Research Square

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Pathogen detection and gut microbiota analysis in subcutaneous abscesses in goats

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Abstract

Subcutaneous abscesses in goats result in carcass condemnation, reduced milk and wool production, growth retardation, and increased mortality, thereby causing substantial economic losses in goat production systems. This study investigated the major pathogens associated with subcutaneous abscesses in goats and characterized alterations in the gut microbiota of infected animals. A cross-sectional survey of 554 Saanen goats from a single farm revealed an overall incidence of clinical abscesses of 13.0% (72/554). The incidence in male goats was 39.6% (21/53), markedly higher than that observed in female goats 10.2% (51/501). Subcutaneous abscesses were predominantly distributed on the cheeks, neck, shoulders, and abdomen. Bacterial isolation and culture of abscess samples identified *Corynebacterium pseudotuberculosis* as the predominant pathogen 68.1%, followed by *Trueperella pyogenes* (18.1%), *Staphylococcus aureus* (16.7%), and *Escherichia coli* (9.7%). Single-pathogen infections accounted for 93.1% of cases, whereas mixed infections involving two or three pathogens accounted for 5.6% and 1.4%, respectively. Furthermore, fecal microbiota sequencing revealed that, compared with healthy goats, the gut microbiota of diseased goats was altered, as evidenced by reduced microbial diversity, changes in community structure, decreased abundance of beneficial genera such as *Lactobacillus*, and an increase in potentially pathogenic bacteria such as *Escherichia-Shigella*. Co-occurrence network analysis indicated substantial alterations in dominant bacterial genera in diseased goats, with a shift in interspecies relationships from predominantly positive to negative correlations. In summary, these results provide new insights into the precise prevention and control of this disease and potential microbiome-based intervention strategies.

1 Introduction

Subcutaneous abscesses represent a major health concern in small ruminant production systems worldwide and are associated with substantial economic losses due to carcass condemnation, reduced milk and wool production, impaired growth performance, and increased mortality[1, 2]. Clinically, these infections are characterized by localized purulent lesions in subcutaneous tissues and lymph nodes caused by bacterial invasion through skin abrasions, mucosal lesions, or hematogenous spread[3, 4]. Previous studies have implicated several bacterial species in goat abscesses, including *Corynebacterium pseudotuberculosis*, *Staphylococcus aureus*, and *Escherichia coli*[5]. However, existing studies have predominantly focused on single-pathogen infections, whereas mixed infections and the relative prevalence of different pathogens under field conditions have received limited attention, which may limit the development of targeted prevention and control strategies.

Mounting evidence suggests that gut microbiota plays an important role in regulating host immune function and resistance to bacterial infections[6–8]. Pathogenic bacterial infections can disrupt the structural homeostasis of the host gut microbiota, potentially leading to more severe pathological outcomes following infection[9]. Correspondingly, dysbiosis of the gut microbiota may contribute to immune dysregulation or persistent inflammation, thereby increasing susceptibility to pathogenic microorganisms[10, 11]. This reflects the complex interplay among gut microbiota function, host

immunity, and pathogenic infection. Previous studies have shown that dysbiosis of the gut microbiota in goats increases susceptibility to diseases such as Orf virus[12]. However, the relationship between gut microbiota dysbiosis and subcutaneous abscesses in goats remains poorly characterized. Elucidating the effects of abscess-causing pathogens on gut microbial composition may improve understanding of disease pathogenesis and facilitate the identification of potential microbiota-based intervention strategies.

Therefore, this study aimed to investigate the prevalence and primary bacterial pathogens associated with subcutaneous abscesses in Saanen goats herd in China. Subsequently, we sought to characterize and compare the gut fecal microbiota between clinically healthy goats and those affected with clinical abscesses. Using 16S rRNA gene amplicon sequencing, we analyzed the alpha and beta diversity, taxonomic composition, and co-occurrence networks of the microbial communities. This integrated approach facilitates a comprehensive assessment of the systemic effects of subcutaneous abscesses and contributes to understanding the relationship between a common clinical infection and gut microbial ecology in goats.

2 Materials and Methods

2.1 Observation and Statistics of Goat Abscesses

Clinical examination of subcutaneous abscess symptoms was conducted on 554 Saanen goats at a farm in Weinan City. The location of abscesses in affected goats was recorded, and the diameter of abscesses was measured using vernier calipers. The clinical incidence rate of abscess symptoms in goats was statistically analyzed.

2.2 Collection of Abscess Samples

After properly fixing the clinically affected goats exhibiting abscesses, the abscess area was disinfected by swabbing with iodophor for 2 to 3 minutes. A 10 mL sterile syringe was used, and the needle was immediately inserted into the center of the abscess to aspirate the pus. The collected samples were labeled with corresponding identification numbers. The exterior of the syringe containing the sample was sterilized by spraying with 75% alcohol, and then stored in a cooling box for transfer to the laboratory for pathogenic bacteria isolation and culture.

2.3 Isolation and Identification of Pathogenic Bacteria

The collected pus samples were diluted with sterile PBS buffer and then streaked onto Luria-Bertani agar plates and plates containing 5% goat blood agar medium using an inoculation loop. The inoculated plates were inverted and placed in a constant temperature incubator at 37°C for cultivation. Single colonies were selected for pure culture. Bacterial suspensions from pure cultures were subjected to Gram staining following the instructions of the Gram staining kit (Anhui Leigen Biotechnology Co., Ltd.), and bacterial morphology was observed under an optical microscope.

Genomic DNA of the bacterial strains was extracted using a genomic DNA extraction kit (Tiangen Biotech (Beijing) Co., Ltd.), strictly adhering to the manufacturer's instructions. The 16S rDNA gene was amplified by PCR using universal primers 27F (forward primer: 5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R (reverse primer: 5'-GGTTACCTTGTTACGA CTT-3'). The PCR reaction mixture consisted of: 12.5 μL of 2X Taq PCR Master Mix, 1 μL each of forward and reverse primers (10 μM), 2 μL of DNA sample, and 8.5 μL of water. The PCR protocol was as follows: pre-denaturation at 95°C for 5 min; 30 cycles of denaturation at 95°C for 30 s, annealing at 55°C for 30 s, and extension at 72°C for 1.5 min; followed by a final extension at 72°C for 10 min. The PCR products were sent to Qingke Biotechnology Co., Ltd. (Xi'an, China) for sequencing. The obtained sequences were subjected to homology analysis using the NCBI BLAST database (https://blast.ncbi.nlm.nih.gov/, accessed on May 16, 2025) to confirm the species information of the strains. Bacterial sequences with homology greater than 99% were downloaded, and phylogenetic tree analysis was performed using MEGA 7.0 software to determine the species of the isolated bacteria and their phylogenetic relationships with known bacteria.

2.4 Comparative Analysis of Pathogenic Bacteria

To further confirm the species of pathogenic bacteria present in the pus samples, specific PCR primers were designed based on the preliminary identification results. DNA was extracted from the collected pus samples and subjected to PCR amplification using the primer sequences listed in Table 2-1. The PCR reaction mixture and cycling conditions are summarized in Table 2-2. The PCR amplification products were analyzed by gel electrophoresis to comparatively analyze the species of pathogenic bacteria in the pus samples.

Table 2-1 Primer sequence information

Bacteria	Gene	Sequence	Product size (bp)
C.pseudotuberculosis	*16S rRNA*	F: 5’-ACCGCACTTTAGTGTGTGTG-3’	816
		R: 5’-TCTCTACGCCGATCTTGTAT-3’	
S. aureus	*nuc*	F: 5’-TTCGAAAGGGCAATACGCAAAGAGG-3’	227
		R: 5’-TAACCGTATCACCATCAATCGCTTT-3’	
T. pyogenes	*fima*	F: 5’-CACTACGCTCACCATTCACAAG-3’	605
		R: 5’-GCTGTAATCCGCTTTGTCTGTG-3’	
E. coli	*phoA*	F: 5’-GGTAACGTTTCTACCGCAGAGTTG-3’	468
		R: 5’-CAGGGTTGGTACACTGTCATTACG-3’	

Table 2-2 PCR system and amplification program				
Reaction system		**Amplification program**		
Component	Content (μL)	Temperature (℃)	Time	Cycles
2×Taq PCR Master Mix	12.5	95	5 min	
Forward Primer (10 μM)	1	95	60 s	32
Reverse Primer (10 μM)	1	58	50 s	
DNA sample	2	72	60 s	
ddH_2O	8.5	72	10 min	

2.5 Analysis of Gut Fecal Microbiota

The collected fecal samples were sent to Novogene for amplicon sequencing analysis of the V3-V4 region of the bacterial 16S rRNA gene. The sequencing results were used to construct libraries and perform quantitative analysis. Based on the required effective library concentration and data volume, quantified libraries were pooled and sequenced on the Illumina MiSeq platform. Raw data were processed using Fastp software to filter and remove chimeric sequences, yielding final high-quality valid data. Additionally, denoising was performed with DADA2 in QIIME2 software (version QIIME2-20202) to obtain Amplicon Sequence Variants (ASVs). Taxonomic annotation was conducted using the QIIME2 software. The relative abundance of microbial taxa was calculated as follows: at a given taxonomic level (phylum, class, order, family, or genus), the relative abundance of a specific species was defined as the number of tags corresponding to an ASV divided by the total number of tags clustered from all ASVs in the sample. The H group represents fecal samples from healthy goats, while the C.p group represents fecal samples from clinically abscess-affected goats.

2.6 Statistical Analysis of Data

The sequencing data of the gut microbiota were analyzed using the data analysis platform (https://magic.novogene.com/). Species accumulation boxplots and rarefaction curves of the sequenced samples were generated to assess sample abundance and sequencing depth. The richness and diversity of microbial communities were evaluated through Alpha diversity, represented by the Chao1 index and Shannon index, calculated using QIIME2. Beta diversity, reflecting the compositional differences between microbial communities, was analyzed via Principal Coordinates Analysis (PCoA) and Non-metric Multidimensional Scaling (NMDS). A T-test was employed to identify species with significant differences ($p < 0.05$) between groups at various taxonomic levels. Data visualization was performed using the analysis platform (https://magic.novogene.com/) and GraphPad Prism 10 software.

3 Results

3.1 Observation and Statistical Analysis of Clinical Abscesses in Goats

A total of 554 goats were surveyed on the farm, among which 72 animals presented with clinical abscesses, corresponding to an overall incidence rate of 13.0%. Among the affected goats, 51 were females, corresponding to an incidence rate of 10.2% (51/501), whereas 21 were males, with an incidence rate of 39.6% (21/53, Table 3-1). The primary clinical manifestation observed in affected goats was the presence of abscesses on the body surface (Figure 1). Most abscesses had a diameter ranging from 2 to 8 cm, accounting for 88.9% of the recorded cases. Abscess were primarily distributed in cheeks, neck, shoulders and abdomen, accounting for 23.3%, 31.3%, 38.9% and 6.7% respectively (Table 3-2). In some goats, superficial abscesses ruptured spontaneously and discharged viscous pus that was creamy or yellowish-white in appearance (Figure 1d). These results showed that the incidence rate of body surface abscesses in male goats was higher than that in female goats, and the common sites of abscesses were cheeks, neck and shoulders.

Table 3-1 Statistics of incidence rate of goat surface abscesses

Variety	Age (month)	Gender	Number (test)	Number (abscess)	Morbidity (%)
Saanen Dairy Goat	>12	female	501	51	10.2
		male	53	21	39.6

Table 3-2 Statistical analysis of the diameter and location of goat surface abscesses

Size of clinical abscess		Location of clinical abscess	
diameter (cm)	proportion	location	proportion
≤ 2	4.4% (4/90)	cheeks	23.3% (21/90)
2~4	52.2% (47/90)	neck	31.1% (28/90)
4~8	36.7% (33/90)	shoulders	38.9% (35/90)
≥ 8	6.7% (6/90)	abdomen	6.7% (6/90)

3.2 Results of Bacterial Isolation and Identification

Bacterial isolation and culture from the pus samples of affected goats revealed four distinct colony morphologies. Gram staining and microscopic examination identified the four pathogenic bacteria as:

Gram-positive short rods, Gram-positive cocci, Gram-negative rods, and Gram-positive long rods (Figure 2).

Sequencing and analysis of the 16S rRNA genes of these four isolates revealed sequence identities exceeding 99.8% with *Corynebacterium pseudotuberculosis* (*C.p*), *Staphylococcus aureus* (*S.a*), *Escherichia coli* (*E.c*), and *Trueperella pyogenes* (*T.p*), respectively. The nucleotide sequences of these four isolates were deposited in the NCBI database under accession numbers PV628296 to PV628299. Sequence alignment was performed using MEGA 7.0 software, and a phylogenetic tree was constructed using the neighbor-joining method (Figure 3). Phylogenetic analysis indicated that the isolates clustered closely with *Corynebacterium pseudotuberculosis* strain PA09 (CP054555.1), *Trueperella pyogenes* strain T002 (LC523903.1), *Escherichia coli* strain 13P477T (CP019273.1), and *Staphylococcus aureus* strain DA70484 (CP139025.1).

3.3 Analysis of Pathogen Distribution in Abscesses

To further determine the prevalence of pathogenic bacteria in the abscess samples, DNA was extracted and subjected to PCR amplification using specific primers. The amplification products were analyzed by gel electrophoresis. *Corynebacterium pseudotuberculosis* was detected at the highest frequency (68.1%), followed by *Trueperella pyogenes* (18.1%), *Staphylococcus aureus* (16.7%), and Escherichia coli (9.7%, Table 3-3). Among the 72 abscess samples analyzed, single-pathogen infections accounted for 93.1% of cases. Mixed infections were also observed, with co-infections involving two pathogens accounting for 5.6% of cases and those involving three pathogens accounting for 1.4% (Figure 4). *Corynebacterium pseudotuberculosis* was the most frequently detected pathogen in clinical abscess samples. Most abscess samples were associated with single-pathogen detection, whereas mixed infections involving multiple bacterial species were less frequently observed.

Table 3-3 The PCR detection results of bacteria in goat abscesses

Number	PCR positivity (%)			
	C. p	*S.a*	*T.p*	*E.c*
72	46 (68.1%)	12 (16.7%)	13 (18.1%)	7 (9.7%)

3.4 16S rRNA Sequencing Analysis

As shown in Figure 5A and 5B, both the species accumulation boxplot and the Shannon index rarefaction curve tend to plateau, indicating that increasing the sampling effort and sequencing depth approached saturation with respect to ASV richness and diversity. These patterns indicate that the sequencing volume and depth of the collected samples are sufficient to meet the requirements for assessing microbial community diversity. Therefore, the sequencing dataset was retained for downstream comparative analyse.

Venn diagram analysis was performed to compare shared and unique Amplicon Sequence Variants (ASVs) between fecal samples from healthy goat (Group H) and those clinically infected with *Corynebacterium pseudotuberculosis* (Group C.p). A total of 1,479 ASVs were shared between Group H and Group C.p. Group H exhibited 3,137 unique ASV sequences, while Group C.p had 2,134 unique ASV sequences (Figure 5C). These findings indicate distinct differences in ASV sequences between the fecal samples of Group H and Group C.p.

3.5 Diversity Analysis of Bacterial Communities in the Fecal Samples

The α-diversity of the bacterial communities in each group was assessed using the Chao1 and Shannon indices, as shown in Figure 6A and 6B. Both indices revealed that the bacterial community richness and diversity in the C.p group were significantly lower than those in the H group ($p < 0.05$). β-diversity, reflecting differences in microbial community composition among sample groups, was assessed using PCoA based on Bray–Curtis distances. The results showed clear separation between the H and C.p groups (Figure 6C), indicating distinct microbial community structures ($p < 0.01$; for details see Supplementary Table S1). Furthermore, NMDS analysis also demonstrated separation between the H and C.p groups, with a stress value of 0.084 (Figure 6D). These findings suggest that clinical abscess disease in goats alters the composition of the gut fecal microbiota, affecting both microbial diversity (α-diversity) and community structure (β-diversity).

3.6 Bacterial Community Composition at Various Taxonomic Levels

To further characterize differences in the gut microbiota associated with clinical abscesses, the composition of fecal microbial communities was analyzed at multiple taxonomic levels. ASVs were clustered and taxonomically annotated, and the relative abundances of the predominant bacterial taxa were summarized. At the phylum level, the dominant phyla were *Firmicutes*, *Proteobacteria*, and *Bacteroidota*. Compared to Group H, all three major phyla were altered in Group C.p (Figure 7A). Further T-test analysis of phylum abundance revealed that, relative to Group H, Group C.p exhibited a significant decrease of *Firmicutes* and *Spirochaetota* ($p < 0.05$), while *Proteobacteria* and *Cyanobacteria* were significantly increased ($p < 0.05$) (Figure 7D). At the family level, the predominantly enriched families included *Oscillospiraceae*, *Rikenellaceae*, *Lachnospiraceae*, *Lactobacillaceae*, *Bacteroidaceae*, and *Spirochaetaceae* (Figure 7B). At the genus level, the genera with higher relative abundances were *Rikenellaceae-RC9-gut-group*, *UCG-005*, *Lactobacillus*, *Bacteroides*, *Clostridia-UCG-014*, and *Alistipes* (Figure 7C). Further T-test analysis showed that, compared to Group H, Group C.p had significantly reduced *Rikenellaceae-RC9-gut-group*, *UCG-005*, *Lactobacillus*, and *Clostridia-UCG-014* ($p < 0.05$), while the relative abundances of *Escherichia-Shigella* and *Hydrogenophaga* were significantly increased ($p < 0.05$) (Figure 7E). Collectively, these results demonstrate significant differences in fecal microbial composition across multiple taxonomic levels between healthy goats and goats with clinical abscesses.

3.7 Comparison of Microbiotas in the Fecal

We employed linear discriminant analysis (LDA) effect size (LEfSe) to identify taxa exhibiting differential abundances between the two groups, enabling comparison of their relative contributions. LEfSe analysis demonstrated significant differences in the abundance of various characteristic microorganisms between the two groups. In Group H, the primarily enriched taxa included *Firmicutes*, *Bacteroidales*, *Rikenellaceae-RC9-gut-group*, and *Clostridia-UCG-014*, among others. In contrast, taxa with higher relative abundances and LDA scores in Group C.p included *Proteobacteria*, *Alphaproteobacteria*, *Burkholderiales*, *Enterobacteriaceae*, and *Comamonadaceae* (Figure 8).

3.8 Correlation Analysis of Microbiota at the Genus Level

Co-occurrence network analysis provides an approach for examining potential associations and community organization within complex microbial environments. By constructing genus-level co-occurrence networks, dominant taxa and patterns of microbial associations in Group H and Group C.p were analyzed. The results revealed that the microbial community structures and interaction relationships differed between the two groups. In Group H, the dominant genera included *Clostridia-UCG-014*, *UCG-005*, and *Lactobacillus*, with most genera exhibiting positive correlations (Figure 9A). In contrast, the dominant genera in Group C.p were *Escherichia-Shigella*, *UCG-002*, and *Alistipes*, with most genera showing negative correlations (Figure 9B). Collectively, these findings indicate that genus-level microbial association patterns differed between healthy goats and goats with clinical abscesses.

4 Discussion

4.1 Identification of Dominant Pathogens in Goat Abscesses

The present study identified four bacterial species—*Corynebacterium pseudotuberculosis*, *Staphylococcus aureus*, *Trueperella pyogenes*, and *Escherichia coli*—as the primary causative agents of subcutaneous abscesses in the studied Saanen goat herd. Among these, *C. pseudotuberculosis* was the most prevalent, with a detection rate of 68.1%, consistent with previous reports highlighting its role as a major pathogen in goat abscesses[5, 13]. This bacterium is well-adapted to survive in host tissues, producing virulence factors such as phospholipase D (PLD) that facilitate its spread through the lymphatic system and promote abscess formation[14]. The high detection rate of *C. pseudotuberculosis* in our study suggests that it may be the primary etiological agent of abscesses in this region, which is consistent with findings from other parts of China[15].

Notably, we found that 93.1% of abscess cases were caused by single-pathogen infections, with mixed infections (2–3 pathogens) accounting for only 7.0%. This contrasts with some previous studies in goat, where mixed infections with *C. pseudotuberculosis* and *S. aureus* were reported in up to 45% of cases[16]. The difference in mixed infection rates may be attributed to variations in farm management practices, such as hygiene standards and antibiotic use, which can influence the diversity of pathogens present in the environment[5, 17]. The low rate of mixed infections in our study suggests that targeted

control measures against *C. pseudotuberculosis*, such as vaccination or improved biosecurity, may be effective in reducing abscess incidence in this herd.

4.2 Gender Differences in Abscess Incidence

Our results revealed a significantly higher abscess incidence in male goats (39.6%) compared to female goats (10.2%), a finding that aligns with previous observations in sheep[18]. Several factors may contribute to this gender difference. First, male goats are often more aggressive and prone to fighting, resulting in more skin injuries that provide entry points for pathogens[19, 20]. Second, hormonal differences between males and females may affect immune function; for example, testosterone has been shown to suppress cell-mediated immunity, increasing susceptibility to bacterial infections[21, 22]. Third, management practices, such as housing males in separate pens with higher stocking densities, may increase the risk of pathogen transmission[17, 23]. These findings highlight the need for gender-specific management strategies, such as reducing stocking density for males and implementing measures to prevent fighting, to minimize abscess incidence.

4.3 Alterations in gut Microbial Diversity in Abscess-Affected Goats

A key finding of this study was the significant reduction in gut microbial diversity (both alpha and beta diversity) in goats with abscesses compared to healthy goats. The alpha diversity indices (Chao1 and Shannon) were significantly lower in the C.p group, indicating a decrease in both the number of species (richness) and the evenness of species distribution (diversity) in the gut microbiota of abscess-affected goats. This is consistent with previous studies showing that bacterial infections can disrupt the gut microbial community, leading to dysbiosis[24, 25]. For example, in mice infected with *Salmonella enterica*, gut microbial diversity was reduced, and the relative abundance of beneficial bacteria (e.g., *Lactobacillus*) was decreased[26]. Similarly, in cattle with bovine respiratory disease, alpha diversity indices were lower in infected animals compared to healthy controls[27].

The beta diversity analysis further revealed distinct clustering of gut microbial communities between healthy and abscess-affected goats, indicating a significant shift in community structure. This shift was associated with changes in the relative abundance of key bacterial phyla, including a decrease in Firmicutes and an increase in Proteobacteria in the C.p group. Firmicutes are known to play a crucial role in nutrient metabolism and maintaining gut barrier function, and a reduction in their abundance has been linked to increased gut permeability and immune dysfunction[28]. In contrast, an increase in Proteobacteria, which includes many pathogenic species (e.g., *Shigella*), is often associated with gut dysbiosis and inflammation[29].

The C.p group exhibited significant gut dysbiosis, marked by decreased beneficial genera (e.g., *Lactobacillus*) and an increase in pathogens like *Escherichia-Shigella*. This shift likely impairs gut barrier function and immune homeostasis[28, 30], suggesting a potential association between abscess status and gut microbial imbalance, which may be relevant to host immune homeostasis. The co-occurrence

network analysis offers a more nuanced view of the microbial interactions. The shift from a network dominated by positive correlations among beneficial genera in the H group to one with more negative correlations in the C.p group indicates a disruption of the stable, cooperative microbial community. This breakdown in ecological structure may reduce the microbiota's resilience and functional capacity, potentially making the host more susceptible to secondary complications[31, 32]. The altered network topology strongly supports the conclusion that pathogenic bacteria infection disrupts the gut microbial homeostasis.

4.4 Limitations and Future Directions

This study has several limitations that should be considered. First, the sample size was limited to a single Saanen goat herd in Weinan city, which may limit the generalizability of the results. Future studies should include multiple herds and different goat breeds to confirm the findings. Second, we did not investigate the temporal dynamics of gut microbiota changes, so it is unclear whether dysbiosis precedes or follows abscess development. Longitudinal studies are needed to address this question. Third, we did not measure host immune parameters (e.g., cytokine levels) or gut barrier function, which would provide further insights into the mechanisms linking gut dysbiosis to abscesses. Finally, the use of 16S rRNA sequencing only provides information on bacterial composition, not function; metagenomic and metatranscriptomic studies are needed to explore changes in microbial function associated with abscesses.

Despite these limitations, our study provides valuable insights into the epidemiology of goat abscesses and the associated gut microbial changes. The identification of *C. pseudotuberculosis* as the dominant pathogen and the observation of gut dysbiosis in abscess-affected goats have important implications for the development of control strategies. For example, targeted vaccination against *C. pseudotuberculosis* and the use of probiotics to restore gut microbiota may help reduce abscess incidence in goat herds.

5 Conclusions

In conclusion, our results demonstrate that the pathogens causing clinical subcutaneous abscesses in goats mainly include *C. pseudotuberculosis*, *S. aureus*, *E. coli*, and *T. pyogenes*. In addition, subcutaneous abscesses are associated not only with localized infection but also with systemic changes, including significant dysbiosis of the gut microbiota. The observed changes are characterized by a decrease in diversity, changes in community structure, depletion of beneficial taxa, and an increase in potential pathogenic bacteria, collectively indicating damage to the gut environment. This study provides new insights into the relationship between common clinical infections in goats and gut microbiota ecology.

Declarations

Consent for publication

Not applicable.

Author Contributions

Conceptualization: D.L., Z.C. and J.L.; Data curation: D.L., L.Z.; Formal analysis: D.L. and L.Z.; Investigation: D.L., J.G., W.S., L.C. and J.L.; Methodology: D.L.,L.Z., Y.W. and J.L.; Validation: L.Z. and Z.C.; Visualization: D.L., L.Z., and Z.C.; Writing-original draft: D.L., L.Z; Writing-review and editing: D.L., Z.C., Y.W. and J.L. All authors have read and agreed to the published version of the manuscript.

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Institutional Review Board Statement

Animal pus samples sampling procedures were approved by the Animal Care and Use Committee of Tongren Polytechnic University (Approval date: 29 August 2024), with informed consent obtained from livestock owners.

Informed Consent Statement

Not applicable.

Data Availability Statement

The authors confirm that all data are fully available without restriction. The source data for this manuscript has been made publicly available through the ScienceDB repository and can be accessed here: https://www.scidb.cn/en/anonymous/dnlJelVq. Further inquiries can be directed to the corresponding authors. The nucleotide sequences of these four isolates were deposited in the NCBI database under accession numbers PV628296 to PV628299.

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Conflicts of Interest

The authors declare that they have no conflict of interest.

References

1. Neaton HJ, Wolf C. Small Ruminant Lentiviruses and Caseous Lymphadenitis. Vet Clin North Am Food Anim Pract. 2025;41:83–92. https://doi.org/10.1016/j.cvfa.2024.11.005.
2. Slosarkova S, Bzdil J, Nedbalcova K, Matiasovic J, Fleischer P, Stanek S. New sequence type ST3756 of Staphylococcus aureus subspecies anaerobius as the causative agent of abscessing lymphadenitis in sheep. Comp Immunol Microbiol Infect Dis. 2019;63:112–6. https://doi.org/10.1016/j.cimid.2019.01.008.
3. Parise D, Teixeira Dornelles Parise M, Pinto Gomide AC, Figueira Aburjaile F, Bentes Kato R, Salgado-Albarrán M, et al. The Transcriptional Regulatory Network of Corynebacterium pseudotuberculosis. Microorganisms. 2021;9:415. https://doi.org/10.3390/microorganisms9020415.
4. Hiller E, Hörz V, Sting R. Corynebacterium pseudotuberculosis: Whole genome sequencing reveals unforeseen and relevant genetic diversity in this pathogen. PLoS One. 2024;19:e0309282. https://doi.org/10.1371/journal.pone.0309282.
5. Didkowska A, Żmuda P, Kwiecień E, Rzewuska M, Klich D, Krajewska-Wędzina M, et al. Microbiological assessment of sheep lymph nodes with lymphadenitis found during post-mortem examination of slaughtered sheep: implications for veterinary-sanitary meat control. Acta Vet Scand. 2020;62:48. https://doi.org/10.1186/s13028-020-00547-x.
6. Cervantes-Barragan L, Chai JN, Tianero MD, Di Luccia B, Ahern PP, Merriman J, et al. Lactobacillus reuteri induces gut intraepithelial CD4+CD8αα+ T cells. Science. 2017;357:806–10. https://doi.org/10.1126/science.aah5825.
7. Djukovic A, Garzón MJ, Canlet C, Cabral V, Lalaoui R, García-Garcerá M, et al. Lactobacillus supports Clostridiales to restrict gut colonization by multidrug-resistant Enterobacteriaceae. Nat Commun. 2022;13:5617. https://doi.org/10.1038/s41467-022-33313-w.
8. Janssen R, de Kleer JWM, Heming B, Bastiaan-Net S, Garssen J, Willemsen LEM, et al. Food allergen sensitization on a chip: the gut-immune-skin axis. Trends Biotechnol. 2024;42:119–34. https://doi.org/10.1016/j.tibtech.2023.07.005.
9. Tun HM, Peng Y, Massimino L, Sin ZY, Parigi TL, Facoetti A, et al. Gut virome in inflammatory bowel disease and beyond. Gut. 2024;73:350–60. https://doi.org/10.1136/gutjnl-2023-330001.
10. Libertucci J, Young VB. The role of the microbiota in infectious diseases. Nat Microbiol. 2019;4:35–45. https://doi.org/10.1038/s41564-018-0278-4.
11. Zhao C, Hu X, Bao L, Wu K, Feng L, Qiu M, et al. Aryl hydrocarbon receptor activation by Lactobacillus reuteri tryptophan metabolism alleviates Escherichia coli-induced mastitis in mice. PLoS Pathog. 2021;17:e1009774. https://doi.org/10.1371/journal.ppat.1009774.
12. Tong J, Ma W, Yang R, Wang T, Chen X, Zhang X, et al. Dysbiosis of the gut microbiota maybe exacerbate orf pathology by promoting inflammatory immune responses. Vet Microbiol. 2020;251:108884. https://doi.org/10.1016/j.vetmic.2020.108884.
13. de Oliveira Zamprogna T, Ribeiro D, Azevedo VAC, Lara GHB, Motta RG, da Silva RC, et al. Bacteriological, cytological, and molecular investigation of Corynebacterium pseudotuberculosis,

mycobacteria, and other bacteria in caseous lymphadenitis and healthy lymph nodes of slaughtered sheep. Braz J Microbiol. 2021;52:431–8. https://doi.org/10.1007/s42770-020-00403-0.

14. El Damaty HM, El-Demerdash AS, Abd El-Aziz NK, Yousef SG, Hefny AA, Abo Remela EM, et al. Molecular Characterization and Antimicrobial Susceptibilities of Corynebacterium pseudotuberculosis Isolated from Caseous Lymphadenitis of Smallholder Sheep and Goats. Animals (Basel). 2023;13:2337. https://doi.org/10.3390/ani13142337.
15. Zhang S, Dao X, Li Y, Ma Y, Yang F. Isolation and Identification of Etiological Bacteria of Subcutaneous Abscess in Goats. China Animal Husbandry & Veterinary Medicine. 2019;46:946–56. https://doi.org/10.16431/j.cnki.1671-7236.2019.03.037.
16. Wang B, Wei Y, Bai X, Wang C, Feng H, Yang Z. Investigation and analysis of pathogenic bacteria in goats and sheep caused by caseous lymphadenit is abscess from Shaanxi and Gansu Province. Chin J Vet Sci. 2022;42:2427–33. https://doi.org/10.16303/j.cnki.1005-4545.2022.12.13.
17. El Khalfaoui N, El Amiri B, Cabaraux J-F, Chentouf M, Raes M, Marcotty T, et al. Rearing Management and Its Impact on Caseous Lymphadenitis in Sheep. Animals (Basel). 2024;14:1504. https://doi.org/10.3390/ani14101504.
18. Lauth EE, White SD, Depenbrock SM, VanHoy G, Heller MC, Chigerwe M, et al. Skin disease in sheep (Ovis aries): A retrospective report of 299 cases at a university veterinary medical teaching hospital (1986-2020). Vet Dermatol. 2025;36:321–31. https://doi.org/10.1111/vde.13338.
19. Barral TD, Mariutti RB, Arni RK, Santos AJ, Loureiro D, Sokolonski AR, et al. A panel of recombinant proteins for the serodiagnosis of caseous lymphadenitis in goats and sheep. Microb Biotechnol. 2019;12:1313–23. https://doi.org/10.1111/1751-7915.13454.
20. Batey RG. Pathogenesis of caseous lymphadenitis in sheep and goats. Aust Vet J. 1986;63:269–72. https://doi.org/10.1111/j.1751-0813.1986.tb08064.x.
21. Wu R, Pettersson C, Demirel I. Testosterone increases the virulence traits of uropathogenic Escherichia coli. Front Microbiol. 2024;15:1422747. https://doi.org/10.3389/fmicb.2024.1422747.
22. McGovern M, Kelly LA, Finnegan R, Murphy JF, Kelleher J, Melo AM, et al. Sex differences in preterm cytokine and inflammasome responses and modulation by exogenous sex steroids. Pediatr Res. 2025. https://doi.org/10.1038/s41390-025-04350-0.
23. Burmayan A, Brundage CM. Caseous lymphadenitis outbreak in a small ruminant herd. Open Vet J. 2021;11:530–4. https://doi.org/10.5455/OVJ.2021.v11.i4.2.
24. Li D, Jiang Y, Cui Z, Ma M, Zhu F, Li G, et al. Lactobacillus acidophilus protects against Corynebacterium pseudotuberculosis infection by regulating the autophagy of macrophages and maintaining gut microbiota homeostasis in C57BL/6 mice. mSystems. 9:e00484-24. https://doi.org/10.1128/msystems.00484-24.
25. Gupta U, Dey P. Rise of the guardians: Gut microbial maneuvers in bacterial infections. Life Sci. 2023;330:121993. https://doi.org/10.1016/j.lfs.2023.121993.
26. Leleiwi I, Kokkinias K, Kim Y, Baniasad M, Shaffer M, Sabag-Daigle A, et al. Gut microbiota carbon and sulfur metabolisms support Salmonella infections. ISME J. 2024;18:wrae187.

https://doi.org/10.1093/ismejo/wrae187.

27. Sabry I, Zeineldin M, Kamal M, Hefnawy A, El-Attar H, Abdelraof Y, et al. Comparative evaluation of lower respiratory tract microbiota in healthy and BRD-affected calves in Egypt. Trop Anim Health Prod. 2025;57:78. https://doi.org/10.1007/s11250-025-04322-w.
28. Dai Y, Lin Z, Zhang X, Wang Y, Sheng Y, Gao R, et al. Probiotic Lacticaseibacillus paracasei E10 Ameliorates Dextran Sulfate Sodium-Induced Colitis by Enhancing the Intestinal Barrier and Modulating Microbiota. Foods. 2025;14:2526. https://doi.org/10.3390/foods14142526.
29. Meng Q, Xu L, Xu F, Shen X, Yue J. HIV-associated gut dysbiosis drives oncogenesis through metabolic-immune crosstalk: mechanisms and therapeutic implications. Front Oncol. 2025;15:1634388. https://doi.org/10.3389/fonc.2025.1634388.
30. Marclay M, Dwyer E, Suchodolski JS, Lidbury JA, Steiner JM, Gaschen FP. Recovery of Fecal Microbiome and Bile Acids in Healthy Dogs after Tylosin Administration with and without Fecal Microbiota Transplantation. Vet Sci. 2022;9:324. https://doi.org/10.3390/vetsci9070324.
31. Bhattarai SK, Du M, Zeamer AL, M Morzfeld B, Kellogg TD, Firat K, et al. Commensal antimicrobial resistance mediates microbiome resilience to antibiotic disruption. Sci Transl Med. 2024;16:eadi9711. https://doi.org/10.1126/scitranslmed.adi9711.
32. Popov IV, Einhardt Manzke N, Sost MM, Verhoeven J, Verbruggen S, Chebotareva IP, et al. Modulation of Swine Gut Microbiota by Phytogenic Blends and High Concentrations of Casein in a Validated Swine Large Intestinal In Vitro Model. Vet Sci. 2023;10:677. https://doi.org/10.3390/vetsci10120677.

Figures

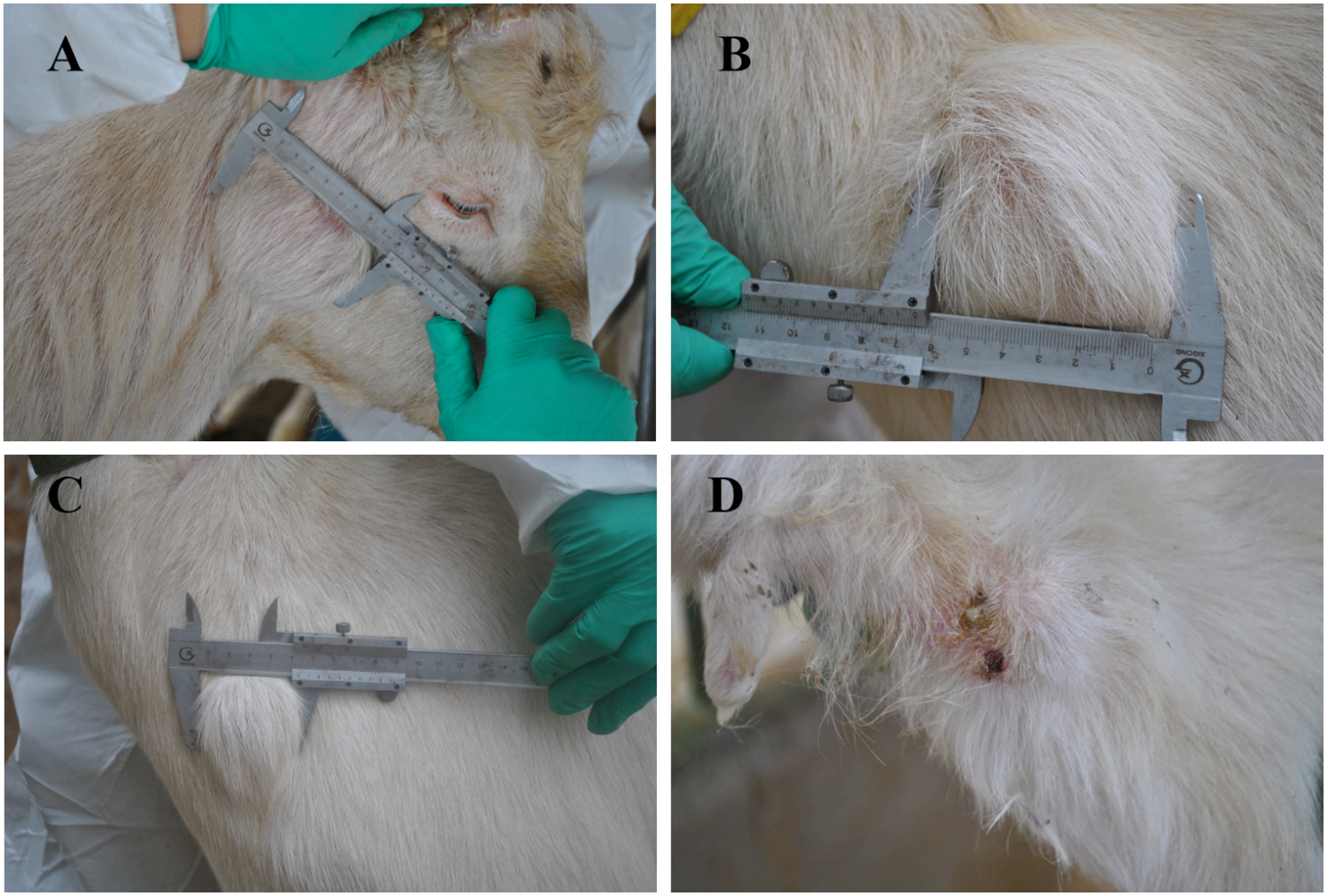


Figure 1

Clinical symptoms of goat surface abscess. Location of clinical abscess, (A) cheeks; (B) neck; (C) shoulders; (D) rupture abscess.

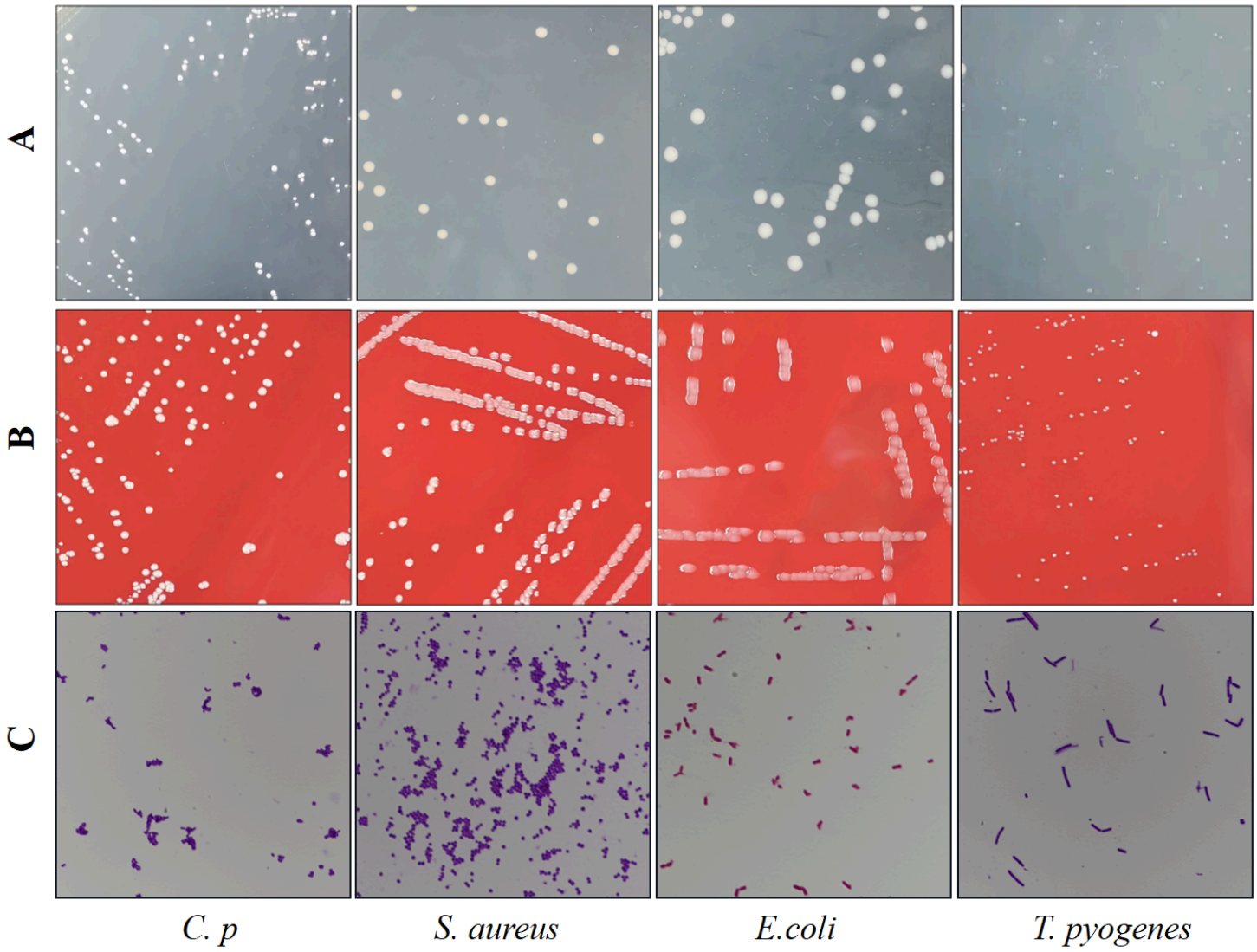


Figure 2

Observation of colony morphology and Gram staining of isolated strains. The bacteria were incubated on the Luria-Bertani agar plates (A) and agar plates containing 5% goat blood (B) overnight at 37 °C; (C) Gram staining and microscopic observation (1000 fold magnification) revealed the morphology of four types of bacteria.

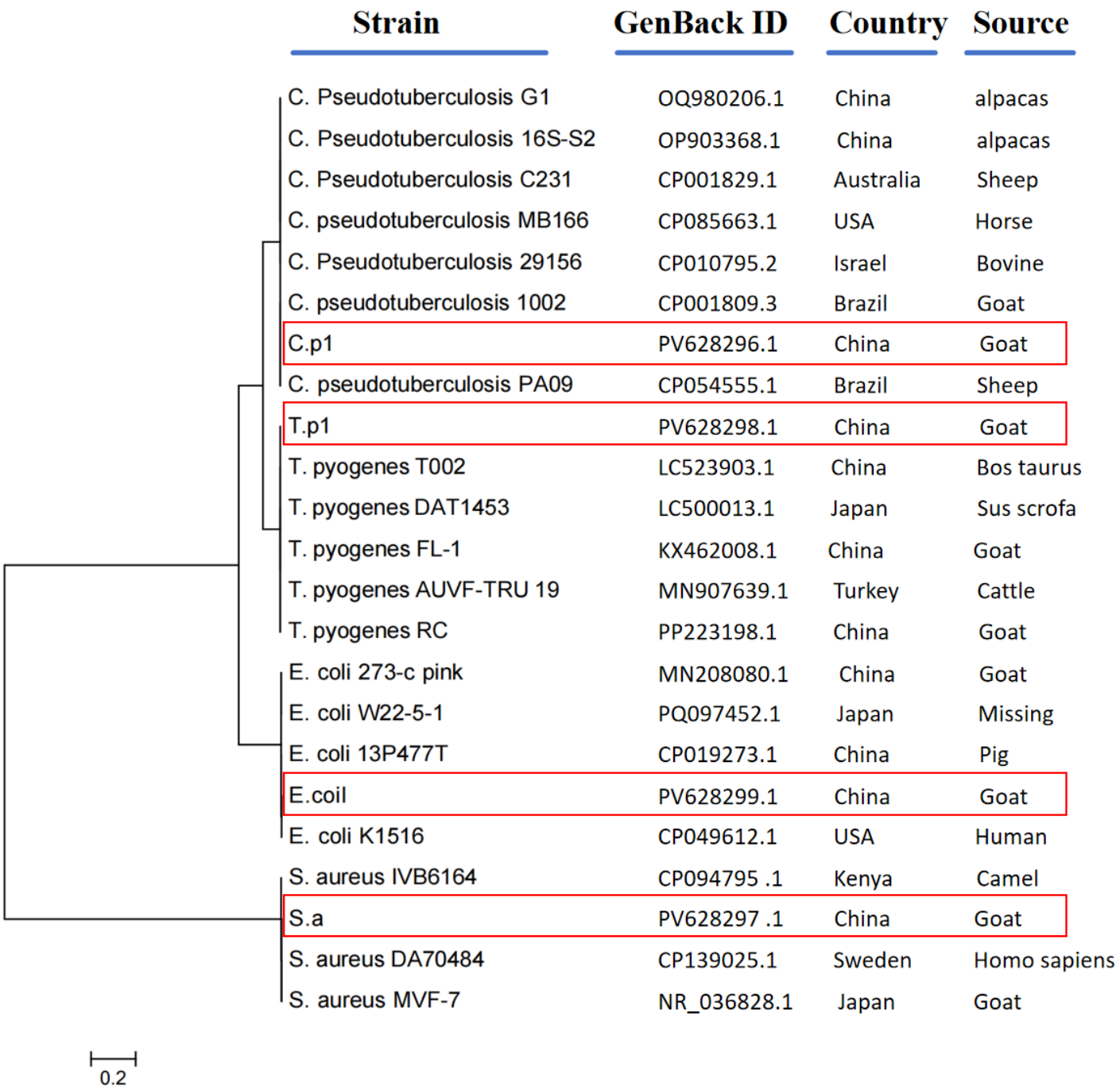


Figure 3

Phylogenetic tree based on 16S rRNA gene sequences of bacterial isolates derived from caprine superficial abscesses. A red line indicates the isolate from this study. The distance bar is the number of nucleotide substitutions per site. The neighbor-joining tree was constructed using MEGA 7.0 software.

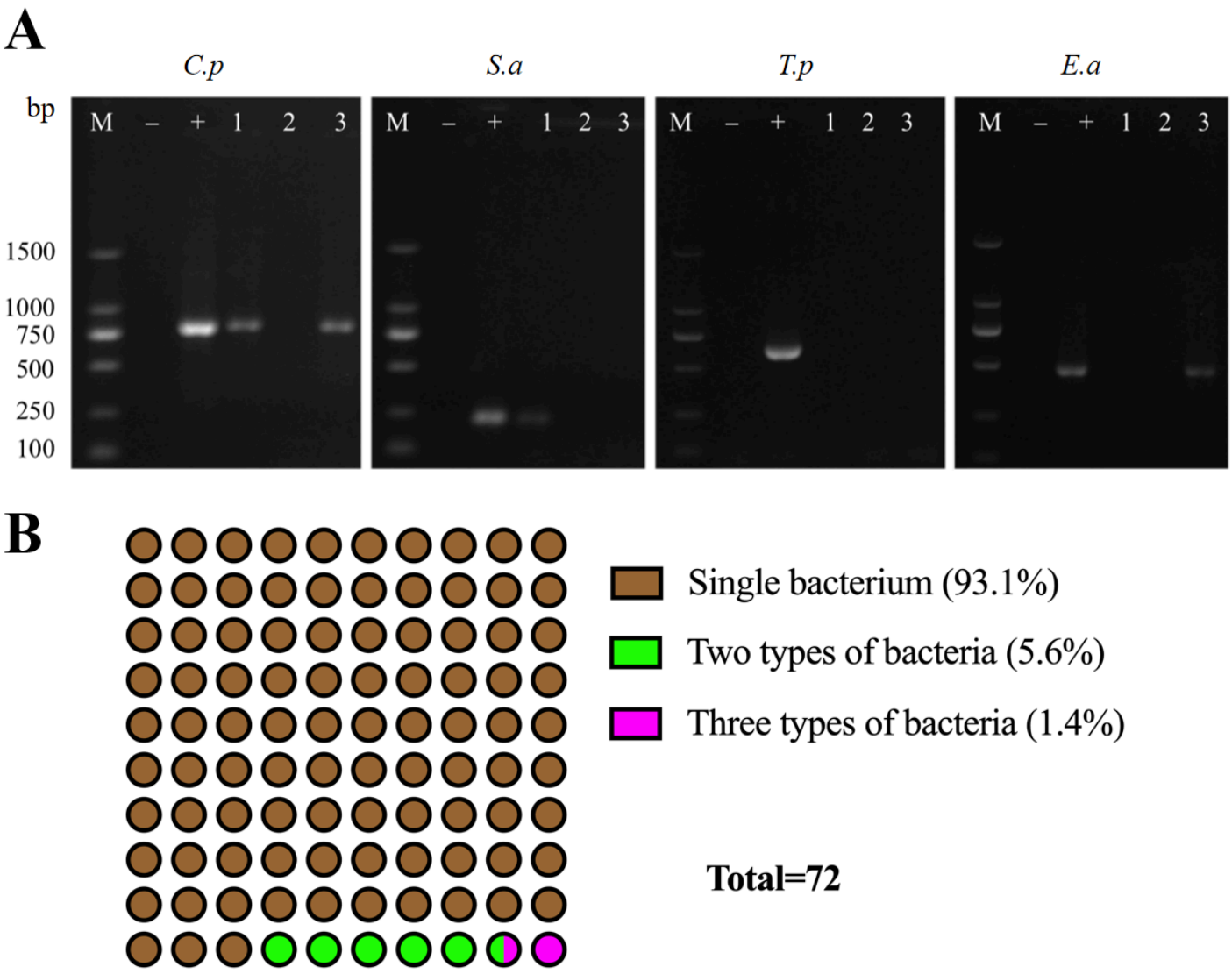


Figure 4

Detection and distribution of bacterial pathogens in caprine subcutaneous abscess samples. (A) Electrophoretic analysis of PCR products amplified from four pathogenic species in goat abscess samples, M: DNA marker, +: positive control (standard strains), −: negative control (double distilled water), 1~3: abscess samples. (B) Statistically analyze the types of bacteria in abscess samples and visualize the results using GraphPad Prism 8 software. A total of 72 samples were included in this study.

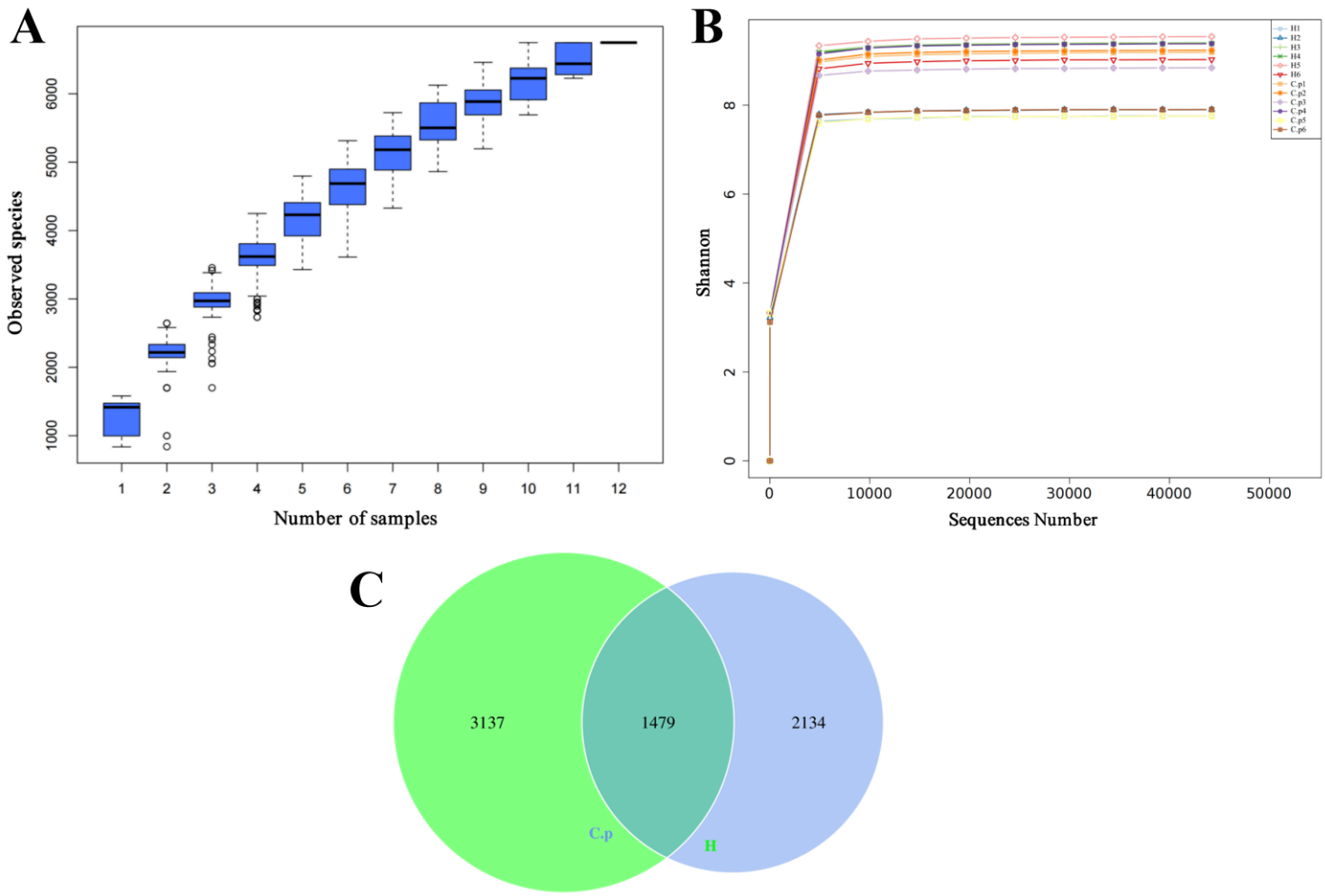


Figure 5

Feasibility analysis of sequencing data. (A) Species accumulation box plot and (B) Shannon rarefaction curve were used to assess the sequencing depth and evenness of the gut microbiota. (C) Venn diagram illustrating differences in ASV between fecal samples from healthy and diseased goats.

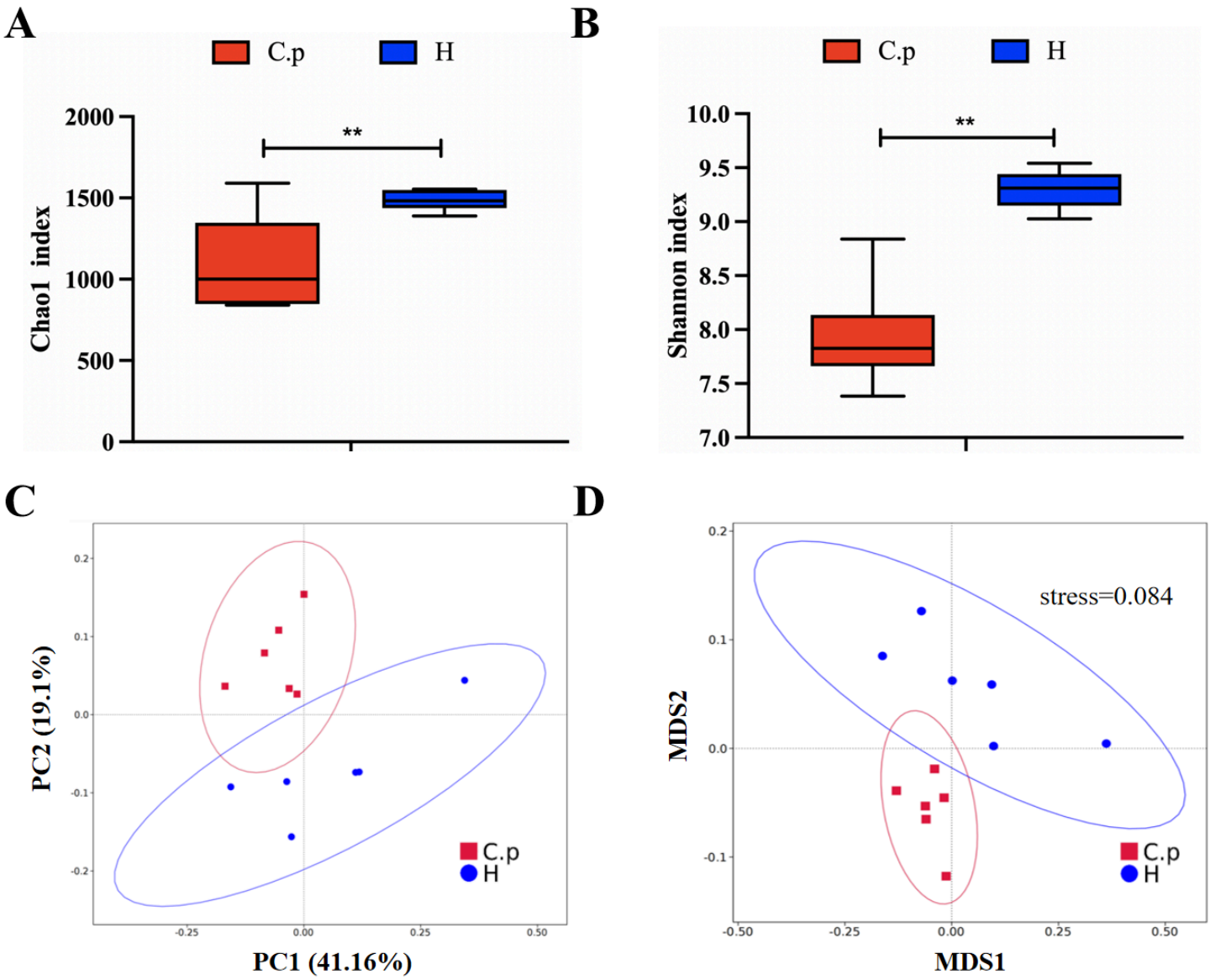


Figure 6

Bacterial community α-diversity (A,B) and β-diversity (C,D). (A) Chao1 index; (B) Shannon diversity index; (C) Principal coordinates analysis (PCoA) on the ASV level based on bray-curtis; (D) Non-metric multidimensional scaling analysis (NMDS) on the ASV level based on bray-curtis (** $p < 0.01$).

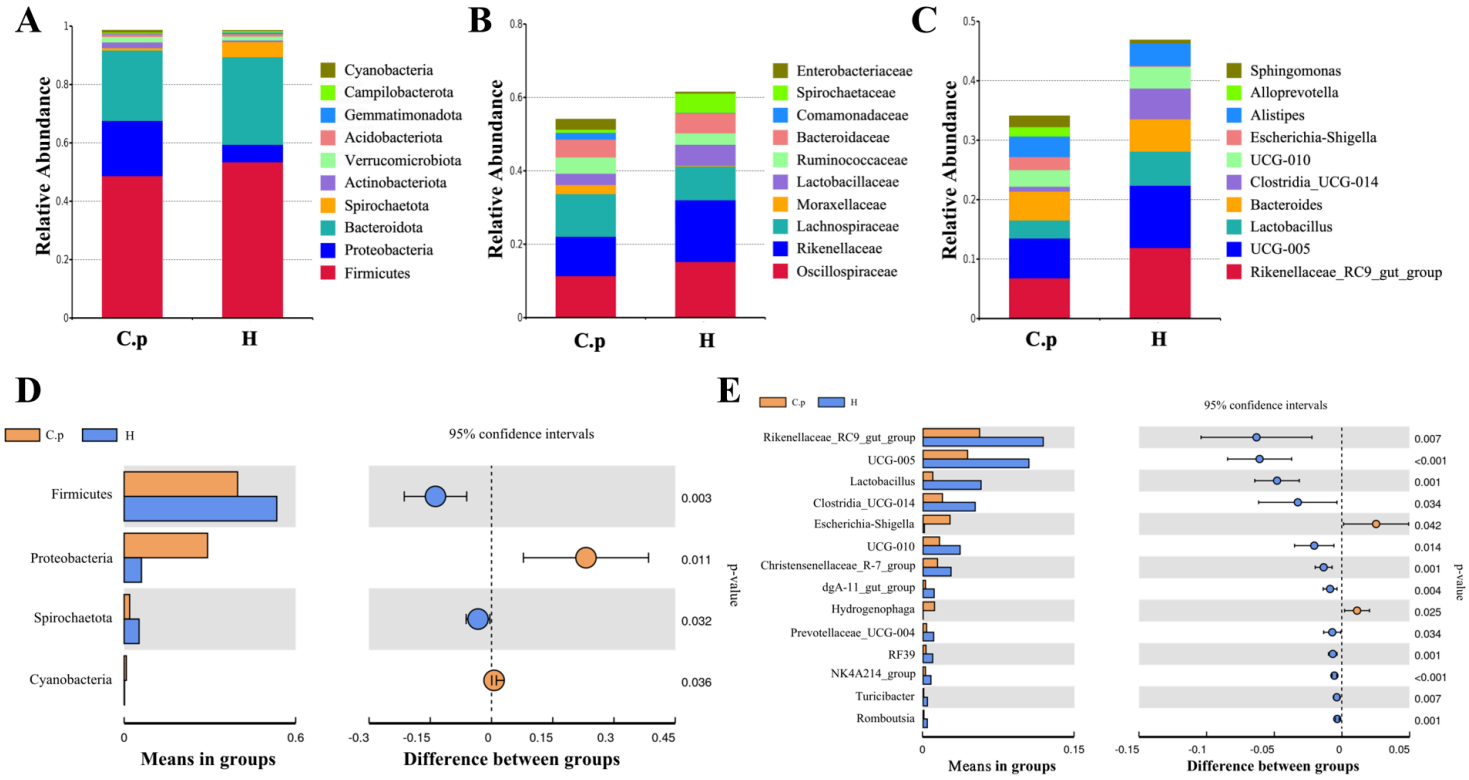


Figure 7

Compositional changes of the bacterial community at different taxonomic levels. Microbial community bar plot of the top 10 genera at different taxonomic levels in fecal (A) at the phylum level, (B) at the family level, and (C) at the genus level. T-test analysis (D) at the phylum and (E) genus levels.

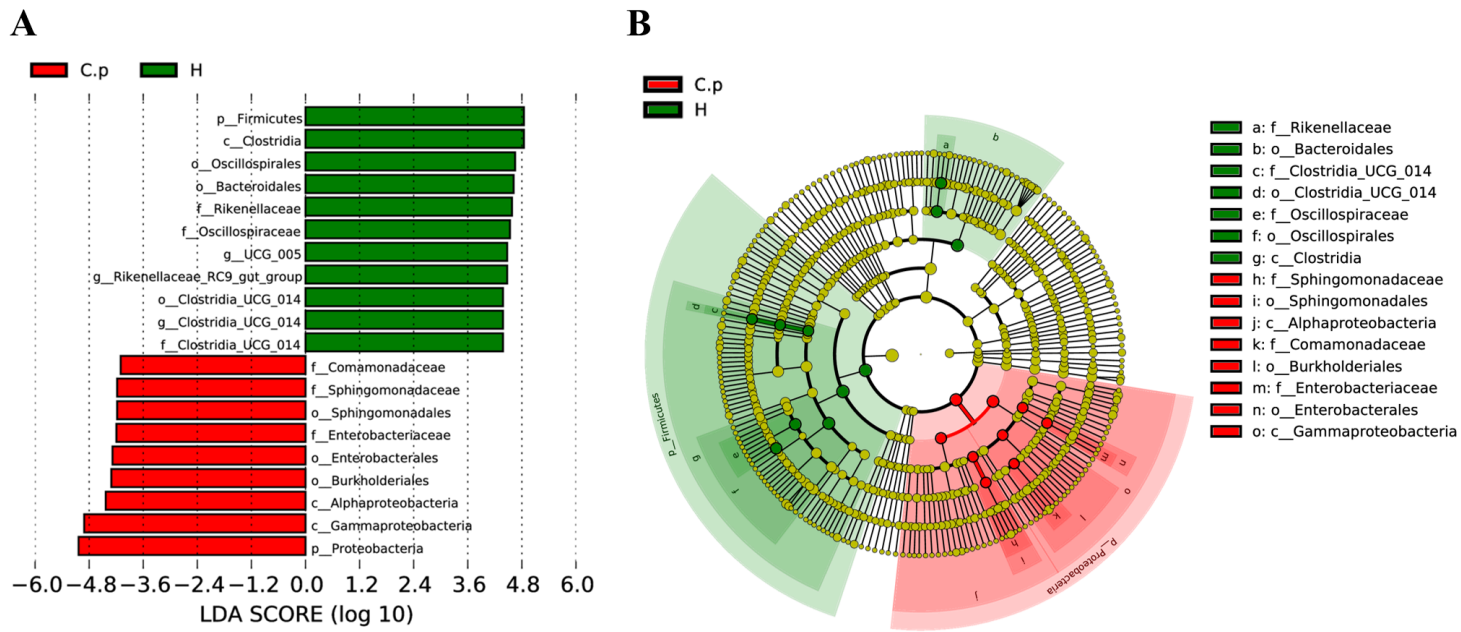


Figure 8

Differential biomarkers in the fecal microbiota of goat associated with Group C.p and Group H. (A) The significance criterion was set at LDA score >4. (B) The cladogram was utilized to visualize the phylogenetic distribution of taxa exhibiting significant differences.

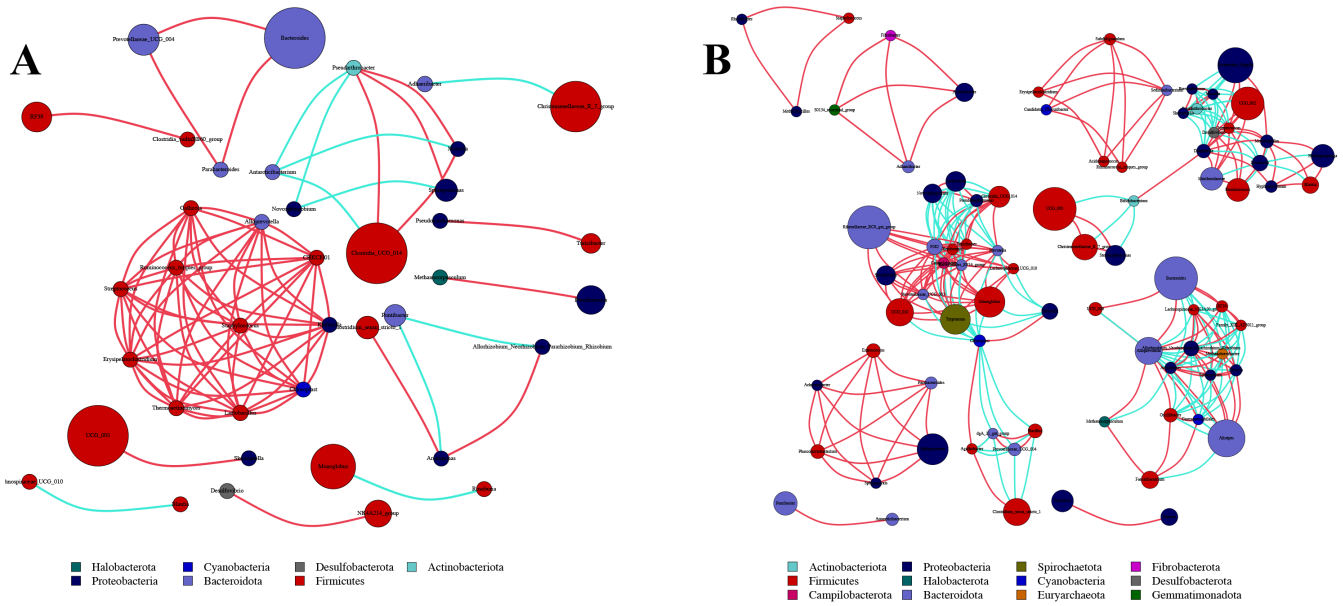


Figure 9

Co-occurrence network of bacterial genera based on correlation analysis. The network was constructed based on Sparman's correlation coefficients ($|\rho| > 0.6$, $p < 0.01$). (A) Group H, (B) Group C.p. Nodes represent bacterial genera, and node size is proportional to relative abundance. Line represent significant positive (red) or negative (blue) correlations.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- supplementaryfile.pdf
- SupplementaryTableS1.docx