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Comparative Vector Susceptibility for Dengue Virus and Their Co-Infection in A. aegypti and A. albopictus

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Abstract : Dengue is now a globally important arboviral disease. Extensive vector surveillance has already established A.aegypti as a primary vector, but A.albopictus is now accelerating the situation through gradual adaptation to human surroundings. Global destabilization and gradual climatic shift with rising in temperature have significantly expanded the geographic range of these species These versatile vectors also host Chikungunya, Zika, and yellow fever virus. Biggest challenge faced by endemic countries now is upsurge in co-infection reported with multiple serotypes and virus co-circulation. To foster vector control interventions and mitigate disease burden, there is surge for knowledge on vector susceptibility and viral tolerance in response to multiple infections. To address our understanding on transmission dynamics and reproductive fitness, both the vectors were exposed to single and dual combinations of all four dengue serotypes by artificial feeding and followed up to third generation. Artificial feeding observed significant difference in feeding rate for both the species where A.albopictus was poor artificial feeder (35-50%) compared to A.aegypti (95-97%) Robust sequential screening of viral antigen in mosquitoes was followed by Dengue NS1 ELISA, RT-PCR and Quantitative PCR. To observe viral dissemination in different mosquito tissues Indirect immunofluorescence assay was performed. Result showed that both the vectors were infected initially with all dengue(1-4)serotypes and its co-infection (D1 and D2, D1 and D3, D1 and D4, D2 and D4) combinations. In case of DENV-2 there was significant difference in the peak titer observed at 16th day post infection. But when exposed to dual infections A.aegypti supported all combinations of virus where A.albopictus only continued single infections in successive days. There was a significant negative effect on the fecundity and fertility of both the vectors compared to control (PANOVA < 0.001). In case of dengue 2 infected mosquito, fecundity in parent generation was significantly higher (PBonferroni < 0.001) for A.albopicus compare to A.aegypti but there was a complete loss of fecundity from second to third generation for A.albopictus. It was observed that A.aegypti becomes infected with multiple serotypes frequently even at low viral titres compared to A.albopictus. Possible reason for this could be the presence of wolbachia infection in A.albopictus or mosquito innate immune response, small RNA interference etc. Based on the observations it could be anticipated that transovarial transmission may not be an important phenomenon for clinical disease outcome, due to the absence of viral positivity by third generation. Also, Dengue NS1 ELISA can be used for preliminary viral detection in mosquitoes as more than 90% of the samples were found positive compared to RT-PCR and viral load estimation.

Keywords : co-infection, dengue, reproductive fitness, viral quantification
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