FECAL GLUCOCORTICOID METABOLITES AND THEIR ASSOCIATION WITH FECAL MICROBIOME IN WESTERN LOWLAND GORILLAS (*GORILLA GORILLA GORILLA*) HOUSED IN US ZOOS

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Abstract

Understanding and mediating health conditions in endangered species under human care is important to optimize welfare and *ex-situ* breeding, as animals experience novel stressors inherent to a captive environment. Some species are able to adapt to their new environment with little consequence, while others respond with behavioral changes and experience health concerns. Western lowland gorillas (*Gorilla gorilla gorilla*) under managed care have historically had moderate to high prevalence of cardiovascular disease, potential insulin resistance, obesity, and various other health concerns that may be linked to captive diet composition and sedentary lifestyles (Lowenstine *et al*., 2016). The gut microbiome of animals is also impacted by management under human care. Animals under human care often have less diverse gut microbiomes than their wild counterparts. Research in humans and model organisms has shown that disruption to the gut microbiome can affect stress, a range of health issues, and has been shown to be important to immune health, metabolism, and hormone regulation. In turn, stress can have an effect on the gastrointestinal tract.

Fecal glucocorticoid metabolites (fGCM) produced by the adrenal cortex function in metabolizing carbohydrates, proteins, and fats, and induce glucose synthesis. It is also often used as a measure of chronic physiological stress in wildlife. Thus, studying the gut microbiome in conjunction with fGCM can provide additional insight needed to help address the welfare and health concerns of gorillas in captivity and contributes to the individualized care of western lowland gorillas under human care. By leveraging an existing fecal sample set for 10 western lowland gorillas housed in three US zoos with existing microbiome data available (Eshweiler *et al*., 2021), this project aimed to measure fGCM and determine associations among fGCM concentrations, age, sex, and stressful life events (*e.g.* breeding, veterinary interventions) with shifts in gut microbiome diversity and composition over a 7-month collection period.

A subset (n = 125) of the original samples (n = 246) was assayed for fGCM. Preliminary analyses focused on assessing gut microbiome diversity using cortisol measurement groups to assess any trends prevalent in the data. These results indicated that, for 6 of the 10 gorillas surveyed, increased levels of cortisol were associated with decreased alpha diversity levels (assessed using Shannon group significance). This trend is significant (P = 0.0455) for one gorilla. Additionally, analysis of alpha diversity by institution showed a similar trend of decreased diversity with increased cortisol, with one institution showing a significant decrease in alpha diversity between specific cortisol groups. These preliminary results indicate a trend of microbiome diversity loss in certain individuals and institutions which will be pursued further. Future directions for this investigation include implementation of TITAN (Threshold Indicator Taxa Analysis) to identify relationships between microbiota and specific fGCM measurements and PERMANOVA analysis of beta diversity.

Literature Cited

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