

Effect of *Aloe arborescens* supplementation in dry cows on rumen and hindgut microbiomes

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Background

The transition period in dairy cows is characterized by reduced immunocompetence, inflammations, oxidative stress with a higher risk of metabolic and infectious diseases. *Aloe arborescens* contains polysaccharides and exhibits anti-inflammatory, immunostimulant, antibacterial, and antioxidant properties. The aim of this study was to investigate the effect of this nutraceutical approach on the rumen and hindgut microbiomes.

M&M

Thirty multiparous dairy cows at the dry off were divided in three different groups: (1) control group (**CTR**) - dry cows following the typical antibiotic treatment and the application of teat sealant; (2) sealant group (**SIG**) - dry cows without antibiotic's treatment and with only teat sealant; (3) *Aloe arborescens* supplementation and sealant group (**ASIG**) – dry cow with teat sealant and oral administration of 10 g of freeze-dried *Aloe arborescens*.

Aloe arborescens was administered in the morning before the distribution of the total mixed ration for 14 days (7 days before up to 7 days after drying). For 16S rRNA-gene sequencing and volatilome analyses, rumen liquor and fecal matter were collected fourteen days before (T0) dry-off, at drying-off (T1) and seven days after dry-off (T2, only fecal samples). The V3-V4 hypervariable regions of the bacterial 16S gene was sequenced in two MiSeq (Illumina) runs with 2×250-base paired-end reads. Rumen liquor volatilome was determined on 10 ml by SPME-GC-MS (32 compounds other than Short Chain Fatty Acids were detected).

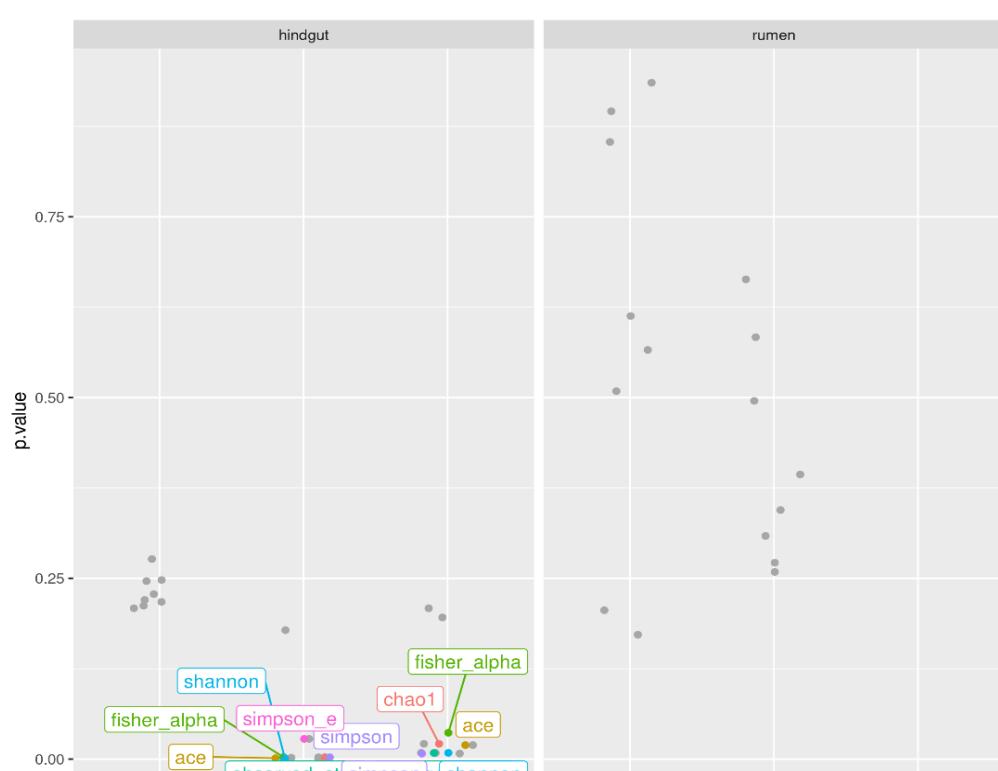


Figure 1: alpha diversity indices calculated for hindgut and rumen samples

Figure 2: bacterial community at phylum level in hindgut and rumen samples at the different timepoints and treatments

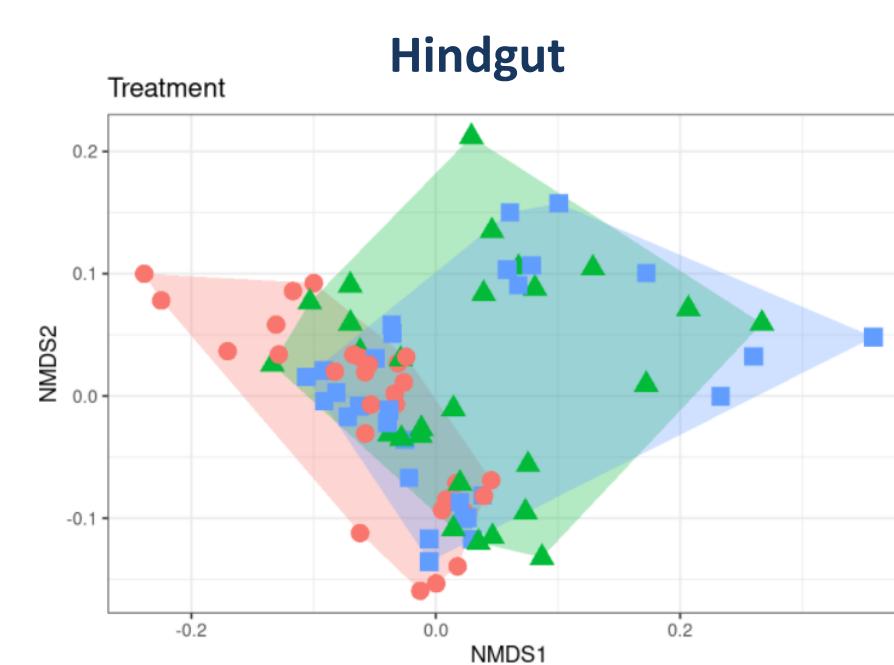
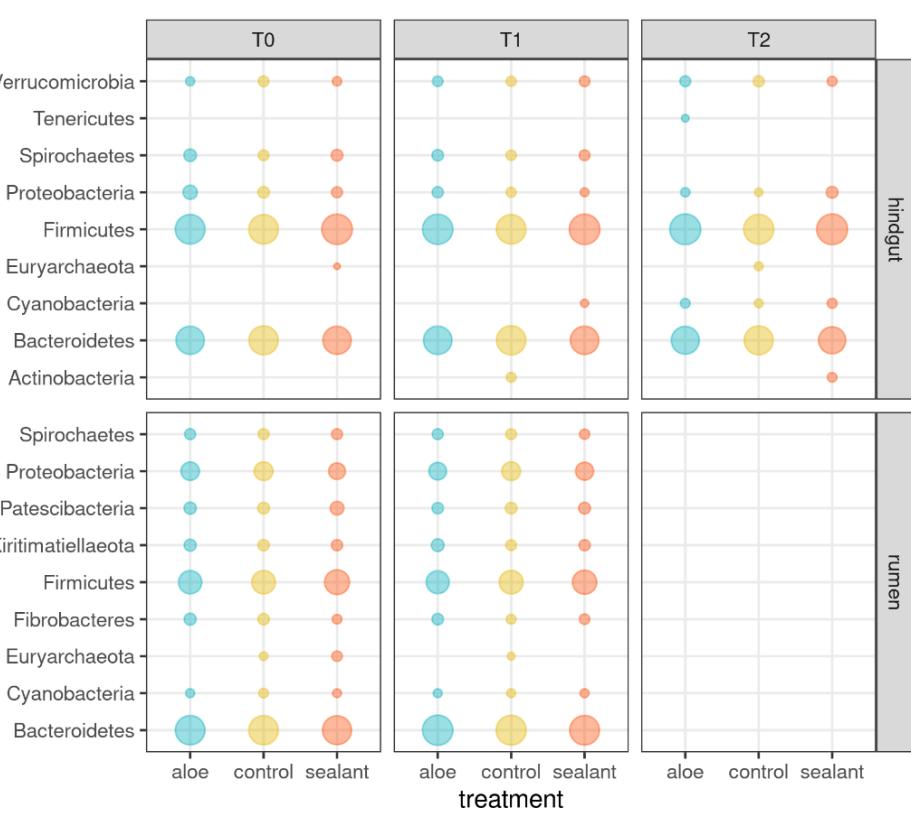
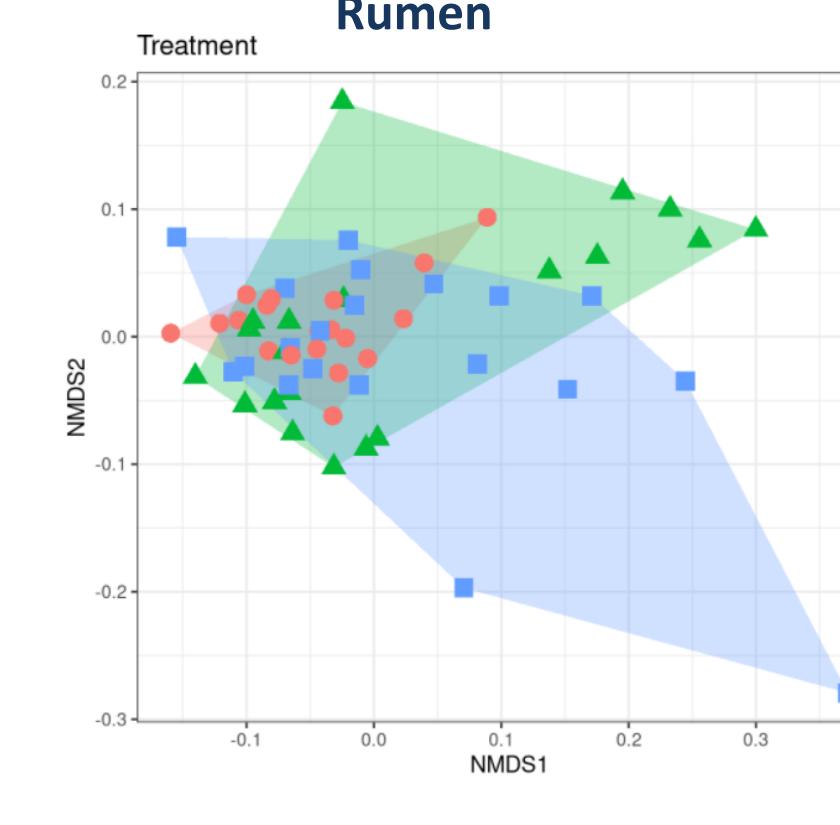


Figure 3: beta diversity for hindgut samples



Results

No significant differences were observed for alpha- and beta-diversity between treatments along the three timepoints in the rumen microbiome. Conversely, according to all indices except evenness (equitability, simpson_e) the alpha diversity of the hindgut microbiome increased significantly (p-values in the range 0.002 – 0.011) in the ASIG group at T2. **Regarding beta-diversity, the hindgut microbiome showed a statistically significant (p-value = 0.0479) separation between treatments.** Independently from sampling time and treatments, the bacterial community of the hindgut was dominated by Bacteroidetes (~40%) and Firmicutes (~48%); rumen showed prevalence of Bacteroidetes (~45%), Firmicutes (~25%) and Proteobacteria (~12%). In rumen, due to the high variability for all the metabolites no significant differences were observed between T0 and T4, in volatilome profile, as for Short Chain Fatty Acid (Fig. 4). In conclusion, the dietary supplementation with *Aloe arborescens* seems to have a sizable effect on the composition of the dairy cow gut microbiome, but not at the rumen level.

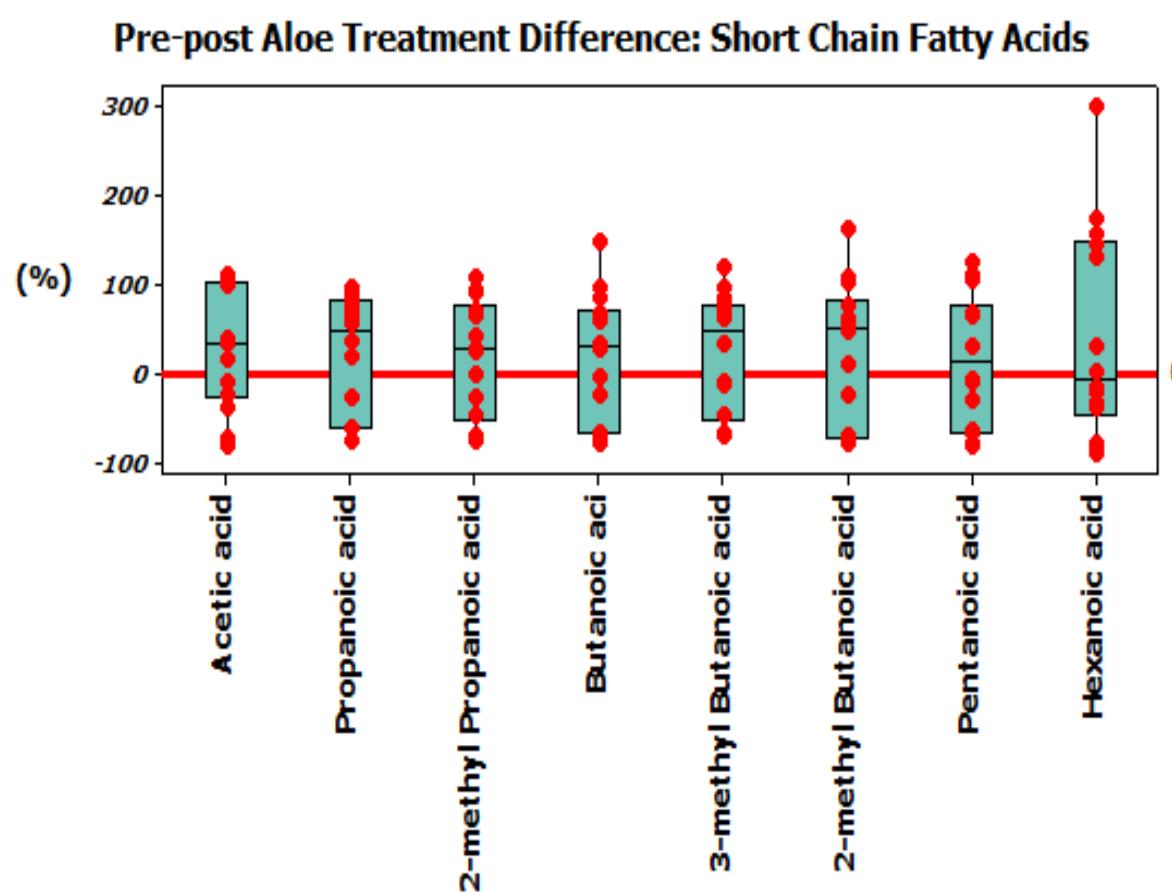


Figure 4: Percent differences from T0 (before treatment) and T4 (after treatment) of Short Chain Fatty Acids in rumen liquor.

Acknowledgements

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