

Giant Panda Microbiome Ill-Suited for Bamboo Diet, Study Finds

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NEW YORK (GenomeWeb) – The gut microbiome of the giant panda more closely resembles that of a carnivore than what a bamboo-eating herbivore would be expected to have, according to researchers from Shanghai Jiao Tong University and the Chengdu Research Base of Giant Panda Breeding in China.

A team led by Chengdu's Zhihe Zhang examined the fecal microbiomes of 45 captive pandas, representing adults, juveniles, and cubs, over the course of a year, and compared them to those from other animals, including herbivores, omnivores, and carnivores. The giant panda microbiome, [they reported in *mBio* today](#), typically exhibited low microbial diversity and was more similar to that of omnivorous or carnivorous bears. Further, it also typically lacked known cellulose-degrading bacteria.

"This result is unexpected and quite interesting because it implies the giant panda's gut microbiota may not have well adapted to its unique diet and places pandas at an evolutionary dilemma," coauthor Xiaoyan Pang, an associate professor at Shanghai Jiao Tong University, said in a statement.

Giant pandas evolved from omnivorous bears, and their ancestors began to exclusively eat bamboo between 2 million and 2.4 million years ago. This switch was likely in conjunction with a number of genomic mutations, including the loss of the umami taste receptor gene. While the researchers noted that the giant panda has morphological features like strong jaws, teeth, and an enlarged radial sesamoid that help it eat bamboo, the giant panda has retained a simple stomach, unlike the elongated ones common to herbivores that increase gut retention time and digestion of plant polysaccharides.

Instead, the microbial residents of the panda gut have been thought to enable the breakdown of the plant matter.

Zhang, Pang, and their colleagues collected 121 samples of giant panda feces from 24 adults, 16 juveniles, and five unweaned cubs — all captive — during three different seasons of one year. Through

barcoded pyrosequencing of bacterial 16S rRNA genes, they generated more than 97,000 reads, which, after filtering, were grouped into 781 operational taxonomic units.

The vast majority of bacteria in the samples belonged to nine phyla and 109 genera, the researchers found, with the most prominent phyla being Firmicutes and Proteobacteria and the most prominent genus being *Escherichia/Shigella*.

However, the amount of these bacteria present in the samples varied wildly: the researchers noted that *Escherichia/Shigella* was the only genus they uncovered in all adult, juvenile, and cub microbiomes, but its abundance ranged from 0.6 percent to 97.1 percent.

The alpha diversity of the adult and juvenile samples was similar to each other, but varied across the seasons. Seven of the 10 dominant genera, the researchers found, fluctuated over the course of the year. For instance, *Klebsiella* was enriched during the summer, but not in the spring or late autumn, while *Streptococcus* and *Clostridium* were more abundant during the late autumn.

There was also a dramatic shift in intra-individual variation between spring and summer to late fall. For each individual, the researchers noted the gut microbiota structure became increasingly dissimilar over time. This change in diversity, they noted, appeared to be linked to what part of the bamboo plant was available to dine on.

The cubs, meanwhile, harbored microbiomes in which *Lactobacillus* numbers exceeded *Escherichia/Shigella* numbers.

To see how these giant panda microbiomes compared to those of other mammals, the researchers combined their dataset with a previously gathered 16S rRNA gene clone library that included eight captive giant pandas and seven wild giant pandas along with 128 other animals, representing nearly 60 species and a dozen orders.

As compared to the other herbivores, omnivores, and carnivores, the giant panda's microbiome had significantly lower alpha diversity. A diverse microbiome, the researchers noted, is typically thought to be beneficial.

The giant panda microbiome was fully differentiated, the researchers added, from non-panda herbivores, but clustered near those of red panda, bears, and a few other carnivores. They added that this indicated that giant pandas have a microbiome composition that's distinct from other herbivores.

By comparing the giant panda microbiome to another 16S rRNA dataset composed of fecal samples from Asian black bears, Siberian tigers, chimpanzees, golden snub-nosed monkeys, hoolock gibbons, and blue peafowl, the researchers found that the giant panda microbiome shared some similarities with the omnivorous bear and carnivorous tiger samples.

Notably, it lacked bacteria that are present in many herbivores and are involved in cellulose digestion and utilization. While a few panda fecal samples contained bacteria that could be related to cellulose-digesting strains, none of these putatively cellulolytic lineages were shared by a majority of pandas.

The giant panda microbiome, then, likely doesn't aid in bamboo digestion, the researchers said. They also speculated that this might put the panda at a higher risk of extinction.

"Unlike other mammalian species that have evolved gut microbiota (and also digestive system

anatomies) optimized for their specific diets, the aberrant coevolution of the giant panda, its dietary preferences, and its gut microbiota remains enigmatic," the researchers concluded.

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