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PEER-REVIEW REPORT

Name of journal: World Journal of Diabetes

Manuscript NO: 76693

Title: Correlation between gut microbiota and glucagon-like peptide-1 in patients with

gestational diabetes mellitus

Provenance and peer review: Unsolicited Manuscript; Externally peer reviewed

Peer-review model: Single blind

Reviewer's code: 03491790

Position: Editorial Board

Academic degree: PhD

Professional title: Professor

Reviewer's Country/Territory: Thailand

Author's Country/Territory: China

Manuscript submission date: 2022-03-26

Reviewer chosen by: AI Technique

Reviewer accepted review: 2022-03-28 04:20

Reviewer performed review: 2022-04-04 09:10

Review time: 7 Days and 4 Hours

Scientific quality	[] Grade A: Excellent [Y] Grade B: Very good [] Grade C: Good [] Grade D: Fair [] Grade E: Do not publish
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	[]Yes [Y]No



Baishideng **Publishing**

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Peer-reviewer	Peer-Review: [Y] Anonymous [] Onymous
statements	Conflicts-of-Interest: [] Yes [Y] No

SPECIFIC COMMENTS TO AUTHORS

The manuscript describes differential microbiota between women with normal pregnancy and gestational diabetes mellitus (GDM). The study included the recruitment of patients and bacterial 16S rRNA gene sequencing. Although the topic is interesting, there are concerns that the authors should take into account. 1. The authors stated that markers of glucose and insulin homeostasis were higher in the GDM group compared with the NGT group (Table 1). The data only showed that HbA1c (%) was significantly different between two groups. For OGTT, it appeared to be different at time = 0. Would it mean that the background of two groups was already different? It'd also be nice if the authors included the dot plots for the significant parameters so the readers can see their distribution. 2. Most of the data were from gene sequencing and the authors analyzed and showed us different aspects of the outputs. The concerns on the accuracy and validity of the data should be pointed out. The authors are advised to elaborate more on this and perhaps include a few validating results to support their findings.



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Title: Correlation between gut microbiota and glucagon-like peptide-1 in patients with

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Provenance and peer review: Unsolicited Manuscript; Externally peer reviewed

Peer-review model: Single blind

Reviewer's code: 05562438

Position: Peer Reviewer

Academic degree: PhD

Professional title: Associate Professor

Reviewer's Country/Territory: Iran

Author's Country/Territory: China

Manuscript submission date: 2022-03-26

Reviewer chosen by: AI Technique

Reviewer accepted review: 2022-04-27 04:14

Reviewer performed review: 2022-05-07 08:32

Review time: 10 Days and 4 Hours

Scientific quality	[] Grade A: Excellent [] Grade B: Very good [Y] Grade C: Good [] Grade D: Fair [] Grade E: Do not publish
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) [] Minor revision [Y] Major revision [] Rejection
Re-review	[Y]Yes []No



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Peer-reviewer	Peer-Review: [Y] Anonymous [] Onymous
statements	Conflicts-of-Interest: [] Yes [Y] No

SPECIFIC COMMENTS TO AUTHORS

In this study, the authors have investigated the changes in the gut microbiota of pregnant women with GDM and compared the changes in the gut microbiota to the GLP-1 level. The outcomes of this study could point to implications of gut dysbiosis in the pathogenesis of GDM and provide further probiotic-based approaches for the treatment of this disease. However, The major concern is that there are not enough findings and the related interpretation about the correlation between the gut microbiota and GLP-1 levels. Hence, this study should be revised before publication, particularly in the interpretation of results and claims in the relation to the gut microbiota composition and GLP-1 level. Moreover, other minor concerns have been listed below. MATERIALS AND METHODS The history of recent antibiotic therapy is an influential factor in microbiome analysis. It should be stated in the exclusion criteria by the authors. RESULTS In the section "Alpha and Beta diversities" the authors mentioned some differences in alpha and beta diversity between GDM patients and NGT subjects, however, they have not stated what are? The authors should remark on any increase or decrease in microbiome diversity in the GDM cohort. There is no need to bring the related Phylum of the families in Paragraph 2 under the heading "Taxonomy". Please omit them. Under the subheading "Functional profiling of the gut microbiome," the authors should provide only microbial-related pathways and there is no need to provide human-related pathways. The entire manuscript has some grammatical and lexical errors.