

A Review on Vector Borne Diseases and Controlling Challenges

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Abstract:

Vector-borne emerging and re-emerging infectious diseases are a serious public health concern worldwide. Some of these diseases are emerging and / or re-emerging and have emerged in new regions over the last two decades. Studies have emphasized that interactions between pathogens, hosts and the environment play an important role in the appearance or recurrence of these diseases. In addition, social and demographic factors such as population growth, urbanization, globalization, trade exchanges and travel, and close interactions with livestock are significantly associated with the appearance and / or recurrence of vector-mediated diseases. increase. Other studies have emphasized that the evolution of progressive pathogens, the growth of reservoir populations, and the use of antibiotics are the major exacerbating factors in the emergence and recurrence of vector-borne infections. Still other studies equivocally claim that climate change has been associated with appearance and resurgence of vector borne infectious diseases. Despite the fact that many important emerging and re-emerging vector borne infectious diseases are becoming better controlled, our success in stopping the many new appearing and resurging vector borne infectious diseases that may happen in the future seems to be uncertain. Hence, this paper reviews and synthesizes the existing literature to explore global patterns of emerging and re-emerging vector borne infections and the challenges for their control. It also attempts to give insights to the epidemiological profile of major vector borne diseases including Zika fever, dengue, West Nile fever, Crimean Congo haemorrhagic fever, Chikungunya, Yellow fever, and Rift Valley fever.

Keywords:

emerging infectious diseases, re-emerging infectious diseases, climate change, zoonotic diseases, vector-borne infectious diseases.

I. INTRODUCTION

Emerging and re-emerging infectious diseases are one of the greatest public health concerns around the world [1]. These diseases are not directly transmitted between humans, but are transmitted when favourable conditions are created for the interaction of vectors, animal hosts, climatic conditions, pathogens, and sensitive human populations [2]. Vector-borne diseases are emerging at an accelerating rate, accounting for a disproportionate proportion of all new infectious diseases, most of which are viruses. Over the last two decades, several vector-borne pathogens have settled in new areas, but the incidence of the corresponding number of endemic diseases has increased. Although the introduction and emergence of endemic pathogens is usually considered a separate event, some endemic pathogens spread at essentially finite levels in synchronization with habitat changes. Previous studies have reported a wide range of vector-borne human infections such as yellow fever and dengue [3]. Outbreaks of vector-mediated disease, although still controversial, appear to be associated with climate factors and climate change. Climate change is obvious and every aspect of nature is affected

by climate [4]. The effects of climate change are very important in the 21st century. Several previous studies have estimated that the global mean temperature will rise by 1.0-3.5 ° C by 2,100 [5], increasing the likelihood of various vector-borne diseases. Changes in weather and the effects of climatic conditions have a direct impact on pathogen carriers and transmission patterns. Human activities, such as the construction of dams and irrigation systems, have the potential to increase food and energy needs in developing countries, but they are steadily increasing infections and introducing new vector-borne infectious diseases. I am concerned [6, 7]. For example, ecological changes associated with water resource expansion and migration may promote the spread of schistosomiasis to non-endemic areas [8, 9]. Recognizing how the once predominant vector-mediated disease is reappearing is a reminder that the world is regularly faced with the challenges of infectious diseases that have received little attention or are ignored. It is important to deal with the damage they cause. Therefore, continued awareness of infectious diseases and advances in management efforts are needed to stimulate appropriate public health responses [10]. Hence this paper aims at reviewing emerging and re-emerging major vector borne infectious diseases and the challenges for their control.

II. DETERMINANTS OF THE APPEARANCE AND RECURRENCE OF VECTOR-MEDIATED DISEASE

The appearance and recurrence of infections occur over time. Before the outbreak occurs, the pathogen goes through various stages of adaptation to mate with a new host [11]. Interactions between pathogens, hosts, and the environment have a strong impact on the appearance or recurrence of infectious diseases. In addition, many factors, including ecological, environmental, and demographic factors, can contribute to the consequences of this adaptation and outbreak of disease. These factors influence by creating favourable conditions, thereby increasing contact with or promoting the spread of previously foreign pathogens or their natural hosts. These factors, coupled with the ongoing evolution of viral and microbial variants and the problem of drug resistance, promote the regular outbreak and possible increase in infection. The spread and colonization of new or revived pathogens can be maintained by multiple driving forces: climatic and non-climatic factors [2]. Climate change and climate factors

Climate change refers to long-term changes in weather conditions and extreme weather patterns. It is part of many interacting determinants of vector infectious diseases. The impact of climate change on the onset, duration, duration, and epidemic of vector-borne diseases constitutes a serious problem [12]. Climate change is indirect by directly affecting the survival, reproduction, and life cycle of the pathogen, or by controlling the habitat, environment, or competitors of the pathogen and altering the contact pattern between human pathogens and human vectors. May affect pathogens. The direct effect of temperature on the duration of the exogenous incubation period of a pathogen in insect-borne organisms is important for the possible presence of insect-borne diseases. Apparently, pathogens require a typical temperature range for their survival and development. Vector development and survival are also significantly influenced by temperature factors [13]. For example, two thresholds, a maximum temperature of 22-23 ° C for mosquito outbreaks and a minimum temperature of 25-26 ° C for transmission of Japanese encephalitis virus [JEV], play important roles in the JEV [14th century] ecosystem. Play., 15]. The development and proliferation of pathogens transmitted within the vector, extrinsic incubation period, or environment also occur more rapidly at high temperatures [16]. Therefore, the direct impact of climate change on habitat and thus ecosystem changes, coupled with increased human invasion of the natural environment, adversely affects biodiversity, thereby affecting the development and transmission of infectious diseases. [17].

That's what studies showed however gambles from vector borne illnesses are naturally vulnerable to changes in climate and environment [18, 19], the contentions around effects of environmental change on them centres around the level to which climate and environment influence their event and force versus human's endeavours to control microbes and their vectors [20]. Then again, a few vectors borne illnesses of general wellbeing significance are zoonotic being kept up with by natural life, and their event is inherently less affected by man's control endeavours [21]. However, they are not the most regularly noted explanations behind rise, climatic and weather conditions related factors are expressly involved in the development of some vector borne zoonotic illnesses. Others revealed that land use changes were the most widely recognized drivers for their rise, representing 26% of all vector borne zoonotic illnesses followed by undefined or obscure drivers and worldwide exchange and business representing 14 and 11%, individually. Nonetheless, environment and weather conditions related factors were accounted for to represent 10% as a driver of those sicknesses [22]. No climatic Variables

Factors other than climatic variables fundamentally affect the development and additionally reappearance of vector borne sicknesses. A portion of the major no climatic factors are worldwide human populaces and urbanization, global

exchange and travel, escalated animals keeping frameworks and extension and modernization of horticultural practices, multiplication of repository populaces, and antimicrobial medication use [23-25]. The relationship between irresistible illnesses and socio-political, and monetary change from the past to the present has been well established and complex social and ecological gamble factors have been accounted for in the event of new irresistible sicknesses including vector borne [26]. The presence of these illnesses and return of the current ones might show that different changes are continuous in human biology including uraturia deluge of individuals bringing about packed metropolitan peripheries, broad deforestation and war and struggle upsetting social capitals. Notwithstanding host and natural variables, changes or transformations in the genome of microbes that happen after openness to synthetics and antibacterial specialists can cause hereditary harm [27] and new sicknesses of medication safe microorganism variations. May prompt appearance [28]. Explicit cycles like quality transformation, quality recombination, or revamp, and factors that influence microbial microorganisms and switch stockpiling has been factors that irresistible microbe develop and adjust to new has in new natural specialties. It gives an amazing chance to spread to [28]. Globalization

A progression of perplexing elements related with human way of behaving and action, microbe advancement, neediness and natural changes, and dynamic human collaborations with creatures are accounted for to be related with the development and spread of irresistible illnesses. Has been [29]. At long last, changes in local area construction, and accordingly powerful cycles answerable for microbe elements at different connection points, seem to lean toward the rise and repeat of irresistible illnesses. Today, there are worries that globalization is influencing the study of disease transmission of vector-borne irresistible sicknesses. Numerous vector-borne viral infections are turning into a worldwide danger because of the regional spread of vectors and infections because of globalization and urbanization [32] [30, 31].

III. URBANIZATION

High flood of rustic to-metropolitan movement has been connected to high-thickness peri-metropolitan ghettos which make helpful environment rearing of vectors. Spontaneous urbanization is regularly connected with unfortunate lodging and nonappearance of fundamental administrations, including water and waste administration, which makes ideal environments for development of vector populaces [33, 34]. Late investigations recommended that urbanization can work with different untamed life domesticated animals' human connection points exhibiting a conclusive point for conceivable event of new microorganisms as well as for cross-species spread [35]. They added that urbanization additionally contribute for the rise of zoonoses, through investigating the environmental intricacy of natural life domesticated animals' human connection points. The cross-species spread and forward transmission might demonstrate a characteristic reaction to the transformative tensions of microbe nature [36]. Conceivable course of transmission can be through food and creature items including meat and dairy items along with water and waste.

IV. AGRIBUSINESS AND IMPROVEMENT TASKS

Human-actuated biological changes have had their portion for the beginning of new diseases or re-appearance of the current ones halfway by horticultural exercises and improvement projects. A few investigations revealed that irresistible illnesses and human-initiated land-use changes in agrarian practice are essentially related [37-40]. For example, infringement on the regular biological system and natural life by rural and land utilizes uncover individuals and their homegrown creatures to a more extensive scope of vectors.

Additionally, the extension of watered cultivating relatively expanded flare-ups of vector-borne illnesses. As per reports farming drivers are related with >25% of arising irresistible sicknesses and >50% of arising zoonotic irresistible infections in people [41]. Development of dams, water system, and comparative advancement projects apparently affected vector populace densities which thusly decide the event of new infections and the resurgence of existing ones. For example, the flare-ups of Break Valley fever have happened following the development of dams and water system channels [42].

V. MAJOR ARISING AND REAPPEARING VECTOR-BORNE IRRESISTIBLE INFECTIONS

All things considered; individuals have been encountering enormous effects of vector-borne irresistible sicknesses. Of these, intestinal sickness and dengue force colossal weight causing an expected 620,000 and 40,500 passings in 2017, for the most part happening in Africa and Asia, separately [43]. It is notable that not all vectors have equivalent importance regarding illness transmission. A few vectors have had moderately a greater number of effects than others. A genuine illustration of mosquito-borne new and old illnesses incorporates those like intestinal sickness, Zika infection fever,

dengue, West Nile fever, Crimean-Congo haemorrhagic fever, chikungunya viral infection, yellow fever, Japanese encephalitis, and Break Valley fever. These irresistible illnesses have been presenting critical medical condition around the world. In this part accentuation will be given to a portion of the generally arising and reappearing vector-borne irresistible illnesses.

A. *Jungle fever*

Jungle fever is a vector-borne illness brought about by five genera of Plasmodium in particular Plasmodium falciparum, P. vivax, P. ovale, P. malariae and P. knowlesi and sent by the female Anopheles mosquitoes [44]. As per World jungle fever report of 2018 around 219 million and 435,000 intestinal sickness cases and passings, individually were kept in 2017. Roughly 80% of overall jungle fever related mortality in 2017 happened in 17 nations in the WHO African Area.

It is deeply grounded that intestinal sickness transmission is affected by ecological factors like geology, precipitation, environment, and financial states of the populace. Therefore, tropical areas with warm temperature, weighty precipitation, high dampness and low elevations are favourable for mosquito reproducing, life span and parasite sporogony. Reports showed that a change in the altitudinal dispersion of intestinal sickness toward higher heights in hotter years has been seen in Colombia and that's what Ethiopia suggesting, without even a trace of mediation, the jungle fever weight will increment at higher rises as the environment warms [45].

Jungle fever is an infection of destitution, and adds to public neediness by means of restricting unfamiliar direct speculation, the travel industry, work efficiency and exchange [46]. Concentrates on announced that the expense of ailment, treatment and sudden passing because of jungle fever was no less than USD\$12 billion every year in Africa alone consequently advancing neediness [47]. Jungle fever establishes the best 10 reasons for horribleness and mortality among the sub-Saharan Africa overall and Ethiopia specifically.

B. *Dengue*

Dengue is brought about by an infection of family Flaviviridae, class Flavivirus and sent by mosquitoes, is extensively spread in tropical and subtropical districts. It is probably the most established illness maybe first recorded in Chinese clinical reference book in 992. The infection got comfortable predominantly after the development of worldwide transportation industry and port urban communities in the eighteenth and nineteenth hundreds of years. Later on, studies showed that dengue fever was brought to the Americas related to the slave exchange during which the tainted slaves from Africa maybe acquainted the disease with the Americas [48]. Dengue infection is a perfect representation of how the collaboration between fast microorganism development, human development, and changing vector biology has driven rise [49, 50].

Epidemiological profile of dengue showed a rising pattern in endemic nations. As per late reports, dengue is the most quickly spreading arbovirus on the planet which compromises a half-billion individuals around the world [51, 52], with dramatical ascend in frequency in the metropolitan and peri urban areas of Americas [53]. Past examinations likewise showed that the biggest dengue pestilence was accounted for in China in 2014, [54] and the primary nearby dengue case report was from Japan before 70 years in 2014 [55]. It has been accounted for that age-normalized DALY rate expanded from 2007 to 2017 for dengue, which made it the sole key vector-borne sickness showing a sharp increment by 26% around the world [43]. From the pattern it tends to be obvious that a constant transmission of the sickness since the 1950s, disturbed by urbanization, globalization and ineffective vector control finishing off with expanded disease and transmission of the infection [32].

C. *Chikungunya*

Chikungunya, and that signifies "infection that curves up the joints" in the Tanzanian Makonde tongue, is a mosquito-borne viral illness brought about by an alphavirus from the Togaviridae family [56, 57]. The beginning of the Chikungunya appears to be questionable as certain reports say that it was first disconnected from the serum of a febrile human dressed in Tanganyika [Tanzania] in 1953 [58] and others from patients with fever, serious joint agony, and skin rash in Uganda in 1959 [56, 57].

Chikungunya has developed quickly after its fruitful prologue to new areas and getting new anthropophilic vectors. Repeat of chikungunya infection is a not kidding general wellbeing worry since the infection has been related with a few episodes of scourges in Africa, Asia, and India [59]. Past investigations affirmed that the Chikungunya infection was

inferable for the flare-up scattered across the Indian Sea which was started in seaside Kenya during 2004 [60]. Indeed, even from ongoing histories, chikungunya appears to be on the ascent as irregular pestilences were recognized in Italy [61] in 2007 and 2017, the principal neighbourhood transmission of the infection in the US in 2014, [62] and most recent flare-ups in the Caribbean, Focal and South American locales [63].

D. Lyme Illness

Lyme illness is brought about by bacterial spirochete alluded to as *Borrelia burgdorferi* and spread to vertebrates including people by the chomp of normally named deer ticks [*Ixodes* species]. It was first depicted in 1977 as "Lyme joint inflammation." Lyme sickness is generally disseminated in the Western and since its recognizable proof; it showed persistent transmission with expanding cases in the north-eastern and north focal US.

It was perceived as a significant arising contamination in the late twentieth 100 years [76]. A few reports showed that the frequency of tick nibbles and instances of Lyme borreliosis has expanded considerably throughout the last many years. As of late, ~20,000-30,000 affirmed instances of Lyme illness each year have been accounted for to the Habitats for Infectious prevention and Avoidance [77]. Around 85,000 instances of Lyme infection are accounted for yearly in Europe and in the Netherlands, yearly north of 1,000,000 individuals report a tick chomp, and more than 25.000 cases are analysed [78].

Biological circumstances helpful for the illness, and the trouble of anticipation, infer that Lyme infection has all the earmarks of being a proceeding with worry to the general wellbeing [79]. Studies show that environmental change has exacerbated the development scope of ticks [80], improving the likelihood of hazard of Lyme sickness, as in areas of Canada in which the vectors were missing previously.

VI. THE WEIGHT OF VECTOR-BORNE IRRESISTIBLE INFECTIONS

Vector-borne irresistible infections represent a colossal weight of horribleness and mortality around the world, especially influencing the asset scant and monetarily lower sections of the general public. In spite of the fact that their obstacle is enhanced across the world, the dismalness and mortality they cause is most noteworthy in tropical and subtropical regions. Indeed, even among the jungles and subtropics they excessively present higher weight devastated populace. It has been noticed that vector-borne irresistible sicknesses represent 17% of assessed worldwide weight of every irresistible infection [107].

The worldwide effect of the vector-borne infections is additionally increased by the intermittent development of new, unnoticed, and reappearance of the current flare-ups. Throughout the course of recent a long time no less than 30 new irresistible specialists influencing people have arisen, the vast majority of which are zoonotic and their starting points were corresponded essentially with financial, natural, environmental and climatic variables.

Vector-borne irresistible infections force a significant worldwide weight on general wellbeing expanding wellbeing disparities. The plague of recently seeming irresistible infections is now indisputable since antiquated times. Vector-borne irresistible illnesses were known to be the most destroying pandemic in the mankind's set of experiences. One counter model such infamous vector-borne illness which killed 25-40 million is bubonic/pneumonic plague [10].

VII. CONTROL MEASURES AND DIFFICULTIES OF VECTOR-BORNE IRRESISTIBLE ILLNESSES

A few devices and control approaches have been polished to moderate arising and reappearing vector-borne irresistible infections. Strengthening dynamic observation, quality guaranteed early determination and powerful case the executives has been of foremost importance. Atomic methodologies like genome sequencing and phylogenetic following examinations can have an unequivocal impact in exactly recognizing the original microorganisms [108].

The control of vector-borne infections is among the significant difficulties across the world wellbeing program. The ongoing quick and uncontrolled urbanization has escalated the worry in settling these issues utilizing organized well thought out plans which can be planned and carried out at worldwide and neighbourhood stages. The high commonness and ascend in rate of endemic vector-borne infections frightened partners for fruitful control and treatment of casualties with related episodes. As needs be, the worldwide weight of irresistible sicknesses including vector-borne ones showed significant decay during the previous many years attributable to the headway of present-day medication, destitution decrease draws near and financial turn of events, and the utilization of more effective intercession and control measures [109]. Among the famous and effective vector control approaches was utilization of compound bug sprays. Regardless of the examples of overcoming adversity of compound insect sprays, insect poison obstruction has arisen as a significant

danger to vector-borne control that primarily relies upon focusing on vector populaces [110]. In any case, propels at a worldwide scale covers huge triumphs acquired locally.

It has been all around saw that few vector-borne infections are zoonotic and their transmission recurrence in vectors is worked with by untamed life repositories. Such peculiarity of coursing among vectors and creature supply has turned into a bottleneck for their control and mediations. Maybe accordingly such complex point of interaction among vector-microbe has, major zoonotic arbovirus sicknesses showed gigantic extension in worldwide conveyance in the previous 10 years [105].

Starting today, however different control and intercession approaches are available to us, the greater part of the control programs are even more tested by one or various factors, for example, ecological change, insect spray opposition, populace development and urbanization and environmental change. Thus, as lack of financing and powerless automatic limit win, a brief requirement for improving association and cooperation is expected for enabling the limit with regards to reconnaissance and control new vector control devices [111]. Monetary imperative additionally wins in propelling turn of events and testing of novel microorganism analytic instruments.

To summarize, vector control has been the vital apparatus in battling against vector-borne sicknesses up to this point nevertheless incredibly compelling, given that it is extensively carried out. As a matter of fact, it stays the sole and suitable control apparatus accessible available to us for some, sicknesses including vector-borne ones.

VIII. SUMMARY

Vector-borne irresistible illnesses force a significant worldwide weight on general wellbeing. For over beyond couple of many years' scourges of vector-borne arising illnesses were rising maybe through numerous main impetuses including financial, natural, a dangerous atmospheric deviation and environmental change. Cooperative examination networks on zoonotic and vector-borne arising and reappearing irresistible infections stay the most significant in tending to the underlying issues for long haul plan. In such manner, enabling One Wellbeing approach enveloping general wellbeing specialists, veterinarians, entomologists, and parasitologists ought to be focused on. In addition, the job of worldwide benefactors and raising money specialists ought to be offer due consideration. These days, various arising, reappearing, and stable vector-borne irresistible illnesses are turning out to be very much overseen yet the future endeavours on obstructing the rise of new infections appear to be unsure. This might caution for continuous battle against arising vector-borne irresistible infections.

REFERENCES

- [1] Gubler DJ. The global threat of emergent/re-emergent vector-borne diseases. In: Atkinson PW, editors. *Vector Biology, Ecology and Control*. Dordrecht: Springer [2010]. Google Scholar
- [2] Savi S, Vidic B, Grgi Z, Potkonjak A, Spasojevic L. Emerging vector-borne diseases incidence through vectors. *Front Public Health*. [2014] 2:267. doi: 10.3389/fpubh.2014.00267 PubMed Abstract | CrossRef Full Text | Google Scholar
- [3] Harvell CD, Mitchell CE, Ward JR, Altizer S, Dobson AP, Ostfeld RS, et al. Climate warming and disease risks for terrestrial and marine biota. *Science*. [2002] 296:2158–62. doi: 10.1126/science.1063699 PubMed Abstract | CrossRef Full Text | Google Scholar
- [4] IPCC. *Intergovernmental Panel on Climate Change the Physical Science Basis*. Cambridge: Cambridge University Press [2007]. Google Scholar
- [5] Watson RT, Zinyowera MC, Moss RH. *Climate Change; Impacts, Adaptations and Mitigation of Climate Change: Scientific-Technical Analysis. Contribution of Working Group II to the Second Assessment Report of the Intergovernmental Panel on Climate Change*. Cambridge: Cambridge University Press [1995]. Google Scholar
- [6] Chu K, Mott KE, Rey L, Hunter J, Adekolu-John E. *Parasitic Diseases in Water Resources Development: the Need for Intersectoral Negotiation*. Geneva: WHO [1993]. Google Scholar
- [7] Kibret S, Lautze J, McCartney M, Nhamo L, Wilson GG. Malaria and large dams in sub-Saharan Africa: future impacts in a changing climate. *Malar J*. [2016] 15:448. doi: 10.1186/s12936-016-1498-9 PubMed Abstract | CrossRef Full Text | Google Scholar
- [8] Gryseels B, Polman K, Clerinx J, Kestens L. Human schistosomiasis. *Lancet*. [2006] 368:1106–18. doi: 10.1016/S0140-6736[06]69440-3 PubMed Abstract | CrossRef Full Text | Google Scholar

- [9] Chala B, Torben W. An epidemiological trend of urogenital schistosomiasis in Ethiopia. *Front Public Health*. [2018] 6:60. doi: 10.3389/fpubh.2018.00060 PubMed Abstract | CrossRef Full Text | Google Scholar
- [10] Morens DM, Folkers GK, Fauci AS. Emerging infections: a perpetual challenge. *Lancet Infect Dis*. [2008] 8:710–9. doi: 10.1016/S1473-3099[08]70256-1 PubMed Abstract | CrossRef Full Text | Google Scholar
- [11] Carruthers VB, Cotter PA, Kumamoto CA. Microbial pathogenesis: mechanisms of infectious disease. *Cell Host Microbe*. [2007] 2:214–9. doi: 10.1016/j.chom.2007.09.007 PubMed Abstract | CrossRef Full Text | Google Scholar
- [12] IPCC. *Climate Change 2014: Impacts, Adaptation, and Vulnerability. Part A: Global and Sectoral Aspects* [eds Field CB, Barros VR, Dokken DJ, Mach KJ, Mastrandrea MD, Bilir TE, Monalisa C, Ebi KL, Estrada YO, Genova RC, Girma B, Kissel ES, Levy AN, MacCracken S, Mastrandrea PR, White LL.], Cambridge University Press [2014]. Google Scholar
- [13] Brady OJ, Johansson MA, Guerra CA, Bhatt S, Golding N, Pigott DM, et al. Modeling adult *Aedes aegypti* and *Aedes albopictus* survival at different temperatures in laboratory and field settings. *Parasit Vectors*. [2013] 6:351. doi: 10.1186/1756-3305-6-351 PubMed Abstract | CrossRef Full Text | Google Scholar
- [14] Mellor PS, Leake CJ. Climatic and geographic influences on arboviral infections and vectors. *Rev Sci Tech*. [2000] 19:41–54. doi: 10.20506/rst.19.1.1211 PubMed Abstract | CrossRef Full Text | Google Scholar
- [15] Tian HY, Zhou S, Dong L, VanBoeckel TP, Cui YJ, Wu YR, et al. Avian influenza H5N1 viral and bird migration networks in Asia. *Proc Natl Acad Sci USA*. [2015] 112:172–7. doi: 10.1073/pnas.1405216112 PubMed Abstract | CrossRef Full Text | Google Scholar
- [16] Reisen WK, Fang Y, Martinez VM. Effects of temperature on the transmission of West Nile Virus by *Culex tarsalis* [Diptera: Culicidae]. *J Med Entomol*. [2006] 43:309–17. doi: 10.1093/jmedent/43.2.309 PubMed Abstract | CrossRef Full Text | Google Scholar
- [17] Keesing F, Belden LK, Daszak P, Dobson A, Harvell CD, Holt RD, et al. Impacts of biodiversity on the emergence and transmission of infectious diseases. *Nature*. [2010] 468: 647–52. doi: 10.1038/nature09575 PubMed Abstract | CrossRef Full Text | Google Scholar
- [18] Medlock JM, Leach SA. Effect of climate change on vector-borne disease risk in the UK. *Lancet Infect Dis*. [2015] 15:721–30. doi: 10.1016/S1473-3099[15]70091-5 PubMed Abstract | CrossRef Full Text | Google Scholar
- [19] Ogden NH, Lindsay LR. Effects of climate and climate change on vectors and vector-borne diseases: ticks are different. *Trends Parasitol*. [2016] 32:646–56. doi: 10.1016/j.pt.2016.04.015 PubMed Abstract | CrossRef Full Text | Google Scholar
- [20] Lafferty KD. The ecology of climate change and infectious diseases. *Ecology*. [2009] 90:888–900. doi: 10.1890/08-0079.1 PubMed Abstract | CrossRef Full Text | Google Scholar
- [21] Ogden NH, Radojevic M, Wu X, Duvvuri VR, Leighton PA, Wu J, et al. Estimated effects of projected climate change on the basic reproductive number of the tick vector of Lyme disease *Ixodes scapularis*. *Environ Health Perspect*. [2014] 122:631–8. doi: 10.1289/ehp.1307799 PubMed Abstract | CrossRef Full Text | Google Scholar
- [22] Swei A, Couper LI, Coffey LL, Kapan D, Bennett S. Patterns, drivers, and challenges of vector-borne disease emergence. *Vector Borne Zoonotic Dis*. [2020] 20:159–70. doi: 10.1089/vbz.2018.2432 PubMed Abstract | CrossRef Full Text | Google Scholar
- [23] Perry BD, Grace D, Sones K. Current drivers and future directions of global livestock disease dynamics. *Proc Natl Acad Sci USA*. [2011] 110:20871–7. doi: 10.1073/pnas.1012953108 PubMed Abstract | CrossRef Full Text
- [24] Jones BA, Grace D, Kock R, Alonso S, Rushton J, Said MY, et al. Zoonosis emergence linked to agricultural intensification and environmental change. *Proc Natl Acad Sci USA*. [2013] 110:8399–404. doi: 10.1073/pnas.1208059110 PubMed Abstract | CrossRef Full Text | Google Scholar
- [25] Tong MX, Hansen A, Hanson-Easey S, Cameron S, Xiang J, Liu Q, et al. Infectious diseases, urbanization and climate change: challenges in future China. *Int J Environ Res Public Health*. [2015] 12:11025–36. doi: 10.3390/ijerph120911025 PubMed Abstract | CrossRef Full Text | Google Scholar
- [26] Weiss RA, McMichael AJ. Social and environmental risk factors in the emergence of infectious diseases. *Nat Med*. [2004] 10:S70–6. doi: 10.1038/nm1150 PubMed Abstract | CrossRef Full Text | Google Scholar

- [27] Lashley FR. Emerging infectious disease: vulnerabilities, contributing factors and approaches. *Expert Rev Anti Infect Ther.* [2004] 2:299–316. doi: 10.1586/14787210.2.2.299 PubMed Abstract | CrossRef Full Text | Google Scholar
- [28] Alcais A, Abel L, Casanova JL. Human genetics of infectious diseases: between proof of principle and paradigm. *J Clin Invest.* [2009] 119:2506–14. doi: 10.1172/JCI38111 PubMed Abstract | CrossRef Full Text | Google Scholar
- [29] Nii-Trebi NI. Emerging and neglected infectious diseases: insights, advances, and challenges. *Biomed Res Int.* [2017] 2017:5245021. doi: 10.1155/2017/5245021 PubMed Abstract | CrossRef Full Text | Google Scholar
- [30] Vasconcelos PF, Monath TP. Yellow fever remains a potential threat to public health. *Vector Borne Zoonotic Dis.* [2016] 16:566–7. doi: 10.1089/vbz.2016.2031 PubMed Abstract | CrossRef Full Text | Google Scholar
- [31] Gubler DJ. Dengue, urbanization and globalization: the unholy trinity of the 21st Century. *Trop Med Health.* [2011] 39:3–11. doi: 10.2149/tmh.2011-S05 PubMed Abstract | CrossRef Full Text | Google Scholar
- [32] Lowe R, Barcellos C, Brasil P, Cruz OG, Honório NA, Kuper H, et al. The Zika virus epidemic in Brazil: from discovery to future implications. *Int J Environ Res Public Health.* [2018] 15:E96. doi: 10.3390/ijerph15010096 PubMed Abstract | CrossRef Full Text | Google Scholar
- [33] Hassell JM, Begon M, Ward MJ, Fèvre EM. Urbanization and disease emergence: dynamics at the wildlife–livestock–human interface. *Trends Ecol Evol.* [2017] 32:55–67. doi: 10.1016/j.tree.2016.09.012 PubMed Abstract | CrossRef Full Text | Google Scholar
- [34] Lindsay SW, Wilson A, Golding N, Scott TW, Takken W. Improving the built environment in urban areas to control *Aedes aegypti*-borne diseases. *Bull World Health Organ.* [2017] 95:607–8. doi: 10.2471/BLT.16.189688 PubMed Abstract | CrossRef Full Text | Google Scholar
- [35] Pearce JC, Learoyd TP, Langendorf BJ, Logan JG. Japanese encephalitis: the vectors, ecology and potential for expansion. *J Travel Med.* [2018] 25:S16–26. doi: 10.1093/jtm/tay009 PubMed Abstract | CrossRef Full Text | Google Scholar
- [36] Karesh W.B. Ecology of zoonoses: natural and unnatural histories. *Lancet.* [2012] 380:1936–45. doi: 10.1016/S0140-6736[12]61678-X PubMed Abstract | CrossRef Full Text | Google Scholar
- [37] McFarlane RA, Sleight AC, McMichael AJ. Land-use change and emerging infectious disease on an island continent. *Int J Environ Res Public Health.* [2013] 10:2699–719. doi: 10.3390/ijerph10072699 PubMed Abstract | CrossRef Full Text | Google Scholar
- [38] Gottdenker NL, Streicker DG, Faust CL, Carroll CR. Anthropogenic land use change and infectious diseases: a review of the evidence. *Ecohealth.* [2014] 11:619–32. doi: 10.1007/s10393-014-0941-z PubMed Abstract | CrossRef Full Text | Google Scholar
- [39] Kock RA. Vertebrate reservoirs and secondary epidemiological cycles of vector-borne diseases. *Rev Sci Tech.* [2015] 34:151–63. doi: 10.20506/rst.34.1.2351 PubMed Abstract | CrossRef Full Text | Google Scholar
- [40] Shah HA, Huxley P, Elmes J, Murray KA. Agricultural land-uses consistently exacerbate infectious disease risks in Southeast Asia. *Nat Commun.* [2019] 10:4299. doi: 10.1038/s41467-019-12333-z PubMed Abstract | CrossRef Full Text
- [41] Rohr JR, Barrett CB, Civitello DJ, Craft ME, Delius B, DeLeo GA, et al. Emerging human infectious diseases and the links to global food production. *Nat Sustain.* [2019] 2:445–56. doi: 10.1038/s41893-019-0293-3 PubMed Abstract | CrossRef Full Text | Google Scholar
- [42] Pepin M, Bouloy M, Bird BH, Kemp A, Paweska J. Rift valley fever virus [Bunyaviridae: Phlebovirus]: an update on pathogenesis, molecular epidemiology, vectors, diagnostics and prevention. *Vet Res.* [2010] 41:61. doi: 10.1051/vetres/2010033 PubMed Abstract | CrossRef Full Text | Google Scholar
- [43] GBD 2017 Causes of Death Collaborators. Global, regional, and national age-sex-specific mortality for 282 causes of death in 195 countries and territories, 1980-2017: a systematic analysis for the Global Burden of Disease Study 2017. *Lancet.* [2018] 392:1736–88. doi: 10.1016/S0140-6736[18]32203-7 PubMed Abstract | CrossRef Full Text | Google Scholar
- [44] Kasetsirikul S, Buranapong J, Srituravanich W, Kaewthamasorn M, Pimpin A. The development of malaria diagnostic techniques: a review of the approaches with focus on dielectrophoretic and magnetophoretic methods. *Malar J.* [2016] 15:358. doi: 10.1186/s12936-016-1400-9 PubMed Abstract | CrossRef Full Text | Google Scholar

- [45] Siraj AS, Santos-Vega M, Bouma MJ, Yadeta D, Ruiz Carrascal D, Pascual M. Altitudinal changes in malaria incidence in highlands of Ethiopia and Colombia. *Science*. [2014] 343:1154–8. doi: 10.1126/science.1244325 PubMed Abstract | CrossRef Full Text | Google Scholar
- [46] Amek N, Bayoh N, Hamel M, Lindblade KA, Gimnig JE, Odhiambo F, et al. Spatial and temporal dynamics of malaria transmission in rural Western Kenya. *Parasit Vectors*. [2012] 5:86. doi: 10.1186/1756-3305-5-86 PubMed Abstract | CrossRef Full Text | Google Scholar
- [47] World Health Organization. World Malaria Report 2017. Geneva: World Health Organization [2017]. Google Scholar
- [48] Laughlin CA, Morens DM, Cassetti MC, Costero-Saint Denis A, San Martin JL, Whitehead SS, et al. Dengue research opportunities in the Americas. *J Infect Dis*. [2012] 206:1121–7. doi: 10.1093/infdis/jis351 PubMed Abstract | CrossRef Full Text | Google Scholar
- [49] Wilder-Smith A, Gubler DJ. Geographic expansion of dengue: the impact of international travel. *Med Clin North Am*. [2008] 92:1337–90. doi: 10.1016/j.mcna.2008.07.002 PubMed Abstract | CrossRef Full Text | Google Scholar
- [50] Lambrechts L, Scott TW, Gubler DJ. Consequences of the expanding global distribution of *Aedes albopictus* for dengue virus transmission. *PLoS Negl Trop Dis*. [2010] 4:e646. doi: 10.1371/journal.pntd.0000646 PubMed Abstract | CrossRef Full Text | Google Scholar
- [51] Bhatt S, Gething PW, Brady OJ, Messina JP, Farlow AW, Moyes CL, et al. The global distribution and burden of dengue. *Nature*. [2013] 496:504–7. doi: 10.1038/nature12060 PubMed Abstract | CrossRef Full Text | Google Scholar
- [52] Brady OJ, Smith DL, Scott TW, Hay SI. Dengue disease outbreak definitions are implicitly variable. *Epidemics*. [2015] 11:92–102. doi: 10.1016/j.epidem.2015.03.002 PubMed Abstract | CrossRef Full Text | Google Scholar
- [53] Musso D, Cao-Lormeau VM, Gubler DJ. Zika virus: following the path of dengue and chikungunya? *Lancet*. [2015] 386:243–4. doi: 10.1016/S0140-6736(15)61273-9 PubMed Abstract | CrossRef Full Text | Google Scholar
- [54] Jin X, Lin M, Shu J. Dengue fever in China: an emerging problem demands attention. *Emerg Microbes Infect*. [2015] 4:e3. doi: 10.1038/emi.2015.3 PubMed Abstract | CrossRef Full Text | Google Scholar
- [55] Kutsuna S, Kato Y, Moi ML, Kotaki A, Ota M, Shinohara K, et al. Autochthonous dengue fever, Tokyo, Japan, 2014. *Emerg Infect Dis*. [2015] 21:517–20. doi: 10.3201/eid2103.141662 PubMed Abstract | CrossRef Full Text | Google Scholar
- [56] Jupp P, McIntosh B. Chikungunya virus disease. In: Monath T, editor. *The Arboviruses: Epidemiology and Ecology*. Boca Raton Florida: CRC Press [1988] p. 137–57.
- [57] Powers AM, Brault AC, Tesh RB, Weaver SC. Re-emergence of chikungunya and o'nyong-nyong viruses: evidence for distinct geographical lineages and distant evolutionary relationships. *J Gen Virol*. [2000] 81:471–9. doi: 10.1099/0022-1317-81-2-471 PubMed Abstract | CrossRef Full Text | Google Scholar
- [58] Karabatsos N. *International Catalogue of Arthropod-Borne Viruses*. 3rd ed. San Antonio, TX: Am Soc Trop Med Hyg [1985]. p. 3.
- [59] Burt FJ, Chen W, Miner JJ, Lenschow DJ, Merits A, Schnettler E, et al. Chikungunya virus: an update on the biology and pathogenesis of this emerging pathogen. *Lancet Infect Dis*. [2017] 17:e107–17. doi: 10.1016/S1473-3099(16)30385-1 PubMed Abstract | CrossRef Full Text | Google Scholar
- [60] Kariuki Njenga M, Nderitu L, Ledermann JP, Ndirangu A, Logue CH, Kelly CHL, et al. Tracking epidemic Chikungunya virus into the Indian Ocean from East Africa. *J Gen Virol*. [2008] 89:2754–60. doi: 10.1099/vir.0.2008/005413-0 PubMed Abstract | CrossRef Full Text | Google Scholar
- [61] Angelini R, Finarelli AC, Angelini P, Petropulacos K, Macini P, Fiorentini C, et al. An outbreak of chikungunya fever in the province of Ravenna, Italy. *Euro Surveill*. [2007] 12:E070906.1. doi: 10.2807/esw.12.36.03260-en PubMed Abstract | CrossRef Full Text
- [62] Staples JE, Fischer M. Chikungunya virus in the Americas—what a vector-borne pathogen can do. *N Engl J Med*. [2014] 371:887–9. doi: 10.1056/NEJMp1407698 PubMed Abstract | CrossRef Full Text | Google Scholar
- [63] Fischer M, Staples JE. Notes from the field: Chikungunya virus spreads in the Americas-Caribbean and South America, 2013–2014. *MMWR Morb Mortal Wkly Rep*. [2014] 63:500–1. Google Scholar

- [64] Ergonul O. Crimean-Congo hemorrhagic fever virus: new outbreaks, new discoveries. *Curr Opin Virol.* [2012] 2:215–20. doi: 10.1016/j.coviro.2012.03.001 PubMed Abstract | CrossRef Full Text | Google Scholar
- [65] van de Wal BW, Joubert JR, van Eeden PJ, King JB. A nosocomial outbreak of Crimean-Congo haemorrhagic fever at Tygerberg Hospital. Part IV. Preventive and prophylactic measures. *S Afr Med J.* [1985] 68:729–32. PubMed Abstract | Google Scholar
- [66] Mardani M, Rahnavardi M, Rajaeinejad M, Naini KH, Chinikar S, Pourmalek F. Crimean-Congo hemorrhagic fever among health care workers in Iran: a seroprevalence study in two endemic regions. *Am J Trop Med Hyg.* [2007] 76:443. doi: 10.4269/ajtmh.2007.76.443 PubMed Abstract | CrossRef Full Text | Google Scholar
- [67] Mishra AC, Mehta M, Mourya DT, Gandhi S. Crimean-Congo haemorrhagic fever in India. *Lancet.* [2011] 378:372. doi: 10.1016/S0140-6736[11]60680-6 PubMed Abstract | CrossRef Full Text | Google Scholar
- [68] Tütüncü EE, Gurbuz Y, Oztürk B, Kusu F, Sencan I. Crimean Congo haemorrhagic fever, precautions and ribavirin prophylaxis: a case report. *Scand J Infect Dis.* [2009] 41:378–80. doi: 10.1080/00365540902882434 PubMed Abstract | CrossRef Full Text | Google Scholar
- [69] Portillo A, Palomar AM, Santibanez P, Oteo JA. Epidemiological aspects of crimean-congo hemorrhagic fever in Western Europe: what about the future? *Microorganisms.* [2021] 9:649. doi: 10.3390/microorganisms9030649 PubMed Abstract | CrossRef Full Text | Google Scholar
- [70] Negrodo A, de la Calle-Prieto F, Palencia-Herrejón E, Mora-Rillo M, Astray-Mochales J, Sánchez-Seco MP, et al. Autochthonous Crimean–Congo hemorrhagic fever in Spain. *N Engl J Med.* [2017] 377:154–61. doi: 10.1056/NEJMoa1615162 PubMed Abstract | CrossRef Full Text | Google Scholar
- [71] Bente DA, Forrester NL, Watts DM, McAuley AJ, Whitehouse CA, Bray M. Crimean-Congo hemorrhagic fever: history, epidemiology, pathogenesis, clinical syndrome and genetic diversity. *Antiviral Res.* [2013] 100:159–89. doi: 10.1016/j.antiviral.2013.07.006 PubMed Abstract | CrossRef Full Text | Google Scholar
- [72] Ince Y, Yasa C, Metin M, Sonmez M, Meram E, Benkli B, et al. Crimean-Congo hemorrhagic fever infections reported by ProMED. *Int J Infect Dis.* [2014] 26:44–6. doi: 10.1016/j.ijid.2014.04.005 PubMed Abstract | CrossRef Full Text | Google Scholar
- [73] McMinn PC. The molecular basis of virulence of the encephalitogenic flaviviruses. *J Gen Virol.* [1997] 78:2711–22. doi: 10.1099/0022-1317-78-11-2711 PubMed Abstract | CrossRef Full Text | Google Scholar
- [74] Griffiths MJ, Turtle L, Solomon T. Chapter 26-Japanese encephalitis virus infection. *Handb Clin Neurol.* [2014] 123:561–76. doi: 10.1016/B978-0-444-53488-0.00026-2 PubMed Abstract | CrossRef Full Text | Google Scholar
- [75] Zhang H, Luo H, Rehman MU, Nabi F, Li K, Lan Y, et al. Evidence of JEV in *Culex tritaeniorhynchus* and pigs from high altitude regions of Tibet, China. *J Vector Borne Dis.* [2017] 54:69–73. PubMed Abstract | Google Scholar
- [76] Steere AC. Lyme disease. *N Engl J Med.* [2001] 345:115–25. doi: 10.1056/NEJM200107123450207 PubMed Abstract | CrossRef Full Text | Google Scholar
- [77] CDC. Centers for Disease Control and Prevention. 2019. Lyme Disease Data Tables: Historical Data. [2019]. Available online at: www.cdc.gov/lyme/stats/tables.html [accessed January 2021].
- [78] Hofhuis A, Harms M, van den Wijngaard C, Sprong H, van Pelt W. Continuing increase of tick bites and Lyme disease between 1994 and 2009. *Ticks Tick Borne Dis.* [2015] 6:69–74. doi: 10.1016/j.ttbdis.2014.09.006 PubMed Abstract | CrossRef Full Text | Google Scholar
- [79] Steere AC, Coburn J, Glickstein L. The emergence of Lyme disease. *J Clin Invest.* [2004] 113:1093–101. doi: 10.1172/JCI21681 PubMed Abstract | CrossRef Full Text | Google Scholar
- [80] Beard CB, Eisen RJ, Barker CM, Garofalo JF, Hahn MM, Hayden AJ, et al. Chapter 5: vector-borne diseases. In: *The Impacts of Climate Change on Human Health in the United States: A Scientific Assessment*. Washington, DC: U.S. Global Change Research Program [2016]. Available online at: <https://health2016.globalchange.gov> Google Scholar
- [81] Daubney R, Hudson JR, Garnham PC. Enzootic hepatitis or rift valley fever. An undescribed virus disease of sheep, cattle and man from east africa. *J Pathol Bacteriol.* [1931] 34:545–79. doi: 10.1002/path.1700340418 CrossRef Full Text | Google Scholar
- [82] Rolin AI, Berrang-Ford L, Kulkarni MA. The risk of Rift Valley fever virus introduction and establishment in the United States and European Union. *Emerg Microbes Infect.* [2013] 2:e81. doi: 10.1038/emi.2013.81 PubMed Abstract | CrossRef Full Text | Google Scholar

- [83] Nanyingi MO, Munyua P, Kiama SG, Muchemi GM, Thumbi SM, Bitek AO, et al. A systematic review of Rift Valley Fever epidemiology 1931-2014. *Infect Ecol Epidemiol*. [2015] 5:28024. doi: 10.3402/iee.v5.28024 PubMed Abstract | CrossRef Full Text | Google Scholar
- [84] Calasans TAS, Souza GTR, Melo CM, Madi RR, Jeraldo VLS. Socioenvironmental factors associated with *Schistosoma mansoni* infection and intermediate hosts in an urban area of northeastern Brazil. *PLoS ONE*. [2018] 13:e0195519. doi: 10.1371/journal.pone.0195519 PubMed Abstract | CrossRef Full Text | Google Scholar
- [85] Hotez PJ. Southern Europe's coming plagues: vector-borne neglected tropical diseases. *PLoS Negl Trop Dis*. [2016] 10:e0004243. doi: 10.1371/journal.pntd.0004243 PubMed Abstract | CrossRef Full Text | Google Scholar
- [86] Mwakitalu ME, Malecela MN, Mosha FW, Simonsen PE. Urban schistosomiasis and soil transmitted helminthiasis in young school children in Dar es Salaam and Tanga, Tanzania, after a decade of anthelmintic intervention. *Acta Trop*. [2014] 133:35–41. doi: 10.1016/j.actatropica.2014.01.012 PubMed Abstract | CrossRef Full Text | Google Scholar
- [87] Klohe K, Koudou BG, Fenwick A, Fleming F, Garba A, Gouvras A, et al. A systematic literature review of schistosomiasis in urban and peri-urban settings. *PLoS Negl Trop Dis*. [2021] 15:e0008995. doi: 10.1371/journal.pntd.0008995 PubMed Abstract | CrossRef Full Text | Google Scholar
- [88] Smithburn K, Hughes T, Burke A. A neurotropic virus isolated from the blood of a native of Uganda. *Am J Trop Med*. [1940] 20:471–92. doi: 10.4269/ajtmh.1940.s1-20.471 CrossRef Full Text | Google Scholar
- [89] Murgue B, Murri S, Triki H, Deubel V, Zeller HG. West Nile in the Mediterranean basin: 1950-2000. *Ann N Y Acad Sci*. [2001] 951:117–26. doi: 10.1111/j.1749-6632.2001.tb02690.x PubMed Abstract | CrossRef Full Text | Google Scholar
- [90] Ronca SE, Murray KO, Nolan MS. Cumulative incidence of West Nile virus infection, continental United States, 1999–2016. *Emerg Infect Dis*. [2019] 25:325. doi: 10.3201/eid2502.180765 PubMed Abstract | CrossRef Full Text | Google Scholar
- [91] CDC. 8 Zoonotic Diseases Shared Between Animals and People of Most Concern in the U.S. Available online at: www.cdc.gov/media/releases/2019/s0506-zoonotic-diseases-shared.html [accessed May 6, 2019].
- [92] Mackenzie JS, Gubler DJ, Petersen LR. Emerging flaviviruses: the spread and resurgence of Japanese encephalitis, West Nile and dengue viruses. *Nat Med*. [2004] 10:S98–109. doi: 10.1038/nm1144 PubMed Abstract | CrossRef Full Text | Google Scholar
- [93] Carter HR. *Yellow Fever: An Epidemiological and Historical Study of Its Place of Origin*. Baltimore, MD: Williams & Wilkins [1931]. Google Scholar
- [94] Gershman MD, Staples JE. Chapter 3: Yellow Book. In: *Infectious Diseases Related to Travel: Yellow Fever* [2014]. Available online at: <http://wwwnc.cdc.gov/travel/yellowbook/2014/chapter-3-infectious-diseases-related-to-travel/yellow-fever> [accessed March 12, 2021].
- [95] WHO. Emergencies: Yellow Fever Situation Report. [2017]. Available online at: <http://www.who.int/emergencies/yellow-fever/situation-reports/2-june-2016/en/> [accessed April, 2021]. Google Scholar
- [96] Chen LH, Wilson ME. Yellow fever control: current epidemiology and vaccination strategies. *Trop Dis Travel Med Vaccines*. [2020] 6:1. doi: 10.1186/s40794-020-0101-0 PubMed Abstract | CrossRef Full Text | Google Scholar
- [97] WHO. Vaccines and vaccination against yellow fever. WHO position paper – June 2013. *Wkly Epidemiol Rec*. [2013] 88:269–83. Google Scholar
- [98] Simpson DI. Zika virus infection in man. *Trans R Soc Trop Med Hyg*. [1964] 58:335–8. doi: 10.1016/0035-9203(64)90201-9 CrossRef Full Text | Google Scholar
- [99] Belluck P, Alvarez L. Zika Cases in Florida Were Likely Spread by Local Mosquitoes, CDC Says. *The New York Times* [2016].
- [100] Duffy MR, Chen TH, Hancock WT, Powers AM, Kool JL, Lanciotti RS, et al. Zika virus outbreak on Yap Island, Federated States of Micronesia. *N Engl J Med*. [2009] 360:2536–43. doi: 10.1056/NEJMoa0805715 PubMed Abstract | CrossRef Full Text | Google Scholar
- [101] Roth A, Mercier A, Lepers C, Hoy D, Duituturaga S, Benyon E, et al. Concurrent outbreaks of dengue, chikungunya and Zika virus infections - an unprecedented epidemic wave of mosquito-borne viruses in the Pacific 2012-

2014. *Euro Surveill.* [2014] 19:1–8. doi: 10.2807/1560-7917.ES2014.19.41.20929 PubMed Abstract | CrossRef Full Text
- [102] Dupont-Rouzeyrol M, O'Connor O, Calvez E, Daures M, John M, Grangeon JP, et al. Co-infection with Zika and dengue viruses in 2 patients, New Caledonia, 2014. *Emerg Infect Dis.* [2015] 21:381–2. doi: 10.3201/eid2102.141553 PubMed Abstract | CrossRef Full Text | Google Scholar
- [103] Fauci AS, Morens DM. Zika virus in the Americas yet another arbovirus threat. *N Engl J Med.* [2016] 374:601–4. doi: 10.1056/NEJMp1600297 PubMed Abstract | CrossRef Full Text | Google Scholar
- [104] Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, et al. Global trends in emerging infectious diseases. *Nature.* [2008] 451:990–3. doi: 10.1038/nature06536 PubMed Abstract | CrossRef Full Text | Google Scholar
- [105] Weaver SC, Reisen WK. Present and future arboviral threats. *Antiviral Res.* [2010] 85:328–45. doi: 10.1016/j.antiviral.2009.10.008 PubMed Abstract | CrossRef Full Text | Google Scholar
- [106] Ryan SJ, Carlson CJ, Mordecai EA, Johnson LR. Global expansion and redistribution of aedes-borne virus transmission risk with climate change. *PloS Negl Trop Dis.* [2019] 13:e0007213. doi: 10.1371/journal.pntd.0007213 PubMed Abstract | CrossRef Full Text | Google Scholar
- [107] WHO. Vector-Borne Diseases. [2020]. Available online at: www.who.int/news-room/fact-sheets/detail/vector-borne-diseases [accessed May 2021]. Google Scholar
- [108] Rabaan AA, Al-Ahmed SH, Sah R, Al-Tawfiq JA, Haque S, Harapan H, et al. Genomic epidemiology and recent update on nucleic acid-based diagnostics for COVID-19. *Curr Trop Med Rep.* [2020] 7:113–9. doi: 10.1007/s40475-020-00212-3 PubMed Abstract | CrossRef Full Text | Google Scholar
- [109] Lozano R, Naghavi M, Foreman K, Lim S, Shibuya K, Aboyans V, et al. Global and regional mortality from 235 causes of death for 20 age groups in 1990 and 2010: a systematic analysis for the Global Burden of Disease Study 2010. *Lancet.* [2012] 380:2095–128. doi: 10.1016/S0140-6736(12)61728-0 PubMed Abstract | CrossRef Full Text | Google Scholar
- [110] Ranson H, N'guessan R, Lines J, Moiroux N, Nkuni Z, Corbel V. Pyrethroid resistance in African anopheline mosquitoes: what are the implications for malaria control? *Trends Parasitol.* [2011] 27:91–8. doi: 10.1016/j.pt.2010.08.004 PubMed Abstract | CrossRef Full Text | Google Scholar
- [111] Wilson AL, Courtenay O, Kelly-Hope LA, Scott TW, Takken W, Torr SJ, et al. The importance of vector control for the control and elimination of vector-borne diseases. *PLoS Negl Trop Dis.* [2020] 14:e0007831. doi: 10.1371/journal.pntd.0007831 PubMed Abstract | CrossRef Full Text | Google Scholar