Reviewer’s report

Title: Abnormal Fecal Microbiota Community and Functions in Patients with Hepatitis B Liver Cirrhosis as Revealed by a Metagenomic Approach

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Reviewer: Matthias Zilbauer

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In their study Wei and colleagues have examined composition of gut microbiota in healthy controls and patients with Hepatitis B liver cirrhosis (HBLC). Specifically, they have extracted bacterial DNA from stool samples and used next generation sequencing to assess composition and partly function of gut bacteria.

Their results demonstrate clear differences in the composition and function of gut microbiota between controls and HBLC patients.

Overall the manuscript is well written, data presented in a concise way and methodologies as well as statistical analysis seem sound.

Major criticism

1) Lack of novelty, i.e. what is new compared to the data published by Chen et al in 2011 (Hepatology. 2011 Aug;54(2): Characterization of fecal microbial communities in patients with liver cirrhosis)

2) What is the relevance to disease - e.g. chronic hepatitis B infection? How can this data be used to improve treatment/management, use as biomarker?

3) One of the main and most important questions that remain is what is cause and consequence? Most likely, changes in gut microbiota are the consequence of cirrhosis; what would be interesting to know is in what way changes in the gut microbiota influence disease progression.

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Needs some language corrections before being published

Statistical review: Yes, but I do not feel adequately qualified to assess the statistics.

Declaration of competing interests:

I declare that I have no competing interests