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Fecal microbiome composition and lactic acid bacteria in Senduro goats revealed by 16S rRNA gene sequencing

GUNTUR TRIMULYONO[1,2], SALAMUN[1,♥], FATIMAH[1], ALMANDO GERALDI[1]

[1]Doctoral Program in Mathematics and Natural Sciences, Faculty of Science and Technology, Universitas Airlangga. Jl. Dr. Ir. H. Soekarno, Surabaya 60115, East Java, Indonesia. Tel.: +62 31-5936501, ♥email: salamun@fst.unair.ac.id

[2]Program of Biology, Faculty of Mathematics and Natural Sciences, Universitas Negeri Surabaya. Jl. Ketintang, Surabaya 60231, East Java, Indonesia

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Abstract. *Trimulyono G, Salamun, Fatimah, Geraldi A. 2026. Fecal microbiome composition and lactic acid bacteria in Senduro goats revealed by 16S rRNA gene sequencing. Biodiversitas 27 (5): d270522. https://doi.org/10.13057/biodiv/d270522.* Senduro goat (*Capra hircus*) is an important breed widely cultivated in Senduro District, Lumajang Regency, East Java, Indonesia. This study aimed to describe the fecal microbiome composition and lactic acid bacteria (LAB) detected in Senduro goats from two age groups (1-2 months and 4-5 years) using 16S rRNA gene sequencing. The 16S rRNA gene amplicons from goat fecal samples were sequenced using next-generation sequencing (NGS), targeting the V3-V4 region. Based on descriptive analysis of two composite samples, variation in microbial diversity indices and taxonomic composition was observed between the two samples. Firmicutes and Bacteroidota were the dominant phyla in both samples, while several other taxa varied between the two samples. In the fecal samples of kid goats, the dominant phyla included Firmicutes, Bacteroidota, Actinobacteriota, Proteobacteria, Campylobacterota, and Fusobacteriota. In the fecal samples of adult goats (FKD), the dominant phyla were Firmicutes, Bacteroidota, Spirochaetota, Verrucomicrobiota, Fibrobacterota, and Desulfobacterota. LAB belonging to the genera *Streptococcus*, *Lactobacillus*, *Ligilactobacillus*, *Limosilactobacillus*, and HT002 were detected only in the kid goat sample (FKA), indicating variation in gut microbial composition between the two samples and providing preliminary insight into potential microbial candidates associated with early gut colonization in Senduro goats. Because each group was represented by a single composite sample, these findings should be interpreted as preliminary descriptive observations rather than evidence of age-related differences. This study provides baseline information on the fecal microbiome composition of Senduro goats and highlights the need for future studies with adequate biological replication and integrated functional analyses.

Keywords: Bacterial diversity, gastrointestinal tract, gut microbiota, Indonesian local goat, next-generation sequencing

INTRODUCTION

Goats (*Capra hircus* Linnaeus, 1758) are among the most common livestock raised in Indonesia for meat and milk production (Sujarwanta et al. 2024). In this context, the Senduro goat is an important breed widely cultivated in Senduro District, Lumajang Regency, as recognized by the Decree of the Minister of Agriculture, which designates the Senduro goat as a local livestock genetic resource of Indonesia (Amam et al. 2022). This breed originated from crossbreeding between Indian Etawah, Kacang, and Jawarandu goats (Almaida et al. 2020). The Senduro goat has been reported to show higher milk production compared with Peranakan Etawa goats. Its milk quality has been reported to differ in terms of protein, lactose, and other physicochemical properties, including dry matter without fat and specific gravity (Arisani et al. 2022). Goat feeding practices vary widely and may include green fodder, tofu dregs, bran, ground corn, cassava, and additional concentrates (Soetriono et al. 2020).

Previous studies have shown that dietary composition is associated with variation in fecal microbiome profiles (Liu et al. 2025). For example, a higher abundance of cellulose-degrading bacteria, such as members of the family Ruminococcaceae, has been observed in goats fed high-fiber diets (Domínguez et al. 2022). Differences in microbiota composition have also been reported between goats raised in confinement and those grazing on pasture (Zhang et al. 2021). Several studies have reported that the goat fecal microbiome is mainly dominated by the phyla Firmicutes and Bacteroidetes (Wang et al. 2018; Domínguez et al. 2022; Mahayri et al. 2022; Li et al. 2022; Zhi et al. 2022). However, variation in dominant phyla has been reported across studies. For instance, Shabana et al. (2021) reported high relative abundances of Firmicutes and Proteobacteria in goat feces. Proteobacteria and Spirochaetota have also been reported as notable phyla in goat feces (Mahayri et al. 2022; Rabapane and Matambo 2024; Wu et al. 2024). Several factors, including diet (Mahayri et al. 2022), age (Luo et al. 2022), breed (Rabee et al. 2025), and environmental management (Fan et al. 2023), are known to influence microbiome diversity in goat feces.

Previous studies have reported that fecal microbiome diversity in goats generally increases with age, accompanied by the expansion of bacterial groups such as Ruminococcaceae and Lachnospiraceae (Jiao et al. 2016; Wu et al. 2024). Initial microbial colonization in sheep and goats is influenced by maternal sources, including vaginal microbiota and milk, and may change as animals grow and are exposed to different diets (Guo et al. 2020). At the phylum level, fecal microbiome composition has been reported to be broadly similar between sheep and goats,

whereas variation at the genus and species levels is commonly observed across developmental stages (Shabana et al. 2021).

Draksler et al. (2004) examined lactic acid bacteria (LAB) in goat feces and reported the presence of *Lactobacillus* and *Enterococcus* strains tolerant to acidic conditions and bile salts. Olaoye and Onilude (2009) also reported LAB diversity in various tissues of West African domestic goats. However, studies focusing on the composition and variation of goat fecal microbiomes are still limited, particularly in local goats from Indonesia. Therefore, information on the composition of the fecal microbiome and LAB in local Senduro goats is crucial.

Recent studies have shown that many factors contribute to variation in goat fecal microbiomes, including diet, age, breed, and environmental management. Many of these studies have focused on commercial or non-local goats, and research on local goats in Indonesia is still limited. The results of this study are expected to provide baseline information for future studies related to animal health, digestive efficiency, feed utilization, and the development of microbial-based nutritional strategies in goat production systems. Furthermore, characterization of LAB and age-related differences in the gut microbiota may support the development of locally adapted probiotic candidates and feed management strategies to improve gastrointestinal health and productivity in the Senduro goat farming system. This study aimed to provide a preliminary descriptive characterization of the fecal microbiome composition and LAB detected in Senduro goat fecal samples using molecular analysis.

MATERIALS AND METHODS

Goats and sample preparation

Fecal samples from Senduro goats were collected at a farm in Senduro District, Lumajang Regency, East Java, Indonesia, and prepared as composite samples for each age group by pooling equal amounts of feces from two individual goats. The samples were grouped into kids (1-2 months old; FKA) and adult goats (4-5 years old; FKD), with two goats per group. Overall, four goats were included in this study, yielding two composite fecal samples (one per age group) for sequencing analysis. This study was designed as a preliminary exploratory investigation to provide baseline information on the fecal microbiome composition of Senduro goats at different ages. Goats were selected purposively from the same farm based on health status and management similarity. Inclusion criteria included clinically healthy animals, normal feeding behavior, and no history of antibiotic treatment within the previous three months. Goats showing signs of gastrointestinal disorders or other clinical illnesses were excluded from sampling. Kids were fed green fodder, concentrates, cassava (*Manihot esculenta*) pulp, and cow's milk, whereas adult goats received green fodder, concentrates, and cassava pulp. These differences reflected distinct feeding management between age groups. The forage-based diet consisted of fresh leaves of *sengon* (*Falcataria moluccana*), *gamal* (*Gliricidia sepium*), and *kaliandra* (*Calliandra calothyrsus*), which were sourced locally and provided ad libitum as the primary source of dietary fiber. Fecal samples were collected immediately after defecation using sterile containers. The samples were transferred into sterile 50 mL centrifuge tubes, placed in an ice box containing dry ice, and transported to the laboratory for further analysis. This study involved only non-invasive fecal sample collection without experimental treatment or invasive procedures causing harm or distress to the animals. Therefore, ethical approval was not required.

DNA extraction and sequencing amplicon gen 16S rRNA

Total DNA was extracted from the composite fecal samples of Senduro goats using the Quick-DNA Magbead Plus Kit (Zymo Research, D4082), and each sample was processed independently for downstream molecular analysis. The concentration and purity of genomic DNA were measured using a NanoDrop 2000 spectrophotometer (Thermo Scientific). The V3-V4 region of the 16S rRNA gene was amplified by Polymerase Chain Reaction (PCR) using primers 341F (5′-CCTAYGGGRBGCASCAG-3′) and 806R (5′-GGACTACNNGGGTATCTAAT-3′), with KOD Multi and Epi DNA polymerase (KME-101). PCR products were visualized using agarose gel electrophoresis. DNA quantification was performed using a Qubit dsDNA HS Assay Kit (Thermo Scientific), and the PCR products were subsequently used for library preparation. The final library was sequenced on the Illumina platform to generate paired-end reads following the manufacturer's instructions (PT. Genetika Science Indonesia).

Sequencing data processing

Sequence adapters and PCR primers were removed from the paired-end reads using Cutadapt version 4.6 (Martin et al. 2011). DADA2 version 1.3.0 was used to correct sequencing errors, remove low-quality sequences, and eliminate chimeric sequences (Callahan et al. 2016). Taxonomic classification was performed using the SILVA ribosomal RNA gene database version 138.1 (silva_nr99_v138.1) based on Amplicon Sequence Variants (ASVs). Downstream analyses and data visualization were performed using packages in R (version 4.2.3) and Krona Tools. Alpha diversity analysis was conducted to evaluate microbial diversity within each composite sample. The Shannon index was used to estimate microbial richness and evenness, whereas the Simpson and InvSimpson indices were used to assess community diversity and dominance patterns. Because only one composite sample per age group was analyzed without biological replication, diversity indices were interpreted descriptively without inferential statistical testing.

RESULTS AND DISCUSSION

DNA sequence data and microbial diversity of goat feces

16S rRNA gene sequencing generated a total of 199,749 raw reads across both samples, with comparable sequencing depth between the kid goat feces (FKA) and adult goat feces (FKD) samples. Sequence processing using the DADA2 pipeline showed that quality control steps

(filtering, merging, and chimera removal) resulted in a substantial proportion of reads being retained in both samples, with overall similar retention patterns between FKA and FKD. After denoising and chimera filtering, more than half of the reads were retained as high-quality sequences for downstream analysis, indicating sufficient sequencing depth for reliable descriptive characterization of the microbial communities in both samples (Table 1).

Differences in ASV composition were observed between the FKD and FKA samples. A total of 1,019 Amplicon Sequence Variants (ASVs) were identified, including 183 ASVs in the FKA sample and 836 ASVs in the FKD sample. Among these, 177 ASVs were uniquely detected in FKA and 830 were unique to FKD, whereas only six ASVs were shared between the two samples.

Alpha diversity metrics were descriptively calculated to evaluate microbial richness and community distribution within each composite fecal sample. The Shannon index, which reflects both richness and evenness, was higher in the FKD sample (5.899) than in the FKA sample (4.081). Similarly, the Simpson index values were 0.994 for FKD and 0.971 for FKA, while the InvSimpson index values were 161.864 and 34.707, respectively (Figure 1). These results suggest variation in microbial diversity and community distribution between the analyzed composite samples. However, because each age group was represented by a single composite sample without biological replication, the observed differences should be interpreted cautiously as descriptive observations rather than statistically supported differences between groups.

The rarefaction curve showed that more than 800 ASVs were detected in the FKD sample, whereas fewer ASVs were detected in the FKA sample (Figure 2). These observations descriptively reflect variation in ASV richness between the two samples.

Composition of goat fecal bacterial community

Given the exploratory nature of this study and the limited sample size from a single farm, the observed patterns in bacterial composition should be interpreted as preliminary descriptive observations rather than evidence of causal relationships. The composition of goat fecal bacterial communities was analyzed at multiple taxonomic levels to describe the two samples (kid and adult goats). The analysis showed that Firmicutes was the most abundant phylum in both samples, accounting for 66% in kids and 65% in adult goats (Figures 3 and 4.A). This high proportion is consistent with previous reports describing Firmicutes as a major component of the goat fecal microbiome. Bacteroidota was the second most abundant phylum in both samples, representing 23% in kids and 25% in adult goats, with slightly different proportions between the two samples. The phylum Actinobacteriota was also detected in both samples. Other taxa varied between the two samples. In the kid sample, the detected taxa included Proteobacteria, Campylobacterota, and Fusobacteriota, whereas in the adult sample, the detected taxa included Spirochaetota, Verrucomicrobiota, Fibrobacterota, and Desulfobacterota.

Table 1. Summary of sequence read processing using the DADA2 pipeline

Sample ID	Trimmed reads	Filtered reads	Merged reads	Non-chimeric reads
FKA	99,867	73,700	66,977	56,632
FKD	99,882	73,804	58,400	54,674

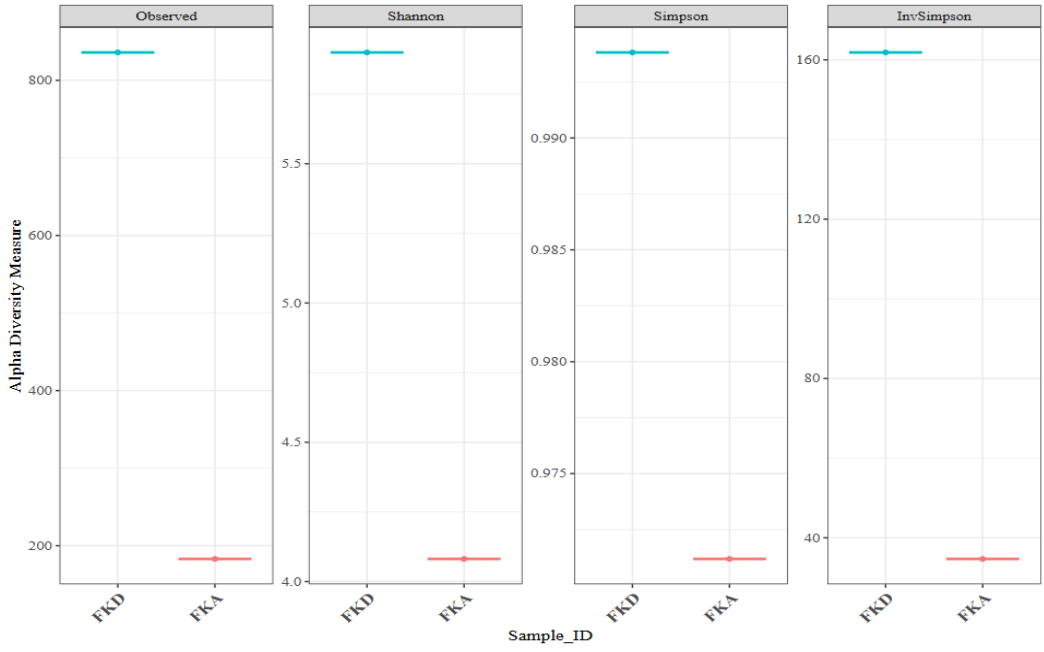

Figure 1. Alpha diversity indices of bacterial communities in the FKA and FKD samples

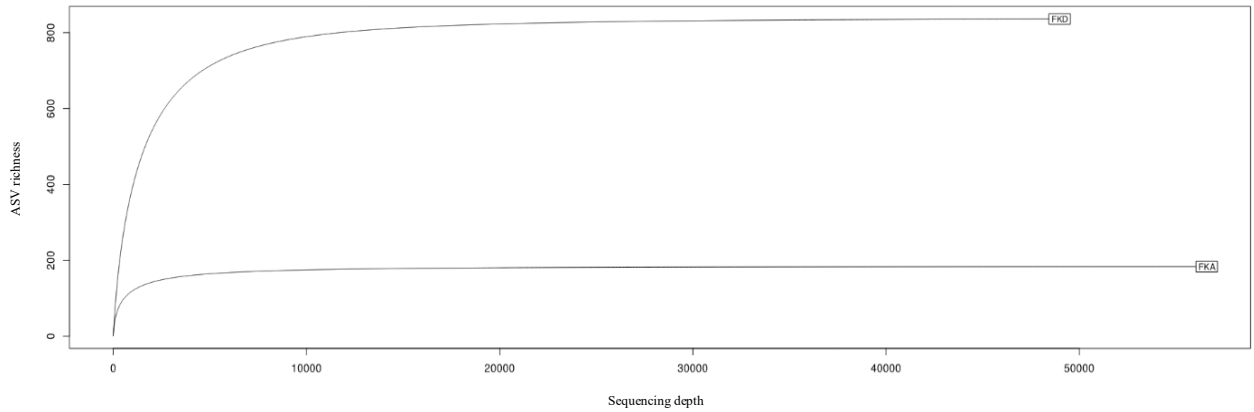

Figure 2. Rarefaction curves of ASV richness in the FKA and FKD samples

Previous studies have reported age-related variation in the diversity and composition of goat fecal microbiota. Firmicutes, Bacteroidetes, and Proteobacteria have been commonly reported as dominant phyla with varying proportions across growth stages (Guo et al. 2020). In maternal goat feces, Firmicutes and Bacteroidetes accounted for 72% and 20%, respectively, whereas in kid goats, the reported dominant phyla included Firmicutes (37%), Bacteroidetes (28%), and Proteobacteria (28%) (Niyazbekova et al. 2025). Previous studies on goat digestive tract microbiota have also reported similar dominant phyla, including Firmicutes and Bacteroidota, followed by Verrucomicrobiota, Proteobacteria, and Spirochaetota (Cao et al. 2023). Other studies have reported the presence of additional phyla such as Fusobacteriota, Fibrobacterota, and Desulfobacterota in different goat populations and feeding conditions (Li et al. 2021; Liu et al. 2024; Rabee et al. 2024). These phyla have been associated with various microbial processes in the digestive system based on previous studies (Gharechahi et al. 2021).

The analysis showed that Clostridia, Bacteroidia, and Bacilli were among the most abundant classes in the two samples. In the kid sample, the detected classes included Gammaproteobacteria, Coriobacteria, Actinobacteria, and Campylobacteria, whereas in the adult sample, the detected classes included Spirochaetia, Verrucomicrobiae, and Negativicutes (Figure 4.B). Previous studies have reported that Bacteroidia becomes enriched in the intestinal microbiota of goats following weaning (Wu et al. 2024). Coriobacteria was detected in the kid sample, and its presence has been described in relation to dietary factors in previous studies (Metzler-Zebeli et al. 2019).

At the order level, Lactobacillales and Oscillospirales were among the most abundant orders in the FKA and FKD samples, respectively. Previous studies have reported that members of the order Lactobacillales are commonly present in the feces of kid goats (Guo et al. 2020). The presence of Oscillospirales in the FKD sample is consistent with previous reports describing this order as commonly detected in the goat digestive tract. Previous studies have also shown that members of the class Clostridia are represented by several orders, including Oscillospirales and Lachnospirales (Cao et al. 2023). In the FKA sample, the detected orders included Oscillospirales, Bacteroidales, Lachnospirales, Clostridiales, Erysipelotrichales, Peptostreptococcales-Tissierellales, and Coriobacteriales. In the FKD sample, the detected orders included Bacteroidales, Lachnospirales, Spirochaetales, Clostridiales, Erysipelotrichales, Peptostreptococcales-Tissierellales, Christensenellales, and Coriobacteriales (Figure 4.C).

The analysis showed that Lachnospiraceae was among the most abundant families in both fecal samples. The presence of Lachnospiraceae in these samples is consistent with previous reports describing this family as commonly detected in the goat digestive tract. Previous studies have reported that Lachnospiraceae is among the abundant bacterial families in different regions of the goat digestive tract, including the stomach, jejunum, and large intestine (Guerra et al. 2022). Lachnospiraceae has also been reported in goat feces and cattle feces, with varying relative abundances across studies (Mahayri et al. 2022). Other families detected in both samples included Bacteroidaceae, Clostridiaceae, Oscillospiraceae, and Ruminococcaceae. Lactobacillaceae was detected in the FKA sample, whereas Spirochaetaceae, Christensenellaceae, and UCG-010 were detected in the FKD sample (Figure 4.D). Lachnospiraceae, Bacteroidaceae, and Ruminococcaceae have also been reported as common bacterial families in the feces of kid goats (Niyazbekova et al. 2025).

The analysis showed that *Bacteroides* was among the most abundant genera in the FKA sample, whereas UCG-005 was among the most abundant genera in the FKD sample. The presence of *Bacteroides* in these samples is consistent with previous reports describing this genus as commonly detected in the goat digestive tract. Previous studies have reported *Bacteroides* as one of the commonly detected genera in goat intestines (Zhi et al. 2022). *Bacteroides* has also been reported in kid goat feces with relatively high proportions in previous studies (Guo et al. 2020). Other genera detected in the FKA sample included *Faecalibacterium*, *Lactobacillus*, *Blautia*, *Ligilactobacillus*, and HT002 (a member of Lactobacillaceae). *Faecalibacterium* has been reported in the downstream sections of the goat digestive tract, such as the colon and rectum (Cao et al.

2023). Other genera detected in the samples included *Alistipes*, *Blautia*, and *Treponema* (Figure 4.E). Previous studies have also reported the presence of genera such as *Alistipes* within the phylum Bacteroidetes and *Lactobacillus* and members of the Ruminococcaceae group within the phylum Firmicutes in goat feces (Guo et al. 2020).

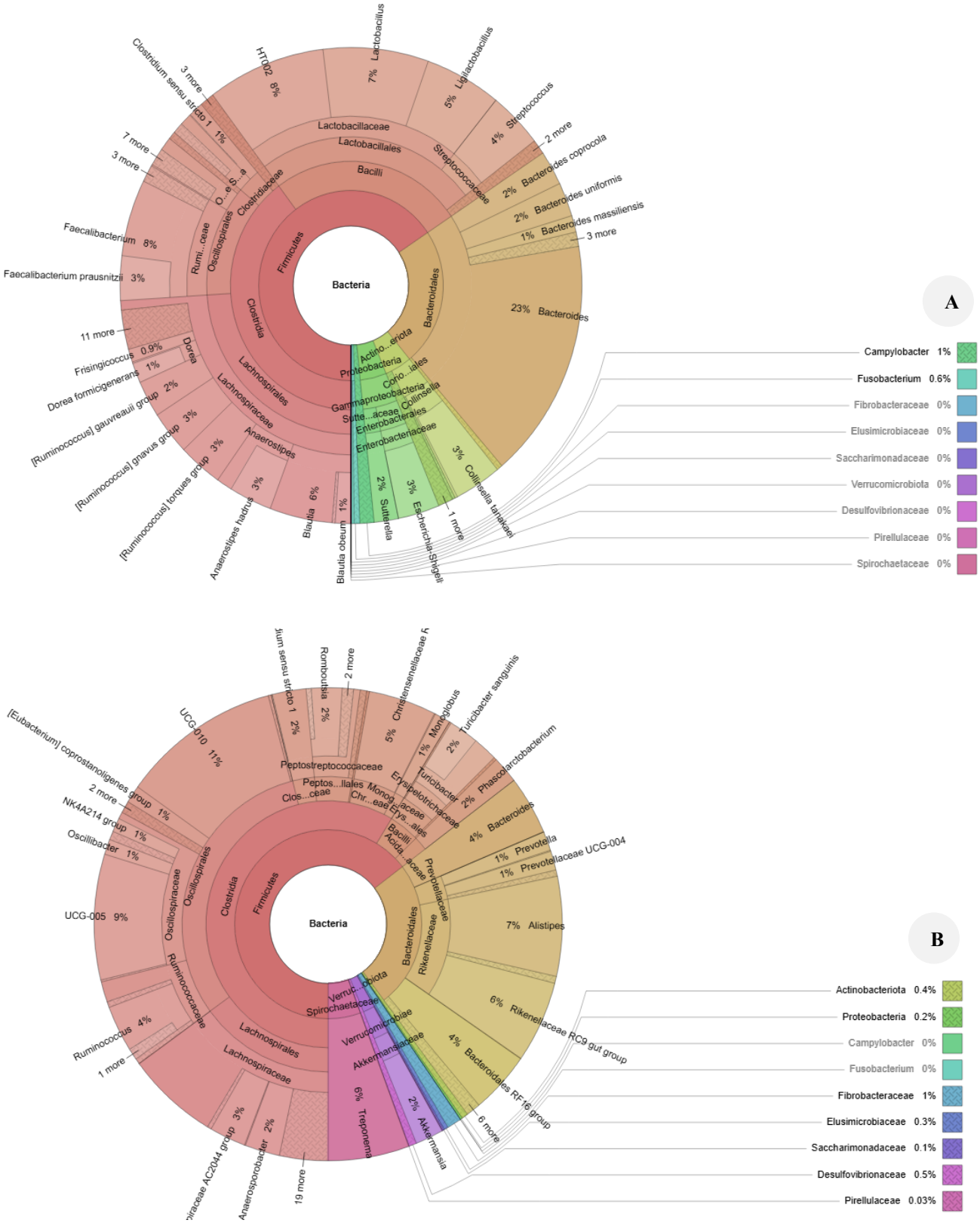

Figure 3. Krona plots showing the taxonomic composition of bacterial communities in: A. FKA and B. FKD samples

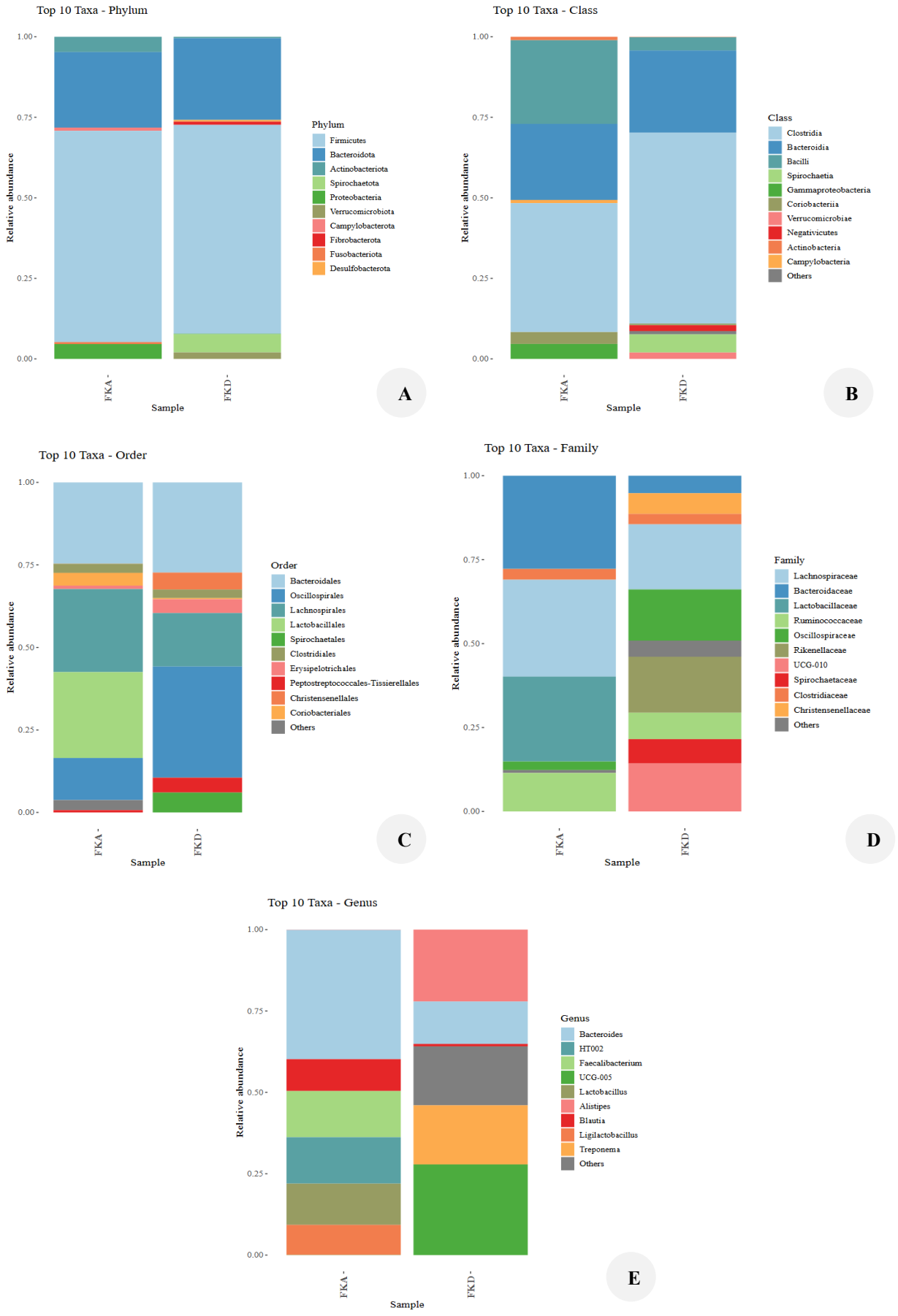

Figure 4. Taxonomic composition of bacterial communities in the FKA and FKD samples at the A. Phylum, B. Class, C. Order, D. Family, and E. Genus levels

Lactic acid bacteria community in goat feces

The LAB diversity analysis showed that LAB were detected in the FKA sample but were not detected in the FKD sample. However, this observation may be influenced by methodological limitations, including sequencing depth and detection sensitivity. The absence of detectable LAB in the FKD sample does not necessarily indicate their absence but may reflect limitations in detection. All LAB detected in the FKA sample belonged to the order Lactobacillales, comprising the families Lactobacillaceae and Streptococcaceae. These bacteria were assigned to the genera *Streptococcus*, *Lactobacillus*, *Limosilactobacillus*, *Ligilactobacillus*, and HT002 (a member of Lactobacillaceae) (Figure 5). Similar genera have also been reported in rumen fluid samples of goats, including *Limosilactobacillus*, *Lactobacillus*, *Ligilactobacillus*, and *Streptococcus* (Poothong et al. 2024). *Streptococcus* was detected in the FKA sample. This genus has also been reported in the feces of various animal species in previous studies. Members of this genus have been associated with probiotic-related characteristics in the literature (Wang et al. 2023). However, no functional validation was conducted in the present study, and therefore no functional roles can be inferred from these observations.

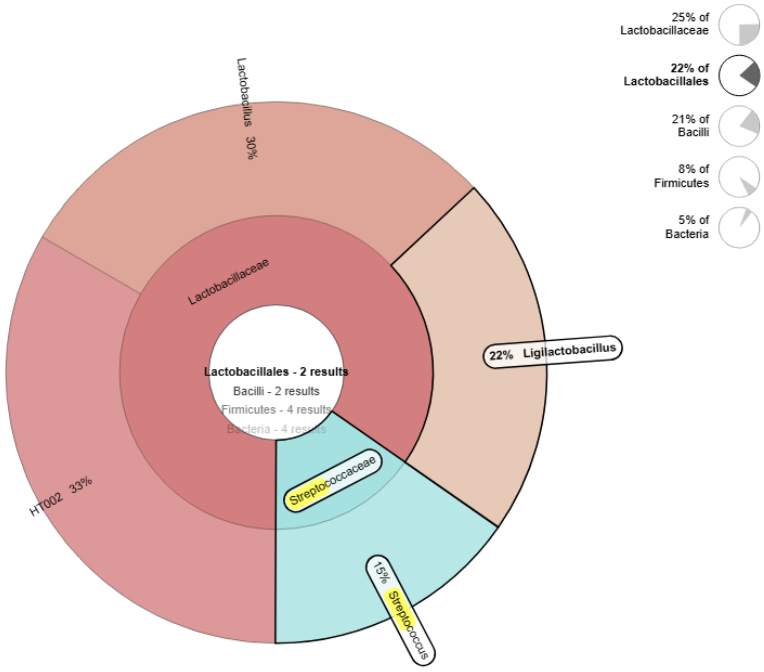

Figure 5. Krona plot showing the taxonomic composition of LAB detected in the FKA sample (*Streptococcus*, *Lactobacillus*, *Ligilactobacillus*, *Limosilactobacillus*, and HT002)

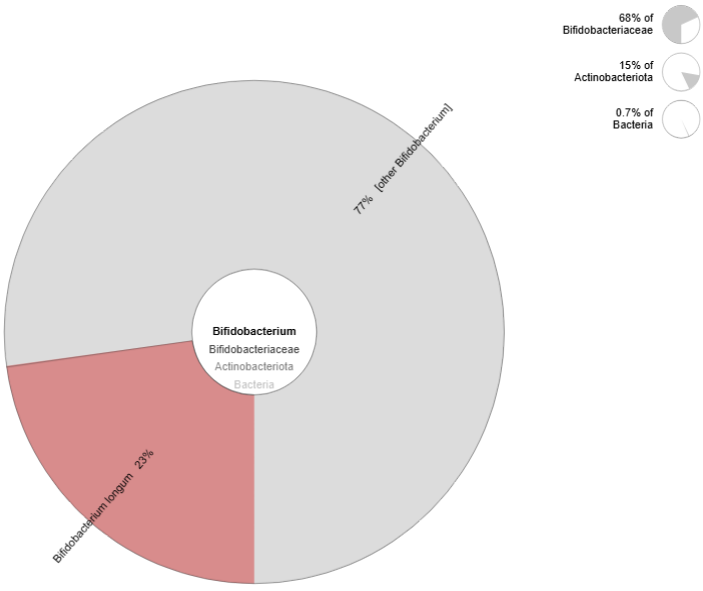

Figure 6. Krona plot showing the taxonomic composition of *Bifidobacterium* detected in the FKA sample

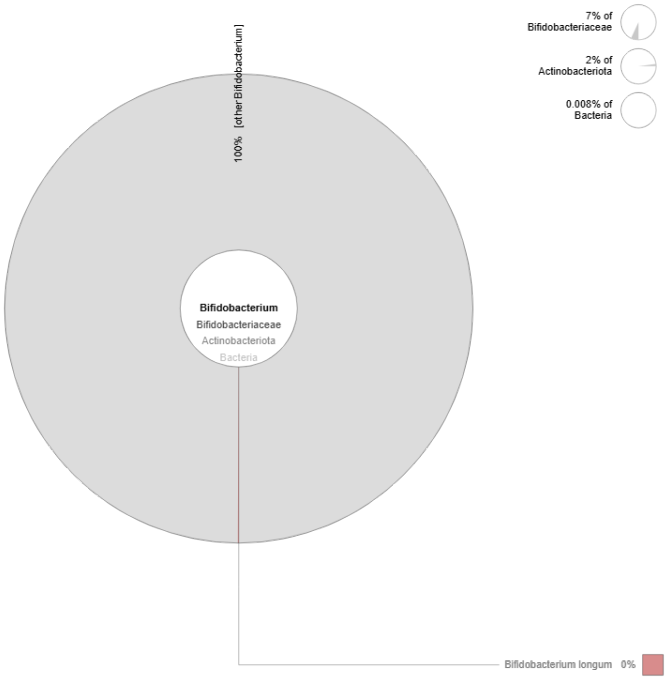

Figure 7. Krona plot showing the taxonomic composition of *Bifidobacterium* detected in the FKD sample

Lactobacillus was detected in the FKA sample, consistent with previous reports describing its presence in goat feces (Wang et al. 2018; Guo et al. 2020). Previous studies have also identified multiple *Lactobacillus* species in goat feces, indicating taxonomic diversity within this genus (Abdou et al. 2023). Early gut microbial colonization in goats has been reported to be influenced by maternal milk and maternal microbiota (Niyazbekova et al. 2025). In this study, kid goats were supplemented with cow's milk, which may contribute to differences in microbial composition observed between the FKA and FKD samples. These observations should be interpreted cautiously, as the present study was based on composite samples without biological replication. In addition to *Lactobacillus*, *Ligilactobacillus* was also detected in the FKA sample. This genus has been reported in the digestive tract and feces of ruminants in previous studies, indicating that members of this group are part of the gut microbial community (Poothong et al. 2024).

Bifidobacterium was also detected in the samples of both kid and adult Senduro goats (Figures 6 and 7). *Bifidobacterium* is a commonly reported genus in the gut microbiota and is often discussed in the context of beneficial microbial groups. However, this genus is phylogenetically distinct from LAB and is classified separately (Axelsson 2004; Burgain and Romond 2024). *Bifidobacterium* and LAB belong to the phyla Actinobacteriota and Firmicutes, respectively. These groups have been reported in previous studies as part of the gut microbial community involved in carbohydrate metabolism (Zhuang et al. 2025).

Age and feed are known to be associated with variation in microbiome composition. In this study, the diversity index observed in the FKA sample was numerically lower than that in the FKD sample. The FKA group (1-2 months old) was fed green fodder, concentrate, cassava pulp, and cow's milk, whereas the FKD group (4-5 years old) received green fodder, concentrate, and cassava pulp. Similar patterns have been reported in other goat studies, where differences in microbial diversity were observed between young and adult animals (Luo et al. 2022). Previous studies have also shown that gut microbiota composition in goats changes over time, particularly during early growth and post-weaning stages (Wu et al. 2024). Differences in fecal microbiota between young goats and adults have also been associated with age and diet in other studies (Guo et al. 2020).

Dietary composition has been widely reported to be associated with variation in the gut microbiota of goats. Previous studies have shown that differences in energy and nutrient levels in feed can influence the composition of fecal bacterial communities at various taxonomic levels (Guo et al. 2022; Liu et al. 2025). Similarly, high-grain or high-concentrate diets have been associated with shifts in microbial composition in different sections of the gastrointestinal tract (Liu et al. 2014; Tao et al. 2017). Changes in feed composition, including the use of alternative dietary components such as dried distillers' grains, have also been reported to influence the relative abundance of specific microbial groups in goat feces (Sorensen et al. 2021). In addition, high-starch feeding in young goats has been associated with alterations in colonic microbiota composition (Jin et al. 2024). These findings suggest that diet may be associated with the variation in microbial composition observed between the FKA and FKD samples in the present study. However, because age and diet differed simultaneously and only composite samples were analyzed, these findings should be interpreted with caution.

Diet modifications have been reported to influence the rumen microbiome of goats (Fliegerova et al. 2021). High-

concentrate feed has been associated with alterations in the structure and composition of the rumen microbiota (Mao et al. 2024). Diet is an important factor shaping fecal bacterial communities, while host-related factors also contribute to microbial community structure (Mahayri et al. 2022). The gut microbiota of kid goats, initially influenced by maternal sources such as milk, continues to develop with age and feeding conditions (Guo et al. 2020). Several studies have reported age-related changes in goat gut microbiota, with microbial abundance generally increasing during early development and stabilizing after weaning (Liao et al. 2021; Wu et al. 2024). Similar age-related patterns have been observed in other ruminants, where gut bacterial diversity and abundance significantly increase from 5 months up to 4 years and 5 months of age (Estrada et al. 2024). These findings suggest that both diet and age may be associated with the variation in microbial composition observed between the FKA and FKD samples in the present study. However, the relative contribution of each factor cannot be distinguished due to the study design.

Differences in microbiome composition observed between the two samples may be associated with multiple factors, including age and diet. However, these factors cannot be disentangled in the present study. The dominance of phyla such as Bacteroidota, Firmicutes, Verrucomicrobiota, Fibrobacterota, and Spirochaetota has been reported in the goat gut microbiota and is often associated with the degradation of complex plant fibers. This pattern may reflect differences in feeding regime and physiological condition between the two groups, although no causal relationship can be established. Members of the genus *Fibrobacter* have been reported as fibrolytic bacteria involved in the degradation of cellulose and hemicellulose in the rumen (Ransom-Jones et al. 2012; Stewart et al. 2018). Members of the phylum Spirochaetota, including *Treponema*, have also been reported in association with polysaccharide degradation in rumen microbial communities (Bekele et al. 2010). Because age and diet differed simultaneously between the two groups, the study design does not allow the individual contribution of each factor to be separated. Therefore, the observed patterns should be interpreted as descriptive rather than indicative of causal relationships.

The presence of LAB in goat fecal samples has been reported in previous studies. In this study, *Streptococcus*, *Lactobacillus*, *Ligilactobacillus*, *Limosilactobacillus*, and *Bifidobacterium* were identified at the genus level using 16S rRNA gene sequencing. However, no strain isolation or in vitro functional assays were conducted to evaluate their potential functional properties. Therefore, these findings should be interpreted as taxonomic observations only, and no functional roles can be inferred from the present data. Further studies involving strain isolation, phenotypic characterization, and functional analyses are required to better understand their potential roles.

As a local Indonesian breed with recognized breeding value, information on the microbiome of Senduro goats remains limited; thus, this study contributes baseline data for future research. A major limitation of this study is the absence of biological replication at the sequencing level, as each age group was represented by a single composite sample. As a result, statistical comparison between groups is not valid, and no inferential conclusions can be drawn. In addition, age and feeding regime differed simultaneously between the two groups, resulting in confounding effects that prevent attribution of observed differences to age alone. Additional limitations include the use of samples from a single location and analyses restricted to the genus level. Future studies should adopt more robust experimental designs with adequate biological replication, multiple sampling locations, diverse feeding systems, and consideration of different physiological conditions. Integrating multi-omics approaches, such as metatranscriptomics, may provide a more comprehensive understanding of microbial functional potential.

In conclusion, this study provides a preliminary characterization of the fecal bacterial communities of kid and adult Senduro goats using 16S rRNA gene sequencing. A total of 1,019 ASVs were identified, with markedly higher ASV richness and alpha diversity observed in the adult goat sample than in the kid goat sample. Firmicutes and Bacteroidota were the dominant phyla in both samples, while several other taxa varied between the two samples. In the fecal samples of kid goats, the dominant phyla included Firmicutes, Bacteroidota, Actinobacteriota, Proteobacteria, Campylobacterota, and Fusobacteriota. In the fecal samples of adult goats (FKD), the dominant phyla were Firmicutes, Bacteroidota, Spirochaetota Fibrobacterota, Desulfobacterota, and Verrucomicrobiota. Lactic acid bacteria belonging to the genera *Streptococcus*, *Lactobacillus*, *Ligilactobacillus*, *Limosilactobacillus*, and HT002 were detected only in the kid goat sample (FKA). The observed differences in microbial composition may be associated with variations in age and feeding regime; however, these factors could not be separated due to the study design. Because each age group was represented by a single composite sample, the findings should be interpreted as descriptive and exploratory. Nevertheless, this study provides valuable baseline information on the microbiome of Senduro goats and highlights the need for future studies with greater biological replication and broader sampling coverage.

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