Title: Associations between interleukin-1 gene polymorphisms and sepsis risk: a meta-analysis

Authors:

An-qiang Zhang (zhangaqiang@126.com)
Wei Pan (qiangwei2@126.com)
Jun-wei Gao (nutdgjw@163.com)
Cai-li Yue (yuecaili8404@163.com)
Ling Zeng (zengling_1025@126.com)
Wei Gu (clgwjm@163.com)
Jian-xin Jiang (hellojx@126.com)

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

Thank you so much for your letter concerning our revised manuscript (1214409578105331) entitled "Associations between interleukin-1 gene polymorphisms and sepsis risk: a meta-analysis". We really appreciate you and the reviewer very much for the insightful and helpful critiques. In response to the comments and recommendations, we have revised our manuscript again. Below please find our point-by-point response to the reviewer.

1. Some language needs to be improved (both grammar and spelling).

We have made all changes according to the reviewer’s suggestion (highlighting these changes in our revised manuscript).

2. Results, IL-1B+3594 subsection: Please add the PFDR value to the overall comparison results and to the results obtained after the removal of the Fang et al study.

Thank you for pointing out. We have added the $P_{FDR}$ value to the overall comparison results ($P_{FDR}=0.12$ in the recessive effect) and to the results obtained after the removal of the Fang et al study ($P_{FDR}=0.12$ for overall studies and $P_{FDR}=0.09$ for Caucasian populations) (Page 10-11).

3. Results, IL-1RN VNTR subsection: Please add the PFDR value to the overall results under the allelic model to Line 6.
Yes, we have added the $P_{FDR}$ value to the overall results under the allelic model ($P_{FDR}=0.12$) (Page 11).

4. **Figure 2: Add a superscript 1 to “Events” and then a definition in the figure legend:**

   **Events1: Number of individuals with TT genotype**

   According to the reviewer’s suggestion, we have revised the Figure 2 and added a definition (Events$^1$: Number of individuals with TT genotype) in the figure legend.

5. **Figures 3: Add a superscript 1 to “Events” and then a definition in the figure legend:**

   **Events1: Number of individuals with 22 genotype.**

   Figure 3 represents the forest plot of sepsis susceptibility associated with IL-1RN VNTR polymorphism under the allelic model (2 vs. L), and the events in the figure indicates the number of 2 allele in the sepsis patients or control group. We have added the annotation in the figure legend (Events$^1$: Number of the 2 allele).

Thank you again for your review and re-consideration. Wish our revision will meet the requirements of the journal and give appropriate answers to the comments of all reviewers.

Sincerely yours,
Jian-xin Jiang, M.D., Professor
Research Institute of Surgery
Daping Hospital
Third Military Medical University
China
Phone/fax: 86-23-68706323
E-mail: hellojjx@126.com