

Accurate monitoring of living and total bacterial populations in milk for improved microbial management

Zhengyao Xue

Ph.D. student

Department of Food Science & Technology

The University of California, Davis

Microbes enter milk from a variety of sources



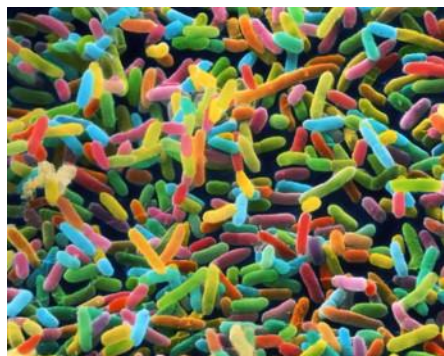
Animal hide
Teat surface
Farm environment



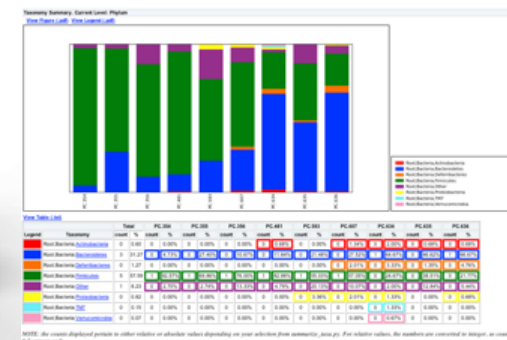
Milking equipment
Handling personnel
Farm storage tanker

Monitoring microbial populations in milk is crucial for milk quality

Comprehensive identification of bacteria

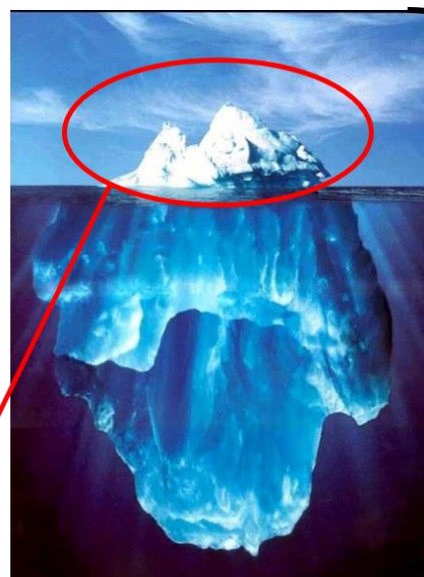


Molecular (DNA)



Identify bacteria
Comprehensive
High throughput (HTP)
Automation is possible

Laboratory culture



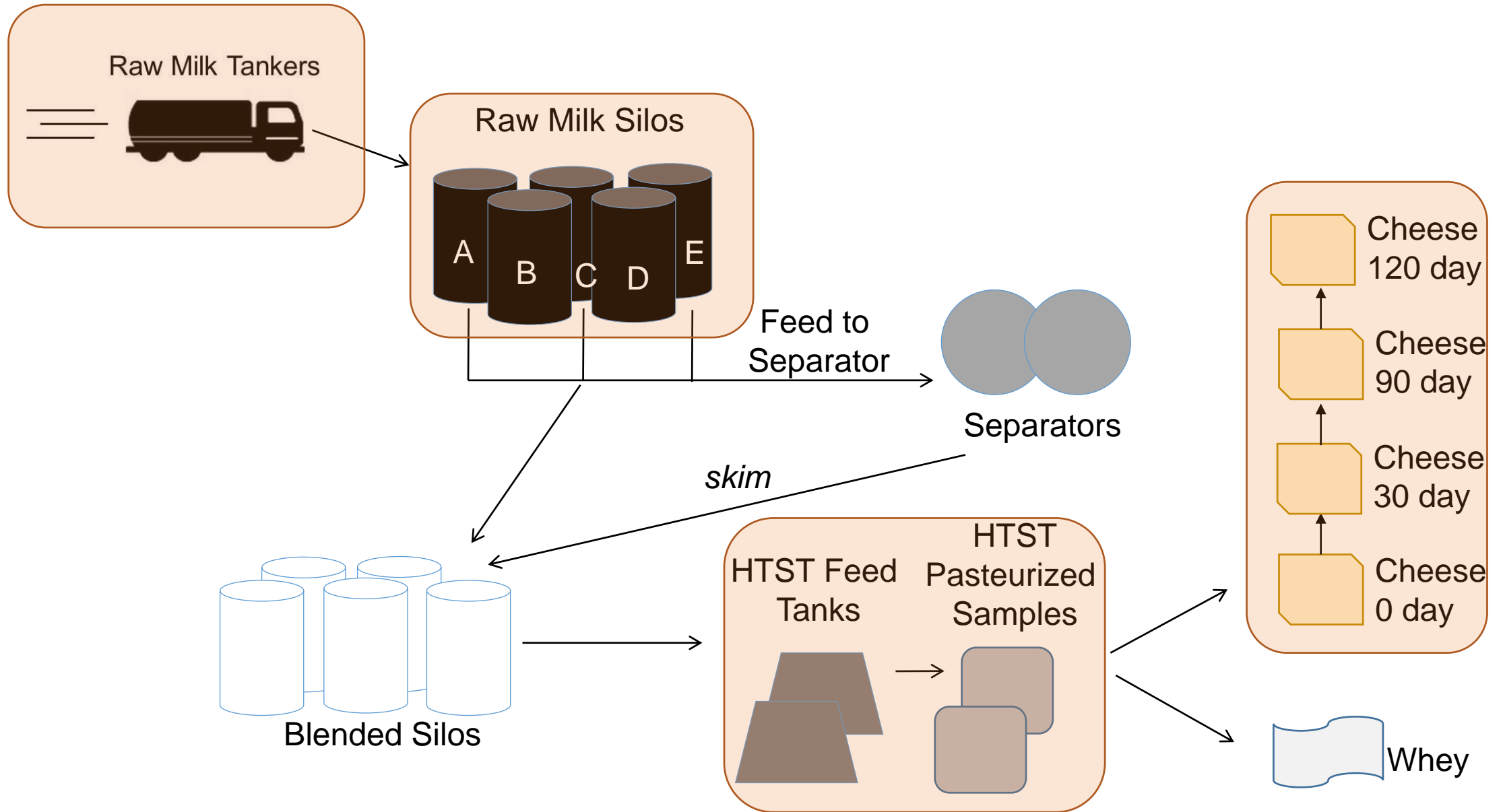
Total bacterial diversity on earth

Quantification
Not useful for identification
Slow/Laborious
Biased

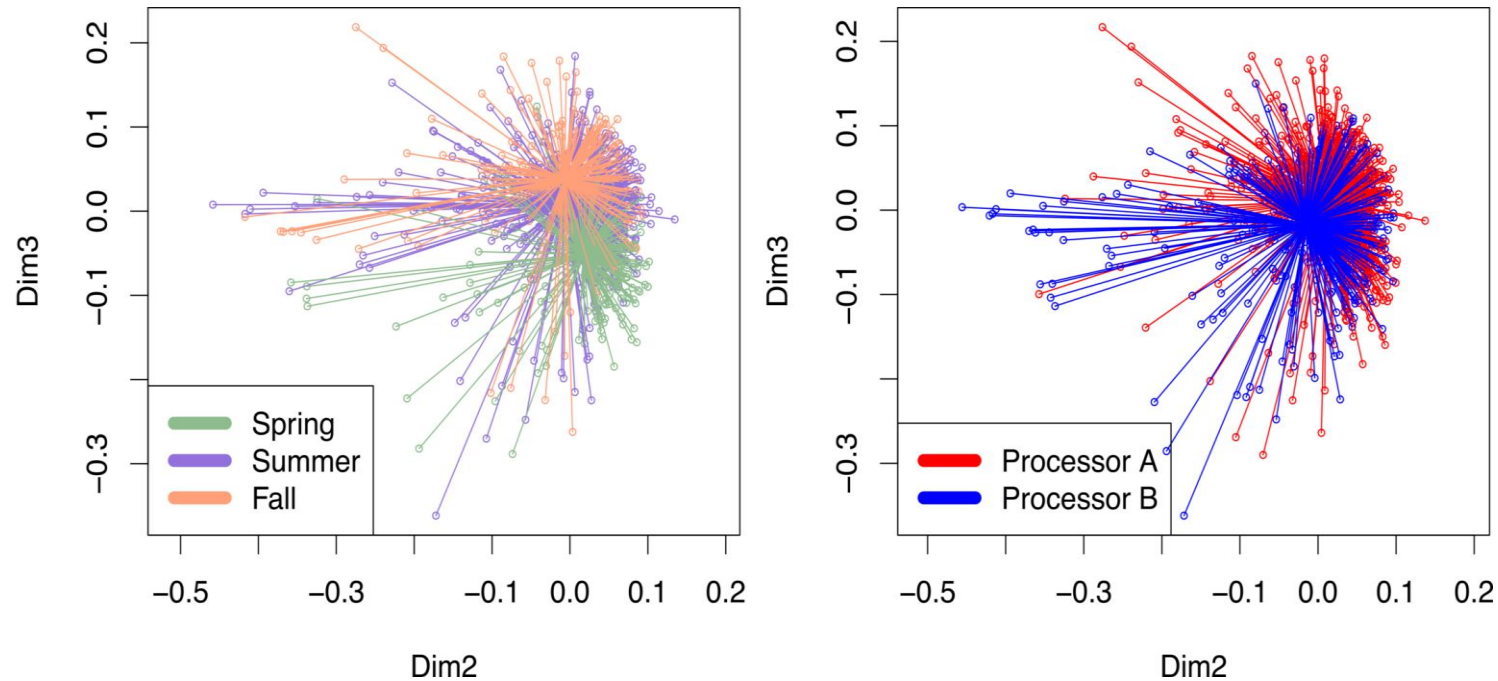


Culturable bacteria

HTP bacterial detection for CA dairy processors



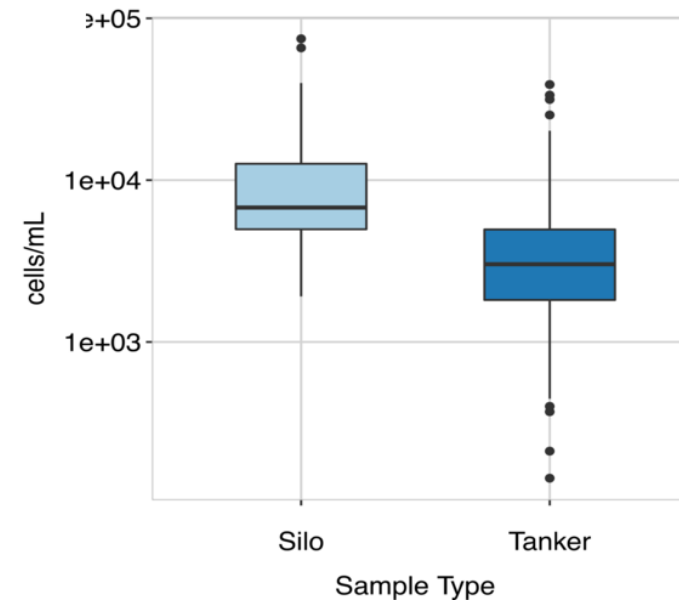
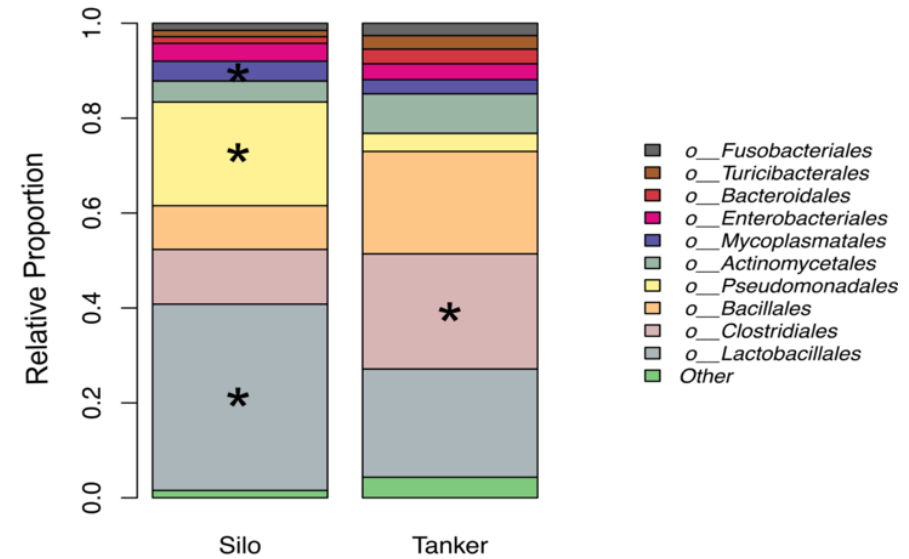
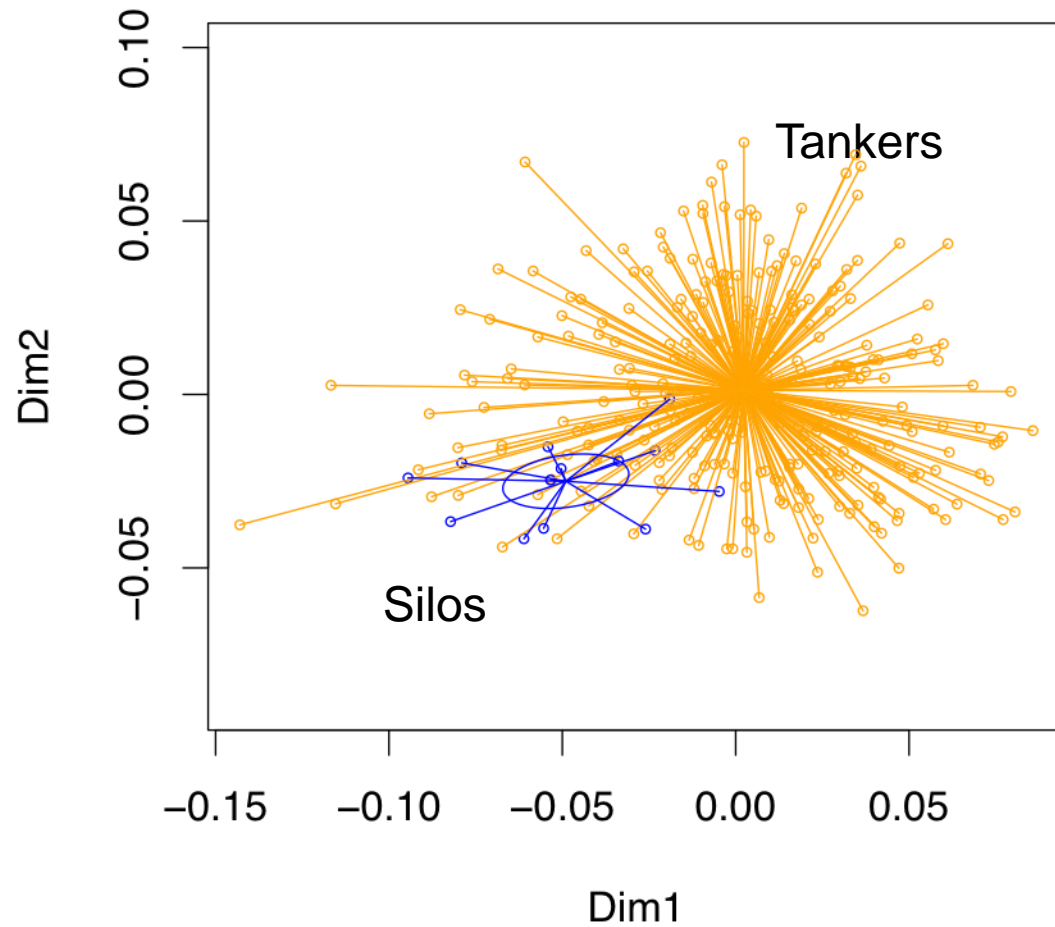
Raw tanker milk contains a core microbiome that fluctuates between seasons



29 bacterial taxa detected in all raw milk

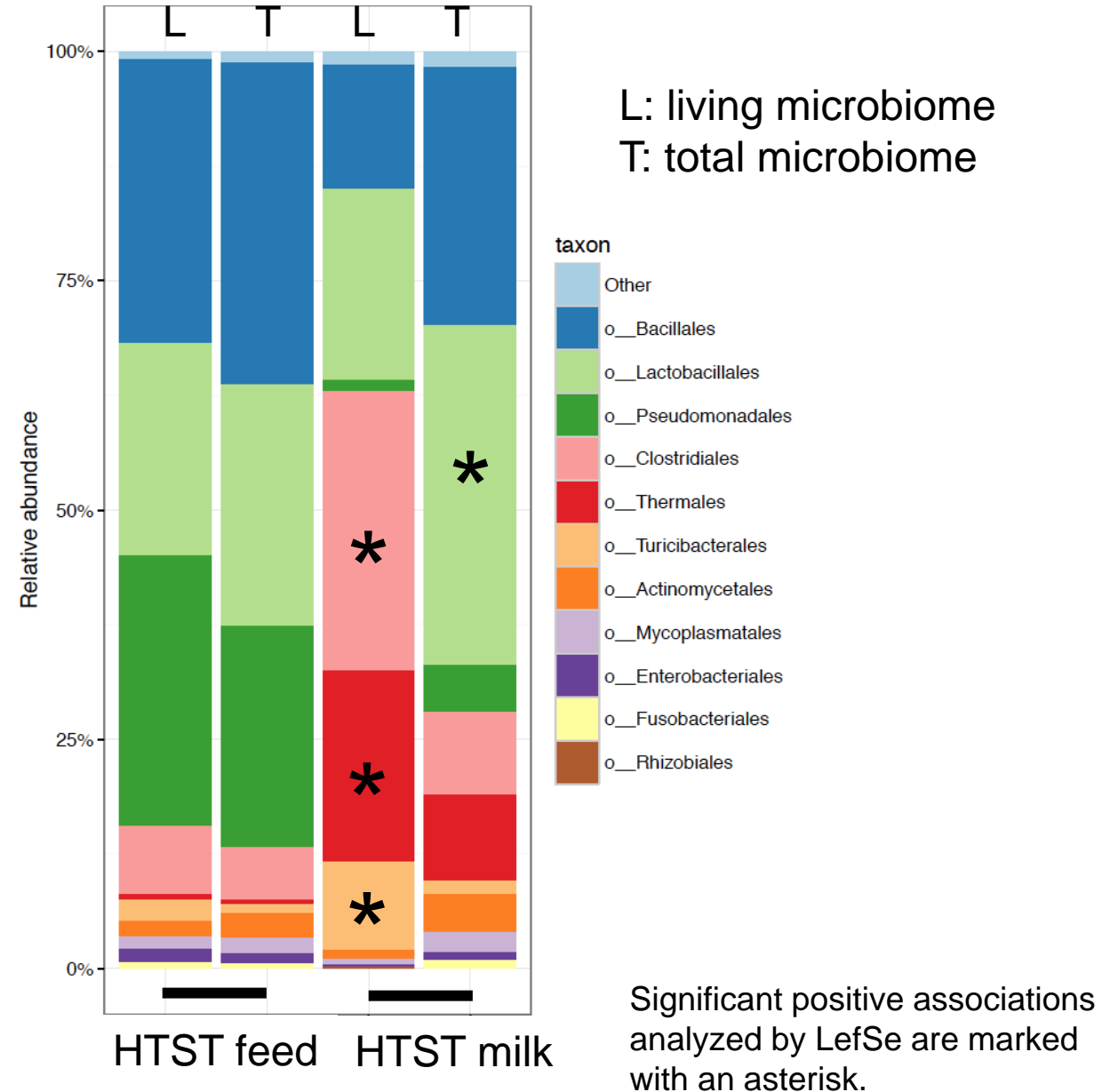
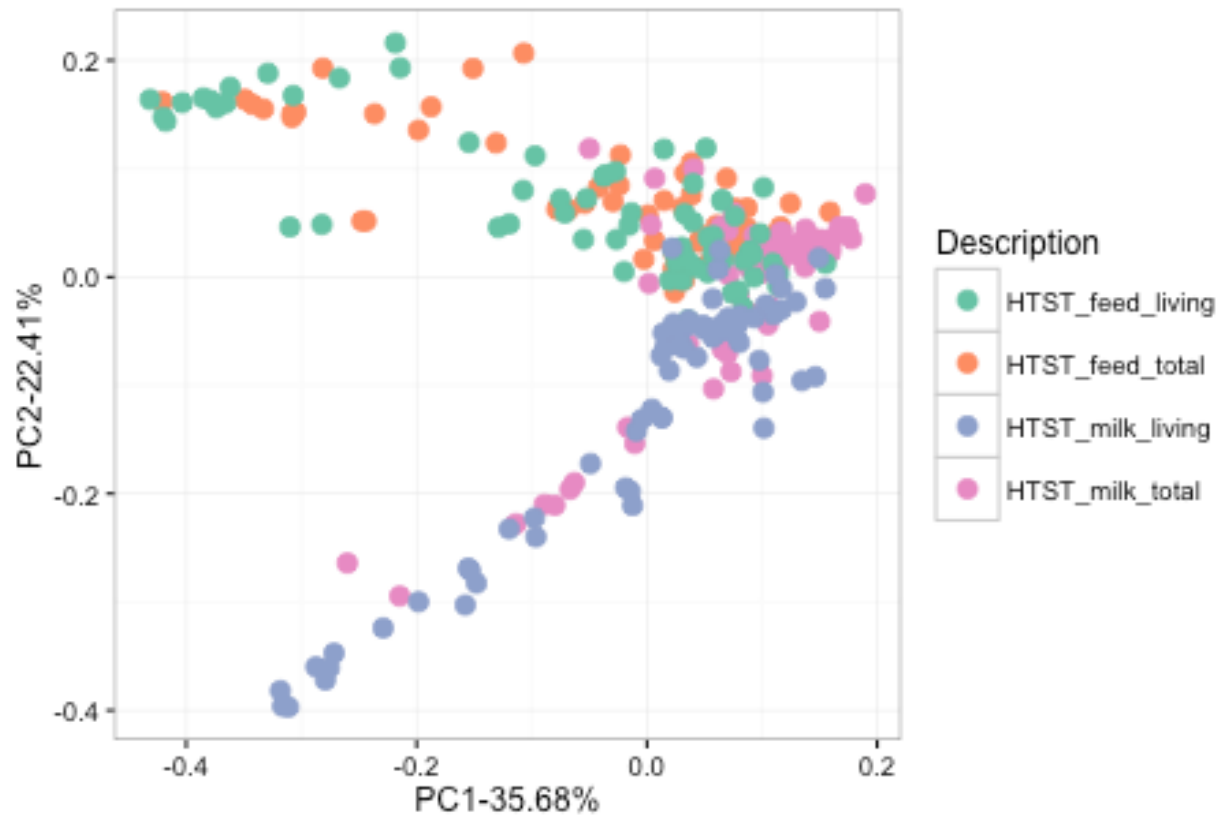
- Milk collected in the spring contained the highest median species richness and total bacterial cell numbers
- No location-dependent differences

Bacterial composition changes at the dairy processor

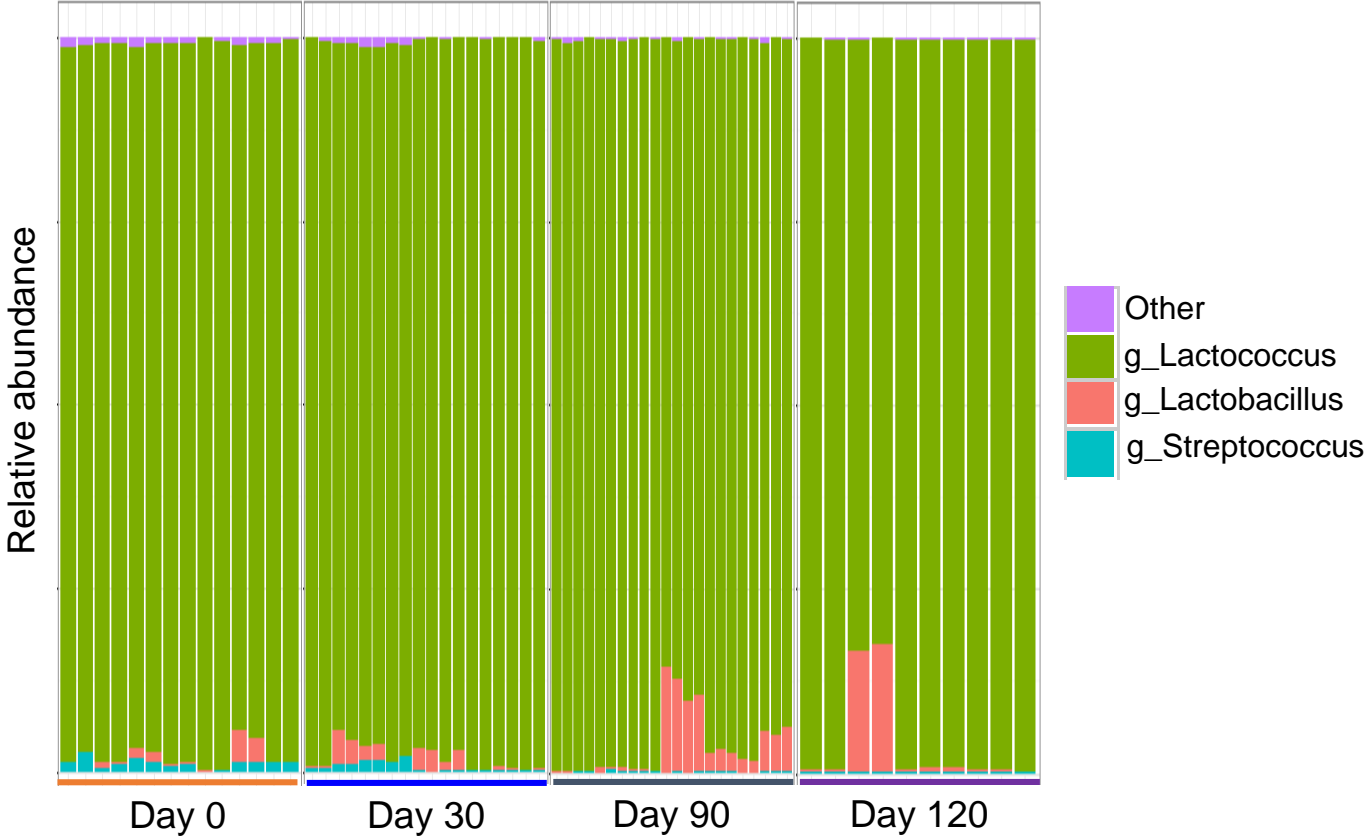


Significant positive associations analyzed by MaAsLin and LefSe are marked with an asterisk.

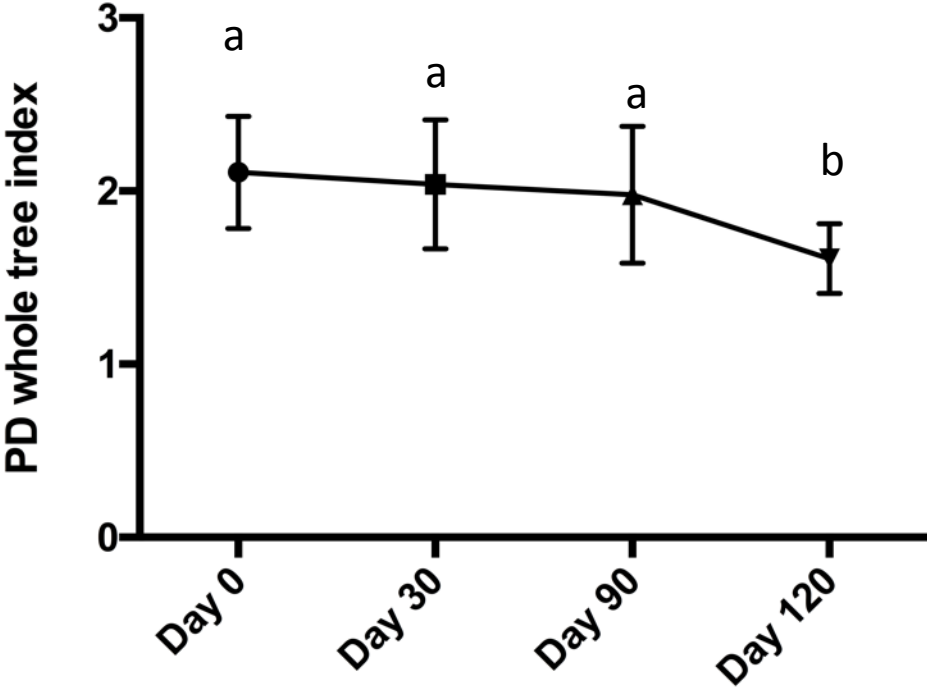
Pasteurization alters the milk microbiota



The cheese microbiota is dominated by a few taxa



Cheddar cheese was sampled in this study.



Cheese microbiota diversity declines with aging period

Significant differences are indicated by the presence of different lowercase letters.

Summary

- The bacterial composition of raw milk is seasonal and changes during storage and processing.
- Cheese microbiota is dominated by a few taxa and the diversity decreases over time.
- With automation, HTP sequencing can have quick turnaround time for identification of total and living bacterial communities.
- Insights into the bacterial species along the dairy processing chain will enable **improved microbial management** for quality assurance.

Acknowledgements



Mary Kable, Ph.D.
Maria Marco, Ph.D.
Dustin Heeney
Annabelle Yu
Zach Bendiks
Xiaochen Yin
Zach Quart
Zhengyuan Zhai, Ph.D.
Brendan McCarthy-Sinclair
Elissa Goldman
Patricia Matus

Jeremy McLeod, Ph.D.
Jessie Heidenreich, Ph.D.

