The Influence of Ketosis on the Rectal Microbiome of Chinese Holstein Cows

Yunfei Huang1,2,4, Yajuan Li1,8, Baoxiang He1,*, Junjing Hu3, Muhammad Ali Mohsin1, Huiru Yu1, Peng Wang1, Peijun Zhang1, Yulan Du1, Lijun Huang1, Wenxiang Shen1 and Xiaojing Zhou1

1Department of Veterinary Medicine, College of Animal Science and Technology, Guangxi University, Nanning, 530004, Guangxi, China; 2Guangxi Key Laboratory of Molecular Medicine in Liver Injury and Repair, Guilin Medical University, Guilin, 541000, Guangxi China; 3Institute of Animal Health, Guangdong Academy of Agricultural Sciences, Guangzhou, 510640, Guangdong, China 
*Corresponding author: hebaox@gxu.edu.cn

ARTICLE HISTORY (18-242)

Received: July 07, 2018
Revised: December 06, 2018
Accepted: January 31, 2019
Published online: March 22, 2019

Key words:
Community structure
Cow
Ketosis
Rectal microbiome

ABSTRACT

This study was conducted to analyze the changes in microbial populations of rectal content of dairy cattle with and without ketosis. The plasma β-hydroxybutyric acid (BHBA) levels of 350 cows were measured and twenty-two post-parturient dairy cows with BHBA levels >1.2 mmol/L were selected and diagnosed with ketosis (KET group). According to statistical pairing rule, 22 dairy cows with BHBA levels <0.60 mmol/L formed the control groups (CON group). The profile of the microbial community of the rectal content samples was detected using high-throughput sequencing analysis of hypervariable V4 region of microbe. The average effective sequences of each sample were 84983, ranging from 64090 to 94470. The Principal Ordinates Analysis (PCoA) showed that there were distinctly different clusters of the rectal microbial community between KET and CON cows. Beta diversity analysis was evaluated differences in samples of species complexity. At the phylum level, the percentage of Euryarchaeota of the KET cows was less than (P<0.05) in the CON group. At the genus level, the percentages of Ruminococcaceae-UGG-014, Methanobrevibacter, Erysipelotrichaceae-UGG-009, and Atopobium of the KET cows were less than (P<0.05) those found in the CON group. The percentage of Lachnospiraceae was greater (P<0.05) in KET cows compared with CON cows. Lachnospiraceae is related to butyrate production and an increased amount may be an important causative agent of ketosis in dairy cattle. Our findings give a complete picture of current knowledge of the population structure of the rectal microbial ecosystem between KET and CON cows and enhance our understanding about the rectal microbial ecology that may be useful in the prevention of ketosis.

INTRODUCTION

Ketosis, a metabolic disorder of carbohydrate and fat, is one of the most prevalent and costly metabolic diseases in post-parturient dairy cows, result in high concentrations of ketone bodies in blood, milk and, urine (Zhang et al., 2013). There are many microbes in the dairy cow’s rumen; in addition, the intestines are also rich in microbes. The gastro-intestinal microbiome is complex and includes many varieties of bacteria, archaea, and fungi that are involved in critical functions within the host, such as immunity, metabolism, digestion (Zhang et al., 2015; Rooks et al., 2016) and other intestine function (Boguslawskatryk et al., 2015). It has been reported that variations in the microbiota may influence the occurrence of ketosis in dairy cows (Luan et al., 2015). Some researchers have used Terminal-restriction fragment length polymorphism (T-RFLP) to investigate the microbe community of ruminant comparisons of small subunit rRNA genes, and correlation between rumen microbe community and marine algae in dairy sheep (Castro-Carrera et al., 2014). The conventional method to investigating gastro-intestinal microbe is by isolation and cultivation, which is insufficient. However, the
composition and diversity of rectal microbe based on high-throughput sequence technology in dairy cows have not been reported. Next-generation sequence of 16S rDNA gene has greatly expanded the ability to obtain more comprehensive and complex information on the microbial community without culture (Logares et al., 2014). In this study, we used next-generation sequence of 16S rDNA gene to characterise and compare the microbiota in the rectum of dairy cows with and without ketosis.

MATERIALS AND METHODS

Animal selection and sample collection: Animals in the present study were selected from Jinguang Dairy Cattle Experimental Farm of Guangxi University in China. These Holstein cows were in early lactation (within 60 days postpartum), were fed the same diet, managed in the same routine had the same body condition scores and were producing a similar amount of milk. The β-hydroxybutyric acid (BHBA) levels of blood plasma of 350 post-parturient dairy cows were detected by kit (Randox Laboratories, UK, Cat. No. FA 115) and, the cows with plasma BHBA greater than 1.2 mmol/L were diagnosed as ketotic (Y Li, 2016). Twenty-two cows were diagnosed with ketosis, two of which exhibited clinical ketosis (having clinical signs of ketosis and with BHBA 5.3 and 5.6 mmol/L respectively) were merged with the subclinical ketotic cows into one group named KET group. According to the pairing rule such as days in milk (DIM), parity etc., 22 healthy cows were assigned to the control (CON) group. Basic information about the enrolled animals including age, DIM, parity, milk yield (MY) and body condition score (BCS) are shown in Table 1. The rectal content of the KET and CON cows were collected by rectal examination and put into frozen tubes, and stored in liquid nitrogen immediately.

DNA extraction, amplification, and sequencing: Every rectal content sample (200 mg) underwent DNA genome extraction by the SDS method (Natarajan et al., 2016). The concentration and purity of DNA samples was monitored on 1% agarose gels. Sterile water was used to dilute DNA to 1ng/μL, and then used a specific primer (515F-806R) with the barcode to amplify the 16S V4 regions, all PCR reactions were carried out with Phusion® High-Fidelity PCR Master Mix (New England Biolabs). The same volume of 1 x buffer (contained SYB green) was mixed to perform quantification and qualification of the PCR production with PCR products and operated the electrophoresis on 2% agarose gel. Those containing 400-450bp bright main strip samples were chosen for further experiments. The PCR products were purified with Qiagen Gel Extraction Kit (Qiagen, Germany) after being mixed in equidensity ratios. The TruSeq® DNA PCR-Free Sample Preparation Kit was used to generate sequence libraries (Illumina, USA) following the recommendations of manufacturer and index codes were added. The Qubit®2.0 Fluorometer and Agilent Bioanalyzer 2100 system were used to assess library quality, which was sequenced on an IlluminaHiSeq2500 platform to generate 250 bp paired-end reads at last. ALL samples were sequenced by Novogene Bioinformatics Technology Co., Ltd (Beijing, China).

Data analysis: The phylogenetic relationship of different operational taxonomic units (OTUs), and the difference in the dominant species in different groups, and the multiple sequence alignment was conducted by MUSCLE software 3.8.31(http://www.drive5.com/muscle/). Species diversity was evaluated by alpha diversity with QIIME 1.7.0. And the difference between samples of species complexity was evaluated by beta diversity analysis (weighted and unweighted unifrac) with QIIME software 1.7.0.

RESULTS

The diversity of rectal microflora of dairy cows: The 44 rectal content samples were confirmed to be qualified after electrophoresis analysis. The mean effective sequences in each sample were 84983, (range 64090 to 94470). According to the sequences in ≥97% similarity, an average of 1721 OTUs was identified with each sample, ranging from 1276 to 1842 (Fig. 1).

In total, the sequences of rectal content samples of CON and KET group were classified into 27 phyla and 368 genera. The complexity of the microbe in the two groups was evaluated based on alpha-diversity as shown in Fig. 2. Chao 1 (Fig 2A) and Shannon (Fig 2B) indexes were used to estimate the community richness and diversity, respectively. The results showed an abundance and diverse range of microbes in both CON and KET groups, however, there was no significant difference.

Comparison of rectal microbial community in dairy cows: In the rectal microbial community, the most abundant taxa microbial at phylum and genus were shown in Fig. 3. The most abundant phyla were Firmicutes and Bacteroidetes, accounting for more than 85% of the total microbial sequences in both CON and KET groups. The remaining taxa at phylum were Proteobacteria, Spirochaetes, Tenericutes, Actinobacteria, Euryarchaeota, Verrucomicrobia, Saccharibacteria and Chloroflexi (Fig. 3A). Both CON and KET groups had similar kinds of microbial phylum, while their proportion of each group differed. There was a difference between CON and KET group at the genus level. Buchnera and Streptococcus were within the top 10 taxa only in the KET group (Fig 3B). The remaining taxa were Ruminococcaceae_UCG-005, Rikenellaceae_RC9_gut_group, Prevotellaceae_UCG-003, Bacteroides, Christens enellaceae_R-7_group, Treponema_2, Eubacterium coprostanoligenes_group, Lachnolosstridium (Fig 3B).

The unique and shared OTUs between CON and KET groups were displayed in a Venn diagram to enable comparison (Fig. 4). A total of 2770 and 2663 OTUs were obtained on KET cows and CON cows, respectively. Ketotic and healthy cows shared 2571 OTUs, and the unique OTUs of KET cows and CON cows were 199 and 92, respectively.

A principal component analysis (PCoA) was used to compare the similarities between the microbial community compositions of the 44 experiment animals. The scatter plot based on PCoA scores showed a clear separation of the community composition between the ketotic and healthy cows (Fig. 5). Samples of the KET formed a cluster and distinctly separated from the CON. The result indicated that the microbial composition of the KET was different from that of the CON.
To identify the specific microbial taxa associated with ketosis, we compared the rectal microbiota of CON and KET cows using the linear discriminant analysis (LDA) effect size (LEfSe) method. A cladogram representative of the structure of rectal microbiota and the predominant microbe was shown in Fig. 6A and 6B; the most significant differences in taxa between the two groups were displayed. The relative abundance of the Firmicutes and Proteobacteria phylum was significantly higher (LDA>4) in the KET group compared with that of the CON group. As shown in Fig. 6C to K, Bacilli, Lactobacillales, Streptococcaceae and Streptococcus belonged to Firmicutes phylum that was significantly higher in KET group than those in CON group; Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae and Buchnera were higher (P<0.05) in the KET group compared with those in the CON group.

In order to identify the significantly different taxa at the different classification level, T-test was performed. As shown in Fig. 7, the different taxa between the CON and KET groups were displayed at phylum and genus level. The proportion of Euryarchaeota of the KET group was significantly different from that of the CON group at phylum level (P<0.05) (Fig. 7A). As shown in Fig. 7B, at the genus level, the proportions of Ruminococcaceae_UCG-014, Erysipelotrichaceae_UCG-009, Lachnospiraceae-UGG-010, and Atopobium were different between the CON and KET (P<0.05). Ruminococcaceae_UCG-014, Erysipelotrichaceae_UCG-009, Lachnospiraceae-UGG-010 belonged to Firmicutes phylum, Methanobrevibacter belonged to Euryarchaeota, and Atopobium belonged to Actinobacteria.
Fig. 4: Unique and shared OTUs in rectal content samples of KET and CON group. The Venn diagram is used to compare with the rectum microbe between CON and KET group.

Fig. 5: Principal coordinates analysis (PCoA) of microbial community compositions of dairy cows rectum content based on unweighted UniFrac distance matrix. The scatter plot based on PCoA scores showed a clear separation of the community composition between the ketotic cows and healthy cows.

Fig. 6: The difference of microbial taxa abundance of the KET compares to the CON was identified by LEfSe. (A) Taxonomic cladogram obtained from LEfSe sequence analysis. Biomarkers taxa are highlighted by colored circles and shaded areas. (B) The difference in taxa abundance between the KET and CON. The cutoff value of $\geq 4.0$ was used for the linear discriminant analysis (LDA). (C) to (K) Details of the difference in taxa abundance between the KET and CON.
DISCUSSION

Microbial composition in the hindgut region of healthy dairy cows: The rumen is the main place that microbes live in dairy cows and these microbes play an essential role to the health and productivity of the host, such as the degradation and fermentation of cellulose and other polysaccharides (Scharen et al., 2017). Gut microbes also underpin the metabolic capability of the host and provide many advantageous effects (Zhang et al., 2015). Lots of studies reported that gut harbored a number of microbes that are very important to the host (Marchesi et al., 2016; Rooks et al., 2016; Sánchez et al., 2017). In the present study, the average effective sequences of each sample were 84983, and the microbes from 22 phyla were identified in rectal content samples of healthy cows. The abundant taxa at phylum level (the top 10) were Firmicutes, Bacteroidetes, Proteobacteria, Spirochaetes, Tenericutes, Actinobacteria, Euryarchaeota, Verrucomicrobia, Saccharibacteria, and Chloroflexi, while Firmicutes and Bacteroidetes made up the vast majority (Fig. 3A). Firmicutes and Bacteroidetes are also dominant in other animals’ gut including humans (Donaldson et al., 2016) and fish (Liu et al., 2016). Firmicutes and Bacteroidetes are the main microbes in most mammals (O Donnell et al., 2017), including adult human (Dinan et al., 2015). At the genus level, Ruminococcaceae_UCG-005, Rikenellaceae_RC9_gut_group, Prevotellaceae_UCG-003, Bacteroides, Christens enellaceae_R-7_group, Treponemata_2, Eubacterium coprostanoligenes_group, and Lachnoclostridium (Fig. 3B) were dominant in dairy cows’ rectal contents. Ruminococcaceae could break down cellulose and disaccharide to formic acid and acetic acid (Gagen et al., 2015). The diet of dairy cows is rich in cellulose and carbohydrates which are digested by ruminal microbes.

Comparison of rectal microbes between the KET and CON groups: It is generally accepted that the vertebrate gut microbiome plays a vital role in host disease (Gao et al., 2017), which is now attracting increased attention regarding its role in the diseased animal. Ketosis is a common metabolic disease of the post-parturient in dairy cow which leads to reduced milk yield, reproductive performance and, increased occurrence of other diseases (Raboisson et al., 2014). It is recognized that ketosis occurs because of excessive mobilization of fat which may induce an imbalance in hepatic carbohydrate and fat metabolism, characterized by elevated concentrations of ketone bodies (BHB, acetocetate, and acetone) and non-esterified fatty acids (Zhang et al., 2016). Lu et al. (2015) reported that cows fed on DFM (direct-fed microbials contained Bacillus pumilus 8G-134 tended to have higher feed conversion and to have a lower prevalence of subclinical ketosis. These studies suggested that microbes play a very significant role in the occurrence of ketosis. As shown in Fig. 5, a scatter plot of KET and CON samples based on PCoA scores shows a clear partition of the community composition between the ketotic cows and controls. It indicated that there was a significant difference between the microbial community composition of the KET and the CON cows. Further more, the results of the T-test at the phylum level (Fig. 7A) showed that the proportion of Euryarchaeota in rectal faeces of the KET cows was significantly decreased compared to the CON cows. Euryarchaeota is implicated in the production of methane through the reduction of CO₂ and H₂ (or formate) (Gaci et al., 2014). It has been reported that increasing the forage in the diet of Bubalus bubalus could increase the proportion of Euryarchaeota in the rumen because the digestion of forage produces CO₂ and H₂ (Singh et al., 2015). In the present study, the percentage of Euryarchaeota in rectal content of ketotic cows was decreased which may indicate a lack of CO₂ and H₂ from forage digestion, which is likely due to the reduced dry matter intake of ketotic cows. In addition, the percentage of Methanobrevibacter, which is a methanogenic microbe, also reduced in dairy cows with ketosis (Fig. 7B), the reason for which may be the same as for the Euryarchaeota. The proportion of Ruminococcaceae of the KET cows was also different from the CON cows based on the T-test (Fig. 7B). Ruminococcaceae is dominant in the rectum of dairy cows (Fig. 3A). It is also dominant in pigs (Argüello et al., 2018), and plays a protective role in cirrhotic human patients (Argüello et al., 2018). The abundance of Ruminococcaceae remarkably reduced in chronic heart failure human patients compared to the controls at the genus level (Luedde et al., 2017). The same occurrence is seen in the abundance of Ruminococcaceae in dairy cows with ketosis (Fig 7B). This may indicate that Ruminococcaceae may play an essential role in maintaining a healthy host. The proportion of Erysipelotrichaceae-UGG-009 of the KET cows was significantly decreased (Fig. 7B). It has been reported that abundant Erysipelotrichaceae of gut microbiota was related to metabolism syndrome and impaired versus normal glucose metabolism in older adults (Lippert et al., 2017). Long-chained fatty acids may cause an increased abundance of Erysipelotrichaceae during the establishment of the human gut microbiota as has been demonstrated in germ-free mice (Nejrup et al., 2017). Erysipelotrichaceae may metabolise fatty acids, and ketosis may be associated with a decreased amount of Erysipelotrichaceae in the gut. Some Lachnospiraceae can produce butyrate by the butyrate kinase pathway or the butyryl-CoA or acetate CoA transferase pathway (Flint et al., 2015) and ketosis occurred with the increase of blood BHBA level. The result based on T-test displayed a significant increase in the abundance of Lachnospiraceae in the KET compared with the CON groups. It is proposed that Lachnospiraceae may be the main microbial taxa that correlates ketosis. To our knowledge, this is the first comprehensive study with high-throughput analysis of rectal microbiota in dairy cows with and without ketosis. These results indicate a strong influence of the ketosis on the diversity and structure of rectal microbiota.

Conclusions: In the current study, the structure of the rectal microbiota of the ketotic cows was different from that of healthy cows. At phylum level, the percentage of Euryarchaeota of the KET cows was significantly decreased compared with that of the CON cows. At the genus level, the percentages of Ruminococcaceae-UGG-014, Methanobrevibacter, Erysipelotrichaceae-UGG-009,
and \textit{Atopobium} were increased (P<0.05) and the percentage of \textit{Lachnospiraceae} was decreased (P<0.05) in the KET cows compared with that of the CON cows. \textit{Lachnospiraceae} is related to butyrate production, the increased percentage of \textit{Lachnospiraceae} in cow’s rectal content may play an essential in ketosis.

**Animal care:** All the experimental procedures were assessed and approved by the Ethics Committee on Animal Experiments of Guangxi University and the care and use of animals complied with the local law and guidelines on animal experiments (Approval No. GXU2016-006).

**Acknowledgments:** This work was supported financially by the grant given by the National Natural Science Foundation of China (NSFC, Approval number: 31260631, 31660697), and the Innovation Project of Guangxi Graduate Education (No. YCBZZ2018005). Special thanks: thanks a lot to my dear English friend Oliver Timms BSc (Hons) BYSc MRCVS who spent a lot of time helping to polish this article.

**Authors contribution:** YH, YL and BH conceived and designed the study. YH, YH, MMA, HY, PW, PZ, YLD, LH, WS and XZ executed the experiment and acquired the data. YFH and YL interpreted and assay the data and drafted the manuscript. BH and MMA critically revised the manuscript.

**REFERENCES**

Arguello H, Estellé J, Zaldívar-López S, et al., 2018. Early Salmonella typhimurium infection in pigs disrupts Microbiome composition and functionality principally at the ileum mucosa. Sci Reports 8.

Boguszewskatryk M, Szmyczko R, Pietrowska A, et al., 2015. Ileal and cecal microbial population and short-chain fatty acid profile in broiler chickens fed diets supplemented with lignocellulose. Pak Vet J 35:212-16.

Castro-Carrera T, Toral PG, Frutos P, et al., 2014. Rumen bacterial community evaluated by 454 pyrosequencing and terminal restriction fragment length polymorphism analyses in dairy sheep fed marine algae. J Dairy Sci 97:1661-9.

Dinan TG, Stilling RM, Stanton C, et al., 2015. Collective unconscious: How gut microbes shape human behavior. J Psych Res 63:1-9.

Donaldson GP, Lee SM, Mazmanian SK, 2016. Gut biogeography of the bacterial microbiota. Nat Rev Microbiol 14:20-32.

Flint HJ, Duncan SH, Scott KP, et al., 2015. Links between diet, gut microbiota composition and gut metabolism. Proc Nutr Soc 74:13-22.

Gaci N, Borrel G, Tottey W, et al., 2014. Archaea and the human gut: New beginning of an old story. World J Gastroenterol 20:16062-78.

Gagen EF, Padmanabha J, Denman SE, et al., 2015. Hydrogenotrophic culture enrichment reveals rumen Lachnospiraceae and Ruminococccaceae acetogens and hydrogen-responsive Bacteroidetes from pasture-fed cattle. FEMS Microbiol Lett 362.