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SCIENCE & BUSINESS SYMPOSIUM

### WHEY PHAGE ECOLOGY IN ARTISANAL TRADITIONAL ITALIAN "HARD" CHEESE: SUSTAINABILITY IN DAIRY PRODUCTION

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Natural whey starters can be considered as a lactic acid bacteria culture, indispensable for the production of Italian traditional "hard" cheeses like Trentingrana. Daily maintained in the dairy activity, the main function of this culture is the acidification during the curd formation, having important effects such as whey drainage from the cocked curd and growth inhibition of photogenic and undesirable bacteria. Loss in whey starter fitness is often associated in poor acidification, mainly due to phage infection, that can strongly affect the cheese production and its final quality. Phage contamination in the dairy environment can not be completely eradicated, and there is fundamentally a co-evolution process that drives an ecological balance between phage and its microbial host, especially in whey starters environments. Therefore knowledge on phages community represent an important aspect to reduce lost in cheese production and to maintain quality and excellence in cheese making.

To study the phage ecology in Trentingrana production chain, we have collected 400 samples in six Trentingrana dairies distributed on the autonomous province of Trento, Italy. Almost 1800 lactic acid bacteria have been isolated and more than 150 phages retrieved. Characterization of phage biotypes as well as phages genome sequencing is ongoing. The gaining knowledge together with the isolation of performing lactic acid bacteria resistant to phage infection, will be important to avoid milk and cheese spoilage, potentially leading to a more sustainable cheese production.

### LACTOBACILLUS RHAMNOSUS GR-1 - THE BEST STUDIED VAGINAL PROBIOTIC STRAIN

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#### Objective

The genome sequences of various gastrointestinal and dairy probiotic *Lactobacillus* strains have been published, however, the vaginal strains are lagging behind. In this study, the complete genome sequence of the vaginal probiotic *L. rhamnosus* GR-1 was determined and compared to other *L. rhamnosus* strains at genomic and phenotypic level. The strain LGR-1 was originally isolated from a female urethra and was assessed with *L. rhamnosus* GG from a feces sample, and *L. rhamnosus* LC705 from a dairy product.

#### Methods

First the genome of LGR-1 was determined, followed by calculating the pan-genome of all publicly available *L. rhamnosus* strains and constructing a high-resolution phylogenetic tree. The phenotypic differences between LGR-1, LGG, and LC705 were evaluated by performing various experiments, such as carbohydrate utilization, adhesion to epithelial cells, detection of pili and EPS molecules, and different stress survival assays.

#### Results

A key difference is the absence in GR-1 and LC705 of the *spaCBA* locus required for pili-mediated intestinal epithelial adhesion. The LGR-1 genome contains a unique cluster for EPS production, which is postulated to synthesize glucose-rich, rhamnase-lacking exopolysaccharide molecules that are different from the galactose-rich EPS of LGG. Compared to LGG, LGR-1 was also genetically predicted and experimentally shown to better metabolize lactose and maltose and to better withstand oxidative stress, which is of relevance in the vagina.

#### Conclusions

Ultimately, this study could thus provide a molecular framework for the selection of the optimal probiotic strain for each targeted niche and condition.