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A scoping review of the prevalence of Rift Valley fever among livestock in East Africa from 1931 to 2025

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Table 7 to 9 are available in the Supplementary Files section.

A scoping review of the prevalence of Rift Valley fever among livestock in East Africa from 1931 to 2025

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Abstract

Rift Valley fever (RVF) is a notifiable, viral zoonotic disease affecting livestock and humans, with significant health and socio-economic effects in East Africa. First isolated in Kenya in 1931, RVF has become endemic in several African countries, causing recurring epidemics with high animal and human mortalities. Despite this, knowledge gaps persist on the prevalence, distribution, and diagnostic tests in the East African Community (EAC). This review synthesizes literature from 1931 to 2025, evaluating prevalence, diagnostic diversity, and future research needs for RVF.

Following PRISMA guidelines, a comprehensive literature search across PubMed, DiscoverEd, Google Scholar, and Web of Science identified articles from 1931 to 2025. Covidence was used to screen, identify duplicates, and extract relevant information. Extracted data included study year, livestock species, diagnostic tests, study period, study design, and prevalence estimates. Spatial-temporal distribution was visualized using QGIS. Pooled and median prevalence were calculated using R and Microsoft Excel.

Fifty-five eligible articles comprising 134 species-specific prevalence and 91 diagnostic test-specific studies were included. Studies focused on cattle, goats, sheep, camels, and some unspecified/mixed species. Overall species pooled prevalence was 11.0%. The highest pooled prevalence was recorded in camels (17.2%), followed by cattle (15.4%), sheep (10.1%), unidentified species/animals (8.5%), and goats (7.8%). Most studies were cross-sectional and carried out during the IEP period. Diagnostic prevalence varied widely, with overall seroprevalence of 9.4% (IgG 11.8%, IgM 3.0%) and molecular prevalence of 3.3%. ELISA, PCR, and virus neutralization tests were the most commonly used. Kenya, Uganda, and Tanzania registered the highest number of studies; Burundi had none.

These findings emphasize RVF's continual threat in the EAC, shaped by ecological conditions, host dynamics, and diagnostic practices that boost RVF vector abundance. The review highlights the need for improved surveillance, all-species-inclusive studies, improved diagnostic capacity, and a one-health approach to controlling and lowering the burden of RVF.

Keywords: Rift Valley Fever (RVF), Prevalence, East Africa, One Health, Scoping Review

1.0 Introduction

Rift Valley fever (RVF) is a viral zoonotic transboundary disease transmitted by arthropods. It is caused by the Rift Valley fever virus (RVFV), a *Phlebovirus* in the family *Phenuiviridae* (1,2). It affects both domestic and wild ruminants, humans, camels, rodents, buffalo, non-human primates, pigs, warthogs, horses, bats, and carnivores. Livestock, particularly sheep, cattle, and goats, play a central role in RVF epidemiology, acting as amplifying hosts during outbreaks(3–5). First recognized in East Africa in the early twentieth century (3), RVF has since emerged as one of the most consequential yet persistently under-addressed diseases affecting livestock-dependent systems. This is evidenced by recurrent epidemics that disrupt human and animal health and food security in Africa and the Arabian Peninsula (4), with the potential to spread to non-endemic areas (6). Despite this geographic expansion and documented impact, its relevance at the human-animal-environment interface remains overlooked.

RVF was first described during an epidemic in Kenya near Lake Naivasha in 1931(7). Since then, RVF outbreaks have recurred across the East African Community(8–14). Shared ecosystems, climate variability, and extensive transboundary livestock movement create conditions conducive for recurrent outbreaks, while animal health governance and surveillance capacity remain uneven across member states. Previous outbreaks in southern and eastern Africa have caused tens of thousands of abrupt livestock deaths and hundreds of thousands of abortions, e.g., between 1950 and 1951, outbreaks in Kenya and South Africa resulted in over 100,000 sheep mortalities and around 500,000 abortions (15). The 2006-2007 outbreak claimed approximately 50,000 animal lives in Tanzania(16). Economic losses attributable to the 2007 RVF outbreak in Kenya and Tanzania were estimated at USD 66 million, reflecting not only animal mortalities but also movement restrictions and trade bans(17,18). The human burden of RVF has similarly been substantial. The largest recorded outbreak occurred in Egypt between 1977 and 1979, resulting in more than 200,000 human infections and 598 deaths(19,20). Subsequent epidemics occurred, e.g., 220 deaths were recorded in Mauritania and Senegal(21), and 478 deaths out of 89,000cases were recorded in eastern Africa(22). In 2008, Sudan recorded 747 human cases and 230 deaths. Since 2016, lesser outbreaks in Niger and eastern Africa have claimed many lives (23).

Despite this well-documented impact, RVF remains a neglected zoonotic disease in Africa. Existing reviews largely synthesise continent-wide evidence or rely on older datasets(24–30), offering limited resolution for regional preparedness and policy decision-making within the EAC. Evidence on RVF prevalence, spatial and temporal distribution, and diagnostic approaches remains fragmented across countries and time periods.

Surveillance systems are frequently fragmented, early warning signals are inconsistently translated into action, and outbreak detection is often delayed, resulting in under-reporting and reactive rather than preventive responses(31). Although RVF is designated a priority emerging pathogen by the World Health Organisation (WHO) (32), listed as a notifiable disease by the World Organisation for Animal Health (WOAH), and classified as a select bioterrorism agent (32,33), its prevention and control efforts remain uneven. Current strategies rely heavily on environmental prediction models (34), movement restrictions (35), and episodic livestock vaccination (36), while persistent gaps in vaccine access, deployment, and sustained coverage limit their effectiveness (36,37). Diagnostic capacity and surveillance infrastructure also vary widely between countries (38), constraining timely detection and coordinated regional response.

The consequences of these evidence gaps extend beyond surveillance failures and affect livestock-dependent communities. Mortality in young livestock can approach 100% while abortion rates exceed 90% during outbreaks, resulting in catastrophic herd losses (39,40). Humans are infected through direct contact or mosquito bites (7,41,42) and are considered dead-end hosts (43). However, case fatality rates can approach 50% in severe cases (3,44), highlighting the virus's capacity to cause substantial morbidity and mortality when outbreaks go undetected or uncontrolled. Beyond the endemic regions, the potential for RVFV introduction into Europe and the Americas remains a growing concern, given the widespread presence of competent mosquito vectors and ongoing climate-driven shifts in vector ecology (45–47).

This review synthesises published evidence from 1931 to 2025 to map RVF prevalence in livestock across the East African Community, characterise spatial and temporal patterns of infection, examine diagnostic methods employed, and identify critical gaps in

surveillance and research. Specifically, we aimed to: (1) determine RVF prevalence and distribution among livestock in East Africa from the literature, and (2) identify gaps and needs in RVF prevalence research for East African livestock. By consolidating nearly, a century of evidence, this study aims to inform risk-based surveillance design, strengthen regional early-warning systems, guide livestock vaccination strategies, and support one health preparedness in one of the regions most vulnerable to RVF globally.

3.0 Methods

3.1 Study design

The search strategy followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines. It involved the use of broad search terms like "Rift Valley Fever" and the specific countries within the East African Community (EAC) ("Uganda, Kenya, Tanzania, Rwanda, Somalia, Burundi, Democratic Republic of Congo (DRC), South Sudan and Sudan").

3.2 Study area and country selection

The study focused on the specific countries within the East African Community (EAC), that is, Uganda, Kenya, Tanzania, Rwanda, Somalia, Burundi, Democratic Republic of Congo (DRC), South Sudan and Sudan (Figure 1). Sudan was included alongside South Sudan and jointly referred to as "Sudan" because the two countries formed a single political entity before 2011 and share a long history of RVF outbreaks, similar ecological conditions, and interconnected livestock systems. These countries were considered due to shared climatic patterns that favor the spread of RVF, livestock-dependent economies, transboundary trade of livestock and livestock products, and high human mobility. RVF's transboundary nature is further supported by outbreak notifications recorded in WOAH's WAHIS website, thereby indicating the recurrent RVF occurrence across multiple countries over time(48).

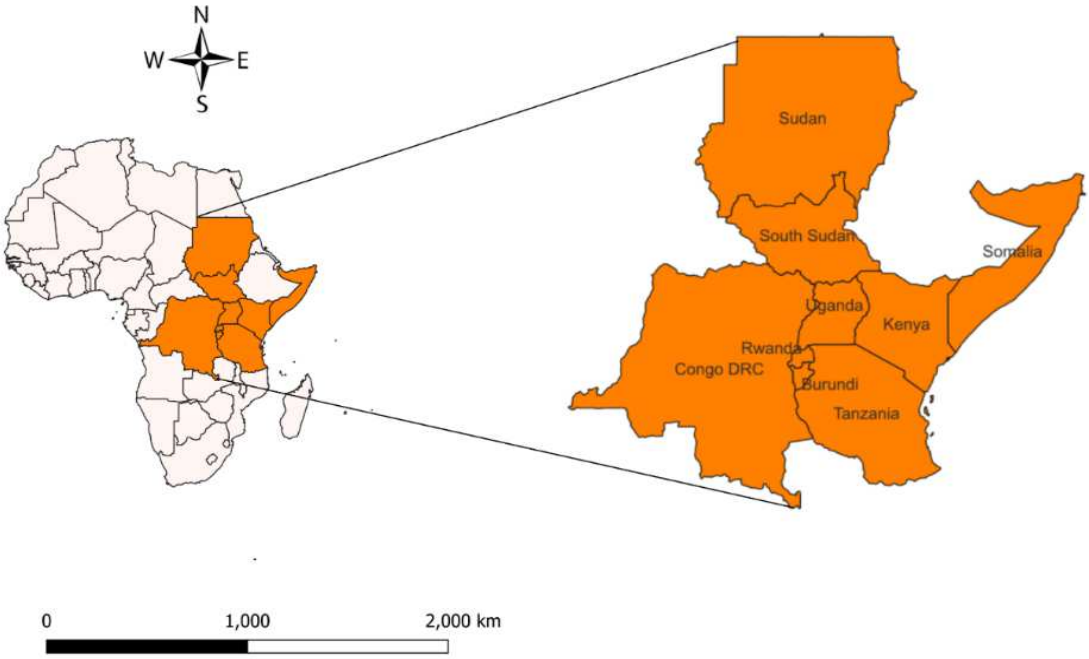


Figure 1: Study area: A map indicating the EAC countries

Specifically, RVF outbreaks have been reported as follows: Kenya experienced major outbreaks between 2006 and 2007, with additional episodes in 2018, 2019, 2021, and most recently in 2024. In the DRC, confirmed cases were reported from 2007 to 2013 and in 2015, followed by suspected cases from 2016 and 2019, as well as in 2021. Tanzania reported suspected RVF activity in 2006 and confirmed cases in 2007. Uganda experienced limited outbreaks in 2007, followed by more widespread occurrences from 2016 through 2023. Rwanda reported cases from 2012 to 2014 and again from 2016 to 2021. Sudan recorded outbreaks between 2007 and 2008 and from 2017 to 2019. Burundi reported cases between 2022 and 2024. No documented information on RVF occurrence in Somalia was identified during this period.

3.3 Search strategy and data sources

A comprehensive data search was conducted using PubMed (due to its structured indexing and ease of access to full texts of peer-reviewed biomedical literature), Google Scholar (to capture grey literature and studies from a wider range of disciplines),

DiscoverEd (to ensure comprehensive access to institutional library resources) and Web of Science (to identify high-impact studies and perform citation-based searches).

3.4 Eligibility criteria

3.4.1 Inclusion criteria

Studies were included if they:

- Were published between 1931 and 2025
- Were written in English
- Originated from one or more countries within the study area.
- Reported original quantitative data on RVF prevalence.

3.4.2 Exclusion criteria

Studies were excluded if they:

- Were not written in English
- Did not include any livestock data.
- Were conducted in areas outside the defined study area.
- Were published outside the specified time frame
- Were abstract-only publications
- Were reviews, systematic reviews, or meta-analyses.
- Were case reports, commentaries, conference proceedings, or newspaper articles.

These exclusions ensured consistency, data completeness, and reliance on primary research.

3.5 Study selection and data management

All identified articles were imported into Covidence (49) for screening and data retrieval, including the PRISMA flow diagram. Titles and abstracts were screened for eligibility, followed by full-text review. Duplicate records were automatically identified and removed, with additional manual duplicate checks performed where necessary. Data extracted from

eligible studies were transferred to Microsoft Excel and R for data management and analysis.

3.6 Data extraction and unit of analysis

Data extraction included country, livestock species, sampling period, outbreak status, diagnostic method, and RVF prevalence. Analyses were stratified by species, epidemiological context (outbreak versus inter-epidemic period (IEP), diagnostic method, and spatial-temporal characteristics.

In multi-species studies, each species was considered a distinct analytical unit. For longitudinal studies, each sampling period was analysed as an independent observation. When species were not disaggregated, populations were classified as “unspecified species” and analysed as a separate category.

When multiple diagnostic methods were applied within a study, each test-specific prevalence estimate was treated as an independent unit. Overall, 55 studies produced 134 species-specific and 91 diagnostic-specific prevalence estimates.

Studies were classified as either outbreak-related or inter-epidemic. If the epidemiological context was not explicitly stated, studies were assumed to represent inter-epidemic periods.

3.7 Data analysis

Prevalence estimates were summarized by country, species, and epidemiological period using Microsoft Excel, from which median prevalence and ranges were calculated descriptively. Pooled prevalence estimates were calculated using R (version 4.4.3).

Spatio-temporal distribution of RVF prevalence was visualized using QGIS (version 3.34.8). When multiple prevalence estimates were available for the same country and period, the median value was used for mapping.

Heterogeneity was assessed among serological studies using Cochran’s Q statistic and the I^2 metric to determine variability across studies.

4.0 Results

4.1 Study selection and characteristics

A total of 55 articles were included in this review following screening and eligibility assessment (Figure 2). Most studies were conducted during inter-epidemic periods (45/55), with fewer undertaken during outbreaks (10/55) (Table 1).

Study output increased over time, peaking in 2018 (Figure 3), however, there were no eligible studies identified from Burundi. Two publications did not specify the year the study was done.

The majority of studies were cross-sectional (83.6%), with fewer outbreak investigations (9.1%) and longitudinal designs (5.5%) (Figure 4). Most studies focused exclusively on livestock (37/55), while the remainder included additional species, primarily humans (11/55), with fewer incorporating vectors (5/55) or wildlife (2/55). Overall, the analytical dataset comprised 134 species-specific prevalence estimates across livestock populations and 91 diagnostic-specific observations.

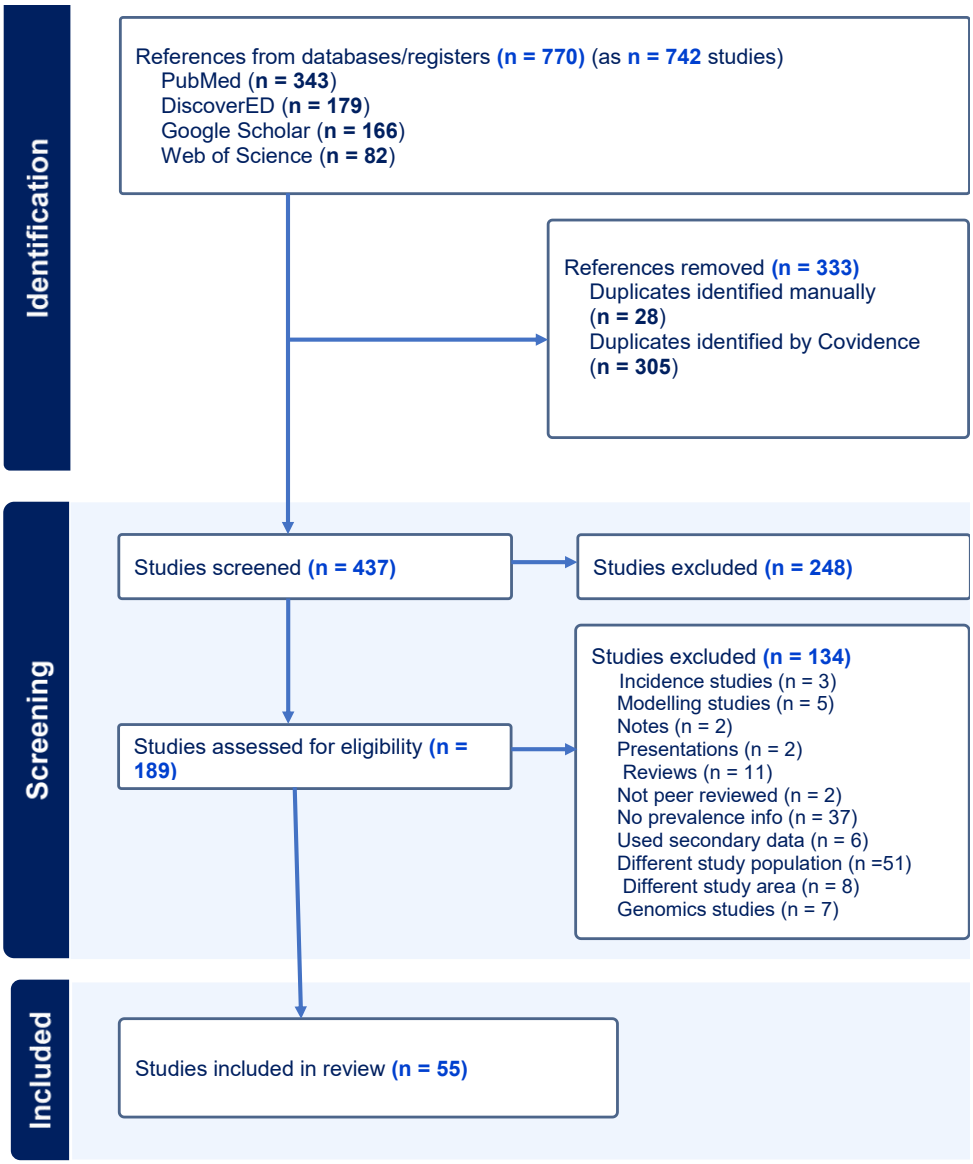


Figure 2: PRISMA flow diagram

Table 1: Number of publications identified in each of the East African Community Countries (n=55)

Country	Inter Epidemic Period (IEP)	Outbreak	Number of publications
Democratic Republic Congo	4	-	4
Kenya	13	4	17
Rwanda	1	-	1
Somalia	3	-	3
Sudan	5	2	7
Tanzania	11	2	13
Uganda	8	2	10
Burundi	0	0	0
Grand Total	**45**	**10**	**55**

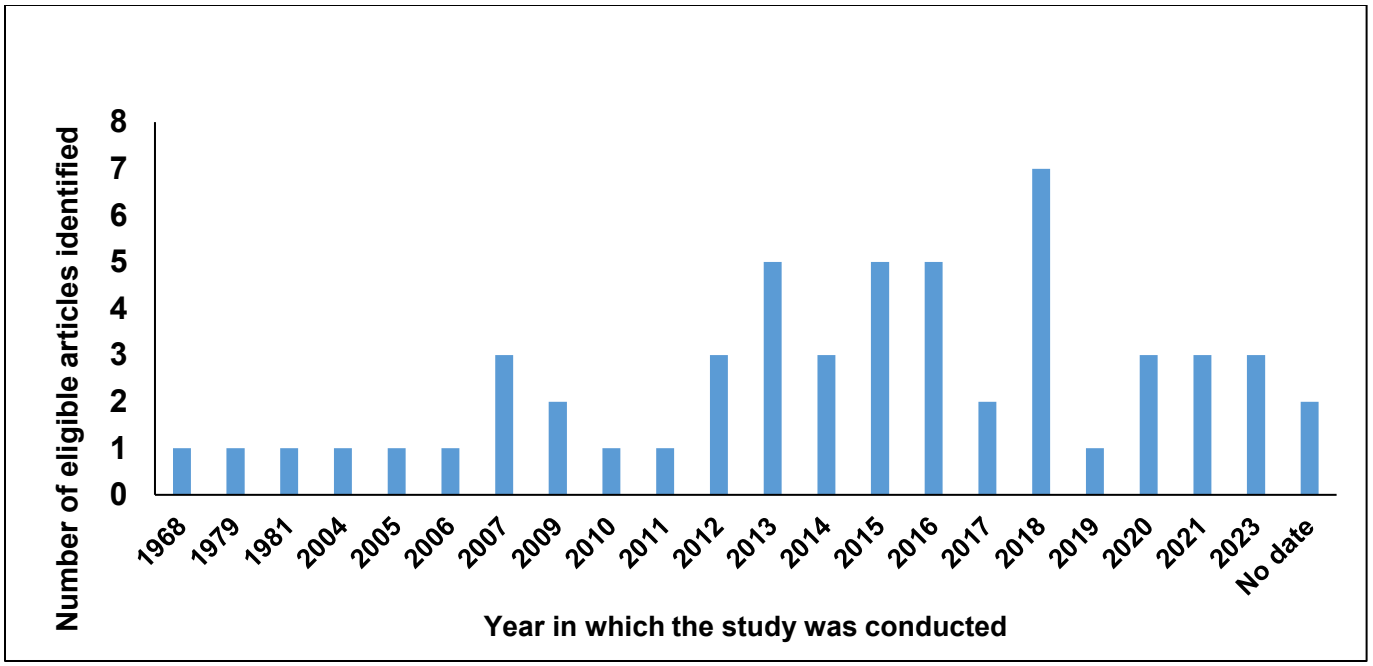


Figure 3: Number of eligible articles identified per year

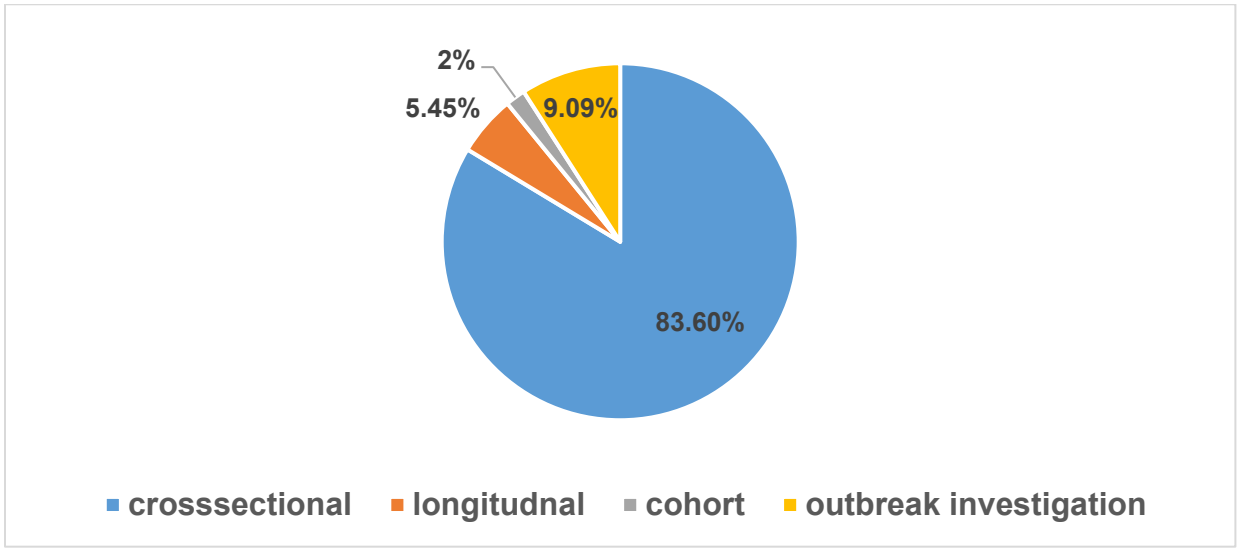


Figure 4: Percentage of study designs among articles included in the review

4.2 Overall RVF prevalence and epidemic context

The pooled prevalence across all livestock species and study periods was 11.0% (95% CI: 9.6–12.6), based on 134 studies (Figure 5 and Table 2). When stratified by epidemic period, the pooled prevalence during outbreak periods was 26.8% (95% CI: 19.7–35.4; *k*

= 24). In contrast, studies conducted during inter-epidemic periods (IEPs) reported a pooled prevalence of 8.8% (95% CI: 7.6–10.2; *k* = 110).

Table 2: RVF pooled prevalence

Analysis	**K**	**Pooled Prevalence**	**95% CI**	**Heterogeneity ($I^{2)}$**
Overall prevalence (All species)	134	11.0%	9.6-12.6%	96.2%
Overall Prevalence during outbreaks	24	26.8%	19.7-35.4%	93.3%
Overall Prevalence during IEPs	110	8.8%	7.6-10.2%	96.2%

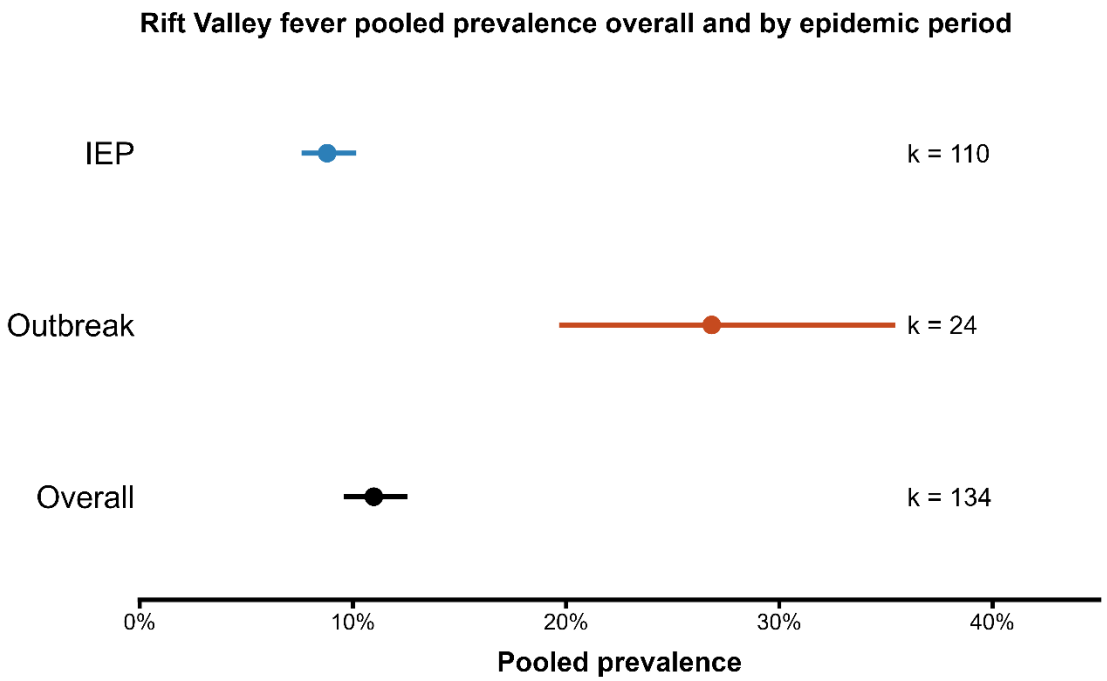
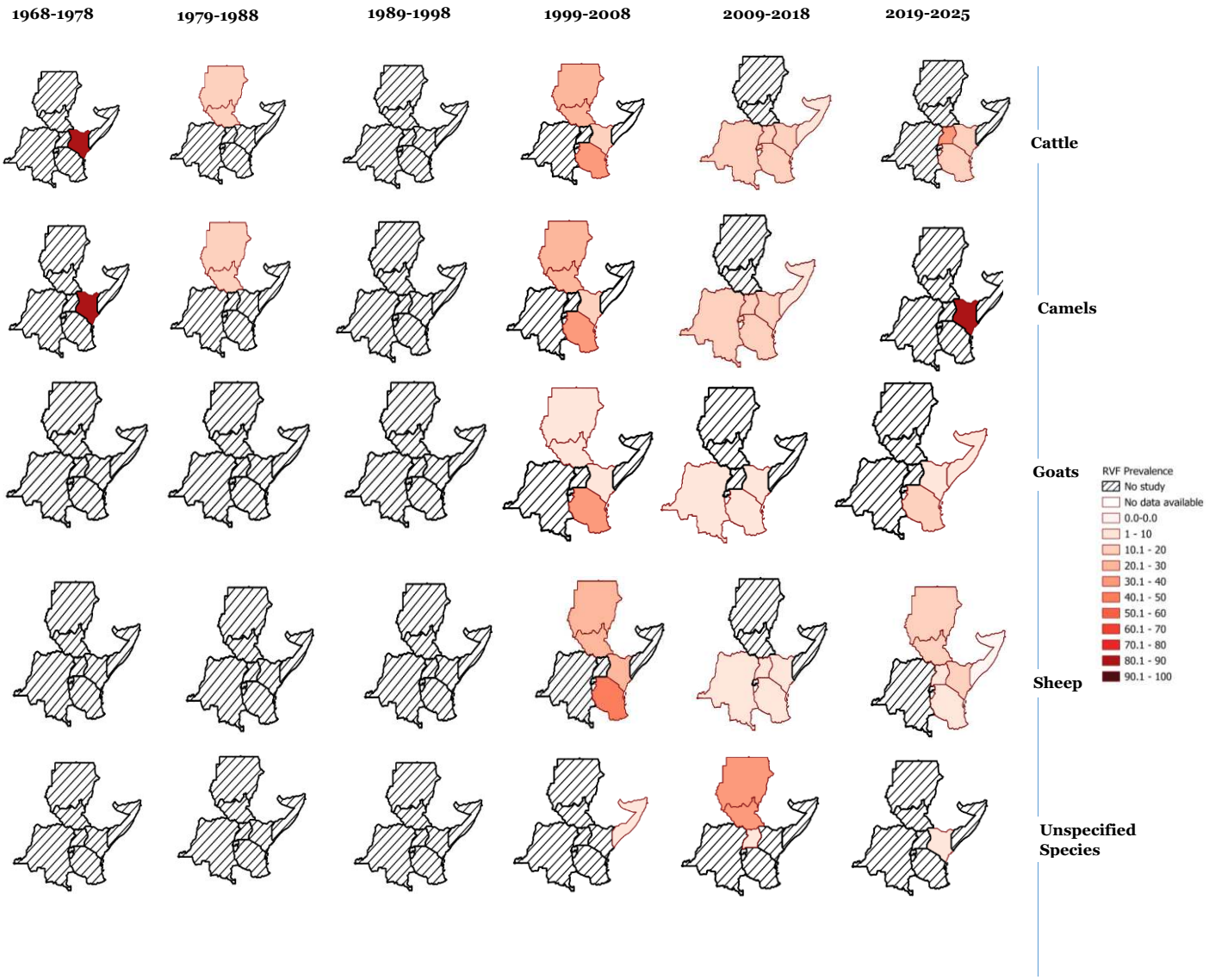


Figure 5: RVF pooled prevalence

4.3 Spatial and temporal distribution of RVF in East Africa

RVF prevalence varied over time and across geographic regions within the East African Community between 1968 and 2025 (Figure 6). Limited data were available for the period 1968-1998, during which prevalence was generally low across reported studies.

From 1999 onwards, prevalence was reported across multiple livestock species, including cattle, sheep, goats, and camels. Outbreak-related studies were identified in Kenya, Sudan, and Tanzania in 2007; in Uganda in 2016; in Kenya, Sudan, Tanzania, and Uganda in 2018; and in Kenya in 2021.



261

262 **Figure 6: Spatial and temporal distribution of RVF in EAC**

4.4 Species-specific RVF prevalence

A total of 134 species-specific prevalence estimates were included (Table 3). These comprised studies on goats (k = 41), sheep (k = 38), cattle (k = 34), and camels (k = 9), with an additional 12 estimates based on mixed or unspecified animal populations.

Most estimates were derived from inter-epidemic periods (110/134), with 24 obtained during outbreaks. Outbreak-period studies were reported from four countries (Kenya, Sudan, Tanzania, and Uganda).

Table 3: Number of RVF prevalence studies by species identified per country (n=134)

Country/Period	Animals	Camels	Cattle	Cattle	Goats	Sheep	Grand Total
IEP	**10**	**6**	**27**		**35**	**32**	**110**
Democratic Republic of Congo			3		1	1	5
Kenya	7	3	7		13	13	43
Rwanda			1				1
Somalia	3		2		2	2	9
Sudan		2	1		1	2	6
Tanzania		1	6		8	7	22
Uganda			7		10	7	24
Outbreak	**2**	**3**	**6**	**1**	**6**	**6**	**24**
Kenya		3	2	1	3	3	12
Sudan	1		1		1	1	4
Tanzania			2		1	1	4
Uganda	1		1		1	1	4
Grand Total	**12**	**9**	**33**	**1**	**41**	**38**	**134**

Pooled prevalence varied by species (Figure 7). The highest estimates were observed in camels (17.2%, 95% CI: 11.4–25.0; k = 9) and cattle (15.4%, 95% CI: 12.7–18.6; k = 34), followed by sheep (10.1%, 95% CI: 7.5–13.4; k = 38) and goats (7.8%, 95% CI: 5.7–10.5; k = 41). Mixed or unspecified animal populations had a pooled prevalence of 8.5% (95% CI: 5.4–12.9; k = 12). Heterogeneity was consistently high across analyses (I^2 range: 90.1%–98.3%) (Table 4).

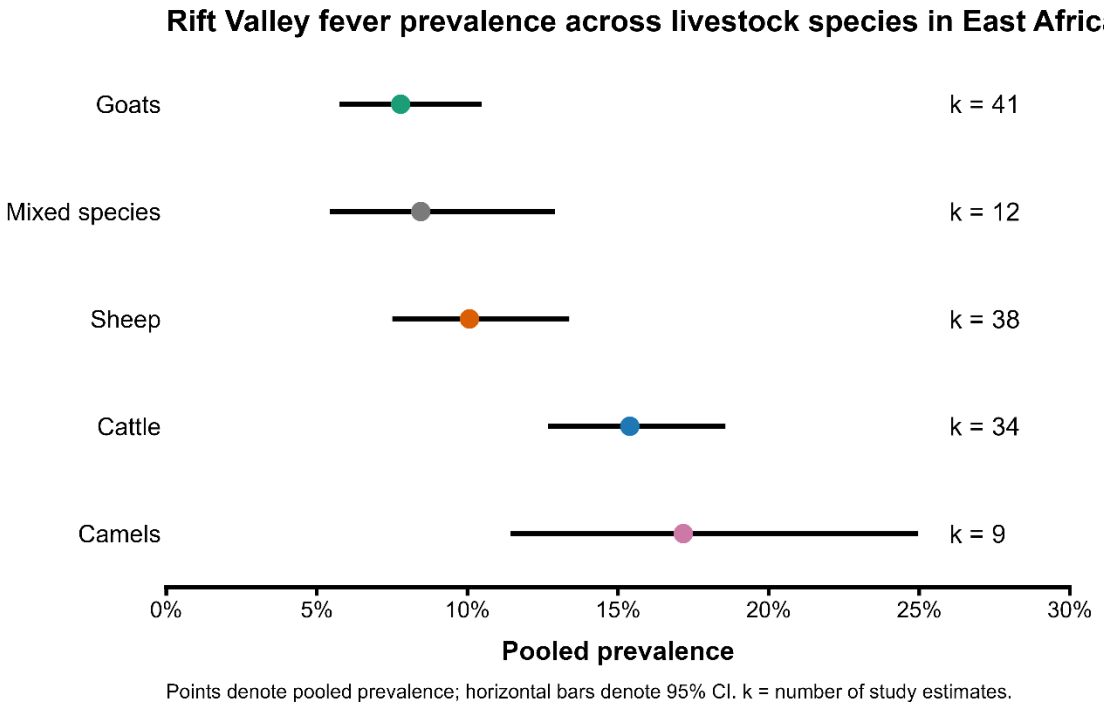


Figure 7: Species Pooled Prevalence

Table 4: Species pooled prevalence

Species	K	Pooled prevalence	95% CI	I^2
Cattle	34	15.4%1	12.7-18.6%	96.5%
Sheep	38	10.1%	7.5-13.4%	92.7%
Goats	41	7.8%	5.7-10.5%	96.4%
Camels	9	17.2%	11.4-25.0%	90.1%
Animals (Mixed/Unspecified)	12	8.5%	5.4-12.9%	96.3%

4.5 Diagnostic methods and prevalence estimates

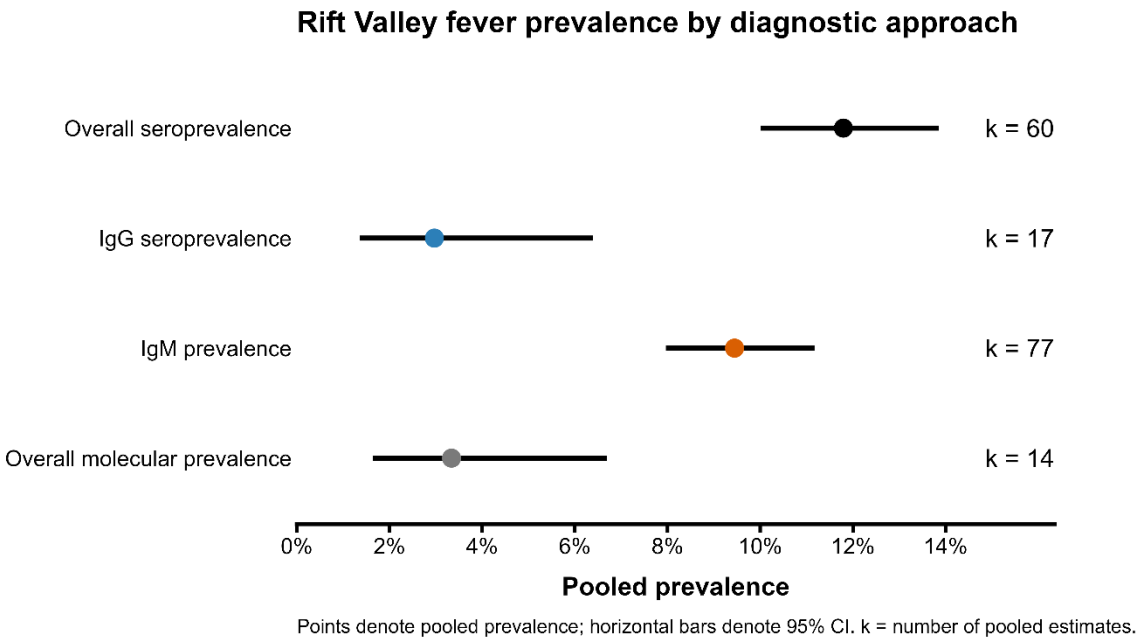
A total of 91 diagnostic-specific prevalence estimates were identified (Table 5). Of these, 77 were based on serological methods (IgG: k = 60; IgM: k = 17), and 14 used molecular methods.

Table 5: Number of RVF prevalence studies

Country	Molecular	Serological		Grand Total
		IgG	IgM	
IEP Total	**10**	**53**	**13**	**76**
Democratic Republic of Congo	3	5	3	11
Kenya	2	13	2	17
Rwanda		1		1
Somalia	1	5	1	7
Sudan	2	5	2	9
Tanzania	2	13	5	20
Uganda		11		11
Outbreak Total	**4**	**7**	**4**	**15**
Kenya	1	4	3	8
Sudan			1	1
Tanzania	2	2		4
Uganda	1	1		2
Grand Total	**14**	**60**	**17**	**91**

Pooled seroprevalence was 9.4% (95% CI: 8.0–11.2; k = 77), with high heterogeneity (I^2 = 97.9%) (Figure 8). Within serological assays, IgG-based prevalence was 11.8% (95% CI: 10.0–13.9; k = 60), while IgM-based prevalence was 3.0% (95% CI: 1.4–6.4; k = 17). Only 29.09% of studies reported diagnostic test performance characteristics (Sensitivity and Specificity), while 70.9% did not.

Molecular methods yielded a pooled prevalence of 3.3% (95% CI: 1.6–6.7; k = 14), with a comparatively lower heterogeneity (I^2 = 85.8%) (Table 6).



312

313 **Figure 8: RVF Prevalence by Diagnostic Test**

314 **Table 6: Pooled prevalence of RVF by diagnostic tests**

Category	***K***	***Pooled prevalence***	***95% CI***	***I^2***
Overall Pooled Serological Prevalence	77	9.4%	8.0-11.2%	97.9%
IgG	60	11.8%	10.0-13.9%	97.7%
IgM	17	3.0%	1.4-6.4%	97.8%
Molecular	14	3.3%	1.6-6.7%	85.8%

315

316 Several serological tests were used in the different studies per country, including indirect
317 immunofluorescence assay (IFA)-1 study, virus neutralization test (VNT)-3 studies,
318 enzyme-linked immunosorbent assays (ELISA)-71 studies, and plaque reduction

neutralization test (PRNT) - 2 studies. Reverse transcription-polymerase chain reaction (RT-PCR) was the only molecular test used.

4.6 Spatial patterns: country-specific prevalence by diagnostic test

Country-level pooled prevalence estimates, stratified by diagnostic test, showed pronounced spatial and methodological heterogeneity across the EAC (Table 7, see additional file 1). ELISA-based seroprevalence estimates were available for multiple countries, including Kenya, Tanzania, Uganda, Somalia, Sudan, and the Democratic Republic of Congo, with pooled prevalence typically ranging from 2.9% to 11.0%, though higher estimates were observed in selected contexts (Table 7, see additional file 1).

Table 7: Pooled prevalence of RVF per country by diagnostic tests

Molecular prevalence estimates were notably sparse, with several country test combinations supported by only one or two studies. Consequently, many pooled estimates were derived from limited evidence, and heterogeneity metrics were not estimable where k = 1.

4.7 Comparative analysis of studies that used both serological and molecular diagnostic tests

Fifteen studies (15/55) from six countries reported both serological and molecular prevalence estimates (Table 8, see additional file 1). Of these, four were conducted during outbreak periods and eleven during inter-epidemic periods. Among the four outbreak studies, only one tested for IgM. This was carried out during the 2007 outbreak in Kenya. IgG prevalence was the highest at 7.80%, IgM at 4.20%, and 2.10% PCR, suggesting that more animals had past infections than recent or active infections.

Table 8: Comparative analysis of studies that used both serological and molecular diagnostic tests

Across studies, serological prevalence estimates (IgG and/or IgM) were higher than molecular prevalence estimates. The highest reported values were from a study in

Tanzania (serological: 93.0%; molecular: 21.0%) (Table 8, see additional file 2). Viral RNA was detected in 6 of 11 inter-epidemic studies, while 5 reported no molecular detection. Two of these five did not test for IgM antibodies; however, the three that tested for IgM recorded a prevalence of 0.20%, and 1.1% in Tanzania, and 1.4% in Somalia (Table 8, see additional file 2), suggesting active infections. Only one study reported strain characterisation, identifying two lineages (Clade B and Clade E), which were similar to those identified in an outbreak in South Africa in 2009(50).

4.8 Comparison of studies that used both IgG and IgM diagnostic tests

Fifteen studies (15/55) also reported both IgG and IgM seroprevalence (Table 9, see additional file 3), with most conducted during inter-epidemic periods (13/15). IgG prevalence exceeded that of IgM across all studies. Reported IgG values ranged from 4.2% to 34.1% during inter-epidemic periods and 7.8% to 13.1% during outbreaks, while IgM prevalence ranged from 0.0% to 10.7% (Table 9, see additional file 1)

Table 9: RVF prevalence among studies that used both IgG and IgM tests

5.0 Discussion

RVF epidemiology and landscape in EAC

Rift Valley fever (RVF) is widely distributed across the East African Community (EAC), with evidence of recurrent outbreaks and ongoing inter-epidemic circulation. The increase in published studies since 1968 likely indicates both increased research interest and advancements in diagnostic capacity, consistent with the recognised endemicity of RVF in Africa(40), which results in under-reporting, under-detection, and misdiagnosis (51). Surveillance data further support this trend, reporting 65 RVF outbreaks comprising 44 animal, 17 human, and 4 human and animal in the EAC between 2010 and 2024 (52). The zoonotic nature of RVF and its grave public health consequences have augmented its research interests, as illustrated by recent human seroprevalence rates of 9.90% in Zambia (53) and 10.5% in Uganda (54), underscoring the disease's ongoing impact.

Despite the growing body of evidence, geographic representation remains inconsistent. Most studies originate from Kenya, Tanzania, and Uganda, while no eligible prevalence studies were identified from Burundi. This absence likely reflects differences in surveillance capacity and diagnostic infrastructure rather than an actual epidemiological absence, as RVF has been reported in Burundi since 2022 (48). The outbreak occurred in 13 provinces in Burundi, affecting mainly livestock, and no human cases were recorded (52). This creates a blind spot in regional risk assessment, especially in a transboundary system characterized by livestock mobility and shared ecological conditions.

The dominance of cross-sectional studies conducted during inter-epidemic periods further shapes the evidence landscape. For example, Kifaro *et al*., (55) detected 12.69% RVF prevalence in Tanzania, Tshilenge *et al.,* (56) detected 1.85% in DRC, and M. Elhaj *et al.,* (57) detected 15.23% in Sudan. These designs provide baseline estimates of exposure but offer limited insight into transmission dynamics and temporal patterns. Furthermore, cross-sectional studies are affordable, can identify associations between exposures and outcomes, can be generalized to the entire population, and are best for prevalence estimation surveys (58). In contrast, outbreak investigations, although fewer, often report higher prevalence, for example, up to 81% among cattle in Kenya(59) and over 40% across multiple species in Uganda(12). This contrast highlights the importance of contextualizing prevalence estimates by epidemiologic period.

The highest number of studies was identified in EAC in 2018, a period marked by increased funding for prioritized zoonotic diseases such as RVF for research and development, by the WHO (60). Coincidentally, according to ProMed data, the highest number of outbreaks was also recorded in 2018 in the EAC(52), indicating that scientific output and observed disease activity track one another closely.

Eastern Africa, especially Kenya, has historically borne the largest share of RVF studies (27), reflecting the region's frequent outbreaks every 5 to 15 years(48). Climate and ecological factors play a central role in shaping RVF epidemiology in the EAC. Outbreaks are strongly associated with periods of heavy rainfall, flooding, and increased vegetation cover, which create favorable conditions for mosquito vector proliferation(59).

Furthermore, according to Situma *et al*. (61), a positive correlation was observed between increasing temperature, rainfall amounts, and NDVI one month prior to outbreaks in East Africa. Notably, over a decade-long longitudinal analysis suggests a shift in RVF occurrence towards highland areas, reflecting broader climatic changes that expand transmission zones (61).

Most studies focused on livestock, and only 32.7% of the publications concurrently examined other species. Notably, no study investigated all hosts and vectors in a single integrated approach. This fragmented approach hinders understanding cross-species transmission dynamics, delays outbreak detection, limits insight into the role of wildlife in the transmission and maintenance of RVF, undermining the practical application of the one health approach (24). Logistical, methodological, and sectoral barriers to integrated studies are often challenging but remain a priority for advancing prevention and control (62).

Temporal and spatial dynamics of RVF

Spatial and temporal patterns reveal considerable variability in RVF occurrence across the EAC over time, with evidence of both geographical spread and recurring outbreaks. Historical data illustrate this spread (63). For example, in Kenya in the early 20th century, RVF activity was largely confined to the Nakuru area, affecting 8/69 administrative units. Still, by the mid-20th century and early 2000s, it had spread to several administrative regions (38/69) (15,63).

ProMed data shows that RVF has since spread to Sudan, Uganda, Rwanda, Burundi, South Sudan, and Tanzania, with up to three-quarters of recent outbreaks recorded in East Africa(52,61). This expansion is closely linked to climate variability, ecological factors, and host movement. Rainfall anomalies, including those associated with El Niño Southern Oscillation (ENSO) events, have been shown to predict outbreak occurrence through their effects on vector ecology (64). Flood-prone areas such as river basins and dambos create hotspots for RVF emergence. For instance, in Sudan, all RVF outbreaks nearly originate in the White Nile State, where annual flooding creates dambos that promote prolific vector breeding and subsequent spread to other states(63,65–67).

Livestock movements and trade further amplify the spread of RVF, particularly in regions with weak surveillance systems. Evidence suggests that a substantial proportion of outbreaks occur near cross-border trade hubs, highlighting the role of livestock mobility in transmission dynamics. Transboundary and informal livestock corridors, such as those connecting Kenya, Somalia, and Ethiopia, enable undetected RVFV spread, with more than 50% of outbreaks occurring near cross-border markets (52,68). Furthermore, in Madagascar, RVF was introduced via cattle imports from the Comoros Islands, with 83% of human RVF cases linked to cattle trade hubs/markets (69).

Vaccination coverage remains insufficient in many high-risk areas, limiting the development of herd immunity. For example, during the 2018 outbreak in East Africa, less than 30% of livestock in hotspot areas were vaccinated (52), yet it would require 79% of the population to be immune to effectively stop RVFV transmission (70).

Delayed reporting, ineffective transboundary coordination, and collaboration among countries during outbreaks may also lead to further spread, e.g., in 2018, the outbreak at the Uganda-Kenya border took 6 weeks to coordinate (52). Disparities in resources and control measures, where wealthier countries implement more robust surveillance and vaccination campaigns than poorer ones, further complicate regional management across regions where import restrictions and testing are inconsistently applied, e.g., some countries accepted entry of livestock from countries with ongoing outbreaks without testing (52). These gaps emphasize the need for harmonized regional protocols for surveillance, vaccination, and movement control (71). While regional analyses provide valuable insights, they may obscure important local heterogeneity driven by ecological, management, and socioeconomic factors; therefore, this warrants finer spatial data to better characterize transmission dynamics (26).

Species-specific patterns of RVF prevalence

Variation in RVF prevalence among livestock species shows differences in host ecology, susceptibility, exposure, and study design. Outbreak studies were confined to four out of the seven EAC countries, which may suggest geographic clustering or country-specific

capacity to carry out outbreak investigations (72). The highest number of studies identified were among goats and sheep, mirroring the central role of small ruminants in small holder production systems and the East African livestock economy. They are widely kept due to their adaptability, shorter lifespan, high turnover, low maintenance costs, and economic importance for small-scale farmers(73,74). Goats and sheep are both highly susceptible to RVF in comparison to other ruminants and often precede human infection; therefore are key indicators of RVF infection during surveillance (75,76). Their high virulence and susceptibility lead to their underrepresentation during seroprevalence studies since dead animals are not sampled, resulting in an underestimation of the true RVF impact(74). In addition, antibodies in small ruminants decline at a faster rate in IEPs than in cattle or camels, further reducing detectability (74). Nevertheless, links between livestock and human infection are evident, for example, being linked to an IgG-positive herd increased the odds of human infection by 3.8 times(9).

The overall pooled RVF prevalence for all species was 11.0%, with marked differences between epidemiological periods 8.8% during the IEP and 26.8% during the outbreak period (Table 2). These findings are similar to other studies carried out elsewhere in Africa. For example, Jarra *et al.,* (77) recorded a prevalence of 13.1% recently in the Gambia during an IEP, while Ksiazek *et al.,* (78) recorded a prevalence of 85% during an outbreak in West Africa, reinforcing the pattern of higher prevalence during outbreaks. In contrast, some South African studies report a higher IEP seroprevalence (34.0% among cattle and 31.7% in goats), which may reflect seroconversion over time (79) or selective sampling of symptomatic animals in high-risk areas (43).

Camels had the highest pooled prevalence, followed by cattle, sheep, unspecified species, and finally goats (Table 4). Similar results were observed in Ethiopia, where the individual apparent seroprevalence was 17.9% in cattle, 42.6% in camels, 6.3% in goats, and 7.4% in sheep (80). Camels are considered sensitive indicators of RVF due to their longevity and movement across large areas, especially in arid areas (81). Notably, high prevalence has been registered among camels even during IEP, for example, 27.5% in Tanzania (82), 22.0% in Kenya (83), and 16.60% in Sudan (84). These results are similar to observations in northern Burkina Faso, where 51.85% of camels tested positive for

RVF (85). This can be attributed to the wide range movement of camels across diverse environments or through transhumance, a longer life span (20 to 40 years) compared to other ruminants, and the tendency of RVF to circulate in subclinical form, which increases their cumulative exposure risk and virus maintenance (86,87). The same applies to cattle, whose prevalence was higher than that of goats and sheep, as documented in Gambia, where cattle had 36.8%. In comparison, goats had 2.1% and sheep had 4.3% (77). This is due to their longer lifespan compared to goats and sheep (88) and movement over longer distances, which exposes them to RVF vectors (89).

Diagnostic approaches and implications for prevalence estimates

RVF prevalence estimates are highly dependent on the diagnostic approach used. In this review, the majority of studies relied on serological tests, predominantly IgG-based assays, which report higher prevalence due to persistence of antibodies after exposure (90). Pooled IgG prevalence was 11.8% compared to 3.0% for IgM and 3.3% (Table 6) for molecular detection, which emphasizes the burden of past infections and the endemicity of RVF in the EAC. IgM antibodies appear 4 to 7 days post-infection, peak around 2 to 3 weeks, and are depleted by 6 weeks; hence are not favorable for the detection of past infections but rather current infections (38,91). In contrast, IgG antibodies appear later (10 to 15 days post-infection) but may persist for years, limiting their ability to distinguish recent from past exposure(90). Human studies have even demonstrated neutralizing antibodies decades after exposure(92).

Molecular methods, such as RT-PCR, confirm the presence of active infection using viral RNA; however, their diagnostic window is narrow because viremia is short-lived. RVFV RNA is detectable in blood only 1 to 2 days post-infection and declines within 10 days of symptom onset (91,93). This contributes to the lower prevalence estimates when molecular methods are used. Although RT-PCR has high specificity and is useful in confirming current infections, its application remains limited in many endemic regions due to logistical and resource constraints (38). Notably, Wilson et al., (94) developed a single tube assay that can detect all three genome segments of the RVFV. This assay is DIVA compatible with a sensitivity of up to 100% (depending on the quality of the sample) and a specificity of 94.6%. This makes it a valuable tool for differentiating infected from

vaccinated animals in endemic and non-endemic settings. The Clone-13 vaccine, which has been registered in South Africa, Kenya, Namibia, and Botswana since 2010, is DIVA compatible due to the deletion of the NSs gene (37,95), making this assay very critical for diagnosis.

The disparities between serological and molecular, and IgG and IgM diagnostic test results, indicate that relying on a single method may either overestimate exposure (using serology) or underestimate/miss active infections (using molecular methods alone). For example, a study by de Glanville et al., (50), reported a 93% IgG and a 21% RT-PCR positivity (Table 8,see additional file 2). It also highlighted the strains from two lineages, Clade B and Clade E, linked to historical outbreaks in East and South Africa(96). Likewise, Munyua *et al.,* (8) detailed the presence of IgM (4.2%), RT-PCR (2.1%), and IgG 7.8% which confirms active transmission during this period (2007 outbreak). Nevertheless, very few studies used both diagnostic methods, limiting the accuracy of prevalence estimates. Regular testing during IEPs is therefore important for the early detection of RVF.

More than half (70.90%) of the eligible articles included in this review did not specify the sensitivity and specificity of diagnostic tests used, which presents bias, shows a lack of methodological rigor, and undermines the reliability of prevalence estimates(97). Furthermore, Thrusfield (2018) emphasizes that if the specificity and sensitivity are not declared, a study's results are questionable and affect the ability to compare findings across different studies(98). In addition, it raises concerns about other aspects of data collection, such as data collection, study design and analysis. The Strengthening the Reporting of Observations in Epidemiology (STROBE) checklist emphasizes the need for complete and transparent reporting, including diagnostic tests and their specificity and sensitivity. A lack of this limits reproducibility and comparison with other studies (99). Like Nanyingi *et al.,* (24) highlighted in a previous review, "the true prevalence of RVF is uncertain" since most studies do not specify the sensitivity and specificity of the tests used, making it difficult to estimate the true prevalence.

Among the serological tests,7//77 used ELISA. Most of these used the competitive ELISA test kit (*ID Screen* RVFV competition multispecies ELISA (ID-Vet, Montpellier, France),

which detects IgG and IgM. It demonstrated a specificity of 100% and a sensitivity of 91%-100% (100). The ELISA test is sensitive, rapid, and can detect IgG and IgM antibodies as early as four days following infection (38).

The high heterogeneity values among the serological studies prove the differences are real rather than random, due to the differences in diagnostic tests used, study designs, sampling procedures, host species, sampling period (IEP vs Outbreak), etc., and therefore, pooled prevalence estimates should be interpreted cautiously. The high heterogeneity likely stems from the variations in the serological tests used, population characteristics, study periods (e.g., IEP or Outbreak periods), and study settings. Kenya showed extremely high IgG pooled prevalence (Table 7,see additional file 1) using IFA, likely due to the targeted outbreak investigation (59) or differences in assay sensitivity, for example, IFA detected anti-RVF IgG antibodies in 8/80 of samples in a study in Italy, yet only 3/8 of these samples were confirmed by serum neutralization assays which highlights the high sensitivity and lower specificity of IFA (101). Somalia reported the lowest serological pooled prevalence (4.08%), probably due to fewer studies carried out.

Key evidence gaps and research needs identified

The determination of research gaps and needs of RVF prevalence among livestock in EAC improves comprehension and intervention strategies for RVF. Therefore, in summary, the research gaps and needs identified include: 1) Geographical Coverage- No research has been done on the prevalence of RVF in Burundi, despite its proximity to other endemic countries. The absence of data from Burundi creates a blind spot in regional risk assessment, particularly given the country's involvement in cross-border trade as discussed earlier. 2) No study looked at all species affected by RVF and vectors concurrently. This fragmented approach hinders understanding of the complex transmission dynamics involving multiple species and vectors, as mentioned earlier.3) Limited genetic characterization of circulating RVFV strains. Only one study typed the identified strains, which limits knowledge of viral diversity and evolution that could influence vaccine efficacy and outbreak severity (54). 4) There isn't any approved DIVA strategy for the available vaccines (40). A few studies have looked at the DIVA compatibility of diagnostic tests (102–104); however, more region-specific field tests are

required. 5) Most studies did not specify the sensitivity and specificity of diagnostic tests used; reasons for this were discussed earlier.6) Most studies did not specify the history of vaccination, probably because it is not widely practiced in the region; according to WAHIS data, 4 out of the 8 countries in EAC have reported official RVF vaccinations. For example, in Kenya from 2007 to 2025, the number of vaccinations ranged from 20,000 to approximately 2.6 million livestock, in Tanzania, vaccinations ranged from 300 to 300,000 and vaccinations were only done in 2014 and 2012, in Sudan, 25,516 cattle and 107,628 goats and sheep were vaccinated in 2007 only, In Rwanda, vaccinations ranged from 2,250 to approximately 190,000 livestock. Yet, these numbers of vaccinations are not enough to create herd immunity. Therefore, this presents a research gap for the lack of vaccination in an endemic region for a disease without a cure that is best prevented by vaccination, as discussed above.

6.0 Limitations

The review focuses on only published data, leading to publication bias where studies with significant or positive results are likely to be published compared to those with negative or inconclusive results(105). This can lead to overestimating certain trends and a skewed understanding of RVF's true prevalence and distribution. Additionally, the review overlooked input from local policymakers, affected communities, and contextual data sources limiting the ability to capture relevant information. Furthermore, language and accessibility barriers to some publications also increased the selection bias.

7.0 Conclusion and recommendations

This review demonstrates that RVF continues to scourge the EAC, affecting livestock and public health with significant variability in prevalence across countries, species, diagnostic tests, and spatial-temporal distribution. The majority of the studies were from Uganda, Kenya, and Tanzania, without any prevalence data from Burundi, which highlights a major geographic research gap. Most studies focused on a single species and lacked corresponding vector data; there was also limited reporting on diagnostic test accuracy, vaccination history, and RVFV strain diversity. The absence of DIVA-compatible vaccines further constrains RVF control endeavors. Therefore, addressing

these gaps through improved surveillance, region-specific research, and integrated control strategies is important in the fight against RVF.

7.1 Suggestions for control and prevention of RVF in EAC

1) Enhance vaccine availability, uptake and documentation in the EAC; Vaccination is considered the most effective prevention strategy for viral diseases like RVF (106) in endemic countries. Commercially available vaccines include: the Smithburn vaccine, which is a live attenuated vaccine that offers long-term immunity with a single dose (Coackley et al.,1967), inactivated vaccines, e.g. the ZH501, Menya (Kamal,2011), and a formalin-inactivated vaccine derived from a cow field strain in South Africa (Barnard and Botha,1977). However, these require booster doses to induce protective immunity (Dungu et al., 2013). Additionally, despite the availability of these vaccines, RVF vaccines are not available in some countries in the EAC, like Uganda. They are also not provided by the government, as with other notifiable diseases. Therefore, RVF vaccines should be made available in all endemic countries.

2) Improve active and passive surveillance and popularize digital event-based systems like ProMed to monitor and report outbreaks in real time (52).However, this might be limited by the fact that ProMed is subscription-based. Nevertheless, real-time disease reporting mobile applications like EMA-I by FAO have been piloted and used in countries like Uganda.

3) One-health approach, which involves cross-sectoral collaboration among medical and veterinary doctors, epidemiologists, public health experts, wildlife experts, environmentalists, entomologists, social scientists, economists, governments, policy makers, vaccinologists, and pharmaceutical companies(62). Still according to Fawzy & Helmy, (2019), the one-health approach encompasses: (a) administering a safe and effective RVFV vaccine to susceptible animals under governmental oversight to mitigate human outbreaks, (b) establishing a robust and consistent surveillance system alongside a rapid reporting program for the disease, (c) employing well-trained and professional personnel, (d) conducting epidemiological investigations to identify risk factors, (e) training veterinary and

medical health specialists in the diagnosis and management of suspected cases, (f) enhancing public health awareness regarding RVFV and its transmission, (g) interrupting the virus transmission cycle by controlling mosquito populations, and (h) regulating animal importation and enforcing quarantine measures for imported animals from Africa.

4) Strengthen diagnostic capacity; there is a need to improve the diagnostic capacity for RVF, including the adoption of DIVA-compatible strategies and identification and characterization of RVFV strains, which is beneficial to vaccine development and targeted control interventions.

List of abbreviations

CI-Confidence Interval

DIVA- Differentiation of Infected from Vaccinated

DRC- Democratic Republic of Congo

EAC- East African Community

ELISA-Enzyme –Linked Immunosorbent Assay

ENSO-El Niño/Southern Oscillation

FAO- Food and Agriculture Organization of the United Nations

HIA- Hemagglutination inhibition

IEP- Inter-epidemic period

NDVI- Normalized Difference Vegetation Index

PCR-Polymerase Chain Reaction

PRNT- Plaque Reduction Neutralization Test

RNA-Ribonucleic acid

RT-PCR- Reverse Transcription-Polymerase Chain Reaction

RVF-Rift Valley Fever

RVFV-Rift Valley Fever Virus

VNT-Virus Neutralization Test

WHO-World Health Organization

WOAH- World Organization for Animal Health

Declarations

Ethics approval and consent to participate

Not applicable to this research

Consent for publication

Not applicable for this research

Availability of data and materials

All data generated or analysed during this study are included in this published article (and its supplementary information files).

Competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Authors' contributions

V.E.N conceived the study and defined the review objectives. V.E.N developed the methodology and search strategy. V.E.N conducted the literature search. V.E.N and D.A performed study selection. V.E.N carried out data extraction and charting. D.A performed

the data analysis. V.E.N synthesized findings. V.E.N drafted the original manuscript. E.M and D.A reviewed and edited the manuscript. E.M supervised the study.

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