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Review

An updated review of the invasive *Aedes albopictus* in the Americas; the minimum infection rate suggests that is more efficient in the vertical than horizontal transmission of arboviruses

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Simple Summary: Currently, the Asian tiger mosquito *Aedes albopictus* Skuse is present on all continents except Antarctica. The vectorial competence of *Ae. albopictus* is different by geographic region. In areas where *Aedes aegypti* is absent, the Asian mosquito is the main vector of arboviruses such as dengue, Zika, and chikungunya. In the Americas, *Ae. albopictus* occupies the same ecological niches as *Ae. aegypti*. It is difficult to incriminate the Asian mosquito as the cause of autochthonous arbovirus outbreaks. However, evidence suggests that *Ae. albopictus* is very effective in transmitting endemic arboviruses such as dengue by transovarial route. *Aedes albopictus* could be useful as a sentinel species to monitor dengue virus in inter-epidemic periods.

Abstract: The aim of the work was to update the distribution range of *Aedes* (*Stegomyia*) *albopictus* Skuse in the Americas, review the blood feeding patterns and compare the minimum infection rate (MIR) between studies of vertical and horizontal transmission of arboviruses. The current distribution of *Ae. albopictus* encompasses 21 countries in the Americas. In eleven published papers on the blood feeding pattern of *Ae. albopictus*, DNA from 16 species of mammals and five species of avian species was found. The most common host is humans, and dogs. We found 24 published papers on the identification of arboviruses in wild populations of *Ae. albopictus* with the potential to infect humans and animals. Eight arboviruses have been isolated in different studies carried out in Brazil, USA, Mexico, Colombia, and Costa Rica. Fifty-eight percent (14/24) of the publications reported vertical transmission of arbovirus. Positive pools were higher in vertical (8.45%) compared to horizontal transmission (0.97%). This was supported by the MIR, which was 3 times greater in vertical (MIR=3.21) than horizontal transmission (MIR= 1.08). In conclusion, *Ae. albopictus* is an invasive mosquito with wide phenotypic plasticity to adapt to broad and new areas, high vectorial competence to transmit several arboviruses mainly by transovarial transmission, it can participate in the endemic transmission, and serve as a bridge vector for emerging arboviruses between sylvan, rural, and urban areas.

Keywords: Blood feeding, Vertebrate host, transovarial transmission, vectorial capacity.

1. Introduction

Aedes (*Stegomyia*) *albopictus* Skuse is a mosquito native to Southeast Asia, colloquially known as the Asian tiger mosquito or Asian mosquito. The mosquito was described by Skuse (1894) in the city of Calcutta, India [1,2]. At the beginning of 2000´s, its importance as a vector of arboviruses was restricted to Asian and African countries [1]. Currently, *Ae. albopictus* is present on all continents except Antarctica [3]. It has been observed that once established in new geographic areas, it is capable of becoming involved in the natural cycles of arbovirus transmission. For example, in Europe it has colonized several countries and was involved in dengue outbreaks in France, Italy, and Spain [4–6]. In Italy, the genome of the chikungunya virus was identified in *Ae. albopictus* and it was incriminated as the vector that caused the local outbreaks of chikungunya fever [7]. Likewise, autochthonous cases of Zika fever occurred in France and *Ae. albopictus* was suspected as the transmitter of the virus [8]. Recently, in Brazil, Yellow Fever virus (YFV) was detected in females mosquitoes in Rio do Janeiro State [9]. Based on the background, the mosquito is considered a species with the potential to increase the risk of arbovirus both in urban and sylvan cycles transmission in the Americas.

Arboviruses of medical and veterinary importance have been isolated in wild populations of *Ae. albopictus* [10–19]. Notably, the Asian mosquito has a great capacity to acquire arboviruses and transmit them to its offspring. The findings of transovarian transmission have been consistent and very frequent [21,22]. Studies carried out in North and South America have found the dengue (all serotypes), Zika and La Crosse viruses in larvae and males of *Ae. albopictus* [20,23–33]. Evidence suggests that the mosquito may have a reservoir role for the dengue virus by keeping it silent in nature [21]. In Brazil, the detection of DENV-3 in males of *Ae. albopictus* was carried out in years in which no autochthonous human cases with this serotype were recorded, suggesting that the silent circulation of DENV-3 occurs by a vertical transmission mechanism [33]. Additionally, also in Rio do Janeiro State, YFV was isolated in *Ae. albopictus* females, which could imply that it could be acting as an additional jungle or rural vector causing a possible transmission bridge to the urban area [9].

Since 1985, when it became known that *Ae. albopictus* had colonized the state of Texas, EE. UU., 36 years have passed since its introduction in America. Despite the importance as a vector of arboviruses, few studies have evaluated the vectorial capacity (e.g., gonotrophic cycle length, daily survival probability, parity index and the proportion of bites made by females on humans). Studies on the blood feeding pattern of *Ae. albopictus* have been carried out in the Unites States of America and Brazil [14,34–43]. The results indicate that it is an opportunistic mosquito. DNA from humans and a diverse range of wild and domestic animals have been identified in the blood meal of the mosquito [36,37,39,43].

Here, we update the distribution range of *Ae. albopictus* in the Americas, review the blood feeding patterns, and compare the minimum infection rate (MIR) between studies of vertical and horizontal transmission of arboviruses.

2. Selection criteria and search strategy

The analysis only included works carried out in the Americas (north, south, central and the Caribbean), with topics focused on the first report of *Ae. albopictus* from each American country, blood feeding patterns and reports of natural infection with arbovirus.

Databases of Google Scholar, PubMed Health (National Center for Biotechnology Information at the National Library of Medicine), SciELO (Scientific Electronic Library Online), and Web of Science (Thompson Reuters) were used for the literature review. The search was done with combination of keywords including "*Aedes albopictus*" AND "first report", "first record", "new records", "blood meal", "feeding pattern", "arbovirus" " dengue", "Zika", "chikungunya", "America". Additional references were facilitated by colleagues.

Importation of references and removal of duplicate references were done using the bibliographical software package, Mendeley version 1.19.8 (Elsevier, Amsterdam, Netherlands). All titles, abstracts and selected full reports were screened independently by two authors based on the inclusion and exclusion criteria. Discrepancies were resolved by consensus.

Test for the difference of proportions was used to compare the positive pools between studies with vertical and horizontal transmission cycle. The values of the minimum infection rate (MIR) of each study were extracted manually and organized in an excel sheet. When the work did not include the MIR, it was calculated with the formula: the ratio between the number of positive pools and the total number of mosquitoes tested, multiplied by 1000.

Host frequencies identified in blood meals of *Ae. albopictus* were extracted from each work and organized in an excel sheet. Statistical analyses were performed using *R* statistical programming language version 4.0.2 and results were considered statistically significant when $p \leq 0.05$.

3. Chronological order of the first reports of *Ae. albopictus* in the Americas

The current distribution of *Ae. albopictus* encompasses 21 of 44 countries in the Americas, although the colonization pattern is different in each country (Table 1). Chile and Peru being the only continental countries where it has not been reported to date. Previously, Kramer and collaborators [3] conducted a global compendium of the distribution of *Ae. albopictus* and described its presence in 16 countries of the Americas. According to reports, the mosquito has presented an erratic distribution, but with great rapidity in its movement through America. The introduction of *Ae. albopictus* in America was divided into four periods. In the first period (1983-1990), the Asian mosquito was reported in three countries. The first report occurred in 1983 in the EE.UU., when a single adult of *Ae. albopictus* was captured in a cemetery in Memphis, Tennessee [44]. Three years later, in Brazil (1986), five male and six female mosquitoes with similar characteristics to the Asian mosquito were captured and their identity was confirmed as *Ae. albopictus* [45]. In Mexico, the Asian mosquito was reported for the first time in 1988, the larvae were collected in tires [46]. In the second period (1993 to 1998), the Asian mosquito was reported in six countries including the Dominican Republic, Cuba, Guatemala, Cayman Islands, Colombia, and Argentina [47–52]. Reiter [44] mentions that *Ae. albopictus* was reported in Bolivia and El Salvador, but there are no reports that confirm it. Their presence in these countries is not currently recognized. In the third period (2000 to 2010), the mosquito significantly expanded its distribution to ten countries including Bermuda, Canada, Trinidad and Tobago, Panama, Uruguay, Nicaragua, Costa Rica, Venezuela, Belize, and Haiti [53–62]. In the fourth period (2011-2021), the presence of the mosquito was only reported in Ecuador in 2017 and in Jamaica in 2018 [63,64]. It is well documented that the introduction of *Ae. albopictus* into America occurred through tires and bamboo stumps from Japan. It is also hypothesized that the massive distribution of the mosquito occurred through the export of used tires between countries in the Americas, Europe and Asia [1,44–46]. Within countries, automobiles are believed to contribute to the distribution [65].

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Table 1. Chronological summary of publications on the first reports of *Ae. albopictus* in American countries

Year of the first report	Country	Collected stage of the mosquito	Author
1983	EE.UU.	A single adult collected	[44]
1986	Brazil	Captured five males and six females	[45]
1988	Mexico	Larvae collected in tires	[46]
1993	Dominican Republic	Larvae collected in tires	[48]
1995	Cuba	Larvae collected	[47]
1995	Guatemala	Larvae collected in tires, glass bottles, and metal drums.	[49]
1997	Cayman island	Larvae collected	[50]
1998	Colombia	Captured adults	[51]
1998	Argentina	Larvae and pupae collected	[52]
2000	Bermuda Island	Larvae collected	[53]
2001	Canada	Two adults captured	[55]
2002	Trinidad and Tobago	Eggs collected with ovitrap	[56]
2002	Panama	Larvae collected	[54]
2003	Uruguay	Adults captured	[57]
2003	Nicaragua	Larvae collected	[58]
2007	Costa Rica	Larvae collected	[59]
2009	Venezuela	Larvae collected	[60]
2009	Belize	Adults captured	[61]
2010	Haiti	Larvae collected	[62]
2017	Ecuador	Captured five males and sixteen females	[64]
2018	Jamaica	Six females captured	[63]

4. Blood feeding pattern of *Ae. albopictus*

In total, there are 11 published papers on the blood feeding pattern of Ae. albopictus; nine of them were carried out in the EE.UU. and two in Brazil. The first four studies used the serological precipitin test and ELISAs to identify the identity of the vertebrate hosts. Seven publications used PCR to identify host DNA. In total, 1,925 individual mosquitos were tested. In 85.56% (1,647/1,925) of the mosquitos, the host was identified at the species level, which comprised 16 species of mammals and 5 species of birds (Table 2). Despite the ability of Ae. albopictus to feed on the blood of different vertebrate taxa, 98.70% (1900/1925) corresponded to mammals. The human (Homo sapiens), the domestic dog (Canis lupus), the brown rat (Rattus norvegicus) and the domestic cat (Felis silvestris) are the most frequent hosts in the publications and with more specimens analyzed.

The frequency of blood feeding of *Ae. albopictus* on a particular host determines the risk of pathogen transmission. According to studies published mainly in the EE.UU., the Asian mosquito has an anthropophilic tendency, although in the absence of humans it can feed on 15 other species of mammals and five species of birds. The method and the place of capture of *Ae. albopictus* was decisive to identify DNA of hosts in the blood meals of the mosquito. Most females of *Ae. albopictus* with human blood were captured with the human bait method and aspirated from mosquitoes inside and outside the houses [35,37,39,41]. The other works captured *Ae. albopictus* in the forest or habitats with abundant vegetation. For this reason, the number of wild species in the blood meals of the Asian mosquito was very diverse [14,34,36,38,40,42,43]. In the EE.UU., the feeding frequency of *Ae. albopictus* on birds and wild mammals partly explains the isolation of zoonotic arboviruses such as VEEE, Keystone virus, La Crosse Virus, West Nile virus, and Cache Valley virus [10–12,14,15,27].

Table 2. DNA of vertebrate hosts identified in blood meals of *Aedes albopictus*

Family	Vertebrate host	Total identified	Author
	Mammalian		
Hominidae	*Homo sapiens*	579	[14,34–37,39–43]
Muridae	*Rattus norvegicus*	227	[14,35–37,42,43]
Felidae	*Felis silvestris*	252	[36,37,39,41,42]
Canidae	*Canis lupus*	217	[14,34,36–39,41–43]
Sciuridae	*Sciurus carolinensis*	110	[39,41]
Leporidae	*Sylvilagus floridanus*	95	[35,36,41]
Cervidae	*Odocoileus virginianus*	52	[34,36,39,42]
Equidae	*Equus caballus*	49	[37–39]
Bovidae	*Bos taurus*	29	[34,36,37]
Didelphidae	*Didelphis virginiana*	8	[40,41]
Sciuridae	*Tamias striatus*	7	[36]
Suidae	*Sus scrofa*	5	[14,37]
Emydidae	*Terrapene carolina*	5	[36]
Phyllostomidae	*Tonatia bidens*	2	[43]
Cricetidae	*Peromyscus leucopus*	1	[41]
Dasypodidae	*Dasypus novemcintus*	1	[35]
	Avian		
Phasianidae	*Gallus domesticus*	4	[37]
Cardinalidae	*Cardinalis cardinalis*	1	[40]
Paridae	*Poecile carolinensis*	1	[40]
Columbidae	*Zenaida macroura*	1	[40]
Tamnophilide	*Taraba major*	1	[43]
Grand total		1,647	

*Unidentified mammals: Leporidae (n=119); Didelphidae (n=68); Procyonidae (n=58); Sciuridae (n= 8); Murid (n=4); ¸); Myomorpha (n=4) = 261. Unidentified birds: Passeriformes (n=10); Columbiformes (n=5); Ciconiiformes (n=1) Quail (n=1) = 17.

5. Natural infections of *Ae. albopictus* with arboviruses

In the Americas there are 24 published papers on the identification of arboviruses in wild populations of *Ae. albopictus* with the potential to infect humans and animals. Ten of the findings were made in Brazil, six in the USA, four in Mexico, three in Colombia and one in Costa Rica (Table 3). The arboviruses identified are Eastern equine encephalitis virus (EEEV), Keystone virus, Cache Valley virus (CVV), La Crosse virus, West Nile virus (WNV), dengue virus (all serotypes), Yellow Fever (YFV) and Zika virus (ZIKV) (Table 3).

Notably, 66.66% (16/24) of the publications reported the genome of the dengue virus in the Asian mosquito, although in only four studies the presence was confirmed by viral isolation. In decreasing order, the most frequent serotypes in the publications are DENV-2 (n = 8), DENV-3 (n = 5), DENV-1 (n = 4) and DENV-4 (n = 3). On the other hand, in six studies carried out in Brazil (n = 4) and Mexico (n = 2), the Zika virus was identified in *Ae. albopictus*.

Aedes albopictus has wide distribution in America, despite this only in five countries has been reported natural infection of *Ae. albopictus* with arboviruses of medical and veterinary importance. Currently, eight arboviruses have been isolated in the Asian mosquito (Table 3). However, experimental studies indicate that *Ae. albopictus* is susceptible to oral infection of 23 arboviruses of the Flaviviridae (dengue virus, Zika virus, Japanese encephalitis virus, West Nile virus, St. Louis encephalitis virus, and yellow fever virus), Togaviridae (chikungunya virus, eastern equine encephalitis virus, Mayaro virus, Ross River virus, Sindbis virus, western equine encephalitis virus, and Venezuelan equine encephalitis virus), Peribunyaviridae (Jamestown Canyon virus, Keystone virus , La Crosse virus, Oropouche virus, Potosi virus, San Angelo virus, Trivittatus virus, and Rift Valley virus), Reoviridae (Orungo virus) and Nodaviridae families (Nodamura virus) [66–68].

In 2013, the chikungunya virus (CHIKV) emerged in the Americas and caused local outbreaks of chikungunya fever. To date, no natural infection with this virus has been reported in *Ae. albopictus* [69,70]. *Aedes albopictus* is an efficient vector of the epidemic mutant strain CHIKV_0621 of the East-Central-South African (ECSA) genotype [71], which, caused autochthonous cases of CHIKV in Indian Ocean [72]. Today, the circulation of the mutant strain in America is not reported.

Aedes albopictus is most abundant in the forest than *Ae. aegypti* and may be involved in virus transmission in rural areas or urban places with a lot of vegetation. Evidence suggests that the Asian mosquito is an extremely important vector because once established it can participate in the transmission of local arboviruses. In United States of America (USA), *Ae. albopictus* is a competent vector of endemic arboviruses such as VEEE, Keystone virus, La Crosse Virus, West Nile virus, and Cache Valley virus [10–12,14,15,27]. On the other hand, more than 70% of the publications of *Ae. albopictus* naturally infected with the dengue and Zika viruses come from Brazil, Mexico, Colombia, and Costa Rica, which are dengue endemic countries and between 2014 and 2018 there was active transmission of the Zika virus. Notably, in nine out of ten studies carried out in Brazil, dengue (all serotypes), Zika and yellow fever viruses were transmitted by transovarial route. Future studies should focus on finding out if there is an evolutionary relationship of arbovirus adaptation with vertical transmission of *Ae. albopictus*.

Table 3. Chronological summary of publications on natural infection of *Ae. albopictus* with arboviruses of medical and veterinary importance

Year	Country	Arbovirus	Detection technique	Author	Observations
1991	EE.UU.	EEEV	IFAA, Viral isolation, PRNT	[10]H	EEEV was isolated from 14 pools of females
1991	EE.UU.	Keystone virus	IFAA, Viral isolation, PRNT	[10]H	Keystone virus was isolated from a pool of females
1993	Brazil	DENV-1	Viral isolation, PCR	[23]V	DENV-1 was isolated from two pools of 30 larvae.
1995	EE.UU.	CVV	Viral isolation, IFAA	[11]H	CVV was isolated from a pool of ~100 females
1995	Mexico	DENV-2 and DENV-3.	Viral isolation, IFAA, RT-PCR	[26]V	DENV-2 and DENV-3 were isolated from a pool of ten males
1999	EE.UU.	La Crosse Virus	Viral isolation, RT-PCR	[27]V	Larvae reared to adults. La Crosse virus was isolated from two pools of 58 females.
1999	Brazil	DENV-3	PCR	[28]V	DENV-3 was isolated from three pools of 30 larvae.
2000	EE.UU.	WNV	RT-PCR	[12]H	WNV was isolated from a pool of two females
2002	Colombia	DENV-1 and DENV-2	RT-PCR	[13]H	Two pools of 26 females were positive for DENV-1, and DENV-2, respectively.

2003	Brazil	DENV-2	RT-PCR	[29]^{V}	DENV-2 was identified from 33 pools of 1,650 larvae. Two Pools of 100 larvae were coinfected with DENV-1 and DENV-2.
2003-2005	EE.UU.	WNV	Viral isolation, ELISA	[14]^{H}	WNV was isolated of females
2010	EE.UU.	CVV	Viral isolation, RT-PCR	[15]^{H}	CVV was isolated from three pools of *Ae. albopictus*
2011	Brazil	DENV-2 and DENV-3	RT-PCR	[30]^{V}	DENV-2 was found in three individual larvae. DENV-2 was found in a pool of six larvae. An individual larva coinfected with DENV-2 and DENV-3.
2007	Brazil	DENV-2 and DENV-3	Viral isolation, IFAA, RT-PCR	[31]^{V}	Larvae reared to adults. DENV-3 was isolated from a pool of 35 adults. One pool of 41 adults coinfected with DENV-2 and DENV-3
2010	Mexico	Dengue, serotype unknown	RT-PCR	[32]^{V}	Larvae reared to adults. DENV was found from a pool of four females.
2014-2015	Brazil	DENV-3	RT-PCR	[33]^{V}	Two pools of 20 males were positive for DENV-3
2015	Costa Rica	DENV-1, DENV-2, DENV-4	RT-PCR	[20]^{H}	Three pools of 60 females were positive for DENV-1, DENV-2, and DENV-4, respectively.
2015	Costa Rica	Dengue, serotype unknown	RT-PCR	[20]^{V}	One pool of 20 males were positive for DENV
2015	Brazil	ZIKV	RT-qPCR	[24]^{V}	One pool of 33 larvae were positive for ZIKV
2016	Colombia	DENV-2	RT-PCR	[16]^{H}	One pool of four females were positive for DENV-2
2016	Mexico	ZIKV	RT-qPCR	[17]^{H}	One pool of six females were positive for ZIKV
2016	Colombia	DENV-2	RT-PCR	[25]^{H}	Twenty pools of females were positive for DENV-2
2017	Colombia	DENV-4	RT-PCR	[25]^{V}	Five pools of 31 males were positive for DENV-4
2017	Mexico	ZIKV	RT-qPCR	[18]^{H}	Seven pools of 78 females were positive for ZIKV
2017	Brazil	DENV-4 and ZIKV	Viral isolation, and RT-PCR	[22]^{V}	Eggs were reared until adulthood. Two pools were positive for DENV-4 and two pools were positive for ZIKV.
2018-2019	Brazil	ZIKV and YFV	RT-PCR	[9]^{V}	Eggs were reared until adulthood. One pool of nine females were positive for YFV. One pool of 32 females and another pool of two males were positive for ZIKV.
2019	Brazil	DENV-1 and ZIKV	RT-qPCR	[19]^{H}	One pool of 10 females and another pool of 15 females were positive for ZIKV and DENV-1, respectively.

Indirect fluorescent antibody assay (IFAA); Polymerase Chain Reaction (PCR); Quantitative reverse transcription PCR (RT-qPCR); Plaque-reduction neutralization Test (PRNT); Eastern equine encephalitis virus (EEEV); Cache Valley virus (CVV); West Nile virus (WNV); Yellow fever virus (YFV); Publications with super index H and V indicates horizontal and vertical transmisión, respectively.

6. The minimum infection rate estimated in vertical and horizontal transmission of arboviruses

Twelve studies reported only vertical transmission and ten only horizontal transmission. Two studies carried out in Costa Rica, and Colombia reported both types of transmission. First findings of dengue virus in the Asian mosquito were through vertical transmission. In Brazil, in 1993, DENV-1 was isolated from two pools of mosquito larvae. Two years later during a dengue outbreak in Mexico, DENV-2 and DENV-3 were isolated from a pool of 10 males of *Ae. albopictus*. In Brazil in 1999, DENV-3 was again identified in three larval pools (Table 3).

In 14 publications on vertical transmission, 19,435 mosquitoes organized in 792 pools were analyzed (Figure 1A, 1B, and 1C). Overall, 8.45% (67/792) of the pools were positive. The overall MIR was 3.45 (67 positive pools/19,435 mosquitoes x 1,000).

In contrast, in 12 publications on horizontal transmission, 53,566 mosquitoes organized in 5,956 pools were analyzed (Figure 1A, 1B, and 1C). Overall, 0.97% (58/5,956) of the pools were positive. The overall MIR was 1.08 (58 positive pools/53,566 mosquitoes x 1,000). The higher percentage of positive pools in vertical transmission contributed to a statistically significant difference compared to horizontal transmission ($X^2 = 215.46$, d.f = 1, $P \leq 0.001$).

In many geographic areas of the Americas, *Ae. albopictus* occupies the same ecological niches as *Ae. aegypti*. It is difficult to incriminate the tiger mosquito as the cause of autochthonous arbovirus outbreaks [13,26]. In horizontal transmission, *Ae. aegypti* is considered the main vector of dengue, Zika and chikungunya viruses in American countries [1,69,70]. In contrast, the evidence suggests that *Ae. albopictus* plays a secondary role in horizontal transmission of dengue and Zika viruses but is very efficient in transmitting them to their progeny [21]. Notably, 11 out of 14 publications refer to transovarial transmission of dengue virus. This has several aspects; the dengue virus can remain and persist silently during inter-epidemic periods [21,33]. The dispersal of eggs and larvae of *Ae. albopictus* infected with dengue and Zika viruses can cause the emergence and re-emergence of arboviruses and modify the local epidemiological pattern [23,24,27–30,32]. Transovarial transmission ensures the presence of arboviruses in *Ae. albopictus* regardless of blood feeding on viremic hosts. The occurrence of male mosquitoes infected by transovarial transmission suggests equal probability of infection of the females of the same batch. Females of *Ae. albopictus* would not have to go through the extrinsic incubation period to transmit the virus to humans, which would enhance the dynamics of dengue transmission [25]. In addition, serotypes and genotypes not associated with autochthonous outbreaks have been detected during transovarial transmission. In Brazil, genotype III of DENV-3 was detected in larvae of *Ae. albopictus* collected in 1999 [28]. However, DENV-3 (genotype III) was first isolated as an autochthonous case from a 40-year-old woman residing in Sao Paulo, Brazil [73]. Which suggests that this serotype was present in Brazil one year before its detection. Similarly, DENV-3 was detected in males of *Ae. albopictus* in years when no human autochthonous cases of this serotype were recorded in São Paulo, Brazil [33].

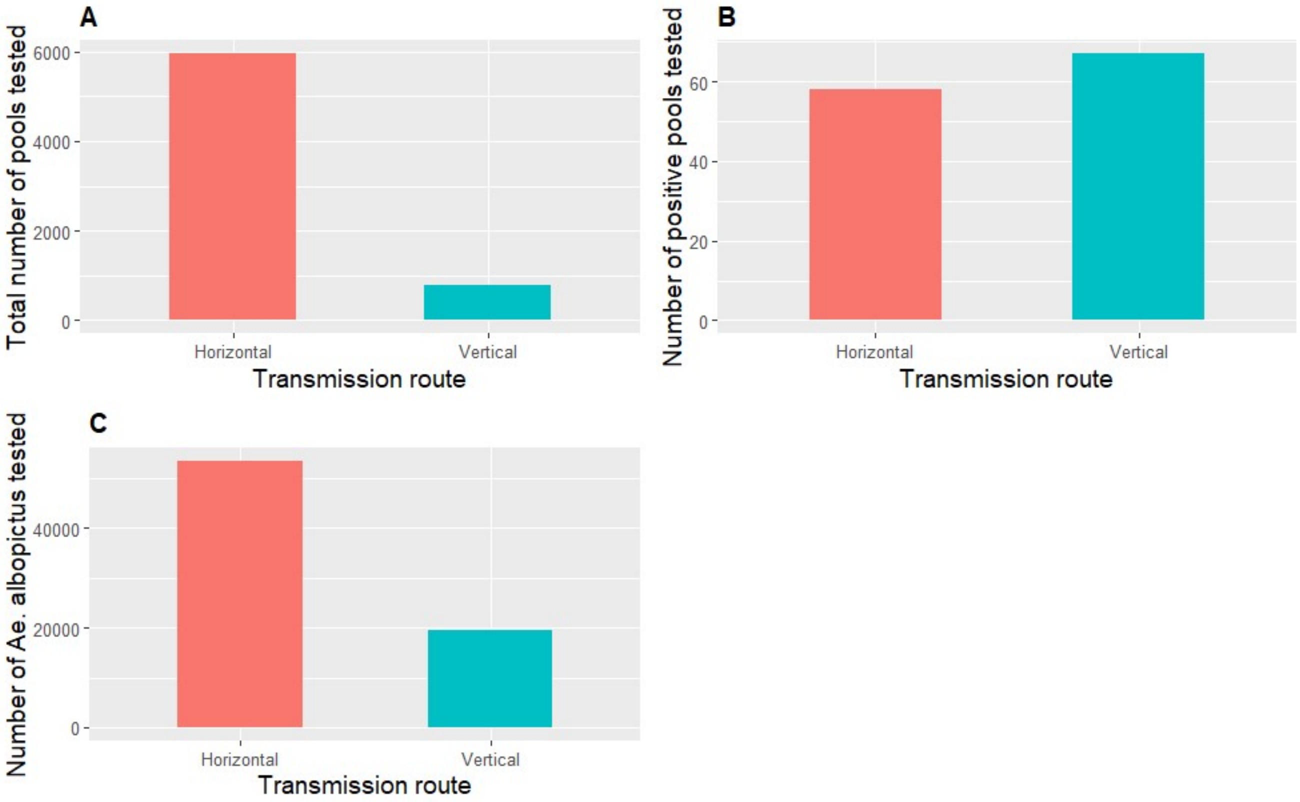

Figure 1. Studies of *Aedes albopictus* with horizontal and vertical transmission of arboviruses. A) Total number of pools tested, B) Number of positive pools tested, and C) Number of *Ae. albopictus* tested.

7. Concluding Remarks and Future Prospects

Despite the importance of *Ae. albopictus* as a vector and reservoir of dengue virus, few studies have evaluated the vectorial capacity in the Americas. Studies should focus on gonotrophic cycle length, dispersion range, daily survival probability, parity index and the proportion of bites made by females on humans. Likewise, in Asian mosquito populations, the susceptibility status and genes associated with resistance to insecticides used by local health services should be monitored. Finally, *Ae. albopictus* is an invasive mosquito with wide phenotypic plasticity to adapt to broad and new areas, high vectorial competence to transmit several arboviruses mainly by transovarian transmission, it can participate in the endemic transmission, and serve as a bridge vector for emerging arboviruses between sylvan, rural, and urban areas. According with the data that of the MIR, which was 3 times greater in vertical (MIR=3.44) than horizontal transmission (MIR= 1.08), this means that *Ae. albopictus* could be maintaining a viral cycle vertically, and also could be useful as a sentinel species to monitor dengue virus in inter-epidemic periods.

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