



HAL
open science

New insights into cow holobiont in relation to heath

Sergine Even, Mahendra Mariadassou, Xavier Nouvel, Fabienne F. Constant, Diego Morgavi, Lucie Rault, Sarah Barbey, Emmanuelle Helloin, Olivier Rué, Sophie Schbath, et al.

► **To cite this version:**

Sergine Even, Mahendra Mariadassou, Xavier Nouvel, Fabienne F. Constant, Diego Morgavi, et al.. New insights into cow holobiont in relation to heath. 16e congrès national de la SFM-MICROBES 2021, Sep 2021, Nantes, France. hal-03361039

HAL Id: hal-03361039

<https://hal.inrae.fr/hal-03361039>

Submitted on 1 Oct 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

New insights into cow holobiont in relation to heath

Sergine Even (sergine.even@inrae.fr)⁶, Mahendra Mariadassou¹, Xavier Nouvel², Fabienne Constant^{3,4}, Diego Morgavi⁵, Lucie Rault⁶, Sarah Barbey⁷, Emmanuelle Helloin⁸, Olivier Rué^{1,9}, Sophie Schbath¹, Frederic Launay⁷, Olivier Sandra⁴, Rachel Lefebvre¹⁰, Yves Le Loir⁶, Pierre Germon⁸, Christine Citti²

¹ Université Paris-Saclay, INRAE, MaIAGE, 78350, Jouy-en-Josas, France ; ² INRAE UMR1225 IHAP

³ Ecole Nationale Vétérinaire d'Alfort, BREED, 94700, Maisons-Alfort, France ; ⁴ Université Paris-Saclay, UVSQ, INRAE, BREED, 78350, Jouy-en-Josas, France ; ⁵ INRAE UMR1213 Herbivores; ⁶ INRAE, Institut Agro, UMR1253 STLO, 35042, Rennes, France; ⁷ INRAE DEP; ⁸ INRAE UMR1282 ISP; ⁹ Université Paris-Saclay, INRAE, BioinfOmics, MIGALE bioinformatics facility, 78350, Jouy-en-Josas, France; ¹⁰ INRAE UMR1313 GABI

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.

This work is part of the MICROCOSM project funded by the INRAE Metaprogramme MEM.

Key words: bovine holobiont susceptibility to mastitis