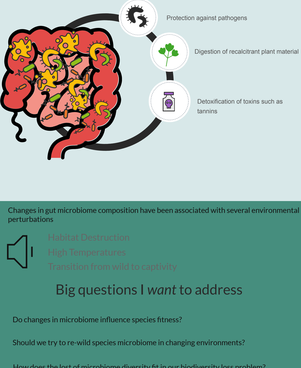
# Ecology and evolution of the gut microbiome of a guild of small mammals

## The gut microbiome provides several functions to its host




Changes in gut microbiome composition have been associated with several environmental perturbations

- Habitat Destruction
- High Temperatures
- Transition from wild to captivity

## Big questions I *want* to address

Do changes in microbiome influence species fitness?

Should we try to re-wild species microbiome in changing environments?

How does the lost of microbiome diversity fit in our biodiversity loss problem?

**Before we can understand the big questions we should address the small ones!**

Someone Smart

## Small questions I **can** address

How are microbiomes assembled across different species?

How does the microbiome changes daily within an individual?

What are general trends in local environment that influences microbiome?

What functions of the microbiome?

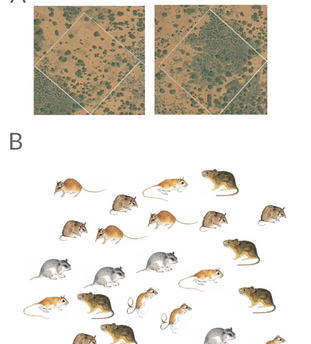
What species of bacteria are constantly associated with an individuals microbiome?

What do we know? Generally speaking, phylogeny, diet and environment influence the gut microbiome


Comparative studies of multiple animals from multiple environments have been useful for identifying factors that contribute to microbiome differences among species . For example, prior studies identified environmental, phylogenetic, and dietary differences among factors that generate dissimilarity in the gut microbiome composition. Yet these prior studies have almost exclusively evaluated the influence of these factors on the microbiome in the context of animals that are kept in captivity or that live in ecologically distinct environment, potentially confounding the results.

## The goal of my thesis is to evaluate each one of these factors influence the gut microbiome of a guild of co-occur small mammals

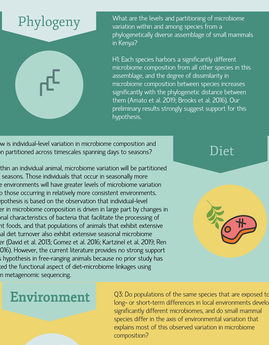
My work will characterize the types of bacteria that occur in the gut microbiome of multiple wild small mammals that live in a Kenyan savanna ecosystem. The environments they live in and the foods that they have access to have been experimentally manipulated in a decades-long experimental manipulation of the environment. This experiment has excluded large mammals such as elephants and giraffes from large plots of land at Mpala Research Center in Kenya, thereby causing an increase in the abundance and diversity of small mammals and small mammal foods (below).



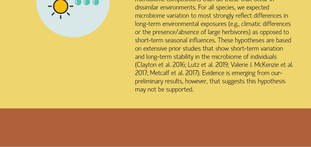
The exclusion of large mammals results in an increased abundance of plants (A) and a speciose guild of small mammals (B).

A


B



## These exclusion plots are located across a 20 km rainfall gradient




# Questions and Hypothesis

## Phylogeny

What are the levels and partitioning of microbiome variation within and among species from a phylogenetically diverse assemblage of small mammals in Kenya?

H1: Each species harbors a significantly different microbiome composition from all other species in this assemblage, and the degree of dissimilarity in microbiome composition between species increases significantly with the phylogenetic distance between them (Amato et al. 2013; Brooks et al. 2016). Our preliminary results strongly suggest support for this hypothesis.

## Diet

Q2: How is individual-level variation in microbiome composition and function partitioned across timescales spanning days to seasons?

H2: Within an individual animal, microbiome variation will be partitioned among seasons. Those individuals that occur in seasonally more variable environments will have greater levels of microbiome variation than do those occurring in relatively more consistent environments. This hypothesis is based on the observation that individual-level turnover in microbiome composition is driven in large part by changes in functional characteristics of bacteria that facilitate the processing of different foods, and that populations of animals that exhibit extensive seasonal diet turnover also exhibit extensive seasonal microbiome turnover (David et al. 2013; Gomez et al. 2016; Kartzinel et al. 2019; Ren et al. 2016). However, the current literature provides no strong support for this hypothesis in free-ranging animals because no prior study has evaluated the functional aspect of diet-microbiome linkages using shotgun metagenomic sequencing.

## Environment

Q3: Do populations of the same species that are exposed to long- or short-term differences in local environments develop significantly different microbiomes, and do small mammal species differ in the axes of environmental variation that explains most of this observed variation in microbiome composition?

H3: Populations of the same species that experience similar local environmental conditions will have more similar microbiome compositions than do those that occur in dissimilar environments. For all species, we expected microbiome variation to most strongly reflect differences in long-term environmental exposures (e.g., climatic differences or the presence/absence of large herbivores) as opposed to short-term seasonal influences. These hypotheses are based on extensive prior studies that show short-term variation and long-term stability in the microbiome of individuals (Clayton et al. 2016; Lutz et al. 2019; Valene I. McKenzie et al. 2017; McCall et al. 2017). Evidence is emerging from our preliminary results, however, that suggests this hypothesis may not be supported.