



ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Gastroenterology

ESPS manuscript NO: 33550

Title: Couples of patients with ulcerative colitis exhibit a biologically relevant dysbiosis in fecal microbial metacommunities

Reviewer’s code: 00225277

Reviewer’s country: Spain

Science editor: Yuan Qi

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CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
<input type="checkbox"/> Grade A: Excellent	<input type="checkbox"/> Grade A: Priority publishing	Google Search:	<input type="checkbox"/> Accept
<input type="checkbox"/> Grade B: Very good	<input type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C: Good	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Duplicate publication	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade D: Rejected	<input type="checkbox"/> Plagiarism	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E: Poor		<input type="checkbox"/> No	<input type="checkbox"/> Major revision
		BPG Search:	
		<input type="checkbox"/> The same title	
		<input type="checkbox"/> Duplicate publication	
		<input type="checkbox"/> Plagiarism	
		<input type="checkbox"/> No	

COMMENTS TO AUTHORS

Gut dysbiosis is considered one of the factors inducing inflammation in chronic inflammatory bowel diseases (IBD), but its role in the etiology of ulcerative colitis is controversial. There have been many studies on fecal microbiota in the last years. The present study using a very sensitive method for assessing bacterial strains and compared the microbiota in patients with inflammatory bowel disease with that of their healthy partners. The study assesses some type of bacteria only found in patients with ulcerative colitis (UC). These bacteria are difficult to detect using less sensitive methods. The study found no significant differences between the microbiota of patients and their partners. These results confirm that long-term habitation has impact on fecal microbiota. Nevertheless, the microbiota of patients with IBD was more similar to that of patients with IBD to that healthy individuals, suggesting that it could play an important role in UC. The aim, material and methods and results are good, nevertheless this reviewer is not familiar with the 16S rRNA sequencing method. The Conclusions are in accordance



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with the Results and Discussion. The paper is interesting and gives new information on etiologic factors related to UC. In my opinion this paper could be admitted for publication as is.