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Exploration of viral diversity in fermented foods of plant origin

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Context/aim:

Fermented food constitutes 30% of the human diet in average. The study of fermented foods of plant origin responds to industrial and economic issues. Indeed, fermentation failure is responsible for important economic losses and can lead to the production of food waste. Furthermore, the upcoming transition in our diet with the reduction of meat consumption and the increase of vegetable consumption leads to the great return of fermentation, a simple and energy efficient food preservation process that generates tasty products with high nutritional value.

The bacterial and fungal communities of fermented foods of plant origin (wine, cabbage, carrot, turnip) are well known, which is not the case for phage communities (i.e. bacterial viruses). The scientific challenges of our project are therefore to provide a detailed description of their composition and to better understand their role in this peculiar type of microbial ecosystems.

The objective of the present study was to evaluate the impact of phages on the microbial dynamics of two different types of fermented foods of plant origin: sauerkraut (solid food) and wine (beverage).

Method:

The viral fraction of the food products collected at different time points during the fermentation process was purified by a specific method relying on the removal of microbial cells by centrifugation and filtration followed by viral particles' concentration using polyethylene glycol (PEG). Viruses were quantified by epifluorescence microscopy and the composition of viral communities was determined through a viral metagenomics approach involving nucleic acids extraction, DNA and RNA amplification and high throughput sequencing.

Results:

Based on epifluorescence microscopy, we estimated the concentration of viruses at 5×10^7 particles/g of sauerkraut after fermentation and 10^7 particles/L of wine. Viral metagenomics analysis revealed that the most abundant viral contigs shared some sequence homology with phages known to infect the principal bacteria responsible for fermentation in the studied systems, for example *Leuconostoc mesenteroides* and *Lactiplantibacillus plantarum* in sauerkraut. Interestingly, few contigs slightly related to RNA phage genomes were detected for the first time in this type of ecosystem, shedding light onto potentially new viruses to be further characterized.