Author's response to reviews

Title: Etiological study of enteric viruses and the genetic diversity of norovirus, sapovirus, adenovirus, and astrovirus in children with diarrhea in Chongqing, China

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Author's response to reviews: see over
On submitting the revised manuscript, we want to thank the reviewers for their comments and suggestions, which have helped to shape an improved manuscript. During this revision, we carefully considered all the comments of the reviewers. Our point-by-point responses to the previous reviewers’ comments are provided below in italic font. The changes are highlighted with underlines in the revised manuscript.

Reviewer #1:

Major comments:
1. In this study, stool specimens were collected only 3 months, from August to November, 2010. This period is too short to describe epidemiology of viral diarrhea in one place. In addition, this period is out of December-March, which is the highly prevalent period of diarrheal viruses. Therefore, study design has essential defect in this manuscript.

Response: In this study, there were 500 samples collected from August to November, 2010. This period is short to describe epidemiology of viral diarrhea. Even up to now, there has been no report of systematic detection of common enteric viruses in children with diarrhea in Chongqing. The aim of this study was to determin common enteric viruses in children <5 years old with diarrhea in this area. On the base of this study, the epidemiology of enteric viruses (Rotaviruses, noroviruses, sapoviruses, astroviruses, and adenoviruses) determined will be studied further.

2. Rotavirus genotypes, G and P types were not determined, although these are epidemiologically very important.

Response: Rotavirus has been recognized as a major pathogen of acute diarrhea in children. A previous study in Chongqing Dr. Xu H attended had showed that Group A rotavirus was the main pathogen of acute diarrhea in children. Group A rotavirus was detected in 257/507 (50.69%) samples collected from 2008.10~2009.2 by RT-PCR. G and P types were analyzed by nested RT-PCR in 147 samples. G-genotypes detected included G1 40.14% (59/147), G2 6.80% (10/147), G3 17.01% (25/147), G4 2.04% (3/147), and G9 0.68% (1/147), respectively. While 49 cases (33.33%) were failed to detect G-genotypes. P-genotypes detected included P[8] 60.54% (89/147), P[4] 6.12% (9/147), P[9] 0.68% (1/147), P[10] 0.68% (1/147), and 47 cases of failed P-genotyping. (Liao Y, Chen J, Zhu C, Xu H, Liu Z. Molecular epidemiologic characterization and related data analysis of rotavirus in infants of Chongqing. Acta Academiae Medicinae Militaris Tertiae, 2010,01:77-80).

The aim of this study is to understand common enteric viruses in children <5 years old with diarrhea in Chongqing which was never reported before. Because the G and P genotype had been studied recently, the molecular characteristics of Group A rotavirus in this area didn’t studied in this study.

3. In the sections of "viral detection", no literatures were written for detection primers of rotavirus and norovirus.
Response: Detection primers for Rotaviruses B and C, noroviruses GI and GII, sapovirus, and astrovirus can be found in References 10, 11 and 12 (Page 2, Line 31).

Reviewer #2:
The figure and analysis are coincidence. I didn't find obvious error, and the conclusion is accord with our studies.

Reviewer #3:
Worldwide viral diarrhea is one of the most common diseases affecting children <5 years old, leading to significant morbidity and mortality, especially in developing countries. Ren et al evaluated the etiology and diversity of viral diarrhea-causing pathogens in children in Chongqing, a metropolitan city in western China. This study included samples from children <5 years of age suffering from both acute and persistent diarrhea in university children’s hospital in Chongqing in August to November 2010. They found that viruses are the main cause of acute diarrhea in Chongqing; rotavirus and norovirus are the two predominant viruses and sapovirus, adenovirus, and astrovirus are responsible for only a small percentage of children with acute diarrhea. The molecular characteristics of the noroviruses, sapoviruses, astroviruses, and adenoviruses were also reported.

They should also include molecular characteristics and serotypes of Rotavirus A, the predominant virus.

Response: Rotavirus has been recognized as a major pathogen of acute diarrhea in children. A previous study in Chongqing Dr. Xu H attended had showed that Group A rotavirus was the main pathogen of acute diarrhea in children. In that study, Group A rotavirus was detected in 257/507 (50.69%) samples collected from 2008.10–2009.2 by RT-PCR. G and P types were analyzed by nested RT-PCR in 147 samples. G-genotypes detected included G1 40.14% (59/147), G2 6.80% (10/147), G3 17.01% (25/147), G4 2.04% (3/147), and G9 0.68% (1/147), respectively. While 49 cases (33.33%) were failed to detect G-genotypes. P-genotypes detected included P[8] 60.54% (89/147), P[4] 6.12% (9/147), P[9] 0.68% (1/147) and P[10] 0.68% (1/147), and 47 cases of failed P-genotyping. (Liao Y, Chen J, Zhu C, Xu H, Liu Z. Molecular epidemiologic characterization and related data analysis of rotavirus in infants of Chongqing. Acta Academiae Medicinae Militaris Tertiae, 2010,01:77-80).

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The GenBank accession number of the sequences should also be included.

Response: The GenBank accession number of the sequences had added in Phylogenetic trees of Fig. 1, Fig. 2 and Fig. 3.