

A direct-fed microbial alters dairy cows' rumen structure and reduces methane intensity



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ABSTRACT

- Methane (CH₄) intensity in dairy cows, a crucial metric in the dairy industry, should be lower when cows eat to their full appetite and maximise milk production.
- A longitudinal study aimed to assess the effects of a direct-fed microbial (DFM) on dairy cattle productivity and rumen microbiome structure.
- Changes in the complexity of the rumen microbiota were observed, and methane production in the treatment group was lower while milk productivity was higher.

INTRODUCTION

- Enteric CH₄ production from cattle contributes to global greenhouse gas emissions.
- CH₄ production in cattle occurs as a consequence of the digestion process in the rumen.
- A placebo-controlled longitudinal study was undertaken with the aim to assess the effects of a direct-fed microbial (DFM), containing one strain of *Lentilactobacillus* and two strains of *Lacticaseibacillus*, on dairy cattle productivity and rumen microbiome structure.

OUR RESEARCH QUESTIONS

1. Does supplementing a cow's diet with a DFM increase productivity and reduce CH₄ intensity?
2. Does DFM supplementation change ruminal microbiota in dairy cows?
3. If the ruminal microbiota changes after DFM supplementation, can this help explain any change in milk production and CH₄ emissions?

METHODS

- 13 Holstein cows were split into two groups (Control, n=3, and DFM, n=10), individually penned and monitored for 23 weeks.
- Cows entered the study between 63-91 DIM and were fed TMR
- The DFM group were supplemented daily with a total of ~7 x 10⁹ cfu of the DFM for the duration of the study. The Control group received a placebo supplement.
- Milk quantity and quality data was gathered daily.
- Ruminal fluid was collected (via oro-gastric tube) at the start of the study and at 2-3 weeks intervals until the study concluded. Samples stored at -80°C for microbiome and VFA analysis.
- Methane values were calculated using VFA measures.

RESULTS AND DISCUSSION

- Average daily milk production (L/day; mean ± SD): Control 24.04 ± 5.94 vs. DFM 24.83 ± 5.99 (p<0.05)
- Average methane yield (g/kgDM; mean ± SD): Control 22 ± 5 vs. DFM 19 ± 5 (p<0.05)
- Total methane production (from total dry matter intake, g/kgDMI): Control: 336 ± 95 vs. DFM 297 ± 103 (p<0.01). Estimated reduction of 11% (range 10-13%) in DFM.
- Microbiota complexity decreased and there were marked changes in microbial diversity in the DFM.
- Pattern searching showed reduction in the relative abundance of methanogens in the DFM.

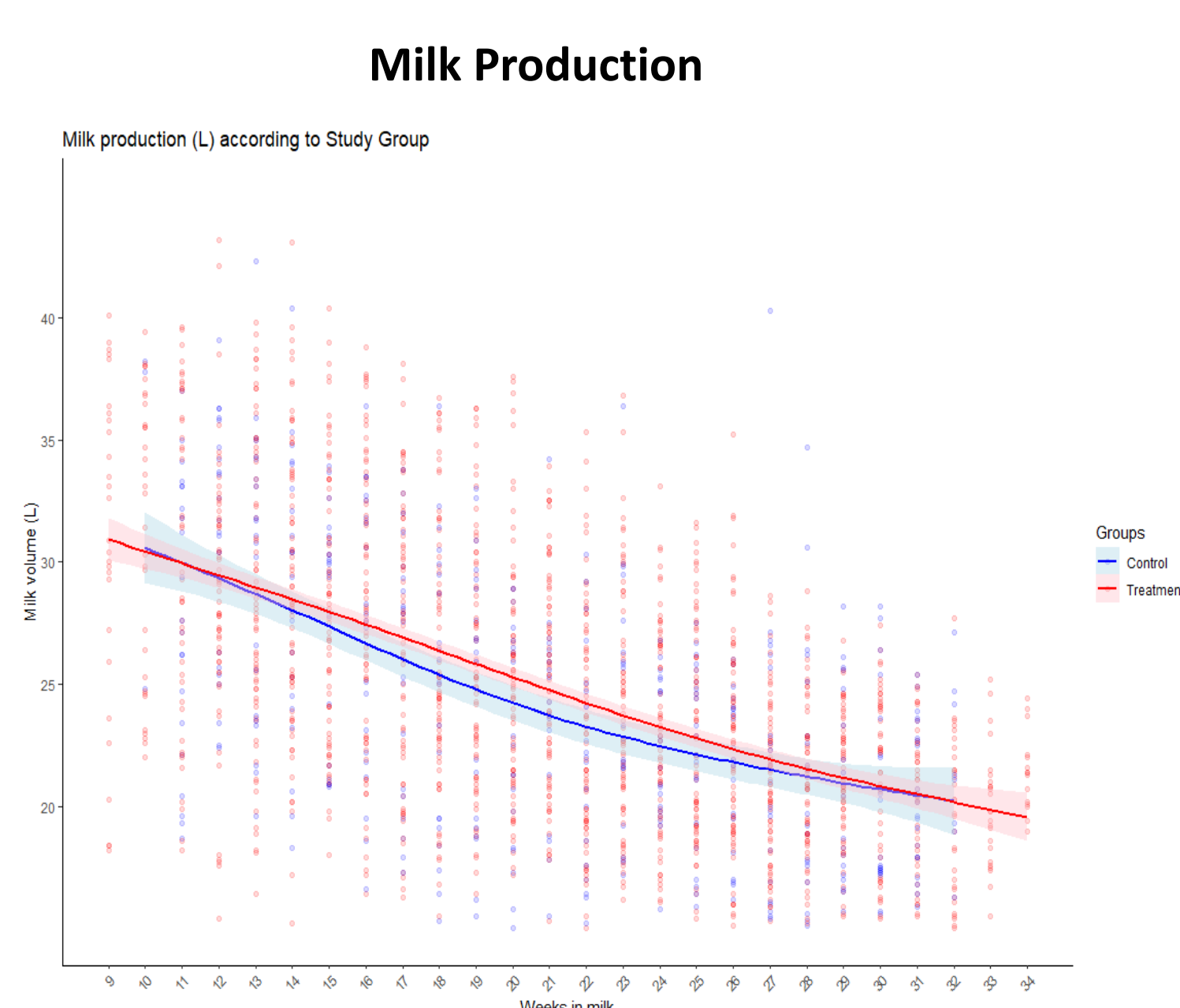


Fig 1. Daily milk production (L/day, mean ±SD) A crude Student's t-test comparing means, indicate significant difference between the Groups (Means difference = 0.79 L (95% confidence interval [CI] = 0.16 - 1.41; t = -2.46, df = 745.95, P = 0.01).

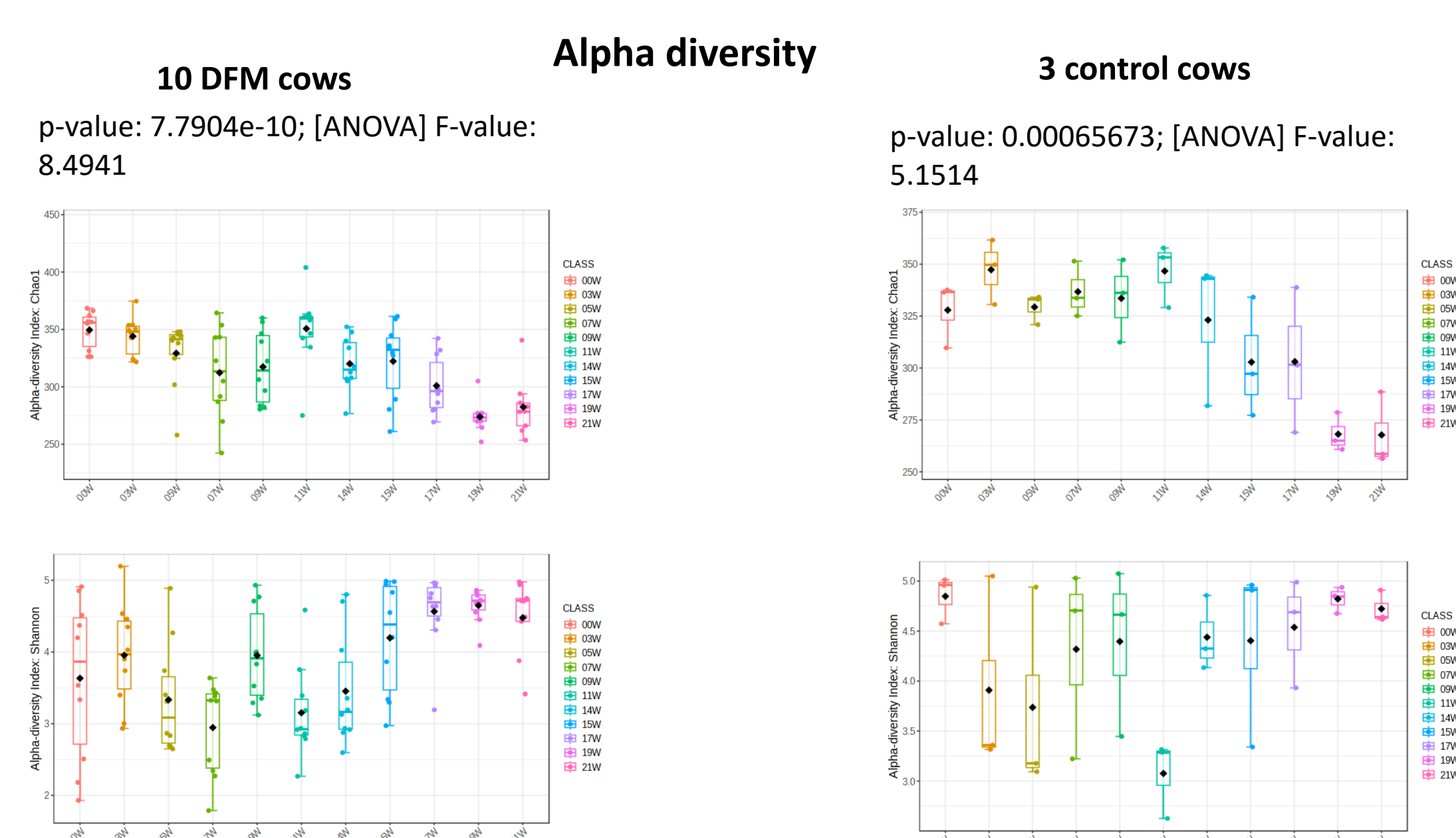


Fig 2. Alpha diversity for the two groups. The Chao1 values trend down over time, indicating a reduction in the raw complexity of the microbiota. The Shannon values move about a lot showing that the interaction of abundance and diversity varies.

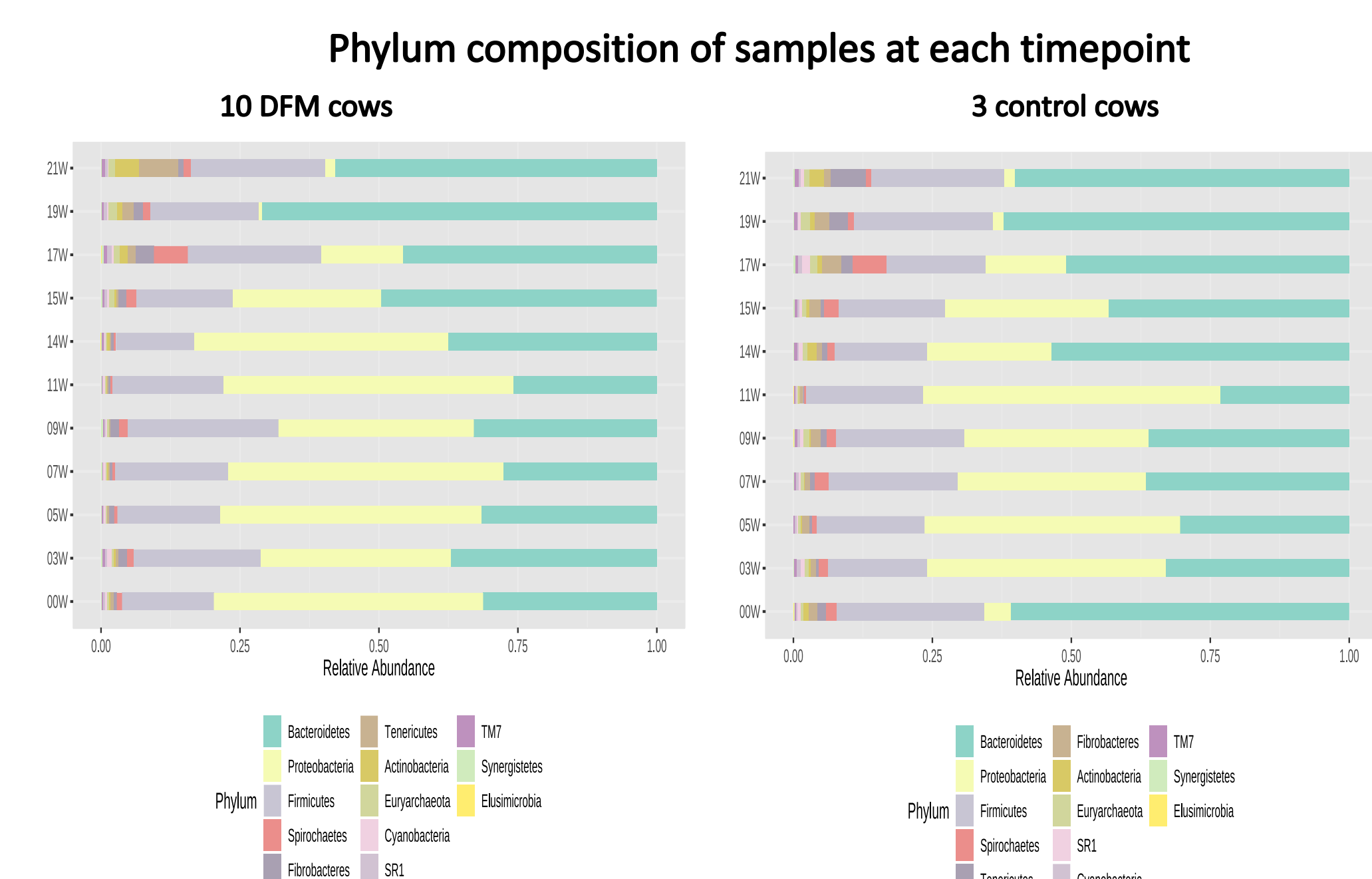


Fig 3. Overall taxonomic composition of rumen samples in the two groups of cows. Visually there are some differences between treated and control groups, e.g., compare the Proteobacteria. However, differences are small and may arise due to small sample sizes

CONCLUSIONS

- In this pilot-scale study, DFM cows showed a significant lift in milk productivity (0.79 L/d, p<0.01).
- Methane production and methane yield were lower in the DFM cows (39 g/kgDMI and 3 g/kgDM respectively).
- The microbiota complexity decreased over the course of the study and there was marked change in β diversity in the DFM.
- Pattern searching showed a reduction in the relative abundance of methanogens in DFM group.
- Further studies are required to elucidate the mechanism driving the change in the relative abundance of methanogens and the reduction in methane intensity.

AFFILIATIONS