

# Analysis of the Intestinal Microbial Diversity of the African Ostrich raised in China

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March 07, 2024

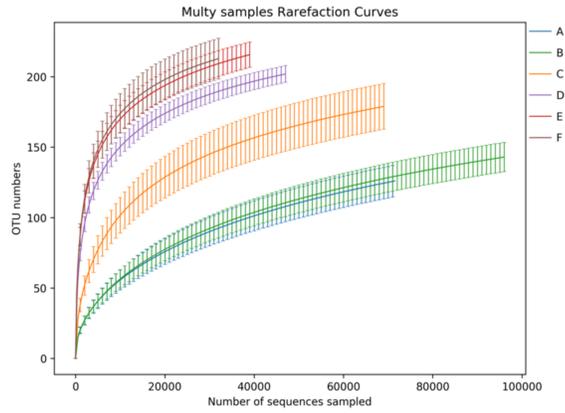
## Abstract

The African ostrich (*Struthio camelus*) is a fast-growing, rough feed-tolerant herbivorous bird. This species has been extensively studied. The aim of this study was to understand the prokaryotic microbial diversity in the intestinal tract of the African ostrich raised in China, and the differences among intestinal segments. To do this, microorganisms in the duodenum, jejunum, ileum, cecum, colon, and rectum were identified and analyzed via 16S rRNA-based macrogenomic sequencing. The microbial abundance and diversity were significantly higher in the cecum, rectum, and especially the colon, than in the duodenum and jejunum. Meanwhile, microbial abundance and diversity in the ileum were between those in the small and large intestines. Proteobacteria and Firmicutes were the most abundant phyla in each segment. Tenericutes and Bacteroidetes were also dominant in the cecum and colon. At the genus level, *Acinetobacter*, *Escherichia-Shigella*, *Pseudomonas*, and *Bacillus* were dominant in the small intestine. In the large intestine, *Acinetobacter*, *Escherichia-Shigella*, *Anaeroplasma*, and *Bacteroides* were dominant. The microflora in each segment differed significantly. Different numbers of microbial groups were responsible for these differences in each segment. Only two main bacterial groups contributed to differences in the duodenum, while 23 different bacterial groups contributed in the colon. The results demonstrated that the intestinal microflora of the African ostrich is complex and diverse, with its composition and abundance differing throughout the system. These findings provide a theoretical basis for further study of intestinal microbial compositions and functions in the African ostrich.

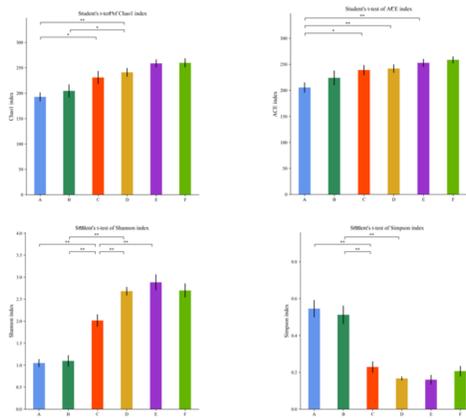
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**Figure. 1**



**Figure. 2**



**Figure. 3**

