

# Microbiome of the Mare and the Foal at Parturition

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## Introduction

The microbiome is a microbial ecosystem that exists in organisms such as mammals (Rosenbaum et al., 2016). It has been assumed that the fetal microbiome starts to develop at parturition. However, long before parturition, microbial populations have been identified in the meconium, fetal membranes and placenta. There has not been a consensus on the origin of the fetal microbiome, but it is believed that the establishment of the microbiome can come from the vagina or maternal circulation (Stinson et al., 2017). The microbiome in the fecal matter of a non-pregnant mare differs from a pregnant mare (Weese et al., 2015). Studies have suggested that the mare shares her bacterial communities with the foal in utero (Quercia et al., 2019) however, the timing of that establishment and the relationship between the microbial communities in the mare and foal are still unknown.

## Objective

The objective of this study was to identify the microbial community in the foal's meconium and to compare it to the microbiome of the mare's placenta, milk, and feces at parturition.

## Materials and Methods

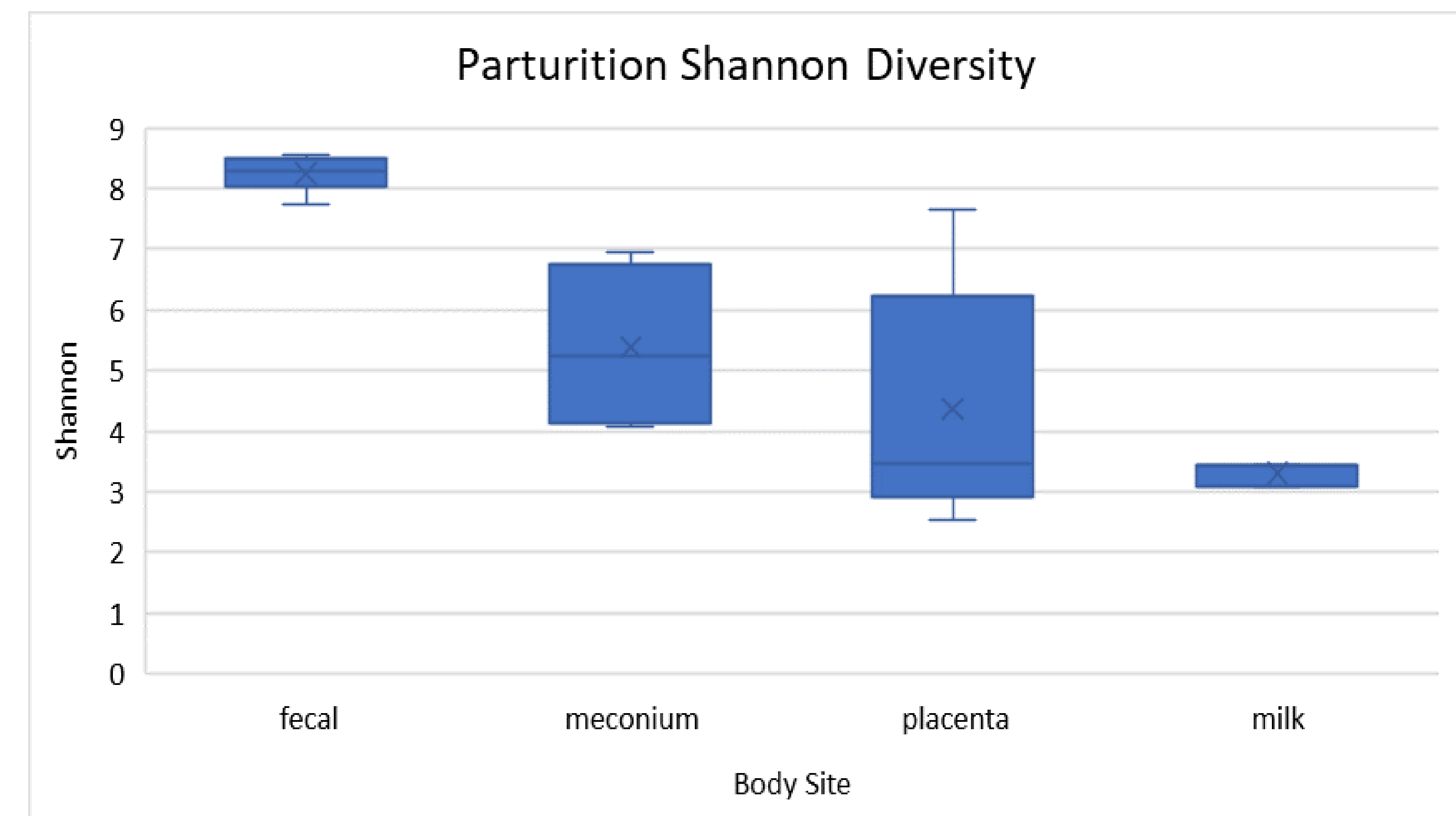
- Six mares were used for this study. Mare fecal, milk, and placental samples, and foal meconium samples were taken at foaling.
- Mare feces were obtained by means of a rectal grab with a lubricated, sterile glove after parturition. Following passage of the meconium, a sample was collected in a similar fashion.
- Prior to nursing, a colostrum sample was taken after disinfecting the teats with iodine.
- When the placenta was expelled, a sample was collected from the internal portion.
- All samples were frozen after collection until they were analyzed with Next Generation Sequencing techniques. Samples were run through a DNA extraction kit, followed by PCR, and then sequenced using Illumina Miseq.
- The sequencing data were analyzed using the QIIME bioinformatics pipeline.

## Results and Conclusions

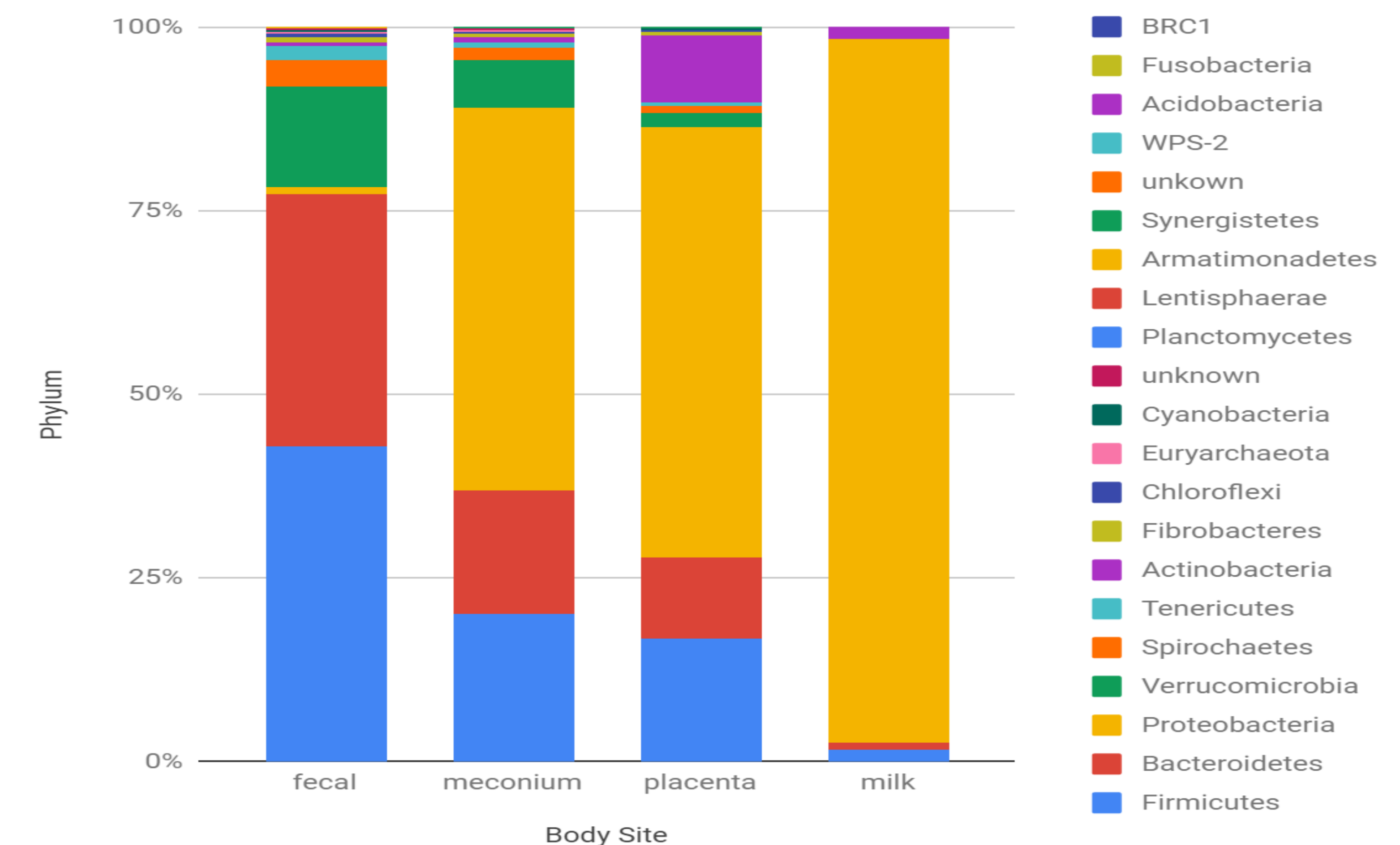
The foal meconium consisted of a unique microbial community that differs from the microbiome of the mare. In the meconium and placenta, the dominant phylum was Proteobacteria, however Firmicutes and Bacteroidetes were also present within the microbial community at lesser relative abundancies. Firmicutes, Bacteroidetes, and Verrucomicrobia comprised the majority of the mare feces. Proteobacteria was the dominant phylum in milk. The mare feces was significantly higher in microbial diversity when compared with meconium, milk and placental samples ( $P < 0.05$ ). Meconium was greater in bacterial diversity than milk ( $P < 0.05$ ), however there was no difference in diversity between meconium and placental samples.

In conclusion, the microbial community of the foal meconium shared taxa with both the mare fecal and placental samples. This indicates the possibility that microbes were transferred between the mare and the foal during gestation, however the timing and methods of transport remain unknown..

## Results and Conclusions, Cont.



## Relative Abundance Parturition



## References

- J.S. Weese and M. Jelinski, 2016. Assessment of the Fecal Microbiota in Beef Calves, *J. of Vet. Internal Med.* 31:1, pg. 176-185.
- Lisa F. Stinson, Matthew S. Payne & Jeffrey A. Keelan. 2017. Planting the seed: Origins, composition, and postnatal health significance of the fetal gastrointestinal microbiota, *Critical Rev. in Microbiology*, 43:3, pg. 352-369.
- Rosenbaum, J.T. & Asquith, M.J. Curr. 2016. The Microbiome: a Revolution in Treatment for Rheumatic Diseases? *Rheumatol. Rep.* 18: 62.
- S. Wright. 2018. Highlights of recent clinically relevant papers, *Equine Vet. Edu.* 30:11, pg. 571-572..