

Assessment of Mucosa-associated Microbiota in the Rumen and Colon of Dairy Calves Fed High Plane of Milk and during Weaning Transition

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Background

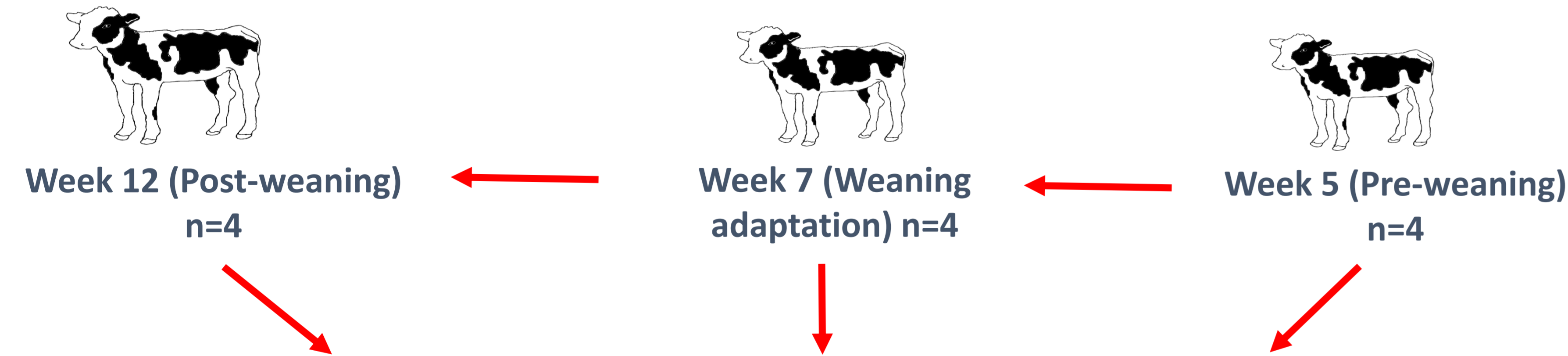
- Weaning is the natural process when the calf's diet gradually shifts from mother's milk to solid feed (Kim et al., 2016).
- How the mucosa-associated microbiota in the rumen and colon shifts during weaning transition is not completely understood.
- The relationship between rumen mucosal microbiota and ruminal pH change during this period is not explored.

Objective

- To explore the effects of weaning on the mucosa-associated microbial community diversity and abundance in the rumen and colon, and their relationship with the rumen and colon mucosa measures of dairy calves using longitudinal biopsies from the same individuals

Materials & Methods

Four Holstein dairy bull calves (weaned at week 6)

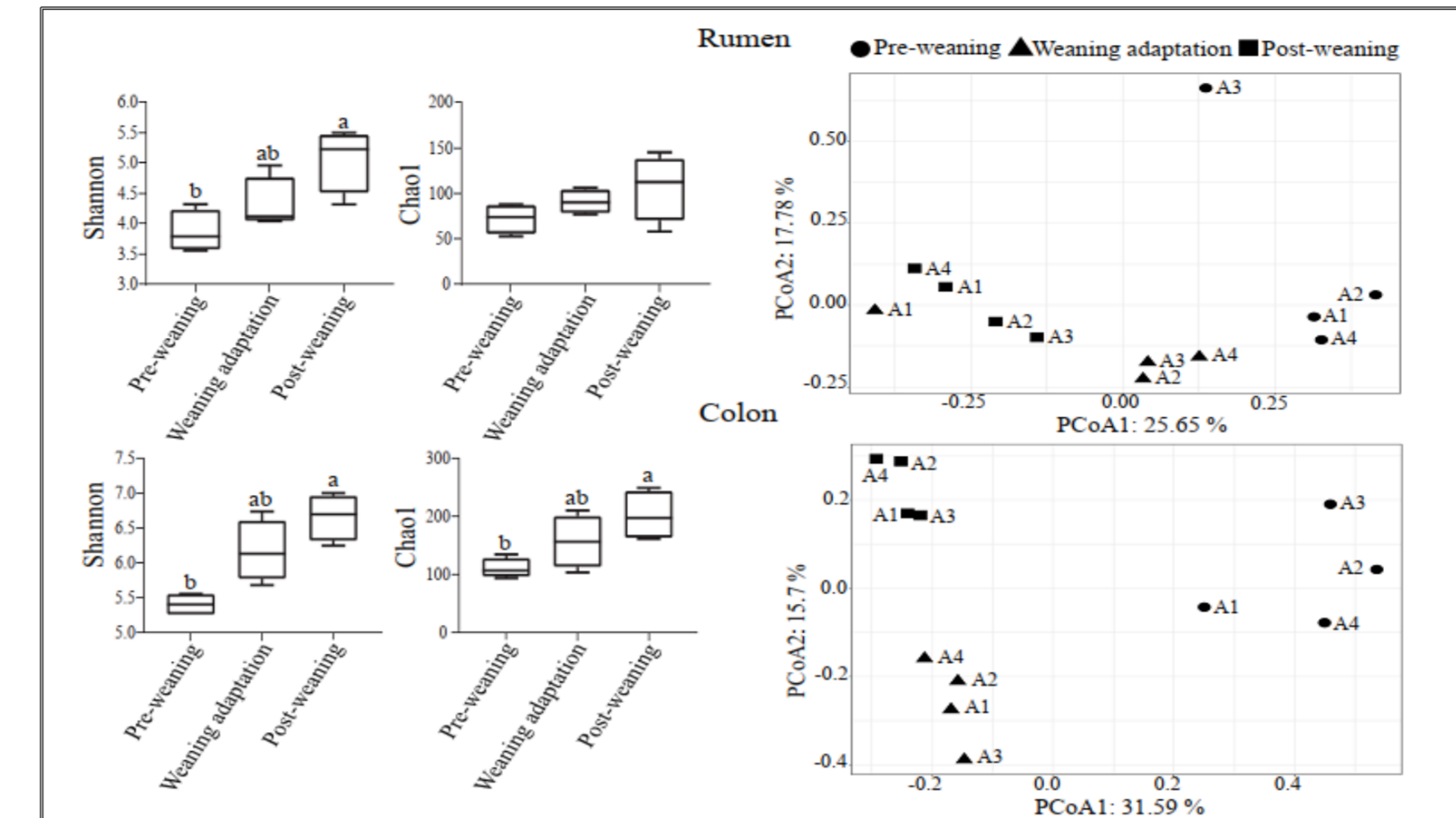


Rumen and colon mucosal tissue sampling of four ruminally cannulated Holstein dairy bull calves at the end of week 5, 7 and 12 (van Niekerk et al., 2018)

Total genomic DNA extraction & PCR amplification of the V1-V3 region of bacterial 16S rDNA

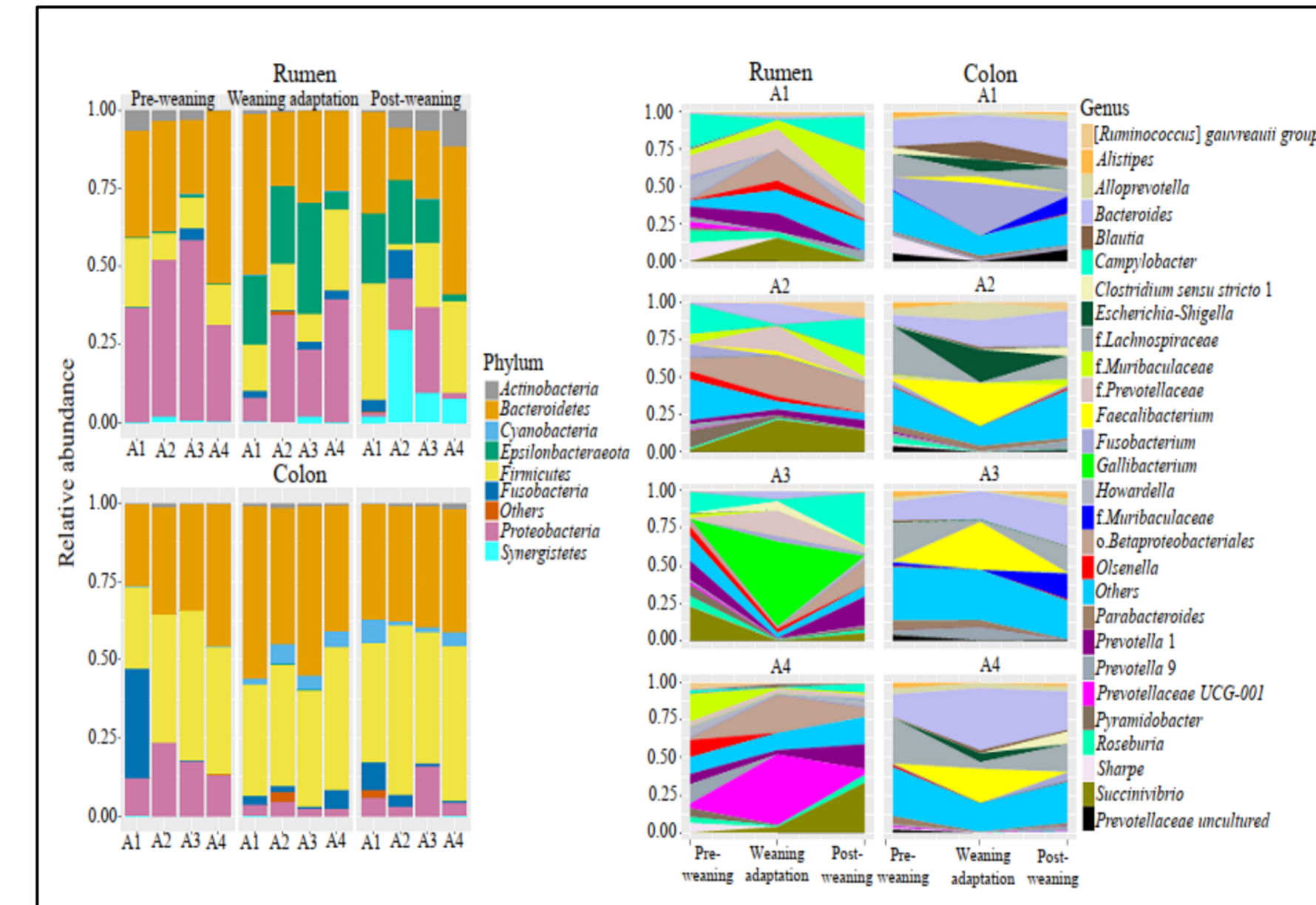
Results & Discussion

A. Diversity of Rumen and Colon Mucosa-associated Microbiota during Weaning Transition



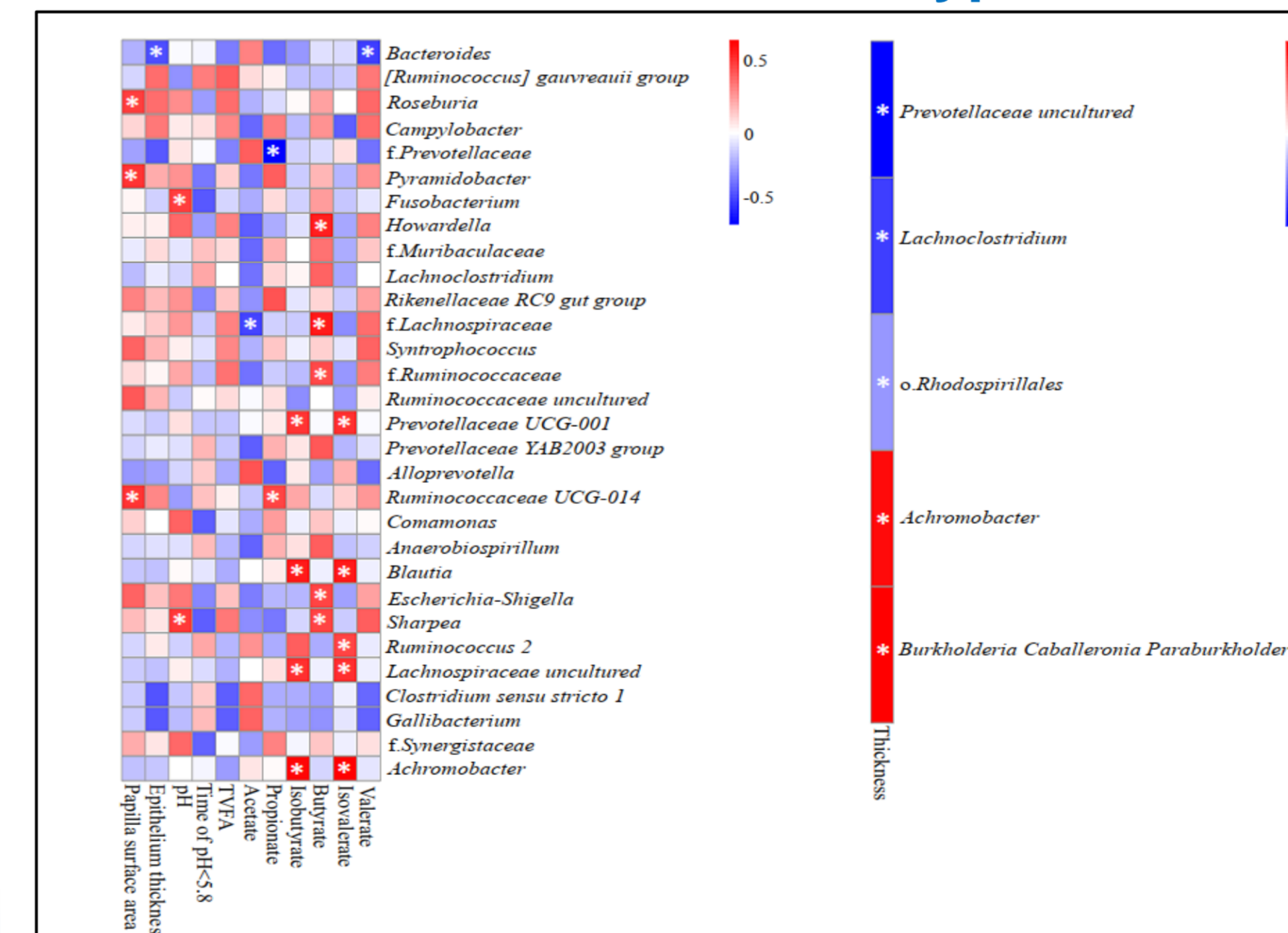
- Both the rumen and colon mucosa-associated microbiota were more diverse (as indicated by Shannon and Chao1 indices; $P < 0.05$) in post-weaning calves, with the exception of Chao1 in the rumen mucosa
- Both rumen and colon microbial profiles clustered together according to particularly weaning period, and the effect of weaning transition on beta diversity of microbiota in the colon mucosa was more noticeable compared to that in the rumen mucosa

B. Effect of Weaning Transition on Rumen and Colon Mucosa-associated Microbiota



- Bacteroidetes (33.1%), Proteobacteria (27.2%) and Firmicutes (17.2%) were predominant irrespective of weaning transition or sampling sites
- Different responses of rumen and colon mucosa-associated microbiota to weaning transition, and region-specific taxa were found in the colon mucosa (Cyanobacteria)

C. Correlation Between Phenotypes and Rumen and Colon Mucosa Associated Microbiota



- Rumen mucosal bacteria such as *Roseburia* and *Pyramidobacter* showed positive associations with rumen papillae surface area
- In the colon mucosa, the relative abundance of *Achromobacter* and *Lachnoclostridium* were correlated with colon mucosal thickness

Note: a,b means within a row with different superscripts differ ($P < 0.05$)

* Indicates $P < 0.05$

Summary & Conclusion

- Weaning transition affects the bacterial community in the rumen and colon mucosa, and the effects of the weaning transition were more obvious in the colon than in the rumen
- *Pyramidobacter* (in the rumen mucosa) and *Lachnoclostridium* (in the rumen mucosa) have positive impacts on rumen and colon mucosa development during the weaning transition

Acknowledgements

