

This study used microarray analysis to identify several candidate biomarkers involved in the development of postoperative peritoneal adhesion and explored the role of TLR4 / MyD88 / NF- κ B. While this study is interesting, there are some major and minor points that should be addressed.

Methods:

1、 Many microarray expression datasets can be downloaded from the GEO database by keyword. Why choose GSE123413, what is the exclusion criterion?

We used the key words: 'RNA', 'peritoneal adhesion', or 'abdominal adhesion' and 'Mus musculus' (organism) searching the GEO database. A total of 16 expression profile numbers were obtained after duplicates removing. After a thorough screening, the accession number GSE123413 was satisfied our inclusion criterion. The others were not about peritoneal abdominal adhesion.

2、 The author mentions in the abstract that PPA can lead to female infertility, and why male mice have been chosen why female mice have not been included?

In our study, we tried to uncover the underlying mechanisms of peritoneal adhesion formation at the transcriptomic and molecular levels. However, we have not yet studied the following complications of PPA. But your good advices give us perfect ideas about the future study on the sex differences in the pathogenesis of PPA formation and the following complications.

3、 In the Beyotime web site, the BCA reagent is used to detect proteins, and not used to detect mRNA.

Thanks for correcting the mistake, we had modified carefully.

Results:

1、 The authors provide the adhesion grades and scores for each group in Table 3. It would be more perfect if pictures of different groups of peritoneal adhesion could be provided.

According to your advices, we had provided the pictures of different groups of peritoneal adhesion, as shown in Figure 4.

We tried our best to improve the manuscript and made some changes in the manuscript. These changes will not influence the content and framework of the paper. We appreciate for Editors/Reviewers' warm work earnestly, and hope that the correction will meet with approval.

Once again, thank you very much for your comments and suggestions.