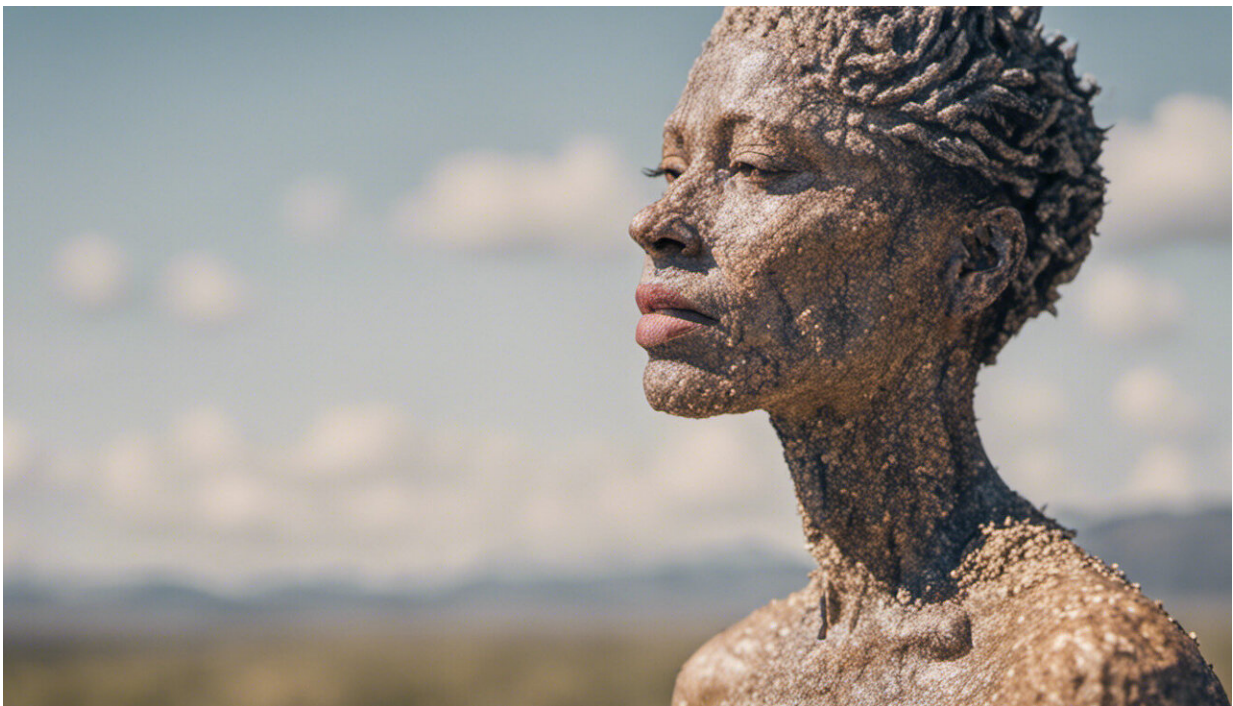


Understanding the microbiome of people transitioning from traditional to Westernized lifestyles

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Credit: AI-generated image ([disclaimer](#))

Ami Bhatt, MD, an associate professor of hematology and of genetics, conducts research on the gut microbiome and infectious-disease transmission. She is a strong advocate of empowering and crediting scientists from diverse groups and a proponent of conducting research on

diverse populations. In a study published Feb. 22 in *Nature Communications*, her group teamed up with South African collaborators to analyze microbiomes in the guts of 169 women from two different South African locales.

The populations represent distinct stages in the transition from traditional to industrialized lifestyles. Stanford Medicine science writer Bruce Goldman asked Bhatt about what motivated her to conduct the study, and about its findings and implications.

1. What did you undertake in this study?

Bhatt: With my co-senior author, Scott Hazelhurst, Ph.D., a professor of electrical and information engineering at the University of the Witwatersrand in Johannesburg, South Africa, and several gifted trainees, we've developed a strong research collaborative spanning language, cultures, countries, spicy-food tolerance and 10,532 miles.

For this study, we collected stool samples from women living in Soweto, an urban township in the Johannesburg area, and Bushbuckridge, a rural, agricultural area near Kruger National Park in eastern South Africa, and compared their microbiome profiles. Health- and demographic-surveillance researchers had been studying these two communities for decades. They'd already collected vast amounts of incredibly useful data: where individuals in these communities live, where they were born, what types of food they eat, details about their housing and sanitation, and who their neighbors are. It seemed natural to build on their impressive research infrastructure for our work. Our very-high-resolution DNA sequencing methods enabled us to analyze our study participants' microbiomes in a much more thorough way than has been possible in the past.

2. Why was it important to do this?

Bhatt: The [human genome](#) of even the most unrelated people on earth is more than 99.9% identical. But the gut microbiomes of two adult identical twins are more different than they are similar, because gut microbiome is strongly affected by diet, environmental exposures and other lifestyle factors.

Thousands of microbiome studies have been published demonstrating relationships between [gut microbiome](#) composition and disease. Although more than 80% of the world's population lives in low- and middle-income countries, almost all previous studies have been carried out in a handful of wealthy countries.

And the little research that exists on people in low- and middle-income countries typically focuses on people who have what most would call "extreme" lifestyles, such as very rural subsistence agriculturalists.

So, we know a lot about the microbiomes of Americans, Europeans, Chinese and Japanese people, and a bit about traditional hunter-gatherer populations, but next to nothing about people who live in huge cities like Nairobi, Kolkata and São Paulo as well as in rural regions scattered throughout the world, all of whom are transitioning from a traditional to a Westernized lifestyle. We sought to understand how their residents' microbiomes change as their lifestyles do.

Ironically, most of the research on nonindustrialized populations hasn't focused on medical issues that mattered to the health of these communities, including obesity.

3. Why did you focus exclusively on women in your screening?

Bhatt: In most [middle-income countries](#), obesity disproportionately affects women. In South Africa, for example, more than 65% of women are overweight or obese. By contrast, about 30% of South African men, who typically have more intensely calorie-burning jobs than South African women do, are overweight or obese. The proportion of women who are obese in South Africa has nearly doubled, to 40%, since 2000.

Over the past three or four decades, as tens of countries around the globe have become industrialized, people have become more sedentary. In addition, many countries, like South Africa and much of the rest of Africa, are transitioning from diets that are high in vegetables and fruit and low in meat and fat to highly processed diets that are rich in meat protein and fat and low in fiber. The prevalence of processed foods has contributed to the worrying increase in obesity in these places.

We anticipate that as obesity increases, disability and death due to health problems such as diabetes and heart disease will disproportionately increase for women in this region. It seems worthwhile to figure out how the microbiome might be contributing to the obesity epidemic.

Our community advisory group—a team of men and women of all ages from several of the villages that participated in our study—also advised us that women would be more interested in and receptive to our study. They were keen that we focus research on women's health, given the importance of women to the family structure.

4. Can you recount a few of the things you found out?

Bhatt: *Prevotella*, a bacterial organism that thrives on fiber, turned out to be abundant in individuals from both Soweto and Bushbuckridge. This is surprising, as many microbiome studies suggest that fiber consumption, which tracks with increased *Prevotella* abundance, is inversely correlated

to body mass. And women living in urban areas tend to be obese or overweight compared with people living in more rural settings. So, we expected to see a corresponding difference in *Prevotella* abundance between the groups. We don't yet know the reasons for the similarity.

We also found more antibiotic-resistance genes in people from Soweto than in Bushbuckridge residents. This could be a result of increased exposure to antibiotics—for example, through medications, meats from animals that were treated with antibiotics to increase their weight, or other environmental exposure.

Curiously, there was more human DNA, as distinct from microbial DNA, in the material extracted from the Soweto group's samples compared with the Bushbuckridge group. While this finding could reflect differences in how those samples were stored or in instructions initially given to patients, for example, it may be a true biological difference. If so, it might be a result of inflammation in the gut, which can lead to a sloughing off of gut epithelial cells or the presence of inflammatory white blood cells in the stool. So, more human DNA in the Soweto versus Bushbuckridge samples could mean individuals from Soweto had more inflammation, possibly related to their more Westernized lifestyle.

5. How might studies such as this one help the globe's transitional populations?

Bhatt: Here's one possible application: Extensive studies demonstrate that vaccines developed for and tested in high-income regions often underperform when they're administered in less-industrialized, lower-income regions. This may be, in part, because of differences in the [microbiome](#) composition of the recipients.

Individuals' immune systems have been routinely "trained" to be tolerant to their bacterial symbionts, and those leading urban, industrial lifestyles have less-robust gut microbiota. Because they aren't exposed to a lot of different bacteria, their immune systems aren't trained to be tolerant of a lot of different bacteria. When they're exposed to a new microbe or microbial component through a vaccine, they mount an aggressive immune response because they recognize some component of the vaccine as foreign.

By contrast, in an individual who has a more diverse microbiota, the [immune system](#) may be tolerant to many more microbial components. That person's immune system may be less likely to recognize a microbial organism or a component a new vaccine contains as foreign, because it's similar to something the person's immune system has become tolerant to.

One way to improve vaccine responsiveness in traditional or transitional populations may be to prepare people's gut microbiota prior to giving them a vaccine. We don't have clear guidance on how to do this, but perhaps future research will inform us. Who knows? Maybe exposure to specific foods, such as fermented foods; probiotics; or even narrow-spectrum antibiotics may help prime the immune system to be more responsive to specific vaccines.

More information: Fiona B. Tamburini et al, Short- and long-read metagenomics of urban and rural South African gut microbiomes reveal a transitional composition and undescribed taxa, *Nature Communications* (2022). [DOI: 10.1038/s41467-021-27917-x](https://doi.org/10.1038/s41467-021-27917-x)

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