Bovine mammary gland microbiota et immune response

Sergine Even[1] (sergine.even@inrae.fr), Lucie Rault[1], Pierre-Alexandre Lévêque[1,2], Sarah Barbey[3], Frederic Launay[3], Hélène Larroque[4], Yves Le Loir[1], Pierre Germon[5], Jocelyne Guinard-Flament[2]

[1] INRAE, Institut Agro, STLO, Rennes, France ; [2] INRAE, Institut Agro, PEGASE, Saint Gilles, France ; [3] INRAE, Domaine Expérimental du Pin, Gouffern En Auge, France ;[4] GenPhySE, Université de Toulouse, INRAE, ENVT, Castanet-Tolosan, France ; [5] INRAE, Université François Rabelais, ISP, Tours, France

Introduction and aims

Bovine mastitis is an inflammation of the mammary gland generally due to an infection. It is responsible for considerable economic losses in dairy farms. Preventive and curative strategies that mainly rely on antibiotic therapies are not totally effective and contribute to antibiotic resistance dissemination, prompting the need for alternative or complementary strategies. We previously established a link between teat cistern microbiota composition and bovine mastitis in quarters which had different histories regarding mastitis [1]. In this study, to further decipher the relationships between teat cistern microbiota and immune and microbial responses, a switch from twice- to once-daily milking (ODM) was used to trigger an udder perturbation.

Material and methods

A switch to ODM was used in 31 initially healthy quarters of dairy cows. Immune and microbial responses including determination of teat microbiota were monitored just prior to the transition (day 0), and 3 and 14 days following transition to ODM.

Results and discussion

A temporal relationship was reported between initial teat cistern microbiota composition and richness, the immune response to ODM, and mastitis development. Quarters with a low initial microbiota richness and taxonomic markers such as Bacteroidetes and Proteobacteria were associated with a higher rate of mastitis during ODM. Quarters with a higher richness and taxonomic markers such as Firmicutes, *Bifidobacterium* and *Corynebacterium* displayed early inflammation following transition to ODM but without developing mastitis (no infection). Short-term evolution of microbiota indicates that microbiota with a higher initial richness were more strongly altered by transition to ODM, with notably the disappearance of rare OTUs. Microbiota modifications were associated with an early innate immune system stimulation, which, in turn, may have contributed to the prevention of mastitis development [2].

These results suggest a role of the bovine teat microbiota composition and richness in the immune response of the mammary gland during perturbations such as transition to ODM or pathogen entrance. They invite us to consider strategies that can preserve teat microbiota diversity and taxa associated to a healthy status for the design of next-generation probiotics.

1- Falentin H, Rault L, Nicolas A, Bouchard DS, Lassalas J, Lamberton P, et al. 2016. Bovine Teat Microbiome Analysis Revealed Reduced Alpha Diversity and Significant Changes in Taxonomic Profiles in Quarters with a History of Mastitis. Front Microbiol. 7:480.

2- Rault L, Lévêque P-A, Barbey S, Launay F, Larroque H, Le Loir Y, et al. 2020. Bovine Teat Cistern Microbiota Composition and Richness Are Associated With the Immune and Microbial Responses During Transition to Once-Daily Milking. Front Microbiol.11:602404.

Key words: mastitis, mammary gland microbiota, immune response