## INRAe



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Other relevant information: UMR545 Fromage contributes to the INRAE metaprogramme HOLOFLUX

The three most important milestones in my scientific career:

- 1. 2000: PhD in microbial ecology
- 2012- : Implementation of metagenomic approaches to highlight the role of teat skin microbiota and milk production practices in the assembly of milk and cheese microbiota.
- 3. 2020: Awarded the INRAE flagship project TANDEM on microbial transfers in the food chain: https://www6.inrae.fr/holoflux/Nos-Actions/Projets-emblematiques/TANDEM

I'm looking forward to the scientific conference on raw milk products because...

... I'm looking forward to meet and exchange with scientists from different disciplines and socio-economic stakeholders committed to developing knowledge about raw milk cheeses and promoting them.

## Short Summary of the talk (max. 300 words)

## Microbial transfers across a food chain: from grassland to cheese using systemic and multidisciplinary approaches

In the context of major changes in production systems (climate, agricultural practices, etc.), a better understanding of the structuring and functioning drivers of microbial communities in a systemic approach is mandatory to reconcile the different dimensions of food quality and global health. This is a major scientific challenge in microbial ecology and fully relevant for farms involved in the production of raw milk cheese, which are mostly associated with a terroir and a complex microbiota. Dairy farming systems represent a set of interconnected ecosystems from the soil to the product, involving a great diversity of holobionts (grassland, ruminant, consumer), environmental and food microbiomes. Through examples selected from the work of our research group and from the literature, integrating different metagenomic approaches but also animal sciences, food technology and socio-anthropology, we will highlight the knowledge on microbial diversity, primary production, milk and cheese processing practices that modulate local microbiota assemblages and potential microbial transfers at the scale of the dairy system.