

AN ANALYSIS OF THE FORESTOMACH BACTERIAL MICROBIOTA IN THE BACTRIAN CAMEL

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ABSTRACT

The digestive systems of ruminant mammals harbour a complex gut microbiome composed of bacteria and archaea, as well as other microorganisms. These microbes influence the health of the animal and provide the host with nutrients. The digestive system of bactrian camels is unique because omasum is absent and it has three compartments. We utilised 16S rRNA gene sequencing to characterise the temporal variations in the forestomach microbiome of Bactrian camels (N=8). Different forestomach compartments had different communities and Firmicutes (34%-43%), Bacteroidetes (26%-30%) and Verrucomicrobia (7%-11%) were the most abundant taxonomic groups. Study also revealed that the forestomach microbiota may be subject to seasonal variations.

Key words: 16S rRNA, bactrian camel, forestomach microbiota, seasonal changes