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► To cite this version:

Lisa Arnalot, Salomé Ducluzeau, Marion Julhes, Laurent Cauquil, Géraldine Pascal, et al.. Fecal microbiota shifts during transition in dairy cows. Séminaire HOLO-AE (Holobiontes des Animaux d'Élevage), INRAE métaprogramme HOLOFLUX, Dec 2024, Paris, France. hal-04872729

HAL Id: hal-04872729

<https://hal.inrae.fr/hal-04872729v1>

Submitted on 8 Jan 2025

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Fecal microbiota shifts during transition in dairy cows

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Introduction: In dairy cows, the transition period around parturition represents a critical phase with the highest incidence of infectious and metabolic diseases compared to the rest of the lactation. In cattle, the ruminal microbiota has been the focus of most research on the gastrointestinal microbiota. In other mammals, the gut microbiota is usually studied by analysing of the fecal microbiota. The composition and evolution of the fecal microbiota of transitioning dairy cows are poorly studied.

Purpose: We aimed to describe the composition of bacterial microbiota in the feces of a large number of dairy cows around parturition on different commercial farms.

Methods: Dairy cows in their 2nd and 3rd lactation were recruited. Fecal samples were collected three weeks before- and in the week post-calving from a cohort of 411 Holstein dairy cows from 25 dairy herds. DNA was extracted from feces, and the 16S rRNA gene (hypervariable region V3-V4) was sequenced after amplification. Bioinformatic analysis was done using FROGS 4.1. Statistical analysis was performed using R software (R-4.3.3). To assess variability, α , and β diversity indices were examined. Subsequently, Analysis of Microbiome Composition using Bias Correction 2 (ANCOM-BC2) was then applied to the composition data, and the relationship between the variables was further explored.

Results: A loss of diversity is observed after calving (mean observed richness 1120.0 *pre-partum* compared to 1027.2 *post-partum*, p -value<0.001), with no difference in association with the lactation rank. However different farms showed different profiles. The ANCOM-BC2 analysis identified different genera when comparing the pre- and post-calving samples, indicating significant changes in the fecal microbiota of dairy cows after calving compared to the dry period. Two unknown genera from the phylum *Verrucomicrobiota* were more abundant in the pre-calving samples (fold change: 4.0 and 3.7). In contrast, the proportions of *Bifidobacterium* (fold change = 6.0) and *Intestinibacter* (fold change = 5.1) were higher after calving than before calving.

Conclusion: Shifts in fecal microbiota around calving, may be due to changes in diet composition and feed intake modifications, or to physiological changes from the dry period to the lactation. However, other factors such as genetic background and health factors may also influence the microbiota composition. This can be further investigated to identify biomarkers for imbalance prediction of states or identify maladaptation to the lactation stage.