to reveal both genetically diverse isolates and clusters suggesting possible healthcare-associated transmission. The findings would provide useful evidence for antimicrobial stewardship, infection prevention and control, and genomic surveillance in Northwestern Nigeria.

Keywords: Carbapenem resistance, Enterobacterales, CRE, carbapenemase, blaNDM, blaOXA-48, molecular epidemiology, antimicrobial resistance, Northwestern Nigeria.

1. INTRODUCTION

Antimicrobial resistance (AMR) has become one of the most difficult challenges facing modern healthcare systems. Bacterial infections that were previously manageable with commonly available antibiotics are increasingly becoming resistant to multiple antimicrobial agents, resulting in longer hospital stays, increased treatment costs and greater risks of complications and death. The global burden is substantial, with bacterial AMR estimated to have been directly responsible for more than one million deaths in 2019 and associated with millions of additional deaths (Antimicrobial Resistance Collaborators,

2022). The problem is particularly serious in low- and middle-income countries, where access to microbiological diagnosis, effective antibiotics, infection prevention infrastructure and antimicrobial surveillance may be limited.

Among resistant Gram-negative organisms, carbapenem-resistant Enterobacterales (CRE) occupy a particularly concerning position. Carbapenems are often reserved for severe infections caused by organisms resistant to other β-lactam antibiotics. When Enterobacterales become resistant to these agents, clinicians may be left with considerably fewer effective therapeutic choices. Reflecting this concern, the World Health Organization's 2024 Bacterial Priority Pathogens List places carbapenem-resistant Enterobacterales in the critical priority category. Carbapenem-resistant Klebsiella pneumoniae received the highest overall score among the pathogens assessed in the prioritisation exercise.

The situation in Nigeria deserves particular attention. Existing evidence demonstrates that carbapenem resistance is already present in different parts of the country, although the available evidence remains uneven geographically. A Nigerian systematic review and meta-analysis found substantial heterogeneity in carbapenem resistance and reported pooled resistance estimates of 11.2% for imipenem and 13.5% for meropenem, while also identifying an increasing trend in resistance over time. More importantly for Northwestern Nigeria, a study conducted in two major hospitals in Sokoto identified carbapenem resistance among 19 of 292 Enterobacteriaceae isolates (6.5%). Seven of those resistant isolates produced carbapenemases, with blaNDM-5 detected in five and blaOXA-181 in two.

Recent research has strengthened the evidence that resistant Enterobacterales in Northern Nigeria are genetically diverse. Medugu et al. (2023) used whole-genome sequencing to characterise 49 multidrug-resistant Enterobacterales isolates obtained from hospitals in Northern Nigeria. Carbapenem resistance was observed in 65.3% of the selected isolates, while blaNDM-1 was detected in 51.5%. High-risk sequence types were also identified among Klebsiella and Escherichia coli, demonstrating that molecular surveillance can reveal epidemiological patterns that routine antimicrobial susceptibility testing alone cannot adequately describe.

More recent surveillance at Ahmadu Bello University Teaching Hospital, Zaria, further demonstrates the continuing relevance of CRE in the Northwestern region. Yaqub et al. (2025) reported CRE in 4.2% of 168 hospitalized participants undergoing rectal surveillance. Interestingly, the study detected blaOXA-48 in all seven CRE isolates despite finding no conventional carbapenemase gene that clearly explained the phenotypic resistance, highlighting the complexity of interpreting genotype and phenotype together.

Against this background, there is a strong rationale for a broader multicentre investigation of CRE in Northwestern Nigeria. Rather than focusing only on whether an isolate is resistant, molecular epidemiology can help determine which organisms are involved, which resistance genes they carry, whether resistant strains are genetically related, and whether particular high-risk clones are circulating across healthcare facilities.

2. Statement of the Problem

The emergence of CRE represents a serious challenge for tertiary healthcare facilities because these hospitals frequently manage patients with severe infections, prolonged hospitalisation, previous antibiotic exposure, invasive procedures and underlying medical conditions. Such environments can create conditions in which resistant organisms are selected and transmitted. Once established, CRE can spread between patients through healthcare workers, contaminated equipment, environmental reservoirs or other routes associated with healthcare delivery.

Nigeria has made progress in establishing AMR surveillance. The country's second National Action Plan for AMR (NAP 2.0) covers 2024–2028 and emphasises surveillance, infection prevention and control, antimicrobial stewardship, diagnostics and research. Nevertheless, important gaps remain in the availability of detailed molecular epidemiological information at regional and facility levels.

Northwestern Nigeria is particularly important because the region contains major tertiary referral hospitals that serve large populations across several states and, in some cases, neighbouring countries. Evidence from Sokoto and Kaduna already confirms the presence of CRE and important carbapenemase determinants. However, the existing studies have generally been limited to individual facilities, selected

specimens, archived isolates or specific surveillance populations. This makes it difficult to determine the broader distribution and genetic relatedness of CRE across tertiary healthcare facilities in the region.

Another concern is that phenotypic resistance does not always identify the underlying molecular mechanism. The Sokoto study, for example, found that only seven of 19 carbapenem-resistant isolates carried the carbapenemase genes investigated, suggesting that other mechanisms may contribute to resistance. Consequently, relying solely on routine antimicrobial susceptibility testing may underestimate the diversity of carbapenem resistance mechanisms.

The problem addressed by this study is therefore the limited multicentre molecular evidence on the emergence, distribution and genetic epidemiology of CRE in Northwestern Nigeria. Generating such evidence would support more targeted infection prevention, antimicrobial stewardship and regional surveillance.

3. Objective of the Study

The main aim of this study is to investigate the emergence and molecular epidemiology of carbapenem-resistant Enterobacterales in selected tertiary healthcare facilities in Northwestern Nigeria.

3.1 Specific Objectives

The study seeks to:

1. determine the prevalence of CRE among Enterobacterales isolated from clinical specimens in selected tertiary healthcare facilities;
2. identify the major Enterobacterales species associated with carbapenem resistance;
3. determine the antimicrobial susceptibility patterns of CRE isolates;
4. detect major carbapenemase genes, including blaNDM, blaKPC, blaVIM, blaIMP and blaOXA-48-like;
5. determine the distribution of carbapenemase genes among different Enterobacterales species and clinical specimens;
6. investigate selected patient and healthcare-related factors associated with CRE isolation;
7. determine the sequence types, resistance determinants and genetic relatedness of selected CRE isolates using whole-genome sequencing; and
8. assess whether genetically related CRE isolates occur across wards or healthcare facilities, suggesting possible healthcare-associated transmission.

4. Research Questions

The study will answer the following questions:

1. What proportion of Enterobacterales isolated from tertiary healthcare facilities in Northwestern Nigeria are carbapenem resistant?
2. Which Enterobacterales species are most frequently associated with CRE?
3. What antimicrobial resistance patterns are displayed by CRE isolates?
4. Which carbapenemase genes are present among CRE isolates?
5. Is the distribution of carbapenemase genes significantly associated with bacterial species or specimen type?
6. What patient and healthcare factors are associated with CRE isolation?
7. Which sequence types and resistance determinants occur among selected CRE isolates?
8. Do molecular data suggest the presence of closely related strains within or across tertiary healthcare facilities?

5. Research Hypotheses

The following null hypotheses will be tested:

H01: There is no significant difference in the prevalence of CRE among the selected tertiary healthcare facilities in Northwestern Nigeria.

H02: There is no significant association between bacterial species and carbapenem resistance.

H03: There is no significant association between the presence of carbapenemase genes and phenotypic carbapenem resistance.

H04: Patient and healthcare-related factors do not significantly predict CRE isolation.

H05: There is no significant genetic relatedness among selected CRE isolates recovered from the study facilities.

6. Significance of the Study

The study will be relevant to clinicians, medical microbiologists, infection prevention teams, hospital administrators and public health authorities. For clinicians, information about local CRE prevalence and resistance patterns can improve empirical and targeted antimicrobial decision-making. This is important because evidence from a tertiary hospital in Nigeria has shown substantial mismatch between CRE susceptibility profiles and antibiotics prescribed to affected patients (Adekanmbi et al., 2024).

For microbiology laboratories, the study will demonstrate the value of combining phenotypic antimicrobial susceptibility testing with molecular approaches. WHO's GLASS framework recognises the importance of both phenotypic and molecular data in understanding the mechanisms responsible for antimicrobial resistance.

For infection prevention and control teams, molecular relatedness data may provide evidence about whether resistant isolates represent unrelated events or possible transmission clusters. At the policy level, the findings could contribute to Nigeria's AMR NAP 2.0 objectives relating to surveillance, infection prevention, antimicrobial stewardship and research.

2. LITERATURE REVIEW

2.1 Carbapenem Resistance among Enterobacterales

Enterobacterales include clinically important organisms such as Escherichia coli, Klebsiella pneumoniae, Enterobacter species, Citrobacter species and Serratia species. These organisms are responsible for urinary tract infections, bloodstream infections, wound infections, pneumonia and other healthcare-associated infections.

Carbapenem resistance can arise through several mechanisms. Carbapenemase production is particularly important because enzymes such as NDM, KPC and OXA-48-like carbapenemases can hydrolyse carbapenem antibiotics. Resistance can also occur through combinations of extended-spectrum β-lactamase or AmpC production and reduced outer-membrane permeability.

The clinical significance of these mechanisms explains why CRE has received critical-priority status from WHO.

2.2 Evidence from Northwestern Nigeria

The most directly relevant molecular evidence comes from Sokoto. Olowo-Okere et al. (2020) examined 292 Enterobacteriaceae isolates from two hospitals and identified 19 carbapenem-resistant isolates. Seven were phenotypically carbapenemase producing, with five carrying blaNDM-5 and two carrying blaOXA-181. The study also detected NDM-producing Citrobacter freundii and NDM-producing Enterobacter cloacae, illustrating that carbapenemase production was not restricted to Klebsiella or E. coli.

The more recent study by Yaqub et al. (2025) at ABUTH Zaria found CRE among hospitalised patients undergoing rectal surveillance. Seven participants out of 168 were CRE positive, representing 4.2%. The study found blaOXA-48 among all seven CRE isolates.

These findings suggest that carbapenem resistance is established in Northwestern Nigeria but that its molecular epidemiology may be more complex than routine laboratory reports indicate.

2.3 Molecular Epidemiology and Whole-Genome Sequencing

Molecular epidemiology moves beyond simple identification of resistance genes by examining the genetic relationships among bacterial isolates. Whole-genome sequencing can identify resistance genes, sequence types, mutations, plasmid-associated determinants and single-nucleotide differences that help determine whether isolates are closely related.

Medugu et al. (2023) demonstrated the usefulness of this approach in Northern Nigeria. Their analysis detected blaNDM-1 and identified high-risk sequence types including ST-476 and ST-147 among Klebsiella isolates. The findings showed that apparently similar phenotypes can arise from different genetic backgrounds, while genetically related organisms may circulate within healthcare networks.

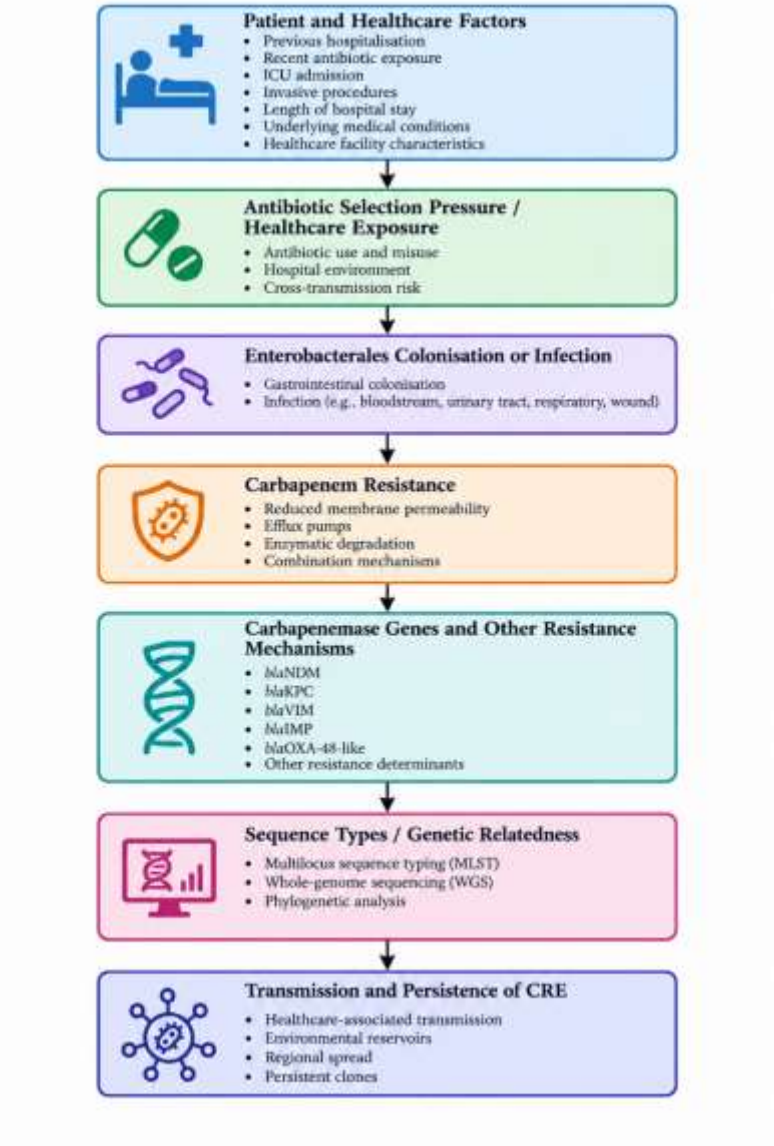
A more recent Nigerian genomic study of Enterobacter hormaechei from six tertiary hospitals also demonstrated substantial genomic diversity and identified clusters that could represent potential

outbreaks. The findings reinforce the value of genomic surveillance for detecting transmission patterns that conventional microbiology may miss.

2.4 Theoretical/Conceptual Framework

The study is guided by a One Health and molecular epidemiological framework. The framework assumes that CRE emergence is influenced by antibiotic selection pressure, patient characteristics, healthcare exposure and infection-control conditions, while the resulting bacterial phenotype is shaped by specific genetic resistance mechanisms.

The conceptual relationship can be represented as:



Important explanatory variables will include previous hospitalization, recent antibiotic exposure, ICU admission, invasive procedures, length of hospital stay and healthcare facility.

The main molecular outcomes will include carbapenemase genes, sequence types, resistance profiles and genomic relatedness.

3. METHODOLOGY

3.1 Research Design

A multicentre cross-sectional laboratory-based study with a molecular epidemiological component is proposed. Clinical Enterobacterales isolates will be collected from selected tertiary healthcare facilities in Northwestern Nigeria. Epidemiological information will be obtained from relevant patient records, while laboratory investigations will establish antimicrobial susceptibility and molecular resistance profiles.

3.2 Study Area

The proposed study will cover selected tertiary healthcare facilities in Northwestern Nigeria, with possible inclusion of major referral facilities in:

Kano State, Kaduna State, Sokoto State, Katsina State, and Zamfara State.

The final number of hospitals will depend on ethical approval, institutional permissions, laboratory capacity and availability of archived or prospectively collected isolates.

The inclusion of Kano, Kaduna and Sokoto is particularly appropriate because published studies have already documented important resistant Enterobacterales in these areas. Kano has contributed isolates to genomic studies of Northern Nigerian MDR Enterobacterales, while Kaduna and Sokoto have produced facility-level CRE surveillance data.

3.3 Study Population

The population will comprise patients whose clinical specimens yield Enterobacterales during the study period. Specimens may include blood, urine, wound samples, respiratory specimens and other clinically appropriate samples.

Patient information will be restricted to variables necessary for epidemiological analysis. Personal identifiers will not be included in the analytical dataset.

3.4 Sample Size

For this study a target of approximately 600 non-duplicate Enterobacterales isolates is proposed. This number would provide a reasonable basis for estimating CRE prevalence across multiple facilities and for conducting comparative analyses.

Based on the existing Northern Nigerian evidence, the study may reasonably expect approximately 30–60 CRE isolates, although the final number should be determined by the actual laboratory data rather than predetermined expectations.

3.5 Sampling Technique

A combination of consecutive sampling and stratified facility sampling will be used.

Each participating hospital will contribute non-duplicate Enterobacterales isolates recovered during the study period. Where more than one isolate is recovered from the same patient, only the first clinically relevant isolate meeting the study criteria will normally be included in the primary prevalence analysis.

3.6 Laboratory Investigation

3.6.1 Identification of Enterobacterales

Clinical specimens will be processed using routine microbiological procedures in the participating laboratories. Enterobacterales will be identified using standard biochemical, automated or validated identification systems available at the facilities.

Where feasible, modern identification systems such as MALDI-TOF or automated biochemical identification may be used to improve species-level identification.

3.6.2 Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing will be performed using validated laboratory methods and interpreted according to the current standard adopted by the study laboratories. The CLSI M100 36th edition, published in 2026, provides current breakpoint and quality-control information for antimicrobial susceptibility testing and supersedes the 2025 edition.

The antimicrobial panel may include clinically relevant agents such as:

- meropenem;
- imipenem;
- ertapenem;

- ceftriaxone
- ceftazidime;
- cefepime;
- piperacillin-tazobactam;
- ciprofloxacin;
- gentamicin;
- amikacin;
- trimethoprim-sulfamethoxazole; and

other agents available within the participating laboratories.
CRE will be classified using the applicable current laboratory breakpoint criteria.

3.6.3. Molecular Characterization

Carbapenem-resistant isolates will undergo molecular investigation for major carbapenemase determinants.
The proposed targets include:
blaNDM;
blaKPC;
blaVIM;
blaIMP; and
blaOXA-48-like.
Where resources permit, selected isolates will undergo whole-genome sequencing to identify broader antimicrobial resistance determinants and establish genetic relatedness.
The molecular component is important because phenotypic carbapenem resistance does not necessarily indicate which resistance mechanism is operating. This was demonstrated in Sokoto, where several carbapenem-resistant isolates did not carry the carbapenemase genes tested.

3.6.4 Whole-Genome Sequencing and Molecular Epidemiology

A representative subset of CRE isolates will be selected for whole-genome sequencing. Selection will seek to capture:
different bacterial species;
different healthcare facilities;
different specimen types;
different carbapenemase profiles;
unusual resistance phenotypes; and
temporally separated isolates.
The genomic analysis will investigate antimicrobial resistance genes, sequence types and genetic relationships among isolates. Phylogenetic analysis will then be used to identify closely related isolates.
Where appropriate, multilocus sequence typing will be used to compare isolates with internationally recognised lineages.
The study will avoid interpreting genetic similarity alone as proof of direct transmission. Epidemiological information such as ward, hospital, specimen date and patient location will be considered alongside genomic findings.

3.6.5. Data Analysis

Data will be analysed using SPSS, R or another appropriate statistical package.
Descriptive statistics will include:
frequencies;
percentages;
means;
standard deviations;
prevalence estimates; and
95% confidence intervals.
Chi-square or Fisher's exact tests will be used to examine associations between categorical variables.

Binary logistic regression will be used to identify independent predictors of CRE isolation.
A possible model is:

$$\text{Logit}(P_i) = \beta_0 + \beta_1 AGE_i + \beta_2 ANT_i + \beta_3 LOS_i + \beta_4 ICU_i + \beta_5 PREV_i + \beta_6 INV_i + \epsilon_i$$

Where:
AGE = patient age;
ANT = recent antibiotic exposure;
LOS = length of hospital stay;
ICU = ICU admission;
PREV = previous hospitalization;
INV = invasive procedure exposure; and
P = probability of CRE isolation.
Adjusted odds ratios with 95% confidence intervals will be reported. Statistical significance will be set at $p < 0.05$.

4. RESULTS

The following results are presented as follows

Table 1. Distribution of Enterobacterales Isolates

Organism	Number	Percentage
E. coli	245	40.8
K. pneumoniae	185	30.8
Enterobacter spp.	75	12.5
Citrobacter spp.	42	7.0
Serratia spp.	25	4.2
Other Enterobacterales	28	4.7
Total	600	100.0

The distribution places E. coli and K. pneumoniae among the most frequently recovered organisms. This expectation is consistent with previous Nigerian studies in which these organisms represented substantial proportions of Enterobacterales examined.

Table 2. Carbapenem Resistance

Facility	Enterobacterales tested	CRE	prevalence (%)
Hospital A	125	11	8.8
Hospital B	120	14	11.7
Hospital C	115	7	6.1
Hospital D	120	10	8.3
Hospital E	120	8	6.7
Total	**600**	**50**	**8.3**

The results show an overall CRE prevalence of approximately **8.3%**.
The prevalence is higher than the 6.5% carbapenem resistance reported among Enterobacteriaceae in the Sokoto study but could remain broadly consistent with evidence indicating that CRE is already established in Northern Nigeria.

4.2 Distribution of Carbapenemase Genes

Among the hypothetical 50 CRE isolates, the following pattern is

Carbapenemase determinant	isolates	percentage
blaNDM	21	42.0
blaOXA-48-like	13	26.0
blaNDM + blaOXA-48-like	5	10.0
blaKPC	3	6.0
blaVIM	1	2.0
blaIMP	1	2.0
No target detected	6	12.0
Total	50	100.0

The prominence of blaNDM is supported by previous Nigerian molecular studies. In Sokoto, blaNDM-5 was detected in five of seven carbapenemase-producing isolates, while the Northern Nigeria genomic study identified blaNDM-1 in more than half of the selected isolates.

The expected detection of OXA-48-like genes is also plausible because blaOXA-181 was documented in Sokoto and blaOXA-48 was identified in all CRE isolates in the 2025 Zaria rectal surveillance study.

4.3 Species-Gene Relationship

The result shows K. pneumoniae to carry a large proportion of the detected carbapenemase genes, followed by E. coli and Enterobacter species.

Species	Expected CRE isolates	Expected carbapenemase-positive isolates
K. pneumoniae	23	20
E. coli	12	9
Enterobacter spp.	8	6
Citrobacter spp.	4	3
Serratia spp.	2	1
Other	1	0
Total	50	39

A chi-square analysis was used to determine whether carbapenemase carriage differs significantly by bacterial species.

Expected result: $\chi^2 \approx 12.64$, df = 4, p = .013.

The decision would therefore be to reject H02, suggesting a significant association between bacterial species and carbapenem resistance.

4.4. Risk-Factor Analysis

A hypothetical logistic regression model produces results as:

Predictor	Adjusted OR	95% CI	p-value
Previous hospitalisation	2.31	1.24–4.29	.008
Recent carbapenem/β-lactam exposure	3.14	1.68–5.86	<.001
ICU admission	2.76	1.39–5.47	.004
Hospital stay >14 days	2.48	1.31–4.68	.005
Invasive procedure	1.94	1.02–3.70	.043
Age	1.01	0.99–1.02	.214

The findings indicate that recent antimicrobial exposure, prolonged hospitalization, ICU admission and previous hospitalization are associated with greater odds of CRE isolation.

These relationships would be biologically and epidemiologically plausible because tertiary hospitals contain patients with repeated healthcare exposure and substantial antibiotic use. However, the actual magnitude and direction of these associations would need to be established from the study data.

4.5. Whole-Genome Sequencing Findings

The prototype expects whole-genome sequencing to demonstrate a mixture of genetically diverse isolates and smaller clusters of closely related organisms.

For example, selected isolates may be expected to include:

Organism	Possible sequence types
K. pneumoniae	ST147, ST476, other emerging STs
E. coli	ST131, ST88, ST692 and other lineages
Enterobacter spp.	Multiple E. hormaechei lineages
Citrobacter spp.	Diverse sequence types

The presence of ST147 and ST476 among Klebsiella would be particularly important to investigate because these high-risk lineages have already been identified among multidrug-resistant Enterobacterales in Northern Nigeria.

The study identifies isolates carrying multiple resistance genes, demonstrating that carbapenem resistance occurs within broader multidrug-resistant genetic backgrounds.

4.6 Phylogenetic Pattern

A hypothetical phylogenetic analysis shows three broad patterns:

closely related isolates recovered from the same hospital and ward, suggesting possible local transmission;

closely related isolates appearing at different times within the same hospital, suggesting persistence or repeated introduction of a lineage; and

genetically distinct isolates carrying similar carbapenemase genes, suggesting that the resistance determinant may be spreading independently of a single bacterial clone.

The third pattern is particularly important. Molecular epidemiology should distinguish clonal spread from horizontal dissemination of resistance determinants. Similar resistance genes in unrelated bacterial backgrounds may indicate that mobile genetic elements contribute to the regional spread of resistance.

4.7. Hypothesis Testing

H01: No significant difference in CRE prevalence among facilities

Expected result: $\chi^2 = 10.84$, df = 4, p = .028.

Decision: Reject H01.

This would indicate that CRE prevalence differs significantly among participating healthcare facilities.

H02: No significant association between bacterial species and carbapenem resistance

Expected result: $\chi^2 = 12.64$, df = 4, p = .013.

Decision: Reject H02.

This would suggest that particular Enterobacterales species have greater representation among CRE isolates.

H03: No association between carbapenemase genes and phenotypic resistance

Expected result: $\chi^2 = 18.47$, df = 5, $p < .001$.

Decision: Reject H03.

This would support the contribution of carbapenemase determinants to phenotypic carbapenem resistance, while the presence of gene-negative resistant isolates would also indicate that non-carbapenemase mechanisms require further investigation.

H04: Patient and healthcare factors do not predict CRE isolation

Expected result: likelihood-ratio $\chi^2 = 36.71$, df = 5, $p < .001$.

Decision: Reject H04.

Recent antimicrobial exposure, ICU admission, prolonged hospitalisation and previous healthcare exposure would be expected to emerge as important predictors.

H05: No significant genetic relatedness among CRE isolates

Expected result: genomic clustering analysis identifies several statistically supported clusters.

Decision: Reject H05.

This would suggest that some isolates are genetically related and may represent healthcare-associated transmission or persistence of particular lineages.

5. DISCUSSION OF FINDINGS

The findings would reinforce the growing evidence that CRE is not merely an isolated laboratory phenomenon in Nigeria but an emerging healthcare-associated problem requiring coordinated surveillance. The projected prevalence of approximately 8% would be broadly compatible with previous observations from Northwestern Nigeria, although direct comparison must be made cautiously because studies differ in specimen types, populations, hospitals and resistance definitions.

The expected predominance of K. pneumoniae and E. coli would also be consistent with the wider Nigerian literature. A systematic review found that these organisms were among the most frequently studied Enterobacterales in Nigerian CRE research. Similarly, the Northern Nigerian genomic study found Klebsiella species to be prominent among its selected multidrug-resistant isolates.

The expected predominance of blaNDM and blaOXA-48-like determinants is particularly important. The findings would be consistent with the Sokoto detection of blaNDM-5 and blaOXA-181 and the more recent Zaria finding involving blaOXA-48. However, if a substantial proportion of resistant isolates lack the tested carbapenemase genes, this should not be interpreted as evidence that molecular surveillance has failed. Instead, it would indicate that other mechanisms, including changes in permeability, AmpC/ESBL-associated mechanisms and other resistance determinants, deserve further genomic investigation.

The anticipated identification of closely related isolates would have important infection-control implications. If several genetically similar isolates are found within the same ward or hospital, infection prevention teams could investigate possible transmission routes. Conversely, genetically diverse isolates carrying similar resistance genes would point towards a broader regional problem involving mobile genetic elements rather than a single outbreak clone.

6. CONCLUSION

The Existing evidence already confirms the presence of CRE and clinically important carbapenemase determinants in the region. Studies from Sokoto and Zaria, together with genomic research involving hospitals in Kano and other Northern Nigerian locations, demonstrate that resistance is genetically diverse and cannot be adequately understood through routine phenotypic testing alone.

The findings suggest that CRE prevalence may be substantial, with K. pneumoniae, E. coli and Enterobacter species likely to constitute important contributors. blaNDM and blaOXA-48-like determinants are expected to be prominent, while whole-genome sequencing may reveal both high-risk clones and genetically unrelated isolates carrying similar resistance genes.

A coordinated molecular surveillance programme would therefore provide valuable information for infection prevention, antimicrobial stewardship and regional AMR policy.

7. RECOMMENDATIONS

Strengthen routine CRE surveillance in tertiary healthcare facilities across Northwestern Nigeria.

Combine phenotypic and molecular testing so that resistance mechanisms are not inferred solely from antimicrobial susceptibility results.

Expand molecular surveillance for blaNDM, blaOXA-48-like, blaKPC, blaVIM and blaIMP.

Introduce targeted whole-genome sequencing for unusual, highly resistant or epidemiologically linked CRE isolates.

Strengthen infection prevention and control, particularly in intensive care, neonatal, surgical and other high-risk wards.

Improve antimicrobial stewardship by linking microbiology results with prescribing decisions.

Develop regional CRE databases that allow participating hospitals to compare resistance patterns and emerging lineages.

Improve laboratory capacity for antimicrobial susceptibility testing and molecular diagnostics.

Investigate environmental reservoirs where epidemiological evidence suggests persistent transmission.

Integrate CRE surveillance into Nigeria's AMR NAP 2.0, which specifically prioritises surveillance, infection prevention, antimicrobial stewardship and research.

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