Nigerian Medical Journal
NIGERIA MEDICAL ASSOCIATION
Print ISSN 0300-1652, E-ISSN 2229-774X

Original Article

Epidemiology and Spatial Dynamics of NIE-ZAS-1 and Related Lineages in Nigeria, 2020–2025

***Tukur Ismail[1], Chukwunonso Nwaokorie[2], Danladi Abubaka[3], Mukhtar Salihu Anka[4], Najaatu Yuguda[5], Bello Arkilla Magaji[6], Tijjani Suleman[1],**

[1]Department of Public Health, Zamfara State University, Talata Mafara, [2]Solina Centre for International Development and Research, 8 Libreville Crescent, Wuse, Abuja, [3]Department of Obstetrics and Gynecology, Federal Medical Centre, Gusau, [4]Department of Public Health, Faculty of Allied Health Sciences, Huda University, Gusau, Zamfara State, [5]Shagari Primary health Zamfara State, Nigeria, [6]Department of Community Medicine, College of Health Sciences, Usmanu Danfodiyo University, Sokoto, [7]Department of Public Health, Zamfara State University, Talata Mafara.

Abstract

Background: Nigeria continues to face persistent circulation of circulating vaccine-derived poliovirus type 2 (cVDPV2), driven by sustained transmission of dominant viral lineages and intermittent emergence of new strains. Since 2020, the NIE-ZAS-1 lineage has remained the most epidemiologically significant strain, with ongoing spread across multiple states. This study describes the temporal, spatial, and lineage-specific transmission dynamics of NIE-ZAS-1 and emerging related lineages between 2020 and 2025.

Methodology: We conducted a descriptive epidemiological and spatial analysis of poliovirus lineage surveillance data across Nigeria from 2020 to 2025. Genetic lineage classifications (NIE-ZAS-1, NIE-YBS-1, NIE-YBS-2, NIE-BOS-1, NIE-KTS-1) were analyzed by state, year, and quarter. Geographic diffusion patterns were reconstructed using state-level detection timelines, frequency counts, and directional spread from presumed origin states.

Results: NIE-ZAS-1 originated in Zamfara State in 2020 and expanded to at least 21 states by 2025, accounting for the majority of detections throughout the study period. Transmission showed marked seasonality, with consistent Q3 peaks. In contrast, newer lineages such as NIE-YBS-1, NIE-YBS-2, NIE-BOS-1, and NIE-KTS-1 demonstrated limited spatial spread and short-lived circulation, largely confined to Borno, Yobe, and Kano states. Despite reductions in case counts in some quarters, no lineage showed sustained interruption of transmission by 2025.

Conclusion: Persistent cVDPV2 transmission in Nigeria is driven predominantly by the long-standing NIE-ZAS-1 lineage, with emerging strains failing to replace but adding complexity to the transmission landscape. These findings underscore the need for geographically targeted, lineage-informed vaccination strategies, enhanced surveillance in origin and amplifier states, and intensified efforts during high-risk seasonal periods.

Keywords: cVDPV2, poliovirus, molecular epidemiology, Nigeria, NIE-ZAS-1, surveillance, spatial transmission

***Correspondence:** Tukur Ismail, Email: tukur.ismail@zamsut.edu.ng

How to Cite: Ismail T, Nwaokorie C, Abubaka D, Anka MS, Yuguda N, Magaji BA, et al. Epidemiology and Spatial Dynamics of NIE-ZAS-1 and Related Lineages in Nigeria, 2020–2025. Niger Med J 2025; 67 (1): 2668-2676. https://doi.org/10.71480/nmj.v67i1.1227

Quick Response Code:

Introduction

The Global Polio Eradication Initiative (GPEI) has made substantial progress toward the elimination of poliomyelitis worldwide, including the interruption of indigenous wild poliovirus transmission in most endemic regions[1]. Nigeria was certified free of wild poliovirus in 2020, marking a major public health milestone[2]. However, the continued circulation of circulating vaccine-derived poliovirus type 2 (cVDPV2) has emerged as a persistent challenge, threatening eradication gains and underscoring gaps in population immunity and outbreak response capacity[3,4].

cVDPV2 outbreaks occur primarily in settings with suboptimal routine immunization coverage, immunity gaps following the global withdrawal of type 2 oral poliovirus vaccine (OPV2), and conditions that facilitate sustained person-to-person transmission[5]. In Nigeria, these risk factors are compounded by large population movements, insecurity in parts of the country, and marked heterogeneity in health system performance across states [6,7]. As a result, Nigeria has experienced recurrent cVDPV2 outbreaks since 2016, often involving prolonged transmission chains rather than isolated, self-limited events[8].

Molecular epidemiology has become central to understanding and responding to cVDPV2 transmission. Genetic sequencing of poliovirus isolates enables classification into distinct lineages based on nucleotide divergence from the Sabin 2 vaccine strain, allowing differentiation between independent emergences and sustained circulation of existing strains [9,10]. In Nigeria, standardized lineage naming conventions (e.g., NIE-ZAS-1, NIE-YBS-1) have been adopted to facilitate real-time tracking of viral evolution, spatial diffusion, and epidemiological linkage across states and over time [11]. These lineage-based analyses provide critical insights into transmission dynamics that are not discernible from case counts alone.

Since its initial detection in 2020, the NIE-ZAS-1 lineage has emerged as the most epidemiologically significant cVDPV2 strain in Nigeria. Unlike many vaccine-derived lineages that fade following targeted outbreak response activities, NIE-ZAS-1 has demonstrated sustained transmission over multiple years[12]. Its persistence suggests entrenched transmission within susceptible populations and highlights potential weaknesses in vaccination coverage or campaign quality in key geographic areas.

In contrast, several newer cVDPV2 lineages detected between 2023 and 2025 appear to have more limited spatial footprints and shorter durations of circulation [13]. While these lineages contribute to the overall complexity of the transmission landscape, they have not displaced NIE-ZAS-1 as the dominant driver of cVDPV2 burden. The coexistence of a long-standing dominant lineage alongside intermittently emerging localized strains raises important questions about lineage fitness, population immunity structure, and the effectiveness of outbreak response strategies.

Spatial dynamics play a critical role in shaping cVDPV2 transmission in Nigeria. Previous studies have shown that certain states act as recurrent sources or amplifiers of poliovirus spread, seeding infections to neighboring regions through population movement [14,15]. Seasonal patterns, particularly increased transmission during specific quarters of the year, further influence outbreak trajectories and response effectiveness [16]. A detailed understanding of where lineages originate, how they spread, and when transmission intensifies is essential for designing geographically targeted and temporally optimized interventions.

Lineages	# of states affected	Last state detected	2023				2024				2025			
			Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4
NIE-BOS-1	1	Borno							4	1	1	1		
NIE-KTS-1	2	Kano			1	2	2	2						
NIE-YBS-1	1	Yobe							2		1			
NIE-YBS-2	1	Borno									1	1	1	
NIE-ZAS-1	21	Zamfara	16	23	75	49	31	23	40	17	17	14	18	12

Table: 1 showing the trend of the circulating lineage

Map of Nigeria showing the movement of different lineages across states - 2025

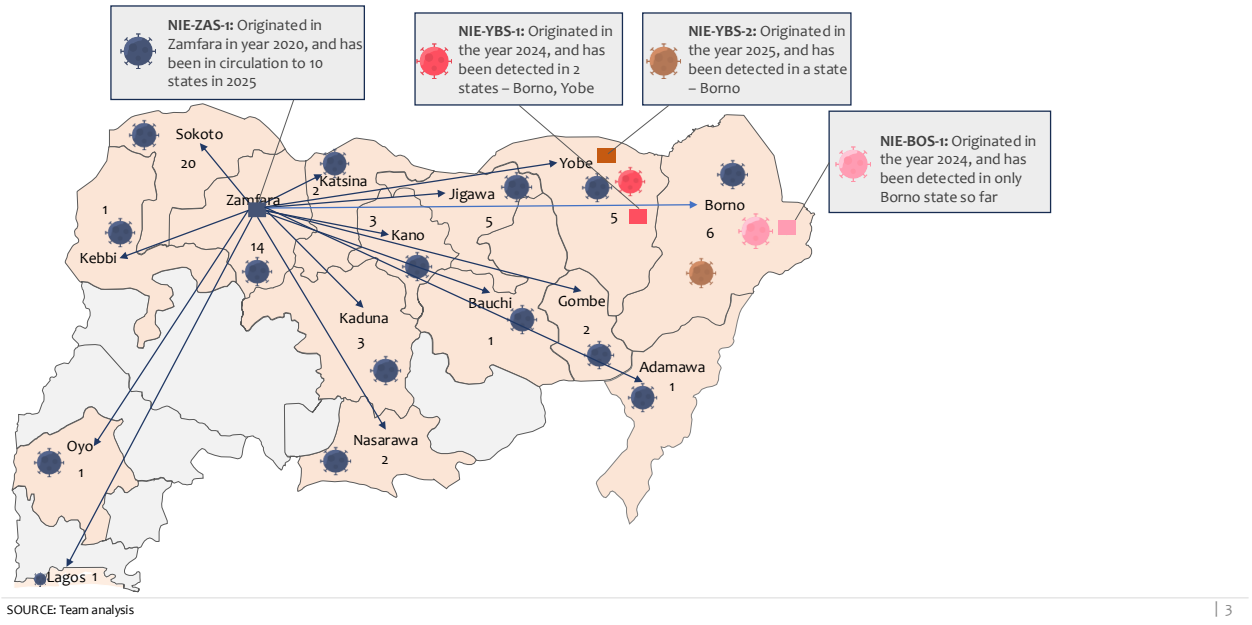

Figure 1: Epidemiological Trend of NIE-ZAS-1 Virus in Nigeria (EPIDEMIOLOGY: The NIE-ZAS-1 virus continues to spread, already affecting 15 states in 2025)

Methods

Study Design

This study was conducted as a retrospective descriptive epidemiological and spatial analysis of circulating vaccine-derived poliovirus type 2 (cVDPV2) transmission in Nigeria between January 2020 and December 2025. The analysis relied on routinely collected national polio surveillance and molecular epidemiology data to characterize lineage-specific temporal trends, geographic diffusion, and persistence over time. A descriptive study design was selected to enable systematic examination of transmission patterns and lineage dynamics across multiple years rather than to test causal hypotheses [17].

Data Sources

Data were obtained from Nigeria's national polio surveillance system, which operates under the Global Polio Eradication Initiative framework and integrates acute flaccid paralysis (AFP) surveillance with environmental surveillance. This system captures laboratory-confirmed poliovirus detections from stool samples collected from AFP cases and sewage samples collected from designated environmental surveillance sites [18].

Genomic sequencing data were used to classify isolates into genetically related lineages based on nucleotide divergence within the VP1 region, following World Health Organization guidelines for poliovirus molecular epidemiology [19]. Surveillance records were aggregated by state, year, and quarter to allow longitudinal assessment of lineage circulation and geographic spread.

This study utilized data from AFP surveillance, a core component of the polio eradication initiative. While AFP surveillance provides high-quality, standardized, and sensitive data for poliovirus detection, AFP cases represent a selected subset of the pediatric population—specifically children presenting with acute flaccid paralysis. As such, AFP cases are not fully representative of the general child population, and findings derived from this dataset should be interpreted within this context.

Case and Lineage Definitions

A cVDPV2 detection was defined as any poliovirus isolate genetically derived from the Sabin 2 vaccine strain with sufficient nucleotide divergence to meet established criteria for circulating vaccine-derived poliovirus [20].

Lineages were defined through phylogenetic clustering of genetically linked isolates, with viruses sharing a common ancestral sequence classified under the same lineage designation.

Data Analysis

Descriptive statistical analyses were conducted to summarize lineage-specific frequency, temporal distribution, and geographic spread. Spatial diffusion patterns were reconstructed by mapping the chronological sequence of first detections across states.

Seasonality was evaluated by comparing quarterly distributions of detections across the five-year period.

Ethical Considerations

This study used secondary, anonymized surveillance data collected as part of routine public health activities. Ethical clearance was obtained from the Zamfara State Ethical Research Committee on 5 December 2025 (Reference number: ZSHREC05122025/357). The analysis did not involve individual-level data and was conducted in accordance with national and international guidelines governing public health surveillance and outbreak investigations[21].

Results

Origin, Geographic Expansion, and Persistence of NIE-ZAS-1

Analysis of state-level detection timelines and genomic lineage classifications identified the NIE-ZAS-1 lineage as the earliest and most persistent cVDPV2 strain circulating in Nigeria during the study period. The lineage was first detected in Zamfara State in 2020, which was therefore classified as its presumed

state of origin. Unlike other lineages identified during the study period, NIE-ZAS-1 demonstrated uninterrupted detection across successive years from 2020 through 2025. This indicates sustained transmission rather than isolated or self-limited outbreaks.

Sequential mapping of first detections by state revealed progressive geographic expansion of NIE-ZAS-1 over time. Initially confined to north-western Nigeria, the lineage spread into north-central and north-eastern states by 2022 and subsequently into southern Nigeria by 2023. By 2025, NIE-ZAS-1 had been detected in at least 21 states, making it the most geographically widespread cVDPV2 lineage identified nationally during the study period.

Zamfara State consistently appeared as a central transmission hub in the reconstructed diffusion pathways. Chronological detection patterns showed repeated outward spread from Zamfara to neighboring north-western states, including Sokoto, Kebbi, Katsina, and Kano, followed by further dissemination to Jigawa, Kaduna, Bauchi, Gombe, Adamawa, and Nasarawa. Later detections in Oyo and Lagos indicated long-distance spread beyond northern Nigeria.

Temporal Trends and Seasonal Patterns of Transmission

Quarterly aggregation of surveillance data demonstrated pronounced seasonality in NIE-ZAS-1 transmission. Across multiple years, detections consistently peaked during the third quarter (Q3), followed by declines in the fourth quarter (Q4) and early first quarter (Q1). This seasonal pattern was observed despite fluctuations in overall detection counts. This indicaes a recurring temporal structure to transmission.

Peak quarterly detection counts for NIE-ZAS-1 were highest in 2023 Q3, with 75 reported detections, followed by 40 detections in 2024 Q3 and 18 detections in 2025 Q3. Although the magnitude of peak detections declined over time, the lineage continued to be detected in every year of the study period, with no quarter meeting criteria for sustained interruption of transmission.

Epidemiological Characteristics of Emerging Lineages

In contrast to NIE-ZAS-1, the other cVDPV2 lineages identified during the study period demonstrated limited geographic spread and short-lived circulation. The NIE-YBS-1 lineage was first detected in Yobe State in 2024 and was subsequently identified only in Yobe and neighboring Borno State. Detections were confined to a narrow time window, with no evidence of continued spread beyond these two states.

The NIE-YBS-2 lineage emerged in 2025 and was detected exclusively in Borno State. At the time of analysis, it showed no evidence of geographic expansion, suggesting a recent emergence without sustained transmission. Similarly, the NIE-BOS-1 lineage, which originated in Borno State in 2024, remained geographically confined to that state and exhibited sporadic detections without onward spread.

The NIE-KTS-1 lineage was first detected in Kano State and was subsequently identified in only one additional state. Its circulation was brief and did not persist across multiple quarters. Compared with NIE-ZAS-1, all emerging lineages showed limited spatial extent, shorter duration of detection, and absence of progressive diffusion, indicating either effective containment or insufficient conditions for sustained transmission.

Spatial Heterogeneity and Transmission Corridors

Spatial reconstruction of lineage movement highlighted heterogeneity in transmission patterns across Nigeria. For NIE-ZAS-1, diffusion pathways frequently followed corridors linking north-western states with north-central and north-eastern regions. States with high population mobility and connectivity, such as Kano, Kaduna, and Bauchi, appeared repeatedly in diffusion sequences and may have functioned as intermediate amplifier states facilitating onward spread.

Although detections in southern states such as Oyo and Lagos were relatively few, their occurrence was epidemiologically significant. These detections indicate long-distance movement of the virus into densely populated urban settings. This underscores the potential for rapid amplification if population immunity is insufficient. In contrast, emerging lineages remained largely restricted to their states of origin, with no clear evidence of comparable transmission corridors.

Discussion

This analysis demonstrates that the epidemiology of circulating vaccine-derived poliovirus type 2 (cVDPV2) in Nigeria between 2020 and 2025 has been significantly shaped by the sustained transmission of a single dominant lineage, NIE-ZAS-1, despite the repeated emergence of additional genetically distinct strains. This prolonged persistence and progressive geographic expansion underscore the challenges in interrupting poliovirus transmission in areas characterized by heterogeneous routine immunization coverage and immunity gaps following OPV withdrawal [22,23]

Subnational disparities in immunization performance are well documented [24]. These immunity gaps create conditions that enable a single lineage to persist and re-seed neighboring areas [25]. Such findings are consistent with previous evidence indicating that cVDPV2 outbreaks are more likely to become prolonged in areas with consistently missed children and suboptimal campaign quality [26,27,28].

The prominent role of Zamfara State as a presumed origin highlights the importance of distinguishing between source and recipient states in eradication strategies[28]. Sustained transmission in origin states can generate new chains of spread if underlying immunity gaps are not adequately addressed [29,30].

The consistent seasonality observed aligns with established patterns of poliovirus transmission in tropical settings [31]. This predictability presents opportunities for anticipatory immunization planning[32].

In contrast, the limited spread of emerging lineages may reflect improvements in outbreak detection and response capacity [33,34]. However, repeated emergences indicate ongoing vulnerability[34].

The coexistence of entrenched and emerging strains underscores the need for lineage-informed programmatic strategies [35]. Detection in southern states, including Lagos, illustrates the national implications of localized transmission failures[29,35].

Limitations

This study has limitations that should be considered when interpreting the findings. First, the analysis relied on routinely collected polio surveillance data, which are subject to variations in surveillance sensitivity across states and over time. Differences in acute flaccid paralysis (AFP) case detection rates, environmental surveillance coverage, and laboratory sampling intensity may have influenced the apparent frequency and geographic distribution of cVDPV2 detections. As a result, periods or areas with fewer reported detections may reflect under-detection rather than the true absence of transmission. A key limitation of this study is the use of AFP surveillance data as a proxy for the general child population. AFP surveillance is inherently case-based and includes only children presenting with acute flaccid paralysis, which may introduce selection bias. Consequently, the findings may not be fully generalizable to all children in the population. However, AFP surveillance remains a valuable data source due to its standardized case definitions, wide geographic coverage, and robust data quality, making it particularly useful for monitoring poliovirus circulation and immunization program performance.

Second, spatial diffusion patterns were inferred using state-level detection timelines rather than formal phylogeographic modeling. While this approach is appropriate for descriptive analysis and programmatic interpretation, it may not fully capture complex transmission pathways, particularly in settings with substantial population movement across state borders. The inferred directionality of spread should therefore be interpreted as indicative rather than definitive.

Despite these limitations, the use of multi-year, lineage-specific surveillance data provides a robust overview of cVDPV2 transmission dynamics in Nigeria and offers valuable insights for guiding geographically and temporally targeted eradication strategies.

Conclusion

This study shows that cVDPV2 transmission in Nigeria between 2020 and 2025 has been dominated by the prolonged circulation of a single lineage, NIE-ZAS-1, rather than by successive replacement with newly emerging strains. The persistence, wide geographic spread, and predictable seasonal peaks of this lineage highlight structural immunity gaps and programmatic challenges that limit the effectiveness of predominantly reactive outbreak responses. These findings emphasize the need to prioritize interruption of entrenched transmission chains, particularly in origin and amplifier states in north-western Nigeria.

Targeted, lineage-informed strategies are essential to achieving sustained interruption of transmission. Strengthening routine immunization, improving the quality and timing of supplemental immunization activities, and maintaining sensitive surveillance capable of detecting silent circulation are critical programmatic priorities. Without sustained investment in high-risk geographies and systematic use of molecular epidemiology to guide interventions, Nigeria risks continued cVDPV2 circulation despite successful containment of new emergences

Acknowledgements

The authors wish to acknowledge the national and state emergency operation centers, surveillance teams, laboratory networks, and field officers whose work made this analysis possible.

References

1. Aylward RB, Tangermann RH. The global polio eradication initiative: lessons learned and prospects for success. *J Infect Dis.* 2011;204 Suppl 1:S280–S285.
2. Fomban Leke RG, Ndzi ES, Same Ekobo A, et al. Certification of the eradication of wild poliovirus in the African Region. *Lancet.* 2020;396(10265):1449–1450.
3. Bigouette JP, Wilkinson AL, Tallis G, et al. Progress toward poliomyelitis eradication — worldwide, 2022–2023. *MMWR Morb Mortal Wkly Rep.* 2023;72(46):1261–1267.
4. Rachlin A, Patel JC, Burns CC, et al. Vaccine-derived polioviruses and the endgame strategy for global polio eradication. *Annu Rev Virol.* 2022;9:1–22.
5. Duintjer Tebbens RJ, Pallansch MA, Kalkowska DA, et al. Characterization of outbreak response strategies and potential vaccine-derived poliovirus emergence. *Risk Anal.* 2016;36(2):262–279.
6. Mangal TD, Aylward RB, Mwanza M, et al. Key issues in the persistence of poliomyelitis in Nigeria. *J Infect Dis.* 2014;210 Suppl 1:S111–S117.
7. Mohammed AJ, Dietz V, Abubakar A, et al. Progress toward poliomyelitis eradication — Nigeria, 2009. *MMWR Morb Mortal Wkly Rep.* 2009;58(24):657–661.

8. Nasir SG, Aliyu GG, Gasasira A, et al. Transmission of vaccine-derived poliovirus in Nigeria. *J Infect Dis.* 2016;213 Suppl 3:S140–S146.
9. Kishore S, Kumar R, Srivastava A, et al. Genomic surveillance of circulating vaccine-derived poliovirus type 2 in endemic settings. *Virus Evol.* 2024;10(1):vead078.
10. Martin J, Burns CC, Jorba J, et al. Molecular epidemiology of polioviruses. *J Virol.* 2022;96(8):e02074-21.
11. Global Polio Eradication Initiative. Standard operating procedures for poliovirus detection and lineage classification. Geneva: WHO; 2004.
12. Lee JY, Morales M, Tangermann RH, et al. Sustained transmission of vaccine-derived poliovirus lineages. *Lancet Infect Dis.* 2023;23(7):e212–e220.
13. Macklin GR, Peak CM, Eisenhawer M, et al. Emergence and control of vaccine-derived poliovirus type 2. *Nat Commun.* 2023;14:1021.
14. Bammeke AO, Oyebanji O, Adebisi YA, et al. Spatial dynamics of poliovirus transmission in Nigeria. *BMC Infect Dis.* 2023;23:412.
15. Gali Y, Ibrahim S, Mohammad S, et al. Role of population movement in poliovirus spread. *Vaccine.* 2016;34(27):3107–3113.
16. Effiong OE, Adebayo A, Okeibunor J, et al. Seasonal trends of poliovirus transmission in sub-Saharan Africa. *Pan Afr Med J.* 2021;39:122.
17. Porta M, editor. *A Dictionary of Epidemiology.* 5th ed. Oxford: Oxford University Press; 2008.
18. World Health Organization. Polio surveillance guidelines. Geneva: WHO; 2022.
19. World Health Organization. Guidelines for environmental surveillance of poliovirus circulation. Geneva: WHO; 2004.
20. World Health Organization. Classification and reporting of vaccine-derived polioviruses (VDPV). Geneva: WHO; 2021.
21. World Health Organization. Ethical considerations in public health surveillance. Geneva: WHO; 2017.
22. Alleman MM, Jorba J, Henderson E, et al. Update on vaccine-derived poliovirus outbreaks. *MMWR Morb Mortal Wkly Rep.* 2023;72(20):543–549.
23. Macklin GR, Goel A, Liao Y, et al. Global epidemiology of circulating vaccine-derived poliovirus type 2. *Emerg Infect Dis.* 2023;29(9):1725–1733.
24. Aheto JMK, Agogo E, Dadzie LK, et al. Subnational inequalities in childhood immunization coverage in Nigeria. *BMJ Glob Health.* 2023;8:e012345.
25. Kalkowska DA, Pallansch MA, Cochi SL, et al. Modeling outbreak response and immunity gaps in poliovirus transmission. *BMC Med.* 2023;21:89.
26. Candido DDS, Quick J, Grubaugh ND, et al. Dynamics of vaccine-derived poliovirus outbreaks. *Nat Microbiol.* 2025;10:145–153.
27. Peak CM, Childs LM, Grad YH, et al. Duration and spread of vaccine-derived poliovirus transmission. *PLoS Pathog.* 2024;20(1):e1011123.

28. Sun H, Patel JC, Burns CC, et al. Epidemiology of prolonged cVDPV2 transmission. *Lancet Glob Health.* 2024;12(2):e300–e309.

29. Adesola RO, Olaniran A, Afolabi MO, et al. Immunization challenges in conflict-affected regions of Nigeria. *Conflict Health.* 2023;17:15.

30. Kalkowska DA, Duintjer Tebbens RJ, Pallansch MA, et al. Strategic responses to persistent poliovirus transmission. *Risk Anal.* 2021;41(4):642–656.

31. Tesfaye M, Gebre H, Desta K, et al. Seasonal variation of poliovirus transmission in tropical settings. *Epidemiol Infect.* 2025;153:e45.

32. Voorman A, O'Reilly KM, Famulare M, et al. Optimizing outbreak response strategies for cVDPV2. *Vaccine.* 2023;41(12):1820–1828.

33. Cooper LV, Bandyopadhyay AS, Jorba J, et al. Advances in surveillance and response to vaccine-derived poliovirus. *J Infect Dis.* 2025;231(Suppl 1):S50–S58.

34. Bricks L, Shulman LM, Manor Y, et al. Recurrent emergence of vaccine-derived poliovirus type 2. *Euro Surveill.* 2024;29(3):2300456.

35. Lopez Cavestany I, Thompson KM, Badizadegan K. Long-term risks of cVDPV2 circulation and eradication strategies. *Vaccine.* 2024;42(5):678–685.