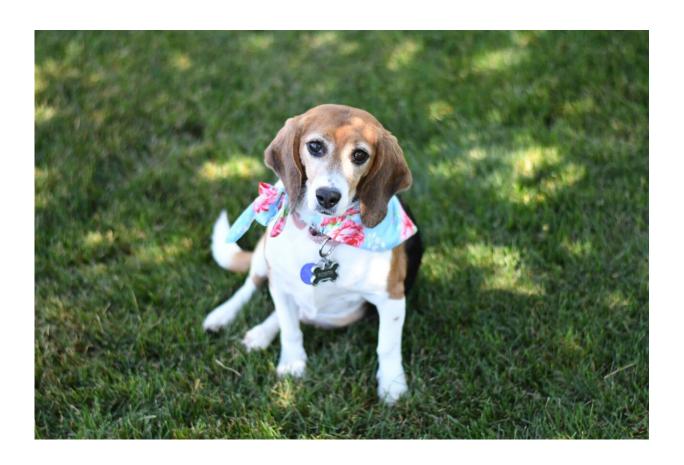


New study investigates the microbiomes of dogs around the world

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Most studies have looked at the microbiome in dogs in veterinary centers, which lead a very different life from dogs that don't live as pets. Credit: Kelly Swanson

Although the microbiome—the collection of all microbes that live in the body—in the fecal matter of dogs has been investigated extensively,



those studies have mostly been limited to domesticated dogs. In a new study, researchers have sampled the fecal microbiomes across diverse geographical populations to better understand what they look like around the world.

"A lot of the studies look at how different diets affect dog microbiomes. Although they are extensive, they work with dogs in veterinary centers, which lead a very different life from dogs that don't live as pets," said Karthik Yarlagadda, a former graduate student in the Malhi group. "It's similar to how studies on the microbiomes of humans have been focused on people who live in cities and eat processed foods."

To sample a diverse range of microbiomes, the researchers collected <u>fecal matter</u> from three geographical locations: pets from South Africa, stray dogs and shelter dogs in India, and dogs from a <u>rural village</u> in Laos. The samples were collected on FTA cards, which contain chemicals that preserve the DNA so it can be sequenced and analyzed later.

"Most of our previous studies have looked at animals that come into a vet clinic or are housed in a research facility; they are vaccinated and eat food that is processed," said Kelly Swanson, a professor of animal and nutritional sciences. "But that is different from animals, like the ones in Laos, that live outside and have a variety of environmental exposures. By carrying out these studies, we can learn what is considered "normal" for different populations around the world."

In each location, the dogs had different diets. The <u>shelter dogs</u> were fed rice, lentils, yogurt, and dog food; the stray dogs likely scavenged human leftovers; the village dogs consumed local agricultural products, including maize, corn, bamboo, sticky rice, and fish from nearby rivers; and the pet dogs were likely fed commercial dog food.



Interestingly, although the microbiomes among the different populations differed, functionally they were the same. "It was cool to see that you can have different microbiomes, but they all fulfill the same metabolic function. For example, dogs that were consuming dairy in the South African and Indian populations had different Lactobacillus species that were probably involved in the same pathway," Yarlagadda said.

In addition to comparing the microbiomes of dogs from different geographical locations, the researchers wanted to contrast these samples with ancient microbiomes, obtained from fossilized dog feces. Presumably, dogs that live in an outdoor environment and have a mixed diet will have similar microbiomes to that of ancient dogs, providing insight into how industrialization affects the fecal microbes.

The researchers indeed observed that the microbiomes from ancient dogs closely resembled the non-US populations, potentially due to overlapping diets and more environmental exposures. Further work will elucidate whether the human microbiome diversity in non-industrialized settings will also follow similar trends.

"Using sequencing techniques from a previous study [in *Scientific Reports*], we want to find more data on ancient microbiomes in various dog species," said Ripan Malhi (GNDP/GSP/IGOH), a professor of anthropology. "Since we know what their diet consisted of, we can make more comparisons to see how <u>diet</u> influences the <u>microbiome</u>."

The new study "Geographically diverse canid samples provides novel insights into pre-industrial microbiomes" was published in *Proceedings* of the Royal Society B: Biological Sciences.

More information: K. Yarlagadda et al, Geographically diverse canid sampling provides novel insights into pre-industrial microbiomes, *Proceedings of the Royal Society B: Biological Sciences* (2022). DOI:



10.1098/rspb.2022.0052

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