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PEER-REVIEW REPORT

Name of journal: *World Journal of Diabetes*

Manuscript NO: 83885

Title: Analysis of N6-methyladenosine-modified mRNAs in diabetic cataract

Provenance and peer review: Unsolicited Manuscript; Externally peer reviewed

Peer-review model: Single blind

Reviewer's code: 06520497
Position: Peer Reviewer
Academic degree: MD, PhD
Professional title: Associate Professor, Research Associate
Reviewer's Country/Territory: Canada
Author's Country/Territory: China

Manuscript submission date: 2023-03-06

Reviewer chosen by: AI Technique

Reviewer accepted review: 2023-03-08 03:21

Reviewer performed review: 2023-03-13 01:43

Review time: 4 Days and 22 Hours

Scientific quality	[ ] Grade A: Excellent [ ] Grade B: Very good [Y] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish
Novelty of this manuscript	[ ] Grade A: Excellent [Y] Grade B: Good [ ] Grade C: Fair [ ] Grade D: No novelty
Creativity or innovation of this manuscript	[ ] Grade A: Excellent [Y] Grade B: Good [ ] Grade C: Fair [ ] Grade D: No creativity or innovation

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Scientific significance of the conclusion in this manuscript	[ ] Grade A: Excellent [Y] Grade B: Good [ ] Grade C: Fair [ ] Grade D: No scientific significance
Language quality	[ ] Grade A: Priority publishing [Y] Grade B: Minor language polishing [ ] Grade C: A great deal of language polishing [ ] Grade D: Rejection
Conclusion	[ ] Accept (High priority) [ ] Accept (General priority) [Y] Minor revision [ ] Major revision [ ] Rejection
Re-review	[Y] Yes [ ] No
Peer-reviewer statements	Peer-Review: [Y] Anonymous [ ] Onymous
	Conflicts-of-Interest: [ ] Yes [Y] No

SPECIFIC COMMENTS TO AUTHORS

The original article conducted by Lei Cai and colleagues aimed to investigate the role of altered M6A and differentially expressed mRNAs in diabetic cataract (DC). The authors used multiple methodologies, including epitranscriptomic microarray analyses, Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses, and qPCR, to verify their hypothesis. The results showed that M6A abundance level in total mRNA increased in patients with DC, providing new insights into the development of therapeutic strategies for DC. Generally, the topic in this paper is timely and pragmatic, and the manuscript is well-written. As such, I recommend its acceptance after minor revision. The specific comments are listed as below. 1. In this manuscript, microarray analyses of the mRNAs extracted from the lens anterior capsule tissues of the DC and NC samples were performed, showing difference in m6A-methylated mRNAs. This result is the footstone of the article and guided the authors' research. To verify the quality of the microarray data, the authors performed MeRIP-qPCR using four randomly selected mRNAs. My point is how to randomly and evenly select the tested mRNAs? And how to guarantee the representativeness of these

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mRNAs? 2. The authors used GO and KEGG enrichment analyses to explore the biological significance of mRNA M6A modification in DC samples. The enriched GO annotations fond three types of mRNAs: biological process (BP), cellular component (CC), and molecular function (MF). Whereas, the KEGG analysis showed that the mRNAs differentially methylated by M6A participated in 27 pathways. So, what is intersection results of these two analyses? Did the authors conduct the contrastive analysis?

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Reviewer's code: 06521203
Position: Peer Reviewer
Academic degree: FRCS, MD, PhD
Professional title: Associate Professor, Instructor, Researcher
Reviewer's Country/Territory: United Kingdom
Author's Country/Territory: China

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Reviewer accepted review: 2023-03-09 08:29

Reviewer performed review: 2023-03-13 02:24

Review time: 3 Days and 17 Hours

Scientific quality	[ ] Grade A: Excellent [Y] Grade B: Very good [ ] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish
Novelty of this manuscript	[ ] Grade A: Excellent [Y] Grade B: Good [ ] Grade C: Fair [ ] Grade D: No novelty
Creativity or innovation of this manuscript	[ ] Grade A: Excellent [Y] Grade B: Good [ ] Grade C: Fair [ ] Grade D: No creativity or innovation

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Language quality	[ ] Grade A: Priority publishing [Y] Grade B: Minor language polishing [ ] Grade C: A great deal of language polishing [ ] Grade D: Rejection
Conclusion	[ ] Accept (High priority) [ ] Accept (General priority) [Y] Minor revision [ ] Major revision [ ] Rejection
Re-review	[Y] Yes [ ] No
Peer-reviewer statements	Peer-Review: [Y] Anonymous [ ] Onymous
	Conflicts-of-Interest: [ ] Yes [Y] No

SPECIFIC COMMENTS TO AUTHORS

Thank you for the opportunity to review the manuscript titled, Analysis of N6-Methyladenosine-modified mRNAs in Diabetic Cataract. Despite successful surgical replacement with artificial lenses, cataract remains to be one of the leading causes of visual impairment and blindness worldwide. It has been recently suggested that m6A plays a role in DC progression. In this study, authors aimed to investigate the role of altered m6A and differentially expressed mRNAs in DC. This manuscript is well written and preparation. Aiming at study the role of altered M6A and differentially expressed mRNAs in DC, this paper showed abundant data. Finally, the concluded that M6A mRNA modifications may be involved in DC progression via the ferroptosis pathway. To increase the readability, the authors could add a hypothetical pathway diagram related to the role of altered M6A in the progression of DC.