A Taste for Diversity: Microbial Community Shifts in Sheep's Milk Cheeses

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Revisiting a study of sheep's milk cheese microbiomes in Brazil.



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Molecular characterization of the bacterial communities present in sheep's milk and cheese produced in South Brazilian Region via 16S rRNA gene metabarcoding sequencing

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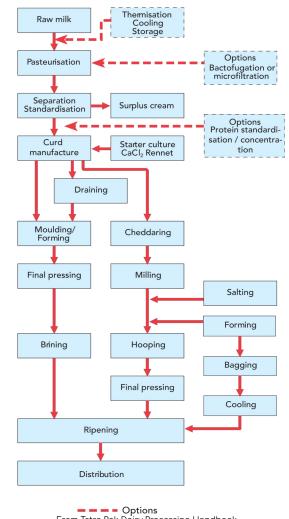
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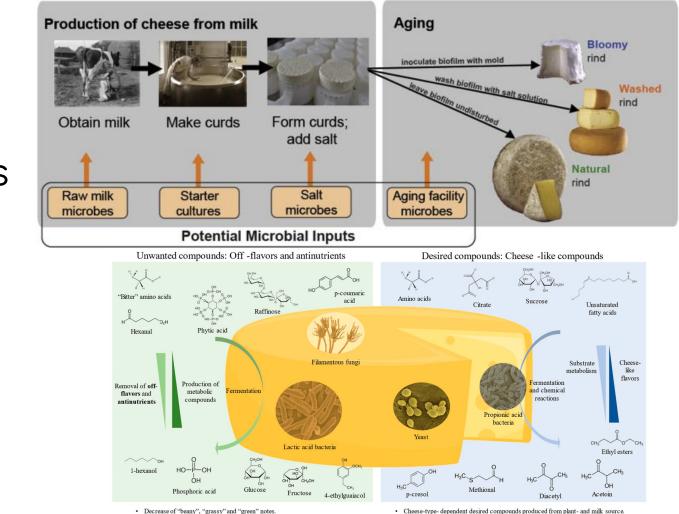


Different types of cheeses have different processing parameters, regulations, and starter cultures.

- Colonial: aged, pressed cheese, similar to cheddar
- Feta-type: brined, crumbly, short/minimal aging
- Fresh: No aging, high moisture, minimal processing
- Pecorino-type: hard, dry-aged



Microbial communities important role in cheese production.



· General "buttery", "sour milk", "sweet" and "floral" in cheeses.

· Specific "sulfurous", "fruity" and "moldy" notes for some cheeses.

· Increase mineral, vitamin and amino acid bioavailability and protein digestibility

· Decrease bitter and astringent tastes.

· Decrease health side-effects such as flatulence.

Top figure from Benjamin Wolf et al., 2014 Bottom figure from Blandine Genet et al., 2023 Does cheese type influence microbial community composition?

And are those differences only visible at finer taxonomic scales?

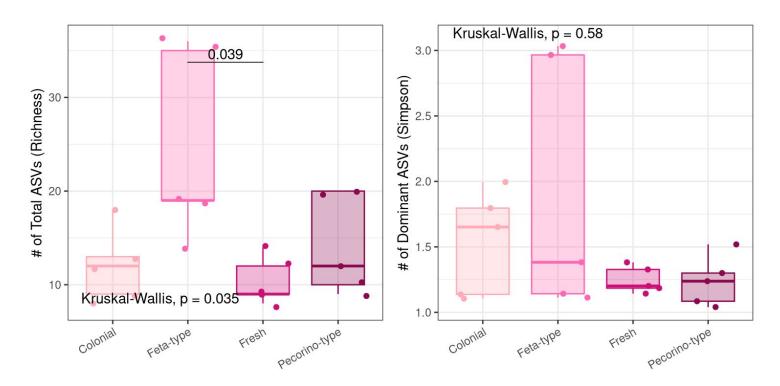
<u>Null</u>

Cheese type does not influence microbial community composition.

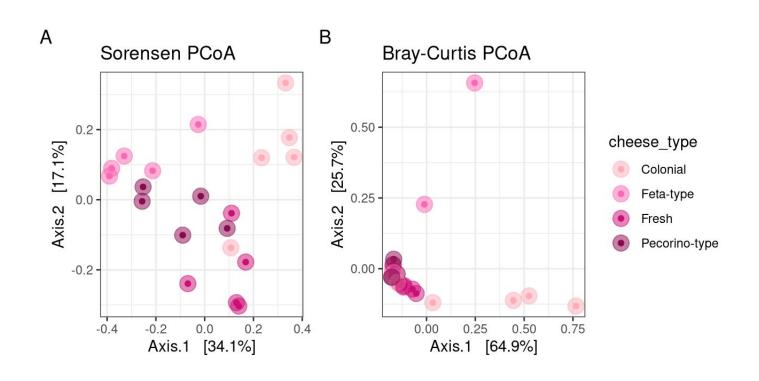
<u>Alternative</u>

Cheese type does influence microbial community composition.

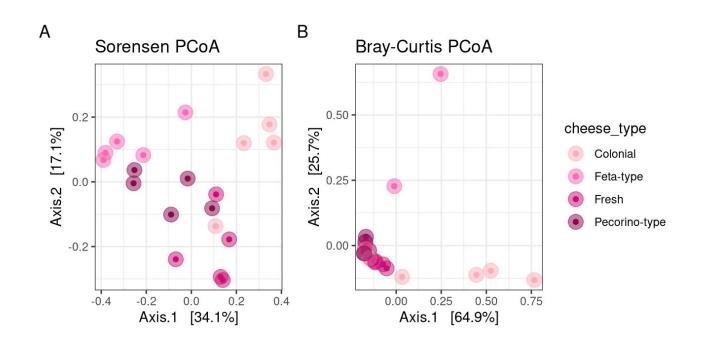
Some cheese types harbor a broader range of microbes, but overall cheese types are dominated by a few taxa.



Community shifts are cheese dependent, but not uniform



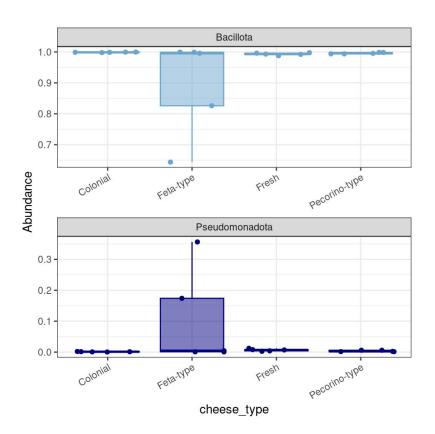
Community shifts are cheese dependent, but not uniform. Batch dependent nature of cheese manufacturing may be a more accurate driver of change.



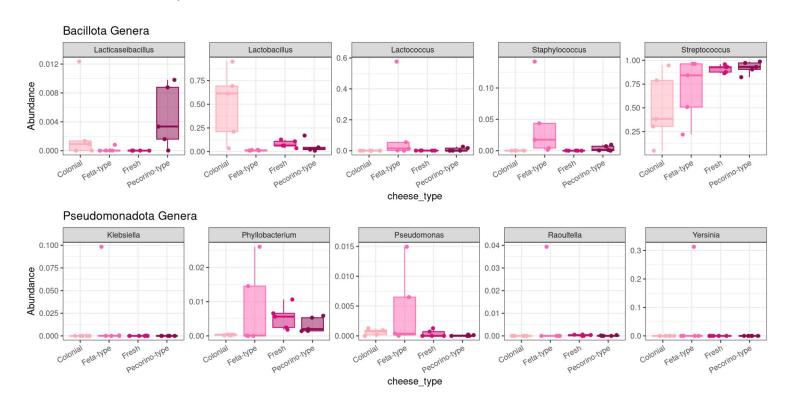
Does cheese type influence microbial community composition? Yes!

And are those differences only visible at finer taxonomic scales?

At the phylum level, cheese type shows limited influence on microbial composition.



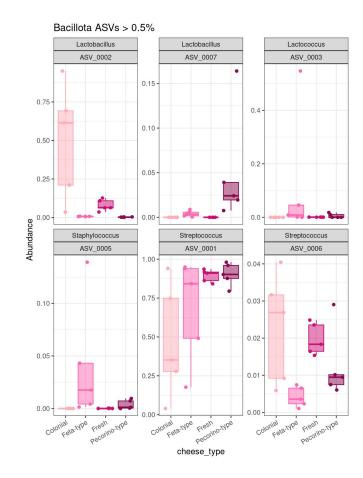
Dominant genera like *Streptococcus* appear across all types potentially as a starter culture. Others like *Pseudomonas* are sporadic and may reflect environmental contamination.



Distinct ASVs dominate different cheese types.

Streptococcus ASV_0001 is most abundant in Pecorino-type, while Lactobacillus ASV_0002 is highest in Colonial

Varience within cheese-types



Does cheese type influence microbial community composition? Potentially!

And are those differences only visible at finer taxonomic scales? Yes!



Cheese type does not influence microbial community composition.

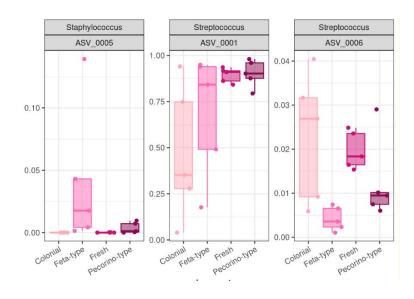
<u> Alternative</u>

Cheese type does influence microbial community composition.

Food microbial communities are a great example as to why absolute data matters!

Who wants to eat cheese that has this in it?!

Indicative of poor pasteurization, mastitis infections, farm/facility sanitation conditions, even phages. Without absolute data it is difficult to draw biological conclusions.



Note: One of these *Streptococcus* ASVs is most likely a probiotic, while another is most likely a pathogen but without context we don't know.

Yersinia in feta-type cheese as a model for the importance of microbial monitoring in food processing.



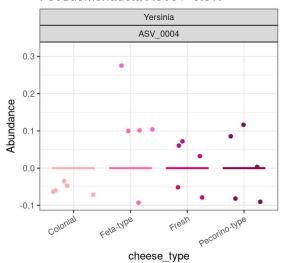




Image generated with Al

Where this dataset falls short and why that matters

<u>Metadata</u> would dramatically change the interpretation of these results.

- Pasteurization and processing (salt!)
- Starter cultures
- Phages

Level of contaminants limit the biological interpretations happening within the system



