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Microbiota of bovine udder and susceptibility to mastitis in dairy cows.

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Mastitis is an inflammatory disease of the mammary gland, which causes huge economic losses in the milk production chain. The involvement of the internal microbiota of the bovine udder in the modulation of pathogens populations and, consequently, of the infection prevalence has never been investigated so far. In this study, the udder microbiota was investigated in 31 quarters (corresponding to 27 cows) whose sanitary status ranged from healthy (i.e. no mastitis during the previous lactations) to susceptible to mastitis (i.e. one to several mastitis episodes during each of the previous lactations). Total bacterial DNA was extracted from foremilk samples and swab samples of the teat canal in each cow. The 16S DNA was PCR-amplified (Variable Regions 3 and 4) and pyrosequenced (GS Flex+, 454 Roche). Phylobiome was analyzed using QIIME, and results were further treated using R, and LEfSe. Clustering of the samples based on their bacterial composition showed a link between udder microbiota and sanitary status. Healthy quarters showed a higher diversity compared to mastitis susceptible ones (Shannon index ~8 and 6 respectively). Discriminant analysis of phylobiomes revealed dysbiosis in mastitis-susceptible quarters and allowed identification of taxonomic markers in relation to mastitis susceptibility. Healthy quarters were associated to a higher proportion of the Clostridia class (including genera such as *Ruminococcus*, *Oscillospira*, *Roseburia*, *Dorea*...), the Bacteroidetes phylum (*Prevotella*, *Bacteroides*, *Paludibacter*...), and the Bifidobacteriales order (*Bifidobacterium*) whereas mastitis-susceptible quarters showed a higher proportion of the Bacilli class (*Staphylococcus*) and Chlamydia class. These results suggest that a diverse and balanced microbiota in the udder contributes to the mammary gland health, likely by exerting a barrier effect with regard to pathogens, as observed in other contexts (e.g. human gut). Mechanisms of interaction between this endogenous microbiota and the mammary gland deserve further investigations, which will help maintain a balanced mammary microbiota e.g. through the development of mammary probiotics.

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