

MILK MICROBIOTA OF HOLSTEIN FRIESIAN COWS PRESENTS HIGHER BIODIVERSITY COMPARED TO RENDENA

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Recently, studies on milk microbiota composition have been intensified, especially concerning the impact that these microorganisms can have on animal health status, as well as on the quality and safety of dairy products (1). Preliminary research performed on the udder microbiota of different ruminant species (cattle, sheep, buffalo) has shown that a complex microbial community is present in raw milk, whose composition is influenced by endogenous and exogenous factors (2).

This study aims to understand the differences in milk microbiota between two different bovine breeds. We compared milk microbial population of 3 Holstein Friesian (HF) and 3 Rendena cows reared in the same farm and under the same management conditions. Quarter milk samples were collected from all cows at dry-off (T1), 1 day after calving (T2), 7-10 days after calving (T3), and 30 days after calving (T4). In order to evaluate the mammary gland health status, somatic cell count and bacteriological analysis were performed on quarter milk samples. Moreover, a NGS approach based on 16S metagenomics was applied to the milk of HF and REN during the peripartum period. Results were assessed by pooling all lactation time points together.

Upon bacteriological analysis, contagious bacteria such as *Staphylococcus aureus* and *Streptococcus agalactiae* were not found, but significant differences were seen in the general composition of the milk microbiota of the two breeds, with the microbiota biodiversity of Rendena milk being clearly lower than the one of HF milk. At the phylum level, REN milk was dominated by Firmicutes (94%, relative abundance), while HF milk contained Firmicutes (65%), Proteobacteria (15%), Actinobacteria (11%) and Bacteroidetes (6%). At the genus level, REN milk showed the predominance of *Streptococcus* (71%), followed by *Lactobacillus* (10%) and *Pediococcus* (6%), while HF milk was dominated by *Streptococcus* (29%), followed by *Lactobacillus* (6%), *Corynebacterium* and *Staphylococcus* (4%). Among streptococci, *Streptococcus thermophilus* was the most prevalent (48%) in REN milk, in comparison with only 2% in HF milk.

Streptococcus thermophilus is a lactic acid bacterium used in the production of fermented milks, yogurt, and many cheeses. Therefore, its presence in higher percentages in Rendena milk may be favorable for dairy processing purposes (2).

The advent of high-throughput technologies capable of providing a complete picture of milk microbial composition enables a better understanding and a more efficient comparison of the characteristics of autochthonous breeds (as in the case of Rendena) promoting the breeding and safeguarding of biodiversity.

1) Addis et al., 2016. "The bovine milk microbiota: Insights and perspectives from -omics studies" *Molecular BioSystems* 12(8):2359-2372.