

Peer Review

Review of: "Molecular Characterization of *Vibrio cholerae* Outbreak Isolates from Western India"

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This study evaluates *V. cholerae* isolates from an outbreak in the Nashik district, Maharashtra, from a cholera outbreak in 2018. Multiple paradigms of phylogenetic analyses were performed based on sequencing PCR products for important markers of El Tor *V. Cholerae* strains, including *ctxB*, *rstA*, *rstB*, and *tcpA*. Analyses of the variants of *ctxB* and *tcpA* genes in the context of currently circulating El Tor strains provide important insights into the molecular epidemiology of sporadic and widespread outbreaks globally. A sharp increase in cholera outbreaks has been reported over the last several years, even in areas where cholera had been previously eliminated; it is critical now more than ever to monitor the genotypes of circulating strains. The focused contributions of this article provide a good example of how targeted sequencing of important toxin genes and virulence markers can inform public health response, especially to highly toxigenic ctx variants of the El Tor lineage.

Declarations

Potential competing interests: No potential competing interests to declare.