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CASE STUDY

A critical assessment of mosquito control and the influence of climate change on mosquito-borne disease epidemics

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Abstract
The world has experienced perceptible climate change for the past 100 years. Global warming enhances the rapid spread of mosquito-borne diseases resulting in unknown consequences in the future. The global economic development, increased urbanization, and climate change have significantly increased the mosquito-borne disease transmission pattern and dynamics. In India, mosquito-borne diseases have been a core public issue for decades. Hence, mosquito control is primordial for preventing the transmission of malaria, lymphatic filariasis, dengue fever, Yellow fever, Zika virus infection, West Nile fever, and chikungunya virus infection in the human population. The mosquito control strategies based on ecology have received much more attention during the 1960s, as chemical pesticides induce negative impacts on human health and the ecosystem. Most of the current approaches in mosquito control have several limitations related to the development of insecticide resistance, lack of long-term sustainability, and negative impacts on the ecosystem and the environment. This review offers invaluable insights into severe mosquito-borne diseases, various vector control strategies, and the influence of climate change in mosquito-borne disease transmission.

Keywords Mosquito-borne diseases · Climate change · Vector control strategies · Mosquito control · Synthetic insecticides · Biological control

1 Introduction

Vector-borne diseases were recognized as one of the pre-eminent health problems that shockingly affected the human populace over the world during the twentieth century. According to the World Health Organization in 2017, about 80% of the human population

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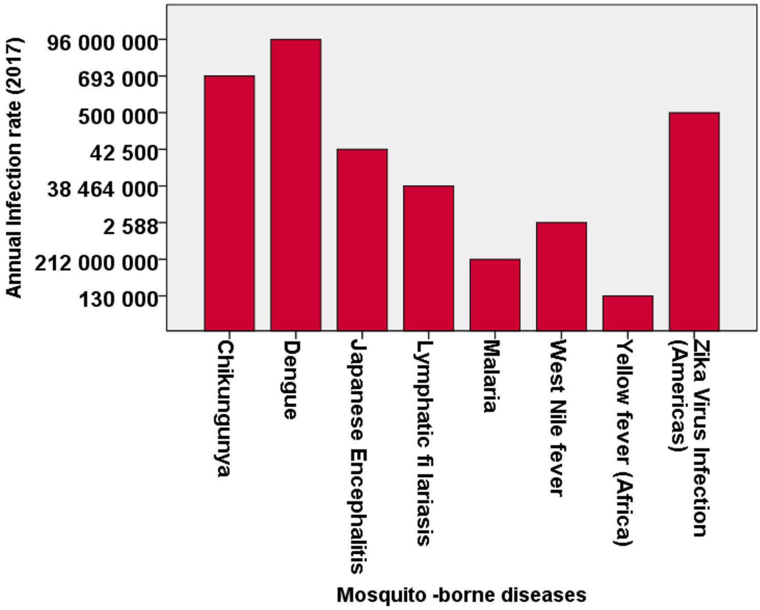

Fig. 1 Adverse impact of mosquito-borne diseases over the world in 2017

were infected by at least one or more vector-borne diseases (Fig. 1). It causes 7,00,000 deaths per year (WHO, 2017). Malaria, dengue fever, Yellow fever, and other deadly diseases caused morbidity, disabilities (Fig. 2), and mortality among the human population.

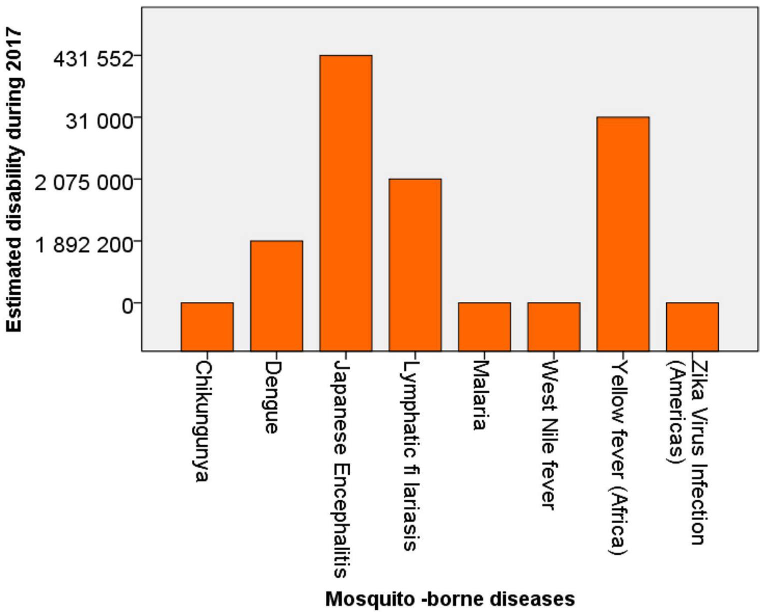

Fig. 2 Disability rates of people infected with mosquito-borne diseases in 2017

The prevention and control of these vector-borne diseases were highly efficient when the control measures were principally focussed on arthropod vectors (Anoopkumar & Aneesh, 2021).

Despite advanced developments in mosquito vector control aspects, infectious diseases remain to continue to spread worldwide, as highlighted by the recent outbreaks in various regions. Moreover, through trade and travel, dangerous mosquito vectors are being introduced into areas that were not threatened by mosquito-borne diseases previously. Due to the critical effort from the scientific community, many chemical products have been developed to offer extensive safety to public health in the current scenario (Anoopkumar et al., 2020a). Apart from their great benefit, the chemical products are also known to instigate toxicity to human beings instigating impairment in the nervous system, skin and eye irritation, swelling, and rashes. As a significant drawback, these synthetic products may also develop insecticide resistance in the target organisms like *Aedes aegypti* and *Culex quinquefasciatus* and the extensively challenging or impossible job of locating and treating all breeding habitats of such mosquito vectors (Anoopkumar et al., 2020e). Owing to the extensive concerns linked with public health and mosquito-borne diseases, researchers across the globe are continuously working hard in investigating the various novel strategies to combat the infection in terms of climate change aspects. As a follow-up, the noticeable focus has been made by the research community on designing and formulating effective diagnostic approaches, drugs, and vaccines together with vector control strategies. Therefore, new discussions regarding the drawbacks, benefits, and developing novel strategies targeting mosquito vectors are urgently imperative.

The intense and frequent extreme climatic events including augmented temperature, droughts, floods, and various environmental factors have exposed detrimental impacts like outbreaks of mosquito-borne diseases. Such events may also develop a large burden on developing countries in terms of social and economic cost. The prominent link between the epidemics of infectious disease together with climate change is investigated in previous studies (Lowe et al., 2020). The influence of climate change and climate-related factors on the dynamics of infectious disease, distribution, and transmission has necessitated the need for significant discussion (Pascual & Bouma, 2009). The four significant facts for efficient vector control programmes include: i) incrimination of the mosquito vector, ii) a better understanding of bio-ecology of the mosquito vector, iii) surveillance, and iv) public awareness programme. In addition to this, the major tools and approaches presently employed to control vector-borne diseases include drugs for its deterrence and treatment and insecticides of natural and synthetic origin to control the vector population. Here we describe the critical assessment of various important mosquito control strategies and whether climate change influences mosquito vector control perspectives. The goal is not only to evaluate the risks of climate change in vector control but also to consider various effective approaches to mosquito control programmes.

2 Literature review

One of the major aspects of this investigation was which are the major mosquito control strategies that are offering minimum risk to the human population in terms of health problems. Moreover, the influence of climate change in mosquito control disease epidemics is also recognized as another major focus of this study. A study by (Katz et al., 2008) revealed that arthropod bites may be considered as a cause of morbidity in many instances since the bite can develop either systemic or local effects that may inflammatory or infectious in nature. Studies that have focussed on the aforementioned aspects have driven us to investigate the most important groups, specifically the mosquitoes that are included in the insect group. The phylum, Arthropoda, includes the invertebrate group of animals such as insects, centipedes, spiders, crayfish, and shrimp. Insects are one of the most important groups of arthropods, in which mosquitoes represent a major threat to public health as they spread severe vector pathogens to the human population. Hence, the World Health Organisation (WHO) in 1996 declared the mosquitoes as 'public enemy number one'. The ability of mosquitoes to transmit various pathogens to humans causes severe diseases such as malaria, dengue fever, chikungunya, lymphatic filariasis, Yellow fever, Japanese Encephalitis, and Zika virus infection. This further leads to millions of deaths every year (A. N. Anoopkumar et al., 2019). The principal vector for malaria and lymphatic filariasis was *Anopheles* mosquito species. More sustained vector control efforts are also necessary to prevent the proliferation of *Culex* species as they spread Japanese Encephalitis, Lymphatic Filariasis, and other viral diseases. *Aedes* spp of vector mosquitoes have the greatest importance in public health (Rozendaal, 1997).

According to (Trampuz et al., 2003), malaria is recognized as a major public health threat and remains one of the principal sources of morbidity and mortality induced by infectious diseases worldwide and early diagnosis along with prompt treatment can block unwanted outcomes. The probable arrival of the disease in Rome (first century AD) was recognized as a turning point in European history. The disease was spread to Fertile Crescent and Greece from the African rain forest. From there, through Greek traders and colonists, it further spread to Italy, Denmark, and England. Plasmodium parasites belonging to the genus *Plasmodium* were recognized as the major pathogen for malaria. The pathogens are primarily transmitted to human beings and other animals through the bites of infected *Anopheles* mosquitoes, principally between dusk and dawn. Ronald Ross in 1897 isolated and identified plasmodial oocysts from mosquito's gut and simultaneously reported the potential of mosquitoes in malaria transmission. For the first time, Charles Louis Alphonse Laveran in 1880 discovered the Plasmodium parasites from the blood sample of patients distressed by malaria (Cox, 2010). The incubation period for malaria infection may vary from 7 to 30 days in most cases.

Geographically specific malaria induces adverse effects such as poverty and economic burden over the human population. In India, a large number of people are infected by malaria (Kumar et al., 2007). Similarly, with the exception of northern and southern extremes of Africa, most of the African countries were seriously threatened by malaria. Haiti, a Caribbean country usually considered as the poorest nation in the Western Hemisphere, is still facing severe risks from malaria (Laumann, 2010). These findings indicate that the risk from malaria is serious and were geographically specific. One of the prominent facts that have arisen behind this is that the African towns have a habit of growing outwards with borders consisting of underdeveloped settlements. Besides this, poorly monitored land use, urban agricultural practices, socioeconomic status, poor-quality housing, uncontrolled urban expansion, and unpaved roads have also been recognized as additional contributing factors for the aforementioned perspective (De Silva & Marshall, 2012).

The Centre for Disease Control and Prevention (CDC) in 2020 has also mentioned the role of local weather conditions, socio-economic instability, and scarce resources in preventing effective malaria control activities (CDC, 2020b). Besides this, relative humidity and temperature have a direct influence on malaria transmission. The statistical analysis by WHO in 2018 revealed that malaria has decreased from 251 to 228 million from 2010 to 2018. However, the latest report in 2019 indicated that more than 80 nations were currently under the threat of malaria and this report offers an ample update on malaria epidemics over the world. Studies conducted in 2019 verified the strong link between the climatic variables and malaria using the convergent cross-mapping technique. They have also reported that the risky weather events (extreme warmer) could augment the risk of malaria re-emergence away from the current distribution. The new developments in high-throughput technologies have assisted the quantification of complete transcriptomes has exposed a significant transcriptional variation. Studies based on the aforementioned aspects have allowed the scientific community to monitor the influence of the transcriptional activity with special inference on malaria infection (Abad-Franch et al., 2017; Solano-Villarreal et al., 2019).

Recent studies indicated that the innate immune response-allied molecular mechanisms and interactions of malaria vectors are prominently associated with the vectorial capacity and prevalence of mosquitoes. Besides this, the diagnosis of malaria infection is vital for accomplishing the aim of malaria eradication proposed by the Government of India. The World Malaria Report by the World Health Organization in 2018 revealed that there is no progress of reduction in global malaria cases from 2015 to 2017. To defeat the hurdles, the novel innovations along with existing strategies concerning disease surveillance, mass drug administration, and mosquito control practices hold the key to resolve the vast problem. The World Health Organisation has provided recommendations regarding the choice of rapid diagnostic tests (RDTs), but the selection concerning the RDTs remains challenging in the endemic provinces. Therefore, the analysis of genetic variability of the Plasmodium has received much more attention than others (Solano-Villarreal et al., 2019).

After malaria, lymphatic filariasis (first described in 1500 B.C.) is recognized as one of the second most common mosquito-borne parasitic diseases. It affects 120 million people in tropical countries (Ramzy et al., 2005). The lymphatic filariasis is caused by three kinds of nematodes such as *Wuchereria bancrofti, Brugia malayi,* and *Brugia timori*. These pathogens were transmitted by *Culex*, *Anopheles* and *Aedes* mosquito vectors, respectively (WHO, 2010). The incubation period for the disease may vary from 4 weeks to 8–16 months. The World Health Organization established a novel concept to start a programme for the eradication of lymphatic filariasis as a public threat by the year 2020 (Ottesen et al., 1997).

Several previous studies have employed ecological niche modelling to find the present status of lymphatic filariasis and its distribution in Africa. Those studies also discover the mechanism of future changes in population and climate leading to the rapid spread, economic loss, and burden to the continents (Slater & Michael, 2012). Based on the report from WHO, approximately 893 million people were infected by lymphatic filariasis. At the start of the Global Programme to eliminate lymphatic Filariasis, about 81 nations were recognized as endemic. Until this moment, the following countries and territories are accredited as accomplishing the eradication of lymphatic filariasis as a public health concern: The Cook Islands, Maldives, Niue, Palau, Tonga, Wallis, Cambodia, Egypt, Marshall Islands, Thailand, Togo, Vietnam, Fortuna, Kiribati, Yemen, Sri Lanka, and Vanuatu. Among the 72 endemic countries, they have eliminated the lymphatic filariasis in more than 11 countries. The successful outcome of the efforts has forced international agencies to design and develop systematic planning with execution for the eradication of lymphatic filariasis. The Global Programme for Elimination of Lymphatic Filariasis (GPELF) targeted and triggered mass drug administration (MDA) using albendazole and diethylcarbamazine to eradicate the disease in 2020. Moreover, as suggested by (Fang & Zhang, 2019), long-term care is essential to prevent the chronic effects associated with filariasis. Good hygiene should be maintained for the treatment of lymphoedema. It includes systematic cleaning with water and soap and the use of specific antifungal or antibiotic agents. Inadequate health infrastructures, the threat of drug resistance, lack of political wills, logistical issues are the significant factors that are linked with the infection rate. Recurrence of lymphatic filariasis owing to the migration of infected individuals into regions with disrupted transmission grants acts as an important challenge in disease eradication efforts.

Mores et al., (2014) discussed the human infection models with special inference on dengue fever transmission, and such aspects can prominently augment the knowledge of the society regarding the significance of some phenotypic traits of viral strains, thereby informing the trial design. The historical perspectives using human infection model have open prominent insight into the transmission mechanisms of dengue viruses. The first clinical report of dengue virus transmission was reported from Philadelphia during 1789–1780 by Benjamin Rush. Prior to 1970, merely nine nations had faced a threat to dengue epidemics. The dengue viruses and their transmitters have become extensively distributed over the tropical and subtropical provinces of the world, especially in Southeast Asia (SEA), Western Pacific region, the region of the Americas, African, and European regions. Now, the infection is endemic in more than 100 nations in the provinces of Western Pacific, South-East Asia, Eastern Mediterranean, and Africa. Recent reports based on cartographic approaches suggest that nearly 400 million people are infected with dengue fever every year. The incidence of dengue infections in 2019 is found to be high than the infection rate reported in 2017–2018. Across the Western Pacific region, an upsurge in infection rates has been found in Singapore, Lao PDR, Australia, Malaysia, Vietnam, China, Philippines, and Cambodia. The disease outbreak has also been reported in the African region (Tanzania, Congo, and Côte d'Ivoire) and the American region (Colombia, Honduras, Brazil, and Nicaragua). Moreover, the rates of infection have dramatically increased in Nepal, Thailand, Bangladesh, Sri Lanka, and various regions of India (WHO, 2019b). This is perhaps because of the presence of multiple other contributing factors such as climate change, travel, globalization, and socioeconomics.

Dengue fever is presently regarded as a severe mosquito-borne viral disease caused by serotypes of dengue virus (DENV-1–DENV-4) primarily transmitted by the *Aedes aegypti* mosquito population (Anoopkumar et al., 2020b, 2020e; Puthur et al., 2018). The virus constitutes seven non-structural and three structural proteins together with a 10.7 kb single strand of ribonucleic acid and a lipid envelope. The infections are usually asymptomatic in most of the infected individuals (75%). The incubation period for the infection can last from 3 to 10 days. However, most dengue patients experience an immediate onset of fever (2–7 days) followed by symptoms such as arthralgia, sore throat, anorexia, headaches, myalgia, and macular skin rashes over the body. A multifaceted interaction of viral factors along with the host after the infection determines whether the infection is severe or asymptomatic. Mainly four criteria were included for dengue fever infections. They are: i) probable dengue, ii) warning signs of dengue, iii) severe dengue, and iv) dengue shock syndrome clinical warnings. The first criterion includes the individuals who live in the dengue-endemic area. The major symptoms for probable dengue infections include fever along with the following conditions such as vomiting, myalgias, nausea, arthralgias, and rash. The second criterion includes persistent vomiting, ascites, lethargy, liver enlargement, mucosal bleeding, thrombocytopenia, and abdominal pain. The third criterion includes dengue fever with haemorrhage, organ dysfunction, plasma leakage, impaired consciousness, pulmonary dysfunction, and myocardial dysfunction. The fourth criterion includes various symptoms and clinical warnings allied with intense abdominal pain, narrowed or lacking blood pressure, and quickly increasing haematocrit (Yacoub et al., 2016).

According to (Chen & Wilson, 2020), many authors have developed and discussed models to predict the threat from yellow fever, its forecasting geographic spread, sudden outbreaks, and significant findings that may be considered beneficial in planning novel strategies to fight against the disease. Yellow fever is an infectious disease caused by Flavivirus, belonging to the family Flaviviridae. The disease was first reported from Africa (first epidemic in 1648) and may instigate a vast clinical spectrum that potentially results in haemorrhagic fever allied with severe damage in the liver. The incubation period for the infection is usually between 3 and 6 days. Yellow fever has primarily been transmitted through the sylvatic cycle and urban cycle. The former cycle involves the transmission of the virus between non-human primates, while the latter one involves the transmission between urban mosquitoes (*Aedes aegypti*) and humans. The disease is endemic in the tropic regions of South America and Africa. An upsurge in the population density and distribution of the *Aedes aegypti* mosquito vector induced the high risk of spread of Yellow fever over the North to Central America and Asia. Due to the adverse impact of Yellow fever, some of the American colonies refused admittance to ships from Yellow fever-infected regions in the 1980s (Pearson & Miles, 1980). The live-attenuated vaccine against Yellow fever was established in 1934. It was discontinued in 1980 as the vaccine generated more risk of encephalitic reaction specifically in children. The low coverage of vaccines permits approximately 80,000–2,00,000 infections and 30,000–60,000 deaths every year over the world. The global supply is inefficient for Yellow fever vaccination; hence, dose-sparing strategies have been implemented including intradermal administration and fractional dosing to overcome such circumstances (Chen & Wilson, 2020).

(de Freitas et al., 2019) reported the inhibiting activity of sofosbuvir against hepatitis C with special emphasis on their practical assumptions. They also discovered that the sofosbuvir diminishes the infected cells count and the production of virus particles carrying infectious properties. Their significant output is specifically relevant in the current scenario since the liver is the major target of the infection. The other added advantages of using sofosbuvir include the protection from weight loss, mortality, and liver injury. As of its antiviral potential (in vitro and in mice) and safety profile in humans, sofosbuvir may be considered as a novel option for the treatment of Yellow fever in the human population. Duarte-Neto et al., 2019 used the orthotopic liver transplantations (OLTs) to treat fulminant Yellow fever hepatitis. Among the seven unvaccinated individuals, four of them died and three of them were recovered. In addition to this, they have also mentioned the autopsy findings of unvaccinated individuals who faced a severe threat from fulminant hepatitis followed by Yellow fever. Faddy et al. 2019 mentioned that the inactivation of the virus can be accomplished by treating the methylene blue, ultraviolet C light, and visible light in platelet concentrates. However, further studies are necessitated to find out the practical assumptions including the determination of threshold concentration to prevent the Yellow fever transmission. Recently, a DNA vaccine was developed against the Yellow fever virus (de Azevedo Marques et al., 2019). Their study is primarily based on the sequences of those codes for the Yellow Fever Virus Envelope protein (p/YFE). The output from their investigation is recognized to be promising for the reason that the constructs can augment T-cell response towards the epitopes prompted by 17DD vaccine.

Before a few years back, the scientific community and news reporting agencies have reported recurrently regarding the Zika fever outbreaks from the world. Several previous studies like an investigation by (Zanluca & Dos Santos, 2016) have reported that the situation during the outbreak is really crucial because of the augmenting panic and fear, exclusively when the clear management guidelines and definitive treatments are unavailable. The Zika virus infection is principally transmitted by *Aedes aegypti*, *Aedes hensilli*, *Aedes africanus*, and *Aedes albopictus*. The incubation period for the disease may vary from 3–14 days. The Zika virus belongs to the *Flaviviridae* family and its evolutionary characteristics revealed that the virus is linked to Asian and African lineage. The isolation of the Zika virus for the first time in the world was performed from a macaque in Uganda's Zika forests. Right after, the Zika virus was isolated from *Aedes africanus* mosquitoes from the same forest. In 1952, the first infection on humans was reported from Nigeria. The first epidemic of ZIKV infection consists of forty-nine confirmed cases from Yap Island, Micronesia, in 2007. The non-mosquito transmission of ZIKV by sexual mode has been reported in 2008. More than 400 cases of ZIKV infections were reported in the second epidemic (French Polynesia).

The link to Guillain-Barré syndrome with Zika virus infection was verified in 2013. The infection rate was drastically increased to be greater than 1.5 million cases in the third epidemic that happened in South America. As a result of the incidence of microcephaly with ZIKV infection in 2015, the WHO in the next year (2016) has announced Zika as a public health threat. The frequency of Zika fever infection in the American regions drastically declined in 2017 and 2018 in comparison with 2016. In 2018, the disease was also reported from the Rajasthan State in India by the Ministry of Health and Family Welfare-Government of India (MoHFW). The central response teams and state health authorities in India continuously paid efforts to prevent the spread of infection over the nation. Mainly two kinds of ZIKV infections are reported: congenital ZIKV syndrome and Zika fever. Congenital Zika syndrome develops serious neurological anomalies associated with microcephaly in the infected person. The Zika fever has exhibited severe manifestations stretching from asymptomatic (80% of infections) to febrile sickness. The symptoms and various other signs of infection imitate "dengue-like" syndrome with bilateral non-purulent conjunctivitis, asthenia, retro-orbital pain, headache, low-grade fever, retro-orbital pain, arthritis, joint pain, vertigo, vomiting, maculopapular exanthema, and muscle pain (Hasan et al., 2019; Weltman, 2016).

Hasan et al. (2019) provided a detailed and comprehensive review of the Zika infection with special inference on public health concern. The non-mosquito transmission of ZIKV infection like sexual mode has been reported by previous studies (Foy et al., 2011). In agreement with their findings, (Musso et al., 2015) reported the point that the viral RNA can be spotted in the semen for 17 days of acute illness followed by 62 days after the symptoms have been observed in the infected individuals. In addition to this, (Dénes et al., 2019) discussed a compartmental model to determine the role of asymptomatic carriers in Zika virus transmission. They mentioned a non-autonomous model that allows the scientific community to explain the epidemics of Zika infection. The ZIKAV is currently circulating in 38 countries including Easter Island, Canada, Japan, Germany, The USA, Australia, and Italy.

During 2008, alarming news was aired on news channels that unveil the re-emergence of kid killer in Uttar Pradesh (UP). Due to a large number of infections and the unavailability of proper medical treatment many peoples have died. Japanese Encephalitis was first reported in 1871 from Japan and is still considered as a neglected tropical disease. The causative agent Japanese Encephalitis virus (JEV) is a member of the Flaviviridae family. Among the five genotypes of JEV, genotype 1 is known to circulate considerably more than others. The size of the virus is about 50-nm spherical particles constituting an electron-dense core surrounded by a lipid layer. The domestic animals including pigs are usually considered as the intermediate hosts, while humans are recognized as dead-end hosts of infection. The incubation period is usually 5–15 days. The significant vector responsible for Japanese Encephalitis transmission includes *Culex* mosquitoes. On account of the infeasibility of eliminating arthropod vectors, vaccination is considered as an effective means of preventing infection (Schiøler et al., 2007).

Various vaccines have been available in the market against the Japanese Encephalitis infection since the 1950s. The various kinds of vaccines include: i) inactivated vaccines cultured on kidney cells, ii) inactivated vaccines derived from mouse brain, and iii) live-attenuated vaccines (strain SA 14–14-2). Owing to the unsatisfactory safety properties, the production of mouse brain-derived vaccines in Europe and the USA has been discontinued. A formalin-based vaccine is widely used as an effective drug against infection in China during 1968. In terms of safety along with effectiveness, a live-attenuated SA14-14–2 vaccine is currently used in Sri Lanka, Nepal, South Korea, Thailand, and India. Also, the second-generation vaccines (chimeric Japanese Encephalitis vaccine and IXIARO®) against JE infections have used a lesser dosage scheme together with an extensive safety profile (Amicizia et al., 2018).

Japanese Encephalitis is endemic in Australasian and Asian regions including India, Nepal, Pakistan, Burma, Sri Lanka, Malaysia, Singapore, Indonesia, Philippines, Maritime Siberia, Korea, Vietnam, and Japan (Vaughn and Hoke Jr, 1992). The outbreak of Japanese Encephalitis has corresponded with two important epidemiological patterns such as monsoons and post-monsoon periods. The density of the vector population has dramatically increased in these periods. Moreover, the population density and abundance of the Japanese Encephalitis vector is strongly dependant on climate change and human activities. Approximately 30,00050,000 clinical cases have been reported every year, causing a mortality of 10—15,000 deaths annually. Fever, abdominal pain, lethargy, headache, vomiting, nausea, hypertension, and papilledema are the foremost signs of Japanese Encephalitis.

There have been several studies reviewed and focussed on West Nile Virus (WNV) infection and mosquito control. West Nile Virus (WNV) infection attained much more attention from 1937 to 1999 since it caused febrile illness throughout Asia, Europe, and Africa. The virus was first isolated from Uganda in 1937. The biggest outbreaks of West Nile Fever happened in Romania, Greece, the USA, Israel, and Russia. One of the major points regarding the WNV outbreaks is that most of the outbreak sites are routes of migratory birds. The pathogens responsible for West Nile Virus (WNV) infection are primarily transmitted by *Culex* vector mosquitoes (*Culex tarsalis, Culex quinquefasciatus, Culex stigmatosoma, Culex thriambus, Culex pipiens,* and *Culex nigripalpus*). The incubation period is usually 2–6 days. However, it may vary from 2 to 14 days for immunocompromised people. The transmission of WNV infection is seasonal (from July to October) in the temperate zones of Europe, North America, and the Mediterranean Basin (Zeller & Schuffenecker, 2004).

The West Nile Virus infections in human beings are mainly subclinical. However, clinical manifestations are also reported from febrile illness to neurological complications including neuroinvasive disease. In 2019, the incidence and drastic effects of WNV-linked anomalies have increased in the European Union with a specific concern for the Mediterranean regions. With the growing distribution of vectors and the extensive endemic potential of infection, the WNV is worldwide renowned and augmenting public health concerns. Alarmingly, there are no specific and effective antiviral treatments or vaccines presently available against WNV (Chianese et al., 2019). Histopathologic studies on WNV-infected human beings indicated that this virus causes severe neurological syndromes including loss of neurons, variable necrosis, and perivascular inflammation (Guarner et al., 2004). The control and prevention of WNV infection are mainly focussed on controlling the vector species by the use of insecticides. However, recent research on the novel concepts has revealed that the scientific community can target the blood-feeding behaviour of mosquito bridge vectors as a vector control strategy (Nguyen et al., 2019). Their study mainly focussed on the IVM-treated bird feed to control and prevent the infection. Laboratory and field trials with special inference on effective endectocide during WNV season have also been performed by them.

A study by (Ganesan et al., 2017) reported that lack of a specific adequate model for testing in both animals and humans is considered as the one of the major tasks in preventing the progressions in research allied with chikungunya virus infection. Chikungunya virus infection is predominantly transmitted by the mosquito vectors such as *Aedes aegypti* and *Aedes albopictus* (Anoopkumar et al., 2017b). The infection has emerged as an epidemic threat and causes a severe form of febrile illness, maculopapular rash, neurological disorders, and polyarthralgia in human beings. The virus was isolated in 1953 from Tanzania (Robinson, 1955). The incubation period for the disease is usually 3–7 days. Comparatively, an extensive range of persistent disability (30%–45%) and fatality rates (17%) were reported among the individuals who faced threats from CHIKV-linked encephalitis. Moreover, the augmented frequency of other neurological anomalies including Guillain-Barré syndrome has also been documented during a chikungunya outbreak in Polynesia (Oehler et al., 2015).

Mainly three kinds of chikungunya virus genotypes have been identified and are: i) Asian, ii) West African, and iii) East/Central/South African (ECSA). The development of A226V mutation in the chikungunya virus (E1- ECSA), as reported in Réunion in 2005, augmented the chance of spread of the virus through the *Aedes albopictus* (Van Bortel et al., 2014). A recent update on the studies concerning chikungunya infection has revealed that interferon-inducible protein (IFI) 16 prominently regulates the CHIKV infection in human skin fibroblasts. They also examined that the induced expression of interferon-inducible protein (IFI) 16 entirely restricted the infection (Wichit et al., 2019). Recent reviews indicated that no licensed effective vaccines are available for chikungunya virus infection. However, several highly auspicious candidate drugs have proceeded for preclinical studies, and only a small number of them have been tested in practical assumptions in humans (Rezza & Weaver, 2019). CHIKV infection has re-emerged in the Reunion Island, Indian subcontinent, South-Eastern Asia, and Africa. During 2014, 2811 clinical cases of chikungunya virus-induced infection were reported from the USA including 12 local clinical infections from Florida. The epidemiology of chikungunya is strongly associated with the weather conditions of Southeast Asia (Fischer et al., 2013). Several scientific reports have emphasized the enhancing climatic constancy for *Aedes* mosquito vectors in the European region as a consequence of changes in the climatic conditions (Caminade et al., 2012). From the review of literature, it was clearly evident that studies that linking various mosquito control strategies, epidemiology, clinical aspects, and barriers in vector control strategies like climate change as a case study are scanty in the current scenario, and this has enhanced the significance of this investigation.

3 Materials and methods

3.1 Data collection

We performed a review concerning the major mosquito-borne diseases, epidemiology, various methods to combat vector-borne disease along with major outbreaks and climate change perspectives. The search was executed using the various databases including Web of Science, ProQuest, ScienceDirect, EbscoHost, ClinicalTrials.gov, Scopus, PubMed, Semantic Scholar, Wiley Online Library, IEEE Xplore Digital Library, JSTOR, Microsoft Academic, Elsevier, Nature, PLOS One, Springer, and Directory of Open Access Journals (DOAJ) and Google Scholar. The keywords used for the search were: “mosquito-borne diseases”, “vector control”, “arboviruses”, “mosquito management”, “predators” “boosted SIT (Sterile Insect Technique)”, “entomopathogenic microorganisms”, “dengue”, “environmental factors”, “Malaria”, “larvivorous fishes”, “sex pheromones”, “sterile insect technique”, “climate change”, “Wolbachia bacteria”, “Africa”, “epidemiology”, “model”, “risk”, “vector-borne diseases”, “Zika virus”, “West Nile virus”, and “Chikungunya virus”. The time line for the selection of article was set from 1900 to 2021. The retrieved articles that are only in English language were then checked for their relevance to this investigation based on the title and the abstract. The reference part of all the important retrieved articles was also reviewed to get additional benefits. The data were then exported to the Microsoft office 2010–2019, R software version 3.0, and SPSS 24.0.0 (Fig. 3). Extraction of data from the collected literature is primarily based on the quality of the database, and the articles that did not meet the sufficient quality are immediately excluded. After the extraction of data, it has been then subjected to cross-checking to ensure the maximum quality of output for this investigation.

3.2 Statistical analysis

The Microsoft office 2010–2019, R software version 3.0, and SPSS 24.0.0. have been used throughout this investigation to perform the statistical analysis. The paired T test for an infection rate and disability/death rate of respective mosquito-borne disease has been performed. The preparation of graphical illustrations has been also done by using the aforementioned software.

4 Case study

WHO directed a global initiative to eliminate malaria between 1955 and 1970. In 1955, the WHO has launched the Global Malaria Eradication Programme (GMEP) to eradicate malaria from endemic provinces. The control strategies mainly focussed on the use of dichlorodiphenyltrichloroethane (DDT) (1960s). The GMEP mainly relied on indoor residual spraying (IRS) followed by systematic detection and treatments. The implementation

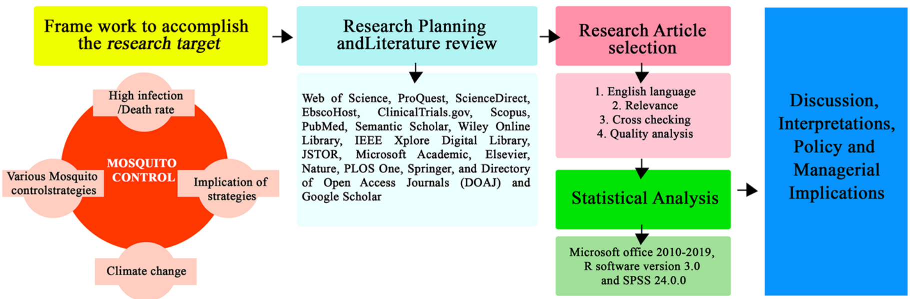

Fig. 3 Experimental framework

of the Global Malaria Control Strategy (1992) and the introduction of the Roll Back Malaria Initiative (1998) have increased financial investment in disease control (Shretta et al., 2017). The Global Malaria Programme (GMP) directed by WHO is liable for organizing WHO's global efforts to eradicate malaria. The Global Technical Strategy for Malaria 2016–2030 (GTS) offers a technical outline for all the malaria endemic provinces struggling against malaria eradication. The main goal of GTS includes: i) diminishing the incidence of malaria infection by at least 90%, ii) reducing the mortality rate to 90%, iii) eradicating malaria from least 35 nations, and iv) preventing the resurgence of the disease in all nations that are malaria-free (Programme, 2016). Likewise, in order to prevent the drastic effects of lymphatic filariasis, the WHO has initiated Global Programme to Eliminate Lymphatic Filariasis (GPELF) (2000). The major focus of the GPELF includes: i) reduce the threats of affected individuals and ii) diminish the intensity of infection.

The Yellow fever initiative and vaccination campaign in 2006 and 2016, respectively, launched by WHO has focussed on diminishing the intensity of outbreaks rapidly together with preventing its spread. The outbreak of Zika in Central, South, and North America with a rapid increase in the intensity of Guillain–Barré syndrome has forced the WHO to declare Public Health Emergency of International Concern (PHEIC) in 2016 (Sikka et al., 2016). Various countries including South Korea and Japan are recognized as prominent nations that gained successful results from Japanese Encephalitis control programmes. The Japanese Encephalitis control programmes principally employed the following four key factors: i) pig immunization, ii) human immunization programmes, iii) improved mechanization, and iv) well-developed living standards. The Ministry of Agriculture and Environmental Protection has initiated WNV surveillance programmes in 2014. The significant objectives of the programmes include the early detection of WNV with special inference on clinical aspects and mosquito control. The major strategy in mosquito vector control programme is the prominent use of either botanical or synthetic insecticides. The present investigation has developed a notion that supports the eco-attractive methods to create a platform to combat mosquito proliferation. One of the major factors to support such aspects is the high cost of synthetic insecticides, the harmful effect of synthetic products on human health, the concern for environmental sustainability, and the lack of essential novel insecticides.

The prominent aspects of this investigation are as follows: first, this study assessed the various mosquito-borne disease and mosquito control aspects that reflect the significance. Second, the data revealed from paired T test of transmission rate and disability/death rate for respective mosquito-borne diseases have verified their threatening effects to the human population, indicating the significance of this investigation in the current scenario.

5 Results and discussion

Here the various vector control strategies that are widely used for mosquito control worldwide are reported and discussed. Based on the statistical analysis from WHO, it was found that the mosquito-borne disease results morbidity and mortality in world, indicating the prominent role of infectious diseases in day today life of human beings. The WHO also reported that about 445,000 deaths have been reported due to malaria in 2016. The other mosquito-borne diseases have also showed their ability to instigate life-threatening effects to human population by augmenting the infection as well as the death rate, as illustrated in the statistical analysis of this investigation (Fig. 4; Tables 1 and 2). The T test analysis of infection rate and disability/death rate for mosquito-borne

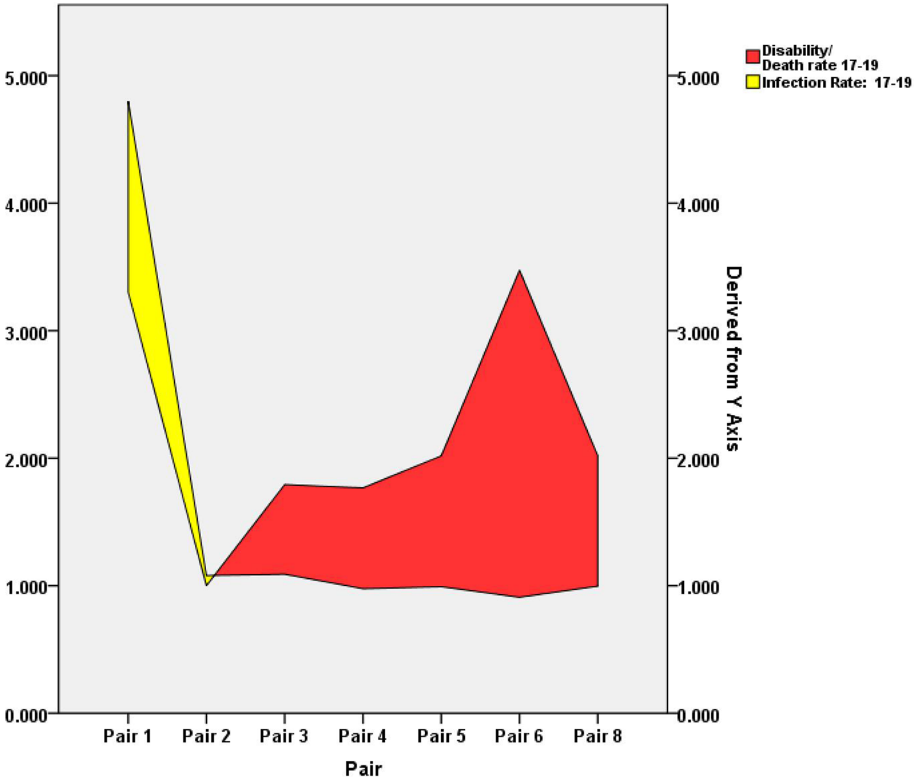

Fig. 4 Paired T test for mosquito-borne diseases infection and disability rate from 2017 to 19

Table 1 Paired T test for mosquito-borne diseases infection rate from 2017 to 2019

Pair	Infection rate from 17 to 19	T value	*P* value	df
Pair 1	Year—Malaria	4.80	0.00140	1
Pair 2	Year—Lymphatic filariasis	1.08	0.00474	1
Pair 3	Year—Dengue	1.09	0.00472	1
Pair 4	Year—Yellow fever (Africa)	0.976	0.00508	1
Pair 5	Year—Zika Virus Infection (Americas)	0.992	0.00502	1
Pair 6	Year—Japanese Encephalitis	0.909	0.00530	1
Pair 8	Year—Chikungunya	0.996	0.00501	1

diseases provided a clear picture of threatened effects in the human population. The prominent results gathered from the analysis have open the door towards the various strategies that can be used to prevent such mosquito-borne diseases. One of the major approaches to accomplish the aforesaid perspectives is targeting the mosquito vector population using different kinds of effective approaches. Hence, here we scrutinized the prominent vector control strategies in terms of their benefits and disadvantages as well

Table 2 Paired T test for disability/death rate of mosquito-borne diseases from 2017 to 2019

Pair	Disability/death rate 2017–2019	T value	*P* value	df
Pair 1	Year—Malaria	3.304	0.0020	1
Pair 2	Year—Lymphatic filariasis	1.000	0.0500	1
Pair 3	Year—Dengue	1.793	0.0032	1
Pair 4	Year—Yellow fever (Africa)	1.767	0.0088	1
Pair 5	Year—Zika Virus Infection (Americas)	2.018	0.0005	1
Pair 6	Year—Japanese Encephalitis	3.473	0.0018	1
Pair 8	Year—Chikungunya	2.018	0.0014	1

as the practical implications. The influence of climate change in mosquito control programme as an important obstacle has also been discussed in this part.

5.1 Chemical methods of vector control

Mosquito control methods have conventionally focussed on killing mosquito populations by using different types of insecticides. The use of chemical insecticides for mosquito control would develop insecticide resistance and generate toxic effects on non-target organisms which might cause damages to the environment (Aneesh & Vijayan, 2010; Puthur et al., 2019, 2021; Strode et al., 2014). Mainly four different kinds of synthetic insecticides (Table 3) such as organochlorines, carbamates, organophosphates, and pyrethroids are used for mosquito control programmes (Rivero et al., 2010).

These chemical insecticides may generate four types of insecticide resistance mechanisms: metabolic resistance, penetration resistance, target site resistance, and behavioural resistance (Hemingway & Ranson, 2000). However, some of the major advantages of chemical methods for vector control are that they are effective within a short period of time and can produce immediate results at a reasonable cost. Therefore, these chemical insecticides are efficiently preferred in emergency situations including disease outbreaks. The World Health Organization in 2006 described a statement encouraging the effective practice of indoor residual spraying (IRS) using dichlorodiphenyltrichloroethane (DDT) for malaria eradication in endemic and epidemic areas (Sadasivaiah et al., 2007).

5.2 Residual spraying, larviciding, and space spraying

Indoor residual spraying (IRS) has been recognized as one of the effective methods of chemical insecticide strategies for malaria control. It involves the controlled and careful spraying of synthetic insecticides on inside walls of a community building or home. World Health Organisation in 2006 recommended that DDT (organochlorine), fenitrothion (organophosphate), malathion (organophosphate), pirimiphosmethyl (organophosphate), propoxur (carbamate), bendiocarb (carbamate), alpha-cypermethrin (pyrethroid), cyfluthrin(pyrethroid), deltamethrin (pyrethroid), etofenprox (pyrethroid), lambda-cyhalothrin (pyrethroid), and bifenthrin (pyrethroid) can be used for indoor residual spraying with limited dose (Pesticides, 2006). But, the agencies for environmental protection have proscribed the use of many synthetic insecticides as they cause serious problems to the

Table 3 Synthetic insecticide and their adverse effects on human population

Chemical group	Chemical names	Adverse health effects
Pyrethroids	Bonthrin, Furethrin, Allethrin, Tetramethrin, Cyclethrin, Cypermethrin, Decamethrin, Alphamethrin, Fenvalerate, Dimethrin, Pyrethrin ,	Sodium channel toxins, neurotoxic hazard. Type I Pyrethroids: Cause reflex hyperexcitability and fine tremor. Type II Pyrethroids: Cause hyperexcitability, salivation, seizures, and choreoathetosis . Sumithrin and permethrin disrupt the endocrine system and influence cellular pathways. Cause headache, facial flushing and swelling, asthmatic breathing, nasal stuffiness, sneezing and convulsions. Sumithrin, fenvalerate, permethrin and d-trans allethrin cause developmental impairment and reproductive dysfunction
Organophosphates	Malathion, Dimefox, Mipafox, Methyl Parathion, Ronnel, enitrothion, Bidrin, Phorate, Fenthion,, Abate, Dichlorovas, Diptrex, caumphos, Phosphomidon, Demetox, Oxydemeton-methyl, Dimethoate, Trichlorofan	Organophosphates cause several health effects such as muscle twitching, vomiting, nausea, blurred vision, headaches, slowed heartbeat, paralysis, respiratory depression, muscular damage and coma
Carbamates	Aminocarb, Bendiocarb, Ethyl-4-bromphenyl-carbamate and ethyl-4-chlorphenyl-carbamate, Carbaryl, Carbendazim, Cartap, carbofuran, Carbofuran, Carbosulfan, Methiocarb, Methomyl, Pirimicarb, Thiodicarb, Carbanolate, Dimetilan,, Dimethan, Aldicarb, Aminocarb. Thiourea, Diallate, Vernolate, Monilate, Cycloate, Trillate, Butylate, Pebulate, Thiram, Ziram Polyran, Amoban, Methan, Naban and Ferban	Toxic effects on lymphoid organs. Degenerative changes on testicular and parenchyma cells. Adverse effects on spermatogenesis.Nephrotoxic effects. Oxidative stress. Liver toxicity. Oxidative damage on kidney and liver. Deleterious effects on cell metabolism
Organochlorines	DDD, DDT, Eldrin, Dicofol,, Dieldrin, Chlorobenziate, BHC, Lindane, Methoxychloro Aldrin, Chlordane, Heptaclor, Endosufan, Chloro propylate, Isobenzan, Isodrin, Toxaphene	Most of organochlorine molecules are neurotoxic and carcinogenic. Organochlorines disrupt endocrine system and generate cardiovascular disorders, Hypertension, and other health related severe problems in human including decrease in birth weight of infants. Increase the risk of gallstone disease
Others	Phenyl Urea, Barban, Carbetamide, Flumeturon, Bromuron, Chlororprofan, Prophan, Fenuron, Monuron, Diuron, Chloroxuron, Neburon, Isopropanil, Nitralin, Trifluralin, Dipropanil, Oryzalin, Isopropanil, Nitralin, Simetryn, Atrazine, Ametryn, Atratone, Simazine, Cynazine, Cyprazine, Propazine, Turbutryn, Metribuzin, Chlorazine, Dichlorobenil, Bromoxynil,, Chloroambin, Neptalan, Dicamba, Tricamba	Affect nucleic acids by barring the activity of RNA polymerase I system. These synthetic pesticides cause endocrine disorders, neurological damage, and have acute and chronic health impacts

environment including human population. In addition to this, some of the synthetic insecticides were directly withdrawn by the manufacturers due to their high cost and norms by the government against them. However, crude kerosene and petroleum oils were also used for killing the mosquito larvae (WHO, 1982). Besides this, mosquito control programmes also recommend space spraying methods to prevent various mosquito-borne diseases.

5.3 Biological and environmental strategies for mosquito control

Vector-borne disease transmission mainly depends on three primary factors such as pathogenicity of the infectious agent, the competence of the vector, and the host organism's susceptibility (Chareonviriyaphap et al., 2013). The transmission is also affected by a diverse number of interconnected environmental factors. Hence, for the successful control of mosquito-borne diseases needs a better understanding of the relation between these three factors and several other environmental and biological factors. This transmission cycle is directly and indirectly driven by a diverse number of inter-related environmental factors (Roberts & Andre, 1994). Environmental methods for the reduction of mosquito breeding sites have been also used along with synthetic insecticides. The notable innovation of the plant-based drug, artemisinin used for malaria treatment and subsequent Nobel Prize award in 2015 explores the significance of screening of plant metabolites against mosquito vectors (Tu, 2011). Recent progress in applied microbiology with special inference on enzymes and aquatic organisms including algae has enabled the development of extensive and inexpensive approaches (Rebello et al., 2018; Rebello et al., 2019; Marten, 1986; Sharrel Rebello, 2019; Rebello et al., 2020a; Anoopkumar et al., 2020c; Puthur et al., 2020). Destruction of mosquito populations can also be achieved by applying biological agents on breeding sites of mosquito larvae.

During the twentieth century, larvivorous fishes were particularly used in peri-urban and urban areas for mosquito control (Gratz & Pal, 1988). But, larviciding did not have a significant role in the complete eradication of *Anopheles gambiae* in Brazil and Egypt. Still, molecules of plant origin ranging from very low concentration to high concentration are often effective against *Aedes*, *Anopheles*, and *Culex* mosquito population as natural ovicides and larvicides. Plant-based natural insecticides might reduce the chance of mosquitocidal nanoformulations. Even a layman can rapidly prepare inexpensive repellents or ovicides with low human toxicity (Anoopkumar et al., 2017a, 2020d; Benelli, 2016; Rebello et al.; Anoopkumar et al., 2021; Rebello et al., 2020b; Vijayan, 2010). It has been found that various natural enemies of mosquito larvae and pupae have a significant role in vector control. The mosquito larvae are preyed upon by various biological control agents such as amphibians, fish, and water bugs.

Currently, vector control programmes based on genetic manipulation to diminish the vectorial capacity of natural mosquito population also received much more attention. Moreover, predatory mosquitoes (toxorhynchites), dragonflies, cyclopoid copepods, nematode worms, fungi, and bacteria have been widely used all over the world to control various mosquito-borne diseases (Rozendaal, 1997). Besides this, zoophylaxis, marsh alteration, and basic sanitary measures have also played a significant role in mosquito vector control as environmental methods (Ault, 1994). There is an extensive eagerness for novel approaches in mosquito control programmes, not only to prevent ZIKAV infections but also to control a wide range of mosquito-borne infectious diseases transmitted by *Aedes aegypti* populations. In 2017, Abad-Franch and his colleagues developed an innovative approach to vector control. This approach uses a potent synthetic analogue (pyriproxyfen) of juvenile hormone from mosquitoes. This material does not develop toxic effects on human population.

5.4 Disease control programme on both international and national level

5.4.1 International level

During 1901–1903 in India, a concept of naturalistic vector control had emerged which was executed in Malaya against *Anopheline* mosquito habitat (Watson, 1921). During the early thirties, pyrethrum extract spray was used as a vector control strategy in South Africa. The notable discovery of the use of DDT as a synthetic insecticide by Paul Muller in 1942 reorganized the field of vector control (Russell, 1963). Based on the history of mosquito control in India, two kinds of eras can be distinguished, viz., pre- and post-DDT era. Several vector control methods have been used prior to 1936. Most of the methods were focussed on the use of oils, paris greens, and larvivorous fishes. The appropriate drainage system may also reduce the mosquito population. During 1944, the DDT was implemented as a residual insecticide for the mosquito control programme in India by antimalarial campaign (White, 1945). During 1950, another synthetic insecticide called hexachlorocyclohexane/benzene hexachloride (HCH/BHC) was introduced for mosquito controlling programmes in Assam, India. However, the continuous transmission of malaria and severe mosquito-borne diseases may lead to the development of the National Malaria Eradication Programme (NMEP) during 1958 in India (Rao, 1958).

The organophosphate insecticide, namely Malathion, was also used to control the population of *Anopheles culicifacies* in 1969 (Rajagopal, 1977). The continuous practice of synthetic insecticides to eliminate malaria using different experiments and methods was not absolutely successful (Sharma, 1984). Excessive and prophylactic use of such synthetic insecticides may lead to management failure by heritable resistance, and this may augment the chance of preventing the successful eradication of malaria (Chandler et al., 2011). Hence, during the 1980s, the insecticides from pyrethroid group were implemented in the public health programme to avoid the rapid spread of mosquito-borne diseases (Singh et al., 1989). At the end of the twentieth-century deltemethrin, lambda cyhalothrin, and cyfluthrin were used as insecticides for public health programme. Various other methods have also been used for the same purpose over India. Advances in computer hardware have strongly reinforced the software development for vector distribution mapping by means of remote sensing (RS), global positioning systems, and digital databases.

Prevention of vector-borne diseases has been intensely influenced by Ross-Macdonald model theory, which emphasizes that the potential for the transmission of the mosquito-borne pathogen principally depends on the abundance of adult vector mosquitoes and human biting rate. For sustained mosquito-borne transmission mitigation, indoor spraying was preferred to residual insecticides (Achee et al., 2015). Nowadays, promising alternative genetic control approaches have been developed for vector control. The genetic approaches for vector control include the implementation of disease-refractory mosquitoes against the vector population. Another genetic approach for mosquito control comprises the discharge of mosquitoes carrying a lethal gene that is responsible for suppressing the target population (Wilke & Marrelli, 2015). Several important problems have been faced before the implementation of these aforesaid techniques for mosquito control. Issues related to transposon stability, drive mechanisms, and sibling species complexes are still recognized as a serious problem while using these genetic techniques. The aforesaid factors need to be considered before the implementation of mosquitoes carrying the lethal gene into the wild population (Riehle et al., 2007). Paratransgenesis is considered as a strategy to prevent mosquito proliferation by using symbiotic bacteria. This approach uses the genetically modified symbiotic bacteria which expressing effector molecules were reintroduced into the mosquito population where they generate desire effect (Coutinho-Abreu et al., 2010). The preferable effective approaches for mosquito control include chemical, biological, and environmental methods (Fig. 5).

5.4.2 National level

In 1947, approximately 22% population of India was estimated to suffer from marking with 0.8 million deaths and 75 million cases of infection due to malaria. In order to fight against the threats from malaria, National Malaria Control Programme (NMCP) was initiated in 1953. Mainly three strategies have been followed for the success of the programme and are: i) insecticidal residual spray (IRS) using DDT, ii) monitoring and surveillance of infections, and iii) treatment of patients. After the success of the programmes, in 1958, the NMCP was then converted to the National Malaria Eradication Programme (NMEP). However, insecticide resistance, the suboptimal monitoring, and logistics together with poor health infrastructure in many parts of the country have instigated the resurgence of malaria (6.46 million cases) in 1976. This has forced the national agencies to launch a modified plan of operations (MPO) in the next year (1977) with three strategies, viz., early diagnosis and prompt treatment, IEC/BCC with public involvement, and mosquito control. In 1997, 2002, and 2005, Enhanced Malaria Control Project (EMCP), National Vector Borne Disease Control Programme (NVBDCP), The Global Fund to fight AIDS, Tuberculosis and Malaria (GFATM), respectively, have been launched to prevent various vector-borne diseases with special emphasis on malaria.

The National Vector Borne Disease Control Programme (NVBDCP) launched in 2002 has also provided importance to prevent other diseases such as dengue, chikungunya, lymphatic filariasis, Kala-azar, and Japanese Encephalitis (Malaria & Ums, 2011; NHM, 2019). In 1955, the National Filaria Control Programme (NFCP) was initiated in India to

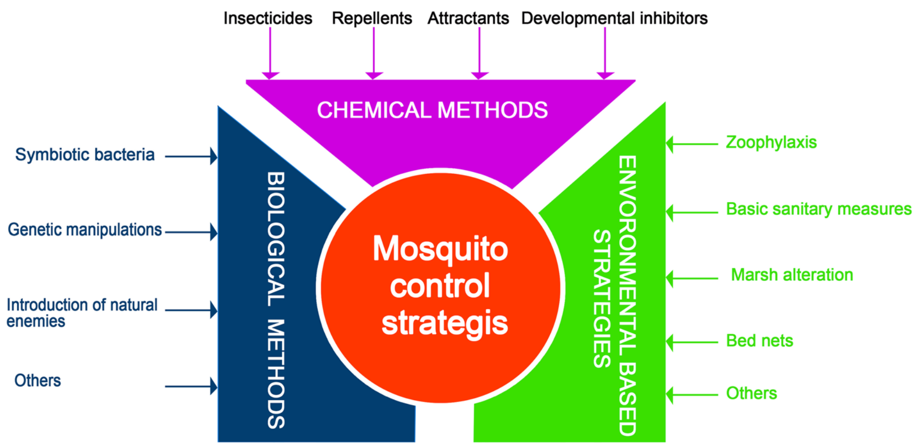

Fig. 5 Various prominent strategies to combat the mosquito-borne diseases

delimit the threats instigated by lymphatic filariasis in India. The control measures were mainly focussed on mass drug administration (MDA) antilarval measures, indoor residual spraying, and annual single-dose co-administration. The dengue fever infection is endemic in most of all the states in India. This indicates that it had a wide distribution in both peri-urban and rural areas. The National Vector Borne Disease Control Programme (NVBDCP) has significantly contributed by combating against the threats of dengue fever. In addition to this, Integrated Disease Surveillance Programme (IDSP), Department of Health Research Associated Research and Programmes (Diagnostic Laboratories (VRDL) and 52 Virus Research Laboratories) have also been involved in the dengue surveillance initiatives (Ganeshkumar et al., 2018). To prevent the rapid spread of Zika infection in India, a well-established Monitoring Group of Technical Experts and a control room were launched at National Centre for Disease Control (NCDC). In 2016, India has launched a vaccination programme against Japanese Encephalitis, which turned into National Immunization Programme in 2014 (Narain et al., 2017). Till now, the afore-mentioned programme has provided vaccines for 179 districts across India. However, the threatening effects of such mosquito-borne diseases have continued in recent years. As depicted in Fig. 4, the paired T test conducted in this investigation has provided a clear illustration of the various mosquito-borne diseases and their drastic effects on human health with strong support of statistical analysis (Tables 1 and 2).

5.5 Climate change and vector control

The various aspects of global change include climate variability, climate change, water storage, land use, urbanization, chemical pollution, travel, trade, and irrigation. The process of climate change exhibits unknown risks in the future to ecosystems including the human population. IPCC (The Inter-Governmental Panel on Climate Change) in 1966 stated that "the scientific studies on climate change suggest that the various activities by human population throughout the last century have led to a discernible consequence on world's climate" (Houghton, 1996). Pathogens carried by vector mosquitoes are principally sensitive to climatic conditions. The relationship between vectors and climatic conditions has been described and quantified during the 1920s and 1950s, respectively. The extreme temperature kills vector mosquitoes. However, the warmer temperature within survival range has been increasing their biting and reproductive activity (Epstein, 2001).

There have been a number of reviews covering various aspects of global change, human health, and infectious diseases that were published in the scientific community (Aneesh EM et al., 2021). Several scientific reviews have been strongly targeted on mosquito-borne infectious diseases. Svante Arrhenius, a Swedish Chemist, predicted that global warming is a slow process that might generate severe consequences on time together with elevated sea levels, fluctuations in global rainfall patterns, modifications to plant and animal inhabitants, and serious harmful health impacts. The global average temperature (1906–2005) has increased by 0.74 °C (Parry et al., 2007). Based on the data from "Global Climate Report—August 2020" the average temperature was reported to 0.94 °C (NOAA, 2020). Based on the aforementioned concepts, without any doubt, we can say that climate change may directly influence the risk of emerging vector-borne diseases all over the world.

According to Uriel Kitron (Professor of Epidemiology at the University of Illinois in Urbana-Champaign), global warming has a significant impact on the transmission of various mosquito-borne diseases, particularly malaria and dengue. The authors also studied the various aspects of global warming as a serious threat in the spread of various vector-borne infectious diseases including dengue and malaria (Suk, 2016). The increased rainfall and the process of global warming may significantly contribute to the distribution and abundance of mosquito vectors. Current studies confirmed that inter-decadal and inter-annual climate variability might have a strong impact on the epidemiology of mosquito-borne diseases. The development, ecology, behaviour and survival of vectors, and the transmission cycle might directly be influenced by several climatic factors such as temperature, humidity, rainfall, and wind too. These factors may play an important role in the transmission rate of pathogens (Fig. 6). Temperature is considered as the major parameter that influences the rate of multiplication in the vector (Reisen et al., 2006).

The insects have various developmental mechanisms that are achieved through evolutionary times to cope with thermal stress. Synthesis of heat-shock proteins, adjusting behavioural activity together with thermoregulation is considered as the afore-mentioned mechanisms to maintain cellular integrity, thereby optimizing their fitness, survival, and adaptations, though their activity and fitness become impaired beyond the critical minimum and maximum temperature range. In addition to this, certain other factors such as the age of the insect, its physical state, and type of species may also influence the afore-mentioned condition. When they overcome such situations, the adaptations would allow them to colonize various habitats, thereby transmitting many infectious diseases to humans and other organisms. As illustrated in Fig. 7, from an environmental perspective of global warming and climate change, the host-seeking behaviour, ecology, population dynamics, spatial distribution, and vector relevance have played a prominent role in the rapid proliferation of *Aedes aegypti* and *Aedes albopictus* mosquitoes.

Aedes aegypti mosquitoes are unable to fly at extreme low temperature (10 °C). However, they were able to fly between 15 °C and 32 °C. A study by (Rowley & Graham, 1968) argues that lower temperature allows them to be active at the early morning and late

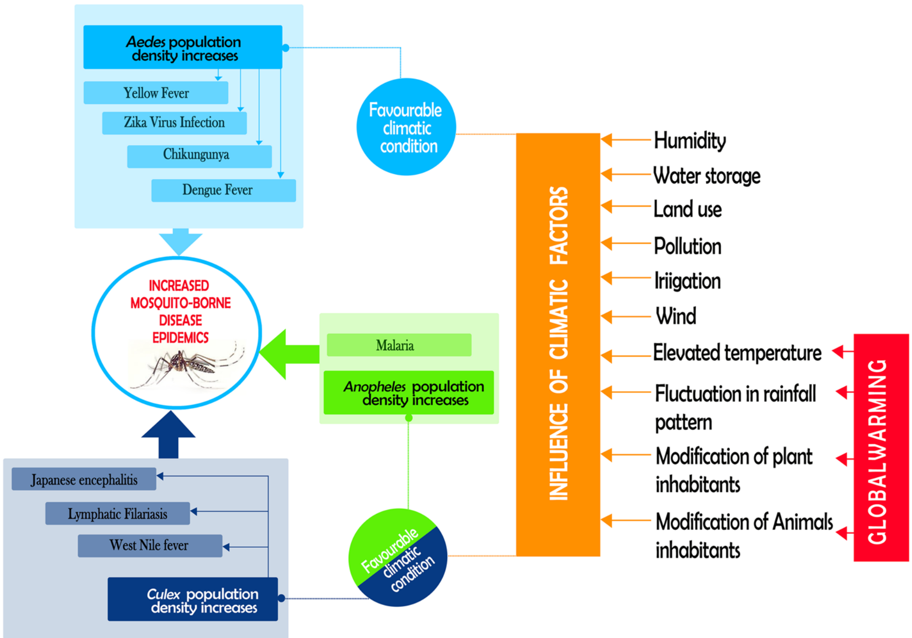

Fig. 6 Influence of climate change on mosquito-borne disease epidemics

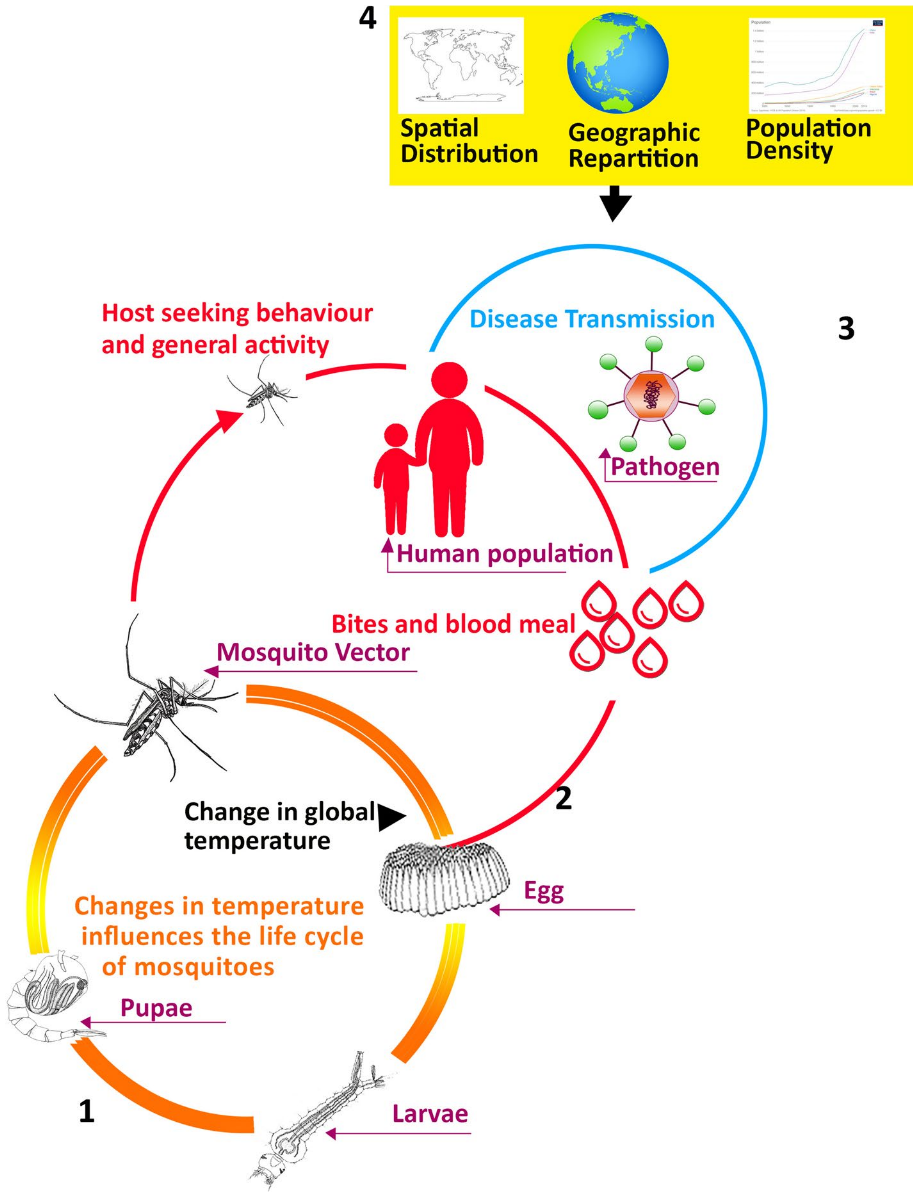

Fig. 7 Prominent role of environmental factors including climate change in mosquito-borne disease transmission: **(1)** the changes in environmental and ecological factors including temperature influences support the development of mosquito vector life cycle. **(2)** The host-seeking behaviour and general activity of the mosquito vector are also influenced by temperature changes. **(3)** The rainfall pattern and other environmental factors augment the disease transmission risk. **(4)** The global temperature change is shown to reveal a prominent role in spatial distribution, geographic repartition, and population density, thereby increasing the chance of spreading mosquito-borne diseases rapidly

afternoon. Mosquito vectors also use several different cues such as chemical, visual, and thermal information to seek and locate the host. Samuel Rickard Christophers, 1960b have verified the link between environmental temperature and wingbeat frequency (367 beat/s at 18 °C vs). In addition to this, Scott et al., 1993 reported that the blood intake in *Aedes aegypti* was positively correlated with the environmental temperature. The environmental temperature has also altered the population dynamics by directly affecting the developmental stages such as eggs, larvae, and pupae as well as general activity and reproduction (Couret & Benedict, 2014). *Aedes* strains from the USA south part had a worse capability to overwinter than those from the northern region indicating the strong ability of *Aedes* mosquitoes to rapidly adapt to a new habitat or thermal conditions, thereby rapidly proliferating their population. The warmer temperature is linked with the pathogen transmission and overwintering strategies by altering both mosquito distribution and biting activity as well as pathogen transmission and development. Beyond the afore-mentioned factors, short days inducing diapause and day length have affected the egg hatching and population dynamics. Based on the above-mentioned facts, it has been clearly evident that climate change can be recognized as an important factor that promotes the quickly increased abundance of mosquito vectors. The yearly pattern of mosquito distribution has been indeed prominently affected in the tropics and subtropics regions all over the world.

The growth rate of vector mosquitoes rapidly upsurges when the temperature rises. It also increases the virus evolution rate too. Previous studies based on the effects of rainfall and temperature on *Aedes albopictus* reported that the populations of warmer regions are likely to produce a large number of adult mosquitoes (Brower, 2001). Besides this, climate change can make alterations in the seasonal transmission and geographic ranges of mosquito-borne infectious diseases such as Yellow fever, dengue fever, and other

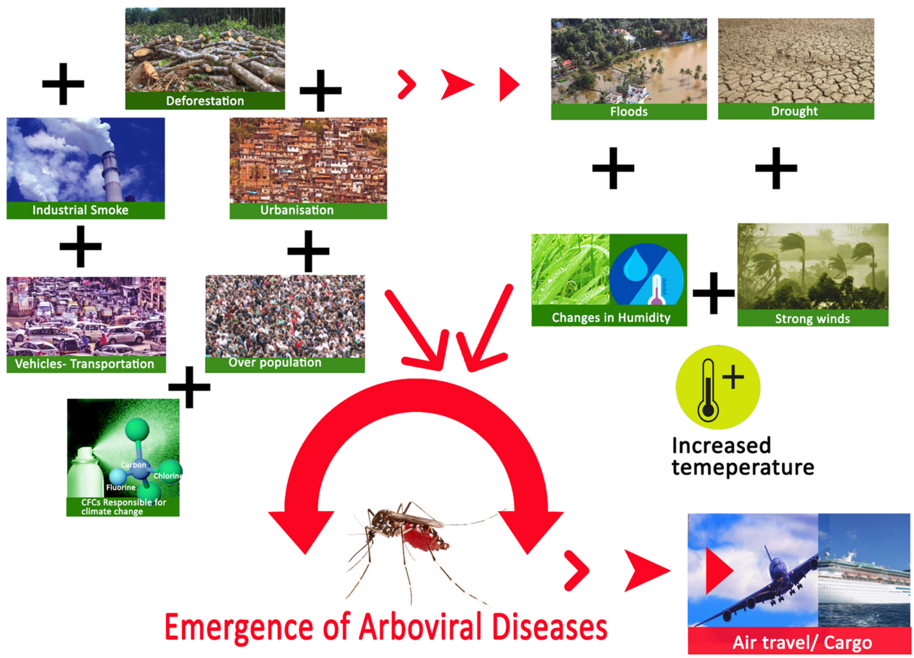

Fig. 8 Climate change and vector-borne diseases

vector-borne diseases too (Fig. 8). Previous studies have reported the impact of climate change on species diversity, distribution, and abundance of *Aedes aegypti* population in Australian regions (Kearney et al., 2009). The link between the life cycle of *Culex* mosquitoes and weather parameters in Northern Italy and Egypt was verified by (Abouzied, 2017). With the help of evolutionary theory and biophysical models in climate change context, (Kearney et al., 2009) found that egg desiccation, water availability, tolerance to colder environmental temperature are prominent factors that drive the establishment of mosquito vector species to new regions of Australia. Kobayashi et al., (2002) reported a significant correlation between the population density of *Aedes* mosquitoes with annual mean temperature in Japan with the help of geographical information system (GIS). They also mentioned that the environmental temperature during their study and global warming allows the *Aedes* mosquito species to expand them to the northern region of Japan. The ability of them to transmit the pathogen to the newer regions primarily depended on two significant factors: (1) whether the infectious agent can disseminate and (2) whether the infectious agent can infect the midgut cells. The major fact is that the changes in global temperature or environmental temperature can affect both the afore-mentioned factors. Global climate change allows the mosquito species to develop and transmit infectious agents and diseases to humans and other organisms more quickly. Previous studies have reported that relatively higher temperatures influence the amplification of West Nile Virus in the mosquito vector, permitting increased transmission rates in warmer regions.

West Nile Fever (WNF) transmissions have increased in Israel during the hot summer (2000 and 2010). This justifies the relationship between climate change and vector control. Climate change would also contribute to an increase in the dengue transmission rate since the rapid increase in global temperature would allow for wide distribution of *Aedes* mosquitoes and increased virus transmission (WHO, 2014). A study by (Thu et al., 1998) with special emphasis on climate change has indicated that the propagation of *Aedes aegypti* and amplification of the virus have increased in warmer environmental conditions. Similarly, the chikungunya transmission by *Aedes albopictus* is strongly influenced by favourable climatic conditions, especially in northwestern Mediterranean. During the 1960s, the local transmission

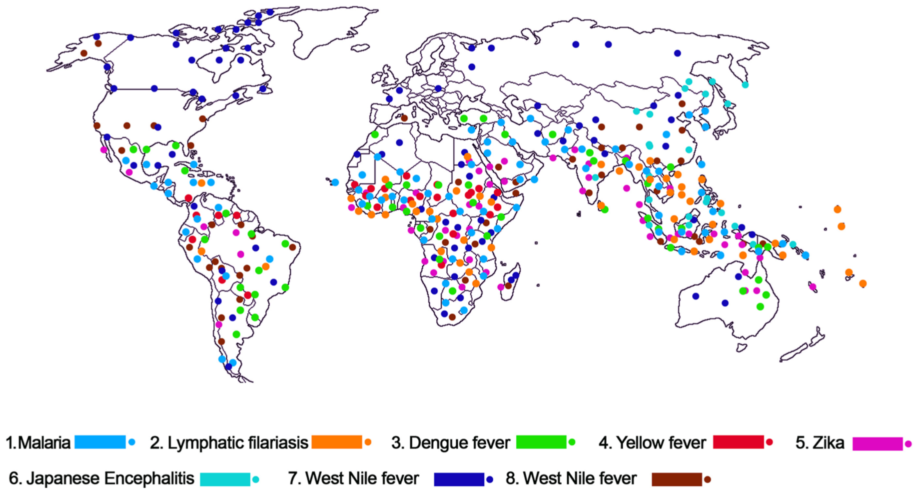

Fig. 9 Distribution of mosquito-borne diseases over the globe

of chikungunya virus was notably reduced due to the lack of reproducing *Aedes aegypti* and *Aedes albopictus* populations in Canada. The limiting factor responsible for the reduced number of *Aedes aegypti* and *Aedes albopictus* population in Canada was the cooler Canadian climate during 1960s (S Christophers, 1960a). But, as a result of climate change, the *Aedes* mosquito population has become established in the Canadian region (Capinha et al., 2014) (Fig. 9). The life cycle of vector population and the reproduction rate of pathogens inside the vectors were directly influenced by the climatic factors. Simultaneously, the temperature rise might boost the transmission risk of infectious diseases through increased vector population. The long-term alterations in the seasons may also affect mosquito vectors and host animals. The population dynamics and distribution of malaria are predominantly directed by abiotic factors than the biotic elements (Southwood, 1977). In addition to this, the rainfall also plays a significant role in the epidemiology of malaria. It offers the aquatic medium for the larval and pupae stages of the mosquito life cycle. The rainfall proves advantageous to mosquito breeding by means of increasing relative humidity.

5.6 Policy and managerial implications

As mentioned in the earlier sections, everyone is at risk because of mosquito-borne diseases to a varying degree depending on the environmental sanitation, rainfall, and temperature (WHO, 2019a). The WHO and PAHO during the twenty-first century have developed frameworks and strategies focussing on current mosquito control. The various perspectives that arisen from this investigation based on the literature survey had illustrated that the following strategies can be implemented to combat mosquito-borne disease. Community participation, advocacy, and social communication have played a prominent role in the vector management programme. Since the vector control strategies vary in effectiveness and coverage, the national and international agencies have advised the travellers to use general protective measures including the use of repellents against mosquitoes. While vaccines are not available for the diseases such as West Nile Encephalitis, Zika, chikungunya, dengue, and filariasis, the CDC recommends the consumers to use the repellent products registered under Environmental Protection Agency (EPA) (CDC, 2020a). CDC also recommends certain general protective measures like: 1) avoid outbreaks, 2) bed nets, 3) insecticides and spatial repellents (DEET, Picaridin, PMD or Oil of lemon eucalyptus (OLE), 2-undecanone, and IR3535), and 4) wear appropriate clothing. Environmental management methods are recognized as the most effective approach in diminishing the number of mosquito breeding sites, thereby effectively preventing the spread of mosquito-borne diseases (CDC, 2019). The reduction of the larval source through "clean-up" campaigns in public spaces, around the house and schools, has also been formed as a significant strategy in vector control approaches. All aspects of integrated vector management as discussed above necessitate well transparent communication. Collaboration with other countries to share the available tools, strategies, and supporting research including larvicides and GIS will provide additional support for effective vector control in practical aspects. In addition to this, the individuals should have trust in national vaccination programmes and should accept both the benefits and risks from it. It is essential to have support from ministries, public health professionals, collaborating institutions, and healthcare professionals collaborating on resource allocation and developing plans to manage the disease outbreaks and seasonal illnesses.

6 Conclusion

While considering the current endemic nature of mosquito-borne infectious diseases all over the world, this investigation evaluates the mosquito-borne diseases, the various strategies for vector control, and the influence of climatic factors governing vector-borne disease transmission. The three important mosquito genera responsible for the transmission of vector-borne diseases to human population include *Aedes*, *Culex*, and *Anopheles*. The increased geographic distribution of mosquito vectors induces the emergence of pathogens and diseases in new regions. Now, the mosquito-borne diseases made epidemics that interrupt health security and cause socioeconomic impacts all over the globe. The various vector control strategies include chemical, biological, and environmental methods. Interestingly, nowadays, micro-organisms including symbiotic bacteria (paratransgenesis) have been used in vector control programmes. For effective vector control, the influence of climatic factors on vector-borne diseases should be studied since the mosquito vectors are also sensitive to the alterations in the climatic condition and the existing vector control approaches are inadequate to combat with the adverse effects of global warming.

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Declarations

Conflict of interest The authors declare that they have no conflict of interest. A.N. Anoopkumar and Embalil Mathachan Aneesh declare that they have no conflict of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

References

Abad-Franch, F., Zamora-Perea, E., Luz, S. L. (2017). Mosquito-disseminated insecticide for citywide vector control and its potential to block arbovirus epidemics: Entomological observations and modeling results from Amazonian Brazil. *PLoS medicine*, 14(1), e1002213.

Abouzied, E. M. (2017). Life table analysis of Culex pipiens under simulated weather conditions in Egypt. *Journal of the American Mosquito Control Association, 33*(1), 16–24.

Achee, N. L., Gould, F., Perkins, T. A., Reiner Jr, R. C., Morrison, A. C., Ritchie, S. A., et al. (2015). A critical assessment of vector control for dengue prevention. *PLoS neglected tropical diseases*, 9(5), e0003655.

Amicizia, D., Zangrillo, F., Lai, P. L., Iovine, M., Panatto, D. (2018). Overview of Japanese encephalitis disease and its prevention. Focus on IC51 vaccine (IXIARO®). *Journal of preventive medicine and hygiene*, 59(1), E99.

Aneesh, E. M., Anoopkumar, A. N., Siva Prasad, M. S., & Rebello, S. (2021). A phylogenomic and evolutionary perspectives of COVID-19. *Journal of Communicable Diseases, 53*(1), 1–8.

Aneesh, E., Vijayan, V. (2010). Laboratory selection of carbofuran tolerant line of Culex quinquefasciatus Say, the filarial vector at Mysore.

Anoopkumar, A., Aneesh, E. M. (2021). Environmental epidemiology and neurological manifestations of dengue serotypes with special inference on molecular trends, virus detection, and pathogenicity. *Environment, Development and Sustainability*, p.1–23.

Anoopkumar, A., Aneesh, E. M., & Sudhikumar, A. V. (2020a). Exploring the mode of action of isolated bioactive compounds by induced reactive oxygen species generation in Aedes aegypti: a microbes based double-edged weapon to fight against Arboviral diseases. *International Journal of Tropical Insect Science, 40*(3), 573–585.

Anoopkumar, A., Aneesh, E. M., & Sudhikumar, A. V. (2020b). Exploring the mode of action of isolated bioactive compounds by induced reactive oxygen species generation in Aedes aegypti: a microbes based double-edged weapon to fight against Arboviral diseases. *International Journal of Tropical Insect Science, 40*(3), 1–13.

Anoopkumar, A., Puthur, S., Rebello, S., & Aneesh, E. M. (2017a). Screening of a Few traditionally used Medicinal Plants for their Larvicidal Efficacy against Aedes aegypti Linn (Diptera: Culicidae), a Dengue Fever Vector.

Anoopkumar, A., Puthur, S., Varghese, P., Rebello, S., Aneesh, E. M. (2017b). Life cycle, bio-ecology and DNA barcoding of mosquitoes Aedes aegypti (Linnaeus) and Aedes albopictus (Skuse). *The Journal of Communicable Diseases*, 49(3): 32-41.

Anoopkumar, A., Rebello, S., Aneesh, E. M., Sindhu, R., Binod, P., Pandey, A., et al. (2020c). Use of Different Enzymes in Biorefinery Systems. *Biorefinery Production Technologies for Chemicals and Energy*, p. 357–368.

Anoopkumar, A., Rebello, S., Devassy, E., Raj, K. K., Puthur, S., Aneesh, E. M., et al. (2020d). Phytoextraction of Heavy Metals. *Methods for Bioremediation of Water and Wastewater Pollution* (pp. 267–276). Cham: Springer.

Anoopkumar, A., Rebello, S., Sudhikumar, A. V., Puthur, S., Aneesh, E. M. (2020e). A novel intervention on the inhibiting effects of Catunaregam spinosa induced free radical formation and DNA damage in Aedes aegypti (Diptera: Culicidae): a verdict for new perspectives on microorganism targeted vector control approach. *International Journal of Tropical Insect Science*, 40(4), 989-1002.

Anoopkumar, A., Siva Prasad, M., Rebello, S., Sini Francis, C., Aneesh, E. M. (2021). An Assessment of ITS rDNA PCR-based molecular identification, and characterization of fungal endophytes isolated from Hypericum japonicum. *Plant Biosystems-An International Journal Dealing with all Aspects of Plant Biology*, https://doi.org/10.1080/11263504.2021.1887958.

Ault, S. K. (1994). Environmental management: a re-emerging vector control strategy. *The American journal of tropical medicine and hygiene*, 50(6_Suppl), 35–49.

Benelli, G. (2016). Plant-mediated biosynthesis of nanoparticles as an emerging tool against mosquitoes of medical and veterinary importance: a review. *Parasitology Research, 115*(1), 23–34.

Brower, V. (2001). Vector-borne diseases and global warming: are both on an upward swing?: Scientists are still debating whether global warming will lead to a further spread of mosquitoes and the diseases they transmit. *EMBO Reports, 2*(9), 755–757.

Caminade, C., Medlock, J. M., Ducheyne, E., McIntyre, K. M., Leach, S., Baylis, M., et al. (2012). Suitability of European climate for the Asian tiger mosquito Aedes albopictus: recent trends and future scenarios. *Journal of the Royal Society Interface*, rsif20120138.

Capinha, C., Rocha, J., & Sousa, C. A. (2014). Macroclimate determines the global range limit of Aedes aegypti. *EcoHealth, 11*(3), 420–428.

CDC (2019). CHAPTER 4 Travel-Related Infectious Diseases. https://wwwnc.cdc.gov/travel/yellowbook/2020/travel-related-infectious-diseases/dengue. Last accessed on 25–10–2020.

CDC (2020a). Environmental Hazards & Other Noninfectious Health Risks. *center for disease control and prevention*, chapter 3. https://wwwnc.cdc.gov/travel/yellowbook/2020/noninfectious-health-risks/mosquitoes-ticks-and-other-arthropods. Last Accessed on 25–10–2020.

CDC (2020b). Malaria's Impact Worldwide. *Global Health, Division of Parasitic Diseases and Malaria*. https://www.cdc.gov/malaria/malaria_worldwide/impact.html#:~:text=Africa%20is%20the%20most%20affected,cause%20severe%20malaria%20and%20death. Last accessed on 23–10–2020.

Chandler, D., Bailey, A. S., Tatchell, G. M., Davidson, G., Greaves, J., & Grant, W. P. (2011). The development, regulation and use of biopesticides for integrated pest management. *Philosophical Transactions of the Royal Society b: Biological Sciences, 366*(1573), 1987–1998.

Chareonviriyaphap, T., Bangs, M. J., Suwonkerd, W., Kongmee, M., Corbel, V., & Ngoen-Klan, R. (2013). Review of insecticide resistance and behavioral avoidance of vectors of human diseases in Thailand. *Parasites & Vectors, 6*(1), 280.

Chen, L. H., & Wilson, M. E. (2020). Yellow fever control: Current epidemiology and vaccination strategies. *Tropical Diseases, Travel Medicine and Vaccines, 6*(1), 1–10.

Chianese, A., Stelitano, D., Astorri, R., Serretiello, E., Della Rocca, M. T., Melardo, C., et al. (2019). West Nile virus: an overview of current information. *Translational Medicine Reports*, 3(1).

Christophers, S. (1960a). Aedes aegypti (L.) the yellow fever mosquito: its life history, bionomics and structure. *Aëdes aegypti (L.) the Yellow Fever Mosquito: its Life History, Bionomics and Structure.*

Christophers, S. R. (1960b). Aedes aegypti: the yellow fever mosquito. CUP Archive.
Couret, J., & Benedict, M. Q. (2014). A meta-analysis of the factors influencing development rate variation in Aedes aegypti (Diptera: Culicidae). *BMC Ecology, 14*(1), 3.
Coutinho-Abreu, I. V., Zhu, K. Y., & Ramalho-Ortigao, M. (2010). Transgenesis and paratransgenesis to control insect-borne diseases: Current status and future challenges. *Parasitology International, 59*(1), 1–8.
Cox, F. E. (2010). History of the discovery of the malaria parasites and their vectors. *Parasites & Vectors, 3*(1), 5.
de Azevedo Marques, E. T., Dhalia, R., & Maciel Filho, R. (2019) 'Dna vaccine against virus of yellow fever'. Google Patents.
de Freitas, C. S., Higa, L. M., Sacramento, C. Q., Ferreira, A. C., Reis, P. A., Delvecchio, R., et al. (2019). Yellow fever virus is susceptible to sofosbuvir both in vitro and in vivo. *PLoS neglected tropical diseases*, 13(1), e0007072.
De Silva, P. M., & Marshall, J. M. (2012). Factors contributing to urban malaria transmission in sub-Saharan Africa: a systematic review. *Journal of tropical medicine*, 2012(1), 10.
Dénes, A., Ibrahim, M. A., Oluoch, L., Tekeli, M., & Tekeli, T. (2019). Impact of weather seasonality and sexual transmission on the spread of Zika fever. *Scientific Reports, 9*(1), 1–10.
Epstein, P. R. (2001). Climate change and emerging infectious diseases. *Microbes and Infection, 3*(9), 747–754.
Fang, Y., & Zhang, Y. (2019). Lessons from lymphatic filariasis elimination and the challenges of post-elimination surveillance in China. *Infectious Diseases of Poverty, 8*(1), 66.
Fischer, D., Thomas, S. M., Suk, J. E., Sudre, B., Hess, A., Tjaden, N. B., et al. (2013). Climate change effects on Chikungunya transmission in Europe: Geospatial analysis of vector's climatic suitability and virus' temperature requirements. *International Journal of Health Geographics, 12*(1), 51.
Foy, B. D., Kobylinski, K. C., Foy, J. L. C., Blitvich, B. J., da Rosa, A. T., Haddow, A. D., et al. (2011). Probable non–vector-borne transmission of Zika virus, Colorado, USA. *Emerging Infectious Diseases, 17*(5), 880.
Ganesan, V. K., Duan, B., & Reid, S. P. (2017). Chikungunya virus: Pathophysiology, mechanism, and modeling. *Viruses, 9*(12), 368.
Ganeshkumar, P., Murhekar, M. V., Poornima, V., Saravanakumar, V., Sukumaran, K., Anandaselvasankar, A., et al. (2018). Dengue infection in India: A systematic review and meta-analysis. *PLoS neglected tropical diseases*, 12(7), e0006618.
Gratz, N., Pal, R. (1988). Malaria vector control: larviciding. *Malaria: Principles and practices of malariology*, p. 1213–1226.
Guarner, J., Shieh, W.-J., Hunter, S., Paddock, C. D., Morken, T., Campbell, G. L., et al. (2004). Clinicopathologic study and laboratory diagnosis of 23 cases with West Nile virus encephalomyelitis. *Human Pathology, 35*(8), 983–990.
Hasan, S., Saeed, S., Panigrahi, R., & Choudhary, P. (2019). Zika virus: a global public health menace: a comprehensive update. *Journal of International Society of Preventive & Community Dentistry, 9*(4), 316.
Hemingway, J., & Ranson, H. (2000). Insecticide resistance in insect vectors of human disease. *Annual Review of Entomology, 45*(1), 371–391.
Houghton, J. T. (1996). *Climate change 1995: The science of climate change: Contribution of working group I to the second assessment report of the Intergovernmental Panel on Climate Change*. Cambridge University Press.
Katz, T. M., Miller, J. H., & Hebert, A. A. (2008). Insect repellents: historical perspectives and new developments. *Journal of the American Academy of Dermatology, 58*(5), 865–871.
Kearney, M., Porter, W. P., Williams, C., Ritchie, S., & Hoffmann, A. A. (2009). Integrating biophysical models and evolutionary theory to predict climatic impacts on species' ranges: the dengue mosquito Aedes aegypti in Australia. *Functional Ecology, 23*(3), 528–538.
Kobayashi, M., Nihei, N., & Kurihara, T. (2002). Analysis of northern distribution of Aedes albopictus (Diptera: Culicidae) in Japan by geographical information system. *Journal of Medical Entomology, 39*(1), 4–11.
Kumar, A., Valecha, N., Jain, T., Dash, A. P. (2007). Burden of malaria in India: retrospective and prospective view. *The American journal of tropical medicine and hygiene*, 77(6_Suppl), p. 69–78.
Laumann, V. (2010). Environmental strategies to replace DDT and control malaria. PAN Germany.
Lowe, R., Ryan, S. J., Mahon, R., Van Meerbeeck, C. J., Trotman, A. R., Boodram, L.-L. G., et al. (2020). Building resilience to mosquito-borne diseases in the Caribbean. *Plos Biology*, 18(11), e3000791.
Malaria, U., & Ums, S. N. (2011) 'National Vector Borne Disease Control Programme'. Control.

Marten, G. (1986). Mosquito control by plankton tnanagetnent: The potential of indigestible green algae. *Journal of Tropical Medicine and Hygiene, 89*, 213–222.

Mores, C. N., Christofferson, R. C., Davidson, S. A. (2014). The role of the mosquito in a dengue human infection model. *The Journal of infectious diseases*, 209(suppl_2), S71-S78.

Musso, D., Roche, C., Robin, E., Nhan, T., Teissier, A., & Cao-Lormeau, V.-M. (2015). Potential sexual transmission of Zika virus. *Emerging Infectious Diseases, 21*(2), 359.

Narain, J. P., Dhariwal, A., & MacIntyre, C. R. (2017). Acute encephalitis in India: An unfolding tragedy. *The Indian Journal of Medical Research, 145*(5), 584.

Nguyen, C., Gray, M., Burton, T. A., Foy, S. L., Foster, J. R., Gendernalik, A. L., et al. (2019). Evaluation of a novel West Nile virus transmission control strategy that targets Culex tarsalis with endectocide-containing blood meals. *PLoS neglected tropical diseases*, 13(3), e0007210.

NHM (2019). Disease Control

NOAA (2020). Global Climate Report - May 2020. *National Centers for Environmental Information*. https://www.ncdc.noaa.gov/sotc/global/202005. Last accessed on October 25, 2020.

Oehler, E., Fournier, E., Leparc-Goffart, I., Larre, P., Cubizolle, S., Sookhareea, C., et al. (2015). Increase in cases of Guillain-Barré syndrome during a Chikungunya outbreak, French Polynesia, 2014 to 2015. *Eurosurveillance, 20*(48), 30079.

Ottesen, E., Duke, B., Karam, M., & Behbehani, K. (1997). Strategies and tools for the control/elimination of lymphatic filariasis. *Bulletin of the World Health Organization, 75*(6), 491.

Parry, M., Canziani, O., Palutikof, J., van der Linden, P. J., Hanson, C. E. (2007). Climate change 2007: impacts, adaptation and vulnerability. Cambridge University Press Cambridge.

Pascual, M., & Bouma, M. J. (2009). Do rising temperatures matter? *Ecology, 90*(4), 906–912.

Pearson, E. F., & Miles, W. (1980). Disinfection of mail in the United States. *Bulletin of the History of Medicine, 54*(1), 111.

Pesticides, W. (2006). *their Application for the Control of Vectors and Pests of Public Health Importance*. WHO.

Puthur, S., Anoopkumar, A., Rebello, S., Aneesh, E. M. (2018). Hypericum japonicum: a Double-Headed Sword to Combat Vector Control and Cancer. *Applied biochemistry and biotechnology*, 186(1), 1–11.

Puthur, S., Anoopkumar, A., Rebello, S., & Aneesh, E. M. (2019). Synergistic control of storage pest rice weevil using Hypericum japonicum and deltamethrin combinations: a key to combat pesticide resistance. *Environmental Sustainability, 2*(4), 411–417.

Puthur, S., Anoopkumar, A., Rebello, S., Aneesh, E. M., Sindhu, R., Binod, P., et al. (2021). Toxic Effects of Pesticides on Avifauna Inhabiting Wetlands. *Sustainable Agriculture Reviews 47* (pp. 335–349). Cham: Springer.

Puthur, S., Raj, K. K., Anoopkumar, A., Rebello, S., Aneesh, E. M. (2020). Acorus calamus mediated green synthesis of ZnONPs: A novel nano antioxidant to future perspective. *Advanced Powder Technology*. 31(12), 4679-4682.

Rajagopal, R. (1977). Malathion resistance in Anopheles culicifacies in Gujarat. *Indian Journal of Medical Research, 66*(1), 27–28.

Ramzy, R. M., Goldman, A. S., & Kamal, H. A. (2005). Defining the cost of the Egyptian lymphatic filariasis elimination programme. *Filaria Journal, 4*(1), 7.

Rao, B. (1958). The national malaria control programme in India and the possibilities of eradication of malaria in India and the tropics. *Bull Nat Soc Mal Mosq Dis, 6*, 5–6.

Rebello, S., Anoopkumar, A., Aneesh, E. M., Sindhu, R., Binod, P., & Pandey, A. (2020a). Sustainability and life cycle assessments of lignocellulosic and algal pretreatments. *Bioresource Technology*, 301, 122678.

Rebello, S., Anoopkumar, A., Puthur, S., Sindhu, R., Binod, P., Pandey, A., et al. (2018). Zinc oxide phytase nanocomposites as contributory tools to improved thermostability and shelflife. *Bioresource Technology Reports, 3*, 1–6.

Rebello, S., Anoopkumar, A., Sindhu, R., Binod, P., Pandey, A., Aneesh, E. M. (2020b). Comparative life-cycle analysis of synthetic detergents and biosurfactants—an overview. *Refining Biomass Residues for Sustainable Energy and Bioproducts* (pp. 511–521). Elsevier.

Rebello, S., Balakrishnan, D., Anoopkumar, A., Sindhu, R., Binod, P., Pandey, A., et al. (2019). Industrial Enzymes as Feed Supplements—Advantages to Nutrition and Global Environment. *Green Bio-processes* (pp. 293–304). Singapore: Springer.

Reisen, W. K., Fang, Y., & Martinez, V. M. (2006). Effects of temperature on the transmission of West Nile virus by Culex tarsalis (Diptera: Culicidae). *Journal of Medical Entomology, 43*(2), 309–317.

Rezza, G., Weaver, S. C. (2019). Chikungunya as a paradigm for emerging viral diseases: evaluating disease impact and hurdles to vaccine development. *PLoS neglected tropical diseases*, 13(1), e0006919.

Riehle, M. A., Moreira, C. K., Lampe, D., Lauzon, C., & Jacobs-Lorena, M. (2007). Using bacteria to express and display anti-Plasmodium molecules in the mosquito midgut. *International Journal for Parasitology, 37*(6), 595–603.

Rivero, A., Vezilier, J., Weill, M., Read, A. F., Gandon, S. (2010). Insecticide control of vector-borne diseases: when is insecticide resistance a problem? *PLoS pathogens*, 6(8), e1001000.

Roberts, D. R., Andre, R. G. (1994). Insecticide resistance issues in vector-borne disease control. *The American journal of tropical medicine and hygiene*, 50(6_Suppl), p. 21–34.

Robinson, M. C. (1955). An epidemic of virus disease in Southern Province, Tanganyika territory, in 1952–1953. *Transactions of the Royal Society of Tropical Medicine and Hygiene, 49*(1), 28–32.

Rowley, W. A., & Graham, C. L. (1968). The effect of temperature and relative humidity on the flight performance of female Aedes aegypti. *Journal of Insect Physiology, 14*(9), 1251–1257.

Rozendaal, J. A. (1997). Vector control: methods for use by individuals and communities. World Health Organization.

Russell, P. F. (1963). *Practical Malariology: By Paul F*. Oxford University Press.

Sadasivaiah, S., Tozan, Y., & Breman, J. G. (2007). Dichlorodiphenyltrichloroethane (DDT) for indoor residual spraying in Africa: how can it be used for malaria control? *The American journal of tropical medicine and hygiene*, 77(6_Suppl), 249–263.

Schiøler, K. L., Samuel, M., Wai, K. L. (2007). Vaccines for preventing Japanese encephalitis. *Cochrane Database of Systematic Reviews*, https://doi.org/10.1002/14651858.CD004263.pub2.

Scott, T. W., Clark, G. G., Lorenz, L. H., Amerasinghe, P. H., Reiter, P., & Edman, J. D. (1993). Detection of multiple blood feeding in Aedes aegypti (Diptera: Culicidae) during a single gonotrophic cycle using a histologic technique. *Journal of Medical Entomology, 30*(1), 94–99.

Sharma, G. (1984) 'Review of malaria and its control in India' *Proceeding of the Indo-UK workshop on malaria education. VP Sharma (MRC ICMR Delhi)*. p. 13–40.

Sharrel Rebello, A. N. A., Embalil Mathachan Aneesh, Raveendran Sindhu, Parameswaran Binod, AshokPandey (2019). Sustainability and life cycle assessments of lignocellulosic and algal pretreatments. *Bioresource Technology Reports*, In Press, Journal Pre-proof, Available online 26 December 2019.

Shretta, R., Liu, J., Cotter, C., Cohen, J., Dolenz, C., Makomva, K., et al. (2017). Malaria elimination and eradication. *Major Infectious Diseases. 3rd edition*: The International Bank for Reconstruction and Development/The World Bank.

Sikka, V., Chattu, V. K., Popli, R. K., Galwankar, S. C., Kelkar, D., Sawicki, S. G., et al. (2016). The emergence of Zika virus as a global health security threat: A review and a consensus statement of the INDUSEM Joint Working Group (JWG). *Journal of Global Infectious Diseases, 8*(1), 3.

Singh, K., Rahman, S., & Joshi, G. (1989). Village scale trial of deltamethrin against mosquitoes. *The Journal of Communicable Diseases, 21*(4), 339–353.

Slater, H., Michael, E. (2012). Predicting the current and future potential distributions of lymphatic filariasis in Africa using maximum entropy ecological niche modelling. *PloS one*, 7(2), e32202.

Solano-Villarreal, E., Valdivia, W., Pearcy, M., Linard, C., Pasapera-Gonzales, J., Moreno-Gutierrez, D., et al. (2019). Malaria risk assessment and mapping using satellite imagery and boosted regression trees in the Peruvian Amazon. *Scientific Reports, 9*(1), 1–12.

Southwood, T. R. (1977). Habitat, the templet for ecological strategies?. *The Journal of Animal Ecology*, 46(2), 337–365.

Strode, C., Donegan, S., Garner, P., Enayati, A. A., Hemingway, J. (2014). The impact of pyrethroid resistance on the efficacy of insecticide-treated bed nets against African anopheline mosquitoes: systematic review and meta-analysis. *PLoS medicine*, 11(3), e1001619.

Suk, J. E. (2016). Climate change, malaria, and public health: accounting for socioeconomic contexts in past debates and future research. *Wiley Interdisciplinary Reviews: Climate Change, 7*(4), 551–568.

Thu, H. M., Aye, K. M., & Thein, S. (1998). The effect of temperature and humidity on dengue virus propagation in Aedes aegypti mosquitos. *Southeast Asian Journal of Tropical Medicine and Public Health, 29*(2), 280–284.

Trampuz, A., Jereb, M., Muzlovic, I., & Prabhu, R. M. (2003). Clinical review: severe malaria. *Critical Care, 7*(4), 1–9.

Tu, Y. (2011). The discovery of artemisinin (qinghaosu) and gifts from Chinese medicine. *Nature Medicine, 17*(10), 1217.

Van Bortel, W., Dorleans, F., Rosine, J., Blateau, A., Rousset, D., Matheus, S., et al. (2014). Chikungunya outbreak in the Caribbean region, December 2013 to March 2014, and the significance for Europe. *Eurosurveillance, 19*(13), 20759.

Vijayan, V. (2010). Laboratory selection of carbofuran tolerant line of Culex quinquefasciatus Say, the filarial vector at Mysore. *Journal of Communicable Diseases, 42*(3), 201–207.

Watson, M. (1921). The prevention of malaria in the Federated Malay States: a record of twenty years' progress. EP Dutton & Company.

Weltman, J. (2016). Medical Microbiology & Diagnosis An Immuno-Bioinformatic Analysis of Zika virus (ZIKV) envelope E Protein. *Journal of Medical Microbiology Diagn, 5*(2), 1–2.

White, R. S. (1945). House spraying with DDT and with pyrethrum extract compared: first results. *Journal of the Malaria Institute of India, 6*(1), 83–93.

WHO (1982). Manual on environmental management for mosquito control, with special emphasis on malaria vectors.

WHO. (2010). World health statistics 2010. World Health Organization.

WHO. (2014). Quantitative risk assessment of the effects of climate change on selected causes of death, 2030s and 2050s. World Health Organization.

WHO. (2017). *Global vector control response 2017–2030*. WHO.

WHO (2019a). Dengue and severe dengue. https://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue. Last accessed on 25–10–2020.

WHO (2019b). Dengue and severe dengue. *Available* at https://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue. Last Acessed on 25 December 2019.

Wichit, S., Hamel, R., Yainoy, S., Gumpangseth, N., Panich, S., Phuadraksa, T., et al. (2019). Interferon-inducible protein (IFI) 16 regulates Chikungunya and Zika virus infection in human skin fibroblasts. *EXCLI Journal, 18*, 467.

Wilke, A. B. B., & Marrelli, M. T. (2015). Paratransgenesis: a promising new strategy for mosquito vector control. *Parasites & Vectors, 8*(1), 342.

Yacoub, S., Mongkolsapaya, J., Screaton, G. (2016). Recent advances in understanding dengue. *F1000Research*, 5, 78.

Zanluca, C., & Dos Santos, C. N. D. (2016). Zika virus–an overview. *Microbes and Infection, 18*(5), 295–301.

Zeller, H., & Schuffenecker, I. (2004). West Nile virus: an overview of its spread in Europe and the mediterranean basin in contrast to its spread in the Americas. *European Journal of Clinical Microbiology and Infectious Diseases, 23*(3), 147–156.

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