

## **Influence of Human Leukocyte Antigens on Altered Immunopathology of Dendue Virus**

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**ABSTRACT** Dengue fever has become one of the most important human viral diseases transmitted by arthropod vector in tropical and subtropical countries of the world. As many as 100 million people are infected yearly resulting in estimated 21,000 deaths. DENV has four antigenically related but genetically distinct serotypes (DENV 1-4). Infection with any of the four serotypes may present as asymptomatic or self limiting mild febrile illness known as dengue fever (DF). However, in some dengue-infected individual, the disease progresses to its severe, life-threatening form, dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS) which may prove fatal without proper early intervention. The pathogenesis of DHF/DSS, however, is not yet completely understood. There are several possible reasons why the primary mild disease progresses to severe form of hemorrhagic manifestations in some individuals. The immune response, Antibody dependent enhancement, virus virulence, and host genetic background are considered risk factors contributing to disease severity. Genetic polymorphisms concerning human leukocyte antigens (HLA) with immunomodulatory effect in dengue infection have been determined in various studies. Human leukocyte antigens (HLA) are highly polymorphic group of genes located on chromosome 6 of human major histocompatibility complex (MHC). HLAs expressed on the cell surface function as antigen presenting molecules and that polymorphism can change individual's immune response. The development of dengue hemorrhagic fever (DHF)/dengue shock syndrome (DSS) has been associated with HLA alleles. Several studies demonstrate the association of various identified versions (alleles) of HLA class I and class II with conferring susceptibility or protection to DHF/DSS. This review discusses recently identified associations of various HLA class I and class II alleles on enhanced or diminished immune response in the course of dengue viral infection, in ethnically and geographically distinct populations.