


# Emergence and Re-Emergence of Arboviruses: When Old Enemies Rise Again

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## Abstract

All arboviruses have complex life cycles that require at least one primary vertebrate host that is not a human and then, an arthropod that serves as the primary vector. They are a diverse group which are well-known in public health due to their widespread ability to produce high rates of illness and death in both animal and human populations. The RNA viruses known as arboviruses are spread by hematophagous or blood-feeding arthropods like mosquitoes, ticks, sandflies, etc. Depending on the severity of the infection, these pathogens can cause hemorrhagic fevers and encephalitis, or they can cause polyarthritis and intermittent fevers. Transient ecosystem dynamics and anthropogenic enablers are pivotal in the emergence and re-emergence of these arboviral diseases as changes in ecological factors can influence vector abundance, behaviour, and viral amplification. These arbovirus diseases are spreading quickly and account for a disproportionate amount of all infectious diseases. It is however imperative that to clearly distinguish the relative contributions of various drivers of global environmental change, it is imperative to assign reported variations in the risk of mosquito-borne disease to non-climatic causes. We provided a comprehensive contextual understanding of the ecosystem dynamics and anthropogenic activities that are playing a pivotal role in the re-emergence of arboviral diseases and the emergence of newer ones with a view to proffering new strategies to decimate this public health concern.

**Keywords:** Arboviruses; Ecosystem dynamics; Anthropogenic activities; Public health; Infectious diseases

## Introduction

All arboviruses have complex life cycles that require at least one primary vertebrate host that is not a human and then, an arthropod that serves as the primary vector [1]. They are a diverse group which are well-known in public health due to their widespread ability to produce high rates of illness and death in both animal and human populations. Mosquitoes, ticks, and sandflies are the most well-known arbovirus vectors [2]. For nutrition or developmental goals, several arthropods also ingest the blood of vertebrates [3]. Typically, each vector has a preference/affinity to blood from particular species, which makes these species serve as primary hosts. The virus hosts are vertebrate species whose blood has been consumed [4]. Throughout this cycle, mammals such as humans are considered to be “dead-end or incidental hosts.” This shows that not enough virus is produced by them in their bloodstream to infect other mosquitoes that bite them. While they cannot produce significant viremia and therefore do not contribute to the natural transmission cycle, domestic animals and humans are often referred to as “terminal” hosts, but they can still show clinical signs [5,6]. Several arboviruses, such as the dengue fever virus, yellow fever virus, Rift Valley fever virus, chikungunya virus, and zika virus, can cause viremia in humans and are spread from person to person by mosquitoes (urban cycle) [7,8]. These viruses have been connected in numerous studies to both domestic animals and non-human primates.

Only six arboviruses were recognized in 1930 and about 500 was discovered by 1980. The international arbovirus library currently lists 537 arboviruses, but as a result of investigations looking into the virosphere, it's anticipated that this number will soon be increased. However,

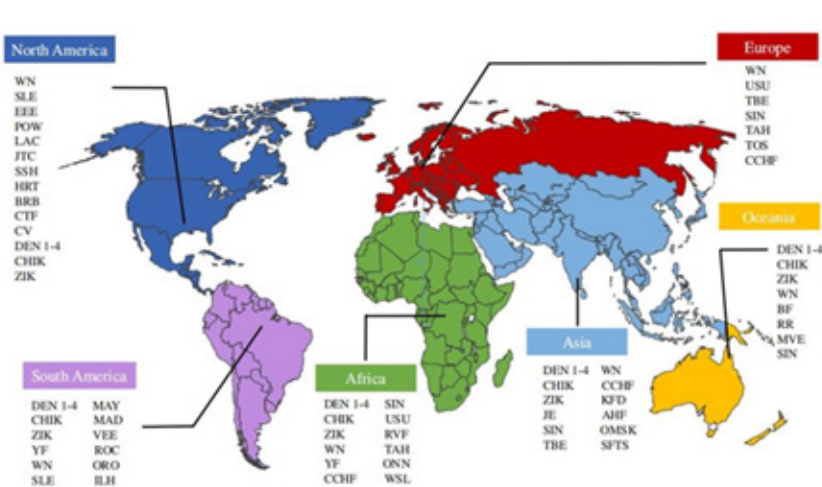
Over 500 distinct arboviruses have been discovered since the beginning [9,10]. One hundred of these have been connected to illnesses in humans and exhibit symptoms such as severe fever with restriction, joint and muscle pain, hemorrhagic symptoms, and/or abnormalities in the nervous system. *Togaviridae*, *Flaviviridae*, *Bunyaviridae*, *Reoviridae*, *Rhabdoviridae*, *Orthomyxoviridae*, and *Asfarviridae* are the seven virus families that makeup animal pathogenic arboviruses, and they are among the frequent causes of arboviral infection in humans and in animals [11]. Their symptoms can range from encephalitis to flaccid paralysis to minor infections such as aseptic meningitis, and one subgroup also affects the Central Nervous System (CNS). According to statistics, 40% of the world's population is susceptible to arboviral infections [12]. They are fairly specific to the specific place. Contrary to this, the majority of human arboviral infections are asymptomatic infections brought on by seroconversion or have mild clinical manifestations. The most typical indicator and symptom of an arboviral infection is fever. Importantly, with their widespread development and reemergence, arboviruses are increasingly posing serious threats to human and animal health [13]. Due to arboviruses' growing impact, continual monitoring and research are required, especially in tropical and subtropical regions, which are home to the majority of the world's low- income countries [14].

Deforestation, which drastically alters the breeding, abundance, and species composition of vectors, is one of the factors for arboviruses to arise. The transformation of the immature stages, as well as variations in resource requirements, predation, survival, and fecundity, are caused by changes in the breeding sites. Arbovirus vectors may benefit or suffer as a result of these alterations [12]. As changes in ecological factors can affect vector abundance, behaviour, and viral amplification, transient dynamics and anthropogenic enablers are pivotal in the re- emergence of arboviruses. Introduction, as well as the re-emergence, of these viruses, are typically viewed in separate lights, however, several endemic viruses continually spread at a slower rate in tandem with

habitat change. These arbovirus diseases are spreading quickly and make up a disproportionate amount of all emerging and re-emerging arboviral diseases. To mitigate the risk of possible future outbreaks, it is essential to identify the transitory dynamics of disease transmission and persistence from within-host to global community-level patterns [15,16]. This broadens the use of dynamic models for outbreak preparedness and management. The review is aimed at providing a comprehensive contextual understanding of the ecosystem dynamics and anthropogenic activities that are playing a pivotal role in the re- emergence of arboviral diseases and the emergence of newer ones with a view to proffering new strategies to decimate this public health concern.

## Epidemiology of Arboviruses

In 1901, the very first human virus was discovered. Since the 15th century, this virus has been common in tropical regions and has been connected with deadly epidemics with high rates of mortality. Although the condition might be mild in some people, more severe occurrences lead to catastrophic failure in the organs, like the liver, causing the formation of yellowish skin in affected individuals. This symptom served as the basis for the disease's name, Yellow fever, which also served as the basis for the name of the related viral genus, *Flavivirus*. Although Yellow fever had a significant impact, nothing was understood about how it was transmitted, however, it was clear that the illness did not spread from one individual to another. Up until Carlos Juan Finlay suggested that a sucking blood insect the mosquito was pivotal in spreading this disease, many theories on origin of the infection including the virus's existence in the air or on bedding were put forth. The study conducted by the Reed Commission in Cuba in 1899 a few years later demonstrated that mosquitoes are the disease's vectors. All arbovirus species, with the exception of African swine disease (*Asfarviridae*), have an RNA genome. Their cycle of transmission alternatively uses a vertebrate host as the virus' reservoir or amplifier and an arthropod vector. Ticks, culicoids, and particularly mosquitoes are arbovirus vectors.



**Figure 1:** Global distribution of arboviral infections.  
Source: Chauhan et al.2022[16].

The virus replicates in the midgut following the ingestion of blood on a host with the infection, the virus invades the tissues close by, leading to an elevated viral count, especially in the salivary glands. The time required by the virus to fully develop in the host organism (vector) is referred to as the extrinsic period. Finally, a further bite allows the arbovirus to infect a vertebrate host. In order to continue the transmission cycle, the virus must once more be able to reproduce successfully in order to cause a significant amount of viremia, at which point it can be taken up by a different vector. This brief period of viremia typically results in host immunity, ensuring a temporary role in the virus' maintenance. While the infected vector can occasionally vertically transmit the virus from one generation to the next, it is infected for the duration of its life (one season for mosquitoes, several years for ticks). There are three epidemiological patterns the sylvatic, urban, and intermediate cycles that some arbovirose, including Yellow fever, can spread through. The primary host of the sylvatic type of Yellow fever is the monkey, and the vectors are numerous species of *Aedes* (*Ae.*) mosquitoes in Africa and mosquitoes of the genus *Haemagogus* in South America. The distribution of arboviral disease around the world is showed in (Figure 1).

## Emergence and Reemergence of Arboviral Diseases

The RNA viruses known as arboviruses are spread by hematophagous or blood-feeding arthropods like mosquitoes, ticks, sandflies, etc. Depending on the severity of the infection, these pathogens can cause hemorrhagic fevers and encephalitis, or they can cause polyarthritis and intermittent fevers. Arboviruses are categorized into six families: (a) the Reoviridae family; (b) the Rhabdovirus family; (c) the Orthomyxoviridae family; (d) the Togaviridae family; (e) the Flaviviridae family; and (f) the Bunyaviridae family [13,17]. These viruses are a diverse group that are well-known in public health due to the substantial morbidity and mortality they frequently cause in both human and animal populations. The Bunyaviridae, Togaviridae, and Flaviviridae families are among them, and they are the most significant groups in Africa and the Eastern Mediterranean. Since most of the members of the flavivirus family are associated with newly emerging and reemerging arboviral infections, they garner more attention. The host and vector cycles, which carry the virus and transfer it to another organism, respectively, are pivotal in debilitating the transmission of these viral diseases. Due to their reliance on vectors to spread, they make up a special class of viruses that exhibit extremely high levels of genetic plasticity, allowing them to select both vertebrates and invertebrates as their primary hosts (this is termed dual-host tropism).

Human epidemics periodically arise every five to ten years for this reason. In the urban setting, mosquitoes pick up the virus from infected humans and pass it on to susceptible individuals. The typical vector is the domestic mosquito *Aedes aegypti*, whose females prefer to deposit their eggs in the still water of containers and live close to their homes. Finally, semi-domestic mosquitoes that nest in the wild and near habitations transmit this intermediary form to both humans and monkeys. In this situation, the virus

may spread from one person to another or from the monkey to the human through the vector. In the intermediate cycle, which involves people who live or work in the jungle's border regions, the latter does occasionally break out of the sylvatic cycle during a trip to or time spent in the jungle. The African savannah is where this epidemiological pattern predominates.

## The emergence of arboviral diseases

When a novel pathogen is discovered or when an existing pathogen establishes an endemic focus in a new location, disease emergence occurs. Even though a number of arboviral zoonoses have been well-known to medicine for hundreds of years, important human infections are still frequently discovered. The advent of a novel arboviral zoonosis in the present day may be best illustrated by the case of SFTSV, a virus that was first identified in humans in South Korea and Japan in 2009 after being initially described in China. According to statistics, China alone has at least 1,500 verified cases with a 7.8% case fatality rate [18]. Arboviral diseases are a recurring hazard that are appearing in new areas. Particularly, two medically relevant arboviruses have demonstrated an unusual capacity to form centres of endemicity far from historical risk zones and produce an enormous disease burden.

## The re-emergence of arboviral diseases

Several arboviruses have shown a predisposition for resurfacing across endemic sites after a protracted period without triggering human disease, in addition to the establishment of vector-borne viruses. Thousands of individuals have been affected by large-scale febrile illness outbreaks linked to both CHIKV and ONNV, yet these outbreaks are usually decades apart. Although there is a chance of misdiagnosis with dengue that could understate the true prevalence, these epidemics appear to be episodic in nature [19]. KFDV, OHFV, POWV, KSIV, CCHFV, and WNV are some arboviruses that have demonstrated the propensity to re-emerge in endemic areas following periods of apparent slumber [20].

## Ecosystem Dynamics as a Driver of the Emergence and Re-Emergence of Arboviral Diseases

According to Tam et al. [21], approximately half of the world's population is in danger from these mosquito-borne viruses, which have a considerable negative impact on global health. In various regions of the globe, arboviral illnesses spread by mosquitoes respond to climatic change in a variety of ways. According to local ecological factors such as seasonal rainfall patterns, sanitary infrastructure, and degree of urbanization, these associations are frequently environmentally different and change [22-24]. Over the past 50 years, the prevalence of dengue has increased more than 30-fold [5]. Global dengue cases were predicted to be responsible for 2,922,630 DALYs in 2017 [25,26]. According to Rocklöv and Dubrow [27], it is a serious concern that the dynamics of the world's ecosystems are to blame for the emergence and reemergence of arthropod-borne viruses. To lessen the catastrophic effects these diseases have on communities all over the world, it is essential to have a better understanding of how these arthropod-borne diseases

are affected by various changes in the ecosystem, including climatic fluctuation.

### **Impact of climate change dynamics on emergence and reemergence of arboviral diseases**

A body of research currently available suggests that the emergence, reemergence, and geographic spread of multiple arboviruses most of which are spread by mosquitoes are being impacted by climate change. Many diseases that were previously limited to warm and hot regions of the world are now resurfacing in areas where incidence had sharply decreased and emerging in previously unaffected regions like regions with cooler temperatures [28-30]. Nevertheless, little is known about how these arboviral illnesses are impacted by ecosystem dynamics, such as shifting climatic suitability and other global environmental change causes.

**Impact of temperature:** The fluctuation in temperature across the globe is an additional significant factor. Many arboviruses and their vectors are thermostatically unequipped. As a result, the factors that affect temperature might change how viruses and their vectors are distributed geographically, encouraging the establishment of new arboviral diseases. Caldwell et al. [31] found that these epidemics of mosquito-borne diseases are significantly predicted by the climate. The development, oviposition, vectorial competence, survival, and abundance of mosquitoes that transmit the zika, chikungunya and dengue viruses all rise with increasing temperatures [32-36]. Higher temperatures also hasten the extrinsic incubation period, which is the amount of period required for the viruses to mature within the vector [37,38].

**a) Impact on the vectors:** According to research from Mordecai et al. [39], Shocket et al. [40], and Caldwell et al. [31], temperature represents certainly one of the key elements that influence the spread of mosquito-borne diseases. *Aedes aegypti*, the primary dengue vector, enhanced oviposition by nearly four times when minimum temperatures were 1 °C higher, according to the current field investigation [41]. Although there exists no extensive evaluation of this, it is likely that the climate sensitivity of these mosquito borne diseases may change based on these different thermal constraints. In reality, there is a complex and not linear relationship between temperature and diseases spread by mosquitoes.

**b) Impact on arboviruses:** Peña-García et al. [42] and Servadio et al. [43] found that elevated temperatures have a negative impact on dengue transmission in both Colombia and South Asia. Generally speaking, dengue disease transmission decreases beyond 32 °C, the temperature at which mosquito development and survival start to be negatively impacted [39,44]. The link between disease and climate is complicated by discontinuities, and average temperature change may not be the best predictor of mosquito-borne viruses. As opposed to this, daily, seasonal, and diurnal temperature variations are more accurate and robust indicators of the probability of contracting a mosquito-borne disease [45,46]. It is very challenging to generalize the effects of temperature on diseases carried by mosquitoes because of these aggravating components.

**Impact of rainfall:** Another significant and well-studied climatic factor that affects the spread of arboviral infections carried by mosquitoes is rainfall. Rainfall is essential for mosquito development and is necessary for completing the phases of their life cycle that depend on water [47]. Rainfall generally increases the number of mosquito breeding sites that are accessible, resulting in higher larval densities and adult abundances during times of high rainfall [48]. The malaria vectors *A. arabiensis* and *A. funestus* were less common in Tanzania due to the drought [49]. However, excessive amounts of rain can wash away mosquito larvae and reduce the spread of disease [50]. According to research conducted in Kenya, rainfall can reduce the loss of *Anopheles gambiae* larvae at night by up to 18% [51]. High rainfall-related overflowing of water containers also decreased the amount of *Aedes aegypti* eggs in Argentina [52]; for every 1mm rise in rainfall, 0.7 fewer eggs were discovered. According to Galardo et al. [53], there are species-specific connections between rainfall and mosquito abundance that reflect the various ecological niches that these mosquito vectors evolved to. Therefore, mosquito species abundance and disease transmission may be at their highest during dry spells or outside of the rainy season. For instance, the *Aedes* vectors that spread arboviruses like dengue and yellow fever differ according to the species in how they react to precipitation. Rainfall in Malaysia was positively connected with the quantity of immature *Ae. albopictus* mosquitoes, but *Aedes aegypti* population had a negative correlation with rainfall [54].

### **Impact of ecosystem dynamics on emergence and reemergence of arboviral diseases**

Socioeconomic variables must be taken into account when examining the connection between disease and climate change. Measures of poverty, such as healthcare, children services, and inadequate sanitation, can account for a large portion of the higher incidence of dengue, Zika, and chikungunya in Colombia and Bangladesh, respectively [55,56]. According to Liu et al. [57], European travel habits accounted for 70% of the variation in imported dengue cases, while population density in China explained roughly 70% of the dengue dispersion. As was previously mentioned, although the risk of contracting dengue fever may rise during periods of intense rainfall, the climate can also affect human behaviour related to water storage. Due to increased use of water containers as a result of water shortages, there are peaks in the likelihood of dengue in Brazil and Puerto Rico in the four months that follow the start of drought conditions [58]. It is however imperative that to clearly distinguish the relative contributions of various drivers of global environmental change, it is imperative to assign reported variations in the risk of mosquito-borne disease to non-climatic causes.

### **Anthropogenic Determinants of Emerging and Re-Emerging Arboviral Diseases**

Human-induced modifications to the environment inevitably lead to a complicated network of connections between people and the environment in the process of meeting their fundamental requirements and enhancing their well-being [59].



As a consequence of such anthropogenically driven climatic, demographic, and technological changes, the environment of viral diseases has changed. Because of habitat deterioration, the manner in which contact between humans and wildlife is changing as human communities spread into formerly unoccupied areas. The consumption of wild meat or intensifying encounters between hosts that are domesticated, and wild animals may be actions that raise the likelihood of spillover [23,60]. Extension and modernization of agriculture may promote the transmission of diseases within domesticated animal populations by employing high-density farming techniques [60,61]. The risk of disease spillover may be influenced by the changing climate. According to several studies [60,62,63], shifting environmental conditions might affect species range and density, resulting in unusual relationships between species and raising the likelihood of infectious emergence. The development of the pulmonary hantavirus in 1993 is thought to have been caused by a confluence of environmental conditions, including a protracted period of dryness followed by intense precipitation [60].

In nations with low or middle incomes, the population growth in overcrowded, subpar housing and accelerated urbanization have facilitated the expansion of most arboviral diseases. Urbanization has increased the prevalence of arboviral illnesses including dengue, Zika virus disease, and chikungunya, which are transmitted by mosquitoes that have become highly suited for urban environments like *Aedes aegypti* and *Aedes albopictus* [60]. Population size and *Aedes aegypti*'s predilection for human odour appears to be connected, which has led to the emergence of arboviral disease transmission through human bites [60]. Despite the notion that natural causes can potentially cause global warming, human action has indisputably accelerated this phenomenon over the past decades. Also, the declining level of biodiversity in aquatic, terrestrial, and marine ecosystems and the decline in ecosystem services are both caused by anthropogenic disruptions such as urbanization, deforestation, and agriculture, which also contribute to the emergence of arboviral diseases. Humans may suffer significant impacts from climate change. There may be other waves of migration in the future to more hospitable environments [64,65]. The average sea level has increased by more than 3 millimetres annually over the past 20 years. A significant factor in accelerating climate change and, thus, interfering with the progression of diseases is deforestation. Because of human activity or the adaptation of a group of species to anthropogenic circumstances, there is an increase in the number of interactions between wild animals and people as a result of the degradation of their natural habitats.

### Tackling the Public Health Threat

Arboviruses have a long history of emerging and reemerging, and this trend is certain to continue. Even if many unidentified arboviruses have not yet been discovered in the wild as epidemic strains, they may nevertheless evolve into pathogens due to the fast rate of mutation. A deeper understanding of the molecular interactions that drives the emergence of arboviruses will greatly

aid in predicting the likelihood of this happening. To increase the control and research programs on arboviral illnesses, governments, academics, and WHO should take note of the public health emergency caused by Zika virus, the threat posed by the Yellow fever, and the resurgence of both Dengue and Chikungunya viruses. An ongoing global and interdisciplinary approach is needed to improve the ability to anticipate, manage, and lessen the threat of emerging and re-emerging arboviruses. Research goals should include the identification of antiviral substances or potential vaccines, as well as an understanding of the mechanisms underlying adaptation to substitute vectors and other factors linked to infection and transmission.

When surveillance projects are initiated, there are more opportunities to find viruses due to the increased variety of viruses in the tropics and the latest developments in sequencing technologies. Although the co-circulation of these viruses requires the establishment of differential diagnostic systems, including more specific serological tests for seroprevalence studies, the similar attributes of these viruses may inspire common ground for research themes in the development of antiviral therapies and vaccines. It is critical to lessen the environmental and socioeconomic conditions that promote vector spread, particularly in urban areas with low incomes. Finding the best tactics and how well they support vaccination requires a review of the vector control tools that are currently in use and those that are being developed. To combine the most efficient and timely treatments against arboviral diseases, new international alliances are required. Two examples of these alliances are the global arboviral and the *Aedes*-related disease consortium. The number of adult mosquitoes and their breeding sites is growing as their resistance to man-made insecticides increases. The resurgence of these diseases has been caused by an increase in the vector (*Mosquito*) in urban agglomerations, which has led to an increase in mosquito resistance to these insecticides [65].

### Conclusion

The impact of arboviral diseases extends far beyond individual health, affecting entire communities and healthcare systems. Arboviral diseases contribute significantly to global morbidity and mortality. Dengue fever alone is estimated to infect millions globally each year, with tens of thousands of deaths. The neurological complications of arboviral encephalitis can lead to permanent disability and long-term care needs. Outbreaks of arboviral diseases can overwhelm healthcare facilities, particularly in resource-limited regions. Thus, there is need for an extensive study into the current prevalence of these viruses, especially in Africa where the endemicity of some of these viruses is prevalent. In addition to already existing control measures, new measures are needed to tackle the spread of the vectors of these viruses.

### References

1. Huang JS, Higgs S, Vanlandingham DL (2019) Arbovirus-mosquito vector- host interactions and the impact on transmission and disease pathogenesis of arboviruses. *Frontiers in Microbiology* 10.

2. Depaquit J, Grandadam M, Fouque F, Andry PE, Peyrefitte C (2012) Arthropod-borne viruses transmitted by phlebotomine sandflies in Europe: A review. *Euro Surveillance* 15(10): 19507.
3. (2020) CDC.
4. Kuno G, Chang GJJ (2005) Biological transmission of arboviruses: Reexamination of and new insights into components, mechanisms, and unique traits as well as their evolutionary trends. *Clinical Microbiology Reviews* 18(4): 608-637.
5. Hunt D (2015) Influenza. In: Hunt R (Ed.), *Microbiology and Immunology Online*.
6. Gregory CJ, Oduyebot, Brault AC, Brooks JT, Chung KW, et al. (2017) Modes of transmission of Zika virus. *Journal of Infectious Diseases* 216(suppl 10): S875-S883.
7. Weaver SC, Barrett AD (2004) Transmission cycles, host range, evolution and emergence of arboviral disease. *Nature Reviews Microbiology* 2(10):789-801.
8. Kuniholm MH, Wolfe ND, Clair YH, Ngole EM, Tamoufe U, et al. (2006) Seroprevalence and distribution of flaviviridae, togaviridae and bunyaviridae arboviral infections in rural Cameroonian adults. *American Journal of Tropical Medicine and Hygiene* 74(6):1078-1083.
9. Hayes E, Mackenzie J, Shope R (2008) Arthropod-borne viral diseases. In: Heymann D (Ed.), *Control of communicable diseases manual 19<sup>th</sup> (edn.)*, pp. 34-62. WHO/American public health association. Antimicrobial and antioxidant properties. *J Microbiol Exp* 10(5): 150-154.
10. Regenmortel VMHV, Fauquet CM, Bishop DH (2010) *Virus taxonomy: Classification and nomenclature of viruses; seventh report of the International Committee on Taxonomy of Viruses*. San Diego, Academic Press, USA, pp. 2000.
11. Hubálek Z, Rudolf I, Nowotny N (2014) Arboviruses are pathogenic for domestic and wild animals. *Advances in Virus Research* 89: 201-275.
12. Zahouli J, Koudou B, Müller P, Malone D, Tano Y, et al. (2017) Effect of land-use changes on the abundance, distribution, and host-seeking behavior of Aedes arbovirus vectors in oil palm-dominated landscapes, southeastern Côte d'Ivoire. *PLOS ONE* 12(12): e0189082.
13. Weaver S, Reisen W (2010) Present and future arboviral threats. *Antiviral Res* 85(2): 328-345.
14. Gould EA, Solomon T (2008) Pathogenic flaviviruses. *Lancet* 371(9611): 500-509.
15. Tao Y, Hite JL, Lafferty KD, Earn DJ, Bharti N (2021) Transient disease dynamics across ecological scales. *Theoretical Ecology* 14(4): 625-640.
16. Chauhan I, Matthews E, Piquet A, Henao A, Paredes F, et al. (2022) Nervous system manifestations of arboviral infections. *Current Tropical Medicine Reports* 9(4): 107-118.
17. King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (2011) *Virus taxonomy, classification and nomenclature of viruses*. In: King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (Eds.), 9<sup>th</sup> (edn.), Elsevier Academic Press, USA.
18. Liu K, Zhou H, Sun X, Yao W, Li Y, et al. (2015) A national assessment of the epidemiology of severe fever with thrombocytopenia syndrome, China. *Scientific Reports* 5: 9679.
19. Powers AM, Logue CH (2007) Changing patterns of chikungunya virus: Re-emergence of a zoonotic arbovirus. *Journal of General Virology* 88(Pt 9): 2363-2377.
20. Service MW, Ashford RW (2001) *Encyclopedia of arthropod-transmitted infections of man and domesticated animals*. CABI Publishers, USA.
21. Tam CC, Khan MS, Quigley HL (2016) Where economics and epidemics collide: Migrant workers and emerging infections. *The Lancet* 388(10052): 1374-1376.
22. Santos IC, Braga C, Souza WVD, Oliveira ASD, Regis LN (2020) The influence of meteorological variables on the oviposition dynamics of *Aedes aegypti* (Diptera: Culicidae) in four environmentally distinct areas in Northeast Brazil. *Memorias do Instituto Oswaldo Cruz* 1156: e200046.
23. Ekpunobi N, Akinsuyi O, Ariri T, Ogunmola T (2023) The reemergence of monkeypox in Nigeria. *Challenges* 14(2): 22.
24. Yuan HY, Liang J, Lin PS, Sucipto K, Tsegaye MM, et al. (2020) The effects of seasonal climate variability on dengue annual incidence in Hong Kong: A modelling study. *Scientific Reports* 10(1): 4297.
25. Bhatt S, Gething PW, Brady OJ, Messina JP, Farlow AW, et al. (2013) The global distribution and burden of dengue. *Nature* 496(7446): 504-507.
26. Zeng Z, Zhan J, Chen L, Chen H, Cheng S (2021) Global, regional, and national dengue burden from 1990 to 2017: A systematic analysis based on the global burden of disease study 2017. *EClinicalMedicine* 32: 100712.
27. Rocklöv J, Dubrow R (2020) Climate change: An enduring challenge for vector-borne disease prevention and control. *Nature Immunology* 21(5): 478-483.
28. Leedale J, Tompkins AM, Caminade C, Jones AE, Nikulin G, et al. (2016) Projecting malaria hazard from climate change in eastern Africa using large ensembles to estimate uncertainty. *Geospatial Health* 11(1 Suppl): 393.
29. Watts N, Amann M, Arnell N, Karlsson SA, Beagley J, et al. (2021) The 2020 report of the Lancet Countdown on health and climate change: responding to converging crises. *The Lancet* 397(10269): 129-170.
30. Ekpunobi NF, Adesanoye S, Orababa O, Adinnu C, Okorie C, et al. (2024) Public health perspective of public abattoirs in Nigeria, challenges and solutions. *GSC Biological and Pharmaceutical Sciences* 26(2): 115-127.
31. Caldwell JM, LaBeaud AD, Lambin EF, Ibarra AMS, Ndenga BA, et al. (2021) Climate predicts geographic and temporal variation in mosquito-borne disease dynamics on two continents. *Nature Communications* 12(1): 1233.
32. Bayoh MN, Lindsay SW (2003) Effect of temperature on the development of the aquatic stages of *Anopheles gambiae sensu stricto* (Diptera: Culicidae). *Bulletin of Entomological Research* 93(5): 375-381.
33. Rodríguez GA, Aybar CAV, Claps GL, Grosso MSLD (2015) Seasonal oviposition activity of *Aedes aegypti* (Diptera: Culicidae) in San Miguel de Tucumán, Northwestern Argentina. *Florida Entomologist* 98(4): 1241-1243.
34. Tesla B, Demakovskiy LR, Mordecai EA, Ryan SJ, Bonds MH, et al. (2018) Temperature drives Zika virus transmission: Evidence from empirical and mathematical models. *Proceedings of the Royal Society B: Biological Sciences* 285(1884): 20180795.
35. Sunmonu AB, Ekpunobi NF (2023) Larvicidal potential of silver nanoparticles synthesized from *Ocimum gratissimum* leaf extracts against *Anopheles* mosquito. *GSC Biological and Pharmaceutical Sciences* 25(3): 041-048.
36. Chu VM, Sallum MM, Moore TE, Lainhart W, Schlichting CD, et al. (2019) Regional variation in life history traits and plastic responses to temperature of the major malaria vector *nyssorhynchus darlingi* in Brazil. *Scientific Reports* 9(1): 5356.
37. Jácome G, Vilela P, Yoo C (2019) Present and future incidence of dengue fever in Ecuador nationwide and coast region scale using species distribution modeling for climate variability's effect. *Ecological Modelling* 400: 60-72.
38. Winokur OC, Main BJ, Nicholson J, Barker CM (2020) Impact of temperature on the extrinsic incubation period of Zika virus in *Aedes aegypti*. *PLoS Neglected Tropical Diseases* 14(3): e0008047.
39. Mordecai EA, Cohen JM, Evans MV, Gudapati P, Johnson LR, et al. (2017)

- Detecting the impact of temperature on transmission of zika, dengue, and chikungunya using mechanistic models. *PLoS Neglected Tropical Diseases* 11(4): e0005568.
40. Shocket MS, Ryan SJ, Mordecai EA (2018) Temperature explains broad patterns of ross river virus transmission. *ELife* 7: e37762.
  41. Gimenez JO, Alvarez CN, Almirón WR, Stein M (2020) Meteorological variables associated with the temporal oviposition rate of *Aedes aegypti* (Diptera: Culicidae). in resistencia city, chaco province, northeastern argentina. *Acta Tropica* 212: 105678.
  42. García VP, Chávez OT, Sánchez SA (2017) Estimating effects of temperature on dengue transmission in Colombian cities. *Annals of Global Health* 833(4): 509-518.
  43. Servadio JL, Rosenthal SR, Carlson L, Bauer C (2018) Climate patterns and mosquito-borne disease outbreaks in South and Southeast Asia. *Journal of Infection and Public Health* 11(4): 566-571.
  44. Mordecai EA, Ryan SJ, Caldwell JM, Shah MM, LaBeaud AD (2020) Climate change could shift disease burden from malaria to arboviruses in africa. *The Lancet Planetary Health* 4(9): e416-e423.
  45. Huber JH, Childs ML, Caldwell JM, Mordecai EA (2018) Seasonal temperature variation influences climate suitability for dengue, chikungunya, and zika transmission. *PLoS Neglected Tropical Diseases* 12(5): e0006451.
  46. Robert MA, Christofferson RC, Weber PD, Wearing HJ (2019) Temperature impacts on dengue emergence in the United States: Investigating the role of seasonality and climate change. *Epidemics* 28: 100344.
  47. Rejmánková E, Grieco J, Achee N, Roberts DR (2013) Ecology of larval habitats. In: Manguin S (Eds.), *Anopheles mosquitoes - new insights into malaria vectors' sylvie manguin*, intechopen.
  48. Reiter P (2001) Climate change and mosquito-borne disease. *Environmental Health Perspectives* 109(Suppl 1): 141-161.
  49. Kreppel KS, Caminade C, Govella NJ, Morse AP, Ferguson HM, et al (2019) Impact of ENSO 2016-17 on regional climate and malaria vector dynamics in Tanzania. *Environmental Research Letters* 14: 075009.
  50. Benedum CM, Seidahmed OE, Eltahir EB, Markuzon N (2018) Statistical modeling of the effect of rainfall flushing on dengue transmission in singapore. *PLoS Neglected Tropical Diseases* 12(12): e0006935.
  51. Benitez EM, Estallo EL, Grech MG, Céspedes MF, Almirón WR, et al. (2021) Understanding the role of temporal variation of environmental variables in predicting *aedes aegypti* oviposition activity in a temperate region of Argentina. *Acta Tropica* 216:105744.
  52. Galardo AK, Zimmerman RH, Lounibos LP, Young LJ, Galardo CD, et al. (2009) Seasonal abundance of anopheline mosquitoes and their association with rainfall and malaria along the matap river, amapí, Brazil. *Medical and Veterinary Entomology* 23(4): 335-349.
  53. Saifur RG, Hassan AA, Dieng H, Ahmad H, Salmah MR, et al. (2012) Update on temporal and spatial abundance of dengue vectors in penang, malaysia. *Journal of the American Mosquito Control Association* 28(2): 84-92.
  54. Paul KK, Chowdhury PD, Haque CE, Amin HMA, Goswami DR, et al. (2018) Risk factors for the presence of dengue vector mosquitoes, and determinants of their prevalence and larval site selection in Dhaka, Bangladesh. *PLoS ONE* 13(6): e0199457.
  55. Morgan J, Strode C, Sora JES (2021) Climatic and socio-economic factors supporting the co-circulation of dengue, zika and chikungunya in three different ecosystems in colombia. *PLoS Neglected Tropical Diseases* 15(3): e0009259.
  56. Liu K, Hou X, Ren Z, Lowe R, Wang Y, et al. (2020) Climate factors and the east asian summer monsoon may drive large outbreaks of dengue in china. *Environmental Research* 18(3): 109190.
  57. Barrera R, Amador M, MacKay AJ (2011) Population dynamics of *Aedes aegypti* and dengue as influenced by weather and human behaviour in san juan, puerto rico. *PLoS Neglected Tropical Diseases* 5(12): e1378.
  58. Petersen TK, Speed JDM, Grøtan V, Frøyen K, Austrheim G (2022) Urbanisation and land-cover change affect functional, but not compositional turnover of bird communities. *Urban Ecosyst* 25: 1679-1698.
  59. Baker RE, Mahmud AS, Miller IF, Rajeev M, Rasambainarivo F, et al. (2022) Infectious disease in an era of global change. *Nature Reviews Microbiology* 20(4): 193-205.
  60. Figueroa DAL, Barboza JJ, Vasquez EAG, Aldana DKB, Torres MD, et al. (2022) Epidemiological situation of monkeypox transmission by possible sexual contact: A Systematic Review. *Tropical Medicine and Infectious Disease* 7(10): 267.
  61. El-Sayed A, Kamel M (2020) Climatic changes and their role in emergence and re-emergence of diseases. *Environmental Science and Pollution Research International* 27(18): 22336-22352.
  62. Ellwanger JH, Leal BK, Kaminski VL, Villegas JMV, Veiga ABG, et al. (2020) Beyond diversity loss and climate change: Impacts of amazon deforestation on infectious diseases and public health. *An Acad Bras Cienc* 92(1): e20191375.
  63. Tazerji SS, Nardini R, Safdar M, Shehata AA, Duarte PM (2022) An overview of anthropogenic actions as drivers for emerging and re-emerging zoonotic diseases. *Pathogens* 11(11): 1376.
  64. Mansouri F (2022) The future of migration, multiculturalism and diversity in Australia's post-covid-19 social recovery. *Social Sciences and Humanities Open* 7(1): 100382.
  65. Enyi EO, Ekpunobi NF (2022) Secondary metabolites from endophytic fungi of *moringa oleifera*: Antimicrobial and antioxidant properties. *Journal of Microbiology & Experimentation* 10(5): 150-154.