

The Power of Poop: Evaluating Gut Microbiome as a Noninvasive Indicator of Animal Health Emma Devereux¹, Dr. Brianna Beechler², Dr. Patricia Conrad¹, Dr. Terra Kelly¹ & Dr. Brian Bird¹



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Question

Monitoring wildlife health in the Kruger National Park (KNP): can gut microbiome provide a noninvasive indicator of herbivore health?

Background

• Assessing wildlife health often relies on capture and sedation of animals – an expensive and often infeasible process. Handling also exposes animals to undue risks such as fractures, capture myopathy and other morbidity or mortality causing events. These challenges underscore the need for a noninvasive strategy for monitoring wildlife health.



- The use of gastrointestinal microbiome analysis is indicated as a potentially viable strategy for noninvasive health monitoring for several reasons:
 - 1) the information required to characterize an animal's gut microbiome can be gathered from fresh feces, which can be obtained easily from most species without handling or exposing the animal to unnecessary risks;
 - 2) recent innovations in metagenomic sequence analysis have reduced the costs of data generation and enabled the characterization of microbiome composition based on a single, taxonomically diagnostic gene (e.g. 16s), making this approach both more cost-effective and feasible;
 - 3) established links between disease status and the gastrointestinal microbiome implicate gut microbiota as a viable potential indicator of animal health (1, 2, 3).
- This project seeks to correlate gut microbial communities with routine health measures to support the use of GI microbiome as an alternative indicator of animal health.

Method

Discussion

- Fecal DNA samples from this project will not be processed and sequenced until the end of September 2018; therefore, microbiome sequencing data is not yet available.
- In the meantime, analyses have focused on describing the sample population (e.g. species, sex and age distribution), as well as evaluating hematological parameters (e.g. hematocrit, total protein, and white blood cell differentials) within and between species groups.
- Body condition score did not prove to be a useful indicator of health in this context due to minimal spread and lack of variance in the data.
- However, hematocrit has been shown to significantly and positively correlate with body condition score in mammals (5). Thus, hematocrit will serve as a proxy for body condition score for the purposes of future analyses. Although these parameters have been previously explored in the literature, understanding the spread of hematological values in our particular sample population was a critical first step towards correlating the diversity, richness and structure of gut microbial communities with traditional, blood-based measures of health in herbivorous host species.



- Feces and blood were collected from all herbivorous animals darted and/or captured by the Veterinary Wildlife Services (VWS) team in the KNP between June 1st and July 18th, 2018. Observations were limited to herbivores as diet
- is known to be a strong predictor of GI microbial community structure (4).
- Body condition scores (1-5), skin condition (i.e. presence of mange), environmental conditions and pregnancy/lactation status were recorded for all captured individuals.
- Hematocrit and total protein were evaluated from blood samples.
- Blood smears were prepared and analyzed under a microscope at the VWS laboratory – total white blood cell count and cell differentials were calculated and recorded.
- DNA was extracted from feces using the MoBio powersoil DNA extraction kit and transported back to Oregon State University for gut microbiome sequencing in the Sharpton Lab (to be completed in Sept). • Hematological data were analyzed using GraphPad Prism 7 software.

Results

• Samples were collected from 99 individuals in the Kruger National



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Park between June 1st and July 18th, 2018.

- Sampled individuals belong to six herbivorous species (Fig 1), including African Buffalo (n=46), Black Rhino (n=6), Elephant (n=1), Impala (n=20), White Rhino (n=24), and Zebra (n=2).
- The majority of sampled individuals are male for all species, except for African Buffalo (Fig 2).
- Hematocrit values were similar across all species for which n>5 blood samples (p=0.5885; Black Rhino=42.67%; Impala=43.91%; White Rhino=42.46%) (Fig 3).
- Total protein varied between species for which n>5 blood samples (p<0.0001; Black Rhino=7.533g/dL; Impala=5.645g/dL; White Rhino=9.492g/dL (Fig 4).
- Total white blood cell count varied between species for which n>5 blood smears (p=0.0002; African Buffalo=14200; Black Rhino=11333; Impala=14545; White Rhino=14400) (Fig 5).
- Lymphocytes were the dominant cell type in African Buffalo and Impala, while neutrophils dominated in both Black and White Rhino.

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