Evolution of dengue viruses on islands

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Abstract

Dengue virus is an emerging infectious mosquito-borne disease that has been expanding worldwide in recent decades. Currently over 3.5 billion people are estimated to be at risk to infection, although a disproportionate number are from low-income tropical populations. Many islands are affected by dengue, either supporting dengue endemically or subject to periodic introductions through traveling humans. *Aedes aegypti* is the primary vector, although *Aedes albopictus* and other relatives are potentially important secondary vectors. Dengue, as a fast-evolving RNA virus, has the ability to adapt rapidly to new ecological opportunities. To understand how dengue viruses evolve in different island systems and identify the major drivers that might lead to endemism, we sequenced viruses for their complete genomes and analyzed evolutionary patterns in a phylogenetic framework. Our findings suggest that higher virus population sizes and resultant genetic diversity are important for dengue establishment and long-term evolving populations. Both endemic and introduced dengue can be associated with severe disease epidemics or outbreaks. These results have major implications for understanding how dengue circulation and its sources through human travel impact diseases on islands.

Keywords: borne, dengue, epidemic, infectious disease, mosquito, vector

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