

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

Alisia Chiadò Rana<sup>1</sup>, Charlotte Valat<sup>2</sup>, Géraldine Cazeau<sup>2</sup>, Kevin Béthune<sup>3</sup>, Vincent Chochois<sup>3</sup>, Corinne Teyssier<sup>1</sup>

<sup>1</sup>Qualisud, Univ Montpellier, CIRAD, Avignon Université, Institut Agro, IRD, Univ de La Réunion, Montpellier, France

<sup>2</sup>Unité Epidémiologie et Appui à la Surveillance, ANSES Laboratoire de Lyon - Université de Lyon, Lyon, France

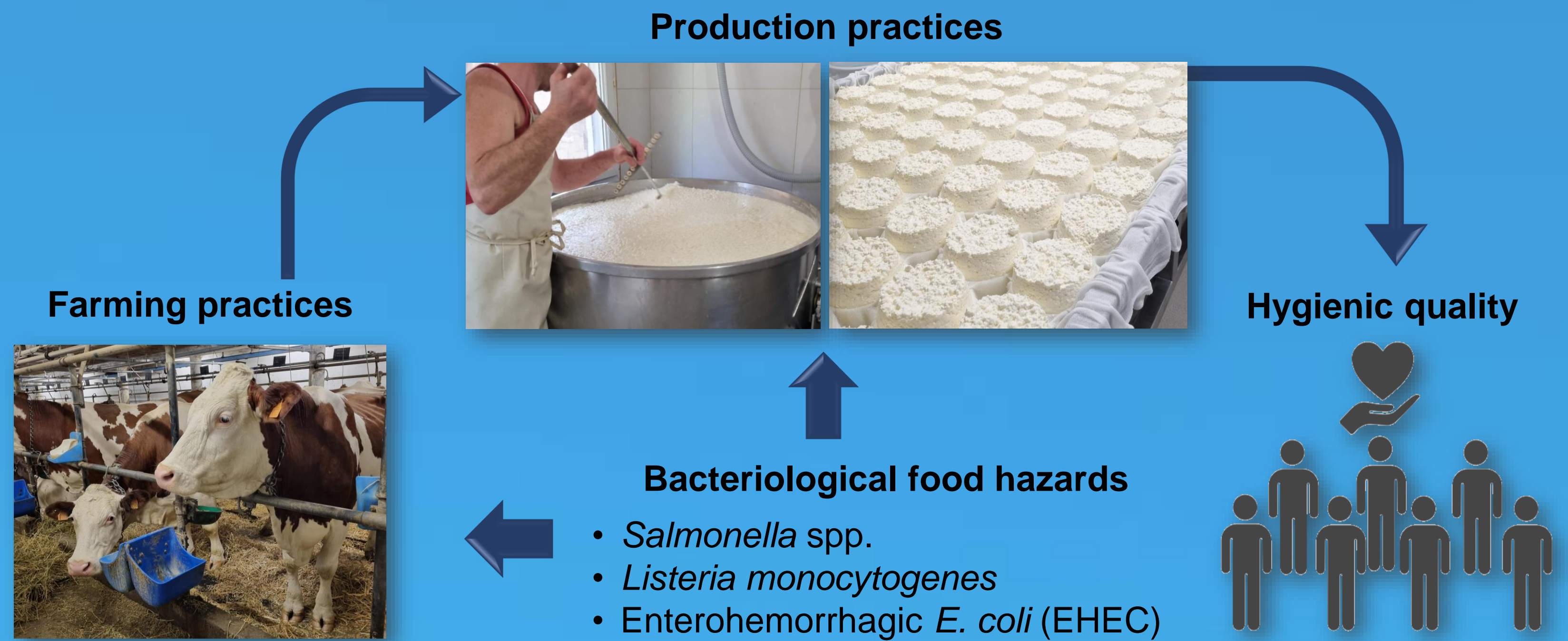
<sup>3</sup>CIRAD, UMR Qualisud, F-34398 Montpellier, France. Qualisud, Univ Montpellier, Avignon Université, CIRAD, Institut Agro, IRD, Université de La Réunion, Montpellier, France  
 alisia.chiado-rana@umontpellier.fr ; charlotte.valat@anses.fr; geraldine.cazeau@anses.fr; kevin.bethune@cirad.fr; vincent.chochois@cirad.fr; corinne.teyssier@umontpellier.fr

## INTRODUCTION

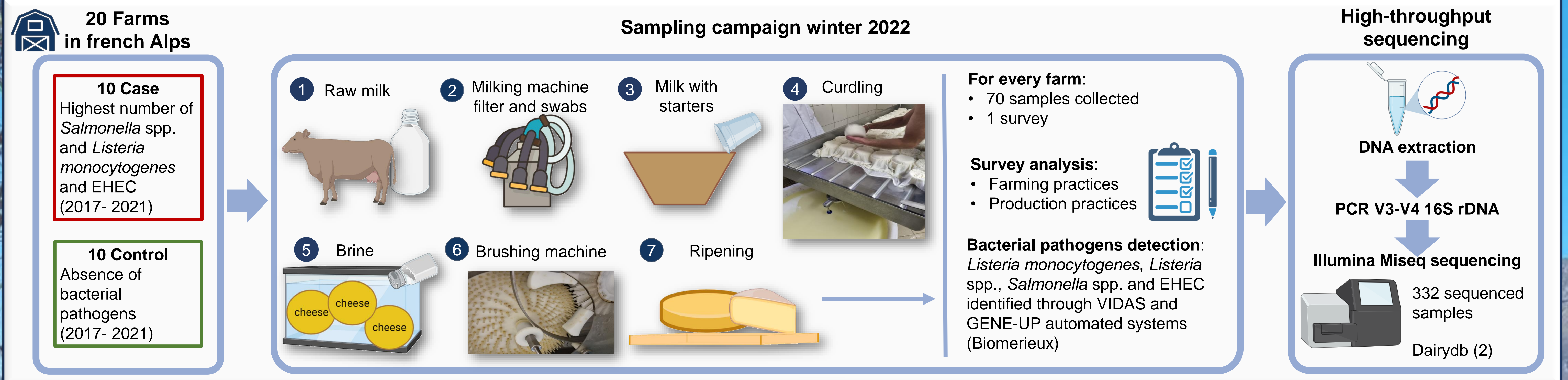
The link between the composition of bacterial communities and the potential contamination of dairy products by bacterial pathogens remains unclear (1). The sources of bacterial contamination of artisanal uncooked pressed cheese (UPC) and the risk factors during farming, milking and processing require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

## OBJECTIVES

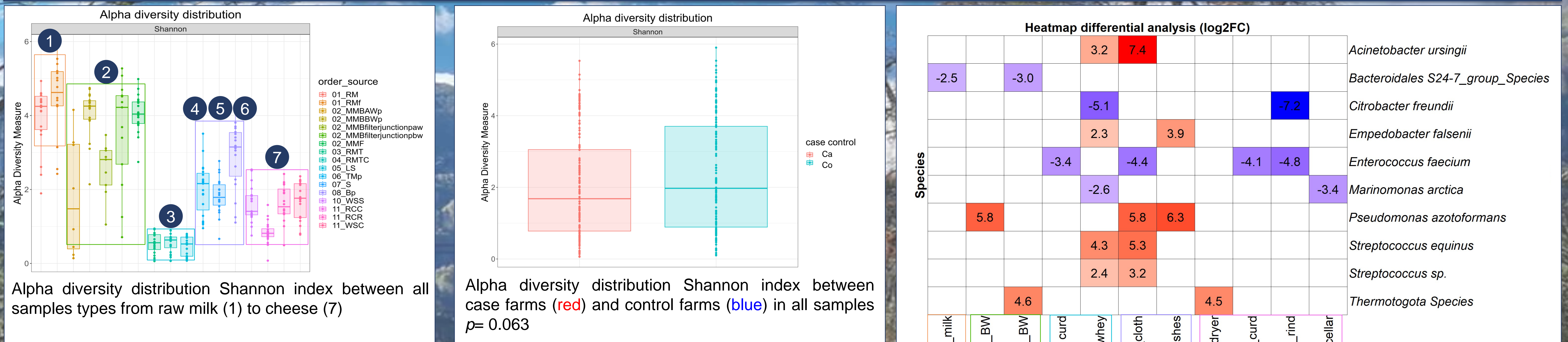
1. Profile the bacterial microflora on contact surfaces and within UPC;
2. Pinpoint farming and production practices impacting the bacterial microflora and the hygienic quality of raw milk and UPC;
3. Evaluate the influence of contact surface's bacterial communities on hygienic quality of UPC.



## 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

- (1) Martin, N. H., Evanowski, R. L., & Wiedmann, M. (2023). Invited review: Redefining raw milk quality—Evaluation of raw milk microbiological parameters to ensure high-quality processed dairy products. *Journal of Dairy Science*, 106(3), 1502–1517. <https://doi.org/10.3168/jds.2022-22416>
- (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>