Cryptosporidiosis in HIV/AIDS Patients: A Review of Species Distribution and Genetic Diversity in Nigeria

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Abstract. Cryptosporidium, a protozoan parasite, is a significant cause of diarrheal diseases and mortality among HIV/AIDS patients in Nigeria. This review synthesises existing publications to provide a comprehensive overview of Cryptosporidium species diversity, genetic variability, and factors influencing their distribution in Nigerian HIV/AIDS patients. Studies reveal a high diversity of Cryptosporidium species, with C. *hominis* and C. *parvum* being the most frequently identified, followed by C. canis, C. felis, C. meleagridis, and C. viatorum. Molecular techniques such as PCR-RFLP and DNA sequencing have enabled the identification of various subtypes within these species. Multiple environmental factors, such as the water source, human-animal contact, hygiene practices, and the host's immune status, influence genetic diversity. Clinical implications of this diversity include variations in disease severity, progression, treatment efficacy, and diagnostic challenges. Public health concerns arise from the parasite's high infectivity, environmental resilience, and contribution to morbidity and mortality in immunocompromised individuals. Control strategies should prioritise water, sanitation, hygiene promotion, consistent antiretroviral therapy, and a One Health approach. Future research must address knowledge gaps in molecular epidemiology, transmission dynamics, clinical outcomes, and targeted interventions to combat cryptosporidiosis among HIV/AIDS patients in Nigeria effectively.

Keywords: Cryptosporidium; HIV/AIDS; Nigeria; Genetic diversity; Species distribution; Immunocompromised; Diarrhoea.

INTRODUCTION

Cryptosporidium is a protozoan parasite that belongs to the Apicomplexa phylum and is classified among neglected tropical diseases due to its significant yet under-recognised public health impact [1]. It is primarily responsible for cryptosporidiosis, a gastrointestinal infection that presents heightened risks in immunocompromised individuals, particularly those with HIV/AIDS [2]. The parasite has a broad host range and a global distribution, affecting various vertebrates, including humans [3]. Although human cases most often involve *Cryptosporidium parvum*, other species such as C. *hominis*, C. *muris*, C. felis, C. canis, and C. meleagridis also cause infections [4]. The global prevalence of *Cryptosporidium* infection varies widely, ranging from 0% to 78.1%, reflecting differences in exposure and detection methods. Several factors contribute to its persistence and transmission, including the excretion of

numerous environmentally resistant oocysts, the limited efficacy of standard water disinfectants, the low infectious dose required for transmission, and the absence of universally effective therapeutic interventions [5]. Notably, authors [6] report that ingestion of as few as 10–30 oocysts may be sufficient to initiate infection, with the parasite exhibiting intracellular yet extracytoplasmic development that renders it particularly resistant to treatment.

Cryptosporidium contributes substantially to the burden of diarrheal illnesses, particularly among individuals living with HIV/AIDS in Nigeria, where it remains a critical public health concern [7]. In immunocompetent hosts, infection is often asymptomatic or presents as a mild, self-limiting illness. However, in immunocompromised individuals, especially those with HIV/AIDS, the infection can lead to severe, persistent, and potentially life-threatening diarrhoea resembling cholera. Affected patients frequently experience prolonged gastrointestinal symptoms that impair the absorption of fluids, nutrients, vitamins, and electrolytes, ultimately leading to malnutrition and further immunosuppression; this is particularly troubling in low-resource settings, where access to effective antiretroviral therapy (ART) remains limited or unaffordable. Although the national HIV prevalence in Nigeria declined from 4.1% in 2010 to an estimated 1.4% by 2019, the incidence of new infections and AIDS-related mortality continues to pose a significant challenge [8].

Despite the global scale-up of antiretroviral therapy (ART), *Cryptosporidium* remains a major contributor to diarrhoeal morbidity in individuals living with HIV, accounting for over 30% of diarrhoea cases in this population. Factors such as the emergence of drug-resistant HIV strains, incomplete virologic suppression, and discontinuation or failure of highly active antiretroviral therapy (HAART) explain this persistence. Diarrhoeal symptoms are reported in approximately 30–60% of HIV-positive individuals in high-income countries, with prevalence rising to as high as 90% in low- and middle-income regions [7].

Although several institutional and region-specific studies in Nigeria have documented *Cryptosporidium* infections among HIV/AIDS patients, there is a lack of comprehensive national surveillance that captures the overall disease burden and the species-specific distribution of this protozoan. With an estimated 2 million Nigerians living with HIV/AIDS and a reported *Cryptosporidium* prevalence of approximately 34%, there is a pressing need to understand the parasite's genetic diversity and epidemiological trends. This review consolidates current literature to present an integrated perspective on the species of *Cryptosporidium* affecting HIV-positive individuals in Nigeria. By analysing data from multiple regions, it identifies circulating species and genotypes, examines factors influencing their distribution, and underscores critical gaps in research, surveillance, and intervention strategies.

METHOD

Search Strategy. The researchers conducted a comprehensive search across seven electronic databases: African Journals Online (AJOL), Google Scholar, PubMed (via NCBI), Wiley Online Library, Frontiers, Elsevier, and Science Direct. The search strategy combined Boolean operators and truncation-based terms to ensure thorough coverage. The search terms included: (HIV OR "HIV-positive" OR "HIV-infected" OR "people living with HIV") AND (*Cryptosporidiosis* OR *Cryptosporidium* OR "*Cryptosporidium infection*") AND ("molecular characterisation" OR "molecular typing" OR genotyping OR genotype OR "genetic diversity") AND ("*Cryptosporidium hominis*" OR "*Cryptosporidium parvum*" OR "*Cryptosporidium canis*" OR "*Cryptosporidium felis*" OR "*Cryptosporidium meleagridis*" OR "*Cryptosporidium viatorum*").

The search was conducted, covering publications from January 2000 to April 2025.

Selection Criteria. Studies were included if they met all the following criteria:

a) Conducted in Nigeria;

b) Published between 2000 and 2025;

c) Described an observational study design (cross-sectional, cohort, or case-control);

d) Specified the geographic location of the study;

e) Reported *Cryptosporidium* infections in HIV/AIDS patients;

f) Identified Cryptosporidium to the species level
g) Clearly stated the diagnostic method used.

Exclusion Criteria. Studies were excluded based on the following:

a) Not identifying *Cryptosporidium* to the species level;

b) Not meeting the inclusion criteria listed above;

c) Duplicates, which were removed after title review;

d) Articles lacking sufficient methodological detail or data on infected individuals;

e) Studies outside the scope of HIV-related cryptosporidiosis in Nigeria.

The screening process consisted of two phases: title and abstract screening, followed by a full-text review. Initial screening of 68 articles resulted in 58 potentially relevant studies. After full-text review and quality assessment, 13 high-quality studies were selected for final analysis.

Overview of Selected Studies. The narrative review identified 13 studies that met the inclusion criteria, representing research conducted across six geopolitical zones in Nigeria. The studies were distributed by region as follows: North-East (n=1), South-East (n=1), South-South (n=2), North-West (n=5), South-West (n=2), and North-Central (n=2). In terms of publication period, three studies were conducted between 2000 and 2010, 4 between 2011 and 2020, and 7 between 2021 and 2025. All 13 studies identified *Cryptosporidium* to the species level, while eight studies further identified genotypic or subtypic variations.

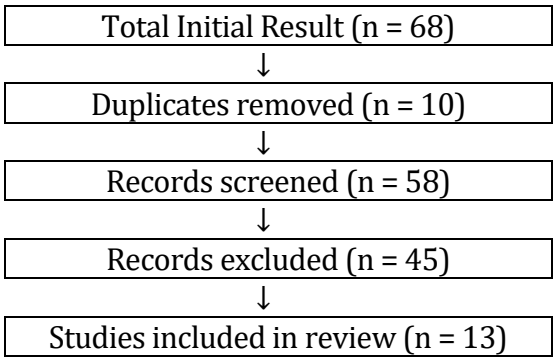

Figure 1 – Search strategy

Table 1 – Regional prevalence of *Cryptosporidium* infection and genetic diversity in HIV/AIDS patients in Nigeria

States	Species Identified	Subgeno type(s)	Subtype(s)	References
Kaduna	C. *parvum* (54.4%), C. *hominis* (45.5%)	IIa IIc IId Ia Id Ie	IIaA15G2R1, IIaA16G2R1, IIcA5G3a IIdA15G1R1, IaA15R3 IdA10G2, IdA10, IeA11G3T3	[9]
Plateau	C. *parvum* (83.3%), C. *parvum* (13.0%)	IIa IIc IId		[10, 11]
Delta	C. *parvum* (2.9%)	IIa IIc IId		[12]
Edo	C. *parvum* (44.4%, 5.1%), C. *hominis* (47.2%), C. canis (2.8%), C. felis (5.6%)	IIa IIc IId Ia Id Ie	C. *hominis*: IaA14R3, IaA16R3 IaA24R3, IaA25R3, IbA13G3 IeA11T3G3 C. *parvum:* IIcA5G3a, IIcA5G3h	[13, 14]
Borno	C. *parvum* (28.6%)	IIa IIc IId		[15]
Kano	C. *parvum* (31.9%)	IIa IIc IId		
Oyo	C. *parvum* (40%)	IIa IIc IId		[16]
Osun	C. *hominis* (44.2%), C. *parvum* (32.5), C. *parvum* (79.0), C. meleagri-dis (6.5%), C. canis (1.3%), rabbit genotype (6.5%), cervine genotype (3.9%)	Ia (29.4%), Ib (29.4%), Id (11.8%), Ie (8.8%) IIa (8.0%), IIc (68.0%), IIi (8.0%), IIm (8.0%)	C. *hominis*; IaA18R2, IaA22R2 IaA24R2, IaA25R2, IaA28R2 IaA21R1, IbA10G2, IbA13G3 IdA11, IdA17, IeA11G3T3, IhA14G1, C. *parvum,* IIaA15G2R, IIaA16G1R1, IIcA5G3a IIcA5G3b, IIiA11, IImA14G1	[17, 18]
Enugu	C. *parvum* (5.4%)	IIa IIc IId		[19]
Zaria (Kaduna)	C. *hominis* (30%), C. *parvum* (70%)	IIa, IIc, IId Ia, Id Ie	IIaA15G2R1, IIaA16G2R1, IIcA5G3a, IIdA15G1R1, IIdA15G1R1, IaA15R3, IdA10G2, IdA10, IeA11G3T3	[9]
FCT, Abuja	C. *parvum* (16.0%)			[20]
Sokoto	C. *parvum* (4.9%), C. *hominis* (3.3%)			[21]
Kano, Kaduna,	C. *parvum* (19.0%)			[22]

States	Species Identified	Subgeno type(s)	Subtype(s)	References
Katsina, Jigawa, Sokoto and Zamfara				

RESULTS AND DISCUSSION

Molecular Techniques for Species Identification and Genetic Characterisation. Although cryptosporidiosis remains highly prevalent in developing nations, molecular studies focusing on the genetic characterisation of *Cryptosporidium* species in HIV/AIDS populations in Nigeria are still limited. Only a few investigations have provided detailed molecular insights [15, 16, 23].

1) Genotyping. Genotyping using PCR-RFLP targeting genes like 18S rRNA and COWP has enabled species-level identification and revealed significant regional variation in *Cryptosporidium* distribution (Table 1).

Table 2 – Worldwide distribution of *Cryptosporidium* genotypes and subtypes [27]

Country	Cryptosporidium spp.	Subgenotype	Subtypes
Nigeria	C. *hominis*, C. *parvum*, C. meleagridis, C. rabbit genotype, C. cervinege, notype, C. canis	Ia, Ib, Id, Ie, Ih, IIa, IIc, IIi, IIm	IaA18R, IaA22R2, IaA24R2, IaA25R2, IaA28R2, IaA21R1, IbA10G2, IbA13G3 IdA11, IdA17, IeA11G3T3, IhA14G1, IIaA15G2R1, IIaA16G1R1, IIcA5G3a, IIcA5G3b, IIiA11, IImA14G1
Japan	C. *hominis*, C. *parvum*	IeIa, IIc, Ib	
Kenya	C. *hominis*, C. *parvum*, C. meleagridis		
India	C. *hominis*, C. *parvum*, C. felis, C. *parvum*, C. meleagridis	Ia, Ib, Id, Ie, If, IIc, IId, IIm, IIn	IaA18, IaA19, IeA11G3T3, IfA13G1, IaA18R3, IaA19R3, IaA21R3, IaA26R3, IaA27R3, IaA29G1T3R3b, IbA9G3, IdA14G1, IdA15G11, IdA16G1, IeA11G3T21, IeA11G3T3, IfA13G1, IIcA5G3a, IIdA14G1, IIdA15G1, IIeA7G1b
Ethiopia	C. *hominis*, C. *parvum*, C. viatorum, C. canis, C. felis, C. meleagridis, C. xioai	Ib, Id, Ie, IIa, IIb, IIc, IId, IIe	IbA10G, IdA20, IdA24, IdA26, IeA11G3T3, IIaA13G2R1, IIaA14G2R1, IIaA15G2R1, IIaA16G2R1, IIaA16G2R1, IIaA17G2R1, IIaA18G2R1, IIaA19G1R1, IIbA12, IIcA5G3, IIdA17G1, IIdA19G1, IIdA22G1, IIdA24G1
South Africa	C. *parvum*, C. *hominis*, C. meleagridis	Ic, Id, Ib, Ie, Ia, IIb, IIc, IId, IIe	IbA12G3R2, IbA10G2, IeA11G3T3, IaA20R3, IaA25G1R3, IaA17R3, IbA9G3, IbA10G1, IdA20, IdA25, IdA26, IdA24, IeA11G3T3b, IfA14G1, IfA12G1, IIbA11, IIcA5G3bb, IIeA12G1, IIIdA4
Ireland	C. *hominis*, C. *parvum*		IIaA18G3R1, IIaA18G3R1, IIaA20G3R1, IIaA15G2R1 IIaA19G3R1, IIaA17G1R1 IIaA10G2R1, IIaA14G2R1 IIaA16G3R1, IIaA17G2R1 IIaA20G5R1, IIaA21G3R1 IIdA26G1
France	C. *hominis*, C. *parvum*, C. meleagridis, C. felis, C. *muris*		
Europe	C. *hominis*, C. *parvum*		IbA10G2, IdA15G1, IIaA18G3R1, IIdA22G1

A genotypic study conducted in Maiduguri detected the 18S SSU rDNA gene in 28.6% (20/70) of analysed samples [15], a figure lower than the 31.9% reported in Kano but higher than the 2.9% recorded in Delta and the 25% observed in Sokoto [12, 24, 25]. In Edo State, RFLP analysis identified

C. *hominis*, C. *parvum*, C. felis, and C. canis among HIV/AIDS patients, with DNA sequencing confirming these profiles [13]. Kaduna studies found C. *parvum* (54.5%) and C. *hominis* (45.5%) [9]. In comparison, Osun recorded C. *hominis* (44.2%) as the most prevalent, followed by C. *parvum* (32.5%), with rare genotypes, such as C. meleagridis and the rabbit genotype, also present [18]. Regionally, C. *parvum* dominated in northern Nigeria (up to 83.3% in Plateau), whereas C. *hominis* prevailed in the south-west. Globally, similar analyses in HIV/AIDS populations have identified species like C. felis, C. canis, C. meleagridis, and C. andersoni, with emerging reports of C. *muris* and C. *suis* in immunocompromised hosts (Table 2) [26].

2) Subtyping (sub-genotyping). Sub-genotyping of *Cryptosporidium* species is crucial for elucidating their population structure and understanding the epidemiological and clinical implications of specific strains [27], as illustrated in Table 1. One of the most commonly employed methods for subtyping involves sequencing the polymorphic region of the gene encoding the sporozoite surface glycoprotein gp60 (also known as cpgp40/15 or gp40) [28]. The gp60 protein, predominantly located at the apical end of invasive parasite stages, serves as a key antigenic target for neutralising antibodies in humans [29]. The gene's polymorphic trinucleotide repeats enable classification into subtype families, with C. *hominis* associated with families Ia, Ib, Id, and Ie, and C. *parvum* with families IIa, IIc, and IId, among others [30]. In Kaduna, C. *parvum* isolates predominantly belonged to IIa (58.3%), followed by IId and IIc, with IIaA15G2R1 being the most common subgenotype [9]. C. *hominis* subtypes included Ia, Id, and Ie, with IaA14R6 and IdA10G2 as frequent variants. A related study revealed broader diversity: C. *hominis* isolates displayed six subtypes within Ia and Ib families, while C. *Parvum* exhibited subtype families IIa, IIc, and IIi. In Edo State, C. *hominis* strains fell into the Ia, Ib, and Ie families, and novel C. *parvum* variants closely resembled C. *hominis* types Ia and Ie [13].

Factors influencing genetic diversity in Nigeria. The genetic diversity of *Cryptosporidium* in Nigeria is shaped by environmental, epidemiological, socioeconomic, and host-related factors [31]. Studies have linked water sources, human-animal interaction, hygiene, and immune status to the spread and variation of genotypes. In Sokoto State, C. *parvum* was found exclusively among individuals using untreated borehole water. In contrast, zero prevalence was recorded among those consuming packaged water [21], highlighting the role of waterborne transmission. Animal contact, though common, may reflect broader issues such as environmental contamination, rather than direct zoonotic transmission. Co-infection with C. *hominis* in these regions suggests anthroponotic transmission as a significant route [21]. Foodborne routes, particularly those involving the use of raw vegetables irrigated with wastewater, have also been implicated [32]. The detection of oocysts in wastewater effluents and seafood products adds to the complexity of infection sources. Host immune status plays a key role. HIV-positive individuals with CD4 counts <200 cells/μL show significantly higher infection rates, potentially acting as reservoirs for persistent or resistant strains [33, 34]. Additionally, inconsistent hygiene practices, such as infrequent handwashing, have been statistically associated with an increased prevalence [35], which facilitates faecal-oral transmission and strain circulation.

Clinical Implications of Genetic Diversity. Genetic diversity in *Cryptosporidium* significantly influences disease severity, treatment response, and diagnostic accuracy, posing challenges in clinical management, especially in Nigeria, where immunosuppression, poor sanitation, and limited resources intersect [36]. Disease presentation varies with both host immunity and parasite genotype. Infections involving both intestines can lead to severe symptoms, including mucosal damage, crypt abscessation, and chronic watery diarrhoea, particularly life-threatening in HIV-positive individuals with CD4 counts <200 cells/μL [33, 34, 37].

Treatment failure with commonly used antibiotics, such as metronidazole and cotrimoxazole, suggests drug resistance and highlights the need for genotype-specific therapy [38]. Although nitazoxanide is the only FDA-approved drug, its availability remains limited in Nigeria [39]. Diagnostic limitations further compound the issue; reliance on microscopy cannot distinguish species or subtypes, obscuring transmission routes and hindering targeted intervention.

Subtyping has shown that both C. *parvum* and C. *hominis* are prevalent, but zoonotic assumptions may be misleading without molecular confirmation. In HIV-prevalent settings with poor ART coverage, the cycle of infection, environmental contamination, and reinfection is intensified, especially among children. These realities

underscore the need for integrated strategies involving treatment, sanitation, surveillance, and education.

Public Health Significance and Control Strategies. The continued burden of cryptosporidiosis in Nigeria's HIV/AIDS population has far-reaching public health implications. The excretion of resilient oocysts by infected individuals perpetuates environmental contamination, particularly in areas where open defecation and inadequate sanitation prevail. Effective control strategies must prioritise water safety, hygiene promotion, ART adherence, and food safety. Integrating molecular diagnosis into HIV care and employing a One Health approach linking human, animal, and environmental health are crucial for breaking the transmission cycle and addressing the zoonotic potential of circulating strains. Investment in molecular diagnostics and surveillance is essential for monitoring emerging variants and informing targeted interventions.

Future research directions. Despite increasing research on *Cryptosporidium* infections in Nigeria, particularly among HIV/AIDS patients, significant knowledge gaps remain. Future investigations must prioritise:

1) Expanding molecular surveillance to cover more regions and populations, enabling a comprehensive understanding of species distribution and genetic diversity across the country.

2) Investigating the transmission dynamics between humans and animals, particularly in rural areas with close human-animal contact.

3) Evaluating the effectiveness of current diagnostic methods and developing more sensitive and specific techniques for species identification.

4) Studying drug resistance patterns among different Cryptosporidium species and subtypes to inform treatment strategies.

5) Exploring potential links between specific Cryptosporidium genotypes and clinical outcomes in immunocompromised individuals.

CONCLUSIONS

This review highlights the significant impact of cryptosporidiosis on HIV/AIDS patients in Nigeria, emphasising the genetic diversity of *Cryptosporidium* species and its implications for public health. Key findings include the predominance of C. *hominis* and C. *parvum*, with regional variations in the distribution of these species. Factors influencing genetic diversity include water sources, human-animal interactions, and host immune status. The review highlights the need for enhanced diagnostics, targeted interventions, and a One Health approach to address this persistent public health challenge.

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