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Effect of *Wolbachia* on Dengue infection in Endemic districts of Odisha

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Abstract

Dengue is the most important arboviral disease posing considerable threat to human and animal health in tropical and subtropical countries. The causative agent for dengue viruses (DENV) are primarily the infectious female *Aedes aegypti* mosquitoes and to a lesser extent its sister taxon infectious female *Aedes albopictus* mosquitoes. Persistent DENV infections play a role in the cycling pattern of dengue outbreaks. Due to lack of proper treatment, strategies for blocking pathogen transmission by mosquito vectors have been proposed as a means of augmenting current control measures to reduce the growing burden of vector-borne diseases. In this scenario, the use of *Wolbachia* has been proposed to reduce dengue transmission. *Wolbachia*, a gram negative endosymbiont bacterium is naturally present in over 20% of all insects including *Aedes albopictus* mosquito. In our study, polymerase chain reaction (PCR) was used to determine the presence of *Wolbachia* from field collected *Ae. albopictus* from various parts of the Odisha using *wsp* primers. *Ae. albopictus* had *Wolbachia* infection ranging from 65 to 100%. Field collected *Wolbachia* infected mosquitoes were challenged with DENV infection. At seven days following infected blood-feeding, an increase in *Wolbachia* densities was displayed to a greater extent compared to control mosquitoes. Our result indicates that virus-blocking is likely to persist in *Wolbachia*-infected mosquitoes suggesting that *Wolbachia* may serve as a successful biocontrol strategy for reducing dengue transmission in the field.

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