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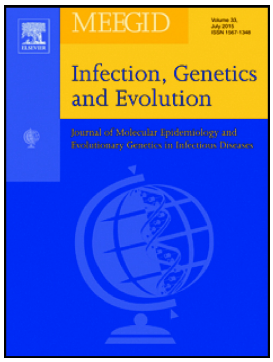

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Host genetics and dengue fever

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Abstract

Dengue is a major worldwide problem in tropical and subtropical areas; it is caused by four different viral serotypes, and it can manifest as asymptomatic, mild, or severe. Many factors interact to determine the severity of the disease, including the genetic profile of the infected patient. However, the mechanisms that lead to severe disease and eventually death have not been determined, and a great challenge is the early identification of patients who are more likely to progress to a worse health condition. Studies performed in regions with cyclic outbreaks such as Cuba, Brazil, and Colombia have demonstrated that African ancestry confers protection against severe dengue. Highlighting the host genetics as an important factor in infectious diseases, a large number of association studies between genetic polymorphisms and dengue outcomes have been published in the last two decades. The most widely used approach involves case-control studies with candidate genes, such as the HLA locus and genes for receptors, cytokines, and other immune mediators. Additionally, a Genome-Wide Association Study (GWAS) identified SNPs associated with African ethnicity that had not previously been identified in case-control studies. Despite the increasing number of publications in America,