

Genomic characterization of long-time persistent *Listeria monocytogenes* strains in dairy facilities

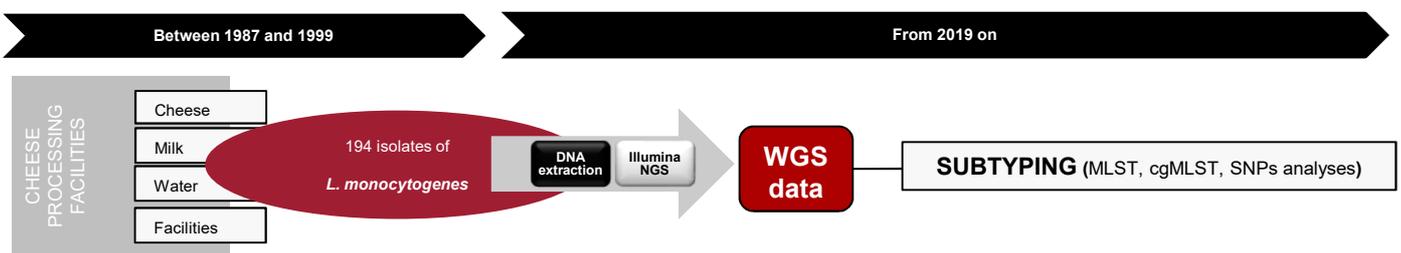
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Introduction

Over the last years, many studies suggested that the persistence of *Listeria monocytogenes* in food processing plants is an important factor in the transmission of this foodborne pathogen to humans via food chain. The ability of *L. monocytogenes* to grow at low temperatures and to tolerate wide pH ranges, high salt concentrations and heat treatment, allow it to persist in many dairy facilities.

OBJECTIVE: To determine the genomic diversity and the persistence of *L. monocytogenes* in Swiss cheese processing companies by applying Whole Genome Sequencing (WGS)

Material and Methods



Results and discussion

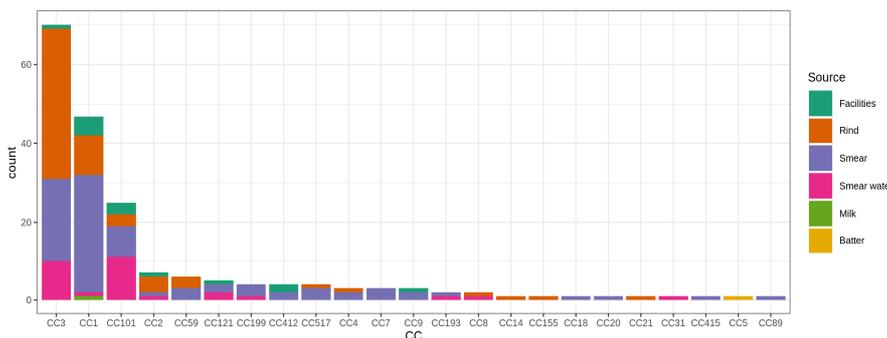


Figure 1: Prevalence of Clonal Complexes in Swiss dairy facilities and products.

- A large number of different Clonal Complexes (CC) was present in Swiss dairy facilities and products
- New Sequence Types (ST) were described for the first time
- Hypervirulent clones are more likely to be found in dairy products → higher ability to colonize the gut lumen and tissue (Maury et al. 2019)
- CC1 is particularly linked with *Lm*-associated ruminant rhombencephalitis and may lead to high prevalence and persistence in dairy cattle farm environments due to prolonged fecal shedding (Dreyer et al. 2016; Maury et al. 2019)

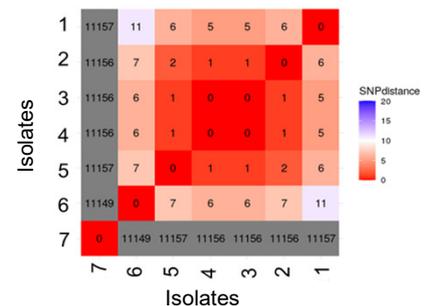


Figure 2: Heatmap of SNP distance between isolates corresponding to CC3 collected in the same facility over 6 years.

- The example in Figure 2 highlights the discriminatory power of WGS & long term persistence of *Lm* isolates that were collected in the same company over 6 years (1988-1994)
- All of them were classified to IIb serotype 1/2b, 3b, and 7; CC3
- Due to the high resolution of WGS, it was possible to show that isolate 7 (1994) is a different strain
- Isolates 1 to 6 are the same strain → after 5 years, a total of 11 different SNPs was determined

Conclusion and future

This work shows the usefulness of WGS to study the persistence of *Lm* subtypes in dairy facilities.

Next analyses will focus on studying the genes involved in adaptation and persistence.

References:
 Dreyer, Margaux, et al. "Listeria monocytogenes sequence type 1 is predominant in ruminant rhombencephalitis." Scientific reports 6.1 (2016): 1-11.
 Maury, Mylène M., et al. "Hypervirulent Listeria monocytogenes clones' adaption to mammalian gut accounts for their association with dairy products." Nature communications 10.1 (2019): 1-13.