



## Incidence of Dengue and Diversity of Dengue Virus

Dylan Xiaoge \*

Department of Pathology, Central South University, Changsha, Hunan, China

### DESCRIPTION

Dengue is a mosquito vector borne viral disease caused by Dengue Virus (DENV) belonging to the family Flaviviridae. It has been estimated that half of the world's population is at the risk of dengue with the most vulnerable zone being the tropical and subtropical regions. Global increase in dengue cases and its geographical expansions to new countries and from urban to rural settings has become a major public health concern drawing serious attention around the world. The epidemics of dengue have been widely reported from Southeast Asia, the Americas, the western Pacific, Africa and Mediterranean regions with the Indian subcontinents considered hyper-endemic to circulation of all the four serotypes of dengue virus (DENV-1 to 4). A unique feature of dengue virus infection is that, primary infection caused by any one of the four serotypes of dengue virus results in mild dengue fever and confers lifelong immunity believed to be protective against re-infection with the same serotype, but secondary DENV infection by a different (heterotypic) serotype may develop a more severe disease weakening immunity to a previous serotype and a factor known to be mediated by Antibody-Dependent Enhancement (ADE) of infection. DENV is transmitted to human by the bite of *Aedes* mosquito. The mosquito acquire virus from infected human, which replicates in the mid-gut of mosquito and reach the salivary gland within 10-14 days post-blood meal. DENV infection in salivary gland regulates the genes that modulate virus replication as well as affect feeding behaviour of mosquito. The infected mosquito then transfer virus to the human host it bites spreading the disease. Although it is mainly transmitted by the primary vector *Aedes aegypti*, the secondary vector *Aedes albopictus* has also been implicated to the transmission of the virus. *Ae. aegypti* are spatially distributed in tropical and subtropical regions while *Ae. albopictus* are known to persist in temperate regions owing to long diapause periods of eggs of the latter in colder environment. An augment in incidence of vector borne diseases such as dengue is linked to the climate change as an outcome of global warming. Temperature, rainfall and humidity are critical to mosquito survival, reproduction and development influencing mosquito existence and abundance. Warmer temperature facilitates development of mosquito and viral replication, while adequate rainfall and humidity influence habitat

availability and survival of vector resulting in their increased population. *Ae. aegypti* reproduces rapidly and bites more frequently at higher temperatures, thus transmission of the dengue virus has been assumed to be influenced by climate change induced rise in temperature. Besides, the multiplication of virus was also found to be stimulated by the rise in temperature since viral replication accelerated when temperature increased from 30°C to 35°C. Climate change has been believed to have contributed to the global spread and persistence of dengue. Rise in temperature by 2°C would simultaneously lengthen lifespan of the mosquito and shorten the incubation period of dengue virus, resulting in more infected mosquitoes for a longer period of time. Thus, rise in global temperatures must have an impact on vector-borne disease. Increased humidity as a result of high rainfall and high temperature is a significant predictor of dengue fever risk. High temperature and high rainfall facilitate in increased humidity which together makes the environment conducive to breeding and survival of vector populations, and rapid replication of the virus.

### CONCLUSION

Several studies have shown that temperature and rainfall have huge impact on dengue incidence. In the year that witnessed highest rainfall, largest proportion of positive cases for dengue was recorded in the post-monsoon period and in some countries it has been a favourable period of mosquito breeding. *Aedes* larvae are abundant in rainy season since rainfall generates vector-breeding sites but heavy rainfall can have adverse effect and reduce the vector density. The analysis of temperature in Nepal has revealed that the maximum temperature has increased by 1.80°C from 1975 to 2006 and the trend of warming is seen at higher rate in mountain. Besides climatic factors, population growth, urbanization and increased rate of long distance travel are augmenting the risk of dengue epidemics as well. The shifts in climate temperatures and globalization can instigate the expansion of vector habitats and prolongation of the transmission season, which in turn contributes to the global spread of DENV. Relating climate variables with vector population and cases of dengue will help predict an outbreak which will aid in taking preventive measures in vulnerable region and increase awareness of the public. Besides, there has been a

**Correspondence to:** Dylan Xiaoge, Department of Pathology, Central South University, Changsha, Hunan, China, E-mail: dylanx@gmail.cn

**Received:** 25-Jun-2022, Manuscript No. JTD-22-17558; **Editor assigned:** 28-Jun-2022, PreQC No. JTD-22-17558(PQ); **Reviewed:** 12-Jul-2022, QC No. JTD-22-17558; **Revised:** 19-Jul-2022, Manuscript No. JTD-22-17558 (R); **Published:** 26-Jul-2022, DOI:10.35241/2329-891X.22.10.337.

**Citation:** Xiaoge D (2022) Incidence of Dengue and Diversity of Dengue Virus. J Trop Dis. 10:337.

**Copyright:** © 2022 Xiaoge D. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

been a shift in the serotype dominating during the outbreak. However, with increase in international travel to dengue endemic countries within Asian region, there is possibility of acquiring genotypically variant strains of virus. Thus, it is essential to study genetic makeup of DENV since genetically

diverse population of this RNA virus is likely to be developed due to rapid evolution resulting from error prone viral encoded RNA-dependent RNA polymerase induced high mutation rate. Genetic diversity have been claimed to increase fitness, thereby facilitating in virus transmission.