**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  

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<th>Scientific quality</th>
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<th>[ ] Grade B: Very good</th>
<th>[ Y] Grade C: Good</th>
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<td>Novelty of this manuscript</td>
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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
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 found 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?
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: 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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### 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.