# Metagenomic analysis of rumen populations in week-old calves as altered by maternal late gestational nutrition and mode of delivery

**T. A. Christensen II[†], K. J. Austin[‡], K. M. Cammack[*], and H. C. Cunningham-Hollinger[‡]**

[†]Department of Chemical Engineering, University of Wyoming [‡]Department of Animal Science, University of Wyoming *West River Ag Center, South Dakota State University

**Abstract #70**

## Introduction

The rumen microbiome is established very early in life, possibly even before birth (Skillman et al., 2004; Alipour et al., 2018). The established population may affect performance, feed efficiency and host health (Myer et al., 2015). In humans, maternal factors such as gestational diet and mode of delivery influence early colonization of the gut microbiome (Rodríguez et al., 2015). Little information on these effects in ruminants is currently available.

## Hypothesis

Late gestational nutrition and mode of delivery influence the calf rumen microbiome

## Objectives

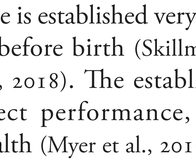
1. Determine if nutrient restriction during late gestation alters the calf rumen microbiome
2. Determine if ruminal microbiome composition differs in calves born vaginally versus those born by caesarean section

## Experimental Design

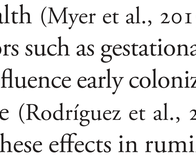
Late-gestating cows treated as:

**CON**
*(Control)*
NRC Requirements Met
—
Vaginal delivery

**CS**
*(Caesarean-section)*
NRC Requirements Met
—
Caesarean delivery



**NR**
*(Nutrient-restricted)*
1.5-2.0 BCS lower than CON
—
Vaginal delivery



Rumen fluid sampled via oral lavage:

- From cows:
  Prior to partution
- From calves:
  At 7 days of age

## Analysis

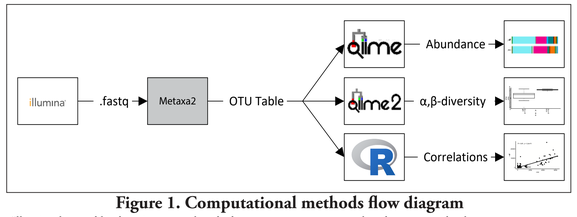



**Figure 1. Computational methods flow diagram**

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- DNA extraction by RBB+C method and QIAmp mini stool kit (Yu and Morrison, 2004)
- Sequencing by Illumina HiSeq 2500
- Taxonomic assignment by Metaxa2 (Bengtsson-Palme et al., 2015)
- Abundance and diversity analyses by QIIME and QIIME2 (Caporaso et al., 2010; Bolyen et al., 2018)
- Correlations by R software

## Results

### Alpha-diversity

### Beta-diversity

### Abundance

**Cows vs. calves**

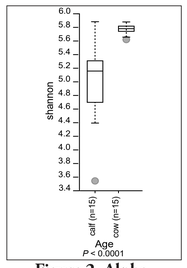


**Figure 2. Alpha-diversity of cows vs. calves.**

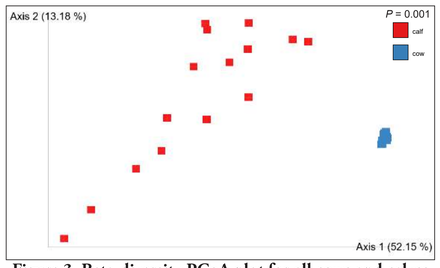


**Figure 3. Beta-diversity PCoA plot for all cows and calves categorized by age group**

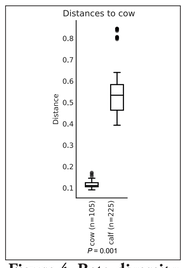


**Figure 4. Beta-diversity of cows vs. calves.**

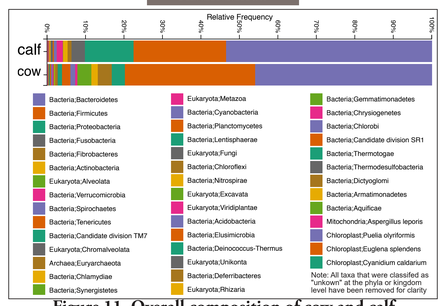


**Figure 11. Overall composition of cow and calf microbiome**

**Cows by treatment**

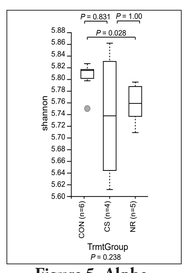


**Figure 5. Alpha-diversity of cows by treatment**

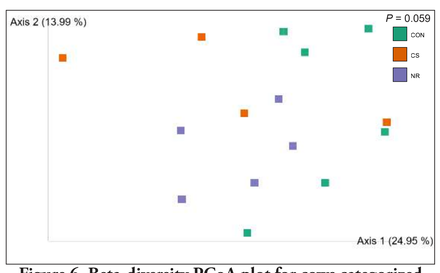


**Figure 6. Beta-diversity PCoA plot for cows categorized by treatment group**

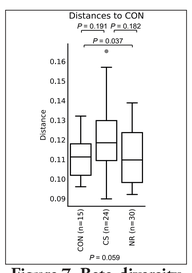


**Figure 7. Beta-diversity of cows by treatment**

**Calves by treatment**

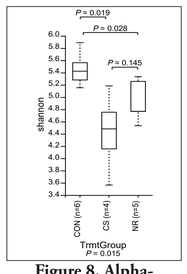


**Figure 8. Alpha-diversity of calves by treatment**

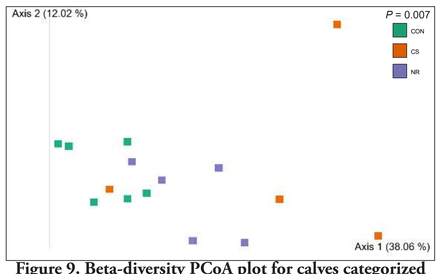


**Figure 9. Beta-diversity PCoA plot for calves categorized by treatment group**

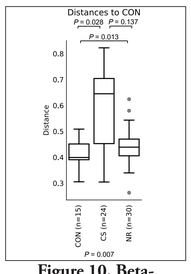


**Figure 10. Beta-diversity of calves by treatment**

**Table 1. Number of differentially abundant species between age & treatment group**

| Subset | Category | # of Differential Species* |
|---|---|---|
| All | Age | 410 |
| Cows | Treatment | 5 |
| Calves | Treatment | 8 |

*$P<0.01$ by Kruskal-Wallis nonparametric analysis of variance

**Table 2. Differentially abundant species in calves by treatment group**

| Species | CS Mean | NR Mean | CON Mean | P-value |
|---|---|---|---|---|
| Unclassified *Intrasporangiaceae* | 0.0 | 3.6 | 0.3 | 0.003 |
| Unclassified *Rhodospirillales* | 0.0 | 1.0 | 3.8 | 0.005 |
| Unclassified *Puniceicoccaceae* | 0.0 | 0.6 | 81.0 | 0.005 |
| Unclassified *Rhodopirellula* | 0.0 | 1.6 | 0.3 | 0.006 |
| *Porphyromonas cangingivalis* | 0.0 | 0.0 | 1.3 | 0.006 |
| *Oscillospira guillermondii* | 0.0 | 0.0 | 1.8 | 0.006 |
| Unclassified *Bifidobacterium* | 2.3 | 0.0 | 0.0 | 0.009 |
| Unclassified *Opitutae* | 0.0 | 7.6 | 100.8 | 0.009 |

### Correlations

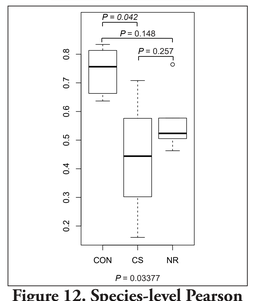


**Figure 12. Species-level Pearson correlation results between cow and calf rumen microbiome**

## Discussion & Conclusions

- Cows had higher microbial richness and greater consistency than calves
- Cows' microbial composition was affected by NR, but not their richness
- Calves' microbial richness and composition were altered by both CS and NR
  - CS and NR were significantly different than CON, but not different from each other
- Age had greater effect on species abundance than treatment
- Delivery by caesarean-section decreased the correlation between a dam's and her calf's rumen populations

These results indicate that it is possible to alter the calf rumen microbiome *in utero* and may provide opportunities to establish a healthy population through dam management and supplemental strategies.

## Literature Cited

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