



ANSWERING REVIEWERS

Title: Proteomics for rejection diagnosis in renal transplant patients: Where are we now?

Author: Wilfried Gwinner, Jochen Metzger, Holger Husi, David Marx

Name of Journal: *World Journal of Transplantation*

ESPS Manuscript NO: 21811

Dear Reviewers,

Thank you for your suggestions to revise our manuscript. We believe your comments have helped to improve the manuscript considerably.

Critiques and responses:

This paper reviews the different proteomic approaches and summarizes results from studies that examined proteomic for diagnosing rejection. It is very well and clearly written.

This review focuses on an interesting and important topic. However is too long and often lacks focus. There is too much text in the first sections that are not directly relevant to the topic.

Response:

We have shortened all parts of the manuscript (see highlighted deletions/changes in the revised document). Although we included a new section with discussion on the identified molecules (part IV) as suggested by the reviewer, the total length of the manuscript has been reduced by 14% (word count is now: 3512).

For example the pathogenesis of rejection can be summarized in a figure rather than a whole text section. There are no specific references for each sentence.

Response:

We have included a new figure (Fig. 1) which summarizes the pathogenesis of rejection and replaces much of the text in part 2 (see highlighted deletions/changes in the revised document). We again checked the text for statements which are not supported by a reference and corrected this (see highlighted changes in the revised document).

Sections I-III can be significantly abbreviated/omitted so that the focus is on section IV. They can also be substituted by figures and tables.

Response:



BAISHIDENG PUBLISHING GROUP INC

8226 Regency Drive, Pleasanton, CA 94588, USA

Telephone: +1-925-223-8242

Fax: +1-925-223-8243

E-mail: bpgoffice@wjgnet.com

<http://www.wjgnet.com>

Shortening of Sections I+II has been commented above. Since Table 1 does give details to the technical platforms which were used to detect the molecules, we believe that some information should be given on the technical aspects. Nevertheless, we have made all efforts to make part III shorter and more concise (see highlighted deletions/changes in the revised document).

In section IV the tables have a lot of info but there is limited synthesis and interpretation of data. There is just a list of proteins and abbreviations but there is no mention of the role of these proteins and how they correlate to the pathogenesis of rejection. Again a figure summarizing the major proteins based on the best evidence and how they are involved in the inflammatory pathways of rejection would increase clarity and the impact of paper. The discussion on the most important section of the paper (IV) is limited with few references and limited interpretation. The manuscript should be shortened appropriately.

This was certainly a very weak point of our paper and therefore, we appreciate your suggestion. To this end, we subjected all the information on the peptides/proteins from Table 1 to a systems biology analysis. The results of this analysis are shown in the new Figure 3A and 3B and we have added appropriate comments in part IV (see revised manuscript, part 4, Figure 3 and Figure Legend).

On behalf of all authors,
Sincerely,
Wilfried Gwinner