Review of: "Regular Consumption of Lacto-fermented Vegetables has Greater Effects on the Gut Metabolome Compared with the Microbiome"

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Potential competing interests: No potential competing interests to declare.

Very interesting work that combines a description of the microbiota composition and a functional readout. The authors found that long-term specific dietary intervention (inclusion of LVF foods in the diet) does not lead to a significant change in microbiota composition, but significantly affects the spectrum of metabolites in the stool. Given the nature of these compounds, these are likely to be microbial metabolites. Similar results have been obtained, for example, in adult European (doi: 10.3389/fnut.2021.783302) or American (doi:10.1136/gutjnl-2014-308209) vegan populations, whose microbiota composition is not fundamentally different from the omnivore population, but there are significant differences in their metabolic performance.

These results seem to support the hypothesis that the microbiota of healthy adults is very stable and does not change due to diet. However, diet can significantly influence the metabolic program of the microbial community and thus the spectrum of metabolites produced what, in turn, may significantly influence the host.

Methodologically the work is very well done, I have only a few comments and questions about the metabolomic part.

1. It is not entirely clear to me what samples were used for LC/MS analysis? The residual fluid (zymoshield) after collection for DNA extraction?

2. It would be great if the "leftover" zymoshiled could be used in this way, but isn't there a risk of losing some group of metabolites by this procedure?

3. The opposite problem with guanidinium isocyanate is that it lyses cells. So we are analyzing the cellular content as well - have you taken this into account?

3. Did you do any normalization of the metabolomics data? Did you relate them to anything (e.g. wet weight of the sample)?

4. Did you do two metabolomic analyses - one untargeted and one targeted to SCFA (after derivatization)?

5. At least for significant metabolites, it would be good to provide the data that led to their identification, here the exact mass, and MS/MS fragments. This should be at least for the unidentified but significant ones.

6. Have the spectra been corrected to blank?