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REVIEW **Open Access**

Viral meningitis in Sub-Saharan Africa: trends in prevalence, etiologies, and diagnostic approaches

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Abstract

Viral meningitis is a significant yet often underreported public health concern in Sub-Saharan Africa (SSA), where diagnostic limitations and surveillance gaps hinder accurate case detection. This systematic review examines epidemiological trends, etiologies, and laboratory diagnostic approaches to viral meningitis across SSA from 1987 to 2024. This data reveal that the prevalence of viral meningitis has shown an overall increasing trend, with a considerable year-to-year variability influenced by seasonal outbreaks, improved diagnostic methods, and enhanced surveillance efforts. Human enteroviruses (HEVs) were the most frequently identified causative agents, accounting for 1,164 confirmed cases, followed by the herpesvirus family, including Epstein-Barr virus (EBV) and cytomegalovirus (CMV). Other detected viral pathogens include mumps virus, adenoviruses, coxsackievirus, and arboviruses such as dengue virus. The shift from traditional viral cultures to polymerase chain reaction (PCR) and multiplex PCR has significantly improved the case detection. Despite these advancements, substantial gaps remain in diagnostic accessibility, surveillance systems, and less research focus on viral meningitis in SSA. Addressing these challenges through improved surveillance, enhanced diagnostic capacity, and targeted public health strategies is crucial for mitigating the burden of viral meningitis in the region.

Key findings

- The prevalence of viral meningitis in SSA has shown an increasing trend, driven by improved diagnostic methods and seasonal outbreaks.
- Human enteroviruses (HEVs) are the predominant causative agents, followed by herpesviruses (EBV, CMV) and mumps virus.
- The shift from traditional viral cultures to PCR and multiplex PCR has significantly improved case detection, though diagnostic accessibility remains limited in many regions.
- There is a critical need for enhanced surveillance, diagnostic capacity, and public health strategies to address the burden of viral meningitis in SSA.

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Key bullet points

Viral meningitis is a significant yet underreported public health issue in Sub-Saharan Africa (SSA), where diagnostic limitations and surveillance gaps hinder accurate case detection. Thus, this systematic review examines the epidemiological trends, etiologies, and diagnostic approaches for viral meningitis in SSA from 1987 to 2024, aiming to highlight the prevalence, causative agents, and advancements in laboratory diagnostics.

Keywords Epidemiology, Viral meningitis, Enteroviruses, Diagnostic methods, Sub-Saharan Africa

Introduction

Meningitis remains a significant public health concern in Africa, particularly in Sub-Saharan Africa (SSA), with recurrent outbreaks, and high morbidity and mortality rates [1]. The region, known as the meningitis belt, stretched across Senegal from the west to Ethiopia in the east, is hit with seasonal epidemics of meningitis, predominantly caused by bacterial [1], and viral pathogens [2]. A significant progress has been made in reducing the meningitis-associated mortality, especially bacterial meningitis, over the past three decades [3], including the MenAfriVac [4]. The surveillance, outbreak investigations, and clinical management of meningitis rely heavily on laboratory confirmation of meningitis-associated bacterial pathogens. However, viral meningitis is often underreported in SSA due to limited diagnostic capacity and inadequate surveillance infrastructure [5]. Despite receiving less attention, viral meningitis has a high associated mortality rate, reaching up to 38% [6], and up to 54% in cases with HIVco-infection [7]. Given the high prevalence of HIV in SSA, it is crucial to consider its role in increasing susceptibility to viral meningitis [8].

The human enteroviruses (HEVs), herpes viruses (HHV), arboviruses (mainly the dengue virus), and the mumps virus are among the common viral etiologies of meningitis, posing significant diagnostic and clinical challenges in SSA [9–12]. Furthermore, environmental and socio-economic factors, including climate change, population displacement, and healthcare accessibility, continue to influence the epidemiology of viral meningitis in the region [13, 14].

The advancements in the laboratory diagnostics, particularly the shift from time-consuming viral cultures [15, 16] to polymerase chain reaction (PCR) [12], and multiplex PCR [17–19], have revolutionized viral meningitis detection. Multiplex PCR enables simultaneous, highly sensitive, and specific pathogen detection, reducing turnaround times and improving detection rates allowing timely interventions, better outbreak management, and enhanced public health strategies to combat viral meningitis in Africa and beyond [20].

We therefore present this review to explore the epidemiological trends of viral meningitis in SSA, as reflected in the available literatures [4, 6, 7, 9–12, 15–19, 21–29], analyzing its prevalence, etiologies, and laboratory diagnostic approaches over years. Understanding these aspects is crucial for guiding public health interventions and enhancing meningitis surveillance and response strategies in the region [19, 22, 24].

Methods

This review synthesizes evidence on the epidemiology, etiologies, and diagnostic approaches for viral meningitis in SSA. All African countries were included except Algeria, Egypt, Morocco, and Tunisia, as per The World Academy of Sciences (TWAS) classification [30]. A comprehensive and systematic search was conducted using PubMed, Science Direct, Web of science electronic data bases, and Google Scholar search engines, with key terms including 'meningitis,' 'viral meningitis,' and individual SSA country names.

The search, unrestricted by publication date, prioritized studies on prevalence, causative agents, and laboratory diagnostics. Primary research studies were included, and data were extracted and organized into thematic categories using Microsoft Excel. Findings were narratively synthesized to provide an overview on the prevalence of viral meningitis in SSA, highlighting the etiologies by countries, and advancements in laboratory diagnosis.

Besides the narrative synthesis, this review also used visual aids such as tables, bar charts, and line graphs to summarize key data points and trends. These visualizations help highlight patterns, relationships, and variations in the data, making complex information more accessible. Additionally, R^2 values are included in the graphs where applicable, providing statistical evidence of the strength and direction of correlations over time.

Considering the broadness of the topic, flexibility, and contextual richness, and the heterogeneity of studies, (Zero prevalence in Guinea [26] vs.52 to 56.7% in South Africa [17]and Malawi [7]), and the use of different diagnostic approaches; we prefer a systematic narrative review over meta-analysis [31]. Our review interest is to provide highlight on the prevalence and patterns of viral meningitis over time, commonest etiologies by country, and conceive laboratory advancements and focus of researches in the resources constrained region, SSA.

17 of the 21 included studies focused on children. The above table shows the patterns where HEVs target children, and the pediatric focus of most research with a possibility underestimation of the adult burden in high-HIV settings.

Results

The figure likely maps out the distribution of viral meningitis cases across different SSA countries, and the variation in cases among countries could highlight disparities in healthcare accessibility, diagnostic capacities, and research priorities. We believe that the regions with fewer reported cases might not necessarily have lower disease burdens but rather insufficient diagnostic or and reporting mechanisms (Fig. 1).

The below figure is likely to display the increasing trend of detection and reporting of viral meningitis cases over time. R-squared value (R^2) is used to see how well the data fits a regression model. A higher R^2 value (closer to 1) would indicate a strong correlation between improved diagnostic capacity and increased case detection (A&B), while a lower R^2 suggests more variability due to external factors like inconsistent surveillance or underreporting (C). Overall, we can appreciate the rise in case identification due to improvements in diagnostic techniques, particularly the adoption of PCR and multiplex PCR in recent years (Fig. 2).

Overall, there were 1,794 viral meningitis cases reported in SSA, with HEV has been the dominant viral pathogen with 1,164 cases (65%), highlighting its significant burden in the region, followed by HHV family with 353 cases (19.7%), 161 EBV, 57 CMV, and 51 HHV6, and Mumps virus with 136 cases (7.6%). Other notable viruses also reported in the region, including Adenovirus and Coxsackievirus (each with 42 cases), and Rabies virus with 14 cases. The less frequent but important pathogens include the echovirus (10 cases) and the arbovirus, dengue (9 cases). This emphasizes the diversity of viral

Table 1 Characteristics of reviewed studies: prevalence, etiology, and laboratory diagnosis of viral meningitis in SSA, 1987–2024

Author	Country	Year published	Prevalence % (*n*/*N*)	Etiologies	Lab diagnosis	Age group
Donald et al. [15]	South Africa	1987	8.8(108/1223)	Not specified	viral culture	children /< 13 years
Donald et al. [16]	South Africa	1996	13.5(395/2920)	HEVs, Mumps, Coxsackie, Echovirus, VZV, CMV, Herpesvirus hominis (HVH)	viral culture	children /< 13 years
Pelkonen et al. [19]	Angola	2012	3(4/142)	HEVs, and Rhinovirus	CSF PCR	Children
Kelly et al. [7]	Malawi	2012	56.7(99/188)	HSV1, EBV, CMV	CSF PCR	Adults
Pelkonen et al. [23]	Angola	2013	26(10/38)	VZV, EBV, HHV7, HHV6A, HHV6B, CMV	PCR	Children
Benjamin et al. [21]	Malawi	2013	32(17/53)	HSV1, EBV, CMV	CSF PCR	Adults
Mallewa et al. [22]	Malawi	2013	26(133/513)	Adenovirus, CMV, HEV, HSV1, HHV6, Mumps, Rabies, EBV, Parvovirus, and HHV 7, and others	CSF PCR	Children/2 months-15 years
Laman et al. [24]	Guinea	2014	14(42/300)	HEV, HSV1, CMV, HHV6, HHV7, Dengue	nested PCR	Children/2 months – 10 years
Thinyane et al. [6]	Lesotho	2015	18(10/56)	negative for Gram stain, culture, and antigenic tests	lymphocyte predominance	Adults
Khumalo et al. [19]	South Africa	2017	32.2(94/292)	HEVs and Mumps	multiplex RT- PCR	Children/2 months-12 years
Page et al. [25]	Uganda	2017	5.9(27/459)	HHV6,VZV, Mumps, CMV, HEV	CSF PCR	Children/2 months-12 years
Barnes et al. [18]	Ethiopia	2018	5.6(12/213)	CMV, HEV, HSV1,HSV2, HHV6, Parechovirus, VZV	Multiplex PCR	All
Adjei et al. [26]	Ghana	2018	0(0/80)	HEVs, Mumps, HSV checked	Real-time PCR	Adults
Kwambana et al. [4]	West Africa #	2020	5.6(40/711)	Parvovirus19, Dengue, CMV, EBV, HEV, HHV6, Mumps	TaqMan Array Card/RT PCR	Children /<5 years
Geteneh et al. [10]	Ethiopia	2021	12.8(11/86)	HEV	conventional RT-PCR	All
Wami et al. [11]	Ethiopia	2021	26.7(39/146)	HEV	conventional RT-PCR	All
Nkosi et al.[27]	South Africa	2021	21.2(742/3497)	HEVs	CSF PCR	All
Fourgeaud et al. [12]	Comoros	2022	11.5(14/122)	HEV, and Parechovirus	CSF PCR	Children and adults
Abdelrahim et al. [28], [29]	Sudan	2022	3.4(17/503)	HSV1, Non-polio HEV, HHV6	CSF real-time PCR	Children /<15 years
Moleleki et al. [17]	South Africa	2024	52(98/188)	EBV, HHV7, HSV1, HSV2, HEV	multiplex PCR	All

#Senegal, Ghana, Togo, Nigeria, and Niger

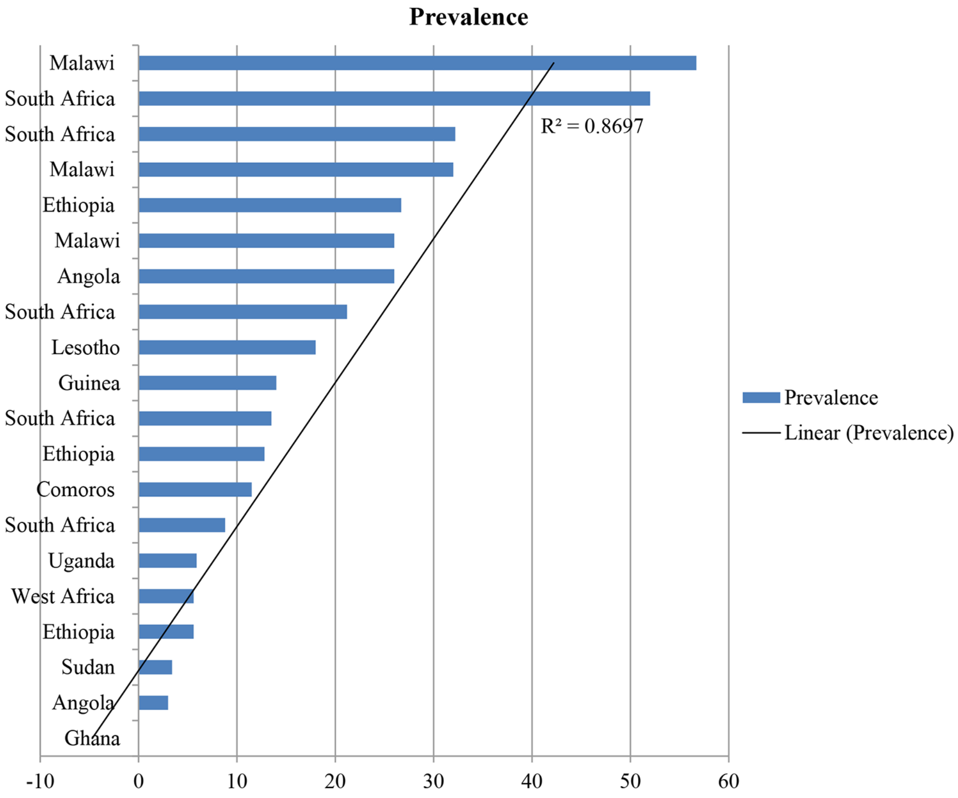

Fig. 1 Country-specific distribution of viral meningitis cases in SSA

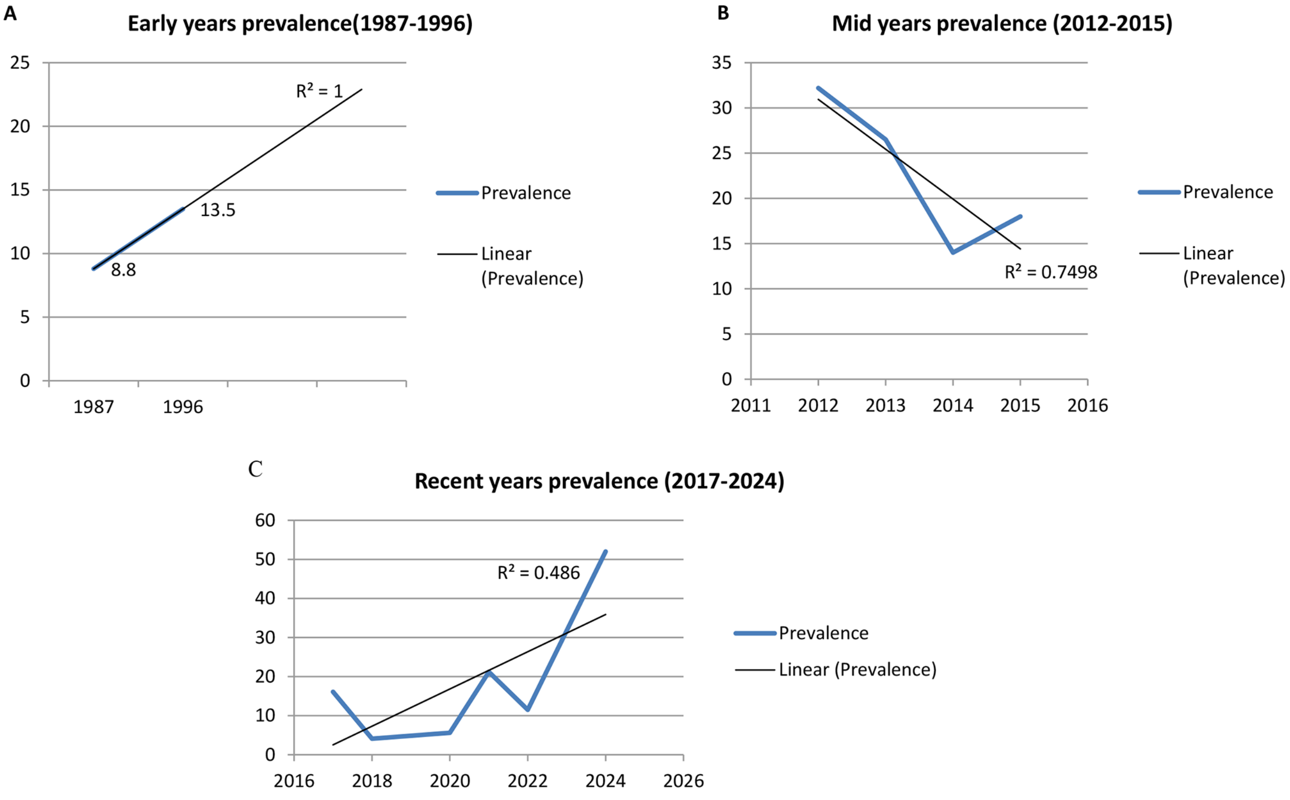

Fig. 2 Trend of viral meningitis by years of publications, 1987–2024

Table 2 Country–wise etiologies of viral meningitis

Country	Confirmed cases	Etiologies
Angola	14	VZV($n=1$), EBV($n=5$), HHV7($n=3$), HHV6($n=2$), CMV($n=2$) HEV($n=3$), and rhinovirus($n=1$)
Comoros	14	HEV($n=13$), and Parechovirus($n=1$)
Ethiopia	62	HEV($=52$), HHV6($n=5$), HSV1($n=3$), HSV2($n=1$), VZV($n=1$)
Guinea	42	CMV($n=16$), HHV7($n=10$), HHV6 ($n=8$), Dengue ($n=3$), HEV($n=1$),HSV1 ($n=1$), HH6/HSV1 ($=n=1$), HHV7/HSV1 ($n=1$), HHV7/CMV($n=1$)
Malawi	249	EBV($n=103$), Adenovirus($n=42$), Mumps($n=29$), CMV($n=25$), Rabies ($n=14$), HSV1($n=13$), HEV($n=8$), HHV6($n=8$), Parvovirus($n=5$) and others($n=2$)
South Africa	1,329	HEV($n=1081$), Mumps ($n=101$), EBV(49), Coxsackie ($n=42$), HHV7($n=22$), HSV1(13), Echovirus($n=10$), HSV2($n=8$) and others($n=3$)
Sudan	17	HHV6 ($n=13$), HSV1 ($n=2$), Non-polio HEV ($n=2$)
Uganda	27	HHV6($n=11$), CMV($n=9$), mumps($n=4$), VZV($n=2$), HEV($n=1$)
West Africa	40	Parvovirus19 ($n=12$), Dengue($n=6$), CMV($n=5$), EBV($n=4$), HEV($n=3$), HHV6 ($n=3$), Mumps ($n=2$), and HIV($n=5$)
Total confirmed isolates in SSA	1,794	HEV($n=1,164$), HHV ($n=353$), EBV ($n=161$), CMV($n=57$), HHV6 ($n=51$), HHV7($n=37$), HSV1($n=34$), HSV2($n=9$), and 4 VZV($n=4$), Mumps($n=136$), Adenovirus($n=42$), Coxsackievirus($n=42$), Parvovirus($n=17$), Rabies($n=14$), Echovirus($n=10$), and Dengue($n=9$)

The HEV accounts for nearly of all isolates, followed by HHV family 19.7% ($n=353/1,794$), and mumps 7.6% ($n=136/1,794$)

etiologies, and the need for targeted prevention and control measures (Table 2).

Discussion

There has been variability in the prevalence and etiologies of viral meningitis across SSA. The high prevalence observed in South Africa, Malawi, Ethiopia, and Guinea may be influenced not only by epidemiological and environmental factors but also by the advancements in the diagnostic capacity, and research priorities in each country [32]. South Africa's high detection rate (1,329/1,794 cases) may aligns with its advancement in laboratory diagnosis from viral culture [16] to multiplex PCR [17], and it might be associated with their surveillance system(the Group for Enteric, Respiratory and Meningeal Disease Surveillance in South Africa (GERMS-SA [33]). Malawi's diverse infections (EBV, adenovirus, rabies) could be a suggestive evidence of its expanding surveillance, and implementation of zoonotic research [34, 35]. To the best of our knowledge; Ethiopia is not known for having a dedicated virology laboratory, but the detection and HEV dominance (52/62 cases) reflect its emerging focus on and recognition of viral meningitis [11, 18].

This review also highlights the considerable emergence of HEVs as the dominant etiologic agents of viral meningitis across multiple studies [11, 16, 27]. The herpes virus family, particularly EBV [7, 17] and CMV [7, 22, 24], follows closely, with mumps virus [16] also contributing significantly. The less frequently occurred dengue could be a critical issue in SSA due to climate change favoring mosquito spread [36], rapid urbanization, limited healthcare infrastructure, low population immunity, and the region's existing burden of other mosquito-borne diseases [13, 36]. However, the current etiological profiles of viral meningitis in SSA underestimate arboviral causes, as most diagnostic algorithms omit these endemic pathogens, with only two exceptions [4, 24]. Thus, our review findings stress the critical need for enhanced laboratory diagnostics to improve case identification and public health responses. The age stratification revealed children (<15 years) dominated enterovirus (HEV) cases (e.g., 1081/1,329 cases in South Africa [16, 17, 19, 27], and 52/62 pediatric cases in Ethiopia [10, 11, 18]) and HSV-6 detection (13/17 cases in Sudan [28, 29]), while adults showed higher HIV-associated mortality (54% vs. 38%)^{7} and EBV predominance (103/249 cases in Malawi) [7, 21].

The transition from viral culture methods [15, 16] to PCR-based techniques, including multiplex PCR [17, 19], has revolutionized the detection of viral pathogens. While PCR enhances sensitivity and specificity compared to cultures, its impact on clinical outcomes depends on timely treatment initiation [37, 38], and its accessibility remains limited in low-resource settings could obscured the true epidemiological scale [39] of viral meningitis. Furthermore, while PCR represents a major advancement, it remains unable to detect novel or unexpected viruses; a gap that could be addressed by Next-Generation Sequencing (NGS). Despite its potential to revolutionize pathogen discovery, NGS remains critically underutilized in SSA due to cost and infrastructure barriers, highlighting an urgent need for investment in NGS capacity to address remaining diagnostic gaps in viral meningitis surveillance [40, 41].

Regardless of the advancement in laboratory diagnosis, Africa still lags behind toward establishing an integrated, comprehensive, and sustainable surveillance [42]. In 2014, the MenAfriNet consortium effectively implemented case-based meningitis surveillance across five countries in the meningitis belt: Burkina Faso, Chad, Mali, Niger, and Togo [43], and this initiative has to be more inclusive for other SSA countries, and has to take lessons from pandemics like COVID-19 [39, 43]. Despite the progress, we believe there are still substantial research gaps in understanding the full spectrum of viral meningitis in SSA. These gaps include limited data on disease burden, underutilization of advanced diagnostics [5, 6], and insufficient surveillance system [42]. Existing frameworks, such as the WHO's Global Meningitis Initiative and the MenAfriNet consortium, is known to successfully strengthened bacterial meningitis surveillance [45, 46] but remain limited in monitoring viral pathogens. Thus, it is very crucial to expand these programs to include viral meningitis. Therefore, future studies should focus on expanding molecular diagnostic capabilities, and strengthening surveillance networks.

While some studies [17, 18] used advanced molecular methods like multiplex PCR for multiple pathogens detection, none implemented (NGS or Sanger) or a culture to sequencing cascade. The reliance on standalone methods (viral culture, PCR, or multiplex PCR) may underscore a critical gap in confirmatory diagnostics. Thus future studies should integrate stepwise diagnostic workflows (culture → PCR → sequencing) to improve unexpected pathogen detection and surveillance in Sub-Saharan Africa.

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Author contributions
AG conceptualized, material preparation, data analysis, methodology, and formal analysis and wrote the main manuscript; MK, ET, AT, YG reviewed and edited the manuscript. SB reviewed and edited the manuscript; and MAR reviewed and edited the manuscript, data curation, and supervision. All the authors read and approved the final manuscript.

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Data availability
Data is provided within the manuscript.

Declarations

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Not applicable.

Consent for publication
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Competing interests
The authors declare no competing interests.

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