

Gastrointestinal microbiome of calves fed solid diets containing different levels and sources of NDF





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INTRODUCTION

Different levels and sources of NDF can modify the gastrointestinal microbiome.

The objective of this work was to evaluate the microbiome of dairy calves fed with solid diets containing different levels and sources of NDF.

MATERIAL E METHODS

- 18 Holstein calves housed in not-bedded suspended individual cages, fed 4L/d milk replacer, and one of the solid diets:
 - 22NDF conventional starter containing 22% NDF (n = 7)
 - 2. 31NDF starter with 31% NDF, replacing part of the corn by soybean hull (n = 6)
 - 3. 22NDF+H conventional starter with 22% NDF + coast-cross hay ad libitum (n = 5)
- Weaned at the 8th wk of age and housed in tropical shelters until 10 wk.
- ruminal fluid samples: oral probe at weeks 2, 4, 6, 8 and 10
- Fecal samples: at birth (0) and at weeks 1, 2, 4, 8 and 10.
- Extracted DNA → V3 and V4 region amplicons of the 16S rRNA gene → Amplified by PCR → Sequenced by the Illumina MiSeq platform.

Table 1. Ruminal and fecal microbial diversity of calves fed solid diets containing different levels and sources of NDF

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Indices	Diet ¹			p-value		
	22NDF	22NDF+H	31NDF	D ²	A^3	DxA ⁴
Ruminal						
Shannon	2.12	2.03	2.10	0.704	0.150	0.654
Simpson	0.77	0.75	0.78	0.650	0.309	0.947
Chao1	39.83	40.05	40.45	0.983	0.157	0.141
Pielou	0.58	0.56	0.58	0.570	0.336	0.950
Feces						
Shannon	2.57 ^b	2.82	2.65 ^{ab}	0.027	< 0.001	0.131
Simpson	0.85 ^b	0.89ª	0.85 ^{ab}	0.022	< 0.001	0.124
Chao1	57.47	56.96	59.31	0.870	< 0.001	0.595
Pielou	0.65 ^b	0.713	0.66ab	0.002	< 0.001	0.068
	0.65 ^b	0.71	0.66 ^{ab}	0.002	<0.001	0.068

^{ab}Means within a row with different superscripts are significantly different ($P \le 0.05$). ²D = diet; ³A age; ⁴Dxl = Interaction between diet and age.

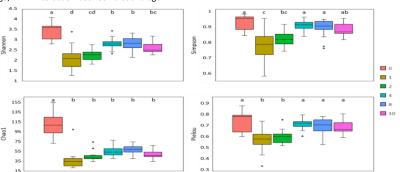


Figure 1 Diversity indices in fecal samples from calves fed solid diets containing different levels of NDF

RESULTS

Bacterial composition

Sixteen and twenty-seven bacterial phyla were identified in ruminal and fecal samples, respectively. And most abundant phyla in both local were:

Bacteroidota: 30.62 and 36.32% Firmicutes_A: 22.97 and 30.32% Firmicutes C: 19.60 and 9.26%

in ruminal and fecal samples, respectively.

CONCLUSIONS

The supply of hay was only effective in modifying the fecal microbiome of dairy calves, suggesting a resilience in the ruminal microbiome.

ACKNOWLEDGMENTS





