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Quick Response Code:

Authors' response

Sir,

We truly value the authors' interest in our recent publication.

We can chart the issue in three parts: *(i)* selection of serum samples for the study; *(ii)* the inclusion of only NS1 positive samples for serotyping of dengue virus; and *(iii)* the scarcity of clinical and demographical data from the study participants.

Regarding the first two concerns raised, it may be noted that through our study[1], we attempted to explain the issues raised regarding the selection of serum samples and the choice of including only NS1 positive serum samples for molecular serotyping of dengue virus. As for the third issue, although we gathered sufficient demographical data for the study, collecting the clinical data was beyond the scope of our study. Our study mainly shed light on the co-circulating dengue serotypes over five yr in West Bengal with the help of Geographic Information System (GIS) and for ethical purposes it was not possible to obtain clinico-pathological data from the study participants. This was mentioned in the discussion section of the article under the term, 'risk factors', since less associated clinical data was available.

The authors believe that the issues raised need more specificity and validation before they can be evaluated on scientific grounds.

(i) According to the Centers for Disease Control and Prevention (CDC), serum specimens are the most thoroughly validated, highly sensitive and can be used to accurately differentiate between dengue and other febrile illnesses and therefore, are the preferred choice for nucleic acid amplification testing (NAAT)[2]. For primary diagnosis of dengue infection, district and sub-divisional hospitals of West Bengal, rely on NS1 sero-reactivity by patients' serum which is in accordance with CDC. So, we deliberately selected serum specimens to detect the serotypes of dengue virus (DENV) through reverse transcriptase PCR (RT-PCR).

(ii) To address the second issue raised, we would like to point out that our aim for this particular study, was mainly focused on the prevalence of co-circulating serotypes of DENV in West Bengal during 2015-2019 and the utilization of GIS for better portraying of our findings. NS1 antigen is used for the early detection of the virus and the presence of NS1 antigen in the blood serum indicates that the viral RNA or infection has not yet been cleared by host immunity[3], thus providing us with better chances for identifying DENV serotypes. To achieve our goal, the serum samples were collected from individuals with ≤5 days of fever and rechecked for NS1 sero-reactivity as already mentioned in the methods section of the article.

(iii) For the third concern stated regarding the paucity of clinical and demographical data collected from the study participants, we partly agree with the authors. Although we managed to collect sufficient demographic data for this study, we were unable to gather detailed clinical data from all the participants. Since most of the participants were enrolled in this study through Outpatient Department (OPD) for the diagnosis of dengue infection only, they lacked reports on any other clinico-pathological data. The major objective of the study was to determine the co-circulating strains in this region over the years, rather than assessing the clinical association with dengue patients, this was beyond the scope of the study for ethical reasons. We have already mentioned the lack of clinical data, terming it as 'risk factors', as one of the limitations of this study in the discussion section.

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