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New insights into cow holobiont in relation to heath

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Introduction and aims

Infectious diseases (ID) have been traditionally considered as the outcome of a bipartite interaction between a given pathogen and its host. Recent advances in high-throughput sequencing technology have uncovered the complexity of the various microbial communities associated with the host, the holobiont, and these have emerged as a key player of the infectious process.

In cattle, major efforts have been devoted to the characterization of the microbiota associated to different anatomical sites in relation to animal performance and health. However, these have mainly focused on the comparison of microbiota of healthy versus diseased animals. The contribution of microbiota associated to the infected organ or to remote body sites towards ID development is one main issue that remained to be addressed.

This study aimed at exploring the bovine holobiont throughout the lactation, in relation to the genetic susceptibility to mastitis.

Material and methods

Over one thousand samples were collected from 45 primiparous prim'Holstein cows selected from two divergent lineages that were respectively more or less susceptible to mastitis. Samplings were done at 4 time points from 1 week pre-partum to 7 months post-partum and from 4 anatomic sites: nasal, genital, buccal (as a proxy for rumen), and foremilk (as a proxy for internal teat microbiota). Sample microbiota were determined through 16S rRNA gene metabarcoding sequencing and analyzed with regard to several metadata : anatomic sites, time of sampling, animal, genotype regarding susceptibility to mastitis.

Results and discussion

Thanks to the specific design of this study, data showed both the independence of the sites and their interdependence. The anatomic site was among the most structuring factors of bacterial communities but overlap of the communities associated to the 4 sites was observed at the individual level. Time was shown to significantly modulate microbiota composition for all sites, with the nasal and buccal microbiota being the most affected. In contrast, the genotype (susceptibility to mastitis) had only a very poor impact on the microbiota composition. Exploration of the relationship between microbiota and health-related metadata is in progress.

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Key words: bovine holobiont susceptibility to mastitis