

Reviewer #1:

Scientific Quality: Grade B (Very good)

Language Quality: Grade B (Minor language polishing)

Conclusion: Minor revision

Specific Comments to Authors: Manuscript ID: 73324 Manuscript Title: Identification of the potential biomarkers and mechanism in dilated cardiomyopathy via bioinformatic analysis Manuscript Type: Basic Study Journal: World Journal of Cardiology Major comments: The author appraised this paper by identifying the potential biomarkers and mechanism in dilated cardiomyopathy via bioinformatic analysis. However, your article is inadequately presented. Furthermore, there are many problems in the different sections as well. Although the article has scientific rigor, several major flows need to be improved before publication.

1. The abstract section is unsuitable—no focus point in the abstract section.

Response: Thank you. The focus point of abstract is that we identified some pathogenesis and potential biomarkers for DCM, and the analysis methods which we used in this study. However, the biomarkers were predicted and need to investigate in the future.

2. No aim found.

Response: Thank you. We have revised and stated the aim of this study.

3. Rewrite the conclusion (in the abstract) in a more straightforward form.

Response: We have rewritten the conclusion (in the abstract) in a more straightforward form to make it easy to understand. Moreover, MogoEdit Company polished whole manuscript with more academic words.

4. Authors are suggested to use the full form when used for the first time throughout the manuscript.

Response: Thank you. We have listed the full form when used abbreviation for the first time.

5. 47 up-regulated and 50 down-regulated genes were screened out. Change this sentence.

Response: Thank you. This sentence has been changed.

6. The introduction section is poorly written. Authors are suggested to develop the introduction section by adding the literature related to cardiomyopathy (marked, risk factor, etc.).

Response: Thank you. We added some literatures related to the biomarker and risk factors of DCM.

7. The introduction section looks concise. Try to include the existing research limitations also, how the present research unravels those limits.

Response: Thank you. We included the existing research limitations and how the present research could unravel those limits in the last paragraph of introduction (“Despite all those findings...and these data can still be used to identify more candidate biomarker and pathways to further explore the cause of DCM”).

8. Need to arrange the introduction section logically—few updated references cited in this section.

Response: Thank you. We added some updated references in this section.

9. Aim of the study need to write in the last paragraph of the introduction section.

Response: Thank you. We added the aim of this study in the last paragraph of the introduction section.

10. Material and methods are written without proper references. Need a logical flow of the writings with enough references.

Response: Thank you. We added the references of the methods and tools used in this study as possible as we can in section of “Material and methods”.

11. Need to write the website and access date for all the websites.

Response: Thank you. We added the website and access date for all the websites.

12. PPI network construction and hub genes identification: Why STRING and Cytoscape?

Response: Thank you. STRING and Cytoscape were the most commonly used tools which constructed PPI network.

13. Some tools used do not represent state of the art, and hence, the quality and confidence of the results may be limited.

Response: Thank you. After reading many similar bioinformatic analysis articles^[1-5], we thought that the tools used in our study were relatively common and reliable in this type of article. So, the quality and confidence of the results in our study could meet the basic standard in similar type of bioinformatic analysis articles.

14. Immune cells infiltration analysis: Need to add details.

Response: Thank you. Immune cells infiltration analysis was mainly performed with “R commands” which used to routine steps. We added necessary details in this part for reader friendly.

15. Function enrichment analysis: Need to add details.

Response: Thank you. GO and KEGG analysis were performed in Metascape website with simple steps which we have listed in this part. Meanwhile, we added more details of GSEA analysis.

16. Many of the tools used are not cutting-edge or represent the best available tools.

Response: Thank you. After reading many similar bioinformatic analysis articles^[1-5], we believed that the tools used in our study were relatively common and reliable in this type of article.

17. The writing of results is good. Need to maintain a logical flow of the writings with the subtitles.

Response: Thank you. In this section, we exhibited subtitles for different part of results. We studied the logical flow by some cardiac diseases bioinformatics researches^[1-5], which arranged the logical flow by the analysis steps. This study flow could be the one of available flows to identify the biomarkers of DCM.

18. Many grammatically problematic sentences are in the results section, which must be checked and corrected precisely.

Response: Thank you. We have precisely checked and corrected those grammatically problematic sentences in the results section. In addition, MogoEdit company polished our revised manuscript.

19. Figures presentation is up to mark.

Response: Thank you.

20. Figure legends are self-explanatory.

Response: Thank you.

21. The discussion is feeble. Please, include the data from other sources about related works.

Response: Thank you. We added more depth discussion and included the data from other sources about related works.

22. A sound discussion includes principal, relationship, and generalizations supported by the results.

Response: Thank you. We discussed our results as required.

23. In the discussion, many concepts already reported in the introduction are repeated, so it is better to avoid unnecessary repetitions.

Response: Thank you. We have checked and delete the unnecessary repetitions between discussion and introduction.

24. The conclusion needs to address future perspectives.

Response: Thank you. We added the address future perspectives in conclusion.

25. Novelty of the work should be added by the author in the conclusion section.

Response: Thank you. We added novelty of the work in the conclusion section.

26. Spacing, punctuation marks, grammar, and spelling errors should be reviewed

thoroughly. I found so many typos throughout the manuscript.

Response: Thank you. We corrected these mistakes. In addition, MogoEdit company polished our revised manuscript.

27. English is modest. The authors need to improve their writing style. In addition, the whole manuscript needs to be checked by native English speakers.

Response: Thank you. MogoEdit company polished our revised manuscript.

Reviewer #2:

Scientific Quality: Grade C (Good)

Language Quality: Grade C (A great deal of language polishing)

Conclusion: Major revision

Specific Comments to Authors: This study demonstrates the identification of the potential biomarkers in dilated cardiomyopathy.

2.4 Function enrichment analysis may be revised to describe that it is gene expression enrichment analysis.

Response: Thank you. We changed “function enrichment analysis” as “gene expression enrichment analysis”

The results of GSEA analysis may be described more in detail.

Response: Thank you. GSEA analysis were performed by R, which have been written in Methods section, and focus on the terms that DCM group enriched which were described in results.

6 EDITORIAL OFFICE’S COMMENTS

Authors must revise the manuscript according to the Editorial Office’s comments and suggestions, which are listed below:

(1) Science editor:

This study demonstrates the identification of the potential biomarkers in dilated cardiomyopathy. However, there are many questions which need to be solved. The language should be checked and revised by the native English speakers. The edited figures should be provided in the PPT format.

Language Quality: Grade C (A great deal of language polishing)

Scientific Quality: Grade C (Good)

Response: Thank you. The manuscript has been polished by professional English language editing company (MogoEdit company, certification has been uploaded). We also uploaded the figures in the PPT format.

(2) Company editor-in-chief:

I have reviewed the Peer-Review Report, full text of the manuscript, and the relevant

ethics documents, all of which have met the basic publishing requirements of the World Journal of Cardiology, and the manuscript is conditionally accepted. I have sent the manuscript to the author(s) for its revision according to the Peer-Review Report, Editorial Office's comments and the Criteria for Manuscript Revision by Authors. However, the quality of the English language of the manuscript does not meet the requirements of the journal. Before final acceptance, the author(s) must provide the English Language Certificate issued by a professional English language editing company. Please visit the following website for the professional English language editing companies we recommend: <https://www.wjgnet.com/bpg/gerinfo/240>. Please provide the original figure documents. Please prepare and arrange the figures using PowerPoint to ensure that all graphs or arrows or text portions can be reprocessed by the editor. Authors are required to provide standard three-line tables, that is, only the top line, bottom line, and column line are displayed, while other table lines are hidden. The contents of each cell in the table should conform to the editing specifications, and the lines of each row or column of the table should be aligned. Do not use carriage returns or spaces to replace lines or vertical lines and do not segment cell content. Please upload the approved grant application form(s) or funding agency copy of any approval document(s).

Response: The manuscript has been polished by professional English language editing company (MogoEdit company, certification has been uploaded). And we have uploaded the tables, figures and grant application forms as required.

References

- 1 Huang H, Luo B, Wang B, Wu Q, Liang Y, He Y. Identification of Potential Gene Interactions in Heart Failure Caused by Idiopathic Dilated Cardiomyopathy. *Med Sci Monit*, 2018; **24**: 7697-7709. [PMID:30368515 DOI:10.12659/msm.912984]
- 2 Cheng C, Hua J, Tan J, Qian W, Zhang L, Hou X. Identification of differentially expressed genes, associated functional terms pathways, and candidate diagnostic biomarkers in inflammatory bowel diseases by bioinformatics analysis. *Exp Ther Med*, 2019; **18**: 278-288. [PMID:31258663 DOI:10.3892/etm.2019.7541]
- 3 Suzuki A, Horie T, Numabe Y. Investigation of molecular biomarker candidates for diagnosis and prognosis of chronic periodontitis by bioinformatics analysis of pooled microarray gene expression datasets in Gene Expression Omnibus (GEO). *BMC Oral Health*, 2019; **19**: 52. [PMID:30922293 DOI:10.1186/s12903-019-0738-0]
- 4 Zhang G, Xu S, Zhang Z, Zhang Y, Wu Y, An J, Lin J, Yuan Z, Shen L, Si T. Identification of Key Genes and the Pathophysiology Associated With Major Depressive Disorder Patients Based on Integrated Bioinformatics Analysis. *Front Psychiatry*, 2020; **11**: 192. [PMID:32317989 DOI:10.3389/fpsy.2020.00192]
- 5 Su Y, Li Q, Zheng Z, Wei X, Hou P. Integrative bioinformatics analysis of miRNA and mRNA expression profiles and identification of associated miRNA-mRNA network in aortic dissection. *Medicine (Baltimore)*, 2019; **98**: e16013. [PMID:31192949 DOI:10.1097/md.0000000000016013]