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Full Length Research Paper

Norovirus Epidemiology in Africa: A Review

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Noroviruses are leading etiological agents of acute gastroenteritis worldwide and represent a major but underrecognized public health burden in Africa, particularly among children under five years of age, leading to inadequate funding and insufficiently adapted intervention strategies. This study aimed to synthesize current evidence on the epidemiology, genetic diversity, transmission dynamics, diagnostic approaches, and control challenges of norovirus infections across the African continent in order to inform context-appropriate prevention strategies. A systematic review of the literature published between 2010 and December, 2025 was conducted using PubMed, ScienceDirect, Google Scholar, ResearchGate, and SpringerLink, with studies selected based on relevance, methodological rigor, and RT-PCR–based detection. Among 155 articles identified, 35 were retained for integrative analysis. The findings indicate an overall norovirus prevalence of approximately 20.3% in Africa, with substantial regional variability and a clear predominance of the GII.4 Sydney genotype, alongside the emergence of recombinant and non-GII.4 strains, which complicate epidemiological surveillance and may impact vaccine effectiveness. Transmission is driven by fecal–oral, foodborne, waterborne, and nosocomial routes, exacerbated by poor sanitation, overcrowding, seasonal factors, and limited access to clean water. Molecular diagnostics have improved detection and surveillance, yet remain unevenly accessible, while management relies largely on rehydration and preventive hygiene measures in the absence of approved antivirals or vaccines. In conclusion, noroviruses constitute a significant and persistent health threat in Africa, underscoring the urgent need for strengthened surveillance, improved sanitation, expanded molecular diagnostic capacity, and the development of vaccines and control strategies adapted to the continent's epidemiological and socio-economic context.

Keywords: Norovirus, Epidemiology, Prevalence, Genetic diversity, Gastroenteritis, RT-PCR, Africa.

Introduction

Noroviruses (NoV) are major pathogens responsible for acute gastroenteritis (AGE). They represent a major public health issue in sub-Saharan Africa (1,2). These viruses, which belong to the Caliciviridae family, exhibit remarkable genetic diversity, with a wide range of genogroups and genotypes, dominated by GII.4 Sydney, which is responsible for the majority of global epidemics (3). In Africa, their overall prevalence is estimated at 20% and contributes to infant mortality (4) in a context of precarious living conditions with limited access to drinking water and healthcare, as well as the circulation of recombinant strains (GII.17 and GII.2) aggravating the

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burden of these infections (5). They are transmitted by a tiny infectious dose and persist for a long time in the environment, leading to frequent outbreaks in closed environments (6). With 685 million cases and 200,000 deaths per year, their impact, despite often being underrecognized, rivals that of many diseases on the "neglected" public health agenda (7, 8). Post-infection immunity is short-lived and there is currently no approved vaccine, although trials are underway, such as the TAK-214 bivalent vaccine, currently in clinical development and targeting GI.1 and GII.4 (9). The fight against NoVs relies on an integrated approach, combining improved hygiene measures, epidemiological surveillance, the development of appropriate vaccines, and community awareness. This study aimed to synthesize current data on the epidemiology, genetic diversity, and control challenges of NoVs in Africa in order to propose realistic and contextualized strategies aligned with global public health objectives.

I. Methodology

1. Type, sources, and search engines

A systematic review of the literature was conducted using the following international scientific databases: PubMed, ScienceDirect, ResearchGate, Google Scholar, and SpringerLink. The keywords used were combined using the Boolean operators "AND" and "OR":

- "Norovirus infection" OR "Norovirus gastroenteritis" OR "norovirus diarrhea";
- "Norovirus epidemiology" OR "Norovirus surveillance";
- "Norovirus genotyping" OR "Norovirus molecular characterization";
- "Norovirus prevalence" OR "Norovirus burden";
- "Africa".

2. Inclusion and exclusion criteria

The following were included:

- Articles published between 2010 and December 2025, in English or French;
- Studies evaluating the prevalence or genotyping of noroviruses in Africa;
- Norovirus detection performed by RT-PCR (reference method);
- Epidemiological or genetic data contextualized to the African continent.

The following were excluded:

- Studies outside the African context;
- Non-verifiable methodologies or those without specific detection by RT-PCR;
- Incomplete or irrelevant data for critical analysis.

3. Selection and analysis steps

A total of 155 articles were initially identified during the literature review. After screening titles and abstracts, 80 records were excluded, and 75 articles were selected for in-depth full-text analysis. Finally, 35 were retained based on the following criteria:

- Level of scientific evidence (cohort studies, cross-sectional studies, or meta-analyses);
- Contextual relevance (relevance to the socio-economic and health realities of Africa);
- Data quality (rigorous methodology, clear and reproducible results).

Figure 1 illustrates the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) flow diagram, detailing the successive stages of study identification, screening, eligibility assessment, and inclusion in this systematic review. The exclusion criteria presented in the flow diagram (including absence of RT-PCR confirmation) are consistent with those described in the methodology section.

A formal quantitative risk-of-bias assessment tool was not applied due to the heterogeneity of the included studies. However, the methodological quality of included studies was assessed qualitatively during the selection process based on predefined criteria, including study design, clarity of case definition, use of RT-PCR for norovirus detection, adequacy of sample size, and transparency of reported methods and results. Studies with unclear methodologies, non-standard diagnostic approaches, or insufficient epidemiological detail were excluded. This approach ensured that only studies with acceptable scientific rigor and relevance to the African context were included in the final synthesis.

II. Epidemiology of norovirus in Africa

1. Prevalence, genetic diversity, and evolution of strains

With an average prevalence of 20.3% and a predominance of the GII.4 Sydney genotype in most countries, noroviruses are a major public health problem in Africa. In Central Africa, studies reveal moderate but worrying prevalence rates. In Congo (Brazzaville), prevalence reaches 27.14% among children with gastroenteritis (10). In the Democratic Republic of Congo (DRC), the lack of direct data has led to the use of a regional comparative approach with neighboring countries (10,11). In Cameroon, a study of children under five hospitalized for gastroenteritis reports a more moderate prevalence of 8.4%, while a longitudinal study conducted in the southwestern part of the country detected infections in 29% of the 283 participants followed over a year (12, 13). Studies in Gabon indicate a prevalence ranging from 9% to 30% (14,15). In the Central African Republic, approximately 7% of severe diarrhea episodes have been attributed to norovirus (16). In addition, a foodborne outbreak confirmed by RT-PCR during a French military deployment in January 2016 showed a prevalence of 22.2% (17). In Angola, the prevalence was approximately 17.4% (18). In Chad and Rwanda, regional data for children under five indicate a prevalence of approximately 10-15% (11). West Africa generally has higher prevalences. In Nigeria, it is around

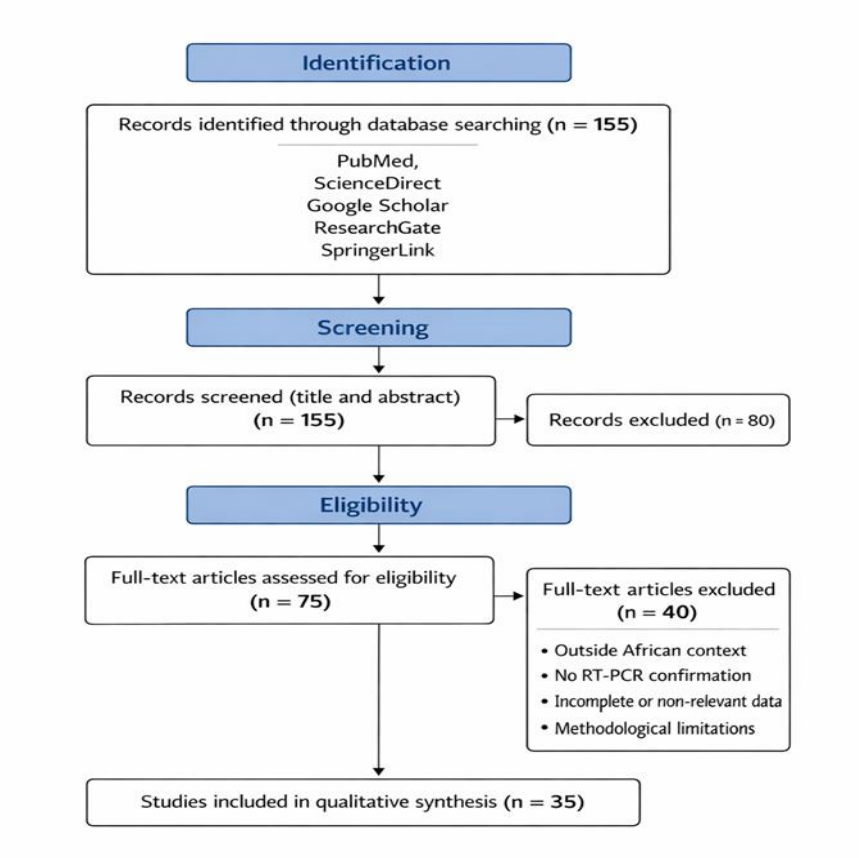

Figure 1. Prisma flow diagram of study selection.

15% (19). In Ghana, studies report prevalence rates ranging from 15.9% to 36.2% (20,21). Studies conducted in Burkina Faso show rates ranging from 16% to 20% (22,23). In Côte d'Ivoire, Mauritania, and Guinea, the lack of direct data has led to the use of a regional comparative approach (11,21,22). In Senegal, prevalence varies between 13% and 20% (24). In Southern Africa, data indicate high circulation of noroviruses. In South Africa, prevalence ranges from 12% to 37% (25). In Malawi, it is estimated to be between 9% and 27% (21,26,27), while in Mozambique, it ranges from 2.7% to 14.2% (28). In Zimbabwe, an estimate of approximately 22% has been established in a regional context (11,21,22). In Botswana, prevalence ranges from 9% to 15% (29,30). In Zambia, it ranges from 11.5% to 15% (31). In Namibia, in the absence of local data, the prevalence of norovirus has been estimated at 15% based on regional data (11,21,22). There are significant disparities in East Africa. In Madagascar, available studies report a prevalence of norovirus of approximately 5.9% in children with acute diarrhea (32,33). In Ethiopia, the reported prevalence ranges from 13% to 25% (34). In Kenya, it is estimated at 15.2% (35). In Tanzania, studies indicate a prevalence of between 10% and 30%, which corresponds to the levels observed in other sub-Saharan African countries (36,37). In Uganda, the lack of direct data has led to an estimate based on regional data (11,21,22). North African countries are not spared. In Morocco, local and regional studies estimate the prevalence of norovirus to be between 8.5% and 16.1%, rates comparable to those observed in other countries in the MENA region (38,39,40). In Tunisia, the prevalence is estimated at 9.3% among children with acute gastroenteritis, while a prospective study of 632 stool samples reports a higher rate of 17.4% (41,42). In Egypt, local studies indicate a prevalence of between 20% and 38% among children with acute gastroenteritis (43,44). In the absence of specific data for Algeria, the prevalence of norovirus has been estimated from regional data (21,22,40).

The GII.4 Sydney genotype is the most prevalent in Africa, but the emergence of new variants and recombinant strains poses a challenge for epidemiological surveillance (21,45). In Central Africa, studies show moderate but worrying prevalence rates. Among children hospitalized for gastroenteritis in Congo-Brazzaville, the GII genotype is predominant (87%), including subtypes GII.3, GII.4, and GII.6 (10). In the DRC, in the absence of direct data, a regional comparative approach was used (10,11,22). In Cameroon, the genotypes identified include, among others, GII.1, GII.3, GII.4, GII.16, GII.17, GII.21, and GI. The GII.4 variant is dominant, particularly GII.4 Sydney, accounting for 97.4% of GII.4-related cases (12,13). In Gabon, studies report that norovirus infections account for approximately 9.1% of cases for the GI genotype and

13.9% for the GII genotype (14,15). In the Central African Republic, data suggest that episodes of severe diarrhea may be linked to norovirus infection of the GII genotype (16,17). In Angola, strains identified in children under 5 years of age with acute gastroenteritis show a predominance of genotype GII.4, followed by GII.6, GI.3, and GII.7 (18). In Chad and Rwanda, genotypic diversity based on regional data indicates a predominance of GII.4 (11,21,22). West Africa shows high genetic diversity. In Nigeria, genetic analyses highlight a predominance of the GII.4 genotype, accompanied by the detection of recombinant strains such as GII. P31 and GII.P30, as well as the Sydney 2012 variant. The GII.P4 genotype accounted for approximately 66.7% of the strains detected in the VP1 region, illustrating the viral diversity of circulating noroviruses (19). In Ghana, the frequent genotypes were GII.4, GII.3, GII.6, GII.17, and GII.5. GII.8/GII.14 recombinants were also detected (20,21). In Burkina Faso, studies conducted among children hospitalized for diarrhea reveal genotypic diversity, with a predominance of genotype GII.4 and significant circulation of genotypes GII and GI, consistent with trends observed in other countries in West and East Africa (22,23). In the absence of local studies, regional estimates for Côte d'Ivoire, Mauritania, and Guinea suggest a predominance of the GII.4 genotype (11,21,22). In Senegal, genotype GII.4 is predominant, followed by GII.6, among the circulating strains detected in children with acute gastroenteritis (24). In Southern Africa, Norovirus circulation is significant, particularly among children with acute gastroenteritis, with a predominance of the GII.4 genotype (11,21,22). In South Africa, noroviruses show marked genetic diversity, dominated by genotype GII.4 and accompanied by other genotypes, such as GII.3, GII.17, GI.3, and GI.7, reflecting similar trends worldwide (25,46). In Malawi, the distribution of genogroups shows the presence of GII and GI noroviruses, with a clear predominance of the GII.4 genotype, followed by the GII.2, GII.6, and GII.12 genotypes, which are frequently detected in children hospitalized for gastroenteritis (21,26,27). In Mozambique, significant genetic diversity is observed, with a predominance of the GII.4 Sydney 2012 [P31] genotype, identified as the most common in children under five years of age, both before and after the introduction of the rotavirus vaccine (28). In Zimbabwe, although direct data are limited, regional estimates indicate a strong representation of the GII genogroup, dominated by the GII.4 genotype (11,21,22). In Botswana, the frequent genotypes are GII.2, GII.12, GI.9, GII.6, GII.10, and predominantly GII.4, as well as recombinant variants such as GII. Pe/GII.4 Sydney 2012, GII.4 Sydney [P31], and GII.4 Sydney [P13] (29,30). In Zambia, various genotypes from the GI and GII genogroups have been identified, with a predominance of the GII.4 genotype (31). In Namibia, in the absence of local data, genetic diversity has been estimated from regional data, with a predominance of the GII.4 genotype (11,21,22). East Africa shows notable disparities. In Madagascar, genogroups GI and GII have been identified in children, with a predominance of genotype GII.4 (32,33). In Ethiopia, norovirus genetic diversity is high, with a predominance of the GII.4 genotype and the presence of GII.6, GII.7, GII.9, GII.10, GII.12/GII.g recombinant-like, GII.13, GII.16, GII.17, GII.20, and GI.3. Genotypes GI.4, GI.5, and GI.8, as well as a GIV isolate, have also been identified (34,47). In Kenya, the genotypes frequently detected in children are GII.4, GII.3, GII.6, and GII.17 (35,48,49). In Tanzania, genotypes GII.21, GII.16, and GII.g were detected, as well as the predominant genotype GII.4 (36,37). In Uganda, in the absence of local data, norovirus diversity was estimated based on regional data (11,21,22). In North Africa, in Morocco, the GII.4 genotype is predominant (38,39,40). In Tunisia, several norovirus genotypes have been identified, with a predominance of genotypes GIIb/II.3 and GII.4. The GII.4 Hunter variant, observed between 2003 and 2007, was subsequently replaced by the GII.4 2006b variant (41,42). In Egypt, the GII.4 genotype is predominant (40,43,44). In Algeria, genetic diversity has been estimated based on regional data (21,22,40). The figure 2 below shows the prevalence (A) and genotypic diversity (B) of Norovirus in Africa.

(A) Map illustrating the prevalence (%) of norovirus infections reported in African countries included in this systematic review. The data are derived from studies conducted in human populations, primarily children under five years of age with acute gastroenteritis, and, in some cases, from general or hospitalized populations, depending on the study protocol. Colored circles represent prevalence categories estimated from RT-PCR–based detection of norovirus in stool samples. When a country is represented by multiple points, these correspond to different studies or epidemiological contexts reported. Countries for which data were absent or insufficient are indicated as such.

(B) Map showing the distribution of the main norovirus genotypes and genogroups identified in the same African countries. Colored symbols indicate the dominant genotype or genogroup reported in the included studies, as determined by molecular characterization methods (RT-PCR and sequencing). The presence of multiple symbols within a single country reflects the co-circulation of several genotypes, as reported in the analyzed publications. Countries without exploitable genetic data are indicated as having insufficient data.

2. Transmission routes

Noroviruses cause highly contagious acute gastroenteritis, which particularly affects children in Africa, but also adults and immunocompromised individuals. Their spread is exacerbated by precarious socioeconomic and environmental conditions. Fig 3.

2.1. Direct fecal-oral transmission

Noroviruses are mainly transmitted through contact with feces, vomit, or contaminated surfaces, as viral particles can remain in the air for several hours (21,36).

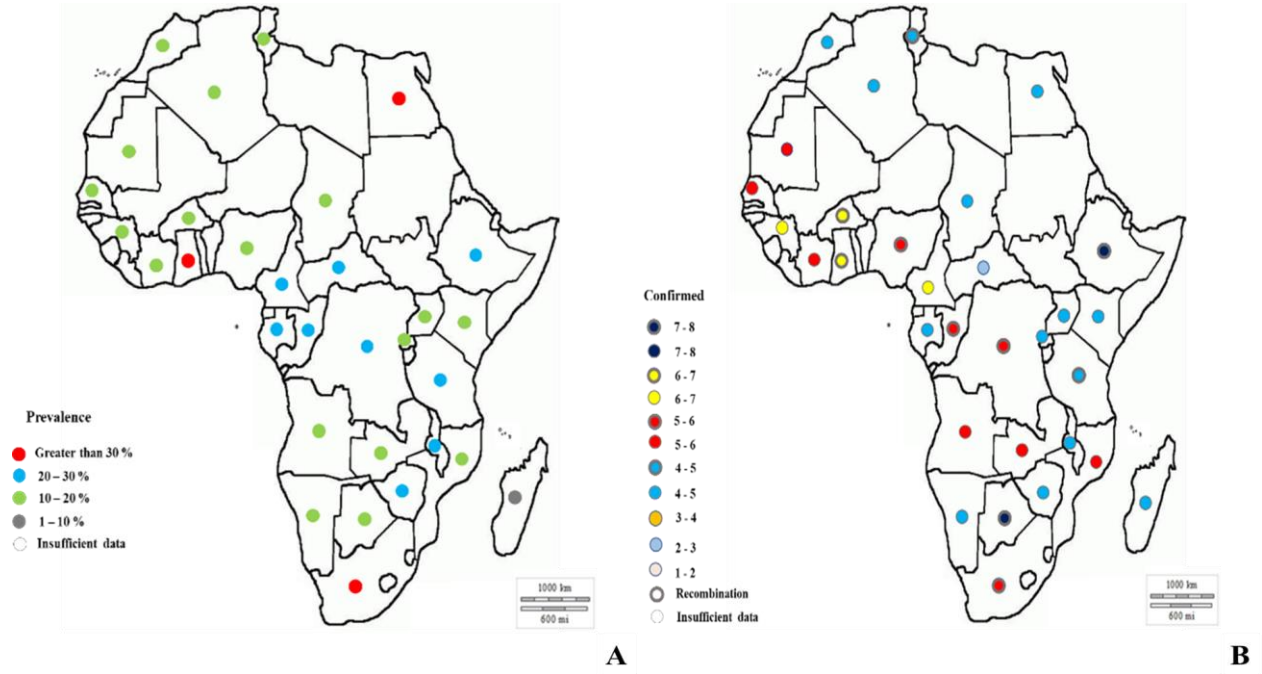

Figure 2. Prevalence (A) and genotypic diversity (B) of Norovirus in Africa.

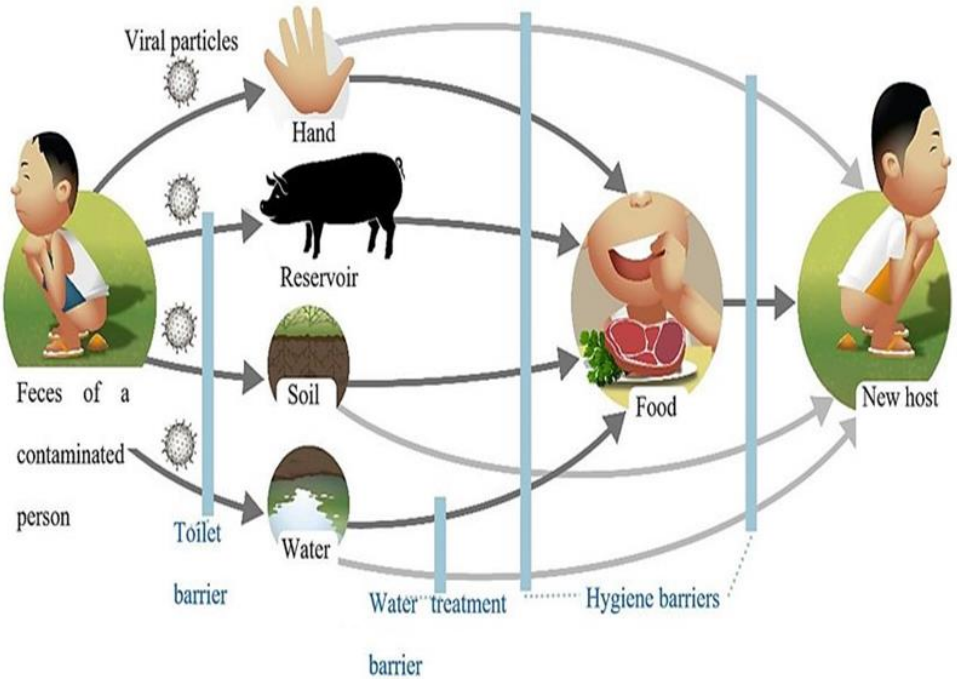

Figure 3. Transmission pathways adapted (50).

2.2. Water and food transmission

Noroviruses are widely transmitted through the ingestion of contaminated food or water (51). Contamination can be direct, through handling by an infected person, or indirect, through the use of untreated water for irrigation (52). Noroviruses are frequently detected in wastewater and surface water in Africa (53,54). Certain foods, such as filter-feeding mollusks, are particularly associated with norovirus infections. Their resistance to many disinfectants complicates prevention in collective settings such as school cafeterias or during community events (51).

Table I. Some risk factors associated with Norovirus.

Factors	Authors	Titles	Years	Countries	References
Military food outbreak, promiscuity on mission (atypical military context)	Watier-Grillot S *et al.*	Challenging investigation of a norovirus foodborne disease outbreak during a military deployment in Central African Republic	2017	Central African Republic	17
Nosocomial infections and genetic circulation	Trainor E *et al.*	Detection and molecular characterisation of noroviruses in hospitalised children in Malawi	2013	Malawi	27
No marked seasonality, present throughout the year. Comparison with rotavirus: cases attributed to NVII were less severe but just as likely to cause dehydration.	Richard Omore *et al.*	Norovirus Disease Among Children <5 Years in 3 Sub-Saharan African Countries: Findings from the Vaccine Impact on Diarrhea in Africa	2023	Kenya, Gambia, Mali	66
Age <5 years (specific to hospitalized children)	Page N.A.	Norovirus epidemiology in South African children <5 years hospitalised for diarrhoeal illness between 2009 and 2013	2017	South Africa	55
Contamination in disadvantaged communities (food/environmental transmission)	Mulondo G *et al.*	Molecular characterization of norovirus strains isolated from older children and adults in impoverished communities of Vhembe District, South Africa.	2020	South Africa	67
Classic factors: children under 5 years of age with gastroenteritis (individual vulnerability and transmission in the community).	Akongnwi EM *et al.*	Molecular epidemiology of noroviruses among children under five years with acute gastroenteritis in Yaoundé, Cameroon.	2018	Cameroon	12

2.3. Nosocomial transmission

Norovirus is a common cause of nosocomial outbreaks, particularly among children and immunocompromised individuals (55). Promiscuity, failure to comply with hygiene protocols, and asymptomatic excretion of the virus promote silent spread, with up to 31% of cases reported as asymptomatic in sub-Saharan Africa (21,22,56).

2.4. Seasonality

Norovirus outbreaks are closely linked to climatic conditions. In temperate regions, infection peaks during the cold season, while in Africa, fluctuations occur mainly during the dry or rainy seasons (56,57). The risk of transmission is particularly high in rural areas and informal settlements, where access to safe drinking water and sanitation infrastructure is limited (25).

3. Demographic and geographic risk factors

Key risk factors associated with norovirus transmission in Africa are summarized in Table I. The burden of infection is highest among children under five years of age, particularly in hospital settings, where nosocomial transmission has been frequently reported. Environmental factors, including poor sanitation, contaminated food and water, overcrowding, and limited hygiene infrastructure, were consistently associated with increased transmission. Several studies also reported variable seasonality and the presence of asymptomatic carriers, supporting sustained community circulation of norovirus across diverse settings (57). In Central and West Africa, water contamination and poor food hygiene are major determinants (22,48). In North Africa, coastal water pollution and irrigation with contaminated water increase the risks (51,58,59).

These findings highlight the need for targeted interventions focused on sanitation and health education (11,21). In Central Africa, several factors contribute to the spread of the virus. In Cameroon, the rainy season and poor food hygiene are among the main risks (11,21,57). In the Republic of Congo, consumption of untreated water and contact with infected individuals are factors associated with infection (10,60). In West Africa, risk factors are also well documented. In Ghana, transmission is influenced by seasonality, with a peak during the dry season, as well as by contact with family members with gastroenteritis (20,21). In Burkina Faso, the onset of cases is strongly linked to the rainy season and consumption of contaminated products, such as vegetables (22,23,52). In Southern Africa, risk profiles vary. In South Africa, overcrowding in schools and poor hand hygiene are frequently reported (25,61). In Botswana, asymptomatic carriers constitute a significant community reservoir (29,30). In Namibia, contamination of wells and poor hand hygiene are aggravating factors (62). In East Africa, several factors contribute to transmission. In Ethiopia, seasonality and consumption of untreated water are predominant (63). In Uganda, overcrowding and poor hygiene conditions in refugee camps significantly increase the risk (64). In Kenya, co-infections with other intestinal pathogens increase the severity of infections (35). In North Africa, certain risk factors are specific to the region. In Morocco, coastal water pollution and the consumption of contaminated shellfish are key drivers of norovirus transmission. Wastewater discharge leads to viral accumulation in filter-feeding mollusks, increasing the risk of foodborne outbreaks from raw or undercooked seafood (65). In Egypt, the risks are amplified by irrigation with polluted water and the inefficiency of wastewater treatment plants (40,59).

III. Diagnostic methods and management of norovirus infections

1. Diagnostic methods

The diagnosis of norovirus in Africa has evolved from simple immunological tests (EIA/ELISA, immunochromatography) to more advanced molecular methods, offering greater sensitivity and specificity. Conventional RT-PCR has enabled reliable detection and identification of genotypes, while real-time RT-PCR (qPCR) and multiplex PCR have improved quantification and simultaneous detection of multiple pathogens (21,27,47). Today, genomic sequencing complements these approaches by enabling in-depth analysis of strains and improved surveillance of emerging variants, thereby enhancing the understanding of norovirus epidemiology in Africa (21,30,68).

2. Management of norovirus infections

Norovirus infections are a public health problem in Africa, particularly among children under five years of age. In the absence of specific antiviral drugs, prevention relies on hygiene and vaccine development (3,21,56). Water treatment, hand washing, and surface disinfection are essential to limit transmission; however, implementing these measures remains difficult in rural areas due to inadequate sanitation infrastructure (21,69,70). Oral Rehydration Therapy (ORT) remains the primary clinical intervention in resource-limited African settings and constitutes the cornerstone of patient management. In terms of treatment, several avenues are currently being explored for the management of norovirus infections, including antivirals such as nitazoxanide, viral protease inhibitors, interferon lambda, and monoclonal antibodies targeting pandemic strains (71,72,73). Complementary approaches, such as probiotics and antiemetics, are also being studied to alleviate symptoms and improve recovery (71,72,73). However, the high genetic variability of noroviruses and the high cost of new molecules complicate the development of universal treatments (71,74,75). With regard to vaccines, candidates based on virus-like particles (VLPs) targeting genotypes GI.1 and GII.4 show promising potential, but their efficacy against African strains remains to be confirmed, particularly due to the high genetic diversity and the circulation of recombinant strains that may not be fully covered by current vaccine formulations, and no large-scale clinical trials have yet been conducted on the continent (3,71). Rehydration remains the basis of treatment. A combination of preventive, therapeutic, and vaccine approaches, adapted to the local context, could improve the management of norovirus infections in Africa (3,56,66).

Conclusion

Noroviruses represent a major and persistent cause of acute gastroenteritis in Africa, with high prevalence dominated by the GII.4 Sydney genotype and increasing genetic diversity. Transmission is closely associated with inadequate sanitation, limited access to safe water, overcrowding, and seasonal factors, while molecular surveillance remains uneven across regions. Key knowledge gaps include the lack of population-based data, continuous genomic monitoring, and evaluation of vaccines and treatments tailored to African strains. Strengthening surveillance systems, diagnostic capacity, and region-specific vaccine trials is essential to inform effective public health policy and future research.

References

1. Omosigho PO, Somtochukwu VW, Okesanya OJ. Prevalence and risk factors of norovirus gastroenteritis in children under five years in Okada, Edo State, Nigeria. J Glob Health Sci. 2025;7(1):e10. doi:10.35500/jghs.2025.7.e10.

2. Omatola CA, Ogunsakin RE, Onoja AB, Okolo MO, Abraham-Oyiguh J, Mofolorunsho KC. Enteropathogenic viruses associated with acute gastroenteritis among African children under 5 years of age: A systematic review and meta-analysis. J Infect. 2024;88(6):106169. doi:10.1016/j.jinf.2024.106169.

3. Omatola CA, Mshelbwala PP, Okolo MO, Onoja AB, Abraham JO, Adaji DM, et al. Noroviruses: Evolutionary Dynamics, Epidemiology, Pathogenesis, and Vaccine Advances-A Comprehensive Review. Vaccines (Basel). 2024;12(6):590. doi:10.3390/vaccines12060590.
4. Carlson KB, Dilley A, O'Grady T, Johnson JA, Lopman B, Viscidi E. A narrative review of norovirus epidemiology, biology, and challenges to vaccine development. NPJ Vaccines. 2024;9(1):94. doi:10.1038/s41541-024-00884-2.
5. Kendra JA, Tohma K, Parra GL. Global and regional circulation trends of norovirus genotypes and recombinants, 1995-2019: a comprehensive review of sequences from public databases. Rev Med Virol. 2022;32(5):e2354. doi:10.1002/rmv.2354.
6. Ge Y, Billings WZ, Opekun A, Estes M, Graham D, Leon J, et al. Effect of Norovirus Inoculum Dose on Virus Kinetics, Shedding, and Symptoms. Emerg Infect Dis. 2023;29(7):1349-56. doi:10.3201/eid2907.230117.
7. Mans J. Norovirus Infections and Disease in Lower-MiddleandLow-Income Countries, 1997-2018. Viruses. 2019;11(4):341. doi:10.3390/v11040341.
8. Lopman BA, Steele D, Kirkwood CD, Parashar UD. The Vast and Varied Global Burden of Norovirus: Prospects for Prevention and Control. PLoS Med. 2016;13(4):e1001999.
doi:10.1371/journal.pmed.1001999.
9. Vesikari T, Saez-Llorens X, Blazevic V, Lopez P, Lopez E, Masuda T, et al. Immunogenicity of a bivalent virus-like particle norovirus vaccine in children from 1 to 8 years of age: A phase 2 randomized, double-blind study. Vaccine. 2022;40(26):3588-96. doi:10.1016/j.vaccine.2022.04.089.
10. Mikounou Louya V, Nguekeng Tsague B, Ntoumi F, Vouvoungui C, Kobawila SC. High prevalence of norovirus and rotavirus co-infection in children with acute gastroenteritis hospitalised in Brazzaville, Republic of Congo. Trop Med Int Health. 2019;24(12):1427-33. doi:10.1111/tmi.13317.
11. Munjita SM. Current Status of Norovirus Infections in Children in Sub-Saharan Africa. J Trop Med. 2015;2015:309648. doi: 10.1155/2015/309648.
12. Mugyia AE, Ndze VN, Akoachere JTK, Browne H, Boula A, Ndombo PK, et al. Molecular epidemiology of noroviruses in children under 5 years of age with acute gastroenteritis in Yaoundé, Cameroon. J Med Virol. 2019;91(5):738-43. doi: 10.1002/jmv.25380.
13. Ayukekbong JA, Fobisong C, Tah F, Lindh M, Nkuo-Akenji T, Bergström T. Pattern of circulation of norovirus GII strains during natural infection. J Clin Microbiol. 2014;52(12):4253-9. doi: 10.1128/JCM.01896-14.
14. Ndjangangoye NK, Lekana-Douki SE, Oyegue-Liabagui SL, Kouna LC, Ndong Ndong KA, Onanga R, et al. Molecular Prevalence of Diarrheal Pathogens in Children with Acute Diarrhea in Southeastern Gabon. Am J Trop Med Hyg. 2023;108(4):829-36. doi: 10.4269/ajtmh.22-0378.
15. Manouana GP, Byrne N, Mbong Ngwese M, Nguema Moure A, Hofmann P, Bingoulou Matsougou G, et al. Prevalence of Pathogens in Young Children Presenting to Hospital with Diarrhea from Lambarche, Gabon. Am J Trop Med Hyg. 2021;105(1):254-60. doi: 10.4269/ajtmh.20-1290.
16. Breurce S, Vanel N, Bata P, Chartier L, Farra A, Favennec L, et al. Etiology and Epidemiology of Diarrhea in Hospitalized Children from Low Income Country: A Matched Case-Control Study in Central African Republic. PLoS Negl Trop Dis. 2016;10(1):e0004283. doi: 10.1371/journal.pntd.0004283.
17. Watter-Grillot S, Boni M, Tong C, Renoult PA, Fournier A, Joie L, et al. Challenging Investigation of a Norovirus Foodborne Disease Outbreak During a Military Deployment in Central African Republic. Food Environ Virol. 2017;9(4):498-501. doi: 10.1007/s12560-017-9312-6.
18. Esteves A, Nordgren J, Tavares C, Fortes F, Dimbu R, Saraiva N, et al. Genetic diversity of norovirus in children under 5 years of age with acute gastroenteritis from Angola. Epidemiol Infect. 2018;146(5):551–7. doi: 10.1017/S0950268818000377.
19. Arovolo KO, Ayolabi CI, Adeleye IA, Lapinski BA, Santos JS, Raboni SM. Genetic Diversity of Norovirus in Children with Acute Gastroenteritis in Southwest Nigeria, 2015-2017. Viruses. 2023;15(3):644. doi: 10.3390/v15030644.
20. Lartey BL, Quaye O, Damanka SA, Agbemabiese CA, Armachie J, Dennis FE, et al. Understanding Pediatric Norovirus Epidemiology: A Decade of Study among Ghanaian Children. Viruses. 2020;12(11):1321. doi: 10.3390/v12111321.
21. Afework DT, Shumie MK, Endalew GF, Adugna AG, Tarekegn BG. Pooled prevalence and genetic diversity of norovirus in Africa: a systematic review and meta-analysis. Virol J. 2022;19(1):115. doi: 10.1186/s12985-022-01835-w.
22. Kuan T, Traore AN, Akapovi M, Ouedraogo N, Ouoba JB, Roques P, et al. Geographical distribution of enteric pathogenic viruses in Burkina Faso: a systematic review and meta-analysis. BMC Infect Dis. 2024;24:756. doi:10.1186/s12879-024-09668-4.
23. Ronneild Y, Bonkoungou IJO, Ouedraogo N, Barro N, Svensson L, Nordgren J. Norovirus and rotavirus in children hospitalised with diarrhoea after rotavirus vaccine introduction in Burkina Faso. Epidemiol Infect. 2020;148:e245. doi:10.1017/S0950268820002320.
24. Kebe O, Fernandez-Garcia MD, Zinsou BE, Diop A, Fall A, Ndiaye N, et al. Prevalence and genetic characterization of noroviruses in children with acute gastroenteritis in Senegal, 2007-2010. J Med Virol. 2022;94(6):2640-4. doi:10.1002/jmv.27496.
25. Khumela R, Kabue JP, Moraes MTB, Traore AN, Potgieter N. Prevalence of Human Norovirus GIL4 Sydney 2012 [P31] between 2019 and 2021 among Young Children from Rural Communities in South Africa. Viruses. 2023;15(8):1682. doi:10.3390/v15081682.
26. Hungerford D, Jere KC, Bar-Zeev N, Harris JP, Cunliffe NA, Iturriza-Gómara M. Epidemiology and genotype diversity of norovirus infections among children

aged <5 years following rotavirus vaccine introduction in Blantyre, Malawi. J Clin Virol. 2020;123:104248. doi:10.1016/j.jcv.2019.104248.
27. Trainor E, Lopman B, Iturriza-Gomara M, Dove W, Ngwira B, Nakagomi O, et al. Detection and molecular characterisation of noroviruses in hospitalised children in Malawi, 1997-2007. J Med Virol. 2013;85(7):1299-306. doi:10.1002/jmv.23589.
28. Chiladie JJ, Munlela B, Mans J, Mabasa VV, Marques S, Bauhofer AFL, et al. Norovirus Genetic Diversity in Children under Five Years Old with Acute Diarrhea in Mozambique (2014–2015). Viruses. 2022;14(9):2001. doi:10.3390/v14092001.
29. Makhaola K, Moyo S, Lechille K, Goldfarb DM, Kebaabetswe LP. Genetic and epidemiological analysis of norovirus from children with gastroenteritis in Botswana, 2013-2015. BMC Infect Dis. 2018;18(1):246. doi:10.1186/s12879-018-3157-y.
30. Makhaola K, Moyo S, Kebaabetswe LP. Next generation sequencing of near-full length genome of norovirus GIL4 from Botswana. Virus Res. 2021;302:198491. doi:10.1016/j.virusres.2021.198491.
31. Howard LM, Mwape I, Siwingwa M, Simuyandi M, Guffey MB, Stringer JS, et al. Norovirus infections in young children in Lusaka Province, Zambia: clinical characteristics and molecular epidemiology. BMC Infect Dis. 2017;17(1):92. doi:10.1186/s12879-017-2206-2.
32. Papaventsis DC, Dove W, Cunliffe NA, Nakagomi O, Combe P, Grosjean P, Hart CA. Norovirus infection in children with acute gastroenteritis, Madagascar, 2004-2005. Emerg Infect Dis. 2007;13(6):908-11. doi:10.3201/eid1306.070215.
33. Randrennanana R, Randrianirina F, Gousseff M, Dubois N, Razafindratsimandresy R, Hariniana ER, Garin B, Randriamanantena A, Rakotonirina HC, Ramparany L, Ramarokoto CE, Rakotomanana F, Ratsitorahina M, Rajatonirina S, Talamnin A, Richard V. Case-control study of the etiology of infant diarrheal disease in 14 districts in Madagascar. PLoS One. 2012;7(9):e44533. doi:10.1371/journal.pone.0044533.
34. Sisay Z, Djikeng A, Berhe N, Belay G, Gebreyes W, Abegaz WE, Njahira MN, Wang QH, Saif LJ. Prevalence and molecular characterization of human noroviruses and sapoviruses in Ethiopia. Arch Virol. 2016;161(8):2169-82. doi:10.1007/s00705-016-2887-7.
35. Wainaina E, Otieno CA, Kamau J, Nyachieo A, Lowther SA. Norovirus infections and knowledge, attitudes and practices in food safety among food handlers in an informal urban settlement, Kenya 2017. BMC Public Health. 2020;20(1):474. doi:10.1186/s12889-020-8401-x.
36. Moyo S, Hanevik K, Blomberg B, Kommedal O, Vainio K, Maselle S, Langeland N. Genetic diversity of norovirus in hospitalised diarrhoeic children and asymptomatic controls in Dar es Salaam, Tanzania. Infect Genet Evol. 2014;26:340-7. doi:10.1016/j.meegid.2014.06.013.
37. Hugho EA, Kumburu HH, Amani NB, Mseche B, Maro A, Ngowi LE, Kyara Y, Kinabo G, Thomas KM, Houpt ER, Liu J, Hald T, Mmbaga BT. Enteric Pathogens Detected in Children under Five Years Old Admitted with Diarrhea in Moshi, Kilimanjaro, Tanzania. Pathogens. 2023;12(4):618. doi:10.3390/pathogens12040618.
38. Tagajdid R, Znady R, Slimani R, Hamou S, Meftah M, Elkochri S, Aabi R, Laraqui A, Elannaz H, Mehichi B, Touil N, Elqatni M, Reggad A, Elkasmi Z, el Hamas, el Youbi A, Driss R, Ennibi K, Amin, I. Gastrointestinal Norovirus Infections at the Mohammed V Military Teaching Hospital, Morocco. J Med Sci. 2024;11(1):12. doi:10.18535/jjmsci/v111.12.01.
39. El Qazoui M, Ounzil H, Baassi L, El Omari N, Sadki K, Amzazi S, Benhafid M, El Aouad R. Rotavirus and norovirus infections among acute gastroenteritis children in Morocco. BMC Infect Dis. 2014;14:300. doi:10.1186/1471-2334-14-300.
40. Kreidieh K, Charide R, Dbaibo G, Melhem NM. The epidemiology of Norovirus in the Middle East and North Africa (MENA) region: a systematic review. Virol J. 2017;14(1):220.doi:10.1186/s12985-017-0877-3.
41. Hassine-Zaafrane M, Sdiri-Loulizi K, Kaplon J, Salem IB, Pothier P, Aouni M, Ambert-Balay K. Prevalence and genetic diversity of norovirus infection in Tunisian children (2007-2010). J Med Virol. 2013;85(6):1100-10. doi:10.1002/jmv.23552.
42. Sdiri-Loulizi K, Gharbi-Khélifi H, de Rougemont A, Chouchane S, Sakly N, Ambert-Balay K, et al. Acute infantile gastroenteritis associated with human enteric viruses in Tunisia. J Clin Microbiol. 2008;46(4):1349-55. doi: 10.1128/JCM.02438-07.
43. Mashaly ME, Alkasaby NM, Bakr A, Zaki MES, Montasser K. Viral pathogens of acute gastroenteritis in Egyptian children: role of the parechovirus. BMC Infect Dis. 2022;22(1):584. doi: 10.1186/s12879-022-07562-5.
44. Kamel AH, Ali MA, El-Nady HG, de Rougemont A, Pothier P, Belliot G. Predominance and circulation of enteric viruses in the region of Greater Cairo, Egypt. J Clin Microbiol. 2009;47(4):1037-45. doi: 10.1128/JCM.01381-08.
45. Mans J, Murray TY, Taylor MB. Novel norovirus recombinants detected in South Africa. Virol J. 2014;11:168. doi: 10.1186/1743-422X-11-168.
46. Mans J, Murray TY, Nadan S, Netshikweta R, Page N.A, Taylor MB. Norovirus diversity in children with gastroenteritis in South Africa from 2009 to 2013: GIL4 variants and recombinant strains predominate. Epidemiol Infect. 2016;144(5):907-16. doi: 10.1017/S0950268815002150.
47. Gelaw A, Pietsch C, Mann P, Liebert UG. Molecular detection and characterisation of sapoviruses and noroviruses in outpatient children with diarrhoea in Northwest Ethiopia. Epidemiol Infect. 2019;147:e218. doi: 10.1017/S0950268819001031.
48. Kiulia NM, Mans J, Mwenda JM, Taylor MB. Norovirus GIL17 predominates in selected surface water sources in Kenya. Food Environ Virol. 2014;6(4):221-31. doi: 10.1007/s12560-014-9160-6.
49. Mans J, Murray TY, Kiulia NM, Mwenda JM, Musoke RN, Taylor MB. Human caliciviruses detected in HIV-

seropositive children in Kenya. J Med Virol. 2014;86(1):75-81. doi: 10.1002/jmv.23787.
50. Cambaza E, Mongo E, Gatambire A, Mateonane E, Chissumba R, Chissaque A, et al. A narrative review on Rotavirus A in Mozambique. Rev Angol Cienc Saude. 2021;2(2):4-9. doi: 10.54283/RACSaude.v2n2.2021.p4-9.
51. Upfold NS, Luke GA, Knox C. Occurrence of Human Enteric Viruses in Water Sources and Shellfish: A Focus on Africa. Food Environ Virol. 2021;13(1):1-31. doi: 10.1007/s12560-020-09456-8.
52. Rouamba SS, Tapsoba F, Kabore B, Soubeiga AP, Bandé M, Kabré E, Savadogo A. Impact of Wastewater Use for Irrigation and Contamination of Lettuce by Enteric Viruses: Case of Ouagadougou Market Gardening Sites, Burkina Faso. Food Environ Virol. 2024;17(1):2. doi: 10.1007/s12560-024-09621-3.
53. Tubatsi G, Kebaabetswe LP. Detection of Enteric Viruses from Wastewater and River Water in Botswana. Food Environ Virol. 2022;14(2):157-169. doi: 10.1007/s12560-022-09513-4.
54. Atsama-Amougou M, Djomsi-Meta D, Ngamaleu MR, Simo FBN, Saha CL, Lamare-Boutgam N, Godwe C, Maidadi-Foudi M, Tongo M, Mpabuka E, Kouanfack C, Ayouba A. First molecular detection of five gastroenteritis viruses in untreated wastewater and impact of seasonal change on their distribution in Cameroon. One Health. 2025;21:101110. doi: 10.1016/j.onehlt.2025.101110.
55. Page NA, Groome MJ, Nadan S, Netshikweta R, Keddy KH, Poonsamy B, Moyes J, Walaza S, Kahn K, Madhi SA, Taylor MB, Mans J, Cohen C. Norovirus epidemiology in South African children <5 years hospitalised for diarrhoeal illness between 2009 and 2013. Epidemiol Infect. 2017;145(9):1942-1952. doi: 10.1017/S0950268817000668.
56. Mans J, Armah GE, Steele AD, Taylor MB. Norovirus Epidemiology in Africa: A Review. PLoS One. 2016;11(4):e0146280. doi: 10.1371/journal.pone.0146280.
57. Nguyen KH, Operario DJ, Nyathi ME, Hill CL, Smith JA, Guerrant RL, Samie A, Dillingham RA, Bessong PO, Rogawski McQuade ET. Seasonality of drinking water sources and the impact of drinking water source on enteric infections among children in Limpopo, South Africa. Int J Hyg Environ Health. 2021;231:113640. doi:10.1016/j.ijheh.2020.113640.
58. Zormati S, Kallel I, Sellami H, Goloura R. Influence of environmental and seasonal factors on microbial contamination levels in clam production areas in southern Tunisia: Escherichia coli, Salmonella spp., hepatitis A virus and norovirus. Rev Sci Tech. 2018;37(3):1049-1070. doi: 10.20506/rst.37.3.2906.
59. Shaheen MNF, Elmahdy EM, Mahmoud LHI, Hammad IA, Soliman ERS. Quantitative RT-PCR detection of human noroviruses and hepatitis A virus in fresh produce and surface water used for irrigation in the Mansoura and Giza regions, Egypt. Environ Sci Pollut Res Int. 2022;29(19):28139-28148. doi: 10.1007/s11356-021-18412-3.
60. Mikounou Louya V, Vouvoungui C, Koukouikila-Koussounda F, Veas F, Kobawila SC, Ntoumi F. Molecular characterization of norovirus infection responsible for acute diarrhea in Congolese hospitalized children under five years old in Brazzaville, Republic of Congo. Int J Infect Dis. 2019;88:41-48. doi: 10.1016/j.ijid.2019.07.034.
61. Nishangase SN, Ghuman S, Haffejee F. Diarrhoeal prevalence and handwashing practices of children attending early childhood development centres in KwaZulu-Natal, South Africa. Health SA. 2022;27:1923. doi: 10.4102/hsag.v27i0.1923.
62. Bauleth MF, Mitonga HK, Pinehas LN. Epidemiology and factors associated with diarrhoea among children under five years of age in the Engela District in the Ohangwena Region, Namibia. Afr J Prim Health Care Fam Med. 2020 Aug 24;12(1):e1-e11. doi: 10.4102/phcfm.v12i1.2361. Erratum in: Afr J Prim Health Care Fam Med. 2024 Jan 24;16(1):4349. doi: 10.4102/phcfm.v16i1.4349.
63. LaPolt, LaPolt D, Smith S, Gazu L, et al. Environmental risk factors associated with community diarrheal diseases in Ethiopia. BMC Public Health. 2025;25:1959. doi:10.1186/s12889-025-23086-4.
64. Nalugya A, Ssempebwa JC, Muleme J, Wafula ST, Tamale BN, Tigaiza A, Nakalembe D, Kansiime WK, Isunju JB, Ssekamatte T, Mugambe RK. Exposure behaviour to Escherichia coli among households in Imvepi refugee settlement, Terego district Uganda. BMC Public Health. 2024 Jul 30;24(1):2041. doi: 10.1186/s12889-024-19525-3. PMID: 39080627; PMCID: PMC11290189.
65. El Moqri N, El Mellouli F, Hassou N, Benhafid M, Abouchoaib N, Etahiri S. Norovirus Detection at Oualidia Lagoon, a Moroccan Shellfish Harvesting Area, by Reverse Transcription PCR Analysis. Food Environ Virol. 2019 Sep;11(3):268-273. doi: 10.1007/s12560-019-09386-0. Epub 2019 Apr 13. PMID: 30982112.
66. Omore R, Powell H, Sow SO, Hossain MJ, Ogwel B, Doh S, Ochieng JB, Jones JCM, Zaman SMA, Awuor AO, et al. Norovirus disease among children <5 years in 3 sub-Saharan African countries: findings from the Vaccine Impact on Diarrhea in Africa (VIDA) study, 2015–2018. Clin Infect Dis. 2023;76(Suppl 1):S114–S122. doi:10.1093/cid/ciac967.
67. Ayukekbong JA, Andersson ME, Vansarla G, Tah F, Nkuo-Akenji T, Lindh M, Bergström T. Monitoring of seasonality of norovirus and other enteric viruses in Cameroon by real-time PCR: an exploratory study. Epidemiol Infect. 2014;142(7):1393-402. doi: 10.1017/S095026881300232X.
68. Mabasa VV, van Zyl WB, Ismail A, Allam M, Taylor MB, Mans J. Multiple Novel Human Norovirus Recombinants Identified in Wastewater in Pretoria, South Africa by Next-Generation Sequencing. Viruses. 2022 Dec 7;14(12):2732. doi: 10.3390/v14122732.
69. Adane M, Mengistie B, Medhin G, Kloos H, Mulat W. Piped water supply interruptions and acute diarrhea among under-five children in Addis Ababa slums,

Ethiopia: a matched case-control study. PLoS One. 2017;12(7):e0181516.doi:10.1371/journal.pone.0181516.

70. Das R, Hossain MN, Levine MM, Kotloff KL, Nasrin D, Hossain MJ, Omore R, Sur D, Ahmed T, Breiman RF, Faruque ASG, Freeman MC. Impact of water, sanitation, and hygiene indicators on enteric viral pathogens among under-5 children in low resource settings. Sci Total Environ. 2025;961:178401. doi:10.1016/j.scitotenv.2025.178401.

71. Okesanya OJ, Eshun G, Ukoaka BM, et al. Water, sanitation, and hygiene (WASH) practices in Africa: exploring the effects on public health and sustainable development plans. Trop Med Health. 2024;52:68. doi:10.1186/s41182-024-00614-3.

72. Dang W, Xu L, Ma B, Chen S, Yin Y, Chang KO, Peppelenbosch MP, Pan Q. Nitazoxanide Inhibits Human Norovirus Replication and Synergizes with Ribavirin by Activation of Cellular Antiviral Response. Antimicrob Agents Chemother. 2018;62(11):e00707-18. doi: 10.1128/AAC.00707-18.

73. Rossignol JF, El-Gohary YM. Nitazoxanide in the treatment of viral gastroenteritis: a randomized double-blind placebo-controlled clinical trial. Aliment Pharmacol Ther. 2006;24(10):1423-30. doi: 10.1111/j.1365-2036.2006.03128.x.

74. Doh H, Lee C, Kim NY, Park YY, Kim EJ, Choi C, Eyun SI. Genomic diversity and comparative phylogenomic analysis of genus Norovirus. Sci Rep. 2025;15(1):5412. doi: 10.1038/s41598-025-87719-9.

75. Tan M. Norovirus Vaccines: Current Clinical Development and Challenges. Pathogens. 2021;10(12):1641. doi: 10.3390/pathogens10121641.