Ruminal microbiome characterization of beef cattle fed with ensiled or not-ensiled total mixed ration

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Introduction

✓Ruminal microbiota is altered by forage proportion, nutritional composition, and methods for diet conservation (Zhang et al., 2021);

✓The characterization of ruminal microorganisms by conventional methods is challenging, and metagenomics emerges as an alternative technique (Morgavi et al., 2013; Kibegwa et al., 2023);

✓Identifying the microbial populations involved in ruminal fermentation allows:

- ✓evaluation of their roles in substrate degradation;
- ✓evaluation of their end products;
- ✓dietary modulation to enhance rumen function and animal performance.

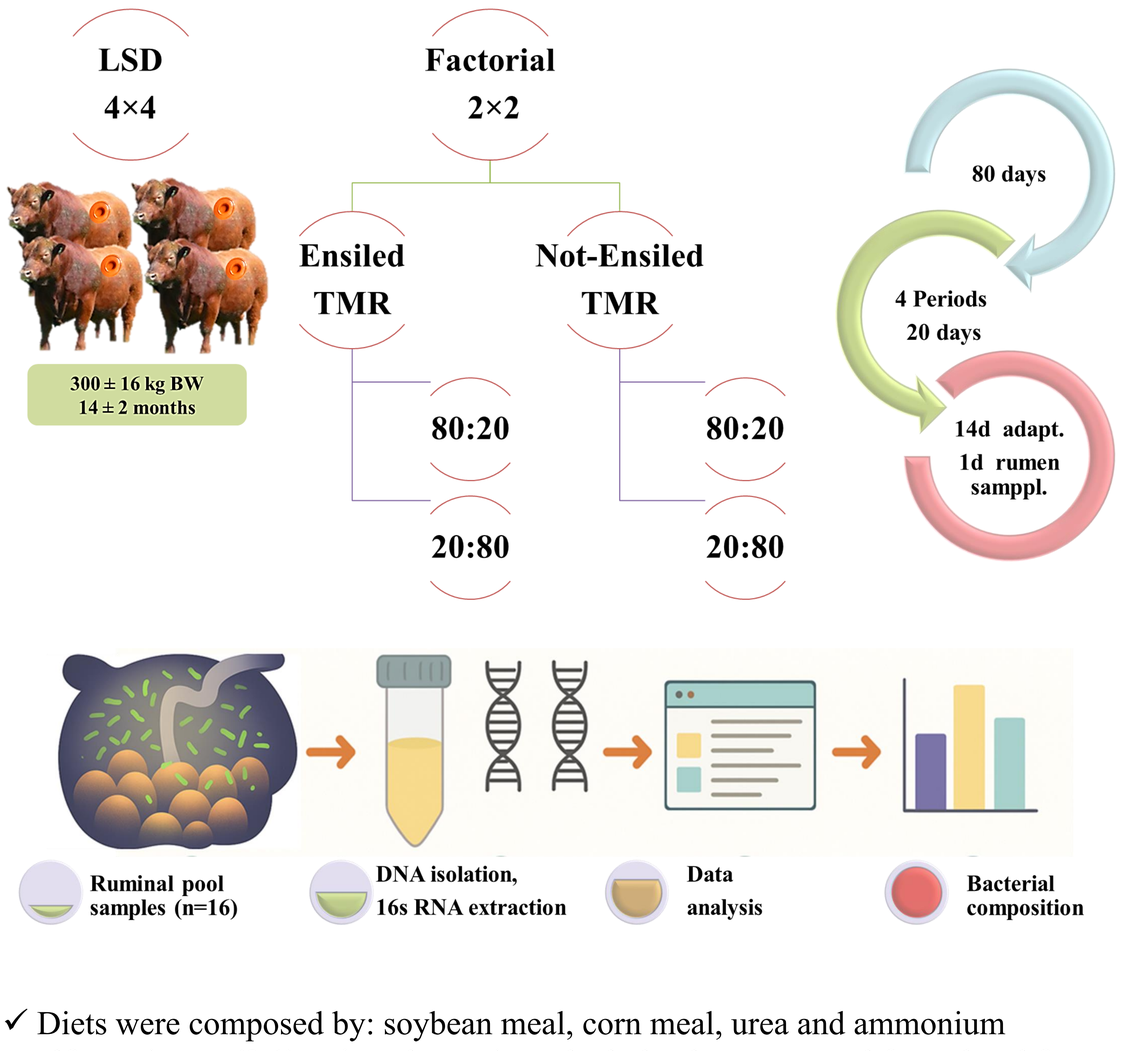
Objective

This study aimed to characterize the ruminal microbiome of beef cattle fed with total mixed ration (TMR) ensiled or not-ensiled, with two forage proportions.

Material and Methods

✓ The experiment was conducted in the Federal University of Viçosa.

✓ All procedures were approved by the by the Ethics Commission on the use of farm animals (40/2024).



✓ Diets were composed by: soybean meal, corn meal, urea and ammonium sulfate mixture (9:1), mineral premix and whole plant corn, and formulated for finishing cattle.

✓Bacterial community analyses: Phyloseq 1.24.2 package in Rstudio and Data were Microbiome Analyst online server.

✓β-diversity analysis: Principal Coordinate Analysis (PCoA) based on the Bray-Curtis.

✓Linear discriminant analysis effect size (LEfSe): identify taxonomic groups classified at the genus level.

Results

✓ We did not observe effects (P > 0.05) when the processing type was analyzed (i.e., ensiled or not-ensiled).

✓ The relative abundance of bacterial taxa at the genus level showed a predominance of *Prevotella*, *Rikenellaceae_RC9*_gut_group, and, *Christensenellaceae_R7*_group for all treatments analyzed, where percentages averaged 18.7%, 11.43%, and 5.45%, respectively (Figure 1).

✓ The β-diversity analysis, revealed significant differences (P < 0.009) for F:C ratio, with the axes varying from 10.5 and 13.6% (Figure 2a).

✓ Genera identified by Lefse analysis (Figure 2b) for the 20:80 F:C ratio were: *Lachnospiraceae_NK3A20*_group, and *Atopobium;*

✓For the 80:20 ratio were: *Candidatus_Soleaferrea*, *Family_XIII*_UCG_001, *Pseudobutyrivibrio*, *Lactobacillus*, *Shuttleworthia*, *Fibrobacter*, *Butyrivibrio*, *Acetobacter*, *Lachnospiraceae_ACC2044*_group, *Lachnospiraceae_XPB1014*_group, *Candidatus_Saccharimonas*, *Saccharofermentans,* and *Succiniclasticum*.

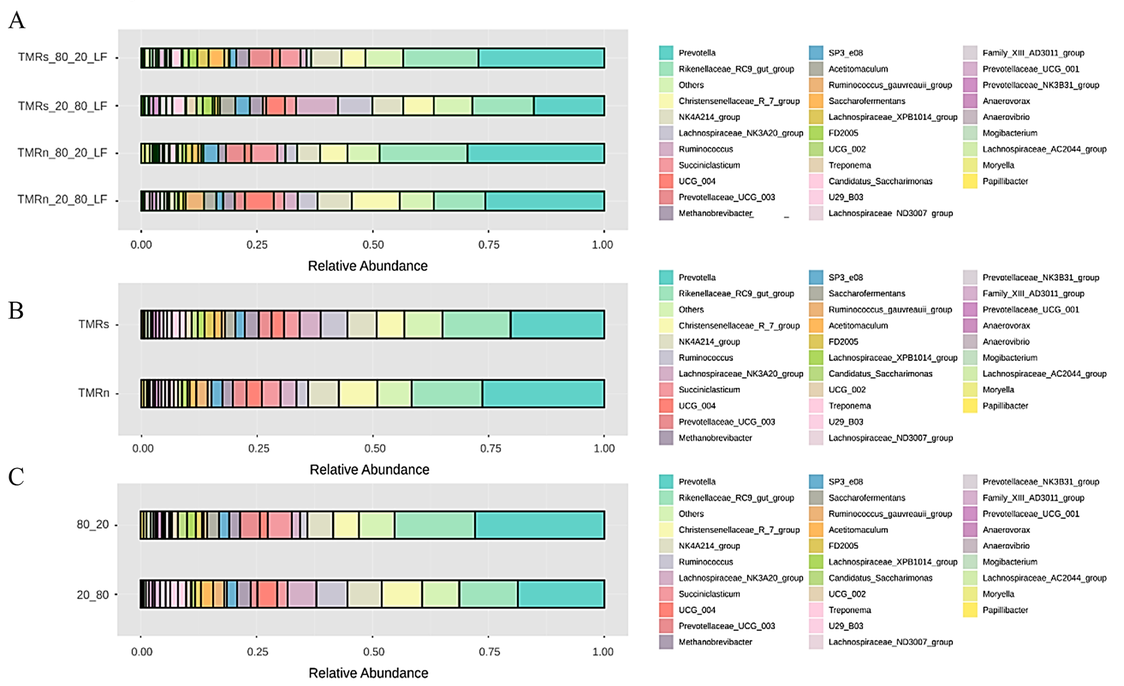


Figure 1. Relative abundance of bacterial genera from the ruminal liquid-phase community according to all treatments (**A**), processing method (ensiled or non-ensiled; **B**), and forage-to-concentrate ratio (20:80 or 80:20; **C**)

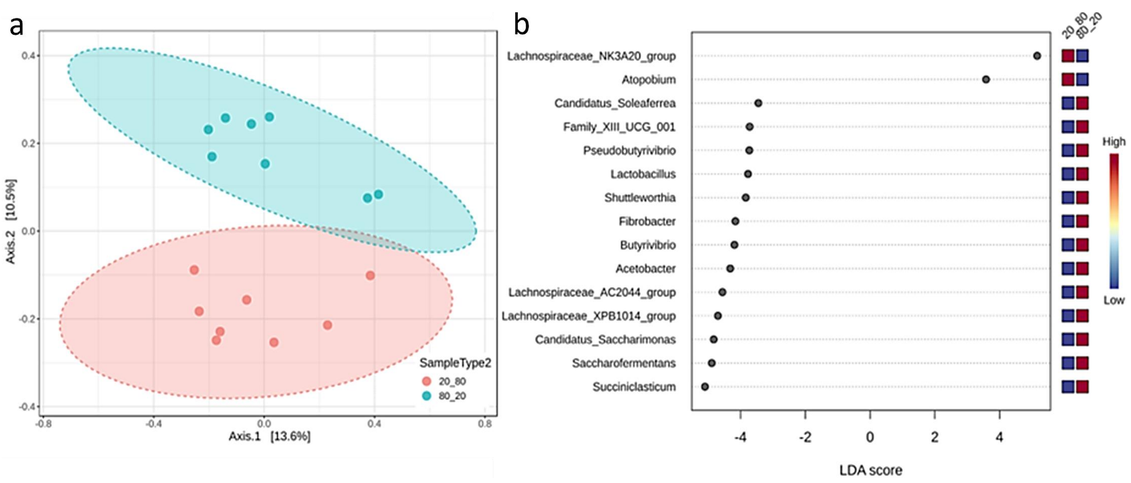


Figure 2. Beta diversity analyses were performed using principal component analysis (PCoA), comparing the different forage:concentrate ratios **(a)**. Lefse analysis shows the taxa representing the significant differences for the different forage:concentrate ratios for the liquid phase, with the F:C ratio 20:80 in red and 80:20 in blue (LDA Score >2; **b**).

Conclusions

✓ The relative abundance of bacterial taxa at the genus level in the liquid phase showed a predominance of *Prevotella*, *Rikenellaceae_RC9*_gut_group, and *Christensenellaceae_R7*_group for all treatments analyzed. The predominance of bacterial populations in treatments with greater forage-to-concentrate ratios highlights the dietary influence on ruminal microbiota. Presenting valuable insights for developing dietary strategies for the optimization of ruminal bacterial activity and achieving animal performance improvements.

Acknowledgements

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