



Thank you for participating in our community science project and sharing your ferment with us! Your food was tested in our lab using established microbiome genetic methods (DNA sequencing targeting the V4 region of bacterial 16S rRNA genes). With this technique, we were able to explore the total bacterial community in your ferments. Below you will find an overview of the microbial community composition in all foods tested followed by a detailed description of the most important bacterial genera.

Bacterial community overview EATLAC fermentations

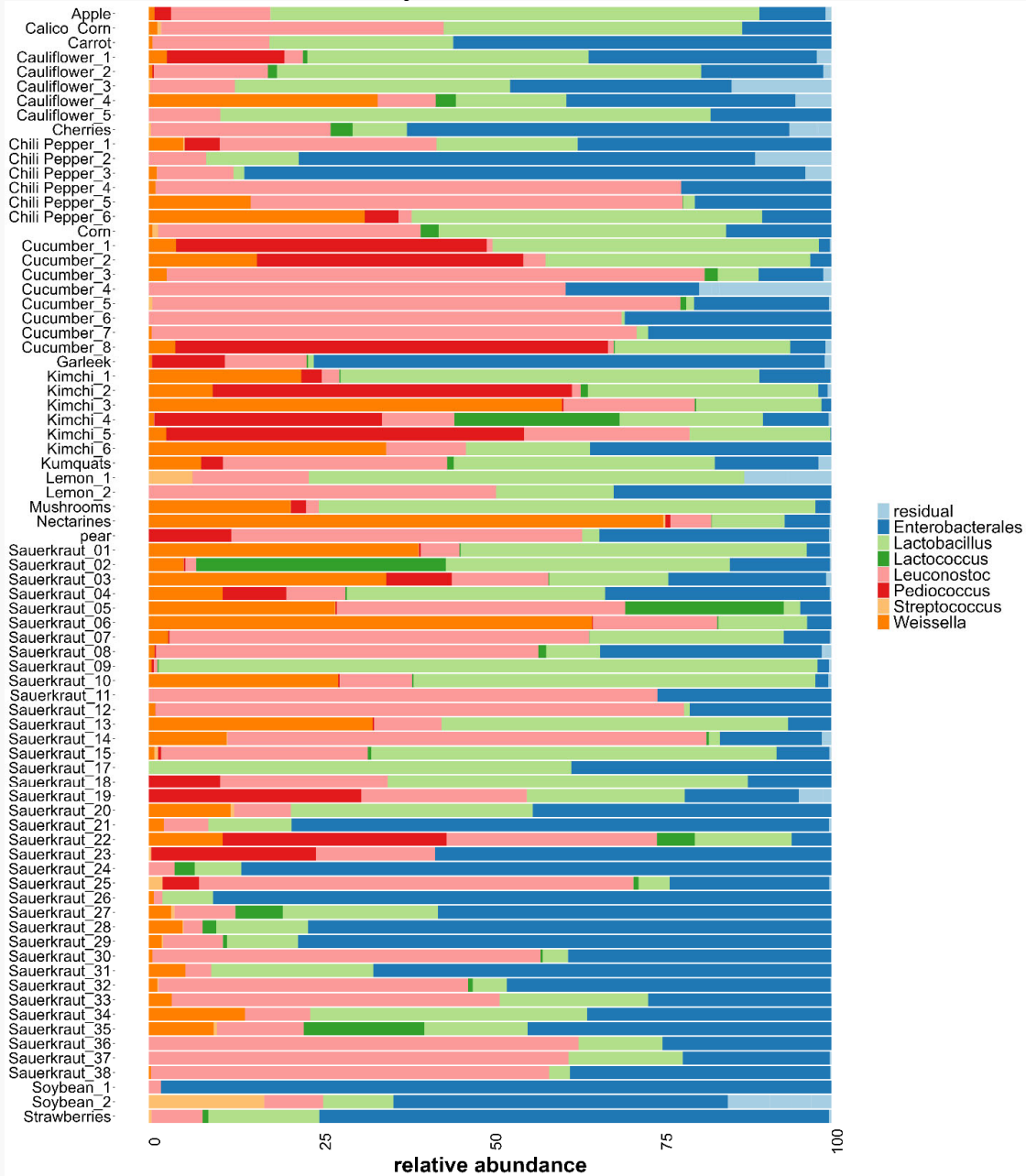


Figure Explanation: The bacterial community is visualized as the relative abundance (%) of different bacterial taxa within each ferment. Fermentations are labeled according to their primary fruit or vegetable ingredient. Your fermentations contained mostly *Lactobacillus*, *Leuconostoc*, *Weissella*, *Pediococcus*, and *Enterobacterales*. Those are also the same bacteria found within most vegetable ferments in other studies. The remaining bacteria identified as “residual” were less abundant and diverse.

Most important bacterial groups

Lactic acid bacteria (LAB)

Leuconostoc

Leuconostoc is a genus of Gram-positive bacteria within the *Lactobacillaceae* family. All species belonging to this genus are heterofermentative, meaning that they break down sugars into lactic acid, acetic acid, ethanol, and CO₂. *Leuconostoc* species are the first LAB commonly found within vegetable fermentations. It is known that they can survive and grow in the presence of a fairly high level of sugar and salt. During their growth they produce acid, resulting in a fast drop in pH, and production of CO₂ (hence you see bubbles during the first days of the fermentation). CO₂ production also makes the environment anaerobic and suitable for subsequent *Lactobacillus* growth. Fast acidification of the fermentation reduces the risk of colonization by unwanted bacteria and pathogens.

Lactobacillus

Lactobacillus is a genus of Gram-positive bacteria within the *Lactobacillaceae* family. *Lactobacillus* species tend to grow after *Leuconostoc* in fruit and vegetable fermentations. They are more acid-tolerant than *Leuconostoc* and mainly use homofermentation, meaning that they break down sugars to lactic acid. This acid production further decreases the pH of the fermented product, reducing the chance of colonization by spoilage bacteria. *Lactobacillus* species can improve the flavor, texture, and functional properties of fermented vegetables by the production of different bioactive compounds. They are often described as the good bacteria and probiotics but they should not be called probiotics until their health benefits have been proven by clinical studies.

Of note, the *Lactobacillus* genus was reclassified and split between 26 new genera. New *Lactobacillus* genera commonly found in fermented vegetables include *Lactiplantibacillus*, *Levilactobacillus*, *Lentilactobacillus*, and *Latilactobacillus*. Fermented vegetables are usually dominated by *Lactiplantibacillus* species at the end of the fermentation. The other genera can be found during the fermentation, but they will rarely reach high levels in the community.

Weissella

Weissella is a genus of Gram-positive bacteria within the *Lactobacillaceae* family. All species belonging to this genus are heterofermentative, meaning that they break down sugars into lactic acid, acetic acid, ethanol, and CO₂. *Weissella* species can be found in a wide range of habitats from the environment to a large variety of fermented foods. Like most lactic acid bacteria, they prefer nutrient-rich environments. *Weissella* species have been isolated from different traditional vegetable ferments such as kimchi and sauerkraut, where they play an important role in reducing the risk of colonization by unwanted bacteria. Studies have been performed exploring the antimicrobial capacity of *Weissella* species through organic acid and bacteriocin production.

Pediococcus

Pediococcus is a genus of Gram-positive bacteria within the *Lactobacillaceae* family. They are commonly found in vegetable based fermentations such as sauerkraut. All species belonging to this genus mainly use homofermentation, meaning that they break down sugars mainly to lactic acid. This acid production further decreases the pH of the fermented product, reducing the chance of colonization by spoilage bacteria. Isolated *Pediococcus* strains have been found to have antimicrobial effects against different spoilage bacteria.

Native vegetable bacteria

Enterobacterales

The surface of fresh fruits and vegetables is inhabited by a wide range of bacteria, native to the host plant. Most members of these native bacteria are classified as *Enterobacterales*, with common genera including *Pantoea* and *Enterobacter*. Members of this bacterial order are important during plant growth and health, but their numbers are typically minimized in fermented products. Due to the addition of salt and anaerobic conditions, these native bacteria are outcompeted by lactic acid bacteria during the fermentation process.

Of note, the presence of these native bacteria within the community profile of your ferment does not indicate failure of the fermentation. Our genetic methods are unable to distinguish between live and dead bacteria within your community. Fermentation parameters such as pH and salinity should always be used to test the success of the fermentation. The use of sufficient salt is crucial to support organic acid production by lactic acid bacteria and results in pH reductions to below pH 4.6. For food safety, it is important that your ferments reach a pH below 4.6 before consumption. Finally, the presence of mold within or on the surface of your fermented vegetable is also unwanted. Dispose of the fermentation and thoroughly clean all your equipment before restarting.

If you have any additional questions, please reach out to us by email: eatlac@ucdavis.edu and follow us on social media to keep up to date with our latest findings.

Thank you for all your support and enthusiasm!