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Global diversity of *Aedes* species (Diptera: Culicidae) relevant to public health

Diversidade global de espécies de *Aedes* (Diptera: Culicidae) relevantes para a saúde pública

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ABSTRACT

Mosquito-borne arboviruses represent one of the main challenges for public health today. The *Aedes* genus includes more than 950 mosquito species, many of which cause discomfort through their bites and are disease vectors. However, little is known about this biodiversity and its role in the context of public health. This study aimed to list the worldwide diversity of mosquitoes belonging to the *Aedes* genus with the potential to transmit pathogens to humans. An integrative literature review was conducted. The articles were searched during July 2024, in the following databases: Lilacs, Scielo, Science Direct and PubMed. A total of 38 species of mosquitoes belonging to the *Aedes* genus with the potential to transmit pathogens to humans were listed. The literature consulted reports a total of 44 pathogens potentially transmitted by *Aedes* mosquitoes, including Dengue, Zika virus, Chikungunya, yellow fever, Rift Valley fever virus, West Nile virus, Ross River virus, Japanese encephalitis virus, Saint Louis encephalitis virus, and equine encephalitis virus. This study provides useful information to support further research and the development of actions to monitor and control mosquito species with vector potential.

Keywords: Arbovirus; vector biogeography; dengue; Rift Valley fever; West Nile vírus.

RESUMO

As arboviroses transmitidas por mosquitos representam um dos principais desafios para a saúde pública atualmente. O gênero *Aedes* reúne mais de 950 espécies de mosquitos, muitas das quais causam incômodo pelas picadas e são vetores de doenças. Contudo, pouco se conhece sobre esta biodiversidade, bem como o seu papel no contexto da saúde pública. Este estudo teve por objetivo listar a diversidade mundial de mosquitos pertencentes ao gênero *Aedes* com potencial para transmitir patógenos para humanos. Foi realizada uma revisão integrativa da literatura e realizada uma busca de artigos durante o mês julho de 2024, nas seguintes bases de dados: Lilacs, Scielo, Science Direct e PubMed. Ao todo foram listadas 38 espécies de mosquitos pertencentes ao gênero *Aedes* com potencial para transmitir patógenos a humanos. A literatura consultada relata um total de 44 agentes patogênicos potencialmente veiculados por mosquitos *Aedes*, com destaque para Dengue, vírus Zika, Chikungunya, febre amarela, vírus da febre do Vale do Rift, vírus do Nilo Ocidental, vírus do rio Ross, vírus da encefalite japonesa, vírus da encefalite de Saint Louis e vírus da encefalite equina. Este estudo contribui com informações úteis para embasar novas pesquisas e para o desenvolvimento de ações de monitoramento e controle de espécies de mosquitos com potencial de vetores.

Palavras-chave: Arbovírus; biogeografia de vetores; dengue; febre do Vale do Rift; vírus do Nilo Ocidental.

INTRODUCTION

Mosquito-borne arboviruses represent one of the main challenges for public health today. The pathogens that cause these diseases are distributed all over the world (Nasir *et al*., 2022). Zika virus, Rift Valley fever virus (RVFV), yellow fever virus (YFV), dengue virus (DENV), and chikungunya virus (CHIKV) stand out in this context. They are considered the most common emerging pathogens transmitted by *Aedes* mosquitoes in tropical and subtropical countries (WHO, 2014). Human activities such as habitat fragmentation, the expansion of urban areas, the growing generation of Municipal Solid Waste (MSW), along with the poor management of this waste, have been identified as factors favoring the proliferation of *Aedes* mosquitoes (Nasir *et al*., 2022). Climate change and the transit of people and goods have been identified as the most relevant factors for the dispersal of vectors (Alan-Barrett, 2010).

Several species of mosquitoes are prominent in the transmission of pathogens of medical and veterinary importance to humans and animals. However, mosquitoes belonging to the genus *Aedes* have stood out in the field of public health, especially *Aedes aegypti* (Linnaeus, 1762) and *Aedes albopictus* (Skuse, 1895) (Tolle, 2009; Guarido *et al*., 2021). The *Aedes* genus includes more than 950 mosquito species, many of which cause discomfort through their bites and serve as disease vectors. However, little is known about this biodiversity and its role in the context of public health. The diversity of *Aedes* is native to temperate and tropical regions and can be found all over the world (Monteiro *et al*., 2019). Mosquitoes of this genus are distinguished from others by their slender, typically black bodies, with unique patterns of light and dark scales on the abdomen, thorax, and legs (Monteiro *et al*., 2019; Nasir *et al*., 2022).

The association between vector-borne diseases and the global movement of humans, animals, and goods, in combination with climate change, has been increasingly highlighted (Leisnham; Juliano, 2012). The distribution, abundance, and seasonality of vectors associated with environmental factors are necessary to develop and implement vector population control strategies (Guarido *et al*., 2021). Understanding the preferences of each vector species is essential to comprehend the circulation of arboviruses between mosquitoes, humans, and other vertebrates. The feeding behavior of *Aedes* mosquitoes is determined by intrinsic and extrinsic factors, and host selection is affected by the presence and abundance of vertebrate species (Kilpatrick *et al*., 2006; Guarido *et al*., 2021). Knowing the diversity of *Aedes* species with the potential to transmit diseases that affect human health is fundamental for developing more effective health policies.

Climate change has been closely linked to the global distribution and burden of infectious diseases (Escobar *et al.*, 2016; Ryan *et al.*, 2019). Mosquito-borne diseases may expand in response to climate change, favored by temperature conditions conducive to infestation and the proliferation of mosquito species with vector potential in latitudes and regions where they did not previously occur (Patz *et al*., 1998). Pathogens can be transmitted by related species, which can be sympatric, or several pathogens can be transmitted by the same vector (Ryan *et al*., 2019). Thus, knowing the species with vector potential, as well as the pathogens that occur in a given region or that can be introduced, represents fundamental knowledge necessary for public health preparedness (Carlson *et al*., 2016).

In the Americas, the relevance of the *Aedes* genus as a potential transmitter of pathogens to humans is restricted to a few species, specifically *Aedes aegypti* and *Aedes albopictus*, although other ecologically relevant species are known. Similar situations exist in Europe, Asia, and Oceania. The greatest known diversity of *Aedes* mosquitoes associated with the transmission of pathogens is found in Africa, the continent of origin of the main vector species that have spread around the world. Considering the importance of knowledge about *Aedes* mosquito species with vector potential in the context of public health and the potential for dispersal of these species to regions where they do not yet occur, this study aimed to list the worldwide diversity of mosquitoes belonging to the *Aedes* genus with the potential to transmit pathogens to humans.

METHODS

Study characterization

An integrative literature review was conducted on the scientific literature concerning the diversity of mosquitoes belonging to the *Aedes* genus with the potential to transmit pathogens to humans. The integrative literature review is a research method that enables the synthesis and analysis of what has been produced on a given phenomenon, in both theoretical and empirical literature (Mendes *et al*., 2008; Souza *et al*., 2010). It also produces new questions, reflections, and criticisms with the potential to identify gaps and consequently advance knowledge.

Search, Selection, and Inclusion of Articles

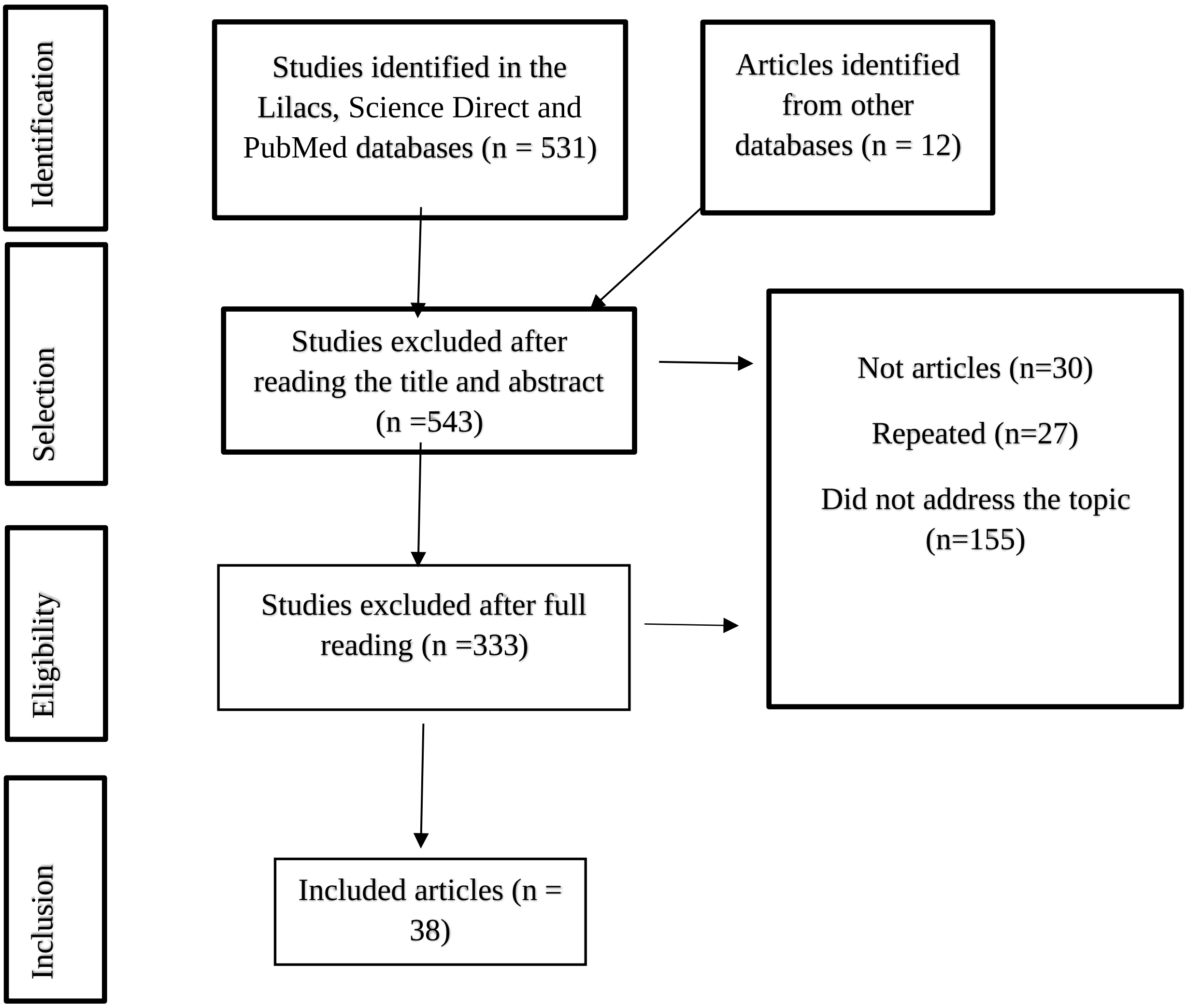
The following steps were followed in the integrative review: 1) Identifying the research question; 2) Searching the scientific literature, establishing inclusion and exclusion criteria, and selecting studies; 3) Categorizing the results found; 4) Evaluating the selected articles; 5) Analyzing, interpreting, and discussing the results; 6) Synthesizing the information and producing knowledge (Mendes *et al*., 2008).

The study question formulated to guide the integrative review was: What is the diversity of *Aedes* mosquitoes with the potential to transmit pathogens to humans? Articles were searched for during July 2024, without limiting the publication date of the works, in the following databases: Lilacs, Scielo, Science Direct and PubMed. The selected descriptors were: "*Aedes* diversity," "*Aedes* vectors," and "pathogens transmitted by *Aedes* mosquitoes," used in Portuguese, English, and Spanish. These terms were used both individually and combined with the Boolean operator "AND."

Only articles and official websites were selected, excluding theses, dissertations, monographs, and abstracts. All the articles were downloaded to an electronic directory in Portable Document Format (.pdf). A total of 531 articles were identified. The preliminary analysis involved reading the titles, abstracts, and keywords. From this pre-analysis, 38 studies that addressed the study question were selected for inclusion in the review (Figure 1).

The studies that met the eligibility criteria were read in full, and the information was extracted and tabulated in an Excel for Windows database (.xlsx). The extracted information included the year of publication, scientific journal, authors, title, objective, and species of *Aedes* and pathogens evaluated.

Figure 1 - Search Strategies for Articles Included in the Research on the Diversity of *Aedes* Mosquitoes with the Potential to Transmit Pathogens to Humans, 2024.



Source: The author (2024)

RESULTS

A total of 38 mosquito species belonging to the genus *Aedes* were identified as having the potential to transmit pathogens to humans. The literature reviewed reports a total of 44 pathogens potentially transmitted by this diversity of *Aedes* mosquitoes, including Dengue fever, Zika virus, Chikungunya, Yellow fever, Rift Valley fever virus, West Nile virus, Ross River virus, Japanese Encephalitis virus, Saint Louis encephalitis virus, and Equine encephalitis virus. Africa, with 26 species, exhibits the greatest diversity of *Aedes* mosquitoes with vector potential, followed by Asia with 11 species, the Americas with 10 species, and Europe and Oceania with six species each (Table 1).

Table 1 - Mosquito species of the genus *Aedes*, occurrence, and associated diseases according to the scientific literature consulted, 2024.

Species	**Global distribution**	**Associated diseases**	**References**
Aedes aegypti (Linnaeus, 1762)	Americas, South of Europe, Asia and Africa	Dengue fever, Zika vírus, Chikungunya, Yellow fever, Rift Valley fever vírus, West Nile virus, Ross River vírus, Murray Valley encephalitis virus, Wesselsbron virus, Babanki vírus, O'nyong Nyong virus	Moritz *et al*., 2015; Kamal *et al*., 2018; Kamgang *et al*., 2018; Kraemer *et al*., 2019; Wint *er al*., 2022; Laporta *et al*., 2023; Padonou *et al*., 2023; Poungou *et al*., 2023
Aedes africanus (Theobald, 1901)	Africa, except Madagascar	Zika vírus, Chikungunya, Yellow fever, Rift Valley fever virus , West Nile virus, Bozo vírus, Bouboui vírus, Babanki vírus, Uganda vírus, Wesselsbron vírus, Orungo vírus, Middelburg vírus, Saboya vírus, Semliki vírus and Yaoundé vírus	Poungou *et al*., 2023
Aedes albopictus (Skuse, 1895)	Americas, parts of Europe, East Africa, Southeast Asia and the Pacific Islands, parts of Australia	Dengue fever, Zika virus, Chikungunya, Rift Valley fever virus, West Nile virus, Usutu vírus, Ross River vírus and Murray Vallée encephalitis virus	Glasser; Gomes, 2002; Kamal *et al*., 2018; Kamgang *et al*., 2018; Kraemer *et al*., 2019; Oliveira *et al*., 2021; Laporta *et al*., 2023; Liu *et al*., 2023; Padonou *et al*., 2023; Poungou *et al*., 2023
Aedes argenteopunctatus (Theobald, 1901)	Sub-Saharan Africa, Central America, parts of South America	Dengue fever, Chikungunya, Ngari vírus, Semliki vírus and Nkolbisson virus	Ochieng *et al*., 2013; Sang *et al*., 2017; Mutisya *et al*., 2021; Poungou et al., 2024; Poungou et al., 2023
Aedes australis (Erichson, 1842)	Australia, parts of southern and eastern Australia	Dengue fever and Ross River virus	New Zealand, 2007
Aedes bromeliae (Theobald, 1911)	Sub-Saharan Africa	Yellow fever	Bennett *et al*., 2015; Weetman *et al*., 2018; Poungou *et al*., 2023
Aedes caballus (Theobald, 1912)	Sub-Saharan Africa and the Middle East	Rift Valley fever vírus, Wesselsbron vírus, Middelburg vírus and West Nile virus	Nejati *et al*., 2024; Poungou *et al*., 2023

Aedes camptorhynchus (Thomson, 1869)	Australia, especially in the coastal region	Ross River virus	Staples *et al*., 2024
Aedes caspius (Pallas, 1771)	North Africa, Europe and the Middle East	*Francisella tularensis*, Usutu vírus and Zika virus	Núñez *et al*., 2019; Poungou *et al*., 2023
Aedes cinereus (Meigen), 1818	North America, Europe and Southeast Asia	Ockelbo virus,Sindbis virus, Tahyna virus and West Nile virus	Medlock *et al*., 2006; Lindström *et al*., 2021
Aedes circumluteolus (Theobald , 1908)	Sub-Saharan Africa	Rift Valley fever virus, Wesselsbron vírus, Pongola vírus, Bunyamwera vírus, Ndumu vírus, Lebombo vírus and Spondweni vírus	Poungou *et al*., 2023; WRBU, 2024
Aedes cumminsii (Theobald, 1903)	Sub-Saharan Africa	Nkolbisson vírus, Rift Valley fever virus and Spondweni virus	Poungou *et al*., 2023; WRBU, 2024
Aedes dalzieli (Theobald, 1910)	Sub-Saharan Africa	Zika vírus, Chikungunya, Middelburg vírus, Ndumu vírus, Kedougou vírus, Bunyawera vírus, Wesselsbron vírus, Simbu vírus, Pongola vírus and Zinga virus	Poungou *et al*., 2023
Aedes dentatus (Theobald, 1904)	Sub-Saharan Africa	Rift Valley fever virus, Pongola vírus, Semliki vírus and Yellow fever	Mohamed *et al*., 2017; Poungou *et al*., 2023
Aedes domesticus (Theobald, 1901)	Central Africa	Bunyamwera virus	Poungou *et al*., 2023
Aedes furcifer (Edwards, 1913)	Central and East Africa	Zika vírus, Chikungunya, Yellow fever, Bunyawera vírus, Bouboui vírus and Bwamba virus	Mondet,1997; Weetman *et al*., 2018; Poungou *et al*., 2023
Aedes hensilli Farner, 1945	Pacific Islands	Dengue fever, Zika vírus and Chikungunya	Ledermann *et al*., 2014
Aedes japonicus (Theobald, 1901)	United States, part of Europe and Asia	Dengue fever, Chikungunya, West Nile virus, Japanese Encephalitis virus, Saint Louis encephalitis virus, Equine encephalitis vírus, La Crosse virus and Rift Valley fever virus	Kampen; Werner, 2014; WRBU, 2024
Aedes koreicus (Edwards, 1917)	Europe and Asia	Japanese encephalitis virus	Nagy *et al*., 2024; WRBU, 2024
Aedes longipalpis (Theobald, 1903)	West and Central Africa	Uganda virus	Poungou *et al*., 2023; WRBU, 2024;

Aedes luteocephalus (Newstead, 1907)	Central Africa	Dengue fever, Zika vírus, Yellow fever and Bnnyamwera vírus	Poungou *et al.*, 2023; WRBU, 2024
Aedes mcintoshi (Huang, 1985)	Africa	Chikungunya, Ngari virus, Rift Valley fever virus, Ndumu vírus, Pongola vírus, Wesselsbron vírus, Babanki virus and Bunyamwera vírus	Poungou *et al.*, 2023; WRBU, 2024
Aedes mediovittatus (Coquillett , 1906)	Central America, parts of South America	Dengue fever	Marcondes;Tauil, 2011
Aedes metallicus (Edwards, 1912)	Africa	Zika vírus and Yellow fever	Weetman *et al.*, 2018; Poungou *et al.*, 2023
Aedes minutus (Theobald, 1903)	Africa	Zika vírus, Ngari virus, Ndumu vírus, Kedougou vírus and Wesselsbron vírus	Poungou *et al.*, 2023
Aedes ochraceus (Theobald, 1901)	West and Central Africa	Rift Valley fever virus, Ndumu vírus and Babanki virus	Poungou *et al.*, 2023
Aedes opok Corbet & Cunningham van Someren, 1962	Africa	Yellow fever, Zika vírus, Chikungunya, West Nile virus, Bouboui vírus, Orungo vírus, Wesselbron vírus, Bozo vírus, Middelburg vírus, Saboya vírus, Semliki vírus and Yaoundé vírus	Weetman *et al.*, 2018; Sang *et al.*, 2022; Poungou *et al.*, 2023
Aedes palpalis (Newstead 1907)	Africa	Rift Valley fever virus, Middelburg vírus and Simbu virus	Poungou *et al.*, 2023
Aedes polynesiensis Marks, 1951	Pacific Islands	Dengue fever, Ross River vírus and Murray Valley virus.	Mercer *et al.*, 2012
Aedes scapularis (Rondani, 1848)	Central America and parts of South America	Yellow fever, Rocio vírus, Mayaro vírus and Equine encephalitis vírus	Campbell *et al.*, 2021
Aedes serratus (Theobald, 1901)	Central and South America	Yellow fever, Mayaro vírus and Venezuelan equine encephalomyelitis virus	Aragão *et al.*, 2017
Aedes simpsoni (Theobald, 1905)	Africa	Ngari virus, Yellow fever, Babanki vírus and Chikungunya	Walter *et al.*, 2014; Poungou *et al.*, 2023
Aedes tarsalis (Coquillett, 1896)	North and Central America and Africa	Zika vírus, Pata virus, Bunyamwera vírus, Middelburg vírus, Pangola vírus, Kedougou vírus and Wesselbron vírus	Poungou *et al.*, 2023; WRBU, 2024
Aedes tricholabis Edwards, 1941	Africa	Ndumu vírus, Pongola vírus, Bunyamwera vírus and Ngari vírus	Poungou *et al.*, 2023

Aedes taeniorhynchus (Wiedemann, 1821)	Central America, Caribbean, parts of South America	West Nile virus, Venezuelan equine encephalomyelitis and Yellow fever	Jiang; Burroughs, 2024
Aedes vexans (Meigen, 1830)	Central America, Central Asia, Africa and parts of East Asia	West Nile fever, Rift Valley fever, Saint Louis encephalitis vírus, Equine encephalitis vírus, Filarial nematodes, Ngari virus eand Wesselsbron virus	Vargas-Espinosa; Aguirre-Obando, 2022; Poungou *et al.*, 2023
Aedes vigilax (Skuse, 1889)	Australia and Pacific Islands	Ross River vírus and Filarial nematodes	Kay, 1982; Poungou *et al.*, 2023; WRBU, 2024
Aedes vittatus (Bigot, 1861)	Central America, East and Central Africa, Central and East Asia	Yellow fever, Zika vírus, Chikungunya, Rift Valley fever vírus, Sindbis vírus, Middelburg vírus, Wesselbron vírus, Semliki vírus, Bunyamuera vírus, Simbu vírus, Saboya vírus and Pongola virus	Weetman *et al.*, 2018; Poungou *et al.*, 2023; WRBU, 2024

Source: The author, 2024

DISCUSSION

Aedes aegypti

Also known as the dengue mosquito, it originated in Africa and is currently distributed throughout most of the world, especially in tropical and subtropical regions. Its spread throughout the tropical and subtropical world began with the advent of transatlantic shipping in the 16th century, when worldwide epidemics of diseases caused by pathogens transmitted by *Aedes aegypti* began. At the height of its distribution in Europe during the early 20th century, the species had well-established populations throughout the Mediterranean Basin (Schaffner; Mathis, 2014).

It is a species well adapted to urban environments, where there is a greater concentration of humans and where it finds places to proliferate. It lays its eggs in artificial containers with small amounts of standing water, preferably in shaded areas (Guarido *et al.*, 2021). *Ae. aegypti* larvae are sensitive to light, which means they also thrive in murky water. The females of the species are hematophagous and can move up to 2,500 meters from where they emerged. This species is considered a vector of serious diseases such as dengue, yellow fever, Zika virus, chikungunya, among others (Kraemer *et al.*, 2015).

Globally, a number of factors are associated with the presence of *Ae. aegypti*, including the process of urbanization, socio-economic factors, the quality of water supply and management, and the quality of other public health infrastructure services. The geographical distribution of *Ae. aegypti* is dynamic and appears to have undergone significant changes over time. In the Americas, efforts to eradicate this species were implemented throughout the 20th century, resulting in a sharp decline in populations (Jansen; Beebe, 2010).

In Southeast Asia, where the introduction of *Ae. aegypti* occurred in the late 19th century, strong economic growth, along with better housing standards and vector control programs, have reduced the populations of this vector in many countries (Halstead, 2006). In Australia, changes in water storage practices have likely contributed to the regression of *Ae. aegypti* to warmer, more tropical regions (Jansen; Beebe, 2010). Studies that have mapped the global or regional distribution of *Ae. aegypti* have focused on different aspects of its ecology. Most have assessed the impacts of climatic conditions, often focusing exclusively on temperature (Kobayashi *et al*., 2002) and, more recently, on the effects of climate change (Escobar *et al*., 2016; Ryan *et al*., 2019).

Aedes africanus

It is a vector species of dengue fever, yellow fever, West Nile virus, Rift Valley fever virus, and a number of other arboviruses, found mainly on the continent of Africa (Poungou *et al*., 2023). It has distinctive black and white stripes along its body that help differentiate it from other species in the genus. The females are hematophagous and can most often be found on mammals living in tropical forests. The *Ae. africanus* species can be distinguished from other mosquitoes in the *Aedes* genus by having white scales on the maxillary palps, a shield with a patch of large white scales, and three large white spots in the middle of the femur (Huang, 1990).

This species lays its eggs in the hollows of trees and bamboos. Its larvae hatch best at 27°C, and the amount of water is not a factor in embryonic development, but it usually lays within 2 cm of the water surface (Sempala, 1981). *Aedes africanus* adults are crepuscular feeders, which means they feed from dusk to dawn. Although this species is a vector for many diseases, it is mainly found in forests, where primates are its main source of blood food (Ross; Gillett, 1950).

Aedes albopictus

Known as the “Asian tiger mosquito,” this species has expanded rapidly due to climate change and international trade (Kobayashi *et al*., 2002). It was first described over a century ago based on specimens collected in Calcutta, India. Its original distribution included Southeast Asia, the islands of the Pacific and Indian Oceans, northern China, Japan, and Madagascar. Today, it has spread to dozens of countries on all continents and is considered one of the most important invasive species in the world (Medlock *et al*., 2007). The trade in used tires containing eggs has probably been a factor favoring the dispersal of this species in recent decades, along with intercontinental traffic in other goods and varied routes (Paupy *et al*., 2010).

Its dispersal from temperate regions such as North America and Europe, as well as from tropical and subtropical regions such as South America and Africa, has been facilitated by the species' biological and behavioral plasticity, including the use of a variety of larval habitats (e.g., artificial habitats) (Paupy *et al*., 2010). Immature forms of this species are found in natural deposits such as bromeliads, tree holes, and bamboos, and their larvae can also co-occur and compete with those of *Ae. aegypti* in man-made containers (Liang *et al*., 2015).

The Asian tiger mosquito, *Ae. albopictus*, is one of the main vectors of arboviruses such as dengue virus (DENV), yellow fever virus (YFV), chikungunya virus (CHIKV), and Zika virus (ZIKV), which are widely distributed in tropical and subtropical regions of the world. These arboviruses infect millions of people every year globally, with almost half of the world's population at risk of infection. The global emergence of these arboviruses is associated with interactions between pathogens, vectors, hosts, and environments (Engering *et al*., 2013). This species of *Aedes* feeds alternately on humans and animals opportunistically and tends to rest outdoors but has also been shown to exhibit strongly anthropophagic behavior (Delatte *et al*., 2010).

Most published predictions of habitat suitability for *Ae. albopictus* are derived from statistical models that relate the known distribution of the species to spatial predictors (Fischer *et al*., 2014). However, this species is among the fastest spreading in the world, exhibits strong environmental adaptability, and can lay diapause eggs that are resistant to cold and dry conditions. The diapause characteristics of *Ae. albopictus* not only help to increase its survival rate in cold and dry periods but also facilitate the rapid invasion of the species globally through long-distance transportation (Laporta *et al*., 2023; Liu *et al*., 2023).

Aedes argenteopunctatus

This species occurs on the African continent. It breeds in small pools of water near the ocean. Being anthropophilic, it is a potential vector for dengue fever, chikungunya, Ngari virus, and Nkolbisson virus. Although zoophilic and preferring to feed on domestic ruminants, it can also feed on humans (Tantely *et al*., 2016; Sang *et al*., 2017; Mutisya *et al*., 2021; Poungou *et al*., 2024; Poungou *et al*., 2023).

Aedes bromeliae

This complex include *Ae. simpsoni* (Theobald) and *Ae. lilii* (Theobald). Molecular techniques are needed to reliably differentiate these species and have confirmed that *Ae. bromeliae* is the most widespread and abundant taxon of the Simpsoni complex in most of central and eastern sub-Saharan Africa. Despite intensive research, only *Ae. bromeliae* has been found in Tanzania, but in neighboring Uganda, *Ae. bromeliae* and *Ae. lilii* are found in sympatry. The *Ae. bromeliae* mosquito is an important vector of yellow fever. Genetic differences have been reported between anthropophilic *Ae. bromeliae* and zoophilic *Ae. lilii* and between forest and domestic populations (Bennett *et al*., 2015).

The females of *Ae. bromeliae* are peridomestic and closely associated with agricultural plots, where they lay their eggs in the axils and hollows of plants. The immatures are found in habitats such as water reservoirs in the axils of palm and banana trees, up to two meters above the ground. This species easily bites humans and other primates who enter the habitats where the species is found. It is a highly efficient vector of yellow fever (Weetman *et al*., 2018; Poungou *et al*., 2023).

Aedes caballus

It is a species considered to be a vector of Rift Valley fever, Wesselsbron virus, Middelburg virus, and West Nile virus (Poungou *et al*., 2023; Nejati *et al*., 2024). Although known as an Afrotropical species, it has also been recorded in the Middle East, including Iran, Saudi Arabia, and Yemen (Nejati *et al*., 2024). This species follows a single-generation breeding pattern and is rarely found indoors, preferring to stay close to its breeding sites. It lays its eggs individually on the ground, between rocks, near rivers or bodies of water. It breeds abundantly in small to medium-sized habitats with vegetation, often periodically flooded by rain or irrigation water. The occurrence of Rift Valley fever epidemics is commonly associated with periods of higher rainfall. The adult mosquitoes emerge in large swarms near their breeding sites and are known for their painful bites. They can attach themselves to humans and clothing, immediately engaging in biting. Humans and some mammals such as horses, cattle, and sheep serve as hosts (Steyn; Schulz, 1955).

Aedes caspius

It is characterized as a species of floodwater mosquito widely distributed in the Western Palaearctic. As an anthropophilic species and an arbovirus vector, it may be associated with certain diseases in Europe, such as Zika virus (ZIKV) (Poungou *et al.*, 2023), although studies on vector competence for ZIKV are still scarce (Núñez *et al.*, 2019).

The immatures of this species are found in a wide variety of coastal locations in the UK, and in lakes and salt pools around the Mediterranean. In the rest of its range, it is found in fresh and salt marshes, but is most abundant in salt marshes. The species winters in colder climates as eggs, which emerge after flooding in spring. Like other salt marsh mosquitoes, the females usually take long-distance flights soon after emergence. Some populations of *Ae. caspius* are autogenous, capable of laying a batch of eggs before the first blood meal. It goes through several generations a year and can become a significant nuisance when abundant, biting during the day and night, both indoors and outdoors. At lower population levels, biting usually occurs outdoors during twilight periods. It is one of the only mosquitoes proven to transmit *Francisella tularensis*, the causative agent of tularemia (WRBU, 2024).

Aedes circumluteolus

It is a species of mosquito found in much of sub-Saharan Africa, often in tropical coastal plains and savannahs. The highest levels of infestation occur after floods. During the dry months, the males of the species mainly disappear, while the females persist at very low levels. Blood feeding and ovarian development occur year-round, with antelope as the preferred host. In populated areas, females have been observed feeding on human, cattle, goat, and dog blood. Immature stages of *Ae. circumluteolus* can be found in shallow temporary pools, and the species hibernates mainly in the form of eggs that are resistant to drought (WRBU, 2024).

This mosquito species is the main vector of the Spondweni virus, a virus related to Zika virus that can lead to an infection known as Spondweni fever. In addition, this species is also a vector for pathogens such as Lebombo virus, Wesselsbron virus, Kedougou virus, Bunyamwera orthobunyavirus, and Rift Valley fever virus (Poungou *et al*., 2023).

Aedes cinereus

The species is opportunistic and can be found in a wide range of larval habitats. It is most often found in permanent and semi-permanent marshes, as well as in various floodwater habitats. The species rarely occurs in great abundance but can be an aggressive stinger. It does not fly very far from its larval habitat and acts as a local pest. It is characterized as a wild species that bites at any time of the day, usually concentrating its feeding activities on the lower extremities of its hosts (ankles). This species has been described as a vector for Ockelbo virus, Sindbis virus, Tahyna virus, and West Nile virus (Lindström *et al*., 2021).

Aedes cumminsi

This species is widely distributed across the African continent, south of the Sahara Desert. It is described as a vector for Nkolbisson virus, Rift Valley fever virus, and Spondweni virus (Poungou *et al*., 2023; Shepherd *et al*., 2023). The larvae develop in temporary pools of muddy water on the edges of swamps. Rain that floods the area tends to trigger the development of larvae in these places. Thus, this species occurs in greater abundance after heavy rains, and adults may be absent between flooding events. Little is known about the biology of this species. The females preferentially feed on the blood of domestic ruminants but can also attack humans (WRBU, 2024).

Aedes dentatus

It is characterized as a predominantly highland species, particularly where rainfall is high. Adult females readily attack humans and other vertebrates such as birds, cattle, and other mammals, including primates (Mohamed *et al*., 2017). It can transmit Rift Valley fever and yellow fever (Poungou *et al*., 2023). It is a diurnal species with peak activity around sunset (Mohamed *et al*., 2017).

Aedes furcifer

Among the *Aedes* species that are potential vectors of yellow fever in the sub-Sudan savannas of West Africa, this is the only species that comes into close contact with both monkeys and humans. This primatophilic behavior is associated with the strong aggressiveness of the females, who are found in both villages and forested areas. They account for one-third of all vectors caught in forest areas and two-thirds of those caught in edge environments. Inside the region's villages, they represent the most abundant mosquito species and the primary vector of the yellow fever virus (Mondet, 1997).

Aedes hensilli

This mosquito species was originally described in 1945. The larvae of *Ae. hensilli* develop in empty coconut shells, tree hollows, bamboo, and artificial containers such as cans, discarded drums, barrels, bottles, tires, tarpaulins, and floats. Water barrels used to collect rainwater are the main breeding grounds for mosquitoes due to the high number of larvae and pupae found in them. Adults are mainly active at dusk. *Aedes hensilli* is described as a potential vector of dengue fever, Zika virus, and chikungunya (Ledermann *et al*., 2014).

Aedes japonicus

Aedes japonicus is considered highly invasive, expanding from its native areas in Korea and Japan to North America and Europe. Females of *Ae. japonicus* lay their eggs on the walls of containers containing fresh water rich in organic matter. Preferred habitats include stone or cement containers with moderate levels of organic matter and turbid water, although immatures have also been collected in tree hollows, bamboo, artificial containers, and in ground pools. In its natural environment, *Ae. japonicus* inhabits forest areas and is active during the day. The females bite humans and large mammals, especially horses. The species hibernates as eggs in cold regions. It is implicated in the transmission of a number of pathogens, including dengue fever, chikungunya, West Nile virus, Japanese encephalitis virus, Saint Louis encephalitis virus, equine encephalitis virus, La Crosse virus, and Rift Valley fever virus (Kampen; Werner, 2014; WRBU, 2024).

Aedes koreicus

The species was described from specimens collected in South Korea and is native to northeastern China, Russia, the Korean Peninsula, and Japan. In 2008, *Ae. koreicus* was discovered outside its native range as an established population in an industrial area of Belgium and was subsequently detected in Italy in 2011 and then in Switzerland. Predictive models suggest that the climatic and environmental conditions of most of northern Europe would support the establishment of this species. *Aedes koreicus* larvae are typically found in small rock pools, tree hollows, and plant axils, containing standing fresh water with decaying tree leaves. The females are highly anthropophilic. The species is commonly found in urban areas, in close proximity to humans, raising concerns about its role in disease transmission. It is associated with the transmission of Japanese encephalitis virus (Nagy *et al*., 2024; WRBU, 2024).

Aedes luteocephalus

Aedes luteocephalus mosquitoes occur widely in sub-Saharan Africa and are significant Afrotropical vectors for Chikungunya, dengue, yellow fever, and Zika viruses (Poungou *et al*., 2023). Adult mosquitoes of this species can be distinguished from other *Aedes* species by the hind femur, which has a large pale band at the base and two large white spots in the anterior median and apical areas. Originally a wild mosquito, it is now also found in towns and urban areas. It bites most often at ground level in villages and forests and is most active during the nocturnal twilight period. Eggs are laid above the waterline in tree hollows and occasionally in broken or cut vertical bamboo stalks. In domestic environments, the species has adapted to artificial containers (WRBU, 2024).

Aedes mcintoshi

This species is widely distributed in Africa and is classified as a floodwater mosquito. Its larvae are typically found in grassy soil puddles and residual pools in streams. The females bite at night, preferring cattle but readily feeding on humans outdoors. They lay their eggs in the top layer of soil in areas likely to be flooded. The eggs can remain dormant for years, hatching only after sustained submersion. Tolerance to egg desiccation in floodwater mosquitoes is often linked to transovarian transmission of viruses between successive generations (WRBU, 2024).

Aedes mcintoshi is an important vector of Rift Valley fever virus and other pathogens, including Chikungunya, Ngari virus, Ndumu virus, Pongola virus, Wesselsbron virus, Babanki virus, and Bunyamwera virus (Weetman *et al*., 2018; Poungou *et al*., 2023).

Aedes mediovittatus

Aedes mediovittatus is a vector of the dengue virus, showing high rates of vertical transmission in laboratory studies. It has been observed feeding mainly on the blood of humans and dogs, but also on chickens, cats, rats, pigs, goats, sheep, cows, and horses. While its broad dietary spectrum may limit its vectorial capacity, the species seems to maintain a sufficiently high rate of vector-human contact to sustain transmission of the virus (Marcondes; Tauil, 2011).

Aedes polynesiensis

Aedes species found in Polynesia include those in the Marquesas, Austral, Society, Cook, Fiji, Pitcairn, Tuvalu, Samoa, Wallis and Futuna, Tokelau, and Tuamotu archipelagos. Morphologically, *Ae. polynesiensis* is very similar to *Ae. albopictus*. This mosquito has been described as a vector for dengue fever, filariasis caused by *Wuchereria bancrofti*, and canine heartworm disease. In laboratory studies, it has also shown potential to transmit filariasis and encephalitis caused by the Murray Valley virus and the Ross River virus. Although originally a semi-domestic species utilizing artificial breeding sites, it also lays its eggs in natural breeding sites such as coconut shells, crab holes, rock pools, cocoa beans, and the axils of coconut and banana trees. It is considered both a semi-domestic and a wild mosquito, usually breeding in clean water and occasionally in polluted water (Mercer *et al*., 2012).

Aedes taeniorhynchus

Aedes taeniorhynchus is reported as a vector for encephalitic viruses, including Venezuelan equine encephalitis, and can also transmit *Dirofilaria immitis*. Found in the Americas, it is known to bite mammals, reptiles, and birds. Adults of *Ae. taeniorhynchus* feed on a combination of blood and sugar, with females typically requiring a blood meal before laying their eggs. This species develops in periodic cycles and is highly sensitive to light. Its flight patterns produce specific wing beat frequencies, which facilitate species detection and sex distinction. The species utilizes habitats with temporary water sources, such as mangroves, salt marshes, and other areas with moist soil, for egg laying and larval development. In unfavorable environmental conditions, the eggs can remain dormant for years. The factors influencing the growth of *Ae. taeniorhynchus* during pre-emergence include environmental conditions, specifically humidity and temperature (Jiang; Burroughs, 2024).

Aedes vexans

Aedes vexans, known as the flood mosquito, is a vector for microfilariae responsible for heartworm disease, setariasis, and viruses such as Rift Valley fever and West Nile fever (Poungou *et al*., 2023). It is distributed across the Holarctic and Eastern regions, with minor extensions into the Australasian Region (excluding Australia). It is also found in the Afrotropical Region, as well as in Central America and South Africa. *Aedes vexans* exhibits increased feeding activity in grassland and meadow habitats compared to forested areas. While light levels alone do not significantly affect its activity, there is a notable increase in activity after sunset, suggesting that reduced lighting may stimulate feeding behavior. The species remains active within a temperature range of 10-34°C, with an ideal temperature for development being 30°C. At this temperature, the transition from larval hatching to adult emergence occurs in 6-8 days (Vargas-Espinosa; Aguirre-Obando, 2022; Poungou *et al*., 2023).

Aedes vigilax

Aedes vigilax is commonly found in salt marshes and mangroves in the Australasian region, noted for its broad white stripes covering its abdomen and tarsus. It breeds in flooded salt marsh environments, with its eggs being more sensitive to desiccation compared to other *Aedes* species. Females lay their eggs up to 4 cm above the ground in damp areas. After flooding, the eggs hatch in batches, and the larvae disperse throughout the marshes (Kay, 1982). The first and second instar larvae actively move to lower areas where water is likely to collect in pools large enough for their development. Adult mosquitoes of this species can fly considerable distances from the salt marshes to find suitable hosts. Females bite at any time of the day or night, with peak biting activity occurring around sunset. Hosts include humans, dogs, birds, possums, cats, and flying foxes (WRBU, 2024). Due to its opportunistic feeding habits, this species is involved in the transmission of several arboviruses and filariasis (Poungou *et al*., 2023).

Aedes vittatus

Aedes vittatus is found in Africa, South Asia, Southeast Asia, Central Asia, the Middle East, Southern Europe, South America, the Caribbean, and North America. The larvae develop in various habitats, including log hollows, hoof prints, boats, wells, bamboo, artificial containers, rock pools, and occasionally, during peak breeding season, in open concrete floodwater drains. This species is known to be a vector for several viruses, including Yellow fever, Zika virus, Chikungunya, Rift Valley fever virus, Sindbis virus, Middelburg virus, Wesselsbron virus, Semliki virus, Bunyamwera virus, Simbu virus, Saboya virus, and Pongola virus (Weetman *et al*., 2018; Poungou *et al*., 2023). Adult females exhibit a short twilight biting period, with peak activity occurring between 6:00 PM and 9:00 PM (WRBU, 2024).

CONCLUSION

The risk of arbovirus transmission by mosquitoes of the genus *Aedes* extends well beyond *Ae. aegypti* and *Ae. albopictus*, including diseases such as Dengue, Zika virus, Chikungunya, and Yellow Fever, which are commonly reported and associated with the Western Hemisphere. Each continent hosts a diverse range of *Aedes* species capable of transmitting pathogens, with Africa being particularly notable in this regard.

Climate change, urbanization, and globalization, characterized by the intense movement of people and goods, heighten the risk of introducing *Aedes* species into regions where they are not currently present, along with the associated pathogens, particularly arboviruses. There is a significant gap in knowledge regarding the biodiversity of the *Aedes* genus within the context of public health and scientific research, as well as regarding the risks to human and animal health. This study aims to provide valuable information to support further research and the development of monitoring and control measures for mosquito species with vector potential. This review does not seek to cover the topic exhaustively but to present an overview based on the available scientific literature.

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REFERENCES

ALAN-BARRETT, D.T. Molecular epidemiology of yellow fever virus. **Revista Biomedica**, v. 21, p. 213–220, 2010. http://www.revbiomed.uady.mx/pdf/rb102138.pdf

ARAGÃO, A. O. *et al*. New Records of Culicidae Species with Medical Importance in the State of Paraíba, Brazil. **Journal of Agricultural Science and Technology**, v. 7, p. 363-368, 2017. doi: 10.17265/2161-6256/2017.05.009

BENNETT, K. L. *et al*. Molecular Differentiation of the African Yellow Fever Vector *Aedes bromeliae* (Diptera: Culicidae) from Its Sympatric Non-vector Sister Species, *Aedes lilii*. **PLoS Negl Trop Dis**, v. 9, n. 12, e0004250, 2015. doi:10.1371/ journal.pntd.0004250

CAMPBELL, L. P. *et al*. Potential Distribution of *Aedes* (*Ochlerotatus*) *scapularis* (Diptera: Culicidae): A Vector Mosquito New to the Florida Peninsula. **Insects**, v.3, n. 12, p. 1-15, 2021. doi: 10.3390/insects12030213.

CARLSON, C. J. *et al*. Uma avaliação ecológica da ameaça pandêmica do vírus Zika . **PLoS Negl Trop Dis**, v. 10, e0004968, 2016. doi:10.1371/journal.pntd.0004968

CARVALHO, R. G. *et al*. Updating the geographical distribution and frequency of *Aedes albopictus* in Brazil with remarks regarding its range in the Americas. **Mem Inst Oswaldo Cruz** [Internet], v. 109, n. 6, p. 787–96, 2014. https://doi.org/10.1590/0074-0276140304

DELATTE, H. *et al*. Blood-feeding behavior of *Aedes albopictus*, a vector of Chikungunya on La Reunion. **Vector Borne Zoonotic Dis**, v. 10, n. 3, p. 249–58, 2010. doi:10.1089/vbz.2009.0026

ENGERING, A. *et al*. Pathogen-host-environment interplay and disease emergence. **Emerg Microbes Infect**, v. 2, n. 2, e5, 2013. doi: 10.1038/emi.2013.5

ESCOBAR, L. E. *et al*. Declining Prevalence of Disease Vectors Under Climate Change. **Sci Rep**., v. 6, n. 39150, 2016. doi: 10.1038/s41598-016-0015-2

FISCHER, D. *et al*. Climatic suitability of *Aedes albopictus* in Europe referring to climate change projections: comparison of mechanistic and correlative niche modelling approaches. **Eurosurveillance**, v. 19, p.1–13, 2014. doi: 10.2807/1560-7917.es2014.19.6.20696.

GUARIDO, M. M. *et al*. *Aedes* species (Diptera: Culicidae) ecological and host feeding patterns in the north-eastern parts of South Africa, 2014–2018. **Parasites Vectors**, v. 14, n. 339, p.1-14, 2021. https://doi.org/10.1186/s13071-021-04845-9.

GERRARD, S. R. *et al*. Ngari virus is a Bunyamwera virus reassortant that can be associated with large outbreaks of hemorrhagic fever in Africa. **J Virol**, v. 78, n. 16, p. 8922-8926, 2004. doi: 10.1128/JVI.78.16.8922-8926.2004.

GLASSER, C. M.; GOMES, A. C. Clima e sobreposição da distribuição de *Aedes aegypti* e *Aedes albopictus* na infestação do Estado de São Paulo. **Revista De Saúde**

Pública, v. 36, n. 2, p. 166–172, 2002. https://doi.org/10.1590/S0034-89102002000200008

HALSTEAD S. B. Dengue in the Americas and Southeast Asia: do they differ? **Rev. Panam. Salud Publica**, v. 20, p.407–415, 2006. doi: 10.1590/s1020-49892006001100007.

HUANG, Y. The subgenus *Stegomyia* of *Aedes* in the Afrotropical region. I. The *africanus* group of species (Diptera: Culicidae**). Contributions of the American Entomological Institute**, v. 26, n. 1, p. 3–90, 1990. Available at: https://apps.dtic.mil/sti/tr/pdf/ADA512452.pdf

JANSEN, C. C.; BEEBE N. W. The dengue vector *Aedes aegypti*: what comes next. **Microbes Infect**, v. 12, p. 272–279, 2010. doi: 10.1016/j.micinf.2009.12.011.

JIANG, Y.; BURROUGHS, S. Interactive effects of salinity and mosquito larvicides toxicity to larvae of *Aedes taeniorhynchus*. **Journal of the American Mosquito Control Association**, v. 40, n. 1, p. 26–31, 2024. https://doi.org/10.2987/23-7151

KAMAL, M. *et al*. Mapping the global potential distributions of two arboviral vectors *Aedes aegypti* and *Ae. albopictus* under changing climate. **PLoS ONE**, v. 13, n. 12, e0210122, 2018. https://doi.org/10.1371/journal.pone.0210122

KAMGANG, B. *et al*. Geographical distribution of *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae) and genetic diversity of invading population of *Ae. albopictus* in the Republic of the Congo. **Wellcome Open Research**, v. 3, p. 1-18, 2018. https://doi.org/10.12688/wellcomeopenres.14659.3

KAMPEN, H.; WERNER, D. Out of the bush: the Asian bush mosquito *Aedes japonicus japonicus* (Theobald, 1901) (Diptera, Culicidae) becomes invasive. **Parasites Vectors,** v. 7, n. 59, p. 1-10, 2014. https://doi.org/10.1186/1756-3305-7-59

KAY, B. H. Three modes of transmission of Ross River virus by *Aedes vigilax* (Skuse). **Aust J Exp Biol Med Sci**, v. 60, n. 3, p. 339-344, 1982. doi: 10.1038/icb.1982.37.

KILPATRICK, A. M. *et al*. West Nile Virus Epidemics in North America Are Driven by Shifts in Mosquito Feeding Behavior. **PLoS Biol**., v. 4, n. 4, e82, 2006. DOI: 10.1371/journal.pbio.0040082

KOBAYASHI, A. M. *et al*. Analysis of northern distribution of Aedes albopictus (Diptera: Culicidae) in Japan by geographical information system. **Journal of Medical Entomology**, v. 39, p. 4–11, 2002 . https://doi.org/10.1603/0022-2585-39.1.4

KRAEMER, M. U. G. *et al*. Past and future spread of the arbovirus vectors *Aedes aegypti* and *Aedes albopictus*. **Nat Microbiol,** v. 4, p. 854–863, 2019. https://doi.org/10.1038/s41564-019-0376-y

LAPORTA, G. Z. *et al*. Global Distribution of *Aedes aegypti* and *Aedes albopictus* in a Climate Change Scenario of Regional Rivalry. **Insects**, v. 14, p. 1-18, n. 49, 2023. https://doi.org/ 10.3390/insetos14010049

LEDERMANN, J. P. *et al*. *Aedes hensilli* as a Potential Vector of Chikungunya and Zika Viruses. **PLoS Negl Trop Dis**., v. 8, n. 10, e3188, 2014. doi:10.1371/journal.pntd.0003188

LEISNHAM, P. T.; JULIANO, S. A. Impacts of climate, land use and biological invasion on the ecology of immature *Aedes* mosquitoes: implications for the emergence of La Crosse. **EcoHealth**, v. 9, n. 2, p. 217–28, 2012. DOI: 10.1007/s10393-012-0773-7

LIANG, G. *et al*. Factors responsible for the emergence of arboviruses; strategies, challenges and limitations for their control. **Emerg Microbes Infect**, v. 4, n. 3, e18, 2015. doi: 10.1038/emi.2015.18

LINDSTRÖM, A. *et al*. Different Hatching Rates of Floodwater Mosquitoes *Aedes sticticus*, *Aedes rossicus* and *Aedes cinereus* from Different Flooded Environments. **Insects**, v. 12, n. 279, p. 1-9, 2021. https://doi.org/10.3390/insects12040279

MARCONDES, C. B.; TAUIL, P. L. Dengue silvestre: devemos nos preocupar?. **Rev Soc Bras Med Trop** [Internet]. v. 44, n. 2, p. 263–274, 2011. Available from: https://doi.org/10.1590/S0037-86822011000200029

MEDLOCK, J. M. *et al*. Possible ecology and epidemiology of medically important mosquito-borne arboviruses in Great Britain. **Epidemiol Infect**., v. 135, n. 3, p. 466-482, 2007. doi: 10.1017/S0950268806007047.

MENDES, K. D. S. *et al*. Revisão integrativa: método de pesquisa para a incorporação de evidências na saúde e na enfermagem. **Texto Contexto Enfermagem**, v. 17, p. 758-64, 2008. doi: 10.1590/S0104-07072008000400018

MERCER, D. R. *et al*. Monitoring temporal abundance and spatial distribution of *Aedes polynesiensis* using BG-Sentinel traps in neighboring habitats on Raiatea, Society Archipelago, French Polynesia. **J Med Entomol**., v. 49, n. 1, p. 51-60, 2012. doi: 10.1603/me11087.

MOHAMED, A. H. *et al*. Mosquitos Aedes na República do Sudão, com chaves dicotômicas para os estágios adulto e larval. **Journal of Natural History**, v. 51, n. 9–10, p. 513–529, 2017. https://doi.org/10.1080/00222933.2017.1285069

MONDET, B. Importance d´*Aedes* (*Diceromyia*) *furcifer* Edwards, 1913 (Diptera: Culicidae) Parmi Les Vecteurs Potentiels d'Arboviroses, dans l'Épidémiologie de la Fièvre Jaune en Savane Sub-Soudanienne de Côte-d'Ivoire. **Annales de La Société Entomologique de France (NS)**, v. 33, *n*. 1, p. 47–54, 1997. https://doi.org/10.1080/21686351.1997.12279177

MONTEIRO, V. V. S. *et al*. *Aedes*-Chikungunya Virus Interaction: Key Role of Vector Midguts Microbiota and Its Saliva in the Host Infection. **Front Microbiol**., v. 9, n. 10, p. 1-13, 2019. doi: 10.3389/fmicb.2019.00492.

MORITZ, U. G. *et al*. The global distribution of the arbovirus vectors *Aedes aegypti* and *Ae. Albopictus*. **eLife**, v. 4, e08347, 2015. https://doi.org/10.7554/eLife.08347

MUTISYA, J. *et al.* Evaluating the vector competence of *Aedes simpsoni* sl from Kenyan coast for Ngari and Bunyamwera viruses. **PLoS ONE**, v. 16, n. 7, e0253955, 2021. https://doi.org/ 10.1371/journal.pone.0253955

NAGY, N. A. *et al.* The updated genome of the Hungarian population of *Aedes koreicus*. **Sci Rep***, v.* 14, n. 7545, 2024. https://doi.org/10.1038/s41598-024-58096-6

NASIR, S. *et al.* A study on the role of *Aedes* mosquitoes in arboviruses and SARS-CoV-2 infection: A new challenge. **J King Saud Univ Sci**., v. 34, n. 6, p. 1-8, 2022. doi: 10.1016/j.jksus.2022.102179.

NEJATI, J. *et al*. The monsoon-associated equine South African pointy mosquito '*Aedes caballus*'; the first comprehensive record from southeastern Iran with a description of ecological, morphological, and molecular aspects. **PLoS ONE**, v. 19, n. 5, e0298412, 2024. https://doi.org/10.1371/journal.pone.0298412

NEW ZEALAND. **New Zealand Miosecure: *Aedes australi***s. 2007, 4 p. Available at: https://www.smsl.co.nz/site/southernmonitoring/files/NZB/Ae.%20australis%20new%20profile%2007.pdf

NÚÑEZ, A. I. *et al.* European *Aedes caspius* mosquitoes are experimentally unable to transmit Zika virus. **Parasites Vectors,** v. 2, n. 363, p. 1-7, 2019. https://doi.org/10.1186/s13071-019-3620-7

OCHIENG, C. *et al*. Mosquito-borne arbovirus surveillance at selected sites in diverse ecological zones of Kenya; 2007–2012. **Virol J**., v. 10, n. 140, p. 110–140, 2013. https://doi.org/10.1186/1743-422X-10-140

OLIVEIRA, S. *et al*. Wide and increasing suitability for *Aedes albopictus* in Europe is congruent across distribution models. **Sci Rep.,** v. 11, n. 9916, p. 1-9, 2021. https://doi.org/10.1038/s41598-021-89096-5

PADONOU, G. G. *et al*. Distribution and Abundance of *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae) in Benin, West Africa. **Trop. Med. Infect. Dis.**, v. 8, n. 9, p. 1-17, 2023. https://doi.org/10.3390/tropicalmed8090439

PAUPY, C. *et al.* Comparative role of *Aedes albopictus* and *Aedes aegypti* in the emergence of dengue and chikungunya in central Africa. **Vector Borne Zoonotic Dis**., v. 10, p. 259–266, 2010. DOI: 10.1089/vbz.2009.0005

PATZ, J. A. Dengue Epidemic Potential as Projected by General Circulation Global Climate Models Change. **Environ Health Perspect**., v. 106, p. 1-7, 1998. DOI: 10.1289/ehp.98106147

POUNGOU, N. *et al*. Mosquito-Borne Arboviruses Occurrence and Distribution in the Last Three Decades in Central Africa: A Systematic Literature

Review. **Microorganisms**, v. 12, n. 4, p. 1-37, 2024. https://doi.org/10.3390/microorganisms12010004

LIU, Q. *et al*. The predicted potential distribution of *Aedes albopictus* in China under the shared socioeconomic pathway (SSP)1–2.6, **Acta Tropica**, v. 248, 107001, 2023. https://doi.org/10.1016/j.actatropica.2023.107001.

ROSS, R.; GILLETT, J. The cyclical transmission of yellow fever virus through the Grivet monkey, Cercopithecus aethiops centralis Neumann, and the Mosquito *Aedes* (*Stegomyia*) *africanus* Theobald. **Annals of Tropical Medicine and Parasitology**, v. 44, n. 4, 351, 1950. doi:10.1080/00034983.1950.11685460

RYAN, S. J. Global expansion and redistribution of *Aedes*-borne virus transmission risk with climate change. **PLoS Negl Trop Dis.**, v. 13, n. 3, e0007213, 2019. https://doi.org/10.1371/journal.pntd.0007213

SANG, R. *et al*. Evolving dynamics of *Aedes*-borne diseases in Africa: a cause for concern. **Current Opinion in Insect Science**, v. 53, 100958, 2022, https://doi.org/10.1016/j.cois.2022.100958

SANG, R. *et al*. Effects of Irrigation and Rainfall on the Population Dynamics of Rift Valley Fever and Other Arbovirus Mosquito Vectors in the Epidemic-Prone Tana River County, Kenya. **Journal of medical entomology**. v. 54, n. 2, p. 460–470, 2017. https://doi.org/10. 1093/jme/tjw206

SCHAFFNER, F. *et al*. VBORNET gap analysis: mosquito vector distribution models utilised to identify areas of potential species distribution in areas lacking records. **Open Health Data**., v. 4, 201, 2017. doi: 10.5334/ohd.27.

SEMPALA, S. Some laboratory observations on the biology of *Aedes (Stegomyia) africanus*. **Insect science and its application**., v. 2, n. 3, p. 189–195, 1981. doi:10.1017/s1742758400001004

SHEPHERD, J. G. *et al*. Emerging Rhabdoviruses and Human Infection. **Biology,** v. 12, p. 1-12, 2023. https://doi.org/10.3390/biology12060878

SOUZA, D. R. *et al*. Field methods for the study of ants in sugarcane plantations in Southeastern Brazil. **Scientia Agricola**, v. 67, p. 651-657, 2010. https://doi.org/10.1590/S0103-90162010000600006

STAPLES, K. *et al*. Development of a regional climate change model for *Aedes vigilax* and *Aedes camptorhynchus* (Diptera: Culicidae) in Perth, Western Australia**. Bulletin of Entomological Research,** v. 114, p. 8–21, 2024. https://doi.org/10.1017/ S0007485323000561

TANTELY, M. L. *et al*. An updated checklist of mosquito species (Diptera: Culicidae) from Madagascar. **Parasite**, v. 23, p. 1-42, 2016. https://doi.org/10.1051/parasite/2016018

TOLLE, M. A. Mosquito-borne Diseases. **Curr Probl Pediatr Adolesc Health Care**., v. 39., n. 4, p.97–140, 2009. https://doi.org/10.1016/j.cppeds.2009.01.001

VARGAS-ESPINOSA, J. H.; AGUIRRE-OBANDO, O. A. Global phylogeography of the flood mosquito, *Aedes vexans* (Diptera: Culicidae), from mitochondrial DNA. **Zoologia (Curitiba)**, 39, e21029, 2022. https://doi.org/10.1590/S1984-4689.v39.e21029

WINT, W. Past, present and future distribution of the yellow fever mosquito *Aedes aegypti*: The European paradox. **Sci Total Environ**., v. 15, n. 847, 157566, 2022. doi: 10.1016/j.scitotenv.2022.157566.

WRBU. Walter Reed Biosystematics Unit. **Site da Walter Reed Biosystematics**. 2024. Available at: http://wrbu.si.edu/vectorspecies/mosquitoes

WEETMAN, D. *et al*. Mosquitos *Aedes* e arbovírus transmitidos pelo *Aedes* na África: ameaças atuais e futuras. **Int. J. Environ. Res. Public Health**., v. 15, n. 2, 220, 2018. https://doi.org/10.3390/ijerph15020220

WHO. World Health Organization. **The top 10 causes of death: The 10 leading causes of death in the world 2011 2000 and 2011**. 2024. Available at: https://www.who.int/news-room/fact-sheets/detail/the-top-10-causes-of-death