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DATA NOTE

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Metagenomic data from the rumen of South African Mutton Merino sheep supplemented with crude or encapsulated Acacia tannin extracts

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Abstract

Objectives This dataset was generated as part of a study investigating the impact of crude and encapsulated Acacia mearnsii tannin extracts on the rumen microbiota of South African Mutton Merino sheep. The aim was to provide high-quality metagenomic data to support methane mitigation strategies through dietary interventions targeting rumen microbial communities.

Data description Rumen fluid was collected from 24 rams (six per treatment) fed a total mixed ration (TMR) supplemented with either distilled water (control), monensin (positive control), crude tannin, or microencapsulated tannin. However, one sample did not yield sufficient sequencing depth, resulting in 23 usable datasets. DNA was extracted and subjected to shotgun metagenomic sequencing on the Illumina NovaSeq 6000 platform. The dataset comprises paired-end reads deposited in the NCBI SRA under accession SRP480487. Taxonomic profiling reveals dominant phyla such as *Bacteroidetes* and *Firmicutes*, and the presence of archaeal genera such as *Methanobrevibacter*. This dataset provides insights into the structural and functional composition of the rumen microbiome and may be useful for comparative studies and biotechnology applications.

Keywords Rumen microbiome, Metagenomics, Acacia mearnsii, Tannins, MG-RAST, Methane mitigation

Objective

This dataset originates from a trial designed to explore the effects of crude and encapsulated tannin extracts on rumen microbial diversity in South African Mutton Merino sheep [1]. The dietary additives aimed to modulate microbial composition to reduce methane emissions. Forty rams (average weight 34 kg) were assigned to four treatments of ten rams per treatment and fed for 105 days. Rumen fluid was collected from six rams per treatment (24 animals in total). However, one DNA extraction did not produce sufficient sequencing depth, resulting in 23 usable datasets.

The data were produced as part of a broader investigation into sustainable feeding strategies and their implications for microbial structure and environmental emissions in ruminants. Although related research paper is available [1, 2], this specific dataset has not been published in its raw, annotated format. Therefore, it serves

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Table 1 Overview of data files/data sets

Label	Name of data file/data set	File types	Data repository and identifier
Data file 1	General information on dataset	MS Excel (.xlsx)	Figshare (https://doi.org/10.6084/m9.figshare.29117828) [9]
Data set 1	Rumen metagenomic reads (23 samples)	fastq.gz	Sequence Read Archive (https://identifiers.org/ncbi/insdc.sra:SRP480487) [10]
Data file 2	Overview of microbial diversity and population from the dataset	MS Word (.docx)	Figshare (https://doi.org/10.6084/m9.figshare.29117831) [11]
Data file 3	Figure 1. Stacked bar chart of rumen microbiome at the phylum level under dietary regimes	PDF	Figshare (https://doi.org/10.6084/m9.figshare.29117834) [12]

as a unique resource for future investigations into the microbial ecology of the sheep rumen and the functional impact of dietary tannins.

Data description

Sampling

The experiment was conducted at the Experimental Farm, Innovation Africa campus, University of Pretoria. Forty South African Mutton Merino rams (average body weight 34 ± 3 kg) were randomly allocated to 20 pens and subjected to four dietary treatments for 105 days, including 28 days of adaptation. At the end of the feeding trial, 24 rams selected based on body weight from each treatment group, were humanely stunned using a captive bolt pistol and immediately slaughtered by severing the major blood vessels in the neck. Rumen contents were the collected post-slaughter for subsequent analysis. But one sample was excluded due to insufficient sequencing depth, leaving 23 datasets for analysis. The rumen content of each ram was emptied into a sterile container, mixed thoroughly, and filtered through four layers of cheesecloth to obtain fluid samples, which were stored at -20 °C. The sampling methodology aligns with the approach used by Ibrahim and Hassen [1] in a similar dietary intervention study on lambs (Table 1).

Meta-DNA extraction and sequencing

Rumen fluid samples were thawed at room temperature prior to DNA extraction. Total genomic DNA was extracted using the ZymoBiomics DNA Miniprep Kit (Zymo Research, USA), following the manufacturer's guidelines. The protocol has been widely used in rumen metagenomic studies due to its effectiveness in recovering high-quality microbial DNA from complex substrates [3, 4]. DNA concentration and purity were verified using NanoDrop spectrophotometry and Qubit 4 Fluorometer (Thermo Fisher Scientific, USA) to ensure suitability for downstream sequencing. Library preparation was performed with standard Illumina protocols, and sequencing was outsourced to Novogene (Singapore). High-throughput paired-end sequencing (2 × 150 bp) was conducted on the NovaSeq 6000 platform, generating approximately 62.2 Gb of raw sequence data, consistent with yields reported in large-scale metagenomic analyses [5].

Data processing

The raw reads were uploaded to the MG-RAST v4.0.3 online platform for annotation and analysis [6]. Pre-processing included adapter trimming, removal of low-quality reads, and filtering of host genomic contaminants. Functional and taxonomic annotations were assigned using the M5NR database, a non-redundant compilation of multiple microbial databases [7]. Alignments were performed using the BLAT algorithm [8], enabling rapid comparisons of metagenomic reads to reference sequences. The processed dataset presented in Fig. 1 revealed 28 bacterial phyla, dominated by Bacteroidetes and Firmicutes. A total of approximately 500 bacterial genera were identified, with Prevotella, Bacteroides, Eubacterium, and Clostridium being the most abundant. Additionally, 41 archaeal genera were identified, predominantly Methanobrevibacter, which plays a key role in ruminal methanogenesis [2].

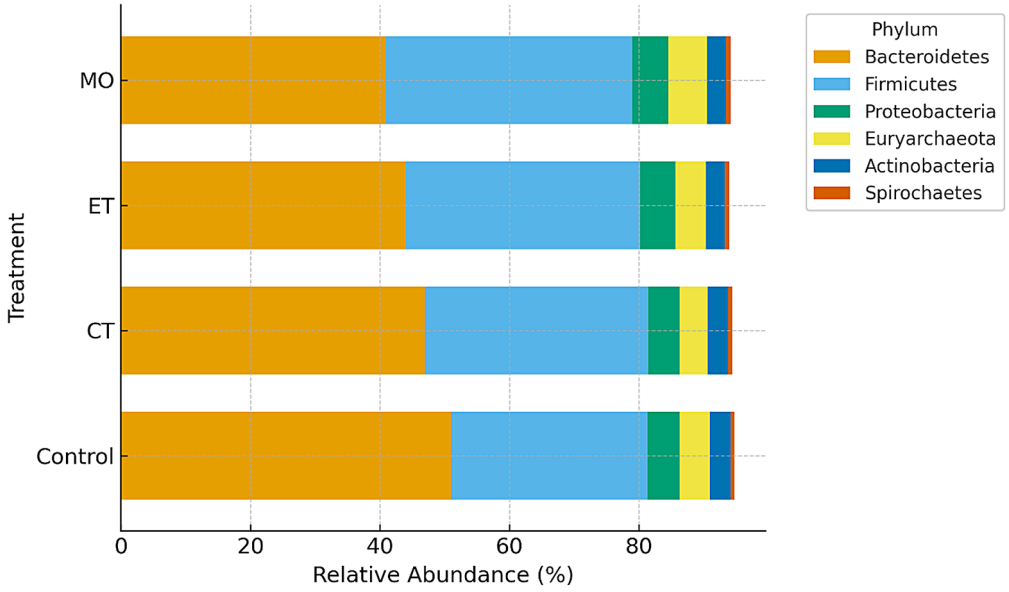

Fig. 1 Stacked bar chart of rumen microbiome at the phylum level under dietary regimes (Total Mixed Ration, monensin, crude tannin and encapsulated tannin). *MO* Monensin; *ET* Encapsulated tannin; *CT* Crude tannin

Limitations

Not applicable.

Abbreviations

TMR	Total Mixed Ration
MG-RAST	Metagenomic Rapid Annotation using Subsystem Technology
SRA	Sequence Read Archive
DM	Dry Matter
bp	Base pairs
BLAT	BLAST-like alignment tool

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Author contributions

AMA: Conceptualisation, Methodology, Software, Validation, Resources, Writing – Reviewing and Editing. IBL: Conceptualisation, Methodology, Software, Writing – Reviewing and Editing. SLI: Conceptualisation, Methodology, Software, Analysis. EVMK: Conceptualisation, Supervision, Writing – Reviewing and Editing. AH: Conceptualisation, Supervision, Resources, Writing – Reviewing and Editing, Project administration, Funding acquisition.

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Data availability

The data described in this Data note can be freely accessed on the NCBI Sequence Read Archive under accession number SRP480487. Please see Table 1 and References [1, 2] for details.

Declarations

Ethics approval and consent to participate

Approved by the Animal Ethics Committee of the University of Pretoria (Approval no. EC075-17). Clinical trial number: not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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