15th International Symposium on Antimicrobial Agents and Resistance
ISAAR 2026
cum HKSID HKSMI Annual Scientific Meetings
Fighting the Ongoing Pandemic of Antimicrobial Resistance
Date: June 12-14, 2026
Venue: Hong Kong Convention and Exhibition Centre, Hong Kong
Hosted by: APFID
Organized by: HKSMI
www.isaar2026.org / www.isaar.org

MOLECULAR CHARACTERIZATION OF RESISTANT DETERMINANT AMONG MULTI-DRUG-RESISTANT BACTERIAL PATHOGENS OF LOWER RESPIRATORY TRACT IN NIGERIAN HOSPITALS

BY
ZAHARADDIN MUHAMMAD KALGO
Department of Microbiology, Federal University Birnin Kebbi, Kebbi State, Nigeria
Zaharaddin.Muhammad@fubk.edu.ng; +2348031367195

Background

World Health Organization Global Burden of Disease Study estimated that lower respiratory tract infections (LRTIs) were responsible for 429.2 million episodes of illness worldwide and also were the leading cause of disease burden measured in terms of disability adjusted life years (DALYs) (Shibl *et al*., 2010).

It is an important cause of death in low and middle income countries (Lozano *et al*., 2012). According to WHO 2006, Lower respiratory tract infection kills more people than human immunodeficiency virus (HIV), TB and malaria combine. LRTI is one of the most frequent reasons for hospitalization (Colloniz *et al*., 2016)

In resource-limited countries, bacteria have been the main cause of LRTI. This could be explained by the inaccessibility of molecular diagnostic tools and antimicrobial susceptibility test thus leading to inadequate antibiotics prescription and consequently contributed to a rapid increase in antimicrobial resistance among bacteria causing LRTIs (Alter *et al.,* 2011; Ouedraogo *et al*., 2014; Simusika *et al*., 2015).

The ESBL and carbapenemase producing/carbapenem resistant organisms are a breed of multidrug-resistant pathogens. Infections caused by these organisms are associated with higher rate of mortality, morbidity as well as health care costs (Bindayna *et al*., 2009; Umadevi *et al*., 2011)

Methodology

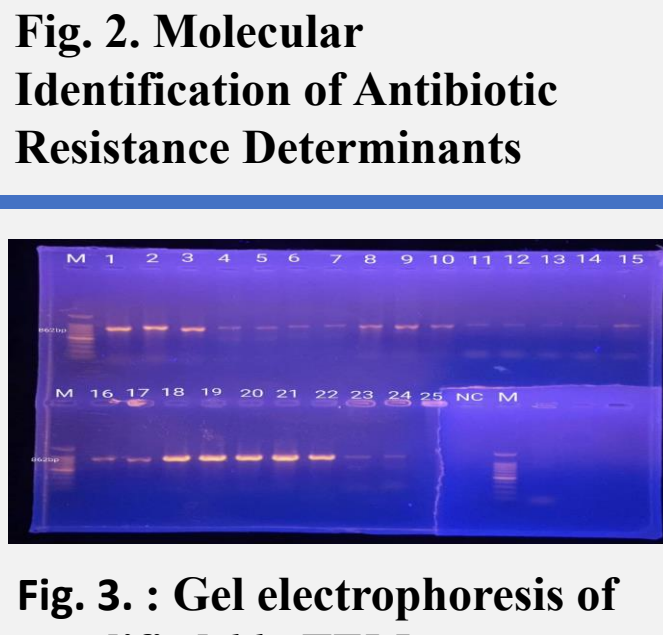

Fig. 1. Antimicrobial Susceptibility Pattern of the Isolated Bacteria

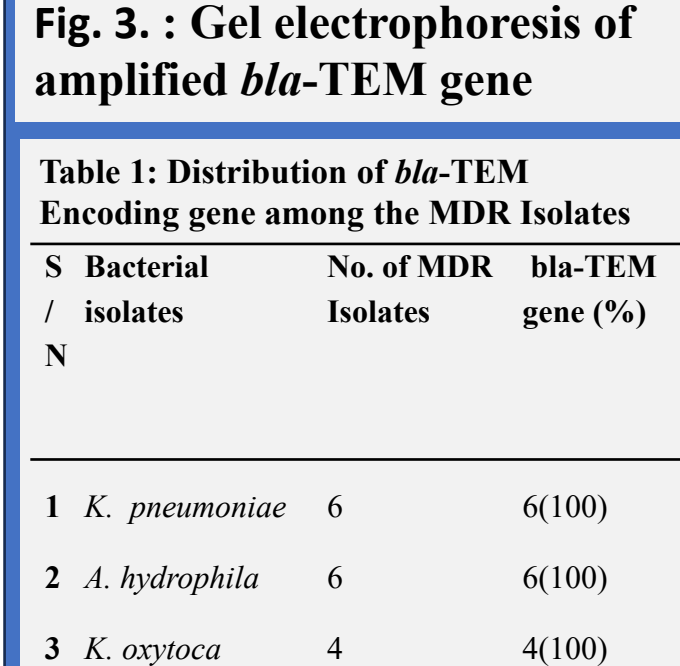

Fig. 2. Molecular Identification of Antibiotic Resistance Determinants

Fig. 3. : Gel electrophoresis of amplified *bla*-TEM gene

Table 1: Distribution of *bla*-TEM Encoding gene among the MDR Isolates

S/N	Bacterial isolates	No. of MDR Isolates	bla-TEM gene (%)
1	*K. pneumoniae*	6	6(100)
2	*A. hydrophila*	6	6(100)
3	*K. oxytoca*	4	4(100)
4	*Pseudomonas aeruginosa*	4	4(100)
5	*Burkholderia psudomallei*	3	3(100)
6	*Escherichia coli*	2	2(100)
	Total	25	25(100)

Table 2: Distribution of MDR among the isolates

S/N	Bacterial isolates	No. of Isolated bacteria	MDR (%)
1	*Staphylococcus aureus*	34	12(35.3)
2	*Klebsiella pneumoniae*	24	9(37.5)
3	*Klebsiella oxytoca*	15	5(41.7)
4	*Escherichia coli*	12	2(16.7)
5	*Aeromonas hydrophila*	6	5(83.3)
6	*Acinetobacter baumannii*	5	2(40.0)
7	*Pseudomonas aeruginosa*	6	5(83.3)
8	*B. pseudomallei*	3	3(100)
	TOTAL	108(100)	43(39.8)

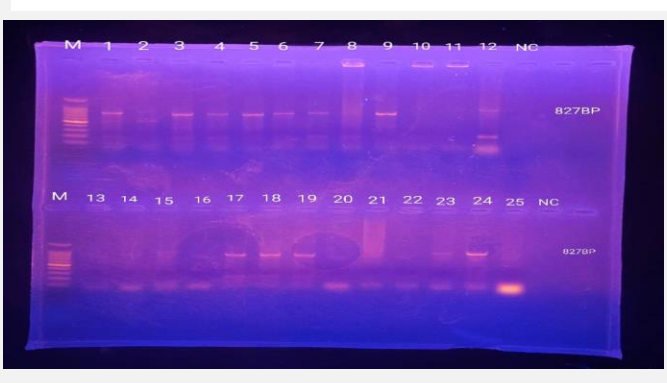

Fig. 4. : Gel electrophoresis of amplified *bla*-SHV gene

Table 3: Distribution of *bla*-SHV Encoding gene among the MDR Isolates

	Bacterial isolates	No. of MDR	Bla-SHV gene (%)
1	*K. pneumoniae*	6	3(50)
2	*Aeromonas hydrophila*	6	3(50)
3	*K. oxytoca*	4	2(50)
4	*Pseudomonas aeruginosa*	4	1(25)
5	*Burkholderia psudomallei*	3	3(100)
6	*Escherichia coli*	2	1(50)
	Total	25	13(52)

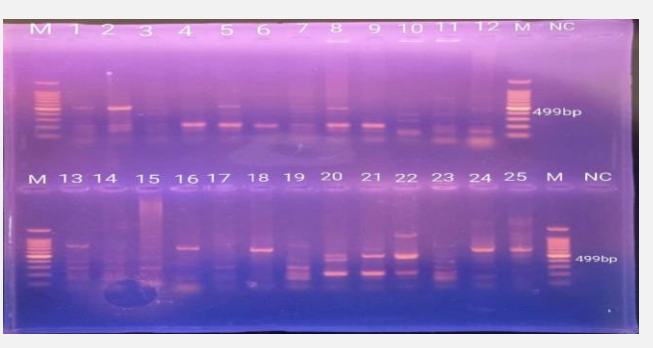

Fig. 5. : Gel electrophoresis of amplified *bla*-CTX-M 1 gene

Table 4: Distribution of *bla*-CTX-M 1 Encoding gene among the MDR Isolates

S/N	Bacterial isolates	No. of MDR	CTX-M 1 (%)
1	*K. pneumoniae*	6	2(33.3)
2	*Aeromonas hydrophila*	6	6(100)
3	*K. oxytoca*	4	3(75.0)
4	*Pseudomonas aeruginosa*	4	3(75.0)
5	*Burkholderia psudomallei*	3	3(100)
6	*E. coli*	2	0(0)
	Total	25	17(68.0)

Fig. 6. : Gel electrophoresis of amplified *bla*-OXA 1 gene

Table 5: Distribution of *bla*-OXA 1 Encoding gene among the MDR Isolates

S/N	Bacterial isolates	No. of MDR	Bla-OXA 1 gene (%)
1	*K. pneumoniae*	6	2(33.3)
2	*Aeromonas hydrophila*	6	6(100)
3	*K. oxytoca*	4	2(50.0)
4	*Pseudomonas aeruginosa*	4	2(50.0)
5	*Burkholderia psudomallei*	3	1(33.3)
6	*Escherichia coli*	2	1(50.0)
	Total	25	14(56.0)

Conclusion

Bla-TEM and CTX-M I genes are the most frequently detected resistance gene among the MDR isolates analysed. The level of resistance exhibited by all the MDR isolates as recorded in this study is of medical concern and occurred as a result of present of more than one ESBL genes among the MDR isolates

Acknowledgements

I would like to sincerely acknowledge my employer (Federal University Birnin Kebbi) and the organizers of ISAAR 2026 for the financial assistance provided to support my travel and participation to this conference.