



Abstract

The dynamics of the community structure and composition of the dairy cow fecal bacterial communities during early lactation is unclear, therefore this study was conducted to characterize the fecal bacterial communities in dairy cows during early lactation using 16S rRNA gene sequencing. Feces were sampled from 20 healthy fresh Holstein dairy cows on day 1 (Fresh1d group) and day 14 (Fresh14d group) after calving. After calving, cows were fed the same fresh diet. The dominated phyla *Firmicutes* and *Proteobacteria* were decreased ($P \leq 0.01$) with lactating progress and phyla *Bacteroidetes* were increased ($P = 0.008$) with lactating progress and dietary transition. At family level, the predominant family were *Ruminococcaceae* (35.23%), *Lachnospiraceae* (11.46%), *Rikenellaceae* (10.44%) and *Prevotellaceae* (6.89%). A total of 14 genera were different between fecal samples from Fresh1d and Fresh14d, included the predominant genera, such as *Ruminococcaceae_UCG-005* ($P = 0.008$), *Rikenellaceae_RC9_gut_group* ($P = 0.043$) and *Christensenellaceae_R-7_group* ($P = 0.008$). All fecal bacterial communities shared members of the genera *Ruminococcaceae_UCG-005*, *Bacteroides* and *Rikenellaceae_RC9_gut_group*. These findings help to improve our understanding of the composition and structure of the fecal microbial community in fresh cows and may provide insight into bacterial adaptation time and dietary in lactating cows.

Introduction

- ❑ The ruminal microbial structure and composition varied with lactation period¹.
- ❑ The bovine fecal microbiota associated with age², diet³, and health⁴ in dairy calves.
- ❑ Lactation was found to be another important factor to shape rumen microbiome in dairy cows⁵.
- ❑ The dynamics of the community structure and composition of the dairy cow fecal bacterial communities during early lactation is unclear, therefore this study was conducted to characterize the fecal bacterial communities in dairy cows during early lactation using 16S rRNA gene sequencing.

Methods

Fecal samples were collected from 20 health Holstein dairy cows at d1 and 14 after calving

DNA was extracted from all fecal samples and PCR was used to amplify the bacterial 16S rRNA gene sequence

The 16S rRNA amplicons were pooled, then sequenced and demultiplexed in an Illumina MiSeq sequencing machine

Sequence processing and Operational Taxonomic Unit assignment was performed in USEARCH and statistical analysis was performed using R

Results

Figure 1. The boxplot of alpha diversity indices (Chao1, Number of OTUs, Shannon and Simpson) of fecal samples. Fresh1d indicates fecal microbiota samples of fresh group on 1d, Fresh14d indicates fecal microbiota samples of fresh group on 14d. Across all samples, Chao1 and number of OTUs differed significantly ($P = 0.03$).

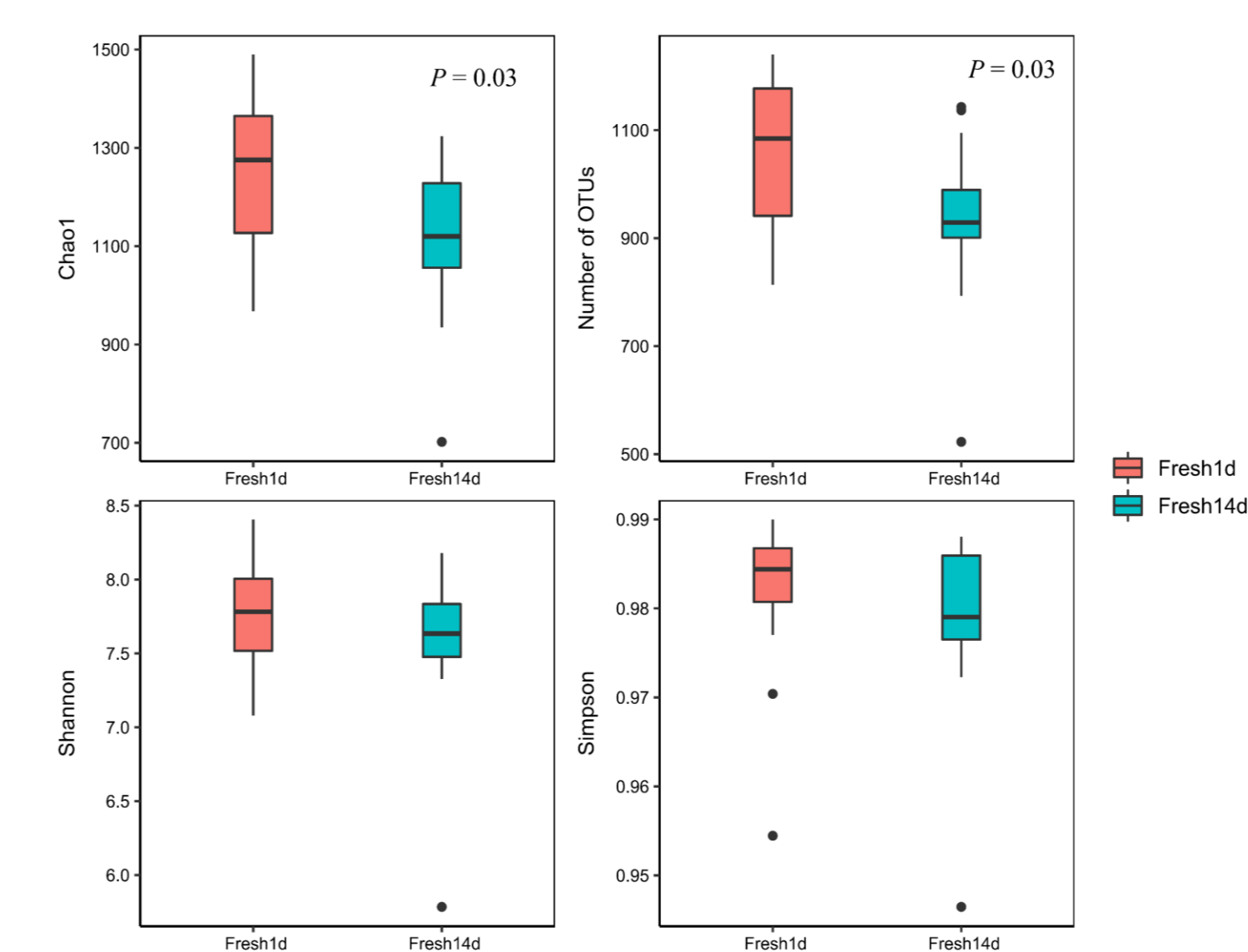


Figure 2. None-metric multidimensional scale analysis based on Bray-Curtis distance. ANOSIM analysis of the samples on d1 and d14, where bacterial communities in dairy cow feces are grouped by lactation period in feces. The overall bacterial community was found to significantly differ between Fresh1d and Fresh14d ($P = 0.001$).

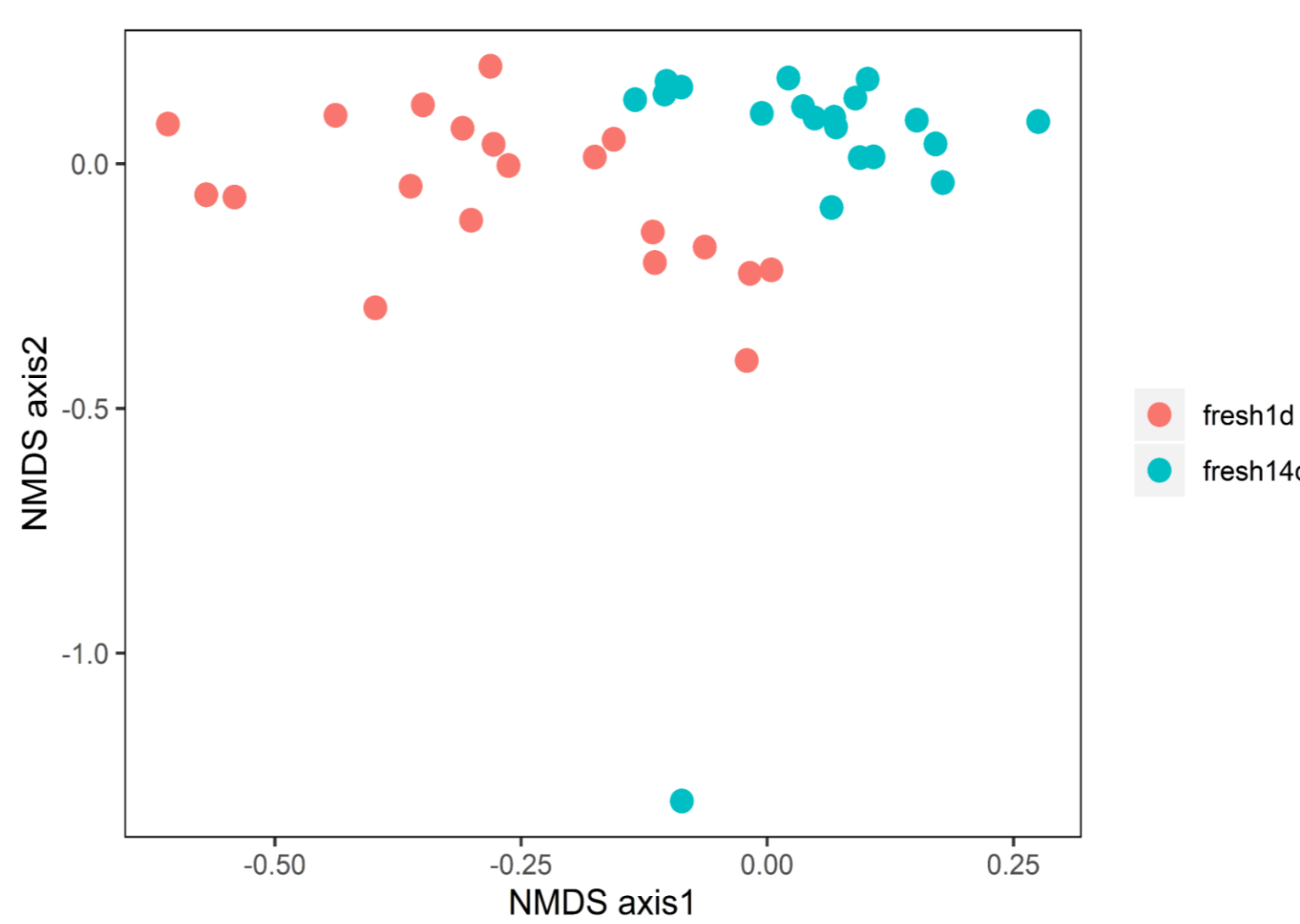


Figure 3. The relative abundance of fecal samples at the phylum, family and genus level. (a) Distribution of predominant phyla, family and genera of all fecal samples (relative abundance > 1% at all samples). (b) The fecal bacterial community composition of all animals at the phyla, family and genus level (relative abundance > 1% at least one sample). Fresh1d indicates fecal microbiota samples from cows on d1, Fresh14d indicates fecal microbiota samples from cows on d14.

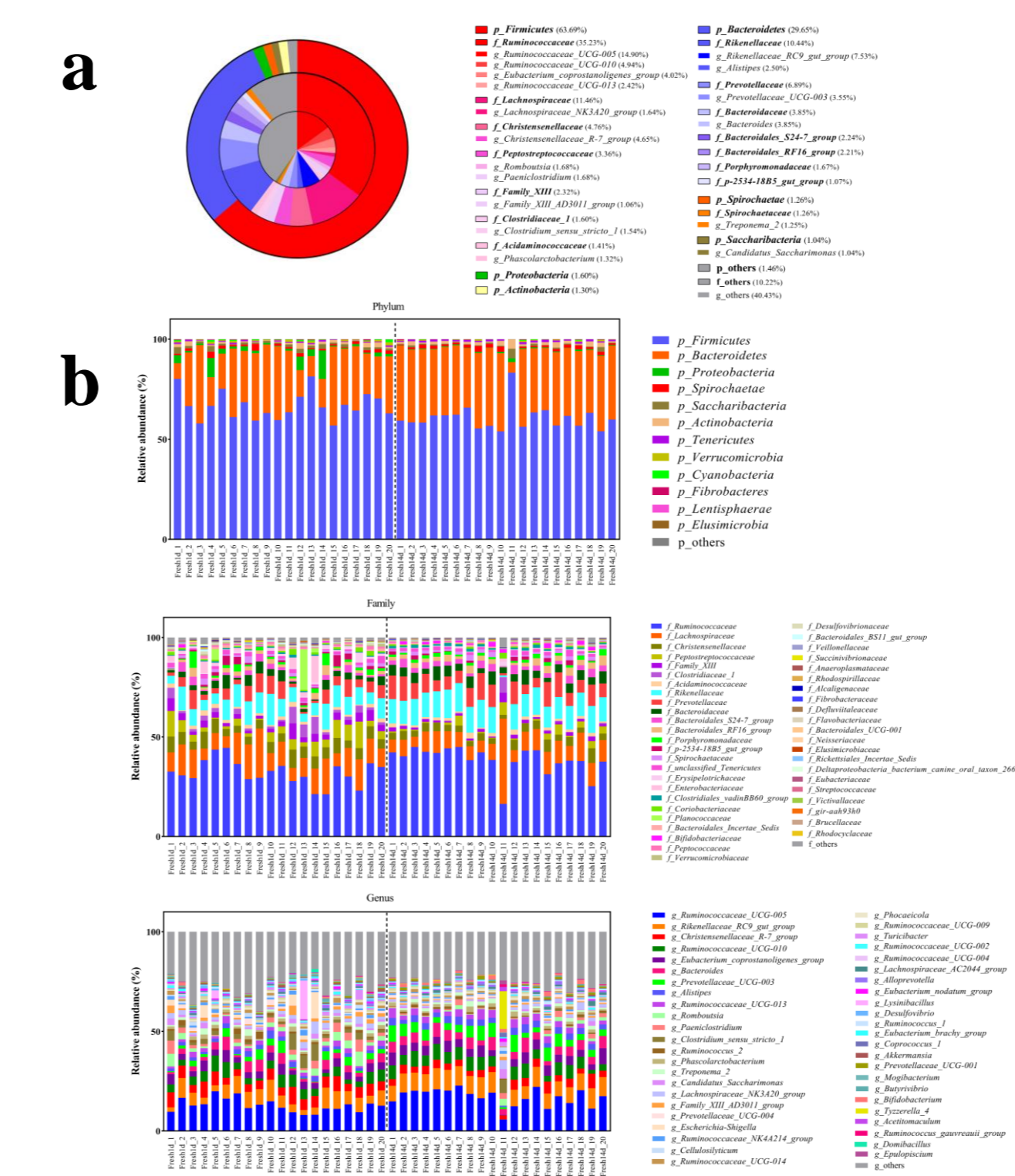
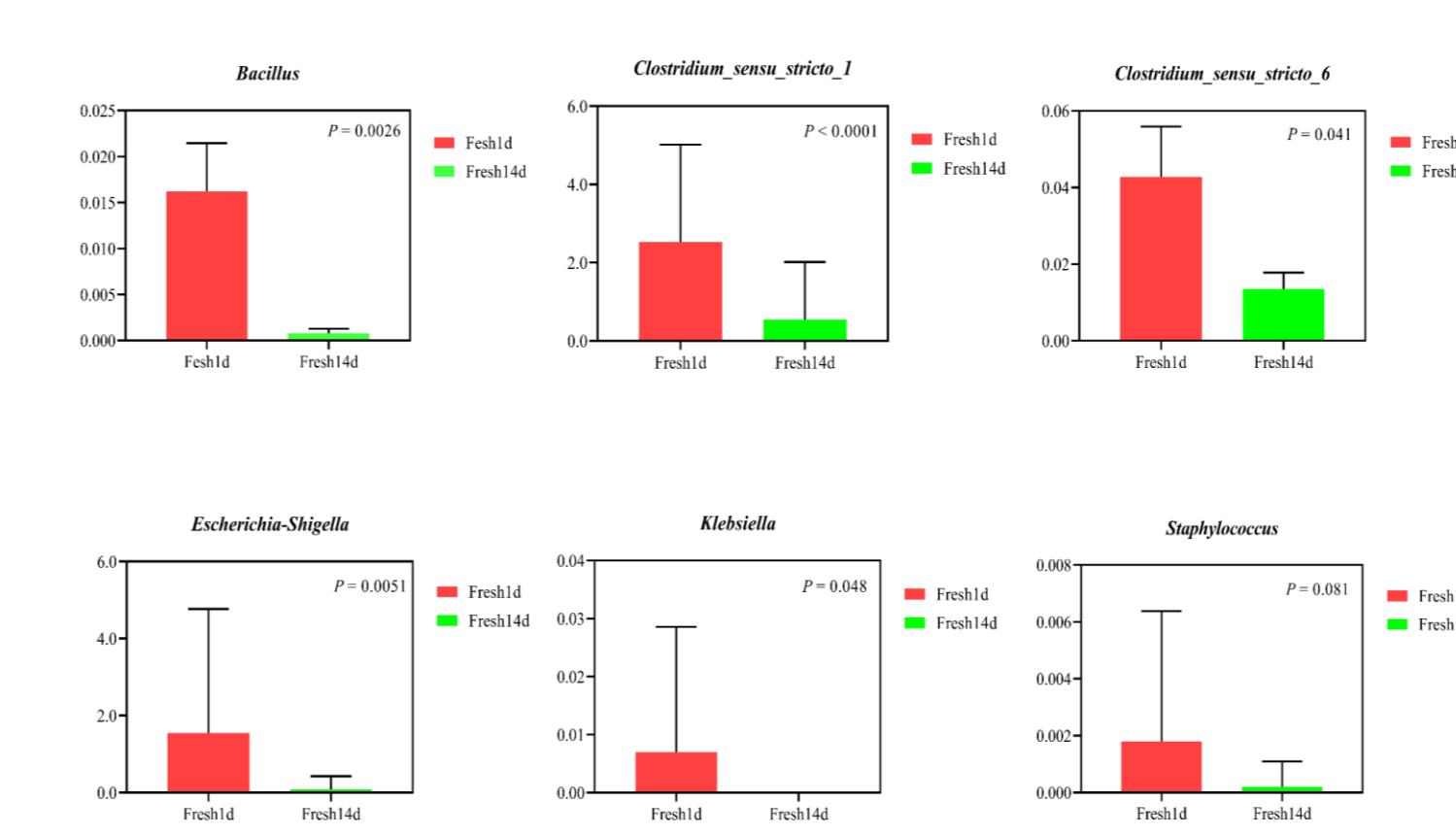


Figure 4. The barplot of the relative abundance of potentially pathogenic bacteria in dairy cows during early lactation. Fresh1d indicates fecal microbiota samples from cows on d1, Fresh14d indicates fecal microbiota samples from cows on d14. The overall potential pathogenic bacteria were decreased by lactation progressed ($P < 0.05$).



Discussion & Conclusion

- ❑ It's clear that the fecal bacterial is dynamic and changing with lactation progress.
- ❑ The bacterial community significantly differed between Fresh1d and Fresh14d.
- ❑ Despite the 16S rRNA sequencing used, the clear decreasing was observed from d1 to d14 after calving.

Future studies

- ❑ The dynamic of fecal microbiome should increase time point and cover one lactation cycle.
- ❑ PCR was used to determine the potential pathogenic bacteria in feces and metagenomic method would more efficient to find the effect of potential pathogenic bacteria on dairy cows' health.

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