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A Systematic Review on *Aedes aegypti* Vector Borne Diseases and its Control Measures

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Abstract: *Aedes aegypti* is the principal transmitter of the four most influential viruses in human health, which include yellow fever viruses, dengue fever, Chikungunya and Zika. Since this insect can easily rear-in-lab and such viruses are growing in tissue-growing cells in labs, many research have been conducted to investigate the relative competence of different mosquito populations for the transmission of many distinct viral strains. A reduction of *Aedes* spp. populations is the primary method to minimize disease transmission with few vaccinations available and with no effective therapeutic therapy for arboviruses. Host-associated microorganisms have lately become a potential topic for research into new vector control methods that are ecologically benign. For example, Darm microbiota has a prospective target for modification in several areas of *Aedes* spp. biology, including vector competency. The current study focuses on control strategies for *A. aegypti* mosquito that engage in viral infection responses. In the last decades it has been widely known that this mosquito is important as a disease vector and its effect on human health. In order to develop effective control measures, it is important for us to enhance our understanding of molecular mechanisms that determine the result of successful viral replication or control of the infection of each arbovirus in the vector.

Keywords: *Aedes aegypti*, Mosquito control, Transmission, Vectors, Biological control

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Introduction

Mosquitoes transmit a substantial share of arboviruses. In recent years, the relevant illnesses have risen and steadily expanded to places not afflicted by Baldacchino *et al.* (2015). Climate change, globalisation, lack of efficient vector management, pesticide resistance, and the

migration of vector populations to the new geographic areas are among the reasons that have contributed to the development of such diseases (Cebrián-Camisón *et al.*, 2020). More than 500 arboviruses, of which about 100 cause human illnesses have been classified (Hustedt *et al.*,

2020).

In the spread and transmission of numerous infectious illnesses including Dengue Fever, Chikungunya, Yellow Fever, and more recently Zika (Hustedt *et al.*, 2020), *Ae. aegypti* is the main culprit. Among them, because of their broad worldwide impact and the accompanying implications of economic losses in public health systems, Dengue Fever was the world's largest mosquito-borne illness (Reinhold *et al.*, 2018). Dengue Fever is the leading disease in the globe. India, together with nearly all nations across equator lines with tropical/subtropical environments, is listed on the current risk map of the WHO for Dengue Fever (Hustedt *et al.*, 2020).

Ae. aegypti has quickly developed in recent decades as exceptionally adaptable species to human settings because to its variable feeding and breeding habitats (Medlock *et al.*, 2015). In comparison to other *Aedes*, *Ae. albopictus*, *Ae. aegypti*'s synanthropic behaviour is very close in humans which leads to much more spreading (Weetman *et al.*, 2018) transmitted by *Ae. aegypti* illnesses. The most sensible manner of managed transmitted illnesses is to reduce *Ae. aegypti* populations and to minimize contacts with people since total eradication of appropriate vectors and/or viruses is unachievable approaches to controls (Slosek, 1986). In addition, adequate vaccines and treatments are still being developed for most human illnesses caused by arboviruses.

The capacity to transmit these four viruses in geographically different *Ae. aegypti* populations has been reported (Takken, 1991). In laboratories and viral strains that are employed to discover underlying patterns, we are striving with the heterogeneity issue. The topic remains unclear how differs between groups the genetic variety which influences phenotypes, such as vector ability. Nevertheless, it is more plausible that *Ae. aegypti* populations are genetically different, compared to genetically homogeneous species, varying in the vector competence (Scolari *et al.*, 2019). The contribution of bacteria in vector competence is also taken into account. Microbiota

is a typical component of vector physiology and it is established that these microorganisms might influence the reactions of mosquitoes to viral infections. Details of the relationships between genetically diverse mosquito populations and how these interactions change remain unclear (Alphey *et al.*, 2013).

Reviews of the literature on *Ae. aegypti* infections, dissemination, and transmission rates of arboviruses have been conducted despite the lack of vector competency testing and the emphasis on mosquito sampling in locations where arboviral infections occur or where there are considerable infections. Martinet *et al.* (2019) studied *Ae. aegypti* and Zika populations, however, total susceptibility to yellow fever tested population was not observed.

The initial dosage of viral infection is strongly correlated to the rate of infection (Sallam *et al.*, 2017). Brazilian *Ae. aegypti* populations are very vulnerable to Dengue. *Ae. aegypti* mosquitoes from the American continent have been proven to be more infective than the ZIKV Asian lineage in Africa. The adaptation of viruses to various mosquito species is still disputed. In 2005, the A226V Amino-Acid Replacement in the E1 envelope Glycoprotein of the Chikungunya was introduced in La Reunion and promoted in the *Aedes albopictus* mosquitoes (Medlock *et al.*, 2012). This is the best known example of vector-based arbovirus adaptation. On co-infections with several viruses or serotypes/genotypes of a single virus species only little data are available. Certain trials with co-infections imply competitive removal of Dengue or interference from superinfection. Other research suggest that one arbovirus of *Ae. aegypti* infection only has a minor effect on another infection (Ferreira-de-Lima and Lima-Camara, 2018).

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