

RE: Serotype of Dengue Virus Causing Dengue Outbreak in Kathmandu

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Dear Editor,

Dear Editor, the publication on "Effects of Virtual Reality-Based Cognitive Behavioral Therapy on Sick Role Adaptation for Patients With Colorectal Cancer: A Randomised Controlled Trial" is discussed here. This study provides crucial epidemiological and molecular data on dengue in Kathmandu, particularly during the 2019 outbreak. However, it has several methodological limitations. First, patient selection from a single laboratory (National Public Health Laboratory) may lead to selection bias and not reflect the overall population situation. Furthermore, although 579 patients were included, only 93 from the NS1-positive group underwent RT-PCR for serotype identification, potentially susceptible to sampling bias in concluding that DENV-2 is the dominant variant. Additionally, immunochromatographic tests have limitations in sensitivity and specificity, which may affect the accuracy of initial screening. From a reinterpretation perspective, the assertion that DENV-2 is the dominant variant (96.77%) may reflect clonal expansion or variant dominance during the outbreak rather than the long-term overall picture of the national outbreak. Moreover, even small amounts of co-infection (DENV-1 and DENV-3) are epidemiologically significant as they may increase the risk of antibody-dependent enhancement (ADE), which is

associated with disease severity. However, the study did not link serotype data to clinical severity, thus missing the opportunity to explain this clinical relationship. Another issue is the analysis focused solely on viral detection and serotype classification, failing to assess environmental factors or vectors such as *Aedes aegypti* and *Aedes albopictus*, which play crucial roles in dengue transmission. Furthermore, it lacked data on temporal dynamics, such as seasonality or viral evolution, which could better characterize outbreaks. For the future, longitudinal and multicenter studies incorporating viral genomic sequencing analysis are needed to track viral evolution and transmission pathways. Additionally, clinical, environmental, and vector data should be integrated to create more comprehensive epidemic models, including an assessment of the relationship between serotype and disease severity, to support effective dengue control planning in the future.

REFERENCES

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