
USE OF PCR-DGGE TO CHARACTERIZE THE DISTRIBUTION OF BACTERIAL POPULATIONS IN FECES OF RETICULATE GIRAFFES (*Giraffa camelopardalis reticulata*), AFRICAN ELEPHANTS (*Loxodonta africana*) AND WHITE RHINOCEROS (*Ceratotherium simum*)

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Abstract

The gastrointestinal microbiota play a vital role in overall health of people and animals by helping break down and digest food, producing vitamins and hormones, training the immune system and preventing pathogenic bacterial overgrowth. Little is known, however, about the ecology of microbiota of large exotic herbivores and basic questions need to be answered. The objectives of this study were to evaluate whether bacterial populations are evenly distributed throughout fecal excretions in three exotic herbivore species and to compare the inter- and intra-species variability of bacterial populations. Fecal samples were collected from reticulated giraffes (*Giraffa camelopardalis reticulata*) (n=6), African elephants (*Loxodonta africana*) (n=7) and white rhinoceros (*Ceratotherium simum*) (n=3) at the Indianapolis Zoo. PCR targeting the 16S rRNA gene was performed followed by denaturing gradient gel electrophoresis (DGGE) to create bacterial community fingerprints for each individual sample. A homogenized sample of an entire bolus (elephants and rhinos) or multiple pellets (giraffes) was compared against five individual samples randomly collected throughout the excretion to evaluate differences in bacterial populations. Pairwise comparisons were made and a cluster analysis performed to evaluate inter- and intraspecies relatedness. The study found that dominant bacterial populations were evenly distributed throughout the fecal excretion in each species, suggesting that a small sample is indeed representative of the entire excretion. This is important to know when collecting samples for microbiologic culture. Differences in microbial communities were observed, with the greatest contributing factor in variability being species, followed by age. One giraffe being treated with antibiotics for a chronic leg infection demonstrated decreased species richness and differed from the other giraffes in the bacterial populations present.

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