RESPONSE TO REVIEWERS

Journal title: World Journal of Clinical Oncology

Manuscript NO: 82533

Title: Integration of molecular testing for the personalized management of patients with B-cell lymphomas

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Dear Editor,

We have carefully considered the reviewers' comments and incorporated changes into the manuscript (marked in red text). We have replied below point-by-point to each comment.

We hope our manuscript is now acceptable for publication in the World Journal of Clinical Oncology.

Sincerely
Dr. Cristina Bilbao-Sieyro, Corresponding author

Reviewer #1:
Dear Editorial Team, Thank you for sharing this manuscript with me. This mini review is very informative and useful. It is written good, but I found one abbreviated word, which is unfamiliar, IHQ was used for immunnohistochemistry instead of IHC. Otherwise it is acceptable.

We would like to thank Reviewer 1 for taking the time to read our article. We have changed IHQ for IHC throughout.

Reviewer #2:
In this mini review, the authors focus on advances in next-generation sequencing in B-cell lymphoma diagnosis, prognosis, and treatment options. This article is comprehensive in content, logical and appropriate in language, which meets the requirements of this journal. But there are still some points worth paying attention to:

1. I see that the author mentioned B-cell lymphoma in the title, but the article is mainly about DLBCL and FL. Although the latter two account for a larger proportion of B-cell lymphomas, they are not substitutes. Hope the author in the article appropriate explanation or choice.

We agree with the Reviewer that the title of B-cell lymphomas is perhaps too general since the minireview focuses on DLBCL and FL. We have modified the title so it more appropriately reflects the review's content.

2. The author used a general sentence at the end of the introduction. I think that as a review article, the introduction should properly explain the following parts of the article and briefly explain why it was written. In this way, readers can quickly understand the author's intention and have a more systematic understanding of the full text.

Thank you for this insight, we agree that the final paragraph of the introduction should mention what the review will include. We have added some additional text to the Introduction (please see pg.5-6).

3. The authors systematically explain in detail the value of NGS in detecting genetic abnormalities in the diagnosis, treatment and prognosis of B-cell lymphoma. As far as I know, molecular biology and cytogenetics are well established in the diagnosis and treatment of hematological tumors. Does this make some of the ideas in this article seem less innovative? It is suggested that the authors should further consider whether relevant methods have other application values such as early diagnosis and prevention of tumors.

It is true that molecular biology and cytogenetics are well established in the diagnosis and treatment of myeloid neoplasms. Indeed, in some neoplasms, like acute myeloid leukemia, the use of an NGS panel is mandatory at diagnosis to define AML subtypes and identify candidates for targeted therapy. This is reflected in the recent WHO and ICC classifications of myeloid neoplasms.

However, neither the WHO or ICC 2022 classifications of lymphoid neoplasms recommend molecular analyses for DLBCL or FL at diagnosis in routine clinical practice. Nevertheless, both consortia acknowledge that molecular analyses in B-cell lymphomas have identified genomic alterations with **diagnostic, prognostic, and predictive impact in different entities and explicitly state that** it is highly probable that more entities will be defined by genomic criteria in the near future. We have included a phrase that addresses this under NGS APPLICATION IN LYMPHOMAS (please see pg.8).

For this reason we believe our minireview is timely. Moreover, our minireview summarizes novel genomic data that have markedly enhanced our understanding of lymphomagenesis, defines disease entities at the molecular level, or has prognostic values in DLBCL and FL for readers.

4. I am puzzled by the author's suggestion that molecular detection can be applied to CAR-T therapy. The only mention in the paper that molecular technology can be applied to monitor the number of CAR-T cells in peripheral blood does not seem to be considered a progress, since qPCR has long been a traditional means of laboratory detection. CAR-T cells can also be detected by immunoassay. I hope the author can give a more detailed explanation.

In the section on CAR-T (starting on pg.13), we mention that qPCR can be used to monitor the number of CAR-T cells in peripheral blood. We do not describe this molecular monitoring of CAR-T or qPCR as progress as such. Rather, the progress can be considered to be the CAR-T therapy itself. As the title of the review is “Integration of molecular testing for the personalized management of patients with diffuse large B-cell lymphoma and follicular lymphoma” and many patients are now receiving CAR-T therapy, we felt that mention of the molecular testing to monitor patients post-CAR-T therapy was relevant. Our apologies if this was not clear in the manuscript. We have modified this paragraph to make this clearer.

5. According to the citation format requirements of the World Journal of Clinical Oncology, the first author's name seems to need to be bold and the name of the cited article needs to be italicized. I hope the author carefully check the full text against the article format requirements. Finally, I noticed that the literature cited by the author is relatively old, so I hope the author can quote more relevant articles in the recent five years to ensure the latest content.

Our apologies for this oversight. We have changed the first author’s name to bold and the title of the journal to italics in the Bibliography. With the changes included in this revised version of the manuscript 4 recent articles (3 published in 2022 and 1 in 2023) have been added.