

49 - Giant and red pandas utilize distinct microbial communities for their bamboo diet degradation

Candace L Williams¹, clw224@msstate.edu, Kimberly A Dill-McFarland², Darrell L Sparks^{1,3}, Andrew J Kouba⁴, Scott T Willard¹, Garret Suen², Ashli E Brown^{1,3}. (1) Department of Biochemistry, Molecular Biology, Entomology, and Plant Pathology, Mississippi State University, Mississippi State, MS 39762, United States, (2) Department of Bacteriology, University of Wisconsin-Madison, Madison, Wisconsin 53706, United States, (3) Mississippi State Chemical Laboratory, Mississippi State, MS 39762, United States, (4) Department of Research and Conservation, Memphis Zoological Society, Memphis, TN 38112, United States

Both giant pandas (*Ailuropoda melanoleuca*) and red pandas (*Ailurus fulgens*) are taxonomically classified and physiologically similar to a carnivore but consume almost an exclusively bamboo diet. Pandas have co-evolved to their bamboo diet through the development of a pseudo-thumb, an enhanced jaw structure, and a unique diet selection behavior. However, neither panda has adapted to a more herbivore-like gastrointestinal tract (GIT). Within a typical herbivores' GIT, microbiota play a major role in the digestion of its plant-based diet as well as host health and immunity. Therefore, the GIT microbiome of these uniquely herbivorous carnivores is of interest. Here, we examine the GIT bacterial microbiota of two adult giant pandas and two adult red pandas using next-generation 16S pyrosequencing of fecal samples. On average, the fecal communities of both giant and red pandas were dominated by the phylum Firmicutes (99 % and 98 %, respectively) with lesser contributions by the Proteobacteria (0.87 % and 1.3 %, respectively). However, distinct clusters in panda GIT microbial communities were found using both the weighted and unweighted UniFrac metric three-dimensional principle coordinate analysis, indicating that microbial communities differ with respect to panda species. The Erysipelotrichaceae family (95 %) dominated the giant panda GIT microbiome, and the *Clostridium* genus (75 %) dominated the red panda. Both taxonomic groups are associated with high fiber diets, and the genus *Clostridium*, in particular, is typically associated with fiber degradation. These data indicate that each panda species utilizes a distinct microbial community to undergo fiber degradation. Currently, analyses are underway to further characterize these microbial communities and determine the degradation efficiency of each species GIT microbial community.

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