Characterisation of lactic acid bacteria in spontaneously fermented camel milk and selection of strains for fermentation of camel milk

The microbial communities in spontaneously fermented camel milk from Ethiopia were characterised through metagenomic 16S rRNA sequencing and lactic acid bacteria were isolated with the goal of selecting strains suitable as starter cultures. The fermented camel milk microbiota was dominated either by Lactobacillales or by Enterobacteriaceae, depending on incubation temperature and the provider of the milk. Strains of species with a potential use as starter cultures i.e., Lactococcus lactis, Lactobacillus plantarum, and Pediococcus acidilactici, were isolated. Fast acidifiers of camel milk have been isolated from the species of Lc. lactis, P. acidilactici, and Streptococcus infantarius. Gram-negative and potentially pathogenic microorganisms were frequent in spontaneously fermented camel milk, indicating the need for improved hygiene in Ethiopian camel farms. The profiled microbiota of spontaneously fermented camel milk and the isolated LAB strains will significantly contribute towards improving food safety and food security in dry regions that depend on camel milk production.

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