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CHARACTERIZATION OF BACTERIAL COMMUNITIES DURING BOVINE RAW MILK AND ARTISANAL UNCOOKED PRESSED CHEESE PRODUCTION: IMPLICATION FOR DAIRY PRODUCTS SAFETY AND QUALITY

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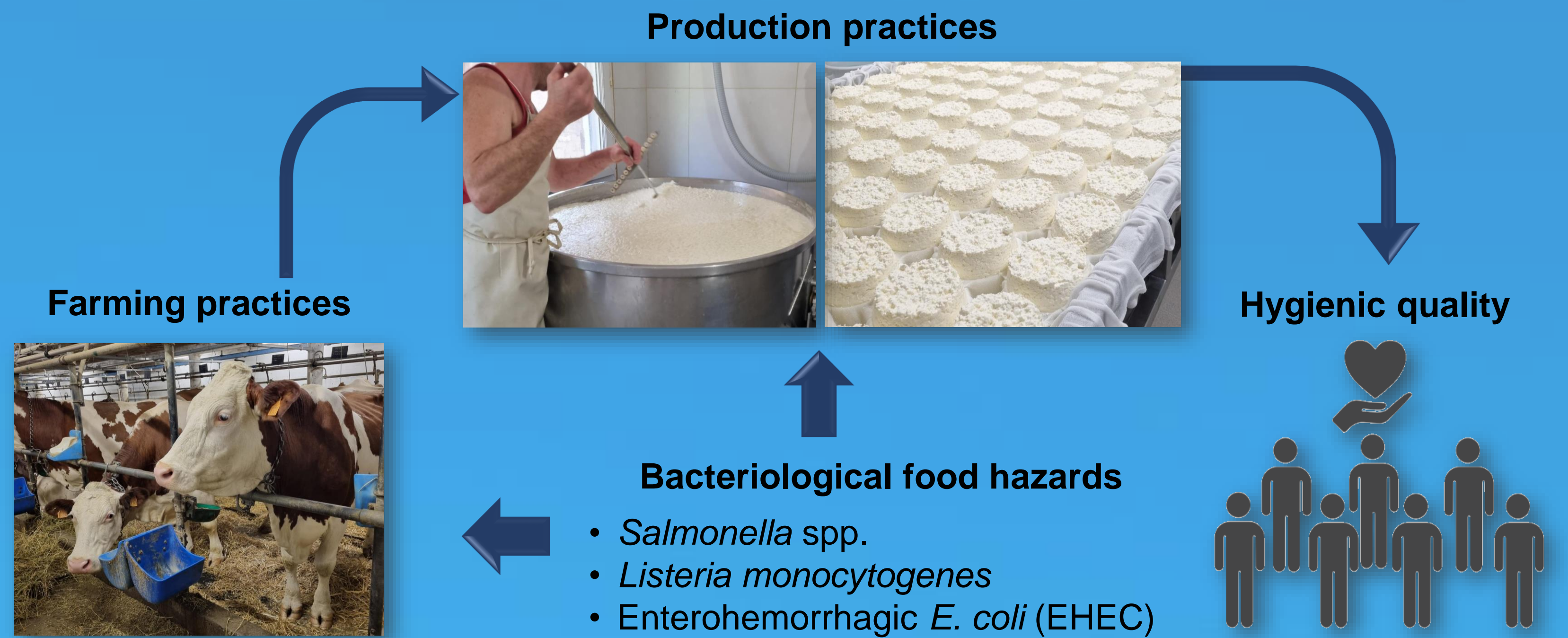
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INTRODUCTION

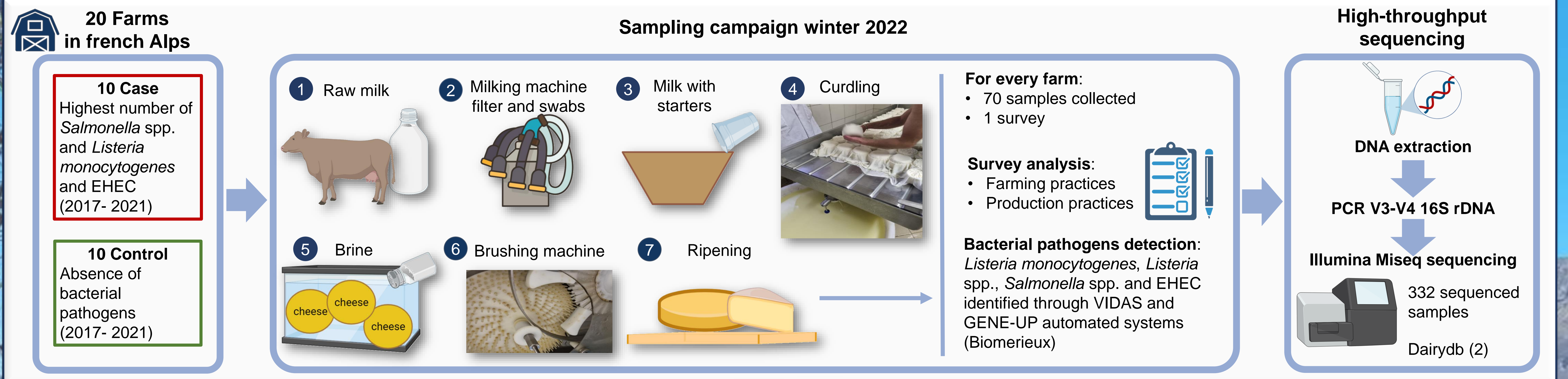
The link between the composition of bacterial communities and the potential contamination of dairy products by bacterial pathogens remains unclear (1). The sources of bacterial contamination of artisanal uncooked pressed cheese (UPC) and the risk factors during farming, milking and processing require further investigation.

OBJECTIVES

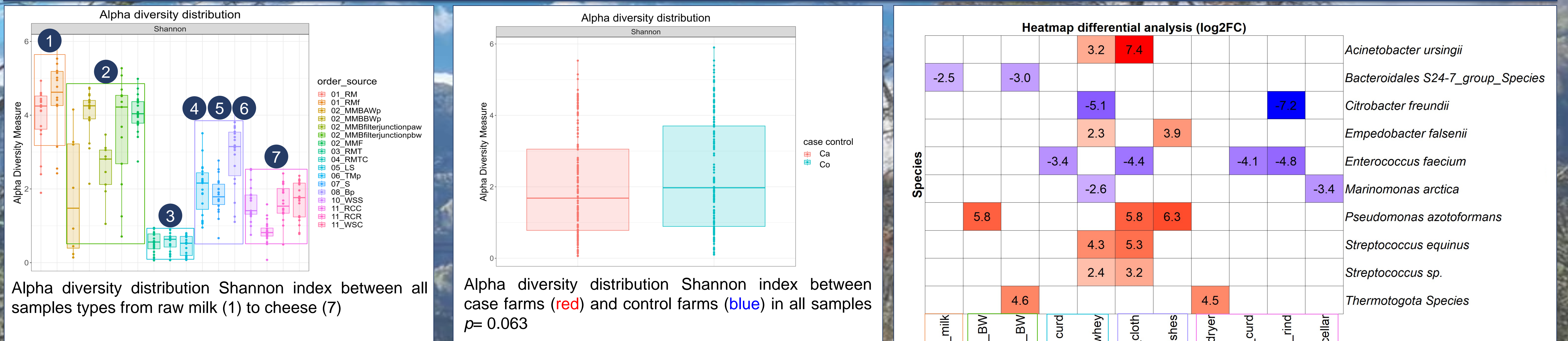
1. Profile the bacterial microflora on contact surfaces and within UPC;
2. Pinpoint farming and production practices impacting the bacterial microflora and the hygienic quality of raw milk and UPC;
3. Evaluate the influence of contact surface's bacterial communities on hygienic quality of UPC.



MATERIALS AND METHODS



RESULTS



Farming and transformation practices (survey analysis)

Significant variables between case and control farms:

• Delay in cheese washing:

- mean case 4.5 days < mean control 5.5 days
- $p=0.028$

• Use of vaccinations other than the required ones:

- control farms used vaccinations more than case
- $p=0.069$

• Ripening time (cellar):

- mean case 8.7 days < mean control 12.3 days
- $p=0.087$



CONCLUSIONS

- The study pointed out high bacterial diversity in raw milk, milk filters, and all contact surfaces. Diversity was reduced after starters addition.
- Samples from control farms showed higher diversity compared to case farms.
- The comparison between case and control farms illustrated significant factors (delay in cheese washing, additional vaccination and ripening time).
- Some bacterial species were associated mainly to control farms (e.g. *Citrobacter freundii*, *Marinomonas arctica*) or case farms (e.g. *Acinetobacter ursingii*, *Pseudomonas azotoformans*) depending on the analysed sample type. Further analyses should be done to analyze the correlations between these bacterial species and the variables related to farming and/or production practices.
- A further sampling campaign was carried out in summer 2023. Analysis are ongoing and results will be integrated to the previous one of the winter campaign.

REFERENCES

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- (2) Meola, M., Rifa, E., Shani, N., Delbès, C., Berthoud, H., & Chassard, C. (2019). DAIRYdb: A manually curated reference database for improved taxonomy annotation of 16S rRNA gene sequences from dairy products. *BMC Genomics*, 20(1), 560. <https://doi.org/10.1186/s12864-019-5914-8>