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Characterization of the gut microbiota in the Bactrian camel

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The gut microbiota of mammals is a complex ecosystem, which is essential for maintaining gut homeostasis and the host's health. The high throughput sequencing allowed us to gain a deeper insight into the bacterial structure and diversity. Bactrian camels may have a unique Gastro-Intestinal Tract (GIT) microbiome because of their distinctive digestive systems, unique eating habits and extreme living conditions. However, our understanding of the microbial communities in the GIT of Bactrian camels remains limited. In order to improve the understanding of the Bactrian camel, we characterized the microbiota of healthy Bactrian camels using high throughput sequencing of the 16S rRNA genes V4 hyper variable regions. Our results showed that, firstly, *Firmicutes* was the predominant phylum in the feces of Inner Mongolian domestic Bactrian camels and Mongolian domestic Bactrian camels, followed by *Verrucomicrobia*, *Bacteroidetes* were abundant. Secondly, several species has specific differences in microbial communities at the genus level, such differences may be related to different eating habits and living conditions and the various camel populations. Thirdly, we describe the bacterial communities from eight different GIT segments (rumen, reticulum, abomasum, duodenum, ileum, jejunum, caecum, colon) and feces, with *Firmicutes*, *Verrucomicrobia* and *Bacteroidetes* predominating. However, there were significant differences in microbial community composition between segments of the GIT. Fourthly, the microbial profile in the large intestine was like that in feces, but feces cannot fully represent the microbial profiles of GITs. The findings provided theoretical basis regarding the gut microbiota of Bactrian camel and may offer new insights to protect this species.

Recent Publications

1. Bhatt V D, Dande S S, Patil N V and Joshi C G (2013) Molecular analysis of the bacterial microbiome in the forestomach fluid from the dromedary camel (*Camelus dromedarius*). *Molecular Biology Reports* 40:3363-3371.
2. Jirimutu, et al. (2012) Genome sequences of wild and domestic Bactrian camels. *Nature Communications* 3:1202
3. Wu H, et al. (2014) Camelid genomes reveal evolution and adaptation to desert environments. *Nature Communications* 5:5188.
4. St-Pierre1 B and Wright A D G (2012) Molecular analysis of methanogenic archaea in the forestomach of the alpaca (*Vicugna pacos*). *BMC Microbiology* 12:1.
5. Ming L, et al. (2017) Comparative analysis of fecal microbial communities in cattle and Bactrian camels. *PloS one* 12:e0173062.

Biography

Jing He has completed her undergraduate degree in Food Science and Engineering from Inner Mongolia Agricultural University in 2014. She is pursuing her Doctorate in Food Science under the supervision of Professor Jirimutu at Inner Mongolia Agricultural University. She is focusing on the application of metagenomics in the gastrointestinal microbiome of camels.

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