Molecular Insights Into Dengue Epidemics And Live Attenuated Vaccine Development

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Abstract
Dengue virus (DENV) is a positive-stranded RNA virus that causes frequent and recurrent epidemics throughout the tropical world. Multiple factors contribute to dengue epidemics. Epidemiological observations have identified the association between the emergence of novel DENV genotypes with epidemic dengue transmission. However, the mechanism by which differences in viral genome sequence result in competitive exclusion or virus survival for epidemic transmission, is unknown. We have been examining one such outbreak in Puerto Rico where the emergence of a new DENV-2 strain coincided with the epidemic of 1994. Our findings suggest a unique way in which viral RNA interacts with host proteins to modulate the host antiviral response during acute infection. Intriguingly, similar mechanisms may also apply in the development of live attenuated viral strains for use as vaccines.

Selected Publications

