Correspondence

To the Editors

DPB1 variant rs9277534 frequency and dengue shock syndrome in Indochina: An observation on population genetic and clinical epidemiology association

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Dear Editors,

Dengue is an important tropical arbovirus infection. This infection is highly prevalent in tropical areas, such as Indochina. The affected paediatric patients usually develop an acute febrile illness with a commonly found haematological aberration, haemoconcentration, atypical lymphocytosis and thrombocytopenia. Severe dengue can lead to death and prompt diagnosis and treatment of dengue is necessary.

There are many factors that are related to severity of dengue. The impact of background population genetics on the severity of dengue is interesting. Recently, the genetic variant of human leucocyte antigen-DPB1 was reported for its association with dengue haemorrhagic fever. The authors hereby analysed public data on genomic databases, gnomAD and GenomeAsia 100k, aiming at assessment on allele frequencies of important DPB1 variant rs9277534 in 5 different countries in Indochina (Thailand, Vietnam, Cambodia, Myanmar and Malaysia).

According to the database analysis, the allele frequencies are different in different population (Table 1).

The association with the report on occurrence rate of dengue shock syndrome in local dengue patient is also assessed by correlation analysis. From such an analysis, there is no observed association between DPB1 variant rs9277534 frequency and dengue shock syndrome (p = 0.69). Although rs9277534 is previously mentioned to have a possible relationship with dengue severity, the results in the present study are totally discordant. In fact, dengue shock syndrome, the most serious form of dengue, is also due to the inappropriate fluid replacement therapy.

References

DPB1 variant rs9277534 frequency and dengue shock syndrome. Sri Lanka Journal of Child Health, 2024; 53(2): 186-187


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