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The Association between Gut Microbiome, Sex, Age and Body Condition Scores of Horses in Maiduguri and Its Environs.

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Abstract

The equine gut harbours complex microbial populations which influence physiology, metabolism, nutrition and immune functions, while disruption to the gut microbiota has been linked with conditions such as lameness, diabetes and obesity. Therefore, the present study was conducted to determine the association between microbial dysbiosis, sex, age and body condition scores (BCS) of horses (*Equus equus caballus*) in Maiduguri and its environs. Forty horses were assessed by convenient sampling, while faecal samples were collected and analyzed to determine the microbiomes in the various age groups with variable BSC in stallions and mares. The present study revealed that there was strong and not significant association between the microbial populations in the gut of horses and the various age groups (Chi-Squared test = 11.809; df = 18; P = 0.8570). There were significant (p < 0.0001) differences in the microbiome population in the guts of the horses. There were significant (p < 0.05) differences in the microbiomes in the various body scores. There were significant (P < 0.047) differences in the microbiomes of the mares and stallions. *E. coli* had the highest burden of microbial populations with $30.38 \times 10^3 \pm 1.04 \times 10^3$ in the guts of horses in the study area, while statistically there were no differences in the populations of *Corynebacterium*, *Klebsiella*, *Salmonella*, *Staphylococcus* and *Streptococcus* in the gut of horses in the study area relative to *E. coli*. This study provides information on the nature of bacterial population present in horses in Maiduguri and its Environs. Therefore, further high-throughput characterization of the faecal bacteria microbiome of horses is essential to enable comparison to disease state and thus develop diagnostic tests, prophylactic measures and appropriate treatments.

Key Words: Gut Microbiome, Sex, Age, Body Condition Score, Horses

Introduction

The intestinal tract contains one of the most dense, dynamic and complex bacterial populations (microbiomes) of any environment on the planet. It has been called the '2nd genome' in testament to its size and complexity. In humans, it is believed that the intestinal microbiome contains up to 1000 different species and approximately 10^{12} bacteria/gram of feces (Mayer *et al.* 2014). This is particularly true for herbivores, including the horse were

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