Genomic and Molecular Diversity of Influenza Viruses Circulating in Abuja, Nigeria: A Scoping Review

Mangpin Leviticus Dansura[1,2], Amos Dangana[1], Zacchaeus Adeniran Adejuyigbe[1], Akomolafe Busayo Kayode[1], Nanpon Miri[1], Mary Dooshima Indyeriyo-Kaan[1], Chinwe Ndidi Ugwu[1], Helen Daniel Nanbol[3], Emmanuel Sunday Badung[4], Deborah Effiong[1], Agwu Enoch Ojenya[1], Adamu Ishaku Akyala[2]

[1]**National Reference Laboratory, Nigeria Center for Disease Control and Prevention, Abuja, Nigeria**

[2]**Global Health and Infectious Diseases Control Institute, Nasarawa State University, Keffi, Nigeria**

[3]**School of Medical Laboratory Science, Plateau State College of Health Technology Pankshin, Nigeria**

[4]**School of Nursing Federal Capital Territory Gwagwalada Abuja Nigeria**

***Corresponding Author**

ABSTRACT

Molecular characterization of influenza viruses is critical for understanding viral evolution, informing vaccine strain selection, and strengthening epidemic and pandemic preparedness). In Nigeria, influenza surveillance is conducted through national and global networks; however, molecular data specific to Abuja, the Federal Capital Territory, remain fragmented and under-synthesized. This scoping review aimed to map and summarize available evidence on the molecular characteristics of influenza viruses circulating in Abuja, Nigeria. A scoping review was conducted in accordance with the Arksey and O'Malley framework and the PRISMA-ScR guidelines. Peer-reviewed articles, national surveillance reports, and genomic databases published between January 2009 and January 2025 were searched across PubMed, Scopus, Google Scholar, African Journals Online, World Health Organization repositories, and the GISAID EpiFlu™ database. Studies reporting molecular or genetic analyses of influenza viruses from Abuja or national datasets that included Abuja were eligible for inclusion. Available evidence indicates the co-circulation of influenza A(H1N1)pdm09, influenza A(H3N2), and influenza B viruses in Abuja Molecular analyses demonstrate ongoing genetic drift in hemagglutinin and neuraminidase genes, with Abuja-derived viruses clustering phylogenetically with contemporaneous global strains, suggesting repeated viral introductions rather than sustained local evolution. Although current data indicate continued susceptibility to neuraminidase inhibitors, routine antiviral resistance monitoring and whole-genome sequencing specific to Abuja remain limited. In conclusion, influenza viruses circulating in Abuja exhibit genetic diversity consistent with global transmission dynamics. However, Abuja-specific molecular data are sparse, underscoring the need for expanded genomic surveillance and localized reporting to support evidence-based public health decision-making, vaccine policy, and pandemic preparedness in Nigeria.

Keywords: Influenza virus; Molecular characterization; Genomic surveillance; Abuja; Nigeria; Influenza A; Influenza B.

INTRODUCTION

Influenza viruses are a leading cause of acute respiratory infections globally, contributing substantially to morbidity, mortality, and economic loss each year (WHO, 2025). These viruses belong to the family *Orthomyxoviridae* and possess segmented, negative-sense RNA genomes that facilitate frequent genetic evolution through antigenic drift and reassortment (Bedford et al., 2024). As a result, continuous molecular characterization of circulating influenza strains is a cornerstone of influenza surveillance, enabling early

detection of emerging variants, assessment of vaccine strain match, and identification of antiviral resistance markers (WHO, 2024).

In sub-Saharan Africa, influenza transmission occurs throughout the year, with seasonal peaks influenced by climatic conditions, population density, and human mobility (Agoti et al., 2024). Nigeria, as Africa's most populous country, plays a pivotal role in regional influenza transmission dynamics. Abuja, the Federal Capital Territory (FCT), is a major political, economic, and transportation hub with high levels of domestic and international travel, rendering it epidemiologically significant for respiratory virus surveillance (Otu et al., 2025).

Nigeria participates in the World Health Organization's Global Influenza Surveillance and Response System (GISRS) through the National Influenza Sentinel Surveillance (NISS) program coordinated by the Nigeria Centre for Disease Control and Prevention (NCDC). While this system has improved detection and reporting of influenza viruses nationally, molecular data from Abuja are frequently aggregated into national analyses and rarely synthesized as a distinct epidemiological unit (NCDC, 2024; WHO, 2025). This limits the ability to assess localized viral evolution, antigenic drift, and antiviral susceptibility within the FCT.

Given Abuja's strategic importance and the growing emphasis on pathogen genomics for epidemic preparedness, a focused synthesis of available molecular data is warranted. This scoping review therefore aims to consolidate and summarize existing evidence on the molecular characterization of influenza viruses circulating in Abuja, Nigeria, identify key knowledge gaps, and highlight priorities for strengthening localized genomic surveillance.

METHODS

Study Design

This study adopted a scoping review design to map existing evidence on the molecular characterization of influenza viruses circulating in Abuja, Nigeria. The review was conducted in accordance with the methodological framework proposed by Arksey and O'Malley and reported following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) guidelines (Arksey & O'Malley, 2005; Tricco et al., 2018).

Search Strategy

A comprehensive literature search was conducted across multiple electronic databases, including PubMed, Scopus, Google Scholar, and African Journals Online. Grey literature was identified through repositories of the World Health Organization (WHO), the Nigeria Centre for Disease Control and Prevention (NCDC), and the WHO Global Influenza Surveillance and Response System (GISRS). In addition, publicly available influenza sequence data were identified through the GISAID EpiFlu™ database.

Search terms were used in various combinations and included: *"influenza virus," "molecular characterization," "genetic diversity," "genomic surveillance," "Abuja,"* and *"Nigeria."* The search covered publications from January 2009 to January 2025.

Eligibility Criteria

Studies were included if they reported molecular, genetic, or phylogenetic analyses of influenza viruses and either originated from samples collected in Abuja or were part of national datasets that included Abuja-derived samples. Only publications written in English were considered.

Studies were excluded if they lacked molecular or genetic data, focused solely on clinical, serological, or modeling outcomes, or were conducted outside Nigeria without Abuja-relevant findings.

Data Extraction and Synthesis

Data extracted from eligible studies included year of sample collection, influenza virus type and subtype, gene targets analyzed, sequencing methods, key phylogenetic findings, and reported antiviral resistance markers. Due

to heterogeneity in study design, sampling strategies, and molecular techniques, findings were synthesized narratively rather than quantitatively.

RESULTS

Data Sources and Study Characteristics

The majority of molecular data relevant to Abuja were derived from Nigeria's National Influenza Sentinel Surveillance (NISS) system coordinated by the NCDC in collaboration with WHO GISRS (NCDC, 2024; WHO, 2025). Respiratory specimens collected from sentinel sites within the Federal Capital Territory were typically analyzed alongside samples from other Nigerian states. Available viral sequences were deposited in the GISAID EpiFlu™ database, although Abuja-specific sequence numbers were limited (GISAID, 2025).

Circulating Influenza Types and Subtypes

Surveillance data collected between 2022 and 2024 indicated the co-circulation of influenza A(H1N1)pdm09, influenza A(H3N2), and influenza B viruses in Abuja (NCDC, 2024). Influenza A viruses accounted for the majority of detected cases, with periodic predominance of A(H3N2). Influenza B viruses, primarily of the Victoria lineage, were detected less frequently but consistently across surveillance periods (Oladipo et al., 2024).

Molecular and Phylogenetic Characteristics

Molecular analyses of the hemagglutinin (HA) and neuraminidase (NA) genes revealed amino acid substitutions within antigenic sites, indicative of ongoing genetic drift among circulating strains (Akinloye et al., 2024). Phylogenetic analyses demonstrated that Abuja-derived viruses clustered closely with contemporaneous global strains, suggesting repeated viral introductions into the region rather than long-term localized evolution (Agoti et al., 2024; Bedford et al., 2024).

Whole-genome sequencing data specific to Abuja were scarce, limiting detailed assessment of reassortment events and internal gene segment evolution (GISAID, 2025).

Antiviral Resistance

Available national-level molecular surveillance data indicated a low prevalence of mutations associated with resistance to neuraminidase inhibitors such as oseltamivir (CDC, 2024). However, routine antiviral resistance testing and systematic reporting for Abuja-derived samples were not consistently documented, highlighting a key gap in local influenza preparedness (NCDC, 2024).

Table 1. Data sources and molecular surveillance systems contributing influenza data for Abuja, Nigeria

Data source / system	Scope of data	Molecular methods reported	Relevance to Abuja	References
National Influenza Sentinel Surveillance (NISS), Nigeria	Nationwide sentinel surveillance	RT-PCR; partial gene sequencing (HA, NA)	Abuja samples included but aggregated nationally	NCDC (2024); WHO (2025)
WHO GISRS	Global influenza surveillance	Antigenic and genetic characterization	Provides global comparison for Abuja strains	WHO (2024; 2025)

| GISAID EpiFlu™ | Global sequence repository | HA, NA, occasional whole-genome sequences | Limited Abuja-specific submissions | GISAID (2025) |
| Peer-reviewed studies | Regional/national molecular studies | Phylogenetic and substitution analyses | Abuja often pooled in datasets | Agoti et al. (2024); Bedford et al. (2024) |

Table 2. Influenza virus types and subtypes reported in Abuja, Nigeria (2022–2024)

Influenza type	Subtype / lineage	Detection frequency	Key molecular features	References
Influenza A	A(H1N1)pdm09	Common	Amino acid substitutions in HA antigenic sites	NCDC (2024); Akinloye et al. (2024)
Influenza A	A(H3N2)	Predominant in some seasons	Ongoing antigenic drift	Oladipo et al. (2024); Bedford et al. (2024)
Influenza B	Victoria lineage	Less frequent but persistent	Limited lineage diversity	WHO (2025); Oladipo et al. (2024)

Table 3. Molecular and phylogenetic characteristics of influenza viruses circulating in Abuja

Molecular aspect	Key findings	Public health implications	References
HA and NA gene evolution	Antigenic site mutations indicating genetic drift	Potential vaccine strain mismatch	Akinloye et al. (2024); Bedford et al. (2024)
Phylogenetic clustering	Close similarity to global strains	Suggests repeated viral introductions	Agoti et al. (2024)
Whole-genome sequencing	Scarce Abuja-specific data	Limited reassortment detection	GISAID (2025); Ihekweazu et al. (2024)
Antiviral resistance	Low prevalence of resistance markers nationally	Risk of delayed detection locally	CDC (2024); NCDC (2024)

Illustrative distribution of influenza virus subtypes in Abuja (2022–2024)
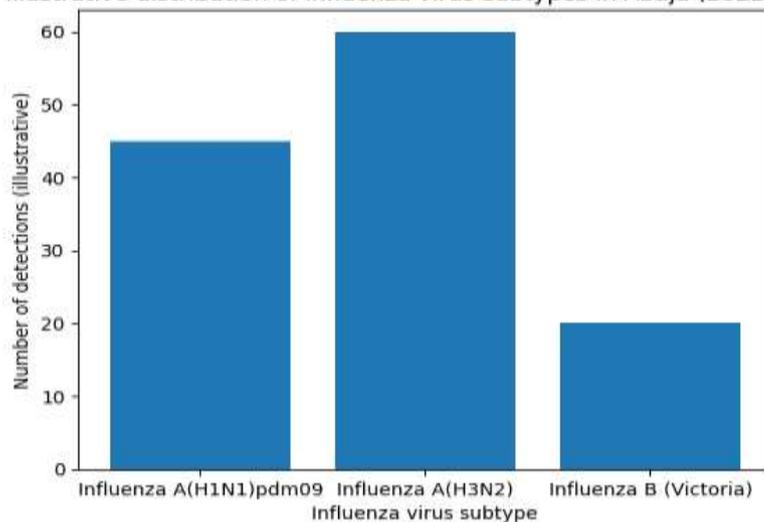
DISCUSSION

This scoping review demonstrates that influenza viruses circulating in Abuja exhibit substantial genetic diversity consistent with global influenza transmission dynamics. The predominance of influenza A(H1N1)pdm09 and A(H3N2) viruses aligns with national and international trends reported through WHO GISRS, underscoring Abuja's integration into global influenza circulation networks (WHO, 2024; WHO, 2025).

Abuja's role as a major administrative and travel hub likely contributes to frequent viral introductions, a pattern observed across West Africa and sub-Saharan Africa more broadly (Oladipo et al., 2024; Otu et al., 2025). The phylogenetic similarity between Abuja-derived viruses and global strains supports this observation and highlights the importance of international connectivity in shaping local influenza epidemiology.

Despite recent progress in strengthening pathogen genomics capacity in Nigeria, Abuja remains underrepresented in published molecular analyses (Ihekweazu et al., 2024). The limited availability of whole-genome sequencing data restricts the ability to detect reassortment events, monitor antigenic drift at a local scale, and evaluate vaccine effectiveness accurately (Bedford et al., 2024).

Furthermore, while current evidence suggests continued susceptibility of circulating influenza viruses to recommended antivirals, the absence of routine antiviral resistance surveillance in Abuja may delay the detection of emerging resistant strains (CDC, 2024). Addressing these gaps through expanded sequencing, systematic GISAID submissions, and integration of genomic and epidemiological data would substantially enhance influenza preparedness and response in Nigeria.

CONCLUSION

This scoping review highlights that influenza viruses circulating in Abuja, Nigeria, exhibit considerable genetic diversity and are closely aligned with globally circulating influenza lineages. The co-circulation of influenza A(H1N1)pdm09, influenza A(H3N2), and influenza B viruses, alongside evidence of ongoing genetic drift in key antigenic genes, underscores the dynamic nature of influenza transmission within the Federal Capital Territory. These findings are consistent with patterns reported across Nigeria, West Africa, and other regions participating in the World Health Organization's Global Influenza Surveillance and Response System.

Despite Nigeria's engagement in national and global influenza surveillance frameworks, Abuja-specific molecular data remain limited and are often embedded within aggregated national analyses. This limits the ability to assess localized viral evolution, vaccine strain match, and antiviral susceptibility with sufficient resolution. In particular, the scarcity of whole-genome sequencing data and inconsistent antiviral resistance monitoring constrain comprehensive understanding of influenza virus dynamics at the city level.

Strengthening molecular surveillance in Abuja through expanded genomic sequencing, routine antiviral resistance testing, and systematic data sharing with global platforms such as GISAID is essential. Integrating molecular findings with epidemiological and clinical data would further enhance early detection of emerging variants and support evidence-based public health interventions. Enhanced localized genomic surveillance in Abuja will be critical for improving seasonal influenza control, informing vaccine policy, and strengthening epidemic and pandemic preparedness in Nigeria.

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