

# Review of: "Meta-Omics Analyses of Organic and Conventional Fermented Vegetables Reveal Differences in Health-Boosting Potential"

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The manuscript by Guse et al. represents an interesting attempt to characterize the microbiome associated with some vegetables: carrots, radishes, and peppers. The authors not only profiled bacterial communities via 16S rRNA short read (V4 region) but also used ITS2 sequencing for fungal communities and even 16S rRNA long read sequencing with an Illumina NovaSeq 6000. On top of that, the authors tried a metabolomic analysis by mass spectrometry.

The authors not only studied the microbiome under conventional farming practices but also from a regenerative organic farm. Autoclaved samples were used as controls.

It is indeed a comprehensive study that deserves attention. However, the authors did not find any clear trend in the evolution of the communities. There is no clear conclusion when peppers, radishes, and carrots are taken together. The division between organic and conventional makes things even more complicated. There are also discrepancies between the short sequencing and the long ones.

On the other hand, metabolomics analysis gives more straightforward conclusions: lactic acid and pyruvate as the major organic acids and GABA as the major amino acid. It is interesting that GABA is present in higher concentrations in the organic fermented vegetables.