

Are We What We Eat?: Identifying Microbial Communities of Fruits and Vegetables

JL Thorsen, KA Grindle, IM Ong, RW Schwartz, JD Barak, JE Gern

BACKGROUND

- Fermenting bacteria metabolize dietary fiber into short chain fatty acids, which can suppress gut inflammation.
- Dietary interventions have been shown to alter the gut microbiome.
- Alterations in gut microbiome has been associated with differential risk of atopic disease.

HYPOTHESIS

High-fiber fruits and vegetables will have unique intrinsic microbial compositions.

- **Among alike produce samples there will be conserved microbial signatures.**
- **External factors including handling practices, farm practices, and grow location will also influence microbial colonization patterns of fruits and vegetables.**

METHODS



- Surface samples were collected from 41 high-fiber produce items and 6 controls.
- Microbes were extracted using 16S rRNA chloroplast-excluding primers and sequenced using Illumina MiSeq platform.
- Data was processed using Divisive Amplicon Denoising Algorithm 2 (DADA2) to obtain amplicon sequence variants.
- Alpha and Beta diversity metrics were calculated to evaluate similarities and differences among produce samples.

RESULTS

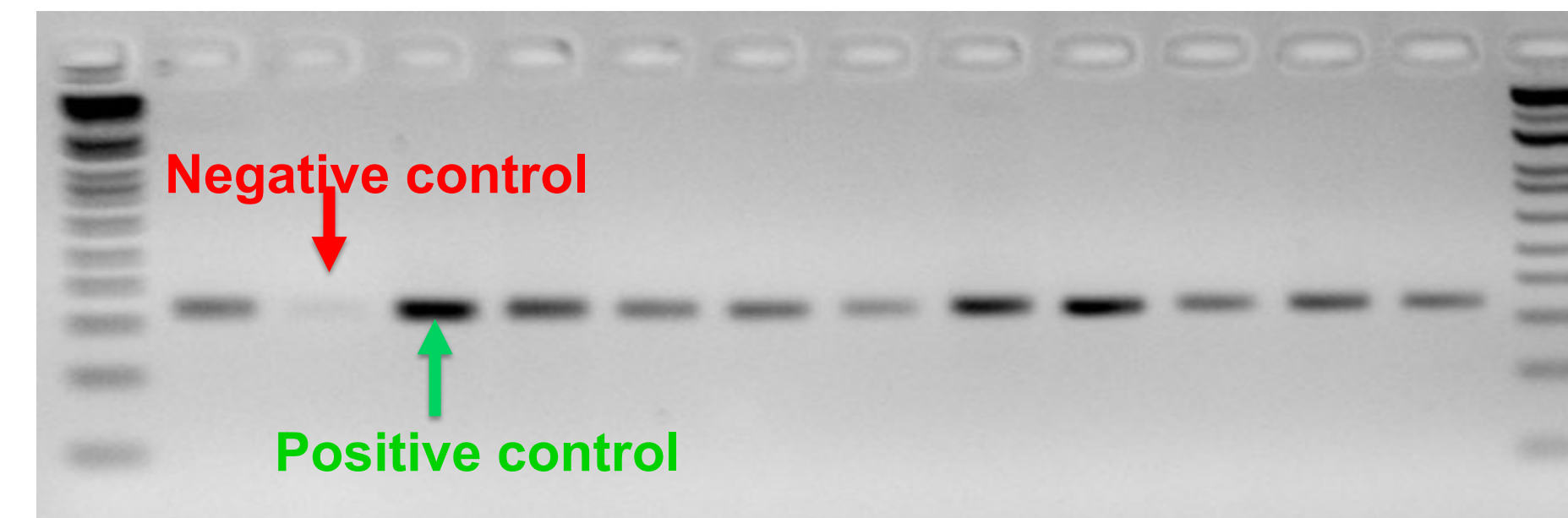


Figure 1. Gel electrophoresis of PCR amplified products using 779F and 1115R primers

Alpha Diversity: Measure of how many microbes are present and how evenly they are distributed *within a sample*

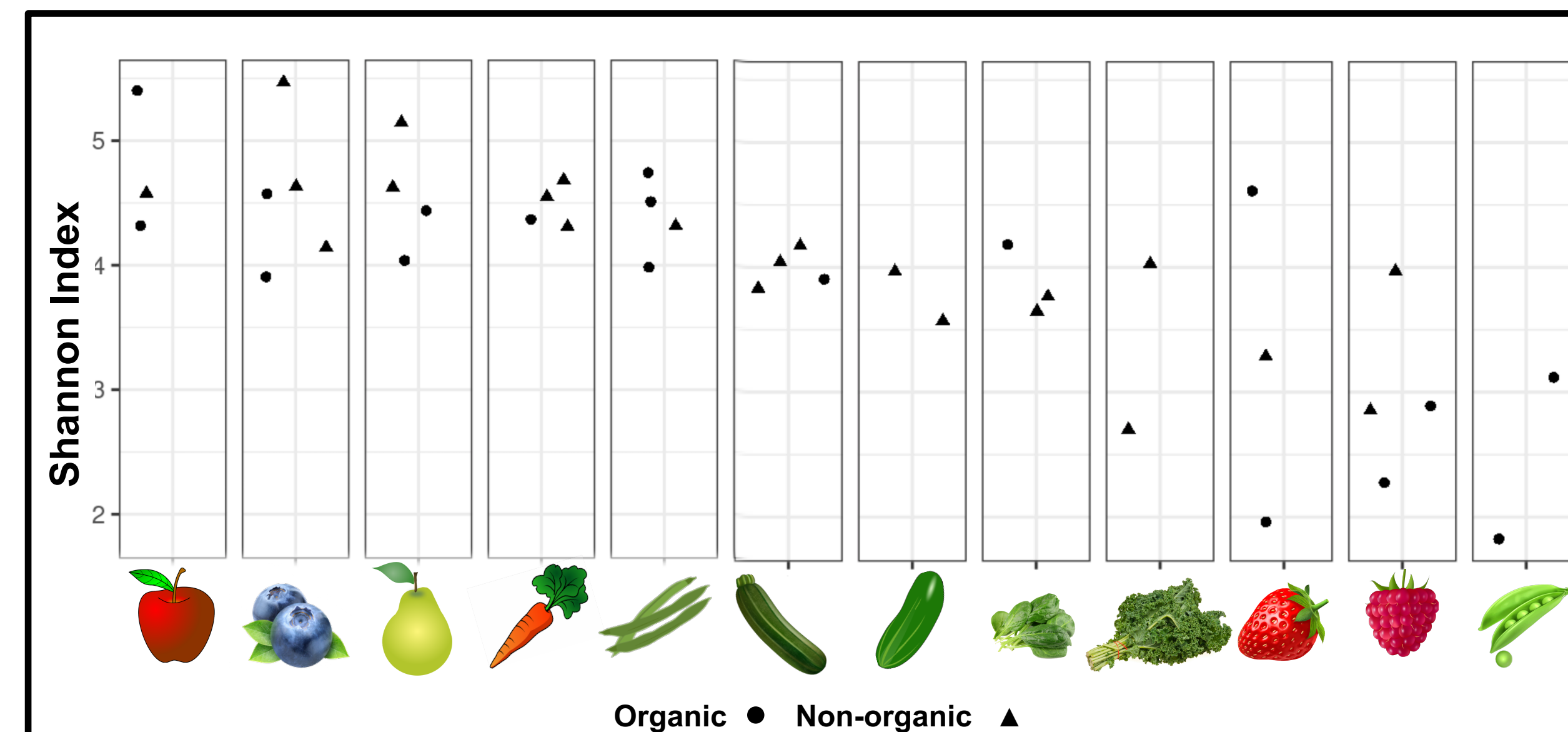


Figure 2. Analysis of alpha diversity by Shannon Index for 41 produce samples

Beta Diversity: Measure of how different microbial communities are *between samples*

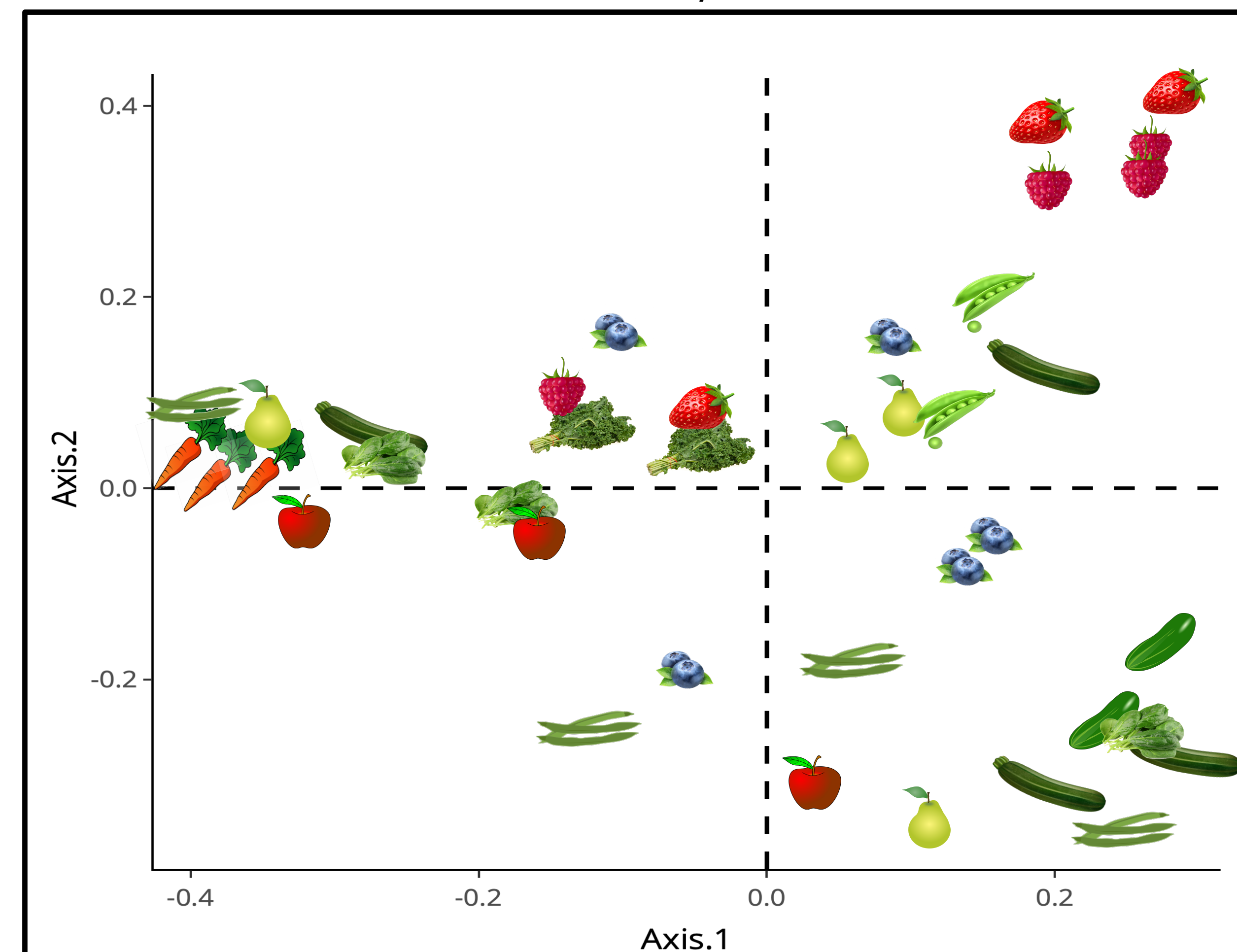
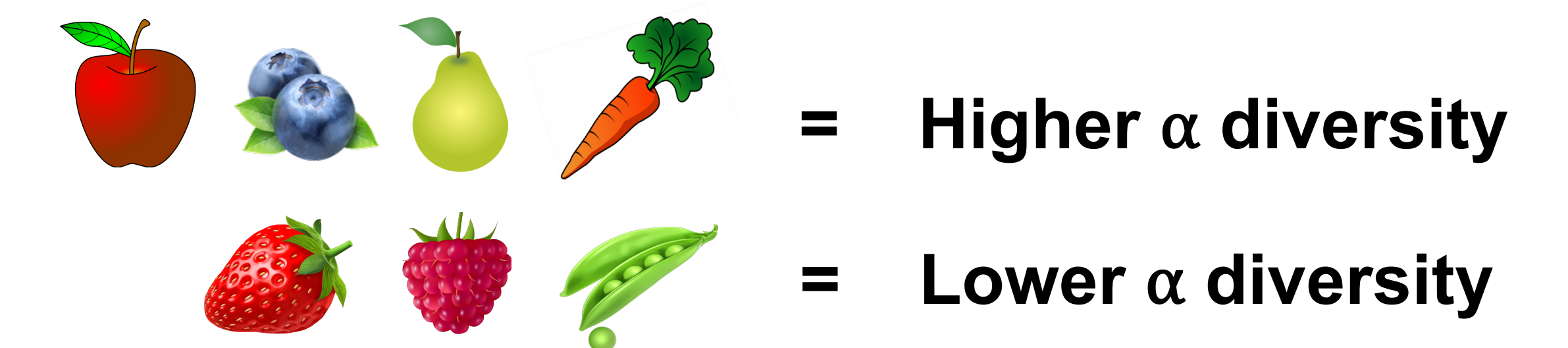


Figure 3. Beta diversity analysis by Principle Component Analysis derived from Bray-Curtis distances

CONCLUSIONS

Among alike produce samples, similarities and differences in microbial composition were observed.

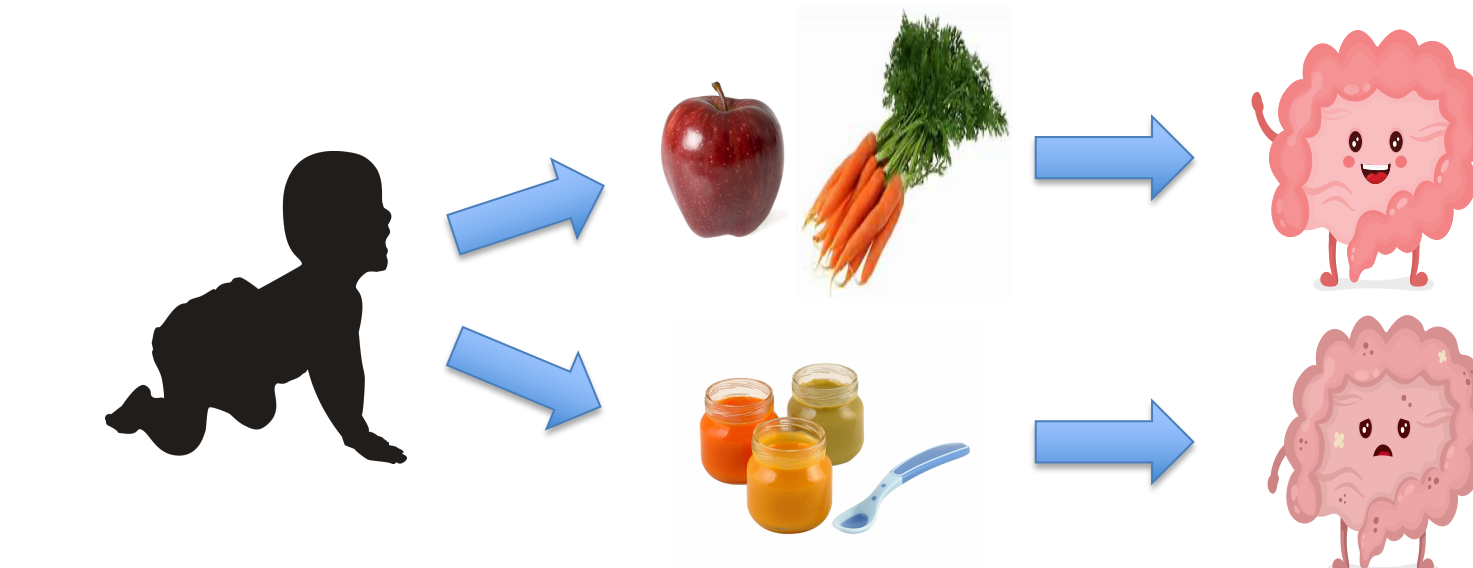
- Alpha diversity as calculated as Shannon index was relatively conserved among alike produce samples.



- Beta diversity showed some clustering among alike produce samples suggesting there is some conservation of microbial communities.
 - However, grouping structure is not well-defined suggesting that microbial communities are influenced by factors other than host type.

DISCUSSION

- Dietary interventions have shown promising results in the alteration of gut microbiome and high-fiber fruits and vegetables may be good sources beneficial bacterial.
- The microbial communities of fruits and vegetables are likely influenced by both the nutritional composition of the food as well as other factors such as pre-purchase handling, farming practices, grow location, soil conditions, and/or seasonal variation.
- Early introduction of fresh fruits and vegetables with rich and diverse bacterial communities may be beneficial to the development of a healthy gut microbiome.



ACKNOWLEDGEMENTS

Thank you to the University of Wisconsin School of Medicine and Public Health for funding this project!