



PEER-REVIEW REPORT

Name of journal: World Journal of Gastroenterology

Manuscript NO: 45236

Title: Characteristics of mucosa-associated gut microbiota during treatment in Crohn’s disease

Reviewer’s code: 02529129

Reviewer’s country: Greece

Science editor: Jia-Ping Yan

Reviewer accepted review: 2019-02-19 10:12

Reviewer performed review: 2019-02-27 22:21

Review time: 8 Days and 12 Hours

SCIENTIFIC QUALITY	LANGUAGE QUALITY	CONCLUSION	PEER-REVIEWER STATEMENTS
<input type="checkbox"/> Grade A: Excellent	<input type="checkbox"/> Grade A: Priority publishing	<input type="checkbox"/> Accept	Peer-Review:
<input checked="" type="checkbox"/> Grade B: Very good	<input checked="" type="checkbox"/> Grade B: Minor language polishing	(High priority)	<input checked="" type="checkbox"/> Anonymous
<input type="checkbox"/> Grade C: Good		<input type="checkbox"/> Accept	<input type="checkbox"/> Onymous
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade C: A great deal of language polishing	(General priority)	Peer-reviewer’s expertise on the topic of the manuscript:
<input type="checkbox"/> Grade E: Do not publish	<input type="checkbox"/> Grade D: Rejection	<input checked="" type="checkbox"/> Minor revision	<input checked="" type="checkbox"/> Advanced
		<input type="checkbox"/> Major revision	<input type="checkbox"/> General
		<input type="checkbox"/> Rejection	<input type="checkbox"/> No expertise
			Conflicts-of-Interest:
			<input type="checkbox"/> Yes
			<input checked="" type="checkbox"/> No

SPECIFIC COMMENTS TO AUTHORS

In this work, He et al. compare the microbiome of patients before and after treatment from endoscopic biopsies from different sites. It is important for the field of metagenomics to gather information on as many different populations as possible due to



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the significant compositional differences those exhibit. The paper is well written and easy to follow. The background section is informative. The discussion is extensive, and the limitations of the paper are described sufficiently. Although, it is an interesting study there are some points to be addressed in methodology and results sections: The methodology is consistent with previous metagenomic studies but lacks in terms of tools used for the analyses and figure generation. For example, it is evident that Figure S4, generated from the PICRUSt results, was created via STAMP, but it is not mentioned anywhere. Furthermore, although they decided to collect samples before and after treatment from the same patients no direct pairwise comparisons were reported. We understand that statistical significance is next to impossible to achieve between two samples, but comparisons could have given a better understanding of the dysbiosis. Regarding the results there are some surprising finds. The authors report that no differences were found between anatomical sites, a finding that contradicts knowledge from previous works (e.g. Tropini C, et al. 2017). Also, there is no characterization of the CD's behavioral phenotypes in their samples or any reference in this point, which recent works have highlighted to be linked to microbial composition and function (e.g. Dovrolis N, et al 2019).

INITIAL REVIEW OF THE MANUSCRIPT

Google Search:

- The same title
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- Plagiarism
- No

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