



LETTER TO THE EDITOR

Dual challenges – the growing burden of dengue and its associated co-infections

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Dear Editor,

Dengue is a viral mosquito-borne infection that is transmitted to humans by *Aedes* mosquitoes; *Aedes aegypti* and *Aedes albopictus*, in tropical and sub-tropical areas.¹ It causes a range of nonsevere to severe clinical manifestations.¹ Around 96 million dengue infections are recorded annually with 21,000 deaths worldwide.² The four serotypes of dengue virus (DEN1-4) can cause the disease with 25% to 40% heterogeneity.³ Infection with one serotype provides lifelong immunity against that specific serotype, but subsequent infection by another serotype often creates fatal outcomes if untreated.³

The number of Dengue cases are significantly increasing.⁴ Between 2000 and 2019, the World Health Organization (WHO) reported a ten-fold increase in dengue infection rate from 500,000 to 5.2 million cases worldwide.⁴ The rate elevated to over 7.6 million cases with 3000 deaths by the end of April 2024 which has already exceeded the 4.6 million cases reported in 2023.⁵ The disease is now endemic in more than 100 countries in the WHO regions of Africa, the Americas, the Eastern Mediterranean, South-East Asia and the Western Pacific.⁵ This increase can be caused by globalization and increased international travel that facilitate the virus spread from dengue endemic regions to previously unaffected areas as well as the crucial role of climate change in elevating the disease cases.^{4,5} Dengue season is found to start 1–2 months earlier due to warmer tem-

peratures, extending the mosquito breeding season and thus making the peak dengue season last longer.⁵

Furthermore, in some endemic regions, dengue co-infection has been reported, making the scenario even worse and complicating patient management.⁵ This problem can be illustrated by the significant overlap in geographic regions of dengue, Zika virus, and chikungunya shown in (Fig. 1). Notably, the areas marked brown and blue on the map represent regions that are particularly burdened by cocirculation of two or more of the viruses, highlighting the increased risk of co-infection. Furthermore, the areas indicating transmission of a single virus for now remain susceptible for possible future co-infection due to the mobility of populations and the adaptability of the *Aedes* mosquito vector. This simultaneous occurrence of dengue co-infections can result in worsening of the symptoms, increasing the severity of the disease and mortality rate.

Additionally, the presence of these simultaneous infections can complicate the diagnosis and treatment course.⁵ Due to similar initial symptoms, misdiagnoses and misreporting as monoinfection are possible in the absence of differential laboratory testing.⁶ For example, a study in Brazil found that 84.4% of the 828,654 suspected arbovirus cases were initially classified as ‘suspected dengue’, while only 15.6% were considered ‘suspected chikungunya’. However, laboratory confirmed cases showed the actual proportions were 65.9% chikungunya and only 34.1% dengue.⁶

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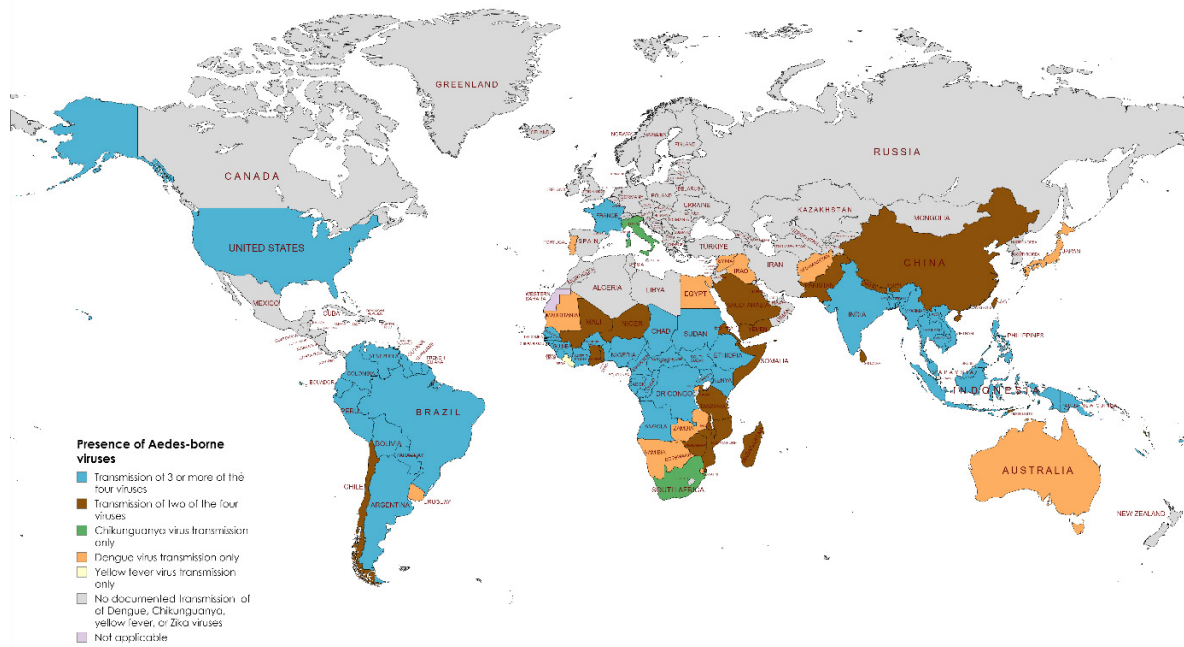


Fig. 1. Countries, territories or areas with previous or current local mosquito-borne transmission of more than one *Aedes*-borne virus (dengue, chikungunya and Zika) as of 30 April 2024

In summary, the increasing trend of dengue infection coupled with increasing cases of its co-infections requires urgent global action. Future studies should focus on addressing preventive strategies and implementing early detection techniques to reduce the risk of dengue and other outbreaks in areas that are currently unaffected. Enhanced surveillance, continued research to find vaccines, early detection of co-infection cases, and integrated clinical management protocols are required to reduce the impact on affected patients and the additional burden on healthcare resources.

Declarations

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Author contributions

Conceptualization, D.K.S.; Data Curation, F.R.K.; Writing – Original Draft Preparation, F.R.K.; Writing – Review & Editing, D.K.S.

Conflicts of interest

All authors declare that they have no conflicts of interest.

Data availability

All data used in this study are publicly available and are obtained from openly accessible websites such as the World Health Organization with the specific sources referenced in the manuscript.

Ethics approval

The study used publicly available data from World Health Organization and no direct human or animal data were used. As the data are openly accessible, no ethical approval was required for the study.

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