

Genetics makes Asians, Europeans susceptible to dengue shock syndrome

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Man in boat. Credit: Luisa Pereira, 2017

As globalization and climate change spread tropical diseases around the globe, not all populations are equally susceptible to infection. Gene variants common in people of Asian and European ancestry, for instance, make them more prone than those of African origin to developing severe dengue shock syndrome, according to a new study in *PLOS Neglected Tropical Diseases*.

Dengue fever is endemic to tropical and subtropical regions of East Asia and the Americas, but the dengue viruses have recently spread to North America and Europe. Dengue can lead to a wide spectrum of illness, ranging from classic [dengue fever](#) (DF) to dengue shock syndrome (DSS). Ethnic diversity has long been considered as one of the factors explaining why the severe forms of dengue are more prevalent in Southeast Asia than elsewhere.

In the new work, Luisa Pereira of the Institute for Research and Innovation in Health-University of Porto (i3S), Anavaj Sakuntabhai of Institut Pasteur-

Paris and colleagues studied the genetics of 411 patients admitted with [dengue virus](#) infection to three hospitals in Thailand between 2000 and 2003. 290 healthy individuals admitted to the same hospitals during the time period were used as controls.

The researchers identified two genes related to blood vessel inflammation that confer risk of DSS, and four genes related to drug metabolism that affect risk of DF. Further experiments showed that variations in the genes led to observable changes in cellular dynamics. Moreover, the prevalence of the genetic variations varies based on ancestry.

"The particular genetic risk conferred by these genes indicates that Southeast and Northeast Asians are highly susceptible to both phenotypes, while Africans are best protected against DSS and Europeans best protected against DF but the most susceptible to DSS," the researchers say.

More information: Oliveira M, Lert-itthiporn W, Cavadas B, Fernandes V, Chuansumrit A, Anunção O, et al. (2018) Joint ancestry and association test indicate two distinct pathogenic pathways involved in classical dengue fever and dengue shock syndrome. *PLoS Negl Trop Dis* 12(2): e0006202.

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