Host and viral factors influencing dengue severity and susceptibility

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Abstract

Dengue is a mosquito-borne viral disease that affects millions of people worldwide every year. The pathogenesis of dengue infection is attributed to a complex interaction between the virus and the host immune response. The study was conducted on different endemic dengue populations in varied geographical regions.

Viral RNA was extracted from the serum samples of dengue-positive patients (NS1-IgG/IgM) and analyzed for dengue and other flaviviruses, including Chikungunya and Zika, using a multiplex panel.

In addition, various host immunological biomarkers known to modulate the immune response in viral infections were assessed in the different clinical phenotypes of the patients. Different dengue serotypes were observed in endemic populations, with serotype-specific temporal and spatial distribution in geographic regions. Host immunologic biomarkers are shown to modulated in patients with varying severity.

Introduction

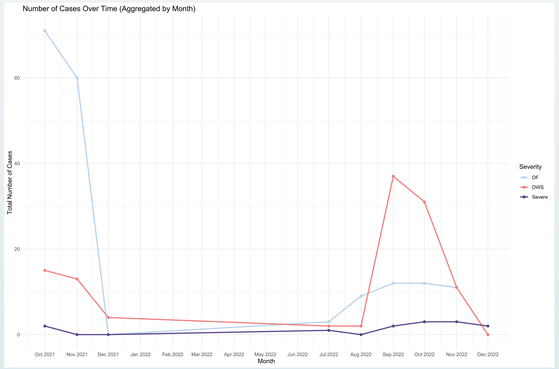
Dengue virus (DENV) is considered a major cause of hemorrhagic fever in tropical countries, including Vietnam. The severity of infection depends on DENV serotypes, patient age, comorbidity, and timing of infection (primary or secondary)[1].

This study aims to examine circulating **DENV serotypes**, spatially and temporally, and analyze host factors associated with viral clearance, **immune modulation**, and further disease complications.

Genetic variants associated with the expression of **inflammatory cytokines** and **chemokines** are being investigated with respect to different disease severities.

Methodology

- Samples are collected from hospitalized patients in central hospital in Hanoi, Vietnam during hemorrhagic fever outbreaks in 2020-2022.

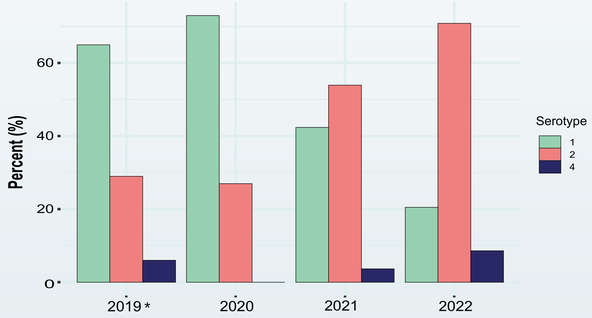


- Viral RNA was extracted from plasma and subjected to dengue serotype differentiation, and to zika and chikungunya screening by RT-PCR.
- Different immunological markers are studied with Bio-Plex Pro Human Cytokine Screening Panel (Bio-Rad).
- DNA from patients' blood was extracted and will be tested for single nucleotide polymorphisms (SNPs) affecting production of cytokines.

Results

- The main cause of haemorrhagic fever during its outbreaks in Hanoi is dengue. Neither zika nor chikungunya were found in tested samples.

Fig. 1 Dengue virus serotypes in Hanoi



** Data for **2019** is collected from previous study* [1]

- The predominant serotype of DENV in Hanoi (central northern Vietnam) is DENV2, followed by DENV1 (Fig.1).
- Significant correlations of various cytokines and chemokines with disease severity and laboratory parameters are observed (Fig.2 and Fig.3).

Fig. 2 Correlation of disease severity and cytokine production

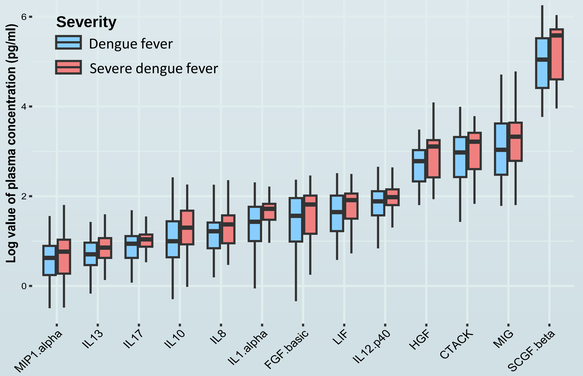
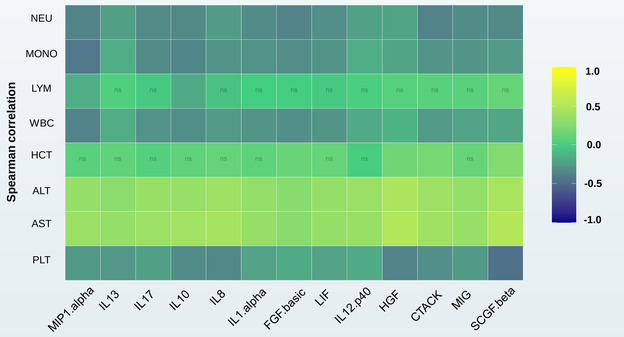


Fig.3: Correlation of laboratory parameters and chemo/cytokines



*Abreviations: **NEU**- Neutrophils; **MONO**- Monocytes; **LYM**-Lymphocytes; **WBC**- White Blood Cells; **HCT**- Hematocrit; **ALT**- Alanine transaminase; **AST**- Aspartate transaminase; **PLT**- Platelets; **ns**- no significant*

Conclusion

- The results show a stable dominance of the two dengue virus serotypes, DENV1 and DENV2 in Hanoi, Vietnam, with DENV2 being the predominant serotype in the last two years. Screening for other arboviruses is important to clarify the possible co-circulation of different viruses during hemorrhagic fever outbreak.
- The study highlights some cytokines and chemokines as potential markers for the severity of dengue infection at the early phase. Human genetic variants (SNPs) could affect the expression of these chemicals and will be further studied.

References

1. Lytton SD, Nematollahi G, van Tong H, et al. Predominant secondary dengue infection among Vietnamese adults mostly without warning signs and severe disease. Int J Infect Dis. 2020;100:316-323.

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