Gut microbiome diversity in wild Kinda baboons using a shotgun metagenomic approach.

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Emerging genomic evidence underscores the complex interplay between host environment, social phenotype, and gut microbiome in humans. However, we know little about how these interactions affect the health and fitness of wild primates threatened by

anthropogenic pressures. Here, we use shotgun sequencing to examine the gut microbiome in Kinda baboons *(Papio kindae)* as a first step to ultimately investigate connections between microbiome, social behavior, and social structure. We collected fecal samples from wild habituated baboons (37 males, 44 females) in Kasanka National Park, Zambia. We predicted that microbiome diversity will be higher in adult females to meet increased metabolic demands of reproduction, and will change seasonally in response to dietary shifts. Permanovas revealed no significant effects of sex and season on taxonomic diversity and functional gene family abundance measures of microbes. Multivariable association employing linear models showed that functional pathways (eg: nucleotide, L-histidine synthesis, ribonucleoside degradation, pyruvate fermentation) were not affected by sex, but by seasons. We speculate that enduring social connections between adult males and females that are emblematic of Kinda baboon social behavior facilitate microbial transmission thereby reducing sex differences, while dietary shifts leading to functional pathway enrichment allow baboons to adapt to seasonal challenges. Future research will test how individual personality traits and group social network characteristics affect their microbiome and overall health and fitness. Supported by NSF (BCS-2141627) & UMass Amherst.