



Data Article

Datasets of shotgun metagenomics evaluation of rumen microbiota of South African mutton merino sheep

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ABSTRACT

The rumen microbial consortium plays a crucial role in the production performance and health of the ruminant animal. They are responsible for breaking down complex plant materials such as cellulose and hemicellulose to release usable energy by the host animal. Rumen microbial diversity manipulation through dietary strategies can be used to achieve several goals such as improved feed efficiency, reduced environmental impact or better utilization of low-quality forages. The dataset, deposited in the National Centre for Biotechnology Information SRA with project number PRJNA775821, comprises sequenced DNA extracted from the rumen content of 16 South African Merino sheep supplemented with different plant extracts. Illumina HiSeq™ 6000 technology was utilised to generate a total of approximately 46.7 Gb in raw nucleotide data. The data consists of 700,318,582 sequences, each with an average length of 184 base pairs. Taxonomic annotation conducted through the MG-RAST server showed the dominant phylum averages are Bacteroidetes (51 %) and Firmicutes (28 %), while Euryarchaeota, Actinobacteria, and Proteobacteria each account for approximately 3 % of the population. This dataset also enables us to identify and profile all expressed genes related to metabolic and chemical processes. The dataset is a valuable tool, offering insights that can lead to enhanced sustainability, profitability and reduced

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environmental impact within the context of ruminant production process.

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Specifications Table

Subject	Microbiology
Specific subject area	Microbiome
Type of data	Figures and Raw NGS data (Fastq files)
How the data were acquired	DNA from rumen fluid extracted and sequenced on Novaseq 6000 platform (2 × 150 paired-end). Raw data were assembled and annotated through MG-RAST, an online service platform.
Data format	Raw data (fasq.gz. file)
Description of data collection	Samples of rumen fluid was collected from 16 South Africa Mutton Merino sheep consuming either of <i>Moringa oleifera</i> , <i>Jatropha curcas</i> , <i>Aloe vera</i> extracts and the control (no additive) as medicinal additives. DNA samples from the rumen fluid samples were extracted using the D4300 ZymoBiomix miniprep (Zymo Research group, USA). NGS on NovaSeq 6000 system (Illumina) and metagenome sequence annotation were carried out using MG-RAST.
Data source location	Institution: Hatfield Experimental Farm, Innovation Africa campus, University of Pretoria, Pretoria, Hillcrest, Pretoria, Gauteng Province, South Africa. Latitude and longitude of the location where animals were housed: (25°44'49.9"S 28°15'31.6"E)
Quality control	This was done via MG-RAST platform and includes: Adapter trimming to remove any primers during library preparations. Quality trimming of low-quality bases. Read filtering to remove sequences that are too short or contain ambiguous characters. De-replication and removal of duplicates/artificial sequences generated during sequencing. Removal of host genomic DNA sequences to focus on microbial content. Contaminant removal.
Data accessibility	Repository name: National Centre for Biotechnology Information SRA Data Identification Number: PRJNA775821 [1] URL: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA775821
Related research article	Akanmu [2]

1. Value of the Data

- It offers a comparative evaluation of ruminal microbiomes within the context of South African Mutton Merino sheep
- The comprehensive dataset elucidates the relative abundance, taxonomic diversity, and functional attributes of rumen microorganisms, unveiling their responses to diverse medicinal plant extracts
- This dataset serves as a valuable resource for identifying phyla-level microbiota responses to interventions in animal nutrition and feeding efficiency, with the potential to enhance feed supplementation strategies.
- Additionally, it enables in depth investigations into the potential effects of plant metabolites on anaerobic microbes, particularly those involved in the production of various fermentation by-products, including methane, within the rumen of ruminant animals.

2. Objective

The overall objective of the study was to assess the effect of medicinal plants on growth performance, nutrient digestibility, methane emission and microbial diversity of South African

Mutton Merino sheep. Improved knowledge of the rumen ecosystem can help optimise live-stock improvement and feeding strategies. High throughput sequencing technology can aid in comprehending the biodiversity and characteristics of the microbial communities in the rumen, enabling researchers to establish connections with feed degradability, greenhouse gas emissions, and feed utilisation.

3. Data Description

The dataset comprises raw data obtained through shotgun sequencing of the rumen metagenome of South African Mutton Merino sheep. All the acquired datasets, available in the fastq.gz file format, have been deposited in the NCBI SRA database under the project accession number PRJNA775821. Details regarding the microbial community and functional structure, determined using SEED subsystem analysis, are illustrated in Figs. 1 and 2, respectively.

4. Experimental Design, Materials and Methods

Rumen fluid samples were collected from 16 Merino sheep, all of which were fed the same base diet. The diet included 3 different plant extracts as additives, and there was also a control group that received the diet without any plant extract additives. The study was conducted at Hatfield Experimental Farm, Innovation Africa campus, University of Pretoria, in the Gauteng Province of South Africa [2]. The entire rumen content was emptied into a container and subsequently strained, and 50–100 mL rumen fluid samples were collected from each rumen

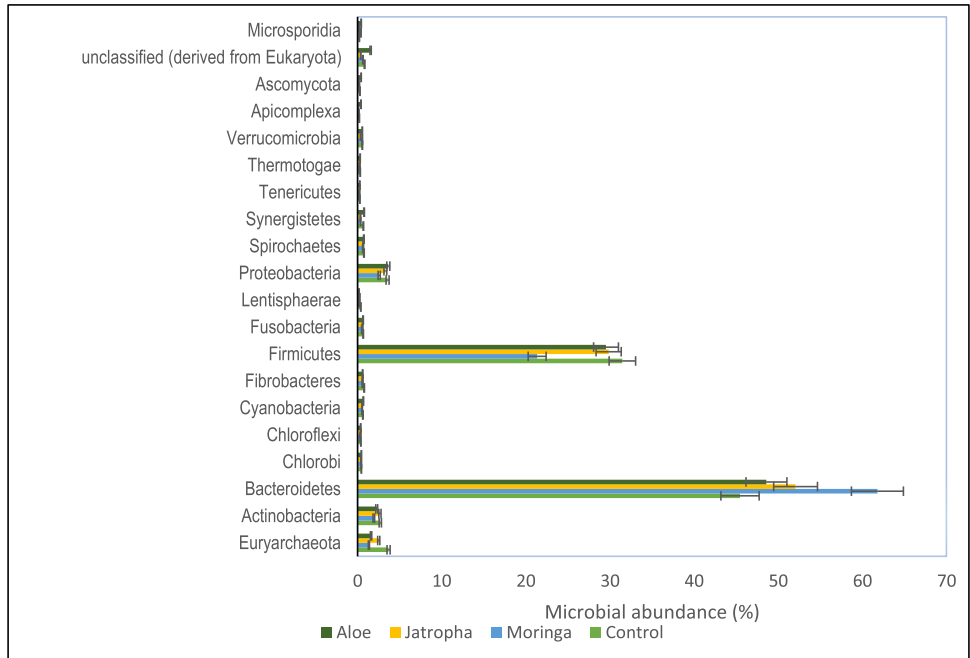


Fig. 1. Phyla obtained according to the taxonomic annotation of rumen fluid microbiome from SA Mutton Merino sheep supplemented with different medicinal plant extracts.

Each bar represents the mean \pm standard error of each phyla component recovered.

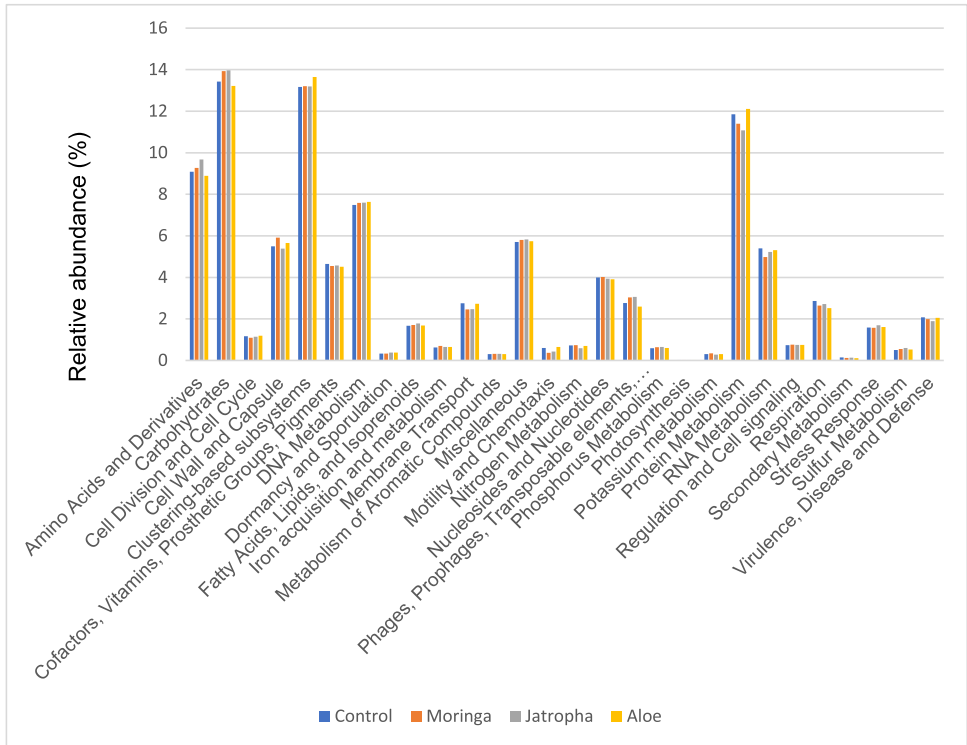


Fig. 2. Functional profiles of rumen fluid microbiome from Merino sheep supplemented with different additives based on Moringa, Jatropha and Aloe plant extracts dataset using SEED subsystem.

within a time frame of 7–10 min after the slaughtering process [2]. Rumen fluid was frozen and DNA extraction was carried out using the D4300 ZymoBiomics miniprep (Zymo Research Group, USA) according to manufacturer's instructions. Shotgun metagenomic sequencing was carried out using NovaSeq 6000 system (Novogene, Singapore). Based on the default metagenomic specifications on MG-RAST online platform, the Rapid Annotation Subsystem was used for structural analysis and functional annotation of the sequenced data [3]. After quality assessment, sequenced data were annotated using a BLAST-like alignment algorithm called BLAT, against the M5NR database [4] which offers a concise alliance with many other databases.

Ethics Statements

This work follows the ethical requirements for publication in Data in Brief. It does not involve human subjects or any data collected from social media platforms. The experiment was carried out under the guidelines and approval of the Animal Ethics Committee of the University of Pretoria (Approval no. ECO-03014), which complies with international requirements for the use of the South African Male Merino sheep.

Data availability

[Methane mitigation using medicinal plant extracts \(Original data\)](#) (NCBI Bioproject)

CRediT Author Statement

Abiodun Mayowa Akanmu: Conceptualization, Methodology, Software, Validation, Resources, Writing – review & editing; **Este van Marle-Köster:** Conceptualization, Supervision, Valida-

tion, Resources, Writing – review & editing; **Abubeker Hassen:** Conceptualization, Supervision, Validation, Resources, Writing – review & editing, Project administration, Funding acquisition; **Festus Adeyemi Adejoro:** Methodology, Validation, Resources, Writing – review & editing, Funding acquisition.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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