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Review

Viruses and Ticks: An Integrative Review of Virological Findings in Ticks

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Abstract

Vector-borne diseases account for over 17% of reported infectious diseases worldwide and are associated with approximately 700,000 deaths annually. The main vectors include mosquitoes, moths, sand flies, black flies, and ticks. Ticks deserve special attention because they transmit a wide range of pathogens, including viruses of major medical importance, such as tick-borne encephalitis virus (*Orthoflavivirus encephalitidis*) and Crimean-Congo hemorrhagic fever virus (*Orthonairovirus haemorrhagiae*), as well as animal-borne pathogens, such as African swine fever virus (*Asfivirus haemorrhagiae*). Recent advances in next-generation sequencing have expanded the ability to detect and characterize tick-borne viruses, revealing increasing viral diversity. However, for many of these viruses, aspects such as pathogenic potential, main vectors, and natural hosts remain unclear. To address this gap, we conducted an integrative literature review using the PubMed, SciELO, BVSalud, and Patuá-IEC databases. We analyzed 336 articles addressing various species of tick-borne viruses. The *Flaviviridae*, *Phenuiviridae*, and *Nairoviridae* families were the most frequently identified among the viral agents detected. Furthermore, we identified that as-yet-unclassified viruses have been frequently detected in different tick species, which sparks significant interest in investigating their potential interactions and public health implications. Investigating viral agents in tick populations is crucial for understanding viral diversity and assessing potential public health risks, especially in the current context of climate change.

Keywords: zoonoses; climate change; ticks; arboviruses; tickborne

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1. Introduction

Vector-borne diseases, according to the World Health Organization (WHO), account for more than 17% of infectious diseases, causing approximately 700,000 deaths annually. In this context, agents transmitted by mosquitoes, culicoides and ticks stand out, such as Dengue virus (*Orthoflavivirus denguei*), *Plasmodium vivax*, Oropouche virus (*Or-*

thobunyavirus oropoucheense) and Tick-borne encephalitis virus (*Orthoflavivirus encephalitidis*), respectively [1,2].

Ticks are important vectors of infectious agents, particularly a diverse range of highly pathogenic viruses for humans, such as *Orthoflavivirus encephalitidis* and *Orthonairovirus haemorrhagiae*, and for animals, such as *Asfivirus haemorrhagiae* [3–6]. The viral families *Flaviviridae*, *Phenuiviridae*, *Orthomyxoviridae*, and *Nairoviridae* are the main viral families of medical and veterinary importance, with several species transmitted by ticks in a cycle involving susceptible vertebrate animals and ticks from the families Ixodidae and Argasidae, with humans serving as accidental hosts [6–9].

Arthropod vectors pose a global threat to public health, as they can spread rapidly and dynamically. Furthermore, climate change and anthropogenic activities, such as human encroachment into wild habitats, have significantly increased the dissemination of vector-borne zoonoses [10]. The recent COVID-19 (SARS-CoV-2) pandemic underscores the importance of identifying novel viruses in wild animal populations [11]. Furthermore, changes in environmental variables, caused by anthropogenic activities such as land use, affect both tick and host populations, thus promoting the spread of zoonoses, which are highly relevant to public health [5,6,8].

Currently, with the introduction of new technologies, novel viruses are being identified in tick species. Recent studies have detected a wide range of new viruses in tick pools, for which hosts, vectors, and pathogenicity remain unknown [12–18]. Therefore, the present study aims to conduct an integrative literature review using data from scientific databases in order to identify viruses already described in tick populations, focusing on those detected/studied through molecular techniques, viral and experimental isolation, and to discuss the impacts of climate change on tick population dynamics and the associated risks to public health.

2. Materials and Methods

2.1. Concept of the Study

This is an integrative and descriptive literature review study. Review papers, as well as other categories of scientific research, are studies that use bibliographic sources or electronic documents to compile research findings from other authors, with the aim of providing theoretical and scientific foundations for a specific purpose [19]. The integrative review is a broader methodological approach that includes both experimental and non-experimental studies to achieve a more comprehensive and complete understanding of the research topic [20]. Moreover, this research method allows for the identification of knowledge gaps and the formulation of new research questions [21].

The integrative review consists of six stages: defining the topic to be discussed; establishing inclusion and exclusion criteria; determining which information will be extracted from the selected studies; evaluating the included studies; interpreting the results; and presenting the findings [19].

2.2. Search Strategies

The bibliographic search was conducted using computerized bibliographic databases, such as the Virtual Health Library of the Evandro Chagas Institute (Patuá), National Library of Medicine (PubMed), Scientific Electronic Library Online (SciELO), and the Regional Portal of the Virtual Health Library (BVSalud), during the period from February 2024 to January 2025.

For the search process, the following descriptors were used: virus, arbovirus, isolation, infection, tick, tick-borne, as well as their equivalents in Portuguese and Spanish. To refine the search, the descriptors were combined using only the Boolean operator AND. The

combinations used were: "arbovirus" AND "tick", "virus" AND "tick", "tick-born" AND "arbovirus", "isolation" AND "arbovirus" AND "tick", "isolation" AND "virus" AND "tick", "infection" AND "arbovirus" AND "tick", "infection" AND "virus" AND "tick". Based on these search strategies, the retrieved articles were saved in PDF format and later organized using the Excel tool (Microsoft Office Professional Plus 2013, version 15.0). In addition, the R software (v.4.5.0) was used to generate illustrations of the results from metagenomic studies.

The review was conducted according to an adaptation of the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) checklist guidelines, with the aim of ensuring the transparency and robustness of the selection, analysis and synthesis process of the included studies (Figure 1).

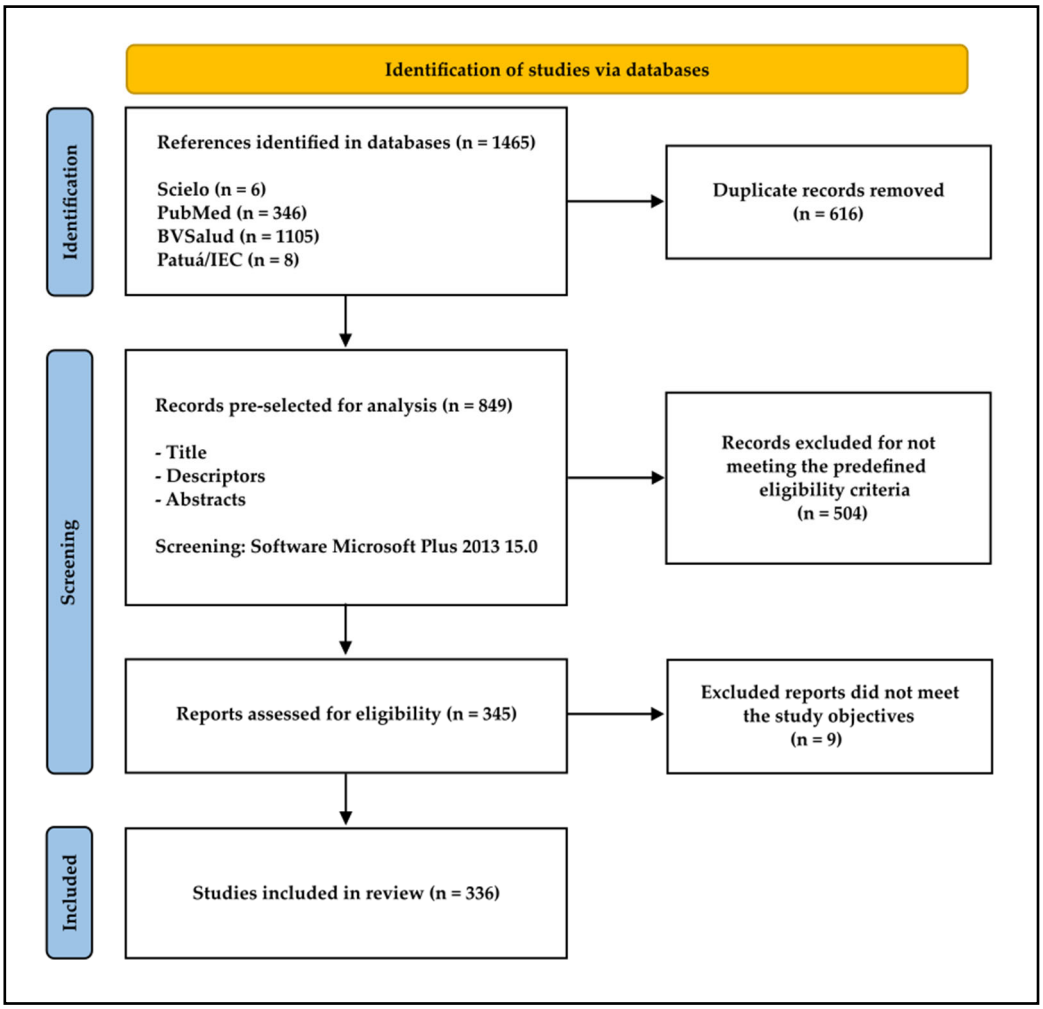


Figure 1. Flowchart of the methodology for bibliographic data collection.

2.3. Inclusion and Exclusion Criteria

The inclusion criteria comprised original, full-text, and open-access articles; studies written in English, Portuguese, or Spanish; and publications with a complete description of the methodology used, including taxonomic identification data of ticks. Articles employing the following methodologies were included: RT-PCR, RT-qPCR, qPCR, PCR, NGS technologies, virus isolation in cell cultures from field-collected tick pools, and experimental infections in ticks and tick cell cultures. No restrictions were applied regarding the year of publication.

The exclusion criteria included review articles, editorials, opinion papers, incomplete studies, paywalled articles, dissertations and theses, articles that mentioned only tick species without providing relevant data for the research, and studies that did not present any information on viruses.

3. Results

A total of 336 articles were evaluated, including 215 studies on virus detection, both previously classified and unclassified. A summary of the main findings of viruses detected in ticks, considering only detections by molecular techniques such as PCR, qPCR, RT-PCR, RT-qPCR, RNA-seq, multiplex PCR, and conventional PCR, as well as the epidemiological significance of the virus and arthropod, is presented in Table 1 (Table S1).

Table 1. Summary of the main virological findings in tick species of importance to public health.

Viral Species	Ticks	Authors/Year
Orthoflavivirus encephalitidis	*I. ricinus* and *I. inopinatus* *Hae. longicornis* *I. persulcatus* *I. ricinus*	Esser et al., 2022 [22] Jung et al., 2024 [23] Klaus et al., 2010 [24] Laaksonen et al., 2017 [25] Ott et al., 2020 [26] Yun et al., 2012 [27] Topp et al., 2022 [28]
Orthoflavivirus loupingi	*I. ricinus* *I. pavlovskyi*	Papa et al., 2008 [29]
Orthoflavivirus nilense	*I. ricinus* *Hy. marginatum*	Korobitsyn et al., 2021 [30] Kolodziejek et al., 2014 [31]
Orthoflavivirus powassanense	*I. scapularis*	Tokarz et al., 2017 [32] Narvaez et al., 2023 [33] Johnson et al., 2018 [34]
Orthoflavivirus kyasanurense	*I. persulcatus* *D. marginatus*, *D. reticulatus*	Wagner et al., 2022 [35]
Asfivirus haemorrhagiae	*O. moubata* *O. porcinus* *O. sonrai*	Vial et al., 2007 [36] Peter et al., 2020 [37] Ravaomanana et al., 2010 [38]
Uukuvirus dabieshanense	*Hae. longicornis*	Han et al., 2024 [39] Xu et al., 2024 [40]
Bandavirus dabieense	*Hae. longicornis* *I. persulcatus* *Rh. microplus* *D. silvarum*,	Wang et al., 2015 [41] Han et al., 2022 [42] Li et al., 2022a [43] Lin et al., 2020 [44]
Bandavirus heartlandense	*A. americanum*	Newman et al., 2020 [45] Tuten et al., 2020 [46] Aziati et al., 2023 [47]
Orthonairovirus haemorrhagiae	*I. ricinus*, *Rh. bursa*, *Hy. dromedarii*, *Hy. marginatum*, *Rh. sanguineus*, *A. variegatum*, *D. nuttalli*, *D. marginatus*, *Rh. sanguineus* s. l.	Hua et al., 2020 [48] Amoah et al., 2024 [49] Schulz et al., 2021 [50] Mohammadian et al., 2016 [51] Moming et al., 2018 [52] Farhadpour et al., 2016 [53] Cuadrado-Matías et al., 2024 [54] Sultankulova et al., 2022 [55]

Table 1. *Cont.*

Viral Species	Ticks	Authors/Year
Alongshan virus	*I. ricinus*, *Rh. microplus*, *Rh. (e.) evertsi*, *I. persulcatus*, *Rh. sanguineus* s. l., *Hae. longicornis*, *D. nuttalli*, *D. marginatus*	Kuivanen et al., 2019 [56] Guo et al., 2020 [57] Ogola et al., 2022 [58] Kholodilov et al., 2020 [59] Dinçer et al., 2019 [60] Liu et al., 2024 [61] Kholodilov et al., 2021 [62]
Yanggou tick virus	*D. nuttalli*, *D. marginatus*	Kholodilov et al., 2021 [62]

Legend: Amblyomma (A.); Ixodes (I.); Ornithodoros (O.); Dermacentor (D.); Rhipicephalus (Rh.); Haemaphysalis (Hae.); Hyalomma (Hy.).

Viruses of public health importance were identified in 32 viral isolation studies. A brief summary of the main viruses identified in batches of tick species of medical and veterinary importance is found in Table 2 (Table S2).

Table 2. Viruses of medical and veterinary importance isolated from batches of tick species in cell cultures.

Viral Species	Ticks	Authors/Year
Orthoflavivirus encephalitidis	*I. persulcatus*, *Hy. dromedarii*, *O. savignyi* *I. ricinus* *D. silvarum*	Adelshin et al., 2015 [63] Mahdi et al., 2011 [64] Danielová et al., 2002 [65] Bai et al., 2024 [66] Yurchenko et al., 2017 [67]
Orthoflavivirus powassanense	*I. marxi*, *I. cookie*, *I. scapularis*, *I. dammini*	Telford et al., 1997 [68] Dupuis II et al., 2013 [69] McLean et al., 1964 [70] McLean et al., 1967 [71]
Orthoflavivirus nilense	*Rh. Pulchellus* *A. gemma*	Lwande et al., 2013 [72]
Bandavirus heartlandense	*A. americanum*	Romer et al., 2022 [73]
Bandavirus dabieense	*Hae. longicornis*	Yun et al., 2016b [74]
Orthonairovirus haemorrhagiae	*Hy. (a.) asiaticum*, *Boophilus* sp., *Rhipicephalus* sp., *Amblyomma* sp.	Hassanein; El-Azazy, 2000 [75] Zhang et al., 2018 [76]
Alphavirus semliki	*Rh. pulchellus*, *A. gemma*, *A. lepidum*, *Hy. truncatum*	Lwande et al., 2013 [72]
Asfivirus haemorrhagiae	*O. moubata*	Wilkinson et al., 1988 [77] Haresnape et al., 1988 [78]

Legend: Amblyomma (A.); Ixodes (I.); Ornithodoros (O.); Dermacentor (D.); Rhipicephalus (Rh.); Haemaphysalis (Hae.); Hyalomma (Hy.).

Among the 336 studies, forty articles were presented as experimental studies on ticks (larvae, nymphs, and adults), considering infection and experimental transmission studies. A brief summary of the main findings is found in Table 3 (Table S3). In addition, seven studies were described as experimental studies of infection in tick cells (Tables 4 and S4).

Table 3. Studies of experimental infection of viruses of medical and veterinary importance in ticks of great epidemiological relevance.

Viral Species	Ticks	Authors/Year
Orthoflavivirus encephalitidis	*I. ricinus*, *D. reticulatus* *I. persulcatus*, *I. ricinus-I. persulcatus hybrids*	Ličková et al., 2020 [79] Liebig et al., 2020 [80] Belova et al., 2023 [81] Bakker et al., 2024 [82] Migné et al., 2022 [83]
Orthoflavivirus nilense	*I. ricinus*, *O. moubata* *A. ovale*, *A. tigrinum*, *A. tonelliae*	Flores et al., 2019 [84] Răileanu et al., 2020 [85] Lawrie et al., 2004 [86]
Orthoflavivirus louisense	*A. ovale*, *A. tigrinum*, *A. tonelliae*	Flores et al., 2019 [84]
Orthoflavivirus powassanense	*I. scapularis*, *A. americanum*, *D. variabilis*, *Hae. longicornis*	Raney et al., 2022 [87] McMinn et al., 2024 [88] Obellianne et al., 2024 [89] Sharma et al., 2021 [90]
Orthonairovirus haemorrhagiae	*Rh. (e.) evertsi*, *Rh. appendiculatus*, *A. variegatum*, *Boo. decoloratus*	Shepherd et al., 1991 [91] Faye et al., 1999 [92]
Asfivirus haemorrhagiae	*O. (p.) porcinus*, *O. (p.) domesticus*, *O. moubata* *O. erraticus* s. s.	Oliveira et al., 2019 [93] Oliveira et al., 2020 [94] Kleiboeker et al., 1999 [95]
Bandavirus heartlandense	*Hae. longicornis*	Raney et al., 2022 [96]
Alongshan virus	*I. ricinus*	Ebert et al., 2023 [97]

Legend: Amblyomma (A.); Ixodes (I.); Ornithodoros (O.); Dermacentor (D.); Rhipicephalus (Rh.); Haemaphysalis (Hae.); Boophilus (Boo.).

Table 4. Viruses of public health importance studied in cell cultures from ticks.

Viral Species	Ticks	Authors/Year
Orthoflavivirus encephalitidis	*O. moubata*	Bell-Sakyi et al., 2009 [98]
Orthoflavivirus nilense	*A. americanun*	Ciota et al., 2015 [99]
Orthoflavivirus louisense	*D. andersoni*	Ciota et al., 2014 [100]
Orthonairovirus haemorrhagiae	*I. scapularis*	Kendall et al., 2020 [101]

Legend: Ornithodoros (O.); Amblyomma (A.); Ixodes (I.); Dermacentor (D.).

High-throughput sequencing is a technology that allows the simultaneous sequencing of millions or even billions of genome fragments, resulting in a large volume of data, which may refer to complete viruses, fragmented viruses, or short viral sequences. Based on this, information from 42 articles that used high-throughput sequencing methods was analyzed using Heatmap to identify the viral families detected in tick samples. The studies used are available in the supplementary files, and a brief summary of the main tick species of public health importance used is summarized in Table 5 (Table S5).

Due to the large volume of data generated by high-throughput sequencing, articles that exclusively used this method were represented by a heat map to demonstrate and visualize the diversity and distribution of viral families detected in different tick species (Figures 2 and 3). The families *Phenuiviridae*, *Hepadnaviridae*, *Nairoviridae*, *Spinareo-viridae*, and *Virgaviridae predominate*, indicating greater diversity or the number of de-tections associated with these groups (Figure 3).

Table 5. The main tick species of medical and veterinary importance used in viral metagenomics studies.

Tick Species	Location/Region/State/Country	Authors/Year
Rh. microplus	Brazil	Souza et al., 2018 [102]
I. ricinus,	Norway	Pettersson et al., 2017 [12]
D. reticulatus,	Croatia	Sameroff et al., 2022 [103]
Hae. concinna	France	Stegmüller et al., 2023 [104]
Hae. longicornis,		
D. everestianus,		Yang et al., 2023 [105]
Rh. microplus,	China	Xia et al., 2015 [106]
Rh. sanguineous,		Yang et al., 2019 [107]
Hy. asiaticum		
Rh. Sanguineus,	China	Wang et al., 2024 [108]
Rh. microplus		
I. persulcatus,	China	Cai et al., 2023 [109]
Hae. japonica,	China	Qin et al., 2023 [110]
D. silvarum,	China	Liu et al., 2022 [111]
Hae. concinna		
Hae. longicornis,	China	Li et al., 2023 [112]
D. silvarum,	China	Qin et al., 2023 [110]
D. nuttalli,	China	Zhao et al., 2020 [113]
D. marginatus		
	New York and Connecticut, USA	Tokarz et al., 2019 [114]
I. scapularis	Wisconsin, USA	Cross et al., 2018 [115]
	Pennsylvania, USA	Sakamoto et al., 2016 [116]

Legend: Ixodes (I.); Haemaphysalis (Hae.); Hyalomma (Hy.); Dermacentor (D.); Rhipicephalus (Rh.).

Based on the virological findings in ticks obtained in the reviewed scientific literature, viral agents of great importance for public health were listed, which are implicated in clinical manifestations that ranged from mild to severe cases, including deaths in humans (Table 6). The suggested severity classification was carried out based on the scientific literature consulted from the bibliographic survey.

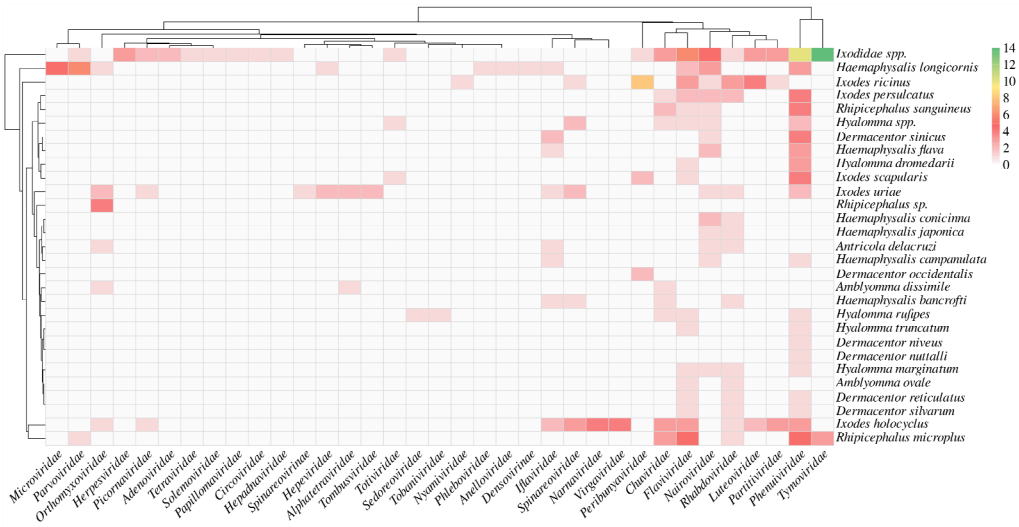


Figure 2. Heatmap of overall record abundance (number of times representatives of viral families appeared throughout the literature search), showing the relationship between viral families and tick species. Legend: Each cell indicates the number of records of viruses belonging to a given viral family (horizontal axis) detected in tick species or genera (vertical axis). Colors range from white (no records) to red and green (highest number of records), according to the intensity scale on the right.

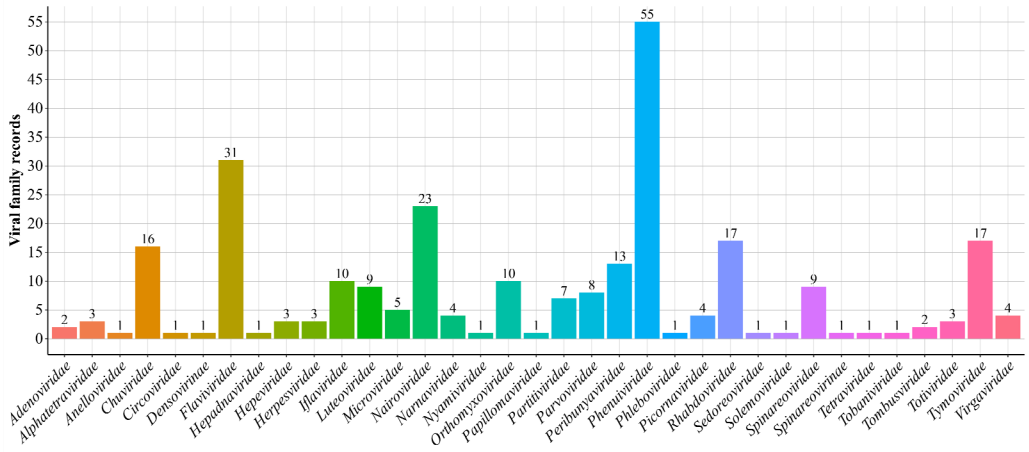


Figure 3. Distribution of records for each detected viral family. The bar graph shows the frequency of records of different virus families (horizontal axis) identified in studies involving ticks. The vertical axis represents the total number of occurrences per viral family. The color variations between the bars correspond solely to the visual differentiation between viral families.

Table 6. Viral agents causing infections in humans.

Viral Family	Viral Species	Severity Classification
Flaviviridae	*Orthoflavivirus encephalitidis*	Severe
	Orthoflavivirus loupingi	Moderate
	Orthoflavivirus powassanense	Severe
	Orthoflavivirus kyasanurense	Severe
	Orthoflavivirus omskense	Moderate
	Orthoflavivirus nilense	Moderate
	Orthoflavivirus usutuense	Moderate
	Orthoflavivirus louisense	Moderate
Nairoviridae	*Orthonairovirus haemorrhagiae*	Severe
	Orthonairovirus dugbeense	Moderate
	Orthonairovirus yezoense	Moderate
	Orthonairovirus kasokeroense	Moderate
	Orthonairovirus nairobiense	Moderate
Phenuiviridae	*Bandavirus dabieense*	Severe
	Bandavirus heartlandense	Moderate
Orthomyxoviridae	*Thogotovirus bourbonense*	Moderate
	Thogotovirus thogotoense	Moderate
	Thogotovirus dhoriense	Moderate/Severe
Togaviridae	*Alphavirus semliki*	Mild
Poxviridae	*Parapoxvirus pseudocowpox*	Mild
	Parapoxvirus bovinestomatitis	Mild
Arenaviridae	*Mammarenavirus choriomeningitidis*	Moderate
Spinareoviridae	*Coltivirus dermacentoris*	Mild
Peribunyaviridae	*Orthobunyavirus bunyamweraensei*	Mild
Paramyxoviridae	*Henipavirus nipahense*	Severe
Ungroup	*Alongshan virus*	Mild/Moderate
	Haseki tick virus	Mild/Moderate

4. Discussion

4.1. Family Flaviviridae: Orthoflavivirus

4.1.1. *Tick-borne encephalitis virus*: *Orthoflavivirus encephalitidis*

Orthoflavivirus encephalitidis is an arthropod-borne virus (arbovirus) first identified in 1937 during scientific expeditions to the Far East [117]. Historically, three subtypes have been recognized: European, Eastern, and Siberian, which exhibit broad and partially overlapping geographic distributions [118]. More recently, two additional subtypes have been described: Baikalian and Himalayan [119,120].

The vectors of *Orthoflavivirus encephalitidis* vary according to geographic region. For example, *I. ricinus* and *I. persulcatus* are responsible for transmission in Europe and Russia, respectively [117]. However, the virus has also been associated with other genera within the family *Ixodidae*, such as *Hyalomma* [27,66,121,122]. In addition, species of the genus *Dermacentor* have likewise been implicated as potential vectors of the agent [66,121,123,124].

4.1.2. *Louping ill virus*: *Orthoflavivirus loupingi*

I. ricinus is considered the natural vector of *Orthoflavivirus loupingi*, and the occurrence of the virus varies according to the distribution of its vectors. Sheep are highly susceptible to infection caused by the virus, often developing encephalitis, which can be fatal [125]. Additionally, the virus has been reported in horses, goats, cattle, and humans [126–128]. Recently, a study described inflammatory lesions and viral distribution in a naturally infected dog that exhibited progressive neurological signs leading to death [129]. Clinical manifestations in humans can be asymptomatic or symptomatic, resembling influenza-like symptoms such as fever and headache [125].

4.1.3. *Powassan virus*: *Orthoflavivirus powassanense*

Orthoflavivirus powassanense comprises two phylogenetically distinct lineages transmitted by different Ixodidae vectors. Both lineages are reported in North America (USA and Canada), with lineage I being disseminated primarily by *I. cookei* and *I. marxi*, while lineage II is transmitted by *I. scapularis* [32,130,131]. The virus was first isolated from *Dermacentor andersoni* specimens collected in Colorado [132]. Since then, the etiological agent has been isolated from *I. cookei*, *I. scapularis*, *I. marxi*, among others [68,133,134]. Furthermore, recent studies have demonstrated that *A. americanum*, *D. variabilis* [90], and Hae. longicornis [87] are competent vectors for the virus, as they are capable of becoming infected, transmitting it to their offspring, and infecting mammalian hosts that present clinical manifestations of infection.

In humans, *Orthoflavivirus powassanense* can cause severe neuroinvasive disease. Most symptomatic cases initially present with febrile illness, but neurological involvement can progress and become fatal. Approximately 10% of patients with neuroinvasive disease caused by the virus die, and survivors often suffer from neurological sequelae [134,135].

4.1.4. *Kyasanur forest disease virus*: *Orthoflavivirus kyasanurense*

Orthoflavivirus kyasanurense comprises two variants, both transmitted by ticks [136]. Lineage I, reported in the Kyasanur forest, Karnataka, India, is transmitted primarily by *Haemaphysalis spinigera*, while lineage II, identified in 1995 after an outbreak of hemorrhagic fever in Jeddah province, Saudi Arabia, has been reported in species of the families Argasidae and Ixodidae, specifically *O. savignyi* and *Hy. dromedarii*, respectively [64,137]. The virus has also been reported in several tick species, including *Hy. marginatum* s. l., *D. auratus*, *I. petauristae*, *Rh. haemaphysaloides*, *A. lepidum*, and *Hae.* [136–139]. The agent is pathogenic for humans, with clinical manifestations ranging from mild symptoms such

as fever, headache and body aches, to more severe cases presenting hemorrhagic and neurological complications [140].

4.1.5. *Omsk haemorrhagic fever virus*: *Orthoflavivirus omskense*

Orthoflavivirus omskense was first identified in batches of *D. reticulatus* ticks collected in Omsk, Russia [141–143]. The agent is endemic in some regions of Russia, such as Omsk, Novosibirsk, Kurgan, and Tyumen [35]. Since its identification, the virus has also been reported in other tick species, such as *I. persulcatus*, *D. reticulatus*, and *D. marginatus*, collected in Akmola, Kazakhstan [35]. These recent findings suggest a possible expansion of the viral agent, as the pathogen was previously restricted to regions of Russia.

The clinical signs caused by infection are well documented; however, information on the pathogen's pathogenesis in humans remains limited. The disease is characterized by a biphasic febrile illness, which can progress to hemorrhagic manifestations and, in more severe cases, neurological symptoms [144].

4.1.6. *West Nile virus*: *Orthoflavivirus nilense*

Orthoflavivirus nilense is predominantly transmitted by mosquitoes; however, the virus has also been isolated from tick species such as *Rh. pulchellus* and *A. gemma* collected in the Ijara District, Kenya [72] and *Argas reflexus hermanni* collected in the Nile Delta, Egypt [145]. Experimental studies involving *O. moubata* [86], *I. ricinus* [85], *A. ovale*, *A. tigrinum*, and *A. tonelliae* [84] suggest a potential role for ticks in virus transmission. Although these results demonstrate transmission potential, studies indicate that ticks are less efficient vectors of Orthoflavivirus nilense compared to mosquitoes [86]. However, the virus has been observed to persist within ticks for a period, suggesting that these arthropods may serve as temporary reservoirs [84,145].

4.1.7. *Kadam virus*: *Orthoflavivirus kadamense*

Orthoflavivirus kadamense was isolated from *Rh. pravus* ticks collected from cattle in Karamoja district, Uganda [146]. Since its discovery, new strains have been detected in ticks such as *Rh. appendiculatus* collected in Nairobi, Kenya [147] and *Hy. dromedarii* collected from a camel in Wadi Thamamah, Riyadh, Saudi Arabia [148]. The identification of antibodies against the virus in humans and cattle, together with the death of a camel from which infected ticks were collected, raises the suspicion that the viral agent may be pathogenic for camels [148–150]. Therefore, it is recommended that future studies be conducted to understand the ecology of the agent, as well as its pathogenic effects on public health.

4.1.8. *Langat virus*: *Orthoflavivirus langatense*

Orthoflavivirus langatense was isolated from tick batches of the genus *Ixodes* collected in Malaysia [151]. Subsequently, it was also isolated from *Hae. papuana* and *I. persulcatus* in Thailand and Siberia, respectively [152]. Experimental studies have evaluated the vector competence of several tick species for *Orthoflavivirus langatense*. For instance, the virus was found in multiple organs of *Hae. longicornis*, with evidence of both horizontal transmission and transmission to susceptible mice [153,154]. Studies on *I. scapularis* showed that the tick acquired the virus during blood feeding on infected mice, transmitted it transstadially to subsequent developmental stages, and that viral infection modulated gene expression changes in the ticks [155].

4.1.9. *Usutu virus*: *Orthoflavivirus usutuense*

The maintenance cycle of *Orthoflavivirus usutuense* involves several bird species as primary hosts, mosquitoes as primary vectors, especially arthropods of the genus *Culex*,

and humans and other mammals as accidental hosts [156–158]. Although mosquitoes are recognized as the main vectors of this virus, a recent study demonstrated that the viral agent adapted to the cells of ticks of the species *I. ricinus* (IRE/CTVM19). Furthermore, the virus survived the molting process, from nymph to adult, and transmission of the agent through saliva was observed [159]. These data suggest that *I. ricinus* may be a competent vector for maintenance and transmission of the agent.

4.1.10. *Saint Louis encephalitis virus*: *Orthoflavivirus louisense*

Orthoflavivirus louisense is transmitted by mosquitoes, especially *Culex* mosquitoes [160]. Furthermore, vector competence studies conducted in Brazil on ticks for this virus [84]. The results demonstrated that ticks of the genus *Amblyomma* (*A. ovale*, *A. tigrinum*, and *A. tonelliae*) acquired the virus. Although transstadial transmission was observed, the arthropods were not competent to transmit the virus to susceptible vertebrate hosts in any case.

4.1.11. *Karshi virus*: *Orthoflavivirus royalense*

Orthoflavivirus royalense was identified in pools of *O. papillipes* ticks collected from *Rhombomys opimus* in Beshkent, Karshinsk Steppe, Uzbek Soviet Socialist Republic [161]. More recently, the viral agent was detected in ticks of the species *Hy. asiaticum*, *Hy. scupense*, and *D. nuttalli* collected in different regions of Xinjiang, China [162]. These findings suggest that these species may serve as potential vectors of the agent in the region. Furthermore, research has shown that the virus can infect a wide range of cells, including several human cell lines. Due to its close phylogenetic relationship with *Orthoflavivirus powassanense* and *Orthoflavivirus kyasanurense*, it is believed that *Orthoflavivirus royalense* can cause infections in humans [163,164]. However, to evaluate this hypothesis, further studies are needed to assess its pathogenicity in mammals.

In adult ticks, an experimental study evaluated the transmission of *Orthoflavivirus royalense* in ticks belonging to the genus *Ornithodoros* [165]. The results indicate that *O. parkeri*, *O. sonrai*, and *O. tartakovskyi* are important arthropods for the maintenance of the agent, as they remained vectors of the virus for long periods, transmitting it to susceptible mice.

4.2. Family Nairoviridae: Orthonairovirus

4.2.1. *Crimean-Congo hemorrhagic fever virus*: *Orthonairovirus haemorrhagiae*

Orthonairovirus haemorrhagiae is a single-stranded, negative-sense RNA virus [166]. It is a zoonotic virus maintained in a tick-vertebrate-tick cycle. The geographic distribution of *Orthonairovirus haemorrhagiae* overlaps with that of Hyalomma ticks, suggesting that members of this genus play a primary role in virus transmission [150,167,168]. Recently, the virus has been detected in several *Hyalomma* species, including *Hy. marginatum*, *Hy. dromedarii*, *Hy. excavatum*, *Hy. anatolicum*, and *Hy. scupense* collected from cattle in Balochistan, Pakistan [169]. However, species from other genera have also been found harboring *Orthonairovirus haemorrhagiae*, such as *Boophilus decoloratus*, *Rh. (e.) evertsi*, collected in regions of Senegal [170], and *A. variegatum* collected in Cameroon [171]. Clinical signs in animals are usually asymptomatic, but the virus is highly lethal in humans [172,173]. Therefore, it is important to expand entomovirological surveillance in ticks to prevent future outbreaks of the disease.

4.2.2. *Dugbe virus*: *Orthonairovirus dugbeense*

Orthonairovirus dugbeense was first isolated from a batch of *A. variegatum* ticks collected from cattle in Nigeria [174]. Since then, the virus has been isolated from several species, including *A. gemma* (Ijara District, Nairobi), *A. lepidum* (Nairobi), *A. variegatum* (southern

Senegal), and *Rh. pulchellus* (Ijara District, Nairobi), leading to the belief that the agent is maintained in nature by many tick species [72,147,175]. However, we emphasize the importance of experimental studies to assess the vectorial competence of the species, since the mere identification of the agent in the arthropod does not mean that it is a vector of the pathogen. Humans are susceptible to infection by *Orthonairovirus dugbeense*, which usually causes a mild febrile illness [176–178].

4.2.3. *Yezo virus*: *Orthonairovirus yezoense*

Orthonairovirus yezoense is transmitted by ticks, with *I. persulcatus* as the main vector. Between 2020 and 2021, only *I. persulcatus* ticks tested positive for the virus in molecular assays, and only tick-derived cells demonstrated viral replication [179]. More recently, the virus was also detected in pools of *I. ovatus* and *Hae. megaspinosa* ticks collected in Hokkaido, Japan [179,180]. A recent study detected *Orthonairovirus yezoense* in *I. persulcatus* ticks collected from migratory birds in Japan; the data suggest that birds may be involved in the virus maintenance cycle. However, further studies are needed to validate this hypothesis [181].

4.2.4. *Kasokero virus*: *Orthonairovirus kasokeroense*

Orthonairovirus kasokeroense was recently detected and isolated from *O. (r.) faini* ticks collected from *Rousettus aegyptiacus* bats in Python Cave, Uganda, in 2013 and 2017 [182]. The research provides evidence supporting *O. (r.) faini* as the vector of *Orthonairovirus kasokeroense*, as no blood meal was observed in ticks, indicating that the arthropods did not feed on actively infected bats, resulting in active viral replication within the ticks. However, we emphasize the importance of experimental studies to evaluate the hypothesis.

4.2.5. *Nairobi sheep disease orthonairovirus*: *Orthonairovirus nairobiense*

Orthonairovirus nairobiense has been identified as the causative agent of the high mortality rates observed in sheep in markets in Nairobi, Kenya. The virus has been isolated from several sheep, and *Rh. appendiculatus* ticks have been implicated as vectors of the agent [183]. Since its discovery, the virus has also been isolated from other tick species, such as *Rh. haemaphysaloides* [184], *Hae. longicornis* [185], and *A. variegatum* [186], collected in India, China, and Kenya, respectively. This virus is of great importance to animal and human health, as it causes hemorrhagic gastroenteritis, fever, abortion, and high mortality in small ruminants, and febrile illness with nausea, headache, and vomiting in humans [187]. The disease has mortality rates of up to 90% in susceptible animals, resulting in significant economic losses in production systems [187,188].

4.2.6. *Hazara virus*: *Orthonairovirus hazaraense*

Orthonairovirus hazaraense was isolated from I. redikorzevi ticks collected in Kaghan Valley, Western Pakistan [189]. Although its natural host is unknown, serological evidence has been detected in rodent serum samples [190,191]. Orthonairovirus hazaraense was classified in the same serogroup as *Orthonairovirus haemorrhagiae* based on cross-reactivity between antibodies and antigens of the two viruses [192]. Although *Orthonairovirus hazaraense* is capable of inducing a disease similar to that caused by *Orthonairovirus haemorrhagiae* in mice, the agent has no association with human disease and is considered nonpathogenic [191,193].

4.2.7. *Antu virus*: *Orthonairovirus antuense*

Orthonairovirus antuense is another recently discovered member of the *Nairoviridae* family. The agent was isolated from *D. silvarum* tick samples collected at the China–North Korea border [194]. Although there is no evidence of infections in humans or domestic

animals, the agent exhibited phylogenetic relationships with *Orthonairovirus tomdiense* and *Orthonairovirus sakhalinense*, both of which are thought to infect humans and domestic animals [195–197].

4.2.8. *Beiji nairovirus*: *Norwavirus beijiense*

Norwavirus beijiense was first detected in *I. persulcatus* collected in Heilongjiang Province, China [14]. More recently, however, the agent has been detected in *I. persulcatus*, *I. pavlovskyi*, and *I. ovatus* collected in Hokkaido, Fukushima, and Nagano, Japan [198]. Norwavirus beijiense has been associated with febrile illnesses in patients with a history of tick bites prior to illness onset. Additionally, the viral agent has also been detected in *I. persulcatus*, *I. crenulatus*, *D. silvarum*, *D. nuttalli*, *Hae. concinna*, and *Hae. longicornis* collected by flagging in regions of China [199]. Thus, an expansion of the agent is observed in a wide variety of species, making it extremely important to intensify entomovirological surveillance, as well as experimental studies to evaluate vector competence for the different tick species.

4.3. Family Phenuiviridae

4.3.1. *SFTS virus*: *Dabie bandavirus*: *Bandavirus dabieense*

Bandavirus dabieense is transmitted by ticks and is characterized by thrombocytopenia, fever, hemorrhage, and gastrointestinal symptoms [200]. The transmission cycle of *Bandavirus dabieense* is not fully understood. Ticks of the species *Hae. longicornis* are considered the primary vectors of the virus [201–204]. However, the agent has also been detected in other species collected in Korea: *I. nipponensis* [205,206], *Hae. flava* [206,207], *A. testudinarium* [206]; China: *Hae. concinna* [43,208], *Rh. microplus* [41], *I. persulcatus*, *Hae. japonica*, and *D. silvarum* [43]; Japan: *Hae. hystricis* [209]. The virus has also been detected in a wide range of vertebrates in China, including sheep, cattle, pigs, chickens, and dogs [210].

4.3.2. *Heartland virus*: *Bandavirus heartlandense*

Bandavirus heartlandense has been identified in *A. americanum* ticks collected in several areas of Missouri, implicating it as a vector [211]. Recently, the virus has been detected in A. americanum in Alabama [45], Illinois [46], and Missouri [47], and has also been isolated in Georgia [73]. *A. americanum* is the primary vector of the agent, but a recent study has shown that *Hae. longicornis* ticks can acquire and transmit the virus to vertebrates [96]. Symptoms of the disease are similar to those of ehrlichiosis and can include fever, anorexia, fatigue, nausea, and diarrhea [212].

4.3.3. *Hunter island group virus*: *Bandavirus albatrossense*

Bandavirus albatrossense was discovered after an outbreak in a colony of albatross (Thalassar-che cauta) on Albatross Island, located in northwestern Tasmania. The virus was isolated from batches of *I. eudyptidis* ticks collected from diseased and healthy birds. However, the maintenance cycle of the agent and its pathogenicity are unknown. Phylogenetic analyses indicated that the viral agent is closely related to *Bandavirus dabieense* and *Bandavirus heartlandense*, classifying it as a new member of the family *Phenuiviridae* [213].

4.3.4. *Bhanja virus*: *Bandavirus bhanjanagarense*

Bandavirus bhanjanagarense is transmitted by metastriate ixodid ticks. The first isolation of the agent occurred in 1954 from ticks of the species *Hae. intermedia* collected in the Ganjam district, Orissa State, India. Furthermore, the pathogen has been reported in other ixodid genera such as *Haemaphysalis* (*Hae. punctata*, *Hae. sulcata*), *Hyalomma* (*Hy. marginatum*, *Hy. detritum*, *Hy. drome-darii*, *Hy. truncatum*, *Hy. asiaticum*), *Dermacentor* (*D. marginatus*), *Rhipicephalus* (*Rh. bursa*, *Rh. appendiculatus*), *Boophilus* (*B. decoloratus*, *B. annulatus*, *B. geigyi*)

and *Amblyomma* (*A. variegatum*) [214]. The viral agent does not cause clinical signs in adult animals; however, it is pathogenic for young ruminants, resulting in central nervous system impairment [215,216].

4.3.5. *Dabieshan tick virus*: *Uukuvirus dabieshanense*

Uukuvirus dabieshanense was identified in ticks of the species *Hae. longicornis* collected in regions of China (Hubei, Zhejiang, Beijing, and Xinjiang) [217]. Since its discovery, the virus has been reported in several tick species, including *Rh. microplus*, *Rh. haemaphysaloides*, and others in Yunnan and Guizhou provinces, southwest China [218]. Recently, molecular epidemiological investigations were conducted in ticks, and *Uukuvirus dabieshanense* was detected primarily in *Hae. longicornis* in other previously unreported provinces of China [39,218–220]. The high detection rate of the virus in ticks, especially *Hae. longicornis*, suggests that this arthropod is the main disseminator of the agent in the provinces of China and Japan [39,221,222]. Therefore, we emphasize the importance of expanding viral investigations in ticks to better understand their dynamics in nature and the risks to public health.

4.3.6. *Lihan tick virus*: *Uukuvirus lihanense*

Uukuvirus lihanense was first identified in a metagenomic study conducted on *Rh. micropulus* ticks collected in Yunnan Province, China. The study described the S segment (GenBank MH814975) and the L segment (GenBank MH814976); to date, there are no records of the M segment. Since its discovery, partial segments of the virus have been reported in molecular studies on ticks in Colombia (*D. nitens* and *Rh. micropulus*) and Brazil (*Rh. micropulus*), with all sequences showing high similarity to the sequence found in China [102,223,224]. To date, there is no clear evidence of the pathogenicity of *Uukuvirus lihanense* in humans, so the public health risk is unknown.

4.3.7. *Kabuto mountain virus*: *Uukuvirus kabutoense*

Uukuvirus kabutoense was isolated and characterized from batches of *Hae. flava* ticks collected in Hyogo, Japan. Furthermore, the study evaluated the infectivity and pathogenicity of the virus in lactating mice. The study found that high pathogenicity was maintained after three passages, demonstrating 100% mortality in this murine model [225]. Furthermore, the viral agent was also detected in a *Hae. formosensis* nymph collected in Wakayama Prefecture [226]. We emphasize the importance of expanding experimental research on the viral agent to assess its pathogenic potential and the risk it poses to public health.

4.3.8. *Uukuniemi virus*: *Uukuvirus uukuniemiense*

Uukuvirus uukuniemiense was isolated from ticks of the species *I. ricinus*, collected during a tick-borne virus investigation in Uukuniemi, Finland [227]. To date, *Uukuvirus uukuniemiense* has not been associated with any human disease [228]. However, its arboviral potential and pathogenicity remain unknown [229].

4.3.9. *Mukawa virus*: *Phlebovirus mukawaense*

Phlebovirus mukawaense was discovered in 2018, when scientists isolated the virus from female I. persulcatus ticks collected in Mukawa, Hokkaido, Japan [230]. Recently, the virus was detected for the first time in Heilongjiang, China, in ticks of the species *I. persulcatus* and *Hae. concinna*, representing the first report of the agent in the region [231]. In the same study, the authors isolated *Phlebovirus mukawaense* in Vero cells, indicating its possible pathogenicity in mammalian cells and potential to cause infections in humans. However, there are no reports of *Phlebovirus mukawaense* directly associated with human

cases. Therefore, studies aimed at assessing its potential risk to public health are of paramount importance.

4.4. Family Orthomyxoviridae

4.4.1. *Bourbon virus*: *Thogotovirus bourbonense*

Thogotovirus bourbonense was described in 2017 after identification in a patient residing in Bourbon, Kansas, USA. Tick samples collected in Andrew, Gentry, and Nodaway, northwestern Missouri, were tested, and three pools of A. americanum were positive. The tick species *A. americanum* is believed to be the likely vector of *Thogotovirus bourbonense* [232]. Experimentally, *A. americanum* ticks were able to become infected and transmit the virus transstadially to the nymphal and adult stages. Vertical transmission was also observed in transstadially infected females [233]. This tick is aggressive and feeds on a variety of vertebrate species, including humans [234–236]. Thus, it becomes an important arthropod for the epidemiology of the agent.

4.4.2. *Thogoto virus*: *Thogoto thogotovirus*: *Thogotovirus thogotoense*

Thogotovirus thogotoense was discovered in two batches of ticks. The first batch contained four tick species (*B. decoloratus*, *Rh. appendiculatus*, *Rh. simus*, and *B. evertsi*), and the second batch contained only *B. decoloratus* (50 individuals), all collected from cattle in the Thogoto Forest, Nairobi, Kenya [237]. Since then, the virus has been reported in other tick species, such as *Hae. longicornis* [238,239], *A. gemma*, and *A. lepidum* [147], Kyoto City, Japan, and Nairobi, Kenya, respectively.

4.4.3. *Dhori virus*: *Dhori thogotovirus*: *Thogotovirus dhoriense*

Thogotovirus dhoriense was identified in ticks of the species *Hy. dromedarii* collected from camels in Dhori village, Kutch district, Gujarat, India. Since its discovery, the pathogen has been reported in other tick species, such as *A. gemma* and *Rh. pulchellus*, implicating them as possible vectors in regions of Kenya [147,240]. This agent has rarely been reported in humans; however, we emphasize the importance of surveillance to assess its spread among arthropod vectors to prevent future outbreaks.

4.5. Family Togaviridae

4.5.1. *Semliki forest virus*: *Alphavirus semliki*

Alphavirus semliki was isolated from ticks of the species *Rh. pulchellus*, *A. gemma*, *A. lepidum*, and *Hy. truncatum* collected from wild animals in Ijara District, Kenya [72]. Experimental studies demonstrated that the virus is lethal to mice, which developed paralysis and seizures followed by death, whereas rabbits exhibited only fever and paralysis [241,242]. Little is known about clinical symptoms in humans, although antibodies against the viral agent have been reported in South Africa and Mozambique. Furthermore, *Alphavirus semliki* has also been reported in Cameroon, the Democratic Republic of the Congo, the Central African Republic, Senegal, Nigeria, and Uganda [242,243].

4.5.2. *Ndumu virus*: *Alphavirus ndumu*

Alphavirus ndumu was described from batches of mosquitoes of the species *Mansonia uniformis* and *Aedes circumluteolus*, collected in Ndumu, KwaZulu-Natal, South Africa [244]. The viral agent was also isolated from other mosquito species of medical and veterinary importance, including *Culex pipiens* [245], *Culex rubinotus*, *Culex cinereus*, *Aedes tricholabis*, *Aedes luridus*, *Anopheles rufipes*, *Anopheles ziemanni*, among others [246,247]. Furthermore, *Alphavirus ndumu* was also isolated from a tick of the species *Rh. pulchellus* collected in Ijara District, Kenya [72]. However, the actual role of ticks in the maintenance and transmission of the virus remains unknown.

4.6. Family Asfarviridae

African swine fever virus: *Asfivirus haemorrhagiae*

Asfivirus haemorrhagiae has been identified in several species of the genus *Ornithodoros* in the regions of South Africa, Tanzania, and Madagascar [37,38,248]. Experimental studies confirm the vectorial competence of eight of these species for viral transmission, highlighting the significant epidemiological role of these ticks in maintaining the viral cycle [93,94,249,250]. *Asfivirus haemorrhagiae* does not pose a risk to humans, but is highly contagious among domestic and feral pigs, causing high mortality and generating substantial economic impacts on the global swine industry [4].

4.7. Family Poxviridae

4.7.1. *Myxomatosum cuniculi virus*: *Leporipoxvirus myxoma*

Leporipoxvirus myxoma has been detected in *Rh. pusillus* and *Hy. lusitanicum* collected from rabbits (*Oryctolagus cuniculus*) and hares (*Lepus granatensis*) in the provinces of Cádiz, Seville, and Badajoz, Spain [251]. *Leporipoxvirus myxoma* is harmless to humans; however, it is lethal to several rabbit species [252,253].

4.7.2. *Milker's node virus*: *Pseudocowpox virus*: *Parapoxvirus pseudocowpox*

In 2020, *Parapoxvirus pseudocowpox* was detected in ticks of the species *A. variegatum*, *Hy. (M.) rufipes* and *Hy. truncatum*, removed from cattle in the provinces of Gourma, Kompienga, and Tapoa, located in eastern Burkina Faso [254]. The natural interaction between the virus and these tick species is unknown.

4.7.3. *Bovine papular dermatitis virus*: *Parapoxvirus bovinestomatitis*

Parapoxvirus bovinestomatitis was detected in ticks of the species *A. variegatum* and *Hy. truncatum*, removed from Cattle in Burkina Faso [254]. Other studies report the detection of *Parapoxvirus* genetic material in tick species such as *Hy. marginatum*, *Hy. scupense* and *Rh. bursa* from cattle in Corsica, France [255]. However, the role of ticks in the epidemiology of this viral agent remains unknown.

4.7.4. *Lumpy skin disease virus*: *Capripoxvirus lumpyskinpox*

Capripoxvirus lumpyskinpox, caused by *Caprivirus*, is a contagious disease that can be transmitted by close contact with infected animals, contaminated food and water sources, and by a wide range of biting vectors, including flies, lice, mosquitoes, and ticks [256]. The agent has been detected in ticks of the genera *Rhipicephalus*, *Amblyomma*, *Hyalomma*, and *Dermacentor* from provinces of Egypt and South Africa [257–260], and experimental studies have been conducted in some ixodid species [261]. However, further studies are needed to understand the true role of arthropods in the epidemiology of this viral agent.

4.8. Family Arenaviridae

4.8.1. *Lymphocytic choriomeningitis virus*: *Mammarenavirus choriomeningitidis*

Mammarenavirus choriomeningitidis is widely distributed in Africa, the Americas, Asia, and Europe [262–264]. It is a pathogen that causes significant neurological infections in humans, including encephalitis, meningitis, and congenital neurological defects [265]. The etiological agent has been detected in some tick species, such as D. silvarum and Hae. japonica collected in Jilin Province, northeastern China [266]. However, the role of ticks in the transmission of *Mammarenavirus choriomeningitidis* remains unknown [266,267].

4.8.2. *Tacaribe virus*: *Mammarenavirus tacaribeense*

Mammarenavirus tacaribeense was isolated from *A. americanum* ticks collected in Florida and showed 99.6% similarity to the original isolate [268]. No natural infections in humans

have been reported; however, the isolation of the virus from mosquitoes and ticks, as well as its maintenance in vertebrate cells, suggests that the virus may use arthropods as vectors, resulting in infections in vertebrates [268,269]. However, the importance of more detailed studies to validate this hypothesis is emphasized.

4.9. Family Sedoreoviridae

4.9.1. *Great Island virus*: *Kemerovo serocomplex*: *Orbivirus magninsulae*

The prototype of the "Big Island virus" complex, *Orbivirus magninsulae*, previously classified as Big Island virus, was originally isolated from *I. uriae* ticks and their seabird host in 1973 in eastern Canada [270]. Since its discovery, new members have been reported, such as "Muko virus," isolated from *I. tudus* ticks in Japan [271].

4.9.2. *Bluetongue virus*: *Orbivirus caerulinguae*

Orbivirus caerulinguae is widely transmitted by specimens of the genus *Culicoides*. Of the 1400 cataloged species, approximately 30 are known to transmit the virus [272,273]. Although members of the genus *Culicoides* are the main vectors of the pathogen, the agent has also been studied in ticks of different species. Serotype 8 was evaluated in five tick species: *I. ricinus*, *I. hexagonus*, *D. reticulatus*, *Rh. bursa*, and *O. savignyi* [274]. The research showed that arthropods of the families Ixodidae and Argasidae can become infected with the pathogen. However, further studies are needed to determine the actual role of ticks in the virus transmission cycle.

4.9.3. *Murid herpesvirus 4*: *Rhadinovirus muridgamma4*

Rhadinovirus muridgamma4 is transmitted through respiratory excretions, urine, and saliva, and vertical transmission can also occur via the transplacental route [275]. Moreover, research provides important data on the sexual transmission of the agent among mice [276,277]. Although studies indicate that the virus is maintained in a vertebrate cycle, a recent study investigated the vector competence of the tick *I. ricinus* for *Rhadinovirus muridgamma4* [278]. The research demonstrated that ticks acquired the virus and were able to transmit it to susceptible mice, and that the agent survived molting, thereby characterizing transstadial transmission. In addition, the pathogen was transmitted to the next generation, characterizing vertical transmission. The study provides information consistent with the criteria for arthropod-borne viruses (arboviruses) [279,280]. Nevertheless, further studies are required to better understand the actual role of ticks in the transmission of this agent.

4.10. Family Spinareoviridae

4.10.1. *Eyach virus*: *Coltivirus ixodis*

Coltivirus ixodis was described from *I. ricinus* tick samples collected in the Federal Republic of Germany [281]. The agent was also isolated from *I. ventalloi* ticks collected in Mayenne, France, thus adding a potential new natural vector of the viral agent [282]. Although the study identified antibodies against *Coltivirus ixodis* in farmers, the pathogen has not yet been isolated from animals or humans. The identification of the agent in ticks does not confirm their status as vectors of the virus; therefore, experimental studies to assess the vectorial competence of these arthropods are of paramount importance to validate this hypothesis.

4.10.2. *Colorado tick fever virus*: *Coltivirus dermacentoris*

The primary vector of *Coltivirus dermacentoris* is the tick species *D. andersoni* [283,284]. The virus is maintained in nature through enzootic cycles between rodents and ticks, and the distribution of the etiological agent overlaps with that of its arthropod vector [283].

The viral agent has been reported in tick species such as *D. albipictus*, *Otobius lagophilus*, *I. sculptus*, *I. spinipalpis*, and *Hae. leporispalustris*, most of which have been removed from wild-caught vertebrates in areas of the USA [285,286].

4.10.3. *Kundal virus*: *Kundal coltivirus*: *Coltivirus kundalense*

Coltivirus kundalense was discovered in 2019 in a tick of the species *Hy. anatolicum* during surveillance for *Orthonairovirus haemorrhagiae* in Gujarat, India. The agent exhibited cytopathic effects in Vero CCL-81 cells, human rhabdomyosarcoma cells, and porcine stable kidney cells, but not in *Pipistrellus ceylonicus* bat embryo cells or *Aedes albopictus* cells. Although the virus shows cytopathic effects in vertebrate cell cultures, it was found to be non-pathogenic to mice [287]. Currently, it is unknown whether *Coltivirus kundalense* is pathogenic to humans.

4.11. Family Peribunyaviridae

Bunyamwera virus: *Orthobunyavirus bunyamweraense*

Orthobunyavirus bunyamweraense is maintained in nature through a cycle involving mosquitoes and susceptible vertebrates. *Ae. aegypti* is believed to be the primary vector of the agent [288,289]. However, the viral agent has also been isolated from tick species such as *Rh. pulchellus*, *A. gemma*, *A. lepidum*, and *Hy. truncatum* collected in Ijara District, Kenya [72]. Research suggests that ticks may contribute to the maintenance, spread, and possibly transmission of the virus.

4.12. Family Picornaviridae

Foot-and-mouth disease virus: *Aphthovirus vesiculae*

Foot-and-mouth disease is caused by *Aphthovirus vesiculae*, which is highly infectious and contagious among domestic and wild cloven-hoofed animals, with outbreaks causing substantial economic losses to the global livestock industry [290]. An unusual finding occurred in 2006 during surveillance of tick-borne arboviruses in Nairobi, Kenya. *Aphthovirus vesiculae* was isolated from ticks of the species *Rh. pulchellus*, representing the first known isolation associated with tick collections [147]. Although *Aphthovirus vesiculae* is not transmitted by ticks of the genus *Rhipicephalus*, there is evidence that the viral agent can persist for several days in ticks fed on infected animals [291].

4.13. Family Rhabdoviridae

4.13.1. *Zahedan rhabdovirus*: *Zarhavirus zahedan*

Zarhavirus zahedan is a recently discovered virus in ticks of the species *Hy. anatolicum anatolicum* collected in Zahedan, Iran, in 2001. However, the full study on the virus was published in 2015 [292]. In the research, the agent was able to infect mammalian Vero cells and demonstrated lethality in mice regardless of the inoculation route.

4.13.2. *Barur virus*: *Ledantevirus barur*

Ledantevirus barur was isolated from batches of *Rh. pulchellus* collected in Mogadishu, Somalia [293] and later from ticks of the species *Hae. intermedia* collected in Saga, Shimoga district, Karnataka, India [294]. The agent was isolated from *Rh. pulchellus* collected from animals at the Njiru and Dagoretti slaughterhouses, outside Nairobi, Kenya [147]. A recent high-throughput sequencing study detected Ledantevirus barur in *Rh. appendiculatus* [295]. Although the agent has not been reported in humans, identification of the virus in ticks and rodents suggests a possible maintenance cycle between hematophagous arthropods and mammals [147].

4.14. Family Paramyxoviridae

Nipah virus: *Henipavirus nipahense*

Henipavirus nipahense is highly pathogenic and infects a wide range of wild and domestic animals, as well as humans, in whom it can cause pulmonary or encephalitic disease with a mortality rate of 92% [296,297]. Transmission of the agent occurs through direct contact with infected pigs, as well as exposure to porcine bodily fluids [298–300]. The hypothesis that ticks may be involved in the agent's transmission cycle led to a recent study evaluating infection in *I. scapularis (IDE8)* embryonic cells [301]. The research demonstrated the presence of viral RNA and antigens, and infectious virus was recovered. These results indicate that ixodid cells can support infection by the agent. However, further studies are required to assess the potential for viral infection in ticks.

4.15. Ungrouped

4.15.1. *Alongshan virus*

Recently, *Alongshan virus* was detected in *I. persulcatus* collected in the Mongolia region of China, where the agent was first described [302,303]. The primary vectors of the virus are ticks, particularly of the genus *Ixodes*, which is most frequently associated with the pathogen [59,104,304,305]. Recently, a study evaluated infection of *Alongshan virus* in ticks of the species *I. ricinus* and *D. reticulatus*. The results provide initial insights into the agent's transmission cycle and reveal the potential of these arthropods to transmit the virus [97].

4.15.2. *Yanggou tick virus*

Yanggou tick virus is another member of the Jingmenvirus group, first detected in *D. nuttalli* ticks in 2018 (GenBank MH688529.1) collected in the Xinjiang Uyghur Autonomous Region, China. Recently, the agent was detected in *D. nuttalli* and *D. marginatus* collected in Russia [62]. Furthermore, for the first time, a study demonstrated the replication of *Yanggou tick virus* in cell cultures of *I. ricinus* (IRE/CTVM19) and *Hy. anatolicum* (HAE/CTVM8) ticks. These results suggest that the pathogen may adapt to different vectors or that the agent may adapt to different tick species. *Yanggou tick virus* and *Alongshan virus* are closely related and cluster separately from other viruses in the JMV group [302]. Although there are no reports of *Yanggou tick virus* in humans, the virus belongs to the JMV group, which includes viruses previously reported in humans, such as *Alongshan virus*, which generally causes mild symptoms [303,306,307].

4.15.3. *Mpulungu flavivirus*

Mpulungu flavivirus (GenBank LC582740.1) is a newly discovered virus in ticks of the species *Rh. muhsamae* collected in different areas of Zambia (Isoka, Mpulungu, and Samfya) [308]. The virus showed 83.2% identity with *Ngoye virus*, previously identified in *Rh. evertsi evertsi* and *Rh. guilhoni* in Senegal [309]. To date, there are no reports of *Mpulungu flavivirus* in humans or other vertebrates, nor in other arthropods.

4.15.4. *Meaban-like virus*

Meaban-like virus (GenBank KJ440085-KJ440090) was detected in *O. maritimus* ticks collected in the Western Mediterranean basin [310]. The detected segment is a partial 124 bp fragment corresponding to the nonstructural protein gene 5 (GenBank KJ440090.1). BLAST analysis identified approximately 95% similarity with a fragment of the NS5 gene of *Orthoflavivirus meabanense*, a virus first detected in *O. maritimus* on islands of South Brittany, France [311].

4.15.5. *Phlebovirus gomselga*

Phlebovirus gomselga was detected in *I. persulcatus* collected in the Chelyabinsk region, Russia, in 2018 [312]. Subsequently, the agent was detected again in *I. persulcatus* collected from the same region [313]. Phylogenetic analysis indicated that *Phlebovirus gomselga* clusters with tick-borne phleboviruses.

4.15.6. *Phenuivirus stavropol*

The first report of *Stavropol virus* occurred in 2020, detected in *D. reticulatus* ticks collected between 2011 and 2012 in Stavropol, Russia (GenBank ON920444-ON920447) [312]. The study identified a preference of *Stavropol virus* for *D. reticulatus*, although the agent was detected once in *Rh. turanicus*. This is an unclassified virus of the family *Phenuiviridae*, with no reported human infections to date, and its pathogenicity remains unknown.

4.15.7. *Okutama tick virus*

Okutama tick virus was first detected in *Hae. flava* nymphs collected from Tokyo, Japan [314]. Subsequently, the agent was also detected in adult *Hae. flava* ticks collected from Cape Toi and Hokuriku, Japan [221,315]. The pathogenicity in humans and animals, as well as the transmission cycle, remain unknown.

4.15.8. *Shibuyunji virus*

Shibuyunji virus was initially detected in *Rhipicephalus* (*b.*) sp. ticks from cattle in the Shibuyunji District, Lusaka Province, Zambia [316] and more recently in *Rhipicephalus* sp. ticks collected from cattle in different districts of Zambia [317]. In this study, the virus showed approximately 99% similarity with the initial report. Although there are no reports of human infections, detection in ixodid ticks infesting cat-tle raises concerns regarding potential zoonotic risk.

4.15.9. *Phlebovirus-like-AYUT*

A molecular study identified a fragment of the L segment of a phlebovirus, provisionally named *Phlebovirus-like-AYUT*, detected in *Rh. sanguineus* s. l. collected from a dog in Phra Nakhon Si Ayutthaya Province, Thailand [318]. The agent exhibited 82.6% similarity with *Brown dog tick phlebovirus 2*, previously detected in *Rh. sanguineus* in Trinidad and Tobago [319]. Additionally, it shares 72.4% and 70.3% identity with *Brown dog tick phlebovirus 1* and *Bole Tick Virus 1*, respectively, both associated with the genus *Phlebovirus*, family *Phenuiviridae*.

4.15.10. *Haseki tick virus*

Haseki tick virus was discovered in *I. persulcatus* ticks collected in Novosibirsk, Russia [320]. Human cases have been reported after tick bites. Human infections have been associated with fever, acute respiratory injuries, and coinfection with other tick-borne agents. Phylogenetic analysis revealed that all *Haseki tick virus* sequences clustered together and were closely related to *Bole tick virus* 4 and *Trinbago virus*.

4.15.11. *Kindia tick virus*

Kindia tick virus was identified in *Rh. geigyi* ticks collected in Guinea, West Africa [321]. Subsequently, the agent was detected in *Rh. geigyi*, *Rh. annulatus*, and *Rh. decoloratus* collected from domestic animals in the Republic of Guinea [322,323]. It is an unclassified flavivirus transmitted by ticks of the JMV group, family *Flaviviridae* [323]. Since it is a member of the JMV group, which includes viruses previously reported in humans, such as *Alongshan virus*, although there are no reports of human cases, we emphasize the importance of experimental studies to evaluate its impact on public health.

4.15.12. *Yichun nairovirus*

Yichun nairovirus is a recently discovered agent in *I. persulcatus* ticks, identified through a metagenomic study that assessed the viral diversity of four tick species collected in northeastern China [111]. Recently, the agent was also detected in *I. persulcatus* and *I. pavlovskyi* ticks collected in Hokkaido and Fukushima, Japan [198]. Although *Yichun nairovirus* is phylogenetically closely related to *Norwavirus beijiense*, little is known about its potential public health risk [111].

4.15.13. *Kinna virus*

Kinna virus is another unclassified virus identified in *A. gemma* ticks collected in Isiolo County, Kenya [324]. Phylogenetic analysis grouped the agent with viruses of the *Bandavirus* genus, showing a strong relationship with *Bandavirus guertuense*. The study also demonstrated that *Kinna virus* is pathogenic to mice. However, further studies are needed to assess the potential risk of *Kinna virus* to public and animal health.

4.15.14. *Sandy Bay virus*

Sandy Bay virus is an unclassified agent isolated from I. uriae ticks collected from the king penguin colony at Sandy Bay, near a king penguin colony at the head of Finch Creek, and from Catch-me Cave on Macquarie Island (Figure 1), a preferred perch for rockhopper penguins [325]. The pathogen showed 94–96% similarity to *Orthoflavivirus gadgetsense*, previously identified in *I. uriae* ticks collected on Macquarie Island, Australia [326]. To date, there are no records of Sandy Bay virus infections in humans. The discovery in ticks parasitizing king penguins suggests that the arthropod has adapted to specific hosts and therefore does not pose a significant threat to human health. However, we emphasize the importance of further studies to evaluate its possible pathogenicity in vertebrates.

Many unclassified viruses have been detected in ticks, but there is a lack of evidence as to whether they are pathogenic to humans and animals. However, some viruses that were initially "unclassified" have subsequently proven pathogenic, such as Bandavirus heartlandense and unclassified *Alongshan virus*. The lack of experimental studies creates a surveillance blind spot, where potentially dangerous viruses circulate unmonitored.

4.16. Climate Change

Atmospheric characteristics and dynamics are important environmental factors, and any changes can significantly impact animal ecology [327]. Changes in climate patterns (temperature and humidity) influence the epidemiology of zoonotic diseases by altering host dynamics, the distribution of clinically important vectors such as ticks, and the pathogens they transmit [328–334]. Climate change can create new niches for hematophagous arthropods such as ticks, facilitating the expansion of their geographic distribution into previously unreported areas [335–338]. Furthermore, changes in environmental variables affect host populations, including rodents, deer, and birds, which in turn alter the abundance and distribution of ticks [339].

Climatic variables also influence specific aspects of etiological agents, including improved climatic adaptation for reproduction, accelerated life cycles, decreased extrinsic incubation time, and increased virulence [340]. Rising temperatures, for example, significantly impacted the replication of *Orthoflavivirus nilense* in mosquitoes, increasing the rate of virus replication and bites, thus improving the arthropod's ability to transmit the agente [341–343].

5. Conclusions

Ticks are globally recognized as important vectors of pathogens with significant impacts on public and veterinary health. These arthropods are expanding their geographic ranges in response to climate change, consequently affecting pathogen transmission cycles. This scenario increases the risk of arbovirus transmission, particularly viruses from the families *Flaviviridae*, *Nairoviridae*, and *Asfarviridae*, which are known to cause serious infections in humans and animals (domestic and livestock), including large-scale deaths. In this review, we demonstrate the wide range of viruses that have been described in tick species, including unclassified viruses such as *Alongshan virus* and *Yanggou tick virus*, which exhibit phylogenetic relationships with viral groups important to public health. We also provide important data on the various studies using viruses and ticks, demonstrating several gaps in knowledge about the interaction between viruses and ticks, as evidenced by the lack of experimental studies to validate theories of tick-borne viral transmission. Therefore, we recommend that viral investigation studies in tick populations, as well as experimental infection and transmission studies using unclassified viruses already identified in ticks, are crucial to understanding potential risks to public and animal health, especially in the context of ongoing climate change.

Supplementary Materials: The following are available online at https://www.mdpi.com/article/10.3390/arthropoda3040016/s1, Table S1: Complete list of viruses detected in ticks, considering only detection by molecular techniques, such as PCR, qPCR, RT-PCR, RT-qPCR, RNA-seq, multiplex PCR and conventional PCR, Table S2: List of unclassified viruses detected in tick species, considering only detection by molecular techniques, such as PCR, qPCR, RT-PCR, RT-qPCR, RNA-seq, multiplex PCR and conventional PCR, Table S3: Viruses isolated from tick species in different regions, Table S4: Viral studies of experimental infection in tick species, Table S5: List of experimental studies in tick cell cultures, Table S6: Metagenomic studies included in the present study from different regions of the globe. References [344–511] are cited in the supplementary materials.

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