

## Responses for reviewers

### Reviewer #1

1. Chapter "The intestinal bacteria of horses compared to those of humans", 1 paragraph, ref [4] - there is no information on gastric acid pH in the reference, it is desirable to clarify the correctness of the citation.

### Response

Thank you for your advice. There was an error in the references, so please refer to the revised version as follows.

4: Beasley DE, Koltz AM, Lambert JE, Fierer N, Dunn RR. The Evolution of Stomach Acidity and Its Relevance to the Human Microbiome. PloS one 2015; 10(7): e013411

2. The same chapter and paragraph, ref [6] is also not cited correctly. The reference report "The bacterial phylotypes were assigned to only two divisions, the Firmicutes (62 phylotypes, 105 sequences) and the Actinobacteria (10 phylotypes, 27 sequences). Although there were no Bacteroidetes 16S rDNA sequences identified in the random assemblies and clone libraries, amplification with species-specific 16S rDNA primers yielded sequences from *Bacteroides fragilis* and *Bacteroides uniformis*". While the author cites the information "It is estimated that this flora contains approximately 500-1000 different species of bacteria, with more than 90% belonging to the two bacterial phyla Bacteroidetes and Firmicutes".

### Response

Thank you so much for pointing it out. That is extremely important point. What I wanted to show was the bacterial species that account for the majority of the intestinal bacterial count. I changed the references and rewrote it as follows.

"It is estimated that this flora contains 500-1000 different species of bacteria[6], with nearly 80% of bacteria belonging to the two bacterial phyla *Bacteroidetes* and *Firmicutes*[7]."

6: Rolhion N, Chassaing B. When pathogenic bacteria meet the intestinal microbiota. Philosophical transactions of the Royal Society of London Series B, Biological sciences 2016; 371(1707)

7: Kobayashi R, Nagaoka K, Nishimura N, Koike S, Takahashi E, Niimi K, Murase H, Kinjo T, Tsukahara T, Inoue R. Comparison of the fecal microbiota of two monogastric herbivorous and five omnivorous mammals. Animal science journal = Nihon chikusan

3. *Table 1. The name was given incorrectly: Enterobacteriaceae is a family that belongs to the class of Gammaproteobacteria, a phylum Proteobacteria. The table shows the diversity of both bacteria and fungi, for which the ability to break down fibers derived from cell walls is described.*

Response

Thank you for your advice. I have changed Enterobacteriaceae to Enterobacteria. Since it was a table that collected bacterial species, the fungi were removed from the Table.

4. *Table 1, ref. [10] used incorrectly. There is no indication of specific species of the genus Bacteroides in this reference.*

Response

Thank you very much for your comment. The reference has been changed. Now I checked the literature carefully and restructured the Table.

5. *Table 1, when describing Ruminococcus flavefaciens, two references are given [8] and [19]. Both references refer to equine microbiota and need to be clarified and adjusted.*

Response

Thank you for pointing that out. The literature has been revised to make it more appropriate and understandable.

6. *Table 1, when describing Ruminococcus albus in humans, apparently, reference is given [20], but in this reference this species is described in cows, while in humans - Ruminococcus bromii (S) and Ruminococcus sp. nov. (C, X)*

Response

Thank you so much. Reference 20 has changed. *Ruminococcus bromii* and *Ruminococcus sp. nov.* have been reported as cell wall-degrading bacteria in humans, so no reports of horses were found but those species were added to the table. I also changed the annotations.

7. *Table 1, ref. For Piromyces equi [13], however, the reference does not indicate this species, only the total amount of fungal gene determined by real-time PCR is presented.*

Response

Thank you for making a comment. Regarding fungi, I deleted them from the table and so

only bacterial species are there.

8. *In general, the table can be expanded by presenting a wider list of species even from those references that are already cited by the author.*

Response

Thank you very much again. I think the contents of the Table have improved because I added the bacterial species according to the advice.