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Chapter

Neglected Arboviruses in Latin America

Alfonso J. Rodriguez-Morales and D. Katterine Bonilla-Aldana

Abstract

Over the last decade, there has been an increasing concern for epidemics in Latin America, as well as in other regions, due to arboviruses causing epidemics. Before 2013, dengue and yellow fever were of major preoccupation in urban and rural areas, respectively. But after that year, the emergence of chikungunya (2013) and Zika (2015) with their widespread in the region, affected millions of individuals, especially in tropical countries. Nowadays, other alpha and flaviviruses, but also bunyaviruses, have been circulating in the region causing small outbreaks, as is the case of Mayaro, Madariaga, Rocio, Oropouche, and St. Louis encephalitis, among others. In the current chapter, we address the situation regarding these other arboviruses that have been neglected by also being a differential diagnosis and an etiology of febrile syndrome in the region.

Keywords: Mayaro, Madariaga, Rocio, Oropouche, St. Louis encephalitis, alphavirus, flavivirus, neglected, Latin America

1. Introduction

Vector-borne diseases and many zoonotic diseases remain significantly relevant in tropical areas, such as Latin America. In the specific case of those caused by viruses, arboviruses, this region, as well as Asia, are particularly affected over time, primarily due to the widespread of competent vectors, as is the case of *Aedes aegypti*, but also *A. albopictus*, and more recently *A. vittatus* [1, 2]. Then, as expected, an integrated One Health approach, considering the environment, and animal and human health, is needed for vector-borne diseases [3].

Over the last decades, multiple arboviral diseases caused by alphaviruses and flaviviruses have been a concern in Latin America [4]. However, since the introduction of yellow fever and dengue, the epidemiological landscape in the region has significantly changed [5]. Dutch slave traders brought yellow fever (YFV) to the America from Africa during the mid-seventeenth century.

For the next two and a half centuries, the disease terrorized seaports throughout the America [6]. Reports describe the possible first introduction in 1648 in Mexico [5, 7–9]. Although some studies suggest dengue (DENV) was introduced in the America, through the Caribbean islands in 1635 [5, 10, 11], before 1981, dengue was considered a public health problem only in Asia and posed little or no threat to the region of the America [11, 12]. This scenario shifted with the 1981 Cuban epidemic,

the first significant dengue epidemic in the area. For the following decade, sporadic cases of dengue were observed. Then, in 1990, Venezuela experienced the second major epidemic in the region. These events marked dengue as an emerging disease in the America [11, 12]. As observed, flaviviruses, such as dengue and yellow fever, have been significant concerns regarding morbidity and mortality in the region [4, 13–27]. Additionally, many of them, as observed with Zika (ZIKV) and chikungunya (CHIKV), lead to chronic consequences, such as central nervous system (CNS) compromise (including congenital microcephaly and other complications of congenital Zika syndrome) [28–32], as well as chronic rheumatic and non-rheumatic diseases (CHIKV) [33–39].

Taxonomically speaking, the essential arboviruses are included in the genus alphavirus, family Togaviridae (**Figure 1**), which consists of a total of 32 species; and in the genus flavivirus, family Flaviviridae (**Figure 2**), where 53 species are currently included.

- Realm: Riboviria	6
- Kingdom: Orthornavirae Realm: Riboviria	6
+ Phylum: Duplomaviricota Kingdom: Orthornavirae	0
- Phylum: Kitrinoviricota Kingdom: Orthornaviroe	0
– Class: Alsuviricetes Phylum: Kitrinoviricoto	0
+ Order: Hepeflviroles Class: Alsuvirketes	0
- Order: Mortellivirates Class: Alsovinicetes	0
+ Family: Bromoviridae Order: Martellivirales	0
+ Family: Closteroviridoe Order: Martellivirales	•
+ Family: Endornoviridae Order: Martellivirales	• •
+ Family: Kitaviridae Order: Martellivirales	•
+ Family: Moyoviridoe Order: Mortellin/roles	6
- Family: Togoviridee Order: Martelliwirales	0
- Genus: Alphovirus Family: Togoviridoe	0
Species: Aura virus Genus: Alphavirus	0
Species: Barnah Forest virus Genus: Alphavirus	0
Species: Bebaru virus Genus: Alphavirus	0
Species: Caaingua virus Genus: Alphavirus	0
Species: Cobassou virus Genus: Alphavirus	0
Species: Chikungunya virus Genus: Alphavirus	0
Species: Eastern equine encephalitis virus Genus: Alphavirus	0
Species: Eilot virus Genus: Alphavirus	0
Species: Everglades virus Genus: Alphovirus	0
Species: Fort Morgan virus Genus: Alphavirus	0
Species: Getah virus Genus: Alphavirus	0
Species: Highlands J virus Genus: Alphavirus	0
Species: Madariaga virus Genus: Alphavirus	0
Species: Mayaro virus Genus: Alphavirus	0
Species: Middelburg virus Genus: Alphavirus	0
Species: Masso das Pedras virus Genus: Alphavirus	0
Species: Mucambo virus Genus: Alphavirus	0
Species: Ndumu virus Genus: Alphavirus	0
Species: Onyong-nyong virus Genus: Alphavirus	0
Species: Phuna virus Genus: Alphavirus	0
Species: Rio Negro virus Genus: Alphavirus	0
Species: Ross River virus Genus: Alphavirus	0
Species: Salmon pancreas disease virus Genus: Alphavirus	0
Species: Semliki Forest virus Genus: Alphavirus	0
Species: Sindbis virus Genus: Alphavirus	0
Species: Southern elephant seal virus Genus: Alphavirus	0
Species: Tonate virus Genus: Alphavirus	0
Species: Trocara virus Genus: Alphavirus	0
Species: Una virus Genus: Alphavirus	0
Species: Venezuelan equine encephalitis virus Genus: Alphavirus	0
Species: Western equine encephalitis virus Genus: Alphavirus	0
Species: Whataroa virus Genus: Alphavirus	0

Figure 1.

Taxonomical classification of viruses belonging to the genus alphavirus (family Togaviridae, order martellivirales, class alsuviricetes). (https://ictv.global/taxonomy).

— Realm: Riboviria		0
- Kingdom: Orthon	aaviraa Realm: Alboviria	0
+ Phylum: Dupi	armavirikata Kiingdom: Orthernavirae	0
— Phylum: Kitri	newhicada Kingdom: Orthernawinae	0
+ Class: Alsi	ndricates Phylum: Kitrinováricata	0
- Class: Flo	auvidicadas Phylum: Ritrinoukicata	0
- Order	Amarillovirales Class: Flassviricetes	0
— Fa	mily: Flaviviridae Order: Amorillovirales	0
_	Genus: Flawlokus Family: Flawlokdore	0
	Species: Apol vitus Gonus: Alov/Wrus	0
	Species: Aroa virus Genus: Flavivirus	0
	Species: Bogaza virus Genus: FlavWirus	0
	Species: Bonzi virus Genus: Flavivirus	0
	Species: Bouboul virus Genus: Florivirus	0
	Species: Bukalasa bat virus Genus: Flavilvirus	0
	Species: Cacipacare Wrus Genus: FlavWirus	0
	Species: Carey Island virus Genus: Florivirus	0
	Species: Cowbane Ridge virus Genus: Flavivirus	0
	Species: Dakar bat virus Genus: Flavivirus	0
	Species: Dengue virus Genus: Flovikirus	0
	Species: Edge Hill Wrus Genus: Flavivirus	0
	Species: Entebbe bot virus Genus: Florivirus	0
	Species: Gadgets Gully virus Genus: Plantinus	0
	Species: Ilhous virus Geneus: Flavivirus	0
	Species: Israel turkay meningoencephalomyolitis virus Genus: Flavivirus	0
	Species: Japanese encephalitis virus Genus: Flavivirus	0
	Species: Jugra virus - Genus: Flavivirus	0
	Species: Jutiopo virus Genus: Flov/w/rus	0
	Species: Kadam vikus Genus: Flavivicus	0
	Species: Kedougou virus Genus: Flavilvirus	0
	Species: Kokobera virus Genus: Flavivirus	0
	Species: Koutango virus Genus: Flavivirus	0
	Species: Kyatamur Forest disease wirus Genus: Flarivirus	0
	Species: Langat virus Genus: Flavivirus	0
	Species: Louping III virus Genus: Flavivirus	0
	Species: Meaban virus Genus: Flavivirus	0
	Species: Modoc virus Genus: Flavivirus	0
	Species: Montana myotis leukaencephalitis virus – Genus: Flavivirus	0
	Species: Murray Valley encephalitis virus Genus: Flowlvirus	0
	Species: Ntaya virus Genus: Flovivirus	0
	Species: Omsk hemorrhogic fever virus Genus: Flav/virus	0
	Species: Phrom Penh bat virus Genus: Flavivirus	0
	Species: Powassan Wrus Genus: Flavivirus	0
	Species: Rio Bravo virus Genus: Flavivirus	0
	Species: Royal Farm virus Genus: Flavivirus	0
	Species: Saboya virus Genus: Flavininus	0
	Species: Saint Louis encephalitis virus Genus: Flavivirus	0
	Species: Sal Vieja virus - Genus: Flavivirus	0
	Species: San Parilta virus Genus: Flavivirus	0
	Species: Saumarez Reef virus Genus: Flavilvirus	0
	Species: Sepile virus Genus: Flavininus	0
	Species: Tembusu vitus Genus: Alavikitus	0
	Species: Tick berne encephalitis wirus Genus: Flavivirus	0
	Species: Tyulaniy virus Genus: Flov/Virus	0
	Species: Uganda S virus - Genus: Flavilinus	0
	Species: Usutu virus Genus: Flavivirus	0
	Species: Wesselsbron virus Genus: Floodvirus	0
	Species: West Nile virus Genus: Flavivirus	0
	Species: Yaounde virus Genus: Flovivirus	0
	Species: Yellow fover virus Genus: Flovinious	0
	Species: Yokase wirus Genus: Flashvirus	0
	Species: Zika virus - Genus: Flavivirus	0

Figure 2.

Taxonomical classification of viruses belonging to the genus flavivirus (family Flaviviridae, order amarillovirales, class flasuviricetes). (https://ictv.global/taxonomy).

Alphaviruses, originally endemic in Latin America, such as the Venezuelan equine encephalitis (VEE) and the eastern equine encephalitis; were described in 1920 in Venezuela and 1972 in Trinidad and Tobago, respectively [5]. Mayaro virus, another



Figure 3.

The number of articles published about arboviruses (alphaviruses, flaviviruses, and orthobunyaviruses) in Latin America, cumulated until November 1, 2022, in PubMed-indexed journals. (https://pubmed.ncbi.nlm.nih.gov/).

alphavirus from Trinidad and Tobago, was described in 1954. In Trinidad and Tobago, an endemic orthobunyavirus, the Oropouche virus, was described in 1955 [5].

Then, as observed in the number of published articles available in PubMed (**Figure 3**), many of these arboviruses in Latin America, such as Mayaro (MAYV), Madariaga (MADV), Saint Louis encephalitis (SLEV), Rocio (ROCV), and Oropuche (OROV) are neglected. Nevertheless, according to the World Health Organization (WHO), only DENV and CHIKV are formally included as neglected tropical diseases (https://www.ho.int/health-topics/neglected-tropical-diseases).

Even the total of articles of them (1364) is much lower than the total of DENV (20.5 times higher), ZIKV (8 times), YFV (6 times), CHIKV (5 times), or VEE (1.4 times) (**Figure 3**). So then, MAYV, MADV, SLEV, ROCV, and OROV may be considered neglected. As a consequence, such arboviruses will be analyzed in the current chapter.

2. MAYV, MADV, SLEV, ROCV, and OROV: neglected arboviruses

Both alphaviruses and flaviviruses included neglected arboviruses. Nevertheless, given the importance of DENV and YFV, flaviviruses have been studied more, and even vaccines for a long time have existed for YFV [25] and recently for DENV [40]. However, there are no vaccines against alphaviruses for humans. Nevertheless, after epidemics of CHIKV in 2014–2015 in the America, their importance increased. However, as a group, the situation is worse regarding investigating orthobunyaviruses. Epidemics of CHIKV and ZIKV, as well as periodical outbreaks of YFV, especially in Brazil and Venezuela, have influenced the attention and research on these alphaviruses and flaviviruses [26, 27].

The region's MAYV, MADV, SLEV, ROCV, and OROV can be considered neglected arboviruses [41–44]. Even in most countries, such arboviruses are not under regular surveillance, laboratory investigation, and confirmation.

2.1 Mayaro (MAYV)

MAYV, an enzootic virus [44, 45], is an alphavirus that shares epidemiological features with YFV, having sylvatic cycles involving animal reservoirs and with sylvatic and urban mosquito vectors. Clinically, MAYV shares characteristics with its genus and family. It is an arthritogenic alphavirus, as occurs with CHIKV, able to generate immune-mediated chronic disease [46, 47] but overlaps in symptoms during the acute phase with other arboviruses [48]. A few years ago, the ChikDenMaZika syndrome was proposed as a mnemotechnic rule to keep in mind Mayaro and other more frequently observed arboviruses, such as CHIKV, DENV, and ZIKV [48]. That would help decrease the negligence of Mayaro, to be considered in the differential diagnosis of febrile syndrome in the tropics or possibly caused by an arbovirus. MAYV is more frequently detected in other countries, in addition to Trinidad and Tobago, Brazil, and Peru. It has also been identified in Panama, French Guiana, Colombia, Argentina, Venezuela, and Paraguay [49, 50]. Studies have reported MAYV positivity in wild mammals, birds, or reptiles, as well as in domestic animals. Also, 12 orders of wildcaught vertebrates, most frequently in Charadriiformes and primate orders, have been identified with MAYV. This alphavirus has been detected in wild-caught mosquito genera, including Haemagogus, Aedes, Culex, Psorophora, Coquillettidia, and Sabethes [49]. Although MAYV has been identified in urban vectors, there is no evidence of sustained urban transmission. MAYV's enzootic cycle could become established in forested areas within cities, similar to the yellow fever virus [51]. Arboviruses in mosquito body pools sampled during the rainy season of 2018 in 21 bird-watching points of Cuiabá and Varzea Grande, south central Mato Grosso, Brazil, highlights the possibility of MAYV detection in urban areas of Latin America [52]. An investigation of arboviruses in patients with acute febrile illness (n=453) for less than 5 days in Mato Grosso state during the period of ZIKV and CHIKV dissemination in Brazil found multiple other neglected arboviruses [53]. Alphaviruses were detected in 2 (0.4%) patients infected with CHIKV genotype ECSA, 1 (0.2%) with Madariaga (EEEV) lineage III, and 34 (7.5%) with Mayaro (MAYV) genotype L. Four (11.4%) patients presented dual infections with DENV-1/ZIKV, DENV-1/DENV4, DENV-4/MAYV, and ZIKV/MAYV. The majority—13/34 positive for MAYV, one for Madariaga virus—are residents in Várzea Grande, the metropolitan region of Cuiabá, the capital of Mato Grosso [53]. Up to June 2015, only 121 articles were published in PubMed-indexed journals, based on a bibliometric analysis [47]. After 7 years, only 230 additional papers have been published on MAYV (Figure 3).

In countries, such as Peru, MAYV has become more critical in epidemiological terms; even MAYV is under surveillance in that country (**Figure 4**). Although that, there is still a lack of research from that country in MAYV (only 28 articles, <8% of the total on MAYV in PubMed). Especially in jungle areas in the country's north and south border with Brazil, Peru has endemic areas where MAYV and other arboviruses cause infection.

During 2017–2020, a total of 36 cases were reported by Peru (**Table 1**), most of them (29, 81%) in 2017 and predominantly in the Madre de Dios department (16, 44%) that year (**Table 1**). At least seven departments of Peru, from a total of 24, reported at least one case of MAYV during that period.



Figure 4.

Geographical distribution of ZIKV, CHIKV, and MAYV in Peru, 2020. (Modified from https://www.dge.gob.pe/epipublic/uploads/boletin/boletin_202043.pdf).

2.2 Oropouche (OROV)

In Peru, there is limited detection of OROV, an orthobunyavirus. But in 2016, at least in three districts of Madre de Dios (2) and Cusco (1), OROV outbreaks were detected (Tambopata, Iñapari, and Ocobamba).

OROV is another neglected arbovirus [54]. OROV is a species in the genus orthobunyavirus, the family Peribunyaviridae (**Figure 5**). That genus includes 103 species, but only OROV is considered of medical importance in Latin America. More relevant in North America, this genus contains the La Cross virus (LACV), which has not yet been identified in Latin America [55].

In another bibliometric study performed in June 2015 [54], only 83 articles were recovered from PubMed (43% from Brazil, 18% from the United States of America, and 6% from Peru) [54]. On May 2016, the Ministry of Health of Peru reported 57 cases of OROV [54]. Cases of OROV have also been reported in nearby countries, such as Panama, Ecuador, French Guiana, Haiti, Suriname, Trinidad and Tobago, Brazil, and Venezuela [56–60]. As occurs with MAYV, OROV is under surveillance in Peru but not in most countries of Latin America. After 7 years of the unique bibliometric assessment of OROV so far [54], only 95 additional articles have been published, showing clearly the lack of research on this orthobunyavirus.

Nevertheless, recent studies (2021–2022) in Colombia have identified OROV as an emerging cause of acute febrile illness in the country [61]. In a study with 2,967 individuals, OROV was identified in 87 of 791 (10.9%) viremic cases, where an RT-qPCR dual-target assay was possible. Those cases were from Cali (the third largest city in the country) (3/53), Cucuta (border with Venezuela) (3/19), Villavicencio (easter lowlands) (38/566), and Leticia (Amazon jungle) (43/153). In parallel, an automated anti-nucleocapsid antibody assay detected IgM in 27/503 (5.4%) and IgG in 92/568 (16.2%) patients screened, for which 24/68 (35.3%) of PCR positives had antibodies [61]. Such findings confirm OROV as an emerging pathogen and recommend increased surveillance to determine its burden as a cause of acute febrile illness in Colombia [61]. A previous assessment in Colombia diagnosed OROV in a woman 28 years of age from Turbaco, Bolivar department (near Cartagena), by viral isolation, quantitative reverse transcription PCR, and phylogenetic analysis of the small,

	Cases per year											
					%			Incidence (cases/100,000 pop.)				
Departments	2017	2018	2019	2020	2017	2018	2019	2020	2017	2018	2019	2020
Madre de Dios	16	0	0	0	55.17	0	0	0	11.14	0	0	0
Loreto	3	0	3	1	10.34	0	50	100	0.28	0	0.28	0.1
San Martin	5	0	0	0	17.24	0	0	0	0.06	0	0	0
Ucayali	4	0	0	0	13.79	0	0	0	0.08	0	0	0
Cusco	0	0	2	0	0	0	33.33	0	0	0	0.15	0
Amazonas	1	0	0	0	3.45	0	0	0	0.24	0	0	0
Ayacucho	0	0	1	0	0	0	16.67	0	0	0	0.14	0
Total	29	0	6	1	100	0	100	100	0.09	0	0.02	0.003

(Modified from https://www.dge.gob.pe/epipublic/uploads/boletin/boletin_202043.pdf).

Table 1.Cases of MAYV in Peru, 2017–2020.



Figure 5.

Taxonomical location of the genus orthobunyavirus (family Peribunyaviridae). (https://ictv.global/taxonomy).

medium, and large genomic segments. That virus was related to a strain isolated in Ecuador in 2016 [62]. That means that in countries, such as Colombia, OROV should be considered in the differential diagnosis of fever and investigated as part of the surveillance [45, 63], especially in possibly endemic areas.

2.3 Saint Louis encephalitis virus (SLEV)

Saint Louis encephalitis virus (SLEV) is a flavivirus, a member of the Japanese encephalitis virus serogroup, initially identified in 1933 in Saint Louis, Missouri, USA, as encephalitis lethargica [64], during an outbreak involving 475 cases with 71 deaths (14.9%) [65]. The encephalitis lethargica occurred in Saint Louis in 1919, 1924, and 1932 [65]. Studies on SLEV in Latin America also lack, regardless of its epidemiological situation [66]. In a bibliometric study performed in December 2016 [64], only 955 articles were recovered from PubMed (44% from the United States of America, 4% from Brazil, and 4% from Argentina) [64]. After 6 years of that bibliometric assessment of SLEV, only 172 additional articles have been published, clearly showing the lack of research on this flavivirus.

Culex species generally transmit SLEV as vectors and birds as animal hosts. Most SLEV infections are asymptomatic, but clinical manifestations range from nonspecific febrile syndrome to febrile headache, aseptic meningitis, and encephalitis, with fatality ranging from 3 to 30% [67]. In the case of Latin America, SLEV is one of the flaviviruses that circulate in Brazil [68]. Reports from Argentina [69, 70], Colombia [71], Cuba [72], Ecuador [73], French Guiana [74], Guatemala [75], Mexico [76], Panama [67, 77], Peru [78], and Uruguay [79] have also been published, among other possible identifications in other Latin countries. The primary SLEV mosquito vectors in some endemic areas include *Culex tarsalis*, *C. pipiens*, and *C. quinquefasciatus* [80, 81]. Like most arboviruses that cause central nervous system (CNS) disease in humans, most SLEV infections are asymptomatic or mild, with symptom onset 5–15 days after exposure and exhibiting a broad range of clinical presentations [80].

	Arboviruses						
Clinical findings	MAYV	MADV	ROCV	OROV	SLEV		
Fever/chills	++++	+	++	++	+++		
Myalgia/arthralgia/fatigue	+++	++	0	++	+/0		
Edema in limbs	0	0	0	0	0		
Maculopapular rash	++	0	0	0	0		
Retro-ocular pain	++	0	0	0	+/0		
Conjunctivitis, non-purulent	0	0	+)	0	0		
Lymphadenopathies		0	0	0	0		
Hepatomegaly	+	0	0	0	0		
Leukopenia/thrombocytopenia	++	0	0	0	0		
Encephalitis	0	++	++	0	++++		
Meningitis	0	0/+	++	0	+++		
Headache	0	++	++	++	+++		
Photophobia	0	0	0	+++	++		
Hemorrhages	0	0	0	0	0		

MAYV, Mayaro; MADV, Madariaga; ROCV, Rocio; OROV, Oropouche; SLEV, St. Louis Encephalitis.

Table 2.

Clinical findings of neglected arboviruses in Latin America and the proposed mnemotechnic of MAMA-ROS syndrome (MAyaro, MAdariaga, Rocio, Oropouche and St. Louis encephalitis).

The discussed neglected arboviruses may overlap clinically, then, initial differentiation between them, may be complex (**Table 2**). Unfortunately, major infectious and tropical diseases books do not cover some of them (e.g., MADV) [82, 83].

2.4 Madariaga (MADV)

Recent ecologic and genetic studies of eastern equine encephalitis virus (EEEV; togaviridae: alphavirus) have demonstrated clear separation between North and South American EEEV strains: North American EEEV cluster in a single genetic lineage—lineage I, in the system proposed by Arrigo et al. [84]—with South American EEEV strains (now known as Madariaga virus [MADV]) clustering in EEEV lineages II, III, and IV. Although there is a reasonable understanding of North American EEE's clinical and epidemiologic features, much less is known about MADV infections. MADV is neglected in multiple ways [85]. Contrasting with other neglected arboviruses, MADV has no previous bibliometric assessments nor for EEE. As shown before, there is a significant lack of studies about it [85–94]. Recent studies in Panama have clinically characterized this emerging encephalitis (Table 2) [90]. Studies from that central American countries suggest that the lack of additional neurological cases may indicate that severe MADV infections occur only rarely. Field studies suggest that over the past five decades, alphavirus infections, such as MADV and VEEV, have occurred at low levels in eastern Panama, but that MADV and VEEV infections have recently increased-potentially during the past decade. In some of eastern Panama, the endemic diseases and outbreaks of MADV and VEEV appear to differ spatially [95].

These neglected arboviruses are usually neglected; in the past, the ChikDenMaZika syndrome helped to decrease the neglect of thinking on Mayaro. Nevertheless, still, that alphavirus, as well as others, and the rest of discussed arboviruses, should be considered for an additional mnemotechnic, as MAMA-ROS syndrome (MAyaro, MAdariaga, Rocio, Oropouche and St. Louis encephalitis) (Table 2) to think in them as differential diagnoses, as also to assess their clinical presentations.

2.5 Rocio (ROCV)

ROCV emerged as a cause of outbreaks of encephalitis in Brazil during 1975–1976. However, as another neglected arbovirus, there are less than 1,000 articles in PubMed (**Figure 3**), with no bibliometric studies.

After initial descriptions, sporadic reports have been identified; nevertheless, no additional outbreaks have been reported. ROCV is probably circulating among wild birds and transmitted by *Psorophora ferox* and *Aedes scapularis* [82, 83]. It has an incubation period of 7–14 days, and illness begins with headache, fever, nausea, and vomiting, sometimes with pharyngitis and conjunctivitis (Table 2). Meningitis or encephalitis follows in many, with altered mental state and cerebellar tremor. Convulsions are uncommon. The case fatality rate is about 10%. Death occurs in patients of all ages with neurological sequelae. Gait disturbances may appear in survivors [1, 2]. Some of these neglected viruses are commonly detected during dengue outbreaks, as with other arboviruses. Patients result negative for DENV and are investigated for multiple other flaviviruses and alphaviruses. Recent seroprevalence studies in animals detected ROCV in regions of Brazil, indicating risk for reemergence of this pathogen. A recent study identified ROCV RNA in samples from two human patients for whom dengue fever was clinically suspected but ruled out by laboratory findings. Then, such results suggest that testing for infrequent flavivirus infections should be considered, including ROCV [96, 97].

A group of maps showing the distribution by countries where neglected arboviruses have been reported (**Figure 6**). Theses maps do not necessarily reflect the real distribution, but just countries that have published cases or studies showing arboviral circulation. In the case of countries, such as Bolivia and Paraguay, is particularly curious that they have not reported most of the neglected arboviral pathogens, although have been described in most of their neighboring countries.



Figure 6.

Distribution map of MAYV, MADV, ROCV, OROV, and SLEV in Latin America. This distribution indicates just circulation in the country, but not necessarily that has been detected nationwide.

	Vector								
Aedes	Culex Culicoides	Haemagogus Psorophora	Coquillettidia	Sabethes					
MAYV x	X	X X	Х	Х					
MADV ?	X	X							
ROCV x	?	Х							
OROV x	x x								
SLEV ?	x			2					
ve reported the detection	n of the arbovirus; ?, j	potential vector.							
SLEV ?	x a of the arbovirus; ?, j	potential vector.		0					

Main reported vectors of neglected arboviruses in Latin America.

A significant problem in the diagnosis of these arboviruses includes the clinical and epidemiological overlapping [4], even with possible coinfections [16, 22, 98], but also the problems derived from potential antibody cross-reactivity that may yield serological false-positive results, now even, including coinfections and cross-reactivity with SARS-CoV-2 [18, 99–102]. Then, molecular diagnosis of them is critical, including multiplex testing to search simultaneously many arboviruses and perform more specific serological testing, using better antigens, such as plaque reduction neutralizing antibody testing (PRNT) [103], especially in patients with risks for severe or complicated disease.

For the control of these neglected arboviruses, vector control is key, especially on *Aedes* and *Culex* species that represent the main mosquito genuses related to their transmission (**Table 3**).

As expected, no vaccines nor antivirals have been developed for these neglected arboviruses [104–106], although there is hope for them in the future. Therefore, symptomatic treatment is indicated with them after establishing a specific and confirmed molecular diagnosis.

3. Conclusions

Vector-borne diseases, particularly those involving virus transmission, continue to be a significant public health problem, especially in tropical countries, but even with climate change in also in subtropical countries. Still, in multiple countries, problems related to accurate diagnosis of the etiology of febrile syndrome are complex. That is in large magnitude related to arboviral pathogens, many of them neglected, as the case of MAYV, MADV, ROCV, OROV, and SLEV, among others. Therefore, after considering major arboviral diseases, such as DENV, CHIKV, ZIKV, YFV, VEE, and EEE, among others, epidemiological and clinical suspicion of them is critical to establishing a differential diagnosis, detecting them, and even identifying possible coinfections. At the same time, as there is a significant gap in knowledge about neglected arboviruses in Latin America, more research is needed to understand their implications and acute and non-acute clinical consequences and impacts.

Conflicts of interest

AJRM has been a consultant/advisor for Takeda, Sanofi Pasteur, Merck Sharp and Dohme, Valneva, and AstraZeneca.

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References

[1] Pagac BB, Spring AR, Stawicki JR, Dinh TL, Lura T, Kavanaugh MD, et al. Incursion and establishment of the Old World arbovirus vector Aedes (Fredwardsius) vittatus (Bigot, 1861) in the Americas. Acta Tropica. 2021;**213**:105739

[2] Rodriguez-Morales AJ, Paniz-Mondolfi AE, Faccini-Martínez ÁA, Henao-Martínez AF, Ruiz-Saenz J, Martinez-Gutierrez M, et al. The constant threat of zoonotic and vector-borne emerging tropical diseases: Living on the edge. Frontiers in Tropical Diseases. 2021;2:676905

[3] Faburay B. The case for a 'one health' approach to combating vectorborne diseases. Infectious Ecology Epidemiology. 2015;5:28132

[4] Rodriguez-Morales AJ, Villamil-Gomez WE, Franco-Paredes C. The arboviral burden of disease caused by co-circulation and co-infection of dengue, chikungunya and Zika in the Americas. Travel Medicine and Infectious Disease. 2016;**14**:177-179

[5] Musso D, Rodriguez-Morales AJ, Levi JE, Cao-Lormeau VM, Gubler DJ. Unexpected outbreaks of arbovirus infections: Lessons learned from the Pacific and tropical America. The Lancet Infectious Diseases. 2018;**18**:e355-ee61

[6] Bryan CS, Moss SW, Kahn RJ.Yellow fever in the Americas. Infectious Disease Clinics of North America.2004;18:275-292

[7] Figueiredo LT. Emergent arboviruses in Brazil. Revista da Sociedade Brasileira de Medicina Tropical. 2007;**40**:224-229

[8] Ortiz-Martinez Y, Patino-Barbosa AM, Rodriguez-Morales AJ. Yellow fever in the Americas: The growing concern about new epidemics. F1000Res. 2017;**6**:398

[9] Rossetto EV, Angerami RN, Luna EJA. What to expect from the 2017 yellow fever outbreak in Brazil? Revista do Instituto de Medicina Tropical de São Paulo. 2017;**59**:e17

[10] Gubler DJ. The changing epidemiology of yellow fever and dengue, 1900 to 2003: Full circle? Comparative Immunology, Microbiology and Infectious Diseases. 2004;**27**:319-330

[11] Brathwaite Dick O, San Martín JL, Montoya RH, del Diego J, Zambrano B, Dayan GH. The history of dengue outbreaks in the Americas. The American journal of tropical medicine and hygiene. 2012;**87**:584-593

[12] Dengue in Central America. The epidemics of 2000. Epidemiological Bulletin. 2000;**21**:4-8

[13] Mattar S, Morales V, Cassab A, Rodriguez-Morales AJ. Effect of climate variables on dengue incidence in a tropical Caribbean municipality of Colombia, Cerete, 2003-2008. International Journal of Infectious Diseases. 2013;17:e358-e359

[14] Rodriguez-Morales AJ,
Paniz-Mondolfi AE. Venezuela: Far from the path to dengue and chikungunya control. Journal of Clinical Virology.
2015;66:60-61

[15] Quintero-Herrera LL, Ramirez-Jaramillo V, Bernal-Gutierrez S, Cardenas-Giraldo EV, Guerrero-Matituy EA, Molina-Delgado AH, et al. Potential impact of climatic variability on the epidemiology of dengue in Risaralda, Colombia, 2010-2011. Journal of Infection and Public Health. 2015;8:291-297

[16] Villamil-Gomez WE, Gonzalez-Camargo O, Rodriguez-Ayubi J, Zapata-Serpa D, Rodriguez-Morales AJ. Dengue, chikungunya and Zika co-infection in a patient from Colombia. Journal of Infection and Public Health. 2016;**9**:684-686

[17] Zambrano LI, Sierra M, Lara B, Rodriguez-Nunez I, Medina MT, Lozada-Riascos CO, et al. Estimating and mapping the incidence of dengue and chikungunya in Honduras during 2015 using Geographic Information Systems (GIS). Journal of Infection and Public Health. 2017;**10**:446-456

[18] Cardona-Ospina JA, Arteaga-Livias K, Villamil-Gomez WE, Perez-DiazCE, KatterineBonilla-AldanaD, Mondragon-Cardona A, et al. Dengue and COVID-19, overlapping epidemics? An analysis from Colombia. Journal of Medical Virology. 2021;**93**(1):522-527. DOI: 10.1002/jmv.26194.

[19] Zambrano LI, Rodriguez E, Espinoza-Salvado IA, Rodriguez-Morales AJ. Dengue in Honduras and the Americas: The epidemics are back! Travel Medicine and Infectious Disease. 2019;**31**:101456

[20] Herrera-Martinez AD, Rodriguez-Morales AJ. Potential influence of climate variability on dengue incidence registered in a western pediatric Hospital of Venezuela. Tropical Biomedicine. 2010;**27**:280-286

[21] Zambrano LI, Sevilla C, Reyes-Garcia SZ, Sierra M, Kafati R, Rodriguez-Morales AJ, et al. Potential impacts of climate variability on dengue hemorrhagic fever in Honduras, 2010. Tropical Biomedicine. 2012;**29**:499-507

[22] Cardona-Ospina JA, Jiménez-Canizales CE, Vásquez-Serna H, Garzón-Ramírez JA, Alarcón-Robayo JF, Cerón-Pineda JA, et al. Fatal dengue, Chikungunya and Leptospirosis: The importance of assessing co-infections in febrile patients in tropical areas. Tropical Medicine and Infectious Disease. 2018;**2018**:3

[23] Rifakis PM, Benitez JA, De-la-Paz-Pineda J, Rodriguez-Morales AJ. Epizootics of yellow fever in Venezuela (2004-2005): An emerging zoonotic disease. Annals of the New York Academy of Sciences. 2006;**1081**:57-60

[24] Rodriguez-Morales AJ, Villamil-Gómez WE. Yellow fever: Still of concern for travelers of Colombia? Infection. 2018;**22**:171-172

[25] Reno E, Quan NG, Franco-Paredes C, Chastain DB, Chauhan L, Rodriguez-Morales AJ, et al. Prevention of yellow fever in travellers: An update. The Lancet Infectious Diseases.
2020;20:e129-ee37

[26] Chaves T, Orduna T, Lepetic A, Macchi A, Verbanaz S, Risquez A, et al. Yellow fever in Brazil: Epidemiological aspects and implications for travelers. Travel Medicine and Infectious Disease. 2018;**23**:1-3

[27] Rodríguez-Morales AJ, Bonilla-Aldana DK, Suárez JA, Franco-Paredes C, Forero-Peña DA, Mattar S, et al. Yellow fever reemergence in Venezuela – Implications for international travelers and Latin American countries during the COVID-19 pandemic. Travel Medicine and Infectious Disease. 2021;**2021**:102192

[28] Cardona-Ospina JA, Zapata MF, Grajales M, Arias MA, Grajales J, Bedoya-Rendón HD, et al. Physical growth and neurodevelopment of a cohort of children after 3.5 years of follow-up from mothers with Zika

infection during pregnancy-third report of the ZIKERNCOL Study. Journal of Tropical Pediatrics. 2021;**2021**:67

[29] Villamil-Gomez WE, Guijarro E, Castellanos J, Rodriguez-Morales AJ. Congenital Zika syndrome with prolonged detection of Zika virus RNA. Journal of Clinical Virology. 2017;**95**:52-54

[30] Alvarado-Socarras JL, Idrovo AJ, Contreras-Garcia GA, Rodriguez-Morales AJ, Audcent TA, Mogollon-Mendoza AC, et al. Congenital microcephaly: A diagnostic challenge during Zika epidemics. Travel Medicine and Infectious Disease. 2018;**23**:14-20

[31] Rodriguez-Morales AJ. Zika and microcephaly in Latin America: An emerging threat for pregnant travelers? Travel Medicine and Infectious Disease. 2016;**14**:5-6

[32] Rodriguez-Morales AJ, Cardona-Ospina JA, Ramirez-Jaramillo V, Gaviria JA, Gonzalez-Moreno GM, Castrillon-Spitia JD, et al. Diagnosis and outcomes of pregnant women with Zika virus infection in two municipalities of Risaralda, Colombia: Second report of the ZIKERNCOL study. Travel Medicine and Infectious Disease. 2018;25:20-25

[33] Rodriguez-Morales AJ, Cardona-Ospina JA, et al. Prevalence of post-chikungunya infection chronic inflammatory arthritis: A systematic review and meta-analysis. Arthritis Care & Research (Hoboken). 2016;**68**:1849-1858

[34] Rodriguez-Morales AJ, Villamil-Gomez W, Merlano-Espinosa M, Simone-Kleber L. Post-chikungunya chronic arthralgia: A first retrospective follow-up study of 39 cases in Colombia. Clinical Rheumatology. 2016;**35**:831-832

[35] Rodriguez-Morales AJ, Gil-Restrepo AF, Ramirez-Jaramillo V, Montoya-AriasCP, Acevedo-MendozaWF, Bedoya-Arias JE, et al. Post-chikungunya chronic inflammatory rheumatism: Results from a retrospective follow-up study of 283 adult and child cases in La Virginia, Risaralda, Colombia. F1000Res. 2016;**5**:360

[36] Rodriguez-Morales AJ, Simon F. Chronic chikungunya, still to be fully understood. International Journal of Infectious Diseases. 2019;**86**:133-134

[37] Rodriguez-Morales AJ. Letter to the Editor: Chikungunya virus infection-an update on chronic rheumatism in Latin America. Rambam Maimonides Med Journal. 2017;**2017**:8

[38] Rodriguez-Morales AJ, Restrepo-Posada VM, Acevedo-Escalante N, Rodriguez-Munoz ED, Valencia-Marin M, Castrillon-Spitia JD, et al. Impaired quality of life after chikungunya virus infection: A 12-month follow-up study of its chronic inflammatory rheumatism in La Virginia, Risaralda, Colombia. Rheumatology International. 2017;**37**:1757-1758

[39] Rodriguez-Morales AJ, Calvache-Benavides CE, Giraldo-Gomez J, Hurtado-Hurtado N, Yepes-Echeverri MC, Garcia-Loaiza CJ, et al. Post-chikungunya chronic arthralgia: Results from a retrospective follow-up study of 131 cases in Tolima, Colombia. Travel Medicine and Infectious Diseases. 2016;**14**:58-59

[40] Biswal S, Borja-Tabora C, Martinez Vargas L, Velásquez H, Theresa Alera M, Sierra V, et al. Efficacy of a tetravalent dengue vaccine in healthy children aged 4-16 years: A randomised, placebocontrolled, phase 3 trial. Lancet. 2020;**395**:1423-1433

[41] Pezzi L, Diallo M, Rosa-Freitas MG, Vega-Rua A, Ng LFP, Boyer S, et al. GloPID-R report on chikungunya, o'nyong-nyong and Mayaro virus, part 5: Entomological aspects. Antiviral Research. 2020;**174**:104670

[42] Pezzi L, LaBeaud AD, Reusken CB, Drexler JF, Vasilakis N, Diallo M, et al.
GloPID-R report on chikungunya,
o'nyong-nyong and Mayaro virus, part
2: Epidemiological distribution of
o'nyong-nyong virus. Antiviral Research.
2019;172:104611

[43] Pezzi L, Reusken CB, Weaver SC, Drexler JF, Busch M, LaBeaud AD, et al. GloPID-R report on Chikungunya, O'nyong-nyong and Mayaro virus, part I: Biological diagnostics. Antiviral Research. 2019;**166**:66-81

[44] Pezzi L, Rodriguez-Morales AJ, Reusken CB, Ribeiro GS, LaBeaud AD, Lourenco-de-Oliveira R, et al. GloPID-R report on chikungunya, o'nyong-nyong and Mayaro virus, part 3: Epidemiological distribution of Mayaro virus. Antiviral Research. 2019;**172**:104610

[45] Rodriguez-Morales AJ, Paniz-Mondolfi AE, Villamil-Gomez WE, Navarro JC. Mayaro, Oropouche and Venezuelan Equine Encephalitis viruses: Following in the footsteps of Zika? Travel Medicine and Infectious Disease. 2017;**15**:72-73

[46] Arenivar C, Rodriguez Y, Rodriguez-Morales AJ, Anaya JM. Osteoarticular manifestations of Mayaro virus infection. Current Opinion in Rheumatology. 2019;**31**:512-516

[47] Patino-Barbosa AM, Bedoya-Arias JE, Cardona-Ospina JA, Rodriguez-Morales AJ. Bibliometric assessment of the scientific production of literature regarding Mayaro. Journal of Infection and Public Health. 2016;**9**:532-534

[48] Paniz-Mondolfi AE, Rodriguez-Morales AJ, Blohm G, Marquez M, Villamil-Gomez WE. ChikDenMaZika Syndrome: The challenge of diagnosing arboviral infections in the midst of concurrent epidemics. Annals of Clinical Microbiology and Antimicrobials. 2016;**15**:42

[49] Celone M, Okech B, Han BA, Forshey BM, Anyamba A, Dunford J, et al. A systematic review and metaanalysis of the potential non-human animal reservoirs and arthropod vectors of the Mayaro virus. PLoS Neglected Tropical Diseases. 2021;**15**:e0010016

[50] Mutricy R, Matheus S, Mosnier É, Martinez-Lorenzi E, De Laval F, Nacher M, et al. Mayaro virus infection in French Guiana, a cross sectional study 2003-2019. Infection, Genetics and Evolution. 2022;**99**:105243

[51] Caicedo EY, Charniga K, Rueda A, Dorigatti I, Mendez Y, Hamlet A, et al. The epidemiology of Mayaro virus in the Americas: A systematic review and key parameter estimates for outbreak modelling. PLoS Neglected Tropical Diseases. 2021;**15**:e0009418

[52] da Silva Neves NA, da Silva FR, Morais DO, Pavon JAR, de Pinho JB, Slhessarenko RD. Chikungunya, Zika, Mayaro, and Equine Encephalitis virus detection in adult Culicinae from South Central Mato Grosso, Brazil, during the rainy season of 2018. Brazilian Journal of Microbiology. 2022;**53**:63-70

[53] de Souza Costa MC, Siqueira Maia LM, Costa de Souza V, Gonzaga AM, Correa de Azevedo V, Ramos Martins L, et al. Arbovirus investigation in patients from Mato Grosso during Zika and Chikungunya virus introdution in Brazil, 2015-2016. Acta Tropica. 2019;**190**:395-402

[54] Culquichicón C, Cardona-Ospina JA, Patiño-Barbosa AM,

Rodriguez-Morales AJ. Bibliometric analysis of Oropouche research: Impact on the surveillance of emerging arboviruses in Latin America. F1000Res. 2017;**6**:194

[55] Rogers MB, Gulino KM, Tesh RB, Cui L, Fitch A, Unnasch TR, et al. Characterization of five unclassified orthobunyaviruses (Bunyaviridae) from Africa and the Americas. The Journal of General Virology. 2017;**98**:2258-2266

[56] Navarro JC, Giambalvo D, Hernandez R, Auguste AJ, Tesh RB, Weaver SC, et al. Isolation of Madre de Dios Virus (Orthobunyavirus; Bunyaviridae), an Oropouche Virus Species Reassortant, from a Monkey in Venezuela. The American Journal of Tropical Medicine and Hygiene. 2016;**95**:328-338

[57] Wise EL, Márquez S, Mellors J, Paz V, Atkinson B, Gutierrez B, et al. Oropouche virus cases identified in Ecuador using an optimised qRT-PCR informed by metagenomic sequencing. PLoS Neglected Tropical Diseases. 2020;**14**:e0007897

[58] Elbadry MA, Durães-Carvalho R, Blohm GM, Stephenson CJ, Loeb JC, White SK, et al. Orthobunyaviruses in the Caribbean: Melao and Oropouche virus infections in school children in Haiti in 2014. PLoS Neglected Tropical Diseases. 2021;**15**:e0009494

[59] van Tongeren HA. Occurrence of arboviruses belonging to the C-, Bunyamwera and Guama groups, and of Oropouche, Junin, Tacaiuma and Kwatta viruses in man in the province of Brokopondo, Surinam: A serological survey. Tropical and Geographical Medicine. 1967;**19**:309-325

[60] Gaillet M, Pichard C, Restrepo J, Lavergne A, Perez L, Enfissi A, et al. Outbreak of Oropouche Virus in French Guiana. Emerging Infectious Diseases. 2021;**27**:2711-2714

[61] Ciuoderis KA, Berg MG, Perez LJ, Hadji A, Perez-Restrepo LS, Aristizabal LC, et al. Oropouche virus as an emerging cause of acute febrile illness in Colombia. Emerging Microbes and Infection. 2022;**2022**:1-49

[62] Gómez-Camargo DE, Egurrola-Pedraza JA, Cruz CD, Popuche D, Ochoa-Díaz MM, Guevara C, et al. Evidence of Oropouche Orthobunyavirus Infection, Colombia, 2017. Emerging Infectious Diseases. 2021;**27**:1756-1758

[63] Watts DM, Lavera V, Callahan J, Rossi C, Oberste MS, Roehrig JT, et al. Venezuelan equine encephalitis and Oropouche virus infections among Peruvian army troops in the Amazon region of Peru. The American Journal of Tropical Medicine and Hygiene. 1997;**56**:661-667

[64] Ortiz-Martínez Y, Vega-Useche L, Villamil-Gómez WE, Rodriguez-Morales AJ. Saint Louis Encephalitis Virus, another re-emerging arbovirus: A literature review of worldwide research. Le Infezioni in Medicina. 2017;**25**:77-79

[65] Encephalitis In St. Louis. American Journal of Public Health and the Nation's Health. 1933;**23**:1058-1060

[66] Mansilla AP, Grande JM, Diaz A. Effect of agroecosystems on seroprevalence of St. Louis Encephalitis and West Nile Viruses in Birds, La Pampa, Argentina, 2017-2019. Emerging Infectious Diseases. 2022;**28**:1393-1402

[67] Kopp A, Gillespie TR, Hobelsberger D, Estrada A, Harper JM, Miller RA, et al. Provenance and geographic spread of St. Louis encephalitis virus. mBio. 2013;4: e00322-e00313

[68] Figueiredo LT. The Brazilian flaviviruses. Microbes and infection. 2000;**2**:1643-1649

[69] Batallán GP, Konigheim BS, Quaglia AI, Rivarola ME, Beranek MD, Tauro LB, et al. Autochthonous circulation of Saint Louis encephalitis and West Nile viruses in the Province of La Rioja, Argentina. Review in Argentina Microbiology. 2021;**53**:154-161

[70] Valinotto LE, Barrero PR, Viegas M, Alvarez López MC, Mistchenko AS. Molecular evidence of St. Louis encephalitis virus infection in patients in Buenos Aires, Argentina. Journal of Clinical Virology. 2012;**54**:349-351

[71] Hoyos-López R, Soto SU, Rúa-Uribe G, Gallego-Gómez JC. Molecular identification of Saint Louis encephalitis virus genotype IV in Colombia.
Memórias do Instituto Oswaldo Cruz.
2015;**110**:719-725

[72] Pelegrino JL, Suárez M, Guzmán MG, Vázquez S, Benítez NR. Surveillance of St. Louis encephalitis, Eastern equine and Western equine in the province of Ciego de Avila. Revista Cubana de Medicina Tropical. 1996;**48**:109-113

[73] Baquerizo Amador L, Marmol Cevallos F. Serological investigation of St. Louis encephalitis in various regions of Ecuador. Revista Ecuatoriana de Higiene y Medicina Tropical. 1959;**16**:249-259

[74] de Thoisy B, Dussart P, Kazanji M. Wild terrestrial rainforest mammals as potential reservoirs for flaviviruses (yellow fever, dengue 2 and St Louis encephalitis viruses) in French Guiana. Transactions of the Royal Society of Tropical Medicine and Hygiene. 2004;**98**:409-412 [75] Scherer WF, Dickerman RW, Ordóñez JV. Serologic surveys for antibodies to Western, Eastern, California, and St. Louis Encephalitis and Dengue 3 arboviruses in Middle America, 1961-1975. Bulletin of the Pan American Health Organization. 1977;**11**:212-223

[76] Laredo-Tiscareño SV,

Garza-HernandezJA,Rodríguez-AlarcónCA, Adame-Gallegos JR, Beristain-Ruiz DM, Barajas-López IN, et al. Detection of antibodies to Lokern, Main Drain, St. Louis Encephalitis, and West Nile Viruses in Vertebrate Animals in Chihuahua, Guerrero, and Michoacán, Mexico. Vector Borne and Zoonotic Diseases. 2021;**21**:884-891

[77] Hayes CG, Dutary BE, Reeves WC, Adames AJ, Galindo P. Experimental studies to determine the susceptibility to infection with St. Louis encephalitis virus of five species of Panamanian mosquitoes. Journal of the American Mosquito Control Association. 1991;7:584-587

[78] Felices V, Ampuero JS,
Guevara C, Caceda ER, Gomez J,
Santiago-Maldonado FW, et al. St. Louis encephalitis virus infection in woman,
Peru. Emerging Infectious Diseases.
2014;20:730-732

[79] Burgueño A, Spinsanti L, Díaz LA, Rivarola ME, Arbiza J, Contigiani M, et al. Seroprevalence of St. Louis encephalitis virus and West Nile virus (Flavivirus, Flaviviridae) in horses, Uruguay. BioMed Research International. 2013;**2013**:582957

[80] Danforth ME, Snyder RE, Feiszli T, Bullick T, Messenger S, Hanson C, et al. Epidemiologic and environmental characterization of the Re-emergence of St. Louis Encephalitis Virus in California, 2015-2020. PLoS Neglected Tropical Diseases. 2022;**16**:e0010664

[81] Reisen WK. Epidemiology of St. Louis encephalitis virus. Adverse in Virus Research. 2003;**61**:139-183

[82] Markoff L. 153 - Alphaviruses. In: Bennett JE, Dolin R, Blaser MJ, editors. Mandell, Douglas, and Bennett's Principles and Practice of Infectious Diseases. Eighth ed. Philadelphia: W.B. Saunders; 2015. pp. 1865-74.e2

[83] Young PR, Ng LFP, Hall RA, Smith DW, Johansen CA. 14 - Arbovirus Infections. In: Farrar J, Hotez PJ, Junghanss T, Kang G, Lalloo D, White NJ, editors. Manson's Tropical Infectious Diseases. Twenty-third ed. London: W.B. Saunders; 2014. pp. 129-61.e3

[84] Arrigo NC, Adams AP, Weaver SC. Evolutionary patterns of eastern equine encephalitis virus in North versus South America suggest ecological differences and taxonomic revision. Journal of Virology. 2010;**84**:1014-1025

[85] Blohm GM, Lednicky JA, White SK, Mavian CN, Márquez MC, González-García KP, et al. Madariaga virus: Identification of a Lineage III strain in a venezuelan child with acute undifferentiated febrile illness, in the setting of a possible equine epizootic. Clinical Infectious Diseases. 2018;**67**:619-621

[86] Luciani K, Abadia I, Martinez-Torres AO, Cisneros J, Guerra I, Garcia M, et al. Madariaga virus infection associated with a case of acute disseminated encephalomyelitis. The American Journal of Tropical Medicine and Hygiene. 2015;**92**:1130-1132

[87] Stechina OS, Oria GI, Torres C,
Diaz LA, Contigiani M,
Stein M. First detection of Madariaga
virus in Mosquitoes Collected in a Wild
Environment of Northeastern Argentina.
The American Journal of Tropical
Medicine and Hygiene. 2019;101:916-918

[88] Buscaglia C. A survey for avian influenza from gulls on the coasts of the District of Pinamar and the Lagoon Salada Grande, General Madariaga, Argentina. Avian Diseases. 2012;**56**:1017-1020

[89] Benvenuto D, Cella E, Fogolari M, De Florio L, Borsetti A, Donati D, et al. The transmission dynamic of Madariaga Virus by bayesian phylogenetic analysis: Molecular surveillance of an emergent pathogen. Microbial Pathogenesis. 2019;**132**:80-86

[90] Carrera JP, Pitti Y, Molares-Martinez JC, Casal E, Pereyra-Elias R, Saenz L, et al. Clinical and serological findings of Madariaga and Venezuelan Equine encephalitis viral infections: A Follow-up Study 5 Years After an Outbreak in Panama. Open Forum Infectious Diseases. 2020;7:ofaa359

[91] Gil L, Magalhaes T, Santos B, Oliveira LV, Oliveira-Filho EF, Cunha JLR, et al. Active Circulation of Madariaga Virus, a Member of the Eastern Equine Encephalitis Virus Complex, in Northeast Brazil. Pathogens. 2021;**10**

[92] Lednicky JA, White SK, Mavian CN, El Badry MA, Telisma T, Salemi M, et al. Emergence of Madariaga virus as a cause of acute febrile illness in children, Haiti, 2015-2016. PLoS Neglected Tropical Diseases. 2019;**13**:e0006972

[93] Vittor AY, Armien B, Gonzalez P, Carrera JP, Dominguez C, Valderrama A, et al. Epidemiology of emergent Madariaga Encephalitis in a Region with Endemic Venezuelan Equine Encephalitis: Initial Host Studies and Human Cross-Sectional Study in Darien, Panama. PLoS Neglected Tropical Diseases. 2016;**10**:e0004554

[94] Silva M, Auguste AJ, Terzian ACB, Vedovello D, Riet-Correa F, Macario VMK, et al. Isolation and characterization of Madariaga virus from a Horse in Paraiba State, Brazil. Transbound Emerging Diseases. 2017;**64**:990-993

[95] Carrera JP, Cucunubá ZM, Neira K, Lambert B, Pittí Y, Liscano J, et al. Endemic and epidemic human alphavirus infections in Eastern Panama: An analysis of population-based crosssectional surveys. The American Journal of Tropical Medicine and Hygiene. 2020;**103**:2429-2437

[96] Saivish MV, da Costa VG, Rodrigues RL, Féres VCR, Montoya-Diaz E, Moreli ML. Detection of Rocio Virus SPH 34675 during Dengue Epidemics, Brazil, 2011-2013. Emerging Infectious Diseases. 2020;**26**:797-799

[97] Saivish MV, Gomes da Costa V, de Lima MG, Alves da Silva R, Dutra da Silva GC, Moreli ML, et al. Rocio virus: An updated view on an elusive flavivirus. Viruses. 2021;**2021**:13

[98] Villamil-Gómez WE, Rodríguez-Morales AJ, Uribe-García AM, González-Arismendy E, Castellanos JE, Calvo EP, et al. Zika, dengue, and chikungunya co-infection in a pregnant woman from Colombia. International Journal of Infectious Diseases. 2016;**51**:135-138

[99] León-Figueroa DA, Abanto-Urbano S, Olarte-Durand M, Nuñez-Lupaca JN, Barboza JJ, Bonilla-Aldana DK, et al. COVID-19 and dengue coinfection in Latin America: A systematic review. New Microbes New Infections. 2022:101041

[100] Patwary MM, Haque MZ, Bardhan M, Rodriguez-Morales AJ. COVID-19 and Dengue Co-epidemic During the Second Wave of the Pandemic in Bangladesh: A Double Blow for an Overburdened Health-Care System. Disaster Medicine and Public Health Preparedness. 2022;**1-3** [101] Mejia Buritica L, Karduss Urueta AJ. Pulmonary mucormycosis. The New England Journal of Medicine. 2021;**384**:e69

[102] Villamil-Gómez WE, Rojas-Torres I, Perea-Vásquez LE, Collazos-Torres LA, Murillo-Moreno MA, Morales-Rudas JD, et al. SARS-CoV-2 and Dengue virus co-infection: A case from North Caribbean Colombia. Travel Medicine and Infectious Disease. 2021;**102096**

[103] Cardona-Ospina JA, Trujillo AM, Jiménez-Posada EV, Sepúlveda-Arias JC, Tabares-Villa FA, Altieri-Rivera JS, et al. Susceptibility to endemic Aedesborne viruses among pregnant women in Risaralda, Colombia. International Journal of Infectious Diseases. 2022;**122**:832-840

[104] da Silva MK, Azevedo AAC, Campos DMO, de Souto JT, Fulco UL, Oliveira JIN. Computational vaccinology guided design of multi-epitope subunit vaccine against a neglected arbovirus of the Americas. Journal of Biomolecular Structure & Dynamics. 2022:1-18

[105] Powers JM, Haese NN, Denton M, Ando T, Kreklywich C, Bonin K, et al.
Non-replicating adenovirus based
Mayaro virus vaccine elicits protective immune responses and cross protects against other alphaviruses.
PLoS Neglected Tropical Diseases.
2021;15:e0009308

[106] Darwish MA, Hammon WM. Preparation of inactivated St. Louis encephalitis virus vaccine from hamster kidney cell culture. Proceedings of the Society for Experimental Biology and Medicine Society for Experimental Biology and Medicine (New York, NY). 1966;**123**:242-246