



# How silage and raw milk affect dairy product quality

Duration: 2013 – 2017

## Highlights

- Raw milk also presents an environment that can be contaminated by thermo-resistant flora and spores from fodder and indigenous flora.
- The microbiological quality of milk is therefore a major commercial issue and a constant technological challenge both on farms and in plants.
- Silage is humid fodder that is preserved through the addition of lactic acid bacteria inoculants.
- These aromatic lactic acid bacteria can have an undesirable impact on milk acidification and on the organoleptic quality of processed dairy products.
- Twenty-four farms divided into five groups that are representative of the primary cow feeding methods were sampled two times to determine the prevalence and diversity of the microbiota of silage and raw milk.
- The lactic acid bacteria selected from 1,400 isolates from silage and raw milk from the 24 farms will be tested for their resistance to heat treatment and their contribution to the production of volatile compounds during the production and ageing of cheddar cheese.
- The anticipated results will help farmers identify the best silage management practices in order to optimize the microbiological quality of milk and help processors control the sources of microbial contaminants.
- While *Lactobacillus buchneri* is prevalent in both inoculated and uninoculated silage, the species is rarely found in raw milk.
- Two of the strains isolated from raw milk—identified as *Lactobacillus casei* and *Lactobacillus plantarum*—were selected for their thermoresistance. In the Pearce test (Cheddar cheese production), these strains did not have an impact on the acidification kinetics of *Lactoccus lactis* SK11 starter culture; however, in a curd model, they were able to produce volatile components during the ripening stage.

## Objectives

- GENERAL OBJECTIVE: Determine the prevalence and diversity of the microbiota of silage and raw milk and their impacts on the organoleptic quality of dairy products.
- HYPOTHESIS 1: Estimating the diversity and prevalence of bacteria will allow us to know if the use of lactic acid bacteria inoculants in silage is responsible for the presence of indigenous flora that alter milk.
- HYPOTHESIS 2: Aromatic lactic acid bacteria that are resistant to heat treatment are responsible for the production of undesirable volatile compounds in cheeses.

## Results and potential benefits

### In terms of new knowledge:

#### Impact of different types of silage in a cow's diet on the microbiological quality of raw milk:

- Overall, 226 bacterial taxons and 648 fungal taxons were identified using metataxonomics.
- The bacterial species found in the milk were also present in the silage and hay at a proportion of approximately 50% to 80% and approximately 60% to 70% for the fungal species.
- While *Lactobacillus buchneri*, is prevalent in both inoculated and uninoculated silage, the species is rarely found in raw milk.

#### Effects of milk's indigenous flora on the organoleptic properties of processed dairy products:

- Two of the strains isolated from raw milk—identified as *Lactobacillus casei* and *Lactobacillus plantarum*—were selected for their thermoresistance. In the Pearce test (Cheddar cheese production), these strains did not have an impact on the acidification kinetics of *Lactoccus lactis* SK11 starter culture; however, in a curd model, they were able to produce volatile components during the ripening stage.
- This link between the activity of the secondary flora and the profile of the volatile components in Cheddar cheese will be evaluated using transcriptome sequencing.



## Results and potential benefits, continue...

### Potential Benefits

- Optimization of the microbiological quality of milk used in cheesemaking.
- Control of the organoleptic quality of dairy products.
- Reduction in numbers of rejections of poor-quality processed dairy products.
- Maintain of quality standards for milk and dairy products.

### Professionals trained

**Ménilie Gagnon** (PhD): Phenotypic and genotypic characterization of isolated lactic acid bacteria in silage and raw milk: antibacterial activity, thermostability and the production of volatile compounds. Ménilie Gagnon has acquired expertise in: i) isolating and identifying lactic acid bacteria in different types of fodder and in raw milk and ii) screening the isolates for different metabolic characteristics. She would like to pursue a career in research in the field of microbiology, in association with dairy products.

**Alexandre Jules Kennang Ouamba** (PhD): Comparative analysis of the prevalence and phylogenetic structure of microbial communities in silage and cow milk. Alexandre is developing expertise in: i) the metagenomic analysis of microbial flora (bacteria, yeasts and moulds) of silage and raw milk through high-output multiplex sequencing and MARISA and PMA-qPCR techniques; and ii) the statistical analysis of metagenomic data (multivariate analyses, ordering, co-occurrence/co-exclusion networks). He is interested in research in food microbiology and related fields.

### For further information

The main project contributions were made available to dairy farmers in the articles published in *Le Producteur de lait québécois* and *La Terre de chez nous*. During the project, results were communicated through presentations and poster sessions at the general assembly of the Op+LAIT strategic cluster and at the Novalait Forum Techno. In 2018, the most salient results will be presented at the Cheese Symposium (Rennes, France) and the Food Microbiology (Berlin) international conferences.

### Financial contributions

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- Novalait

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