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The transcriptomic response of a *Liquorilactobacillus mali* strain from French cider to a lytic phage infection.

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Insights into the interactions between phages and their bacterial hosts are crucial for understanding ecosystems equilibria. Although many works are dedicated to the study of the microbial diversity and fluxes within fermented food matrices, phage-bacteria interactions are still poorly described in these ecosystems. This is especially true when it comes to cider, an alcoholic fermented apple beverage. The current work aimed at studying the transcriptomic response of the lactic acid bacterium (LAB) *Liquorilactobacillus mali* UCMA 16447 during the lytic infection by phage UCMA 21115, both originating from cider.

A RNAseq approach was used to monitor the transcriptomic response of *L. mali* UCMA 16447 after fifteen minutes (T_{15}) and after one hour (T_{60}) of phage infection, a non-infected culture being used as a control. More than 100 and 200 genes appeared to be up or down regulated at T_{15} and at T_{60} , respectively. Overall, genes involved in cell motility, translation, carbohydrates metabolism and signal transduction were down regulated, while genes implicated in nucleotide metabolism and in the control of DNA integrity were upregulated, and this phenomenon increased over time. The current study is the first report regarding the impact of a lytic phage on a LAB isolated from a fermented beverage. Getting knowledge about host response to phage infection is crucial to better control and understand microbial population equilibria throughout fermentation processes. This will contribute to guaranteeing the production of safe and sustainable foods.