

Peer Review

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

Melanie N. Cash¹

1. University of Florida, United States

In my opinion, this manuscript addresses an important topic—molecular characterization of *Vibrio cholerae* outbreak isolates from a tribal population in Western India. This study provides regional data that may be useful for understanding cholera epidemiology. However, in its current form, the manuscript requires significant revisions before it can be considered for publication.

Major Issues

1. *Scope and sample size restriction.* Only five isolates from a single outbreak in one tribal population (2018) were analyzed. This limited sampling significantly restricts the conclusions that can be drawn. Expanding the number of isolates, including multiple time points and locations, would strengthen the study. If this cannot be done, the manuscript should acknowledge this limitation in the discussion.
2. *Antibiotic resistance analysis lacking.* There appears to be no antibiotic resistance data presented. Given the importance of antimicrobial susceptibility in cholera outbreaks, this would link the relevance of this study to public health.
3. *Public health and future directions lacking.* The manuscript would benefit from a stronger discussion on the public health implications of this study and suggestions for future research. Connecting the molecular data to outbreak surveillance strategies would enhance its impact.

Minor Issues

1. *Clarity of molecular methods needed.* The molecular methods are not sufficiently detailed. It is unclear whether whole-genome sequencing (WGS) or a targeted sequencing approach was used,

and the mention of a Bioanalyzer is misleading, as it is not a sequencing platform. The sequencing methods, instruments, and quality control measures should be specified.

2. *Laboratory and bioinformatic pipelines missing.* Laboratory protocols are generally lacking in detail. The bioinformatic analysis and clustering methods are particularly unclear; the pipelines, parameters, and software used to generate the phylogenetic trees should be described in sufficient detail for reproducibility.
3. *Manuscript structure could be revised.* Results and Discussion are currently blended. These should be separated for clarity and better flow.
4. *Data presentation could be clarified.* A summary table comparing the key features of the isolates (serotype, virulence genes, phylogenetic clustering, etc.) would improve clarity for the reader.
5. *Language and grammar need to be revised.* The manuscript contains multiple grammatical and structural issues. Careful editing for English usage and sentence flow is recommended.

Other Suggestions

1. *Clarify what is novel about this study.* Emphasizing its unique contribution (e.g., characterization of outbreak isolates from a tribal region) would help deflect from the weaknesses of small sample size and limited scope.
2. *Make comparisons to what was circulating in 2018.* Compare the data to what was circulating in India in 2018, and briefly link this to *V. cholerae* serotypes/lineages at that time worldwide.

Conclusion

This manuscript addresses an important and timely subject but requires substantial revision. Improvements in methodological clarity, data presentation, contextual analysis, and language will be essential before the work is suitable for publication.

Declarations

Potential competing interests: No potential competing interests to declare.