Reviewer’s report

Title: MOLECULAR AND EVOLUTIONARY CHARACTERIZATION OF NOROVIRUS GII.17 IN THE NORTHERN REGION OF BRAZIL

Version: 0 Date: 17 Jul 2019

Reviewer: Juan Degiuseppe

Reviewer's report:

The present manuscript describes the emergence and evolutionary analysis of norovirus GII.17 strains detected in the northern region of Brazil.

Although the aspects that authors mention are relevant and represent useful data for understanding the evolutionary dynamic of noroviruses, there some considerations that must be addressed to improve it.

First, there are several misspellings, grammatical errors and/or awkward sentence structuring along the text. Therefore, language editing by a native English speaker or experienced English editor would benefit the manuscript.

Authors should describe better the epidemiological data from the samples tested: how many samples come from the sporadic panel and how many related to acute gastroenteritis outbreaks, the ages of these patients, if they were hospitalized and so. Also, it would be better if authors state if samples were tested for other bacterial or viral enteropathogens (i.e. Group A Rotavirus, Shigella sp) for understanding if NoV GII.17 strains were associated with co-infections or if they are associated with some age group or type of sample (i.e., sporadic vs. outbreak) in particular. In this manner, a full description of the NoV genetic diversity must be addressed to understand the global prevalence of GII.17 strains considering that authors remark its circulation and therefore have analyzed them.

It is not clear why authors needed to use a new pair of primers designed for this study. These new primers are used for NoV detection in samples or for amplification and further sequencing of the NoV positive ones?

Also, it does not seem that these new primers went under proper validation assays. They were designed taking a strain from Hong Kong as reference when probably it would be more useful to use one of the Brazilian circulating strains. Also, as it is not clear the aim of this new strategy, if they were used for detection, they should be validated with a set of human samples besides the referred controls. If the new set of primers were only designed to amplify a partial genome segment for sequencing purposes, it is not needed to validate the assay. Authors should clarify this aspect.
Other considerations:

Background section:

It is desirable to avoid the structure description paragraph and describe the NoV genetic diversity (i.e., authors state the characteristics of NoV GII.4 strains when no references on the genetic diversity where mentioned before). In this section, authors should center in the aspects that are relevant for this manuscript.

It is not clear the purpose and the meaning of the statement 'Whereas most GenBank sequences…' (page 4, line 21).

Methods section

The Genotyping Norovirus Tool 1.0 is not really updated currently. Authors should consider using https://norovirus.phiresearchlab.org for better results.

The description of the 138 sequences retrieved from GenBank that were used for phylogenetic analysis should be part of the Evolutionary analysis subsection.

It is not clear why authors conduct protein modeling analysis considering that in the Background section there is no reference about epitopes or how changes could implied an impact in the spreading pattern.

Results section

When there is evidence of regional circulation activity, it is not clear why authors do not compare their detected strains with the Brazilian and the Argentine ones.

Discussion section

Statements already mentioned in the Background section should be eliminated to avoid duplicated information.

Limitations are not addressed (i.e. why the number of genotyped strains are below 50%, the results of the validation process and that no clinical samples were used to test this new pair of primers). The strength of every research relies in identifying the weaknesses and the assumptions that were made.

Figures

Authors should state when analysis were conducted on partial or complete sequences.

Argentine strain is described in the Background and Discussion sections but is not taken into account in the phylogenetic or evolutionary analysis.
Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

No

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

No

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

No

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

Not relevant to this manuscript

Quality of written English
Please indicate the quality of language in the manuscript:

Not suitable for publication unless extensively edited

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