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Review Article

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Evolving dynamics and antimicrobial resistance of *Vibrio cholerae* in Nigeria: An integrative epidemiological and microbiological review

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Abstract:

Background: Cholera remains recurrent in Nigeria, with outbreak location and magnitude varying over time in relation to population displacement, flooding, rapid urban growth, and constraints in water and sanitation services. Published microbiological and genomic studies describe circulation of seventh-pandemic *Vibrio cholerae* O1 El Tor lineages in Nigeria, with antimicrobial resistance (AMR) reported in multiple isolate series and occasional reports of non-O1/non-O139 strains.

Methodology: We conducted an integrative review combining Nigeria cholera surveillance reporting (January 1, 2017 to December 31, 2024) with microbiological and genomic literature relevant to Nigeria. State and year outbreak patterns were synthesized from national and partner reports. Microbiological characteristics, lineage assignments, and resistance mechanisms were summarized from peer reviewed literature and selected grey literature.

Results: Across 2017 to 2024, Nigeria experienced recurrent cholera surges with shifting geographic concentration. Northern states frequently contributed a large share of reported cases, particularly in conflict-affected and displacement settings, while recent reports also indicate risk in densely populated urban settlements. Microbiological evidence describes predominance of *V. cholerae* O1 El Tor, including atypical El Tor variants, with resistance patterns commonly involving trimethoprim-sulfamethoxazole and reduced fluoroquinolone susceptibility, linked to mobile genetic elements and target-site mutations in some isolate series. Genomic analyses that include Nigerian isolates place them within West African seventh-pandemic transmission clusters, including T12 and AFR12 lineage designations reported by study authors.

Conclusion: Available genomic literature supports sustained transmission of seventh-pandemic lineages and persistent AMR risks. Nigeria's cholera control planning for 2025 to 2029 provides an opportunity to link surveillance, diagnostics, WASH, and targeted vaccination, but impact will depend on implementation capacity and sustained financing.

Keywords: Evolving dynamics; Antimicrobial resistance; Integrative epidemiology; *Vibrio cholerae*

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Dynamique évolutive et résistance aux antimicrobiens de *Vibrio cholerae* au Nigéria : une revue épidémiologique et microbiologique intégrative

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Résumé:

Contexte: Le choléra demeure récurrent au Nigéria, et la localisation et l'ampleur des épidémies varient au fil du temps en fonction des déplacements de population. Inondations, croissance urbaine rapide et contraintes liées aux services d'eau et d'assainissement. Des études microbiologiques et génomiques publiées décrivent la circulation des lignées de *Vibrio cholerae* O1 El Tor, responsables de la septième pandémie, au Nigéria. Une résistance aux antimicrobiens (RAM) a été observée dans de nombreuses séries d'isolats, ainsi que des cas occasionnels de souches non-O1/non-O139.

Méthodologie: Nous avons réalisé une revue intégrative combinant les données de surveillance du choléra au Nigéria (du 1er janvier 2017 au 31 décembre 2024) avec la littérature microbiologique et génomique pertinente. Les schémas épidémiques par État et par année ont été synthétisés à partir des rapports nationaux et de ceux de nos partenaires. Les caractéristiques microbiologiques, l'identification des lignées et les mécanismes de résistance ont été résumés à partir de la littérature scientifique et de la littérature grise.

Résultats: De 2017 à 2024, le Nigéria a connu des flambées épidémiques de choléra récurrentes, avec une concentration géographique variable. Les États du nord ont souvent contribué de manière significative aux cas déclarés, en particulier dans les zones de conflit et de déplacement de population, tandis que des rapports récents indiquent également un risque dans les zones urbaines densément peuplées. Les données microbiologiques décrivent la prédominance de *V. cholerae* O1 El Tor, y compris des variants atypiques d'El Tor, avec des profils de résistance impliquant fréquemment le triméthoprim-sulfaméthoxazole et une sensibilité réduite aux fluoroquinolones, liés à des éléments génétiques mobiles et à des mutations du site cible dans certaines séries d'isolats. Les analyses génomiques incluant des isolats nigériens les situent au sein des clusters de transmission de la septième pandémie en Afrique de l'Ouest, notamment les lignées T12 et AFR12 rapportées par les auteurs de l'étude.

Conclusion: La littérature génomique disponible confirme la transmission soutenue des lignées de la septième pandémie et la persistance des risques de résistance aux antimicrobiens. Le plan de lutte contre le choléra au Nigéria pour la période 2025-2029 offre l'opportunité de coordonner la surveillance, le diagnostic, l'accès à l'eau, à l'assainissement et à l'hygiène (EAH) et la vaccination ciblée, mais son impact dépendra des capacités de mise en œuvre et d'un financement durable.

Mots-clés: Dynamique évolutive; Résistance aux antimicrobiens; Épidémiologie intégrative; *Vibrio cholerae*

Introduction:

Cholera is an acute diarrhoeal disease caused by toxigenic *Vibrio cholerae*, and it remains a major public health problem in many low- and middle-income settings. Global estimates suggest 1.3 to 4.0 million cases and 21,000 to 143,000 deaths annually, with a large proportion of reported burden occurring in sub-Saharan Africa (1). In 2024, a multi-country resurgence was documented, with substantial numbers of cases and deaths reported across multiple WHO regions (2). Nigeria has experienced recurrent outbreaks over the last decade, with substantial variation in timing, geography, and reported severity across years (3,4,5). Epidemiological risk is shaped by overlapping vulnerabilities, including population displacement and insecurity in parts of Northern Nigeria, flooding and disruption of water services, and rapid urban expansion with inadequate sanitation in informal settlements (6,7,8).

In parallel, microbiological and genomic studies show that outbreaks in Nigeria are largely associated with seventh-pandemic *V. cholerae* O1 El Tor lineages, including atypical El Tor variants described in Nigerian isolate collections, and antimicrobial resistance determinants linked to mobile genetic elements and quinolone resistance mechanisms in some datasets (9-13). Reports of non-O1/non-O139 *V. cholerae* associated with diarrhoeal illness also have im-

lications for diagnostics, because O1-targeted rapid tests may not detect them (9,12).

Despite long-standing recognition of cholera risk in Nigeria, three gaps keep showing up across the literature and outbreak reporting. First, outbreak reports often provide large suspected case counts but limited microbiological confirmation and sparse reporting of isolate-level details. This makes it hard to distinguish true cholera from other causes of acute watery diarrhoea, and it weakens confidence in comparisons across states and years when case definitions, testing access, and reporting completeness vary (3,4,7).

Second, while several Nigerian studies describe serogroup distribution, virulence markers, and antimicrobial susceptibility patterns, the evidence is heterogeneous. Studies differ in sampling frames, culture methods, susceptibility methods, and interpretive standards, and they are often limited to single outbreaks or a small number of sites. This makes pooled estimates of resistance prevalence unreliable and creates uncertainty about how laboratory findings should inform empiric care and stewardship during outbreaks (9,10,13).

Third, genomic evidence relevant to Nigeria is growing but remains uneven over time. A substantial part of the genomic picture comes from regional or multi-country studies that include Nigerian isolates rather than continuous Nigeria-only sequencing. Even so, the available

phylogenomic work provides useful insights into seventh-pandemic lineage circulation, regional connectivity, and the likely movement of strains across West Africa, including lineage labels used by study authors such as T12 and AFR12 (11,12,14).

The practical challenge is converting these insights into operational tools that can be used during outbreaks, including specimen referral pathways, routine susceptibility testing linked to case management, and feasible sequencing or genotyping strategies integrated into surveillance (7,15). A synthesis that links the Nigeria Center for Disease Control and Prevention (NCDC) reporting with isolate and sequencing data is needed to interpret shifting hotspots and resistance risk. Nigeria's cholera control planning for 2025 to 2029 also makes the timing useful, because priorities such as targeted vaccination, water, sanitation and hygiene (WASH) investments, and improved surveillance can be better aligned when evidence is summarized in a way that is actionable for both public health and clinical decision-making (7,16).

This integrative review aims to synthesize epidemiological, microbiological, and genomic evidence on cholera in Nigeria, with a focus on the period January 1, 2017 to December 31, 2024 for outbreak epidemiology, and inclusion of earlier microbiological or genomic studies where needed to interpret circulating lineages and antimicrobial resistance patterns (17). Specifically, we address four questions; (i) What are the state-level and year-to-year patterns of reported cholera burden in Nigeria from 2017 to 2024 based on national surveillance reporting, and how do geographic concentrations shift across outbreak years (3,4,5)? (ii) What microbiological characteristics are reported from Nigeria outbreaks, including serogroups, biotype descriptors, and virulence markers, and what is the consistency of these findings across studies (10,14,18)? (iii) What antimicrobial susceptibility patterns and resistance mechanisms have been described in Nigerian *V. cholerae* isolate series, and what are the main limitations that affect interpretation for clinical guidance and stewardship (9,10,13)? (iv) What do genomic studies that include Nigerian isolates indicate about lineage assignments and regional clustering, and what are the implications for surveillance design and outbreak response in Nigeria (11,12,14)?

We summarize state-level outbreak patterns (2017 to 2024) and link them to what is known about circulating lineages and resistance in Nigeria, consolidates a state-by-year summary of surveillance-reported suspected cholera burden using a defined approach to selecting

the last available sitrep for each year, summarizes microbiology and AMR evidence with attention to methods and comparability, situates Nigeria within the regional genomic context described by major Africa-wide and West Africa-focused sequencing work.

Materials and method:

We conducted an integrative review of cholera in Nigeria that combined surveillance-derived epidemiological reporting with microbiological and genomic evidence on *V. cholerae*. The epidemiological component covered January 1, 2017 to December 31, 2024. Microbiological and genomic studies published within the same period were included, and earlier studies were also included where needed to interpret circulating lineages and antimicrobial resistance patterns reported in Nigeria.

Evidence was compiled from three source streams; (i) Peer reviewed literature (PubMed, Web of Science, African Journals Online, and Google Scholar), (ii) National and global surveillance reports (NCDC weekly and annual cholera situation reports and outbreak updates, and World Health Organization cholera updates where applicable (2,4), and (iii) Grey literature and humanitarian or environmental reports (UNICEF and ReliefWeb reports and other humanitarian updates used to extract contextual information on flooding, displacement, WASH conditions, and response activities relevant to cholera transmission and control) (19,20,21).

Search strategy:

A structured search strategy was applied using combinations of organism, disease, geography, and thematic terms. Core terms included; "cholera", "*Vibrio cholerae*", "Nigeria", "outbreak", "epidemic", "antimicrobial resistance", "AMR", "genomics", "whole genome sequencing", "phylogeny", "lineage", "El Tor", "atypical El Tor", "non-O1", "non-O139", "integrative conjugative element", "ICE", "ctxB", "tcpA", "cholera vaccine", "oral cholera vaccine", and "WASH". Boolean operators (AND, OR) were used to restrict results to Nigeria and to prioritize microbiology, AMR, genomics, vaccine, and response literature. Reference lists of included articles and key Nigeria-focused papers were hand searched to identify additional eligible studies.

Database searches were last run on 20 February 2025. Google Scholar screening was restricted to the first 200 results sorted by relevance due to the high volume and variable quality of retrieval. For grey literature, targeted searches were performed within NCDC, WHO,

UNICEF, and ReliefWeb repositories using the same core keywords, and additional relevant documents were identified through citations and embedded links within retrieved reports. We included articles and reports available in English. Preprints were eligible if they provided sufficient methodological detail and Nigeria-specific extractable results. Where included, they were clearly identified as preprints and interpreted cautiously (14).

Eligibility criteria:

To map the breadth of evidence regarding *V. cholerae* in Nigeria, we included sources that met the following criteria: (i) Geographic relevance - studies reporting primary data from Nigeria at the national, state, local government area (LGA), or facility level; (ii) Content relevance - sources addressing one or more of the following key domains; (a) epidemiological indicators such as case counts (suspected/confirmed), mortality data (CFR), temporal trends, and geographic distribution; (b) microbiological and genomic characteristics such as serogrouping (O1, O139, non-O1/non-O139), biotyping, virulence determinants, antimicrobial susceptibility (AMR) phenotypes, and phylogenetic lineage assignments; (c) environmental and contextual drivers such as impact of flooding, population displacement, and WASH infrastructure on outbreak dynamics; (iii) Evidence type - adoption of inclusive approach including peer-reviewed primary research (observational, cross-sectional, and genomic studies), official surveillance reports (NCDC, WHO), and grey literature from reputable humanitarian agencies (UNICEF, ReliefWeb) to capture real-time outbreak data.

We excluded studies that did not provide extractable Nigeria-specific findings, duplicate reports of the same dataset, and opinion pieces or editorials that lacked primary data or systematic synthesis.

Case definitions and outcomes:

We extracted suspected and confirmed cholera counts as reported by each source, recognizing that definitions vary by reporting system and time period. Where case definitions were provided, they were extracted into the evidence table. Case fatality rate (CFR) was extracted as reported. When not explicitly stated, CFR was calculated as deaths divided by cases for that source and reporting period, provided both numerators and denominators were available. When multiple sources reported overlapping national counts for the same reporting period, NCDC situation reports were treated as the primary reference for national totals to reduce

double counting. WHO and partner reports were used mainly for triangulation and contextual information (2,4).

Study selection and screening process:

The study selection process followed the Preferred Reporting Items for Systematic reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) (22). All retrieved records were deduplicated prior to screening. Titles and abstracts were screened first, followed by full-text assessment against eligibility criteria. Two reviewers (NM and OIA) screened records independently. Discrepancies were resolved by discussion, and where consensus was not reached, a third author (BA) adjudicated. The study selection process is summarized in the PRISMA-ScR flow diagram (Fig 1).

Surveillance dataset for state-by-year analysis:

For each calendar year from 2017 to 2024, state-level case distributions were extracted from the last available NCDC cholera situation report published within that year. Where a year did not have a report close to epidemiological week 52, the most recent sitrep available for that year was used. Counts are cumulative suspected cases as at the epidemiological week covered by the sitrep and do not necessarily represent full-year totals. Percent contributions were calculated within each year using the year total shown in Table 1 as the denominator (4).

Data extraction:

Data were extracted using a standardized form developed a priori and piloted on a sub set of records. Extracted variables were grouped into epidemiological and microbiological or genomic domains. Epidemiological variables included year and, where available, epidemiological week or month; State and LGA; suspected and confirmed cases; deaths; CFR; outbreak duration markers (start and end dates when reported); setting descriptors (community, health-care facility, IDP setting); and contextual drivers reported by sources (flooding, displacement, WASH disruptions, insecurity, population density, or access constraints).

Microbiological and genomic variables included specimen source (clinical or environmental), isolate counts, confirmation method (culture, PCR, RDT with confirmatory testing where stated), serogroup and biotype descriptors, virulence determinants when reported, antimicrobial susceptibility results and method used (disc diffusion, MIC, automated systems where stated), interpretive standards (CLSI, EUCAST, or not stated), resistance genes or mechanisms (including mobile genetic elements

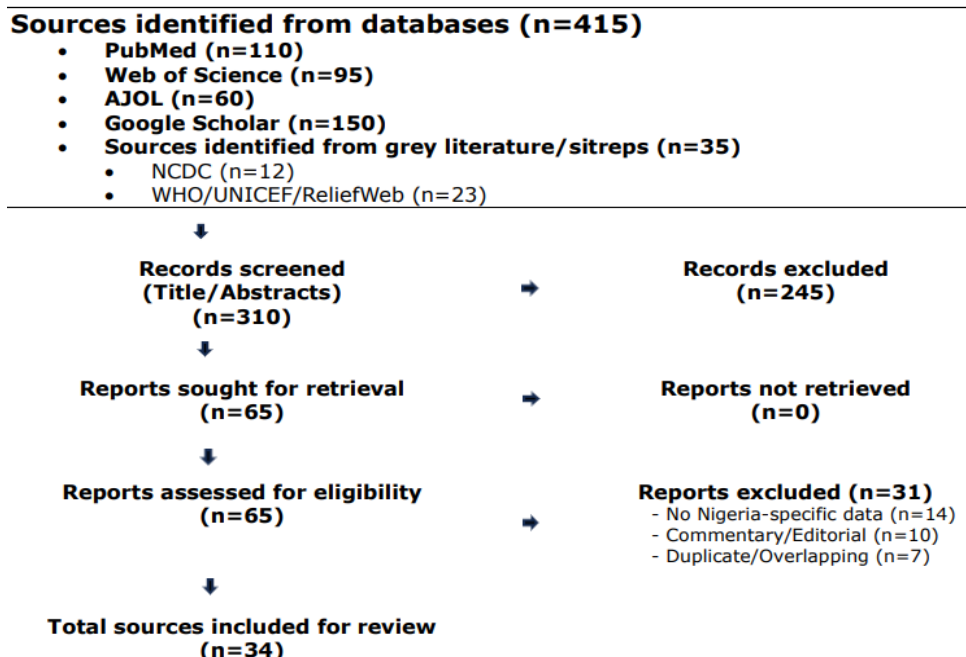


Fig 1: PRISMA-SCR flow diagram

such as ICEs), and reported genomic lineage or clade assignments with the analytical approach described by the original authors. Where multiple publications described overlapping isolate collections or outbreak episodes, we retained the most complete dataset as the primary record and used the others to supplement missing fields.

Quality appraisal and credibility assessment:

Given heterogeneity in evidence types, we applied a structured credibility assessment rather than a single quantitative score. For surveillance and outbreak reports, we assessed clarity of case definitions, reporting completeness, and internal consistency across reporting periods. For microbiology and AMR studies, we assessed clarity of laboratory methods, antimicrobial susceptibility testing methodology, and interpretive criteria. For genomic studies, we assessed transparency of sequencing and analysis methods, including whether lineage assignment and resistance mechanism inference were supported by described pipelines and adequate metadata. Lower-credibility sources were not automatically excluded, but their findings were interpreted cautiously and were not used as the sole basis for key conclusions.

Data synthesis and analysis:

We used narrative and descriptive synthesis. Epidemiological data were summarized by year and state to identify recurrent hotspots and major surge periods. Outbreak timelines

were descriptively compared with documented environmental and humanitarian events such as flooding and displacement. Microbiological and genomic findings were synthesized by serogroup, lineage, and resistance mechanism categories. No formal statistical hypothesis testing or meta-analysis was performed. Quantitative results presented are descriptive counts, proportions, and simple derived measures such as CFR when not reported.

Results:

A total of 34 sources were included in the final synthesis. This comprised 21 peer-reviewed primary research articles (covering microbiology, genomics, and epidemiology), 7 NCDC national situation reports (2017–2024), and 6 humanitarian or strategic policy documents providing contextual WASH data. The distribution of cumulative suspected cases across the study period is summarized in Fig 2.

Epidemiology: temporal trends and reporting spread (2017 to 2024):

Across 2017 to 2024, Nigeria reported recurrent cholera surges with substantial year-to-year variation in magnitude and geographic spread (Table 1) (3,4,5). Surveillance analyses covering 2020 to 2021 indicate that cholera affected multiple states with heterogeneous outcomes, including variation in reported mortality across settings and time periods (6). Broadly,

national reporting over the review period reflects recurring multi-state outbreaks rather than isolated events, with the number of affected States varying across years (5).

Where demographic distributions were reported in national analyses, children and adolescents accounted for a substantial proportion of cases across multiple outbreak periods, and sex distribution was broadly balanced with modest year-specific differences (3). These demographic patterns are consistent with cholera transmission in contexts where exposure risks are shaped by household water sources, sanitation access, and community-level WASH conditions (23,24).

Geographic clustering and shifting hotspots:

State-level distributions derived from national situation reports indicate repeated high caseloads in northern states across several outbreak years, though the specific States contributing the largest share varied significantly (Table 2). Between 2018 and 2022, the rep-

orted burden was frequently concentrated in the North. For instance, in 2018 (week 43), Bauchi, Zamfara, and Katsina together accounted for nearly 60% of the 42,446 suspected cases reported by that period. Similarly, the massive surge in 2021 (week 52), the largest in the study period with 94,886 cases, was driven primarily by Bauchi (20.6%), Jigawa (16.0%), and Kano (12.8%) (4).

However, the geographic concentration shifted notably in 2024. As of week 39, Lagos contributed the largest share (51.2%) of the 9,110 cases reported, marking a significant increase in burden within a densely populated southern urban settlement compared to previous years. This shift contrasts with 2022 (week 52), where Borno alone accounted for 56.1% of the national burden. These state-by-year distributions describe where the reported burden was concentrated at the time of reporting and allow for comparison of relative state contributions, though they do not provide direct year-to-year incidence comparisons due to differing reporting weeks.

Table 1: State distribution of reported suspected cholera cases in Nigeria (2017 to 2024)

Year (last sitrep week)	State	Cumulative suspected cases, n	Share of yearly total, %
2017 (week 36)	Kwara	1,629	31.0
2017 (week 36)	Borno	1,380	26.3
2017 (week 36)	Kebbi	1,263	24.0
2017 (week 36)	Zamfara	430	8.2
2017 (week 36)	Kano	362	6.9
2017 (week 36)	Lagos	70	1.3
2017 (week 36)	Kaduna	39	0.7
2017 (week 36)	Gombe	35	0.7
2017 (week 36)	Jigawa	17	0.3
2017 (week 36)	Oyo	13	0.2
2017 (week 36)	Ebonyi	9	0.2
2017 (week 36)	Ondo	7	0.1
2017 (week 36)	Total	5,254	100.0
2018 (week 43)	Bauchi	9,405	22.6
2018 (week 43)	Zamfara	8,311	20.0
2018 (week 43)	Katsina	7,358	17.7
2018 (week 43)	Borno	6,439	15.5
2018 (week 43)	Adamawa	2,700	6.5
2018 (week 43)	Yobe	2,133	5.1
2018 (week 43)	Kano	1,905	4.6
2018 (week 43)	Sokoto	1,609	3.9
2018 (week 43)	Niger	584	1.4
2018 (week 43)	Gombe	432	1.0
2018 (week 43)	Kaduna	401	1.0
2018 (week 43)	Plateau	347	0.8
2018 (week 43)	Total	41,624	100.0
2019 (week 43)	Adamawa	810	51.2
2019 (week 43)	Bayelsa	526	33.2
2019 (week 43)	Katsina	131	8.3
2019 (week 43)	Kano	58	3.7
2019 (week 43)	Plateau	48	3.0
2019 (week 43)	Ebonyi	9	0.6
2019 (week 43)	Delta	1	0.1
2019 (week 43)	Total	1,583	100.0
2021 (week 52)	Bauchi	19,558	20.6
2021 (week 52)	Jigawa	15,141	16.0
2021 (week 52)	Kano	12,116	12.8
2021 (week 52)	Zamfara	11,931	12.6
2021 (week 52)	Katsina	9,209	9.7
2021 (week 52)	Sokoto	8,477	8.9
2021 (week 52)	Kebbi	5,959	6.3

2021 (week 52)	Borno	5,672	6.0
2021 (week 52)	Yobe	4,002	4.2
2021 (week 52)	Niger	2,821	3.0
2021 (week 52)	Total	94,886	100.0
2022 (week 52)	Borno	12,465	56.1
2022 (week 52)	Yobe	1,888	8.5
2022 (week 52)	Katsina	1,639	7.4
2022 (week 52)	Gombe	1,407	6.3
2022 (week 52)	Taraba	1,153	5.2
2022 (week 52)	Kano	1,131	5.1
2022 (week 52)	Cross River	802	3.6
2022 (week 52)	Bauchi	653	2.9
2022 (week 52)	Zamfara	652	2.9
2022 (week 52)	Jigawa	417	1.9
2022 (week 52)	Total	22,207	100.0
2023 (week 52)	Zamfara	914	28.9
2023 (week 52)	Cross River	718	22.7
2023 (week 52)	Katsina	343	10.8
2023 (week 52)	Bayelsa	319	10.1
2023 (week 52)	Ogun	295	9.3
2023 (week 52)	Ebonyi	236	7.5
2023 (week 52)	Niger	195	6.2
2023 (week 52)	Jigawa	84	2.7
2023 (week 52)	Adamawa	62	2.0
2023 (week 52)	Total	3,166	100.0
2024 (week 39)	Lagos	4,667	51.2
2024 (week 39)	Jigawa	870	9.5
2024 (week 39)	Kano	809	8.9
2024 (week 39)	Borno	588	6.5
2024 (week 39)	Katsina	559	6.1
2024 (week 39)	Adamawa	553	6.1
2024 (week 39)	Bayelsa	513	5.6
2024 (week 39)	Bauchi	307	3.4
2024 (week 39)	Ebonyi	244	2.7
2024 (week 39)	Total	9,110	100.0

Source: Nigeria Center for Disease Control and Prevention (NCDC) sitrep for each year

Note: Counts are cumulative suspected cholera cases reported in NCDC cholera situation reports as at the stated epidemiological week.

Percentages are calculated within each year block using the year total shown in the table.

2020 sitrep was not available.

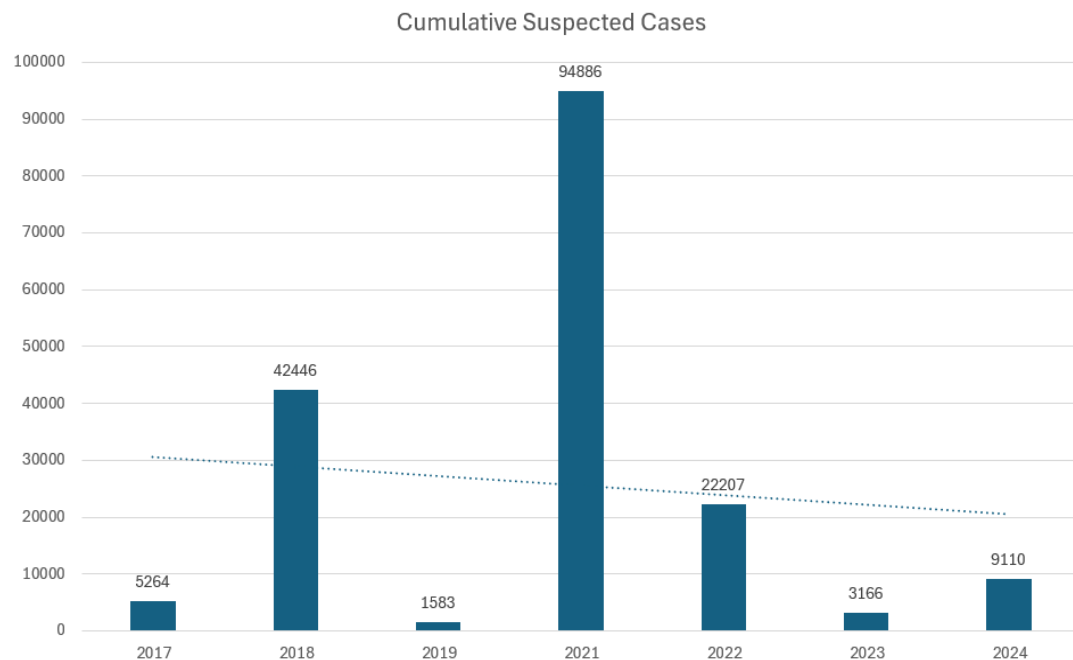


Fig 2: Cumulative cases of suspected cholera cases in Nigeria (2017-2024)

Table 2: Top contributing States by cumulative suspected cholera cases in Nigeria (2017–2024)

Year (Sitrep Week)	Total Cases (N)	Top 3 States	Cases (n)	Share (%)
2024 (week 39)	9,110	Lagos; Jigawa; Kano	4,667; 870; 809	51.2; 9.5; 8.9
2023 (week 52)	3,166	Zamfara; Cross River; Katsina	914; 718; 343	28.9; 22.7; 10.8
2022 (week 52)	22,207	Borno; Yobe; Katsina	12,465; 1,888; 1,639	56.1; 8.5; 7.4
2021 (week 52)	94,886	Bauchi; Jigawa; Kano	19,558; 15,141; 12,116	20.6; 16.0; 12.8
2020	—	Data Unavailable	—	—
2019 (week 43)	1,583	Adamawa; Bayelsa; Katsina	810; 526; 131	51.2; 33.2; 8.3
2018 (week 43)	42,446	Bauchi; Zamfara; Katsina	9,405; 8,311; 7,358	22.2; 19.6; 17.3
2017 (week 36)	5,264	Kwara; Borno; Kebbi	1,629; 1,380; 1,263	31.0; 26.2; 24.0

Note: Total annual cases represent cumulative suspected cases of cholera as of the reported epidemiological week. Data for 2020 was not captured in the standardized format used for this analysis

Contextual settings described in surveillance and partner reporting:

Across the review period, multiple sources link cholera risk in Nigeria to overlapping contextual drivers, including flooding and displacement in some settings and sanitation constraints in rapidly growing urban areas (6,8,19, 20). The 2022 flooding emergency is repeatedly cited as a major WASH-disrupting event with implications for diarrhoeal disease risks, including cholera (25). In conflict-affected areas, particularly in the Northeast, reports describe constraints on access to safe water and health-care, with implications for outbreak response capacity in displaced populations (6,26).

In urban settings, literature describing sanitation conditions in informal settlements in Lagos highlights plausible transmission risks where sanitation access is limited and water sources may be contaminated (27,28). These contextual descriptions provide interpretive background but should not be treated as causal inference for specific year patterns without linked analytic designs.

Microbiological and genomic evidence from Nigeria: serogroups, lineages, and AMR patterns:

Predominant serogroups and biotype descriptors reported in Nigeria:

Across published outbreak and laboratory studies that included Nigerian isolates, toxigenic *V. cholerae* O1 has been the dominant serogroup reported in association with cholera outbreaks, most commonly described within the El Tor biotype framework (9,10,18). Studies reporting characterization of isolates from Nigeria describe circulation of El Tor strains and variants with mixed classical and El Tor molecular features, consistent with descriptions of atypical El Tor in West Africa and other cholera-affected regions (9,10).

In addition to O1, non-O1/non-O139 *V. cholerae* strains have been reported from Nig-

eria in association with diarrhoeal illness or outbreak investigations, although these reports are less frequent than O1-based outbreak reports and are not necessarily captured by routine O1-focused rapid test algorithms (9,12).

Atypical El Tor variants and virulence marker patterns:

Molecular analyses of Nigerian O1 isolates have identified variants described by study authors as atypical El Tor, including strains carrying cholera toxin B subunit alleles associated with classical-like toxin genotypes within an El Tor background (9,10). These findings are relevant because they indicate that Nigerian outbreaks have involved seventh-pandemic lineages with evidence of genetic exchange or replacement events in virulence-associated loci, consistent with patterns described across Africa during the seventh pandemic (11,12). Across studies, the interpretability of virulence marker reporting depends on the methods used (culture confirmation, PCR targets, sequencing), and not all outbreak investigations report comparable marker panels (11,18).

Non-O1/non-O139 isolates and implications for confirmation pathways:

Reports that include non-O1/non-O139 *V. cholerae* isolates from Nigeria emphasize that these strains may be associated with diarrhoeal illness despite lacking the classic O1/O139 serogroup designation used for many cholera surveillance definitions (1). Where such strains are present, outbreak confirmation systems that rely primarily on O1/O139 antigen-based rapid tests may fail to detect them, creating potential under-ascertainment of *V. cholerae* in diarrhoea outbreaks that are clinically and epidemiologically compatible with cholera-like illness (9,12). The practical implication for Nigeria is that surveillance-confirmation pathways benefit from integrating culture and/or nucleic acid detection workflows that can identify *V. cholerae* beyond O1/O139, especially during outbreaks where

rapid tests are negative but clinical suspicion high (3,7).

Antimicrobial susceptibility patterns reported in Nigerian isolate series:

Across isolate series reported from Nigeria, antimicrobial resistance patterns commonly include resistance to older, widely used agents, particularly trimethoprim-sulfamethoxazole and related folate pathway inhibitors, with additional reports of reduced susceptibility to quinolones and other agents depending on outbreak and study period (9,10,13). The systematic review evidence from sub-Saharan Africa supports that resistance in *V. cholerae* is heterogeneous across settings and time, and that variation in testing methods and interpretive criteria limits direct comparability of resistance prevalence estimates across studies (8). Nigeria-specific reports similarly differ in antimicrobial panels tested, susceptibility testing approach, and reporting standards, which constrains attempts to infer national resistance trends from the published literature alone (10,29).

Where resistance mechanisms were explored, studies describe roles for mobile genetic elements, including integrative conjugative elements (ICEs), and for target-site mutations relevant to quinolone susceptibility, consistent with established mechanisms in seventh-pandemic *V. cholerae* (1,2,3). However, because many outbreak reports do not include isolate-level antimicrobial susceptibility testing, the degree to which published resistance profiles represent contemporaneous national outbreak strains is uncertain (3,7).

Genomic lineage assignments and regional clustering including Nigerian isolates:

Genomic studies that include Nigerian isolates place them within seventh-pandemic El Tor diversity and identify regional clustering patterns across Africa and West Africa. The Africa-wide genomic reconstruction of seventh-pandemic spread identifies multiple introductions and lineages circulating on the continent, providing context for Nigerian isolates within broader transmission histories (11). West Africa focused sequencing work reports persistence of regional lineages over time and includes Nigerian isolates within lineage groupings described by study authors, including T12, with continuity into AFR12 designations in more recent multi-country analyses (4,9). These studies support that Nigerian outbreak strains are part of regional transmission systems rather than isolated national lineages, although the density of Nigeria-only sequencing across all outbreak years is limited, constraining fine-scale inference about within-country transmission routes and

state-to-state connectivity in some years (12, 14).

Laboratory confirmation gaps as a cross-cutting limitation for microbiological interpretation:

Across surveillance reports and published analyses, limited laboratory confirmation is repeatedly identified as a constraint for characterizing outbreak strains and tracking AMR during response (3,7). Over-reliance on rapid diagnostic tests without systematic confirmatory culture and susceptibility testing can delay detection of resistance patterns and limit the ability to link epidemiological hotspots to pathogen characteristics. This limitation also affects interpretation of whether observed epidemiological shifts reflect true changes in pathogen circulation, changes in exposure and vulnerability, or changes in testing and reporting completeness (3,7).

Public health responses reported (OCV, WASH and outbreak operations)

Vaccination activities and constraints (oral cholera vaccine):

Across the reviewed sources, oral cholera vaccine (OCV) is consistently described as a key outbreak control and prevention tool, but with operational constraints that affect coverage and timing in Nigeria. Reports and analyses cite limited vaccine availability and distribution challenges as barriers to achieving coverage levels considered programmatically useful in high-risk settings, particularly during periods of global OCV supply constraint (30,31). Implementation barriers are described as more pronounced in insecure settings, where access limitations and displacement complicate campaign logistics (16,32). Where campaigns were implemented, sources describe temporal associations between targeted vaccination activities and subsequent reductions in reported cases, although these accounts are typically descriptive and not designed as causal evaluations (4,16).

WASH interventions documented during outbreaks:

Water, sanitation and hygiene interventions reported during outbreak periods include emergency water point chlorination, hygiene kit distribution, and WASH service strengthening in high-risk communities. UNICEF and partner reports describe chlorination and hygiene support activities implemented in outbreak-prone areas, including north-west settings, alongside broader WASH response efforts in the northeast through collaboration with international and national partners (21,33,34). Humanitarian updates and analytical reviews also link major flooding events to WASH disruption and subsequent out-

break risk, and they describe scale-up of emergency response activities during flooding-associated crises (19,20,25). These sources emphasize operational challenges in sustaining safe water access over time, particularly when infrastructure damage, population displacement, and monitoring constraints limit consistent water quality control (33,35).

Outbreak operations, insecurity, and access constraints:

Several sources describe how conflict and insecurity affect cholera response operations in Nigeria, particularly in the Northeast. These constraints include disrupted water and sanitation infrastructure, limited access for responders, and fragmentation of routine health-care services in displaced populations (6,8). Situation reporting from affected areas describes concurrent challenges from flooding and health system strain during outbreak response periods, with implications for timely detection, case management, and implementation of community-level interventions (26,32). These contextual reports are consistent with broader analyses linking conflict and cholera in Nigeria and emphasizing the compounding effects of displacement and service disruption on outbreak dynamics (6,15).

Diagnostic and laboratory capacity in response reporting:

Across surveillance analyses and policy-focused reviews, diagnostic gaps are repeatedly described as a limiting factor for outbreak confirmation and for microbiological characterization during response. Sources describe reliance on suspected case reporting and variable laboratory confirmation, with implications for differentiating cholera from other acute watery diarrhoea causes and for linking epidemiological patterns to pathogen characteristics such as lineage and antimicrobial resistance (6,7). This limitation is presented as operational rather than purely technical, reflecting specimen referral constraints, uneven culture capacity, and inconsistent linkage between field detection and laboratory confirmation workflows.

National strategic planning for cholera control:

The reviewed sources also point to an increased focus on national-level planning that aims to integrate surveillance, laboratory strengthening, WASH, and vaccination strategies within defined implementation frameworks. Recent analyses discuss enabling factors and barriers for cholera intervention implementation, emphasizing governance, logistics, and community engagement as determinants of feasibility

(7,16). These sources describe strategic intent to align prevention and response activities with global cholera control approaches, while acknowledging that execution is shaped by financing, operational capacity, and the realities of insecurity and climate-related shocks in high-risk settings (7,15).

Discussion:

This integrative review synthesizes surveillance reporting (2017 to 2024) alongside microbiological and genomic evidence relevant to Nigeria and supports five main findings. First, cholera in Nigeria during 2017 to 2024 was characterized by recurrent surges with shifting geographic concentration. State-by-year distributions derived from NCDC sitreps show that reported burden frequently clustered in northern states across multiple years, while later reporting also highlighted large burdens in densely populated urban settings, including Lagos in 2024 within the extracted distribution (4). National surveillance analyses similarly describe multi-state outbreaks with heterogeneous outcomes and recurring transmission across years rather than isolated, self-limited events (3,5).

Second, multiple sources consistently describe contextual conditions that plausibly amplify transmission and complicate response, including conflict-related displacement and access constraints in parts of the North, and flooding-linked disruption of water and sanitation services in several regions (6,8,25,32). In urban informal settlements, published work describing sanitation constraints in Lagos provides a plausible environmental and social basis for sustained diarrhoeal disease transmission risks, although these sources are not designed to attribute causality to specific outbreak years contaminated (27,28).

Third, the microbiological literature indicates that outbreaks in Nigeria are predominantly associated with seventh-pandemic *V. cholerae* O1 El Tor, including atypical El Tor variants described in Nigerian isolate series (9,10,18). These findings align with broader African genomic reconstructions that place West African outbreaks within seventh-pandemic spread and persistence patterns (11). Fourth, antimicrobial resistance patterns reported from Nigerian isolates commonly include resistance to agents such as trimethoprim-sulfamethoxazole, with reports of reduced quinolone susceptibility in some datasets and mechanistic evidence implicating mobile genetic elements and target-site changes, consistent with established resistance mechanisms in seventh-pandemic *V. cholerae* (9,10,11,13). However, the Nigeria-specific evi-

dence base is methodologically heterogeneous, and isolate series are often outbreak- or site-specific, limiting inference about national resistance prevalence or temporal trends (13,29).

Fifth, genomic studies that include Nigerian isolates support regional clustering and connectivity within West African seventh-pandemic transmission systems. West Africa-focused sequencing and more recent multi-country genomic analyses include Nigerian isolates within lineage groupings described by study authors such as T12 and AFR12, reinforcing the interpretation that Nigeria's outbreak strains are part of regional transmission networks (4,9). The main limitation is that Nigeria-only sequencing density remains insufficient across all years to consistently resolve within-country transmission pathways or to link state-by-state epidemiology to fine-scale phylogenetic structure (12, 14).

Nigeria's surveillance patterns and the wider contextual evidence suggest that cholera burden is shaped by the intersection of environmental shocks, population movement, and structural limitations in safe water and sanitation. Analyses linking conflict and cholera in Nigeria emphasize how insecurity and displacement can increase exposure risks through crowded living conditions and disrupted WASH infrastructure, while simultaneously limiting access for responders and reducing health system capacity for prompt case management and outbreak control (6,8). In these settings, even when suspected case reporting is strong, laboratory confirmation and isolate characterization may lag due to specimen referral constraints, limited culture capacity, and operational risk, which in turn reduces the ability to generate real-time microbiological intelligence to guide response (3,7).

Flooding is repeatedly described as a major WASH-disrupting event in Nigeria with implications for diarrhoeal disease outbreaks, including cholera. The 2022 flooding emergency is consistently highlighted in the literature and humanitarian reporting as a large-scale displacement and infrastructure disruption event that plausibly increased exposure through contamination of water sources and interruption of routine sanitation services (19,20,25). Such flood-linked amplification does not negate the importance of endemic persistence and recurrent introductions, but it underscores why outbreak magnitude may vary sharply by year even when underlying vulnerabilities remain similar.

The contribution of urban informal settlements to cholera risk is supported by sanitation literature describing high-risk environmental conditions in parts of Lagos, including limited access to improved toilets and reliance

on compromised water sources in some communities (27,35). These conditions are compatible with cholera transmission pathways and may become increasingly relevant as urban populations expand. The implication for cholera control is that surveillance and prevention strategies should not assume that risk is confined to rural or conflict-affected northern settings, even if those settings account for large reported burdens in many years (4,7).

A consistent operational weakness across sources is limited laboratory confirmation relative to suspected case reporting. This has direct consequences. When confirmation is delayed or absent, outbreak response may proceed without clear pathogen characterization, limiting the ability to detect and respond to changes in serogroup distribution, virulence profiles, or antimicrobial susceptibility (3,7). It also complicates rational antibiotic policy for severe cases. Even if antibiotic therapy is not indicated for most mild cholera cases, severe disease and hospitalized patients may require antimicrobial therapy to reduce stool volume and duration, and local susceptibility data are needed to support empiric guidance and stewardship (7,13).

The presence of non-O1/non-O139 *V. cholerae* reports in Nigeria further supports strengthening confirmation pathways beyond O1/O139-focused antigen testing. While O1 remains predominant in cholera outbreaks, non-O1/non-O139 isolates associated with diarrhoeal illness introduce a diagnostic vulnerability if confirmation workflows depend mainly on O1-targeted rapid tests, particularly when clinical suspicion is high but initial antigen testing is negative (9,12). Practical approaches include ensuring culture capacity at reference laboratories, predefined specimen referral routes during outbreaks, and targeted molecular testing panels where feasible to support timely identification and characterization (3,7).

The available Nigeria-specific microbiology indicates that resistance to trimethoprim-sulfamethoxazole and related agents is common in reported isolate series, while reduced quinolone susceptibility and other resistance patterns appear in some datasets, supported by described mechanisms including mobile genetic elements and target-site changes (9,10,13). These findings suggest that empiric antibiotic guidance for severe cholera in Nigeria should not assume susceptibility to older oral agents and should be based on locally generated susceptibility data where available, interpreted with awareness of methodological variability (13,29). They also support the inclusion of antimicrobial stewardship principles in outbreak response planning, especially where inappropriate antibiotic expo-

sure may be common in informal care settings, potentially selecting for resistant strains and complicating management of other bacterial infections (7).

Genomic studies that include Nigerian isolates provide evidence for regional clustering and connectivity within West Africa and support the interpretation that Nigeria's outbreaks are linked to broader transmission systems rather than confined national lineages (11,12,14). The operational value of genomics for Nigeria depends on shortening the distance between sequencing outputs and outbreak decision-making. For many outbreak years, sequencing evidence remains retrospective or dependent on external collaborations, limiting real-time utility (12,14). Priority steps include establishing minimum metadata standards for isolate submission, ensuring integration between surveillance reporting and laboratory information systems, and defining practical sequencing triggers, such as a defined number of isolates per outbreak cluster or per high-burden state to support lineage and resistance mechanism tracking (7).

Sources consistently describe OCV as an important tool but emphasize supply and operational constraints, including global shortages and access barriers in insecure areas (10,31, 32). Where implemented, vaccination campaigns are described as potentially impactful, but most available reporting is descriptive rather than evaluative (4). WASH interventions such as water point chlorination and hygiene kit distribution are widely reported, often implemented in emergency response contexts, but sustained safe water provision remains challenging where infrastructure damage, displacement, or monitoring constraints limit continuity (21,35). The practical implication is that cholera control strategies require alignment between immediate emergency WASH measures and longer-term sanitation and water infrastructure improvement, with prioritization of settings repeatedly identified in surveillance reporting (7,15).

This review has important limitations. First, the epidemiological findings rely largely on routine outbreak reporting, which is affected by under-ascertainment, variable case definitions over time and across settings, and uneven access to laboratory confirmation. These issues reduce comparability across states and years and can bias apparent geographic concentration toward locations with stronger reporting systems or better access to care and testing (3,4, 7). Second, the State-by-year distributions in Table 1 were extracted from the last available NCDC situation report within each calendar year. The counts are cumulative as at the epidemiological week covered by that report and

may not represent full-year totals. Because the last reporting week differs by year, data in Table 1 are most appropriate for within-year state comparisons rather than direct year-to-year comparisons of incidence or national burden.

Third, the microbiological and antimicrobial resistance evidence is heterogeneous. Studies differ in outbreak context, sampling frames, isolate selection, antimicrobial panels, susceptibility testing methods, and interpretive standards. This limits comparability across studies and prevents reliable pooled estimates of resistance prevalence or inference of true temporal trends (13,29). Fourth, the genomic evidence relevant to Nigeria is uneven over time and often derived from multi-country datasets that include Nigerian isolates rather than continuous Nigeria-only sequencing. While these data support lineage assignment and regional clustering, they limit fine-scale inference about within-country transmission dynamics in some years and settings (12,14).

Finally, grey literature and humanitarian reporting add valuable context on flooding, displacement, and response activities, but these sources vary in methodological detail, outcome definitions, and reporting consistency. They are useful for triangulation and operational interpretation but should be treated cautiously for quantitative inference (19,20,25).

Implications and recommendations:

The evidence in this review points to practical priorities that connect surveillance, laboratory confirmation, antimicrobial stewardship, and prevention. Outbreak response needs dependable confirmation. Rapid specimen referral from treatment sites to culture-capable laboratories should be pre-defined, with minimum confirmation targets per outbreak cluster, routine susceptibility testing on a subset of confirmed isolates, and standardized reporting that links confirmation method, serogroup, and AST results to surveillance line lists. Where RDTs are used widely, confirmatory testing should be built into routine outbreak workflow so results can inform case management and messaging in real time (3,7).

Antibiotic guidance for severe cholera should reflect Nigeria-relevant susceptibility data and be updated periodically. Where local data are limited, guidance should state uncertainty and avoid agents with frequent resistance in reported isolate series. Stewardship should be integrated into outbreak case management because outbreaks often drive inappropriate antibiotic use in communities and informal care settings (7,9,10,13,29).

Genomics should be used for defined operational decisions, not only retrospective description. Priority uses include distinguishing linked outbreaks from multiple introductions, tracking resistance mechanisms and mobile genetic elements, and enabling regional co-ordination through comparable sequence data and metadata. A feasible minimum is a tiered sequencing plan with a standard subset of isolates from high-burden states and major outbreaks each year (7,11,12,14).

Prevention should concentrate on repeatedly high-risk settings, including conflict and displacement contexts and flood-affected communities with WASH disruption, while also addressing urban informal settlements. Packages should combine predictable emergency WASH actions during outbreaks, sustained safe-water strategies where feasible, and targeted OCV when doses are available, adapted- to insecurity and access constraints (6,7,16,25,27). Finally, reporting comparability needs improvement. A minimum national outbreak dataset with consistent case definitions, denominators, confirmation counts, and key response actions would reduce confusion across years and partners and allow clearer linkage between epidemiology and laboratory outputs (3,7).

Conclusion:

Nigeria experienced recurrent cholera surges from 2017 to 2024 with shifting geographic concentration and persistent vulnerability in settings affected by displacement, flooding, and inadequate sanitation. The microbiological and genomic literature indicates that outbreaks are predominantly associated with seventh-pandemic *V. cholerae* O1 El Tor lineages, including atypical El Tor variants, and that AMR determinants reported in Nigerian isolate series have implications for empiric management of severe disease. Genomic studies that include Nigerian isolates support regional clustering within West Africa, but Nigeria-only sequencing density remains insufficient for consistent within-country resolution across all outbreak years.

Strengthening outbreak-linked confirmation, routine susceptibility testing, and feasible sequencing pathways, alongside integrated WASH and targeted vaccination strategies, would improve both response effectiveness and the evidence base needed for sustained cholera control in Nigeria (3,7,12).

Contributions of authors:

BA conceived the study; NM prepared the first draft of the manuscript; NM, OIA, and

RE performed data curation and descriptive analysis; and all authors (NM, OIA, IJ, RE, RDG, BA) critically reviewed, revised, and approved the final manuscript.

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