Author's response to reviews

Title: Emergence of dengue virus 4 genotype II in Guangzhou, China, 2010: Survey and molecular epidemiology of one community outbreak

Authors:

Qin-Long Jing MD (jingqinlong@126.com)
Zhi-Cong Yang MD (gdgzc@163.com)
Lei Luo PHD (llyeyq@163.com)
Xin-Cai Xiao PHD (biotin2001@163.com)
Biao Di MD (biao65di@yahoo.com)
Peng He MD (emailhepeng@foxmail.com)
Chuan-Xi Fu PHD (fuchuanxi@gmail.com)
Ming Wang MD (wangming@gzcdc.org.cn)
Jia-Hai Lu PHD (jiahailu@yahoo.com.cn)

Version: 5 Date: 23 March 2012

Author's response to reviews: see over
Dear Editors and Reviewers:

Thank you for your precious proposals.

We resubmit our case report, *Emergence of dengue virus 4 genotype II in Guangzhou, China, 2010: Survey and molecular epidemiology of one community outbreak*, which we wish will meet the requirements of *BMC Infectious Diseases*. It has been revised carefully on copyediting in accordance with the reviewers’ and editors’ suggestions, with point-by-point responses attached. All changes made to the text are in red color in the manuscript. In addition, we have this paper revision professionally edited by Edanz before the submission.

If you have any questions about this paper and changes, please don’t hesitate to contact me. Correspondence should be directed to Jing Qinlong:
Address: Guangzhou Center for Disease Control and Prevention, No. 1, Qide Road, Baiyun District, Guangzhou City, People’s Republic of China 510440
Tel: 86-20-36055821
Fax: 86-20-36055833
E-mail: jingqinlong@126.com

Thanks again and best wishes!

Yours sincerely,

Qin-Long Jing
Responses to Editors and Reviewers

For your guidance, point-by-point responses are appended below. The original comments are in black, and our responses are in blue.

Reviewer Ng Lee Ching: The authors have addressed all the issues raised. I enjoyed reading this more concise and straightforward manuscript. Just need minor editorial improvement.

Additional editor note: Professional copyediting is required. Examples are as follows:
1. Pg 3, para 2, line 4: 'and partially progress' to 'and may progress'
2. pg 4, last para, line 4: 'uppermost vector' to 'predominant vector'; the whole para should be rewritten.
3. pg 6, subtitles: 'Imported case confirmation' to 'Imported case'; 'Secondary autochthonous cases information' to 'Secondary autochthonous cases'
4. pg 8, para 1, line 5: 'colonisation' to 'spread'

Response: we have made the language a substantial improvement in this revised manuscript, and professionally copyedited by Edanz. The examples listed by editors were amended accordingly. More specific details are displayed in main modifications below.
Main modifications in the manuscript

The red color denotes the changes in the manuscript.

1. Pg 2, para 3, line 1: “On the basis of” to “Based on”.
2. Pg 3, para 1: “Dengue is the most globally prevalent arthropod-borne viral disease in humans [1], with approximately 2.5 billion people living in regions at risk and 50-100 million infections annually, resulting in one-half million individuals suffering from dengue hemorrhagic fever (DHF) and more than 25,000 deaths [2].” to “Dengue is the most globally prevalent arthropod-borne viral disease in humans [1]. Approximately 2.5 billion people live in regions at risk and 50-100 million infections occur annually, resulting in half a million individuals suffering from dengue hemorrhagic fever (DHF) and more than 25,000 deaths [2].”
3. Pg 3, para 1, line 5: “in five countries” to “based on figures from five countries”.
4. Pg 3, para 1, line 6: “El Salvador” to “El Salvador”.
5. Pg 3, para 2: “The agent of dengue virus (DENV), a member of the genus Flavivirus family Flaviviridae, is a single-stranded, positive-sense, RNA virus with a genome of about 11kb, antigenically divided into four serotypes (DENV-1, DENV-2, DENV-3, DENV-4), all of which commonly cause a mild febrile illness and partially progress to dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS) [5].” to “The agent of dengue virus (DENV) is a member of the genus Flavivirus family Flaviviridae. It is a single-stranded, positive-sense, RNA virus with a genome of about 11 kb, which can be antigenically divided into four serotypes (DENV-1, DENV-2, DENV-3, and DENV-4). All four serotypes commonly cause a mild febrile illness which may progress to DHF and dengue shock syndrome (DSS) [5].”
6. Pg 3, para 3, line 4: “was placed in” to “was serotyped as”.
7. Pg 3, para 3, line 7: “DENV-4 including genotypes I, II and III,” to “genotypes I, II, and III of DENV-4”.

3
8. Pg 3, para 3, line 12: “had replaced” to “took over”.
9. Pg 4, para 2, line 2: “which plays” to “Viral genetic changes play”.
10. Pg 4, para 2, line 6: “reflecting” to “which are reflective of”.
11. Pg 4, para 3, line 2: “that accounted for more than 50% of cases” to “accounting for more than 50% of the DENV cases”.
12. Pg 4, para 4 was rewritten. “In this paper, we investigated the DENV-4 outbreak in the Jingtai Street community which covered 11.4 square kilometres with a population of 32,567 in 2010. There was a high density of Aedes albopictus which was identified as the predominant vector for dengue in Guangzhou, with an average Breteau index (BI) of 8.67 in the first three days after the first autochthonous case was distinguished on September 13, 2010. The survey enabled analysis of the epidemiological distribution, laboratory testing and phylogenetic analyses of envelope gene sequences, using 2 sequences extracted from isolates and 32 sequences published in GenBank.”
13. Pg 5, para 1: “All patients identified from passive surveillance when seeking medical services or identified by active searches should be reported to the Notifiable Infectious Disease Report System (NIDRS) within 24 hours after diagnosis, followed by a face-to-face interview conducted by the Center for Disease Control and Prevention (CDC).” to “All patients were identified from passive surveillance when seeking medical services or recognized by active searches that were reported to the Notifiable Infectious Disease Report System (NIDRS) within 24 hours after diagnosis, and were followed by a face-to-face interview conducted by the Center for Disease Control and Prevention (CDC).”
14. Pg 5, para 1: “and written informed consent from all patients upon seeking medical service.” to “Written informed consent was obtained from all patients upon seeking medical service.”
15. Pg 6, para 1: “with 16 cases hospitalized, 16 cases from passive reports and 2 cases among 18324 persons from active searches, which produced an incidence rate of 5.53 per 10,000 residents” to “Of these 18 cases, 16 patients were hospitalized. Sixteen cases were identified from passive reports and 2 cases
among 18,324 residents from active searches, which produced an incidence rate of 5.53 per 10,000 people.”

16. Pg 6, subtitles: “Imported index case confirmation” to “Imported case”; “Secondary autochthonous cases information” to “Secondary autochthonous cases”.

17. Pg 6, para 3: “However, she visited a friend living on fifth floor in Jingtai Street on September 2.” to “After her return, on September 2, she visited a friend living on a fifth floor apartment in Jingtai Street community.”

18. Pg 6, para 3, line 12: “where” to “Interestingly”.

19. Pg 7, para 2: “including two in age group 10–19 years,” to “The ages included two people aged 10-19 years”.

20. Page 7, para 3: “were fever” to “All patients had fever”; “Other main symptoms” to “The other reported symptoms included”.

21. Pg 7, para 5: “The isolate Guangzhou 10660 (GenBank accession no. JN599977), the first isolate of the autochthonous cases, shared 100% homology with D10168-GZ that was isolated in China in 2010 and imported from Thailand and shared 98.9% homology with 02-12-1HuNIID strain isolated in 2002 in Japan and imported from Thailand (see Additional file 3 for homology details).” to “The first isolate of the autochthonous cases was the isolate Guangzhou 10660 (GenBank accession no. JN599977). Guangzhou 10660 shared 100% homology with D10168-GZ that was isolated in China in 2010 and imported from Thailand, and also shared 98.9% homology with the 02-12-1HuNIID strain isolated in 2002 in Japan which also was imported from Thailand (see Additional file 3 for homology details).”

22. Pg 8, para 2: “but were distantly related to strain CN78-56 grouped into genotype II isolated in China in 1978 and remarkably remote from Guangzhou B5 grouped to genotype I isolated in China in 1990.” to “These strains are distantly related to strain CN78-56 which was grouped into the genotype II clade which was isolated in China in 1978, and remarkably remote from the Guangzhou B5 strain which isolated in China in 1990 and was grouped to the genotype I clade.”
23. Pg 8, para 3 was rewritten. “DENV-4 has not been identified in mainland China since the 1990 DENV-4 genotype I outbreak. Based on epidemiological and phylogenetic analyses, this current outbreak was confirmed as DENV-4 genotype II and initially traced to a the imported index case, a Guangzhou resident who travelled back from Thailand. The DENV-4 genotype II Spread rapidly (Figure 3), but was not classified as a re-emergence of the DENV-4 outbreaks from 1990 and 1978.”

24. Pg 8, para 4: “As indicated though divergent cases, sampling time and patient addresses, the DENV-4 isolates were determined to be from the same origin.” to “Though the cases were divergent, based on sampling time and patient addresses, the DENV-4 isolates were determined to be from the same origin.”

25. Pg 9, para 2: “which acted as the most important export countries of dengue to adjacent areas” to “from which dengue was exported to adjacent countries.”

26. Pg 9, para 4: “was considered to have been the result of the virus spreading from Yuexiu District where it was located in the metropolitan region in Guangzhou,” to “spread the virus from the Yuexiu District in Guangzhou.”

27. Pg 9, para 4: “such importations leading to outbreaks” to “the import of a dengue virus which may then lead to an outbreak.”

28. Punctuation marks and minor changes such as prepositions, articles, and tenses are not listed all in cover letter, but in red color in the manuscript.