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Abstract

A multiomic microbiome approach to decipher drivers of bitterness in French blue-veined PDO cheeses

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Bitterness is a defect frequently observed in blue-veined cheeses. This study aims to better understand the origins of excessive bitterness in blue-veined Bleu d’Auvergne (BA) PDO cheeses. Thirty-day-old BAs with high and low bitterness scores (HB vs. LB) were selected and analysed through metabarcoding (16S and ITS), shotgun sequencing and RNA sequencing (n=60) at 30 and 60 days of ripening. Microbiomes were more diversified in LB than in HB cheeses. LB cheeses presented higher abundance in 5 bacterial species assigned to *Turicibacter*, *Leuconostoc*, *Paucilactobacillus*, *Delftia* and *Streptococcus* genera and 15 fungal species, including *Debaryomyces hansenii*, *Geotrichum candidum*, *Diutina catenulata* and *Yarrowia lipolytica*. *Lactococcus sp.* and *Penicillium roquefortii* were more abundant in HB cheeses. Shotgun sequencing confirmed highest diversity in LB cheeses and provided an insight in the balance and diversity of the bacterial, fungal and viral kingdoms. Gene expression in the microbial community differed according to bitterness and highlighted metabolic pathways associated with ripening time and bitterness level.