Reviewer's report

Title: Ulcerative colitis and irritable bowel patients exhibit distinct abnormalities of the gut microbiota

Version: 1 Date: 25 January 2010

Reviewer: S H Duncan

Reviewer's report:

Noor et al have examined differences in the composition of the microbiota of stool samples from IBS and UC samples whilst in remission compared to that of healthy controls using DGGE. The paper is well written and the authors acknowledge that their results are surprising, in that Bacteroides species were less prevalent in stool samples from the disease state compared to healthy controls. The authors could perhaps speculate on this more than has been covered in their discussion.

Minor essential revisions

1. Are the p values not actually “equal to” rather than “less than” in the abstract

2. In the background section, the authors should add additional references which do attempt to assign particular bacterial species into those that may be beneficial or detrimental to gut health. For example, see Sartor et al 2008 (PNAS) and Sokol et al 2008 (PNAS).

3. The level of uncultured bacterial species in the human large intestine is probably not as high as has been suggested in this article. Eg See paper by Tap et al 2009 (Env Microbiol).

4. The power of DGGE should not be overstated as it is generally considered as a low resolution method.

5. There would merit in comparing the profiles of faecal samples from patients during active disease and in remission.

6. Freezing the samples prior to extracting DNA may have resulted in differential loss of particular bacterial groups including the Gram negative Bacteroidetes. The authors should comment on this.

7. Did any of the sequenced bands give multiple products?

8. Given the surprising results in this study, it would have been valuable to employed an independent technique to analyse the samples too.

9. Figure 1a. Please add labels to the sample lanes to indicate which samples were derived from control, IBS or UC subjects.
10. Table 1. Define what you mean by average similarity and state how many bases were sequenced per sample.

11. Figure 2 is too small and therefore difficult to see.

12. How were the samples for these profiles selected?