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Determinants of dengue virus phylodynamics.

Dengue fever (DF) and the more severe dengue haemorrhagic fever (DHF) are mosquito borne viral infections which have seen a major increase in terms of global distribution and total case numbers over the last few decades. There are currently four antigenically distinct and potentially co-circulating dengue virus (DENV) serotypes and each one shows substantial genetic diversity, organised into phylogenetically distinct lineages (genotypes). While there is some evidence for positive selection, the molecular evolution of DENV is supposed to be mostly dominated by purifying selection due to the constraints imposed by its two-host life-cycle. Results from our previous work demonstrated that although small differences in viral fitness can explain the rapid expansion and fixation of novel genotypes, their fate is ultimately determined by the epidemiological landscape in which they arise. Using a stochastic, spatially explicit model we revisit previous conclusions and address the impact of host and vector population structure on DENV molecular evolution and disease epidemiology.