Author’s response to reviews

Title: Genetic Diversity and Epidemiology of Genogroup II Noroviruses in Children with Acute Sporadic Gastroenteritis in Shanghai, China, 2012-2017

Authors:

Lijuan Lu (lu5223085@126.com)
Huaqing Zhong (zhonghuaqing66@163.com)
Menghua Xu (xmh0111@163.com)
Liyun Su (weicheng_39@163.com)
Lingfeng Cao (hawking_clf@126.com)
Ran Jia (goodbye_sea@126.com)
Jin Xu (jinxu_125@163.com)

Version: 2 Date: 31 Jul 2019

Author’s response to reviews:

Aug 1, 2019

BMC Infectious Diseases

Dear Editor in chief,

Thank you for the second opportunity to revise this paper for resubmission. We have revised the manuscript in accordance with the editors’ and reviewers' comments, and carefully proof-read the manuscript to minimize typographical, grammatical, and bibliographical errors.

Please see below our detailed responses to individual comments made by the reviewers. We hope you will find these changes acceptable. Thank you for considering this revised manuscript for publication in BMC Infectious Diseases. We welcome further suggestions to improve the clarity of our manuscript for publication in your journal.
Sincerely yours,

Jin Xu, Ph.D.
Director, Department of Clinical Laboratory
Children’s Hospital of Fudan University
399 Wanyuan Road, Shanghai 201102
China

Response to Reviewers

Editor:

Critique 1: Is there any specific reason why not showing GII.4 variants in Figure 3? Although tree topology is not the focus of the current work, I always found it very interesting and informative to show how GII.4 sequences map on a phylogenetic tree. For example, a step-wise topology can to some extent indicate human-to-human spread, whereas identical sequences may be reflecting a point-source outbreak.

Response: Thank you for the good suggestion. Because NoVs strains detected in our study are too large to be shown in a single figure, GII.4 variants could not be shown well in Figure 3. Thus, GII.4 variants were analyzed using the Norovirus Genotyping Tool v.2.0 (https://www.rivm.nl/mpf/typingtool/norovirus/) in this study. But we have added the phylogenetic trees of GII.4 variants in an additional figure which is Figure 4 in part of Figures. The quotes and figure legends were changed accordingly in part of Results and Figure Legends on Page 7, Line 158, Page 8, Line 167-168, Page 8, Line 181, Page 9, Line 191 and Page 22-23, Line 483-494. Your advice is very useful and we will make more analysis in our next study.

Reviewer:

Jing Lu (Reviewer 1):

Critique 1: Although the finding is of some interest, I found few improvements in the revised manuscript and not all reviewer's questions were well addressed. At least, the GII.4_2006b and GII.4_Sydney_2012 phylogenetic clusters should be clearly marked in Figure 3 or an additional
figure if author wanted to mention the dynamic change of these two GII.4 sub genotypes in AGS cases. In fact, I couldn't find authors make any efforts to improve their results in the revised manuscript.

Response: Thank you for your comments. We are so sorry for not understanding and addressing well your question. We have added the phylogenetic trees of GII.4 variants in an additional figure which is Figure 4 in part of Figures according to your suggestion. The quotes and figure legends were changed accordingly in part of Results and Figure Legends on Page 7, Line 158, Page 8, Line 167-168, Page 8, Line 181, Page 9, Line 191 and Page 22-23, Line 483-494. We will modestly accept your suggestion to conduct more detailed and in-depth analysis in our following work.

Yuanyun Ao (Reviewer 2):

Critique 1: Although in several work they did not conducted on my comments, which I can respect, the authors have responded to my suggestions and/or questions. It is suggested to be published in this journal.

Response: Thank you for your recognition of our research work. We will do our best to make improvements in our next work according to your suggestions.