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Understanding Dengue – the need for basic epidemiological research

Dengue disease is caused by dengue virus that includes four serotypes antigenically distinct viruses belonging to the family Flaviviridae. The viruses are transmitted by the prolific urbanized mosquito vector, Aedes aegypti. Dengue has become a major international public health concern and one of the most important arthropod-borne diseases. The majority of symptomatic cases are classified as Dengue fever (DF), an acute viral infection characterized by fever, rash, headache, muscle and joint pain, and nausea. Occasionally, DF progresses to dengue hemorrhagic fever (DHF), a potentially life-threatening illness associated with vascular leakage, haemorrhage, and shock. Escalations in the number of outbreaks and people involved have and the 'population-at-risk' is increasing yearly. More than 3.5 billion people (approximately 55% of world's population) are at risk of dengue infection, including asymptomatic infections, which potentially increase the risk for the individual to develop severe disease following subsequent. It is estimated that every year, there are 70-500 million dengue infections, generating 36 million cases of DF and 2.1 million cases of DHF, with more than 20,000 deaths per year. This prolific increase has been connected to societal changes such as population growth, increasing urbanization generating intense applomeration leading to proliferation of synanthropic species. In addition, it has been suggested that rising temperatures and global climate change may lead to the expansion of the range of major mosquito vectors into new areas, extension of the transmission season in areas with currently circulating dengue virus and increase in the mosquito species' vectorial capacity. Human migration and international travel provide a continued source of virus (and potentially mosquito vectors), feeding the potential for invasion and eventual colonisation.

Despite this rapidly developing public health disaster, our knowledge of dengue epidemiology is rudimentary, with focus primarily on clinical dengue. A significant investment in gathering community-based data is, however, required to understand dengue epidemiology. The incontrovertible fact is that it is impossible to develop appropriate intervention strategies if the epidemiology is not understood. Here I will outline the recent progress in developing the necessary tools, highlight several key unknowns and benefit from the largely theoretical audience to urge increased collaborative efforts between empiricists and theoreticians to prioritise data acquisition.