Author’s response to reviews

Title: Genomic characterization of a large plasmid containing a blaNDM-1 gene carried on Salmonella enterica serovar Indiana C629 isolate from China

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Version: 1 Date: 02 May 2017

Author’s response to reviews:

Dear Editor of BMC Infectious Diseases

We greatly appreciate your efforts and consideration of our manuscript for possible publication. Please convey our heartfelt thanks to all the referees for reviewing our manuscript. There are no suggestions from the referees. However, editor himself raises several importance suggestions so i have revised this manuscript carefully according to editor suggestions. Detailed responses to his comments and questions are provided below.

Comment 1:

Can you determine the copy number of pC629? How stable is the plasmid-is it easily cured?
Response

Yes we already did it. Detail has been given below

To evaluate the stability of the plasmid, the C629 strain was inoculated into 5 mL LB broth and 5 mL LB broth with 2 mg/L meropenem, incubated at 37°C 200 rpm, respectively. The culture was then transferred to a new 5 mL LB broth and 5 mL LB broth with 2 mg/L meropenem after 12 h incubation, respectively. The stability of the plasmid would be evaluated after 5 times subculture. The culture was tested the blaNDM-1 gene by PCR each time to detect the transferability of the plasmid C629 according to previous report.

Finally, the blaNDM-1 gene could still be stably transferred after 20 times subculture.


Comment 2:

Figure 2 is incomplete. I could not locate the various panels a-e.

Response:

Sorry for creating miss understand in understand the fig 2. In our old version we divided fig 2 into several panels (a-e) but we merge all the panels into single in the final version of manuscript. Therefore, there are no panels in figure 2. It was writing mistake. Now I edit all the panels. Everything we present in figure 2.

Comment 3:

Some description of the virulence factors encoded by pC629 should be provided.
Response:

To identify potential virulence genes in the plasmid pC629 genomes, the virulence factors listed in the Virulence Factors Database (VFDB) were aligned to the ORF protein sequences using BLASTP and filtered with 50% identity and 90% match length. By using this approach, two virulence genes, both named as dDE_Tnp_1, matched abzi_00085 and abzi_00086, were identified on plasmid pC629 (Fig. 1), both have already been characterized in Acinetobacter baumannii MDR-ZJ06, this is a multidrug-resistant bacterium detected and isolated from patient in China. These two genes were participated in composition of the capsule gene cluster, which plays an important role in protecting bacteria from the host innate immune response.


Comment 4:

Please carefully edit your paper as there are numerous grammatical and structural problems.

Response:

I requested one Australian person Dr. Syed Jabir Hussain of Guangzhou Institute of Geochemistry, Chinese Academy of Science Guangzhou China to revise our article English language, I am so thankful to him for his help. I also try my best to improve the language of my whole article. You can read it I hope now it will fulfil the required standard of the journal.

I revised my manuscript according to referee recommendation. However if still there is any mistake please inform me I will make it correct. Thank you again for your attention on these revisions. I look forward your last decision.

Sincerely Yours,

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