Host and altitude factors affect rumen bacteria in cattle

Dongwang Wu¹ · Paramintra Vinitchaikul² · Mingyue Deng¹ · Guangrong Zhang¹ · Liyuan Sun¹ · Xiao Gou¹ · Huaming Mao¹ · Shuli Yang¹

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Abstract

There are many kinds of microorganisms in the gastrointestinal tract of mammals, some of which are closely related to the host. Rumen microorganisms are essential for normal physiological activities of their host by decomposing plant crude lignin and providing essential nutrients. The composition and diversity of this microbial population are influenced by the host, environment, and diet. Despite its importance, little is known about the effects of factors such as altitude variation on rumen microbial population abundance and diversity in different ruminants. Here, we described the changes in overall rumen bacteria in four groups of cattle, including the Zhongdian yellow cattle and Zhongdian yaks, grazing at high altitudes (3600 m); the Jiangcheng yellow cattle and Jiangcheng buffalo were kept at an altitude of 1100 m. We found that there was a significant difference in rumen bacterial abundance of the Zhongdian yellow cattle and Zhongdian yaks at high altitude and there was obvious homogeneity in rumen bacterial abundance and diversity in the Jiangcheng yellow cattle and Jiangcheng buffalo at low altitude. Therefore, our research concluded that under the same dietary environment, there were differences in the abundance and diversity of certain bacteria in the rumen of different breeds of cattle, indicating that host genetic factors and intestinal microorganisms related to altitudinal variation had a greater influence on rumen bacterial abundance in the cattle.

Keywords Rumen microbiology · Microbiome · Bacteria · Altitudinal variation · Host type

Introduction

There are very complex interactions between mammals and microbial community in the gut. Gut microbiota play an important role in keeping mammals healthy [1–3]. Intestinal microorganisms affect the host endocrine system function through a variety of bacteria-derived metabolites [4]. There are many factors that affect mammalian gut microbiota, such as variations in the altitude, diet, breed, and genetic factors. There are many new ideas about the effects of microbial

population and host, altitude, and diet. Presently, much microbial diversity in mammalian gut is unknown because most microorganisms cannot be cultured in vitro. Most ruminant anaerobe are very sensitive to oxygen due to their diverse and complex composition, coordination among microorganisms, and poorly understood relationships [5].

In general, animal-related intestinal microbial communities vary in different species and within and between populations. According to a recent study, altitude can affect the composition and function of the gut microbiota in wild mammals [6]. Altitude has been found to significantly influence the diet and gut microbial community in mammals [7]. Diet can affect the acquisition of ancient and large microbial lineages in the host gut [8]. Both host diet and phylogeny affect bacterial diversity [9]. Diet has a greater effect on the composition of rumen microbial communities than animal species [10]. The physiological evolution of the diversity of different mammals is accompanied by the formation of intestinal microbial diversity, and it influences the filtration or selection of specific types of intestinal bacteria [11]. The host can influence the rumen archaea abundance and the expression of microbial genes through genetic control [12]. Some studies have shown that the abundance and composition of microbial communities

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Dongwang Wu, Paramintra Vinitchaikul and Mingyue Deng contributed equally to this work.

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✉ Shuli Yang
yangshuli77@163.com

¹ Key Laboratory of Animal Nutrition and Feed Science of Yunnan Province, Yunnan Agricultural University, Kunming 650201, People's Republic of China

² Faculty of Veterinary Medicine, Chiang Mai University, Chiang Mai 50100, Thailand

have distinct species-specific characteristics [13]. Changes in the composition of microbes among populations have been found in house mice [14] and chimpanzees [15]. Species differences in gastrointestinal microbes have been found in both wild and captive animals [13, 16].

Exploring how host and environmental factors affect the composition and diversity of gut microbiota is of great significance in the understanding of the health of mammals [17, 18]. Given the critical role of gut microbes in the physiology of different species of animals, it is important to determine whether the composition and diversity of gut microbes are determined by the host type or the host's habitat. The main way of identifying these factors is to study the intestinal microbial diversity of host species. Therefore, the rumen bacterial flora of ruminants at high (3600 m) and low (1100 m) altitudes were analyzed using amplification sequencing method through species classification and abundance analysis, sample diversity, and differential analysis. The results showed that host type and elevation gradient affected the abundance and diversity of rumen bacteria. Different types of hosts have the same dominant flora, but with different proportions.

Materials and methods

All experiments performed in this study were approved by the Institutional Animal Care and Use Committee of Yunnan Agricultural University (Contract 2007-0081), China. The study complied with the guidelines of the institutional administrative committee and ethics committee of laboratory animals.

Animal handling and sampling

There were 24 experimental animals, $n = 6$ for each group, both for the adult animals. The experimental animals used in this study were selected from Shangri-La, Yunnan province, China (3600 m), wild grazing of Zhongdian yaks ($n = 6$) and Zhongdian yellow cattle ($n = 6$), and Jiangcheng County, Puer, Yunnan province, China captive (1100 m) of Jiangcheng yellow cattle ($n = 6$) and Jiangcheng buffalo ($n = 6$). After feeding in the morning, gastric tube with rumen vacuum sampler was used to extract the rumen liquid. In each animal, 30 mL of rumen gastric juice was obtained, placed in a labeled centrifuge tube and transferred immediately into a liquid nitrogen tank.

DNA extraction and sequencing

The microbial community DNA was extracted using EZNA Stool DNA Kit (Omega Bio-Tek, Norcross, GA, USA) following the manufacturer's instructions. DNA was quantified with a Qubit Fluorometer by using Qubit dsDNA BR Assay

kit (Invitrogen, USA), and the quality was checked by running aliquot on 1% agarose gel. Variable regions V1–V9 of bacterial 16S rRNA gene were amplified with degenerate PCR primers, 27F(5'-AGRGTTYGATYMTGGCTCAG-3') and 1492R (5'-RGYTACCTTGTTACGACTT-3'). Both forward and reverse primers were tagged with Illumina adapter, pad, and linker sequences. PCR enrichment was performed in a 50 μ L reaction containing 30 ng template, fusion PCR primer, and PCR master mix. PCR cycling conditions were as follows: 94 °C for 3 min, 30 cycles of 94 °C for 30 s, 56 °C for 45 s, 72 °C for 45 s, and final extension for 10 min at 72 °C. The PCR products were purified with AmpureXP beads and eluted in elution buffer. Libraries were qualified by the Agilent 2100 bioanalyzer (Agilent, USA). The validated libraries were used for sequencing on Illumina MiSeq platform (BGI, Shenzhen, China) following the standard pipelines of Illumina and generating 2×300 bp paired-end reads. The raw reads were submitted to the NCBI Sequence Read Archive database under ID number PRJNA630991.

Sequence analyses

Raw data were filtered to eliminate adapter pollution and low quality to obtain clean reads, and paired-end reads with overlap were merged to tags. Moreover, tags were clustered to operational taxonomic unit (OTU) at 97% sequence similarity. Taxonomic ranks were assigned to OTU representative sequence using the Ribosomal Database Project (RDP) Naïve Bayesian Classifier v.2.2. Finally, alpha diversity, beta diversity, and different species screening were analyzed based on OTU and taxonomic ranks.

The tags were clustered to OTU by scripts of the software USEARCH (v7.0.1090) [19]. OTU representative sequences were taxonomically classified using the RDP Classifier v.2.2 and trained on database Greengene_2013_5_99, using 0.5 confidence values as cutoff. Filtered tags were clustered into OTU (operational taxonomic units) at 97% similarity, and OTU number per sample primarily represents the degree of sample diversity. Based on OTU abundance, the OTU of each group was listed, Venn diagram was drawn using the Venn diagram software R (v3.1.1), and then common and specific OTU IDs were summarized. Based on the information on OTU abundance, the relative abundance of each OTU in each sample was calculated, and the PCA of OTU was done with the relative abundance value. The software used in this step was package "ade4" software R (v3.1.1). Good's coverage index and alpha diversities including inverse Simpson and Shannon indices, richness (observed number of OTUs), and evenness (Shannon evenness) were calculated using Mothur V.1.31.2. Beta diversity analysis was done using software QIIME (v1.80). There were differences in sequencing depth in different samples, and normalization was introduced as follows: Sequences was extracted randomly according to the

minimum sequence number for all samples, the extracted sequences formed a new “OTU table biom” file, and then the beta diversity distance was calculated based on the “OTU table biom” file.

Results

Rumen bacterial composition in different altitudes and host types

We collected rumen fluid from 24 animals from the four groups. We then used bacterial tag-encoded amplicon sequencing generated from the V1 and V9 regions of 16S rRNA gene to identify and characterize the overall rumen bacterial composition from each of our samples. In total, 241,841 raw reads were obtained from all 24 rumen fluid samples. After filtration, 170,091 high-quality sequences were produced, with an average of $13,436 \pm 5035$ reads per sample. Filtered tags were clustered into OTU at 97% similarity. The abundance of OTU initially indicated the species richness of the samples. The number of OTUs produced from 24 animal samples was 2200. The observed species value, *chao1* value, and *ACE* value reflected the species richness in community, and the rarefaction curve based on the three values used to evaluate obtained data was enough to cover all species in the community. To assess whether the sampling provided sufficient OTU coverage for accurate description of the bacterial composition of each group, sample- and individual-based rarefaction curves were generated for each group. We found that when the curve was smooth, it suggested that the sequencing depth covered all the species in the sample. The comparison of non-metric multidimensional scaling of community OTU showed that the samples were clustered according to their specific feeding patterns, host types, and changes in altitude, indicating that each group had its unique bacterial community and that different host types had their bacterial distribution in common; however, they all had high common clustering (Fig. 1). The number of OTU from large to small and the proportion of OTU in the total OTU are in the order of Zhongdian yellow cattle (183,327.99%), Zhongdian yaks (179,427.39%), Jiangcheng buffalo (150,923.04%), and Jiangcheng yellow cattle (141,321.58%). The endemic numbers of Zhongdian yellow cattle, Zhongdian yaks, Jiangcheng buffalo, and Jiangcheng yellow cattle are 96, 95, 21, and 46, respectively, accounting for 1.47%, 1.47%, 0.69%, and 0.32% of the total OTU, respectively, while the total OTU is 969, accounting for 14.80% of the total OTU. Among the 24 samples collected, we detected 14 phyla, among which Bacteroidetes and Firmicutes were the dominant phyla (Fig. 2). The dominant bacterial phylum in the rumen of the yellow cattle and yaks grazing in Shangri-La city was consistent, but the abundance of bacterial phylum composition was

Fig. 1 Shared OTU across different groups. Venn diagram displays the number of common/unique OTUs in multi-samples/groups. Different color represents different samples or groups. The interior of each circle symbolically represents the number of observed OTUs in the certain sample/group. The overlapping area or intersection would represent the set of OTU commonly present in the counterpart samples/groups. Likewise, the single-layer zone represents the number of OTUs uniquely found in the certain sample/group. A (Zhongdian yellow cattle), B (Zhongdian yellow yaks), C (Jiangcheng yellow cattle), and E (Jiangcheng buffalo)

different. The content of these two dominant phyla is highest in Zhongdian yaks and lowest in Jiangcheng yellow cattle among the four groups. The ratio of Bacteroidetes and Firmicutes in the rumen of Zhongdian yellow cattle and Jiangcheng yellow cattle was 1:0.99, 1:0.92, and 1:0.98, and the ratio of buffalo in Jiangcheng was 1:0.88. The rumen bacterial abundance and composition in the yellow cattle

Fig. 2 Taxonomic composition distribution of samples at the phylum level. A (Zhongdian yellow cattle), B (Zhongdian yaks), C (Jiangcheng yellow cattle), and E (Jiangcheng buffalo)

and buffalo in Jiangcheng County were similar. The host type and elevation gradient had certain effects on the composition and abundance of rumen bacteria.

Diversity analysis of rumen bacteria in different altitudes and host types

Alpha diversity was applied in analyzing the complexity of species diversity using a sample through several indices, including the observed species, chao1, ace, Shannon, and Simpson indices. The complexity of sample was proportional to the first four values, while it correlated negatively with the Simpson value. Bacterial community diversity was measured in different altitudes and hosts using the observed species, chao1, ace, Shannon, and Simpson indices (Fig. 3). These five indices reflected variations in the rumen bacterial community at different altitudes and in different hosts. The results showed that, in the same habitat, compared with the yaks, the rumen bacterial abundance and diversity in the yellow cattle in Shangri-La County were higher, while that in the yellow cattle and buffalo in Jiangcheng County were similar. The diversity of beta directly showed the differences in bacterial species in each sample at different altitudes and among different hosts (Fig. 4).

Differences in rumen bacteria in different altitudes and host types at the genus level

We observed that in the four experimental groups, rumen bacteria showed certain generality and differences at the genus level (Fig. 5). Thirteen genera of rumen bacteria were detected in the 4 groups, of which more than 60% were unclassified in each group. *Prevotella* was the dominant genus of rumen bacteria in all 4 groups. Interestingly, in the same habitat, the abundance of *Comamonas* was significantly higher in buffalo than that in the yellow cattle. This suggests that *Comamonas* has a distinct host specificity. We considered the genera that were present in all the samples from at least one group and analyzed the genera that showed three times or more variation of the same species in the high-altitude and relatively low-altitude groups. Therefore, we examined the genera such as *Butyrivibrio*, *Pseudobutyrvibrio*, or *Selenomonas*, which were significantly present in the high-altitude group but were at a comparatively low level in all the animals in the relatively low-altitude group. *Butyrivibrio* and *Pseudobutyrvibrio* fermentation metabolism can decompose a variety of carbohydrates. The rumen bacteria of the yellow cattle and yaks in the Shangri-La region were significantly different at the genus level. Noteworthy, the rumen bacteria of the yellow cattle and buffalo in the Jiangcheng County were similar in distribution and abundance at the genus level. Owing to the

Fig. 3 Alpha diversity indices boxplot among groups (description). Diversity was measured using the Shannon index; richness and evenness were measured by the Chao 1 and Simpson evenness indices,

respectively. A (Zhongdian yellow cattle), B (Zhongdian yaks), C (Jiangcheng yellow cattle), and E (Jiangcheng buffalo)

Fig. 4 Beta diversity heat map (description, bray_curtis). The Bray-Curtis distance is a commonly used index to show the differences between two communities, and its value is between zero and one. Zero Bray-Curtis represents the exact similar community structure. A (Zhongdian yellow cattle), B (Zhongdian yaks), C (Jiangcheng yellow cattle), and E (Jiangcheng buffalo)

altitudinal variation, the abundance of yaks ruminal bacteria at the genus level was significantly different. At the genus level, the results show that both the Zhongdian yellow cattle, the Zhongdian yaks, the Jiangcheng yellow cattle, and the Jiangcheng buffalo contain a large number of unclassified

Fig. 5 Taxonomic composition distribution of samples at the genus level. The ratio of each species in certain samples is directly displayed. The species of which abundance is less than 0.5% in all samples were classified into “others” in other ranks. A (Zhongdian yellow cattle), B (Zhongdian yaks), C (Jiangcheng yellow cattle), and E (Jiangcheng buffalo)

bacterial genera, 66.88%, 61.62%, 73.40%, and 76.29%, respectively. The rumen of the Zhongdian yellow cattle and the Zhongdian yaks are rich in *Prevotella* (9.65% vs 11.70%), *Butyrivibrio* (3.14% vs 3.42%), and *Clostridium* (2.99% vs 2.70%), and the species with high abundance of Jiangcheng yellow cattle and Jiangcheng buffalo are *Prevotella* (5.40% vs 3.98%) and *Fibrobacter* (4.90% vs 3.78%). The main rumen fibrous bacteria in genera *Prevotella*, *Vibrio butyrate*, *Ruminococcus*, *Treponema*, and *Clostridium* are Zhongdian yaks (24.4%) and Zhongdian yellow cattle (20.74%), respectively. It can be seen that among the four groups of cattle, the rumen fibrous bacteria of Zhongdian yaks was the most abundant, while the fibrous bacteria of Jiangcheng buffalo was the least abundant.

Prediction of bacterial function and differential microorganisms

A prediction of bacterial functional abundance was made from sequencing data of marker 16S rRNA gene, so as to infer the functional information of the biological community under the condition that it cannot be observed. The results showed that the main functions of the 16s rRNA gene were carbohydrate metabolism, membrane transport, amino acid metabolism, replication, and repair (Fig. 6). Cladogram shows the species with significant differences in abundance among the four experimental groups, phylum, class, order, family, genus, and

Fig. 6 Heat map of PICRUSt gene predicted function. A (Zhongdian yellow cattle), B (Zhongdian yaks), C (Jiangcheng yellow cattle), and E (Jiangcheng buffalo)

species (Fig. 7). Altitude and host, dietary factors, give each group of animals the advantage of microorganisms that differ significantly from one another. The four groups of host animals contained differentially labeled microorganisms with high abundance; Zhongdian yellow cattle include the Lachnospiraceae, *Butyrivibrio*. Zhongdian yaks include the Firmicutes, Bacteroidetes, and *Prevotella*, and Jiangcheng buffalo includes the Verrucomicrobia. Jiangcheng yellow cattle include the Planctomycetes, Proteobacteria, and Lentisphaerae. All of which are differential species biomarkers among the groups.

Discussion

The objective of this study was to evaluate the effects of differences and changes in altitude on total rumen bacteria of ruminants. Our results showed that each sampled group had its advantageous microbiome, which could be used to cluster samples from each experimental group using NMDS (non-metric multidimensional scaling). 16S rRNA is the most commonly used “molecular clock” in the taxonomic study of bacteria, and is used in the classification and identification of microorganisms and the study of microecology will play an important role. As for the universal primers, this experiment

Cladogram

Fig. 7 Cladogram for marking different species. The circle radiating from inside to outside represents the classification level from phylum to genus (or species). Each small circle at different classification levels represents a classification at that level. The diameter of the small circle is proportional to the relative abundance size. There was no significant difference of species uniform color yellow, biomarker follows differences between

species group of staining, red nodes play an important role in the red group of microbial groups, green nodes represent microbial groups and play an important role in the green group, and the other circle color means similar species name in English letters in the figure on the right side to display in the legend

referred to Zhang et al. method of microbial research [20]. By extracting the total genomic DNA of the samples, PCR amplification was conducted using the common primers of the 16S rRNA gene, and then the microbial diversity in the samples could be analyzed by sequencing. Because the similarity of 16S rRNA gene sequence is closely related to the evolution distance of microorganism, so the degenerate PCR primers of bacterial gene are used. Although Zhongdian yellow cattle and yaks received the same diet, their microbiota differed to some extent, which might indicate a dynamic change in the rumen microbiota independent of the same diet among different animal species at high altitudes. The composition of the rumen flora in ruminants is partially influenced by host genes [21]. The genetics and physiology of ruminants are related to the structure of rumen microbiome, and the host genes may shape the composition of the rumen microbiome. At the same time, another study on 709 beef cattle of three different breeds showed that the relative abundance and the total bacterial number of rumen flora diversity index of 34% (59/174) had heritability [22]. In the process of animals adapting to the extreme environment of the plateau, co-evolution between the host and the microbiome occurred. However, under the influence of the same feeding method and diet, the microbiota of the yellow cattle and buffalo in Jiangcheng County had certain homogeneity, and the differences in the rumen microbiota composition among different breeds were relatively low in the lower altitude area. The abundance of rumen bacteria in yaks reared in different habitats changed greatly, which may have been affected by altitude [23]. Compared with low-altitude vegetation types, the number of ruminant bacteria in the rumen of high-altitude grazing animals increased, and the acetic acid ratio decreased [24]. The results showed that the changes of rumen microorganisms in high-altitude animals were influenced by vegetative nutrients [25]. Compared with plain animals, intestinal microbes in high altitude were different and played more efficient roles. Altitude difference is related to intestinal microbial community, and high altitude environment affects the composition and function of intestinal flora in wild mammals [6].

The dominant phyla found in all the experimental groups were Bacteroidetes and Firmicutes. The two phyla differed greatly in abundance and the diversity of their genera composition; the yellow cattle and yaks living on the plateau exhibited more prominent abundance of the two phyla. The rumen bacteria Planctomycetes and Verrucomicrobia were more abundant in the yellow cattle and buffalo at low altitudes. A study comparing the intestinal flora of Tibetans and Han Chinese living at high altitudes reported similar changes in the composition of Firmicutes and Bacteroidetes [26]. The results showed that Chinese Han had a low relative abundance of Firmicutes and a high relative abundance of Bacteroidetes compared with those in Tibetans living at high altitude. However, there was no difference in the abundance of

Firmicutes and Bacteroidetes between the two groups of people living at the same altitude. The atmospheric oxygen content in the plateau area may be responsible for these factors [27]. The results of this study showed that the abundance of Firmicutes and Bacteroidetes in rumen bacteria of the yellow cattle and yaks in high altitude was higher than that of yellow cattle and buffalo in low altitude. The differences in these outcomes were likely to be influenced by diet and environment. In addition, animals in high altitude had a high abundance of vibrio butyrate, which can perform organic nutrition of chemical energy, fermentation, and metabolism, and the main metabolites were formate, butyrate, and lactate. The rumen abundance of Planctomycetes and Verrucomicrobia was relatively high in yellow cattle and buffalo in low altitudes, and Verrucomicrobia in particular may be related to the altitude and diet. Studies have shown that Verrucomicrobia decreases in abundance with high-fiber intake [28]. It was evident that cattle and yaks grazing on the plateau had a higher fiber intake.

All animals have the same core microorganisms in the gastrointestinal tract in the same grazing environment and in the dormitory feeding environment, while different microorganisms in the gastrointestinal tract of different host types have their different characteristics. In the rumen of yellow cattle and yaks grazing in Shangri-La, Yunnan province, China, there were 267 species and 228 species of unique bacteria respectively that could be classified and 1566 species of common core microorganisms. The number of common core bacteria in yaks in different altitude habitats was 940 species, and the number of bacteria unique to the rumen of yaks in high altitude areas was 854 species. In low-altitude area of Jiangcheng County, Yunnan province, China, the number of common bacteria in the rumen of yellow cattle and buffalo was 1202 species, and the number of unique bacteria was 211 species and 307 species, respectively. Unlike the shared communities of the low-altitude groups, the high-altitude groups had a larger number of shared communities, but within them, they had a similar number of different microbes. However, there were significant differences in the number of microorganisms in yaks alone in different habitats, which may indicate that the microbial changes were caused by altitude variation after migration. Some studies have shown that the host's genes play a key role in influencing intestinal microorganisms [29], but variations in altitude also have a significant effect on the host's intestinal microorganisms. A study on intestinal microecology of wolves supports this idea. Altitude, human disturbance, age, climate, and other factors affected the microecology in the wolf [30]. Both the genera *Vibrio* and *Succinicum* and the genus *Turicibacter* were affected by altitude.

Among the samples collected from the rumen of the three breeds, the number of anaerobes was significantly higher, and they were considered permanent residents of the mature

rumen bacterial community. The main function of *Prevotella*, *Butyrivibrio*, *Clostridium*, *Ruminococcus*, *Fibrobacter*, and *Treponema* is to decompose crude fibers. In the four groups, the proportions of some bacteria were as follows: Zhongdian yaks (24.4%), Zhongdian yellow cattle (20.74%), Jiangcheng yellow cattle (15.28%), and Jiangcheng buffalo (12.72%). Therefore, among the four groups, the rumen fibrous bacteria of Zhongdian yaks had the highest abundance, while the fibrous bacteria of Jiangcheng buffalo had the lowest abundance. The effect of host type on the microbial abundance of crude fiber degradation resulted in the difference in the utilization efficiency of crude fiber degradation. The most important of these is *Prevotella*, a genus that is the most abundant in adult rumen and is considered a major component of the genetic and metabolic diversity of rumen microbes [31]. In general, compared with *Prevotella* and *Butyrivibrio* in the rumen of cattle and buffalo at low altitude, the proportion of the two phyla in the rumen of yellow cattle and yaks at high altitude was higher. *Prevotella* is associated with carbohydrate and monosaccharide digestion. In individuals on high-fiber diet, *P. copri* in the gut has a greater ability to break down carbohydrates [32]. One of the main functions of *Butyrivibrio* in the rumen is to participate in the decomposition of xylem. There are varieties of fiber that are consumed by grazing animals in plateau areas; therefore, dietary factors may lead to a high abundance of *Prevotella* and *Butyrivibrio* in the rumen. *Selenomonas* is the main succinic acid decarboxylated microorganism in the rumen, which can ferment different soluble carbohydrates under different dietary conditions and use decarboxylated succinic acid to produce propionic acid [33]. *Succinimonas* in the rumen of yellow cattle and yaks were significantly different, with an average difference of 30 times. The diet was similar, while the abundance of microorganisms was significantly different, indicating that the type of host was closely related to rumen microorganisms. *Comamonas* showed significant differences in host type. In our study, this genus was not detected only in the rumen of yaks, and its abundance in the rumen of buffalo was high relatively compared with that in other cattle. Owing to the biological characteristics of the host, the theory needs to be extended to consider the feedback effect of flora on host's behavioral development and evolution. The essence of understanding the differences between different individuals (hosts) is to understand the ecological mechanisms underlying them [34]. At the same time, there are microorganisms among different individuals that affect the productivity of ruminants. Some studies have shown that the individual microbial species in rumen of ruminants may affect the structure and function of microbial flora to some extent and ultimately change the production efficiency of the host [35, 36]. Therefore, in the process of production practice, attention should be paid to screening rumen microorganisms to improve production efficiency.

Conclusion

Our findings led to the conclusion that some bacteria in the rumen of cattle of different breeds under the same dietary environment have certain differences in both abundance and diversity, indicating that the genetic factors of the host are related to intestinal microorganisms. Altitudinal change had a great influence on the rumen bacterial abundance in yaks. However, the significant similarities observed between the yaks rumen and the rumen of other animals, along with human intestinal bacterial communities, in this study in terms of reproduction and its variation with the host type, altitude, and diet suggest that the development and function of intestinal bacteria are somewhat homogenous for different organisms. Each individual is an ecosystem with a unique microbial community. Therefore, recognition of the differences between individuals is, in essence, a comprehensive scientific problem. The present results provide an attractive topic for in-depth discussion on the synergistic effects of intestinal flora and host genetics on physiological mechanisms, nutrient decomposition and utilization, and elevation changes.

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Authors' contributions WDW, MHM, and YSL made substantial contributions to the conception or design of the experiments. WDW, ZGR, DMY, SLY, and GX performed the experiments. WDW and VP analyzed the data. WDW, VP, and YSL wrote the paper. All authors read and approved the final manuscript and ensure that issues relating to the accuracy or completeness of any part of the work are properly investigated and resolved.

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Compliance with ethical standards

All experiments performed in this study were approved by the Institutional Animal Care and Use Committee of Yunnan Agricultural University (Contract 2007-0081), China. The study complied with the guidelines of the institutional administrative committee and ethics committee of laboratory animals.

Conflict of interest The authors declare that they have no conflict of interest.

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