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Correspondence

Chikungunya, zika, and dengue: Three neglected re-emerging Aedes-borne diseases

Dear Editor;

Vector-borne and zoonotic infections (VBZI) should be considered a serious biological threat to humans that can affect global travel. Vectorborne diseases originate from non-human vertebrates, especially livestock, as well as wildlife animals that can be transmitted to humans. There are approximately 2.5 billion cases as well as 2.7 million deaths from zoonotic diseases worldwide, not including economic losses [1]. Although emerging vector-borne diseases mainly affect developing countries, these infectious agents do not spare richer regions due to travel, migration, and climate change, as well as other multiple implicated factors. However, it is obvious that the diversity of geographical differences as well as economic status mainly influence the distribution of zoonotic and vector-borne emerging tropical infectious diseases in the world [2]. Rapid control as well as global elimination of these diseases requires measures such as evidence-based surveillance, veterinary medicine, herd immunization, and other countermeasures.

According to the World Health Organization (WHO) in recent years, the growing recognition of Aedes-borne viruses particularly chikungunya virus, zika virus, as well as dengue virus has become a global concern across the world, especially in West Africa [3]. Unfortunately, due to lack of vector-borne disease surveillance, there is no a comprehensive knowledge about the arboviral diseases, accordingly these are lurking behind the malaria. Underestimation of arboviral diseases may lead to misdiagnosis as well as unnecessary health care expenditures, especially in febrile illnesses suspicious to malaria. Thus, there is an urgent need to better understanding about the epidemiology of arboviral transmission using implementation some strategies such as nationwide surveillance system, detection of relevant vectors, and also recognition of high transmission risk areas to establish travel ban rules.

Developing countries are more affected by emerging arboviral diseases for reasons including high poverty, rapid urbanization, vector habitat, climate changes, poorly documented epidemiology of these infectious agents, as well as travels [4]. In addition, the emergence of vector-borne zoonotic diseases can even co-circulate and co-infest a large portion of residents in such regions as Africa [5]. This may obscure medical suspicion, as the clinical manifestations and symptoms of many of these pathogens may overlap; as expected, coinfection between arboviral pathogens e.g. dengue virus and SARS-CoV-2 variants is also now increasingly reported, exacerbating the current situation [6,7].

Zika virus (ZIKV) is an arthropod-associated virus that has been sporadically identified from infested mosquitoes and humans in sub-Saharan Africa and Southeast Asia over the past 60 years [8]. Nevertheless, ZIKV outbreaks were reported from Micronesia and Latin America in short-span [9]. ZIKV infection may be easily misdiagnosed with dengue fever, Japanese encephalitis, as well as other arthropod-borne diseases in the absence of exclusive serological assays [10]. However, the increase in Guillain–Barré syndrome (GBS) and microcephaly is strong evidence for the emergence of ZIKV in new areas. Since the virus has spread around the world, healthcare authorities need to launch national boundaries, medical disciplines, as well as wide-spread awareness of the clinical manifestations of ZIKV and the *Aedes aegypti* mosquito.

Dengue virus is considered as another Aedes-borne disease, and several outbreaks of this infectious disease have been reported from South Asia and Latin America [11]. According to the literature, dengue virus has so far affected nearly 390 million people across the world [12]. Tropical countries with high population density, unplanned urbanization, as well as humid climates experience more severe outbreaks. During monsoon season, the re-emergence of dengue is associated with over-burdened health care systems, particularly in developing countries, where there is a vulnerable healthcare system with high population density [13]. Furthermore, chronological congruence of the monsoon season with the SARS-CoV-2 Omicron variant wave leads to catastrophe in healthcare facilities in tropical as well as subtropical regions. We hypothesize that coinfection could mask this suspicion due to the similarity in laboratory features and symptoms between dengue fever and COVID-19 [14].

Chikungunya virus (CHIKV) is an arthropod-borne virus transmitted to susceptible individuals by *Aedes aegypti* and *Ae. Albopictus* mosquitoes. The first Chikungunya outbreak was reported from Tanzania in 1952 [15]. Further sporadic outbreak was detected from Africa and Asia in 1950s–1960s; subsequently, there was a global distribution of CHIKV in 2000s [9,16]. According to the literature, there are four different genotypes of CHIKV: Asian, West African, East/Central/South African (ECSA), and Indian Ocean Lineage (IOL) [17]. Harapan et al. recently revealed the globalization of Chikungunya due to the spread of the ECSA sub-lineage worldwide [18].

Approximately 3.9 billion people from 120 different territories appear to be at risk from these three major arboviruses [19]. Buchwald et al. suggested that the epidemiology of arboviral disease has shifted; widespread *Ae. Albopictus* mosquito to human transmission plays an important role in the re-emergence of arthropod-related outbreak in non-endemic regions [20]. In the current situation, it is necessary to monitor and control the arbovirus diseases. There are several gaps in vector surveillance, identification of Aedes-borne viruses, and distribution of Aedes vectors. Understanding the epidemiologic changes as well as the ecology of Aedes-vector sheds light on a new approach for predicting further outbreaks of Aedes-borne diseases in non-endemic areas.

Finally, there is an enlightening shift in the epidemiology of Aedesborne diseases. In general, new outbreaks have occurred in urban areas and compared to previous observational studies, we are experiencing an increase in seroprevalence. *Ae. aegypti and Ae. Albopictus* play a critical role in the exacerbation of arboviral-related outbreaks. Rapid urbanization, climate change, and suitable habitat for arbovirus vectors

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all seem to have combined effects in the globalization of Aedes-borne disease in non-tropical regions. Vector surveillance is likely to reflect the risk of arboviral disease and evaluate effective control strategies to rapidly combat Aedes-borne diseases.

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