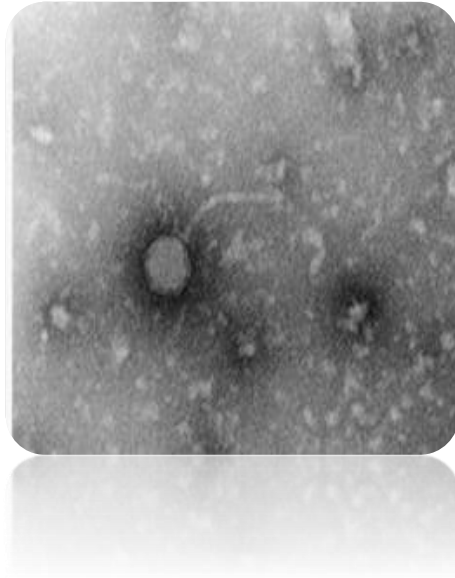


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**Genomic characterization and evolutionary relationships among  
Bacteriophages in the dairy industry and applications to detect phage  
Contamination**



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## Abstract

The prevalence of bacteriophages and their pernicious effects on the *Lactococcus* starter culture in the dairy industry has been an ongoing problem for several decades.

The main purpose of this investigation was to understand the relationship, evolutionary history and the sources of the phages that have been isolated from the different fermentative units of Fonterra. We report the genomic comparison results of 15 phages in this study that were isolated on the host bacteria, *Lactococcus lactis cremoris*. These phages can be grouped in two clusters namely P335 and 936, commonly encountered tailed bacteriophages in the dairy industries. The majority of the phages belong to the P335 species with just one phage clustering with the 936 species. Although phages of the P335 group display a high level of synteny with one another, we report nine different types of P335 phages in this study. A prophage integrated in the host strain has been identified. The prophage and the phages show homology to the temperate P335 phage, R1T isolated in Netherlands in 1996. The genetic makeup of these phages is suggestive of their source and evolution from other prophages in strains that may have been co-cultured with the strain that was used in this study. Furthermore, we identified that horizontal gene transfer events and homologous recombination have played a role in the evolution of phages in our study.

Phage annotation was carried out for representatives in both the clusters and forty eight to fifty seven ORFs have been identified in these phages. Our analyses indicate that majority of the genes are conserved across these phages. For further detection of phages, this project also suggests rapid tools like PCR that can be used to better understand the phage species and the type of phage infecting the starter culture. With the availability of whole genome sequences, we are hoping that the genome analysis will enlighten our knowledge on the current distribution of phages and their relationship with one another in the dairy industry.

## Abbreviations

DNA	Deoxyribonucleic acid
LAB	Lactic acid bacteria
RNA	Ribonucleic acid
PCR	Polymerase Chain Reaction
RPM	Revolutions per minute
bp	Base pair
CRISPR	Clustered regularly interspaced palindromic regions
TMP	Tape measure protein
MCP	Major capsid protein
MTP	Major tail protein
HGT	Horizontal gene transfer
TR	Transcriptional regulator

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