

Long distance travelers likely contributing to antibiotic resistance's spread

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Swedish exchange students who studied in India and in central Africa returned from their sojourns with an increased diversity of antibiotic resistance genes in their gut microbiomes. The research is published 10 August in *Antimicrobial Agents and Chemotherapy*, a journal of the American Society for Microbiology.

In the study, the investigators found a 2.6-fold increase in genes encoding resistance to sulfonamide, a 7.7-fold increase in trimethoprim [resistance genes](#), and a 2.6-fold increase in resistance to beta-lactams, all of this without any exposure to [antibiotics](#) among the 35 exchange [students](#). These resistance genes were not particularly abundant in the students prior to their travels, but the increases are nonetheless quite significant.

The germ of the research was concern about the burgeoning increase in [antibiotic resistance](#). "I am a physician specializing in infectious diseases, and I have seen antibiotics that I could safely rely on ten years ago being unable to cure my patients," said principal investigator Anders Johansson, MD, PhD, Chief, Infection Control, Umeå University and the County Council of Västerbotten, Sweden.

However, Johansson also questioned the conventional wisdom that overuse of antibiotics was entirely responsible for the surge in resistance, despite the fact that overuse is a huge problem. "Currently, I head an [infection control](#) department, and from this position it is very evident that resistance is no longer generated primarily in the hospital," he

explained. Instead, patients bring bacteria carrying resistance genes into the hospital as part of their own microbial communities, he said. "We hypothesized that the gut microbiome of humans serves as a vehicle for moving many different resistance genes very large distances, even in the absence of [antibiotic treatment](#)."

And in fact, the increases the investigators observed in abundance and diversity of resistance genes occurred despite the fact that none of the students took antibiotics either before or during travel. The increase seen in resistance genes could have resulted from ingesting food containing resistant bacteria, or from contaminated water, the investigators write. Providing further support for the hypothesis that resistance genes increased during travel, genes for extended spectrum beta-lactamase, which dismembers penicillin and related antibiotics, was present in just one of the 35 students prior to travel, but in 12 students after they returned to Sweden.

Collecting samples of resistance genes was simple. "We asked students going abroad on exchange programs to provide a sample of their feces before and after traveling," said Johansson. But the study was different from previous studies of this issue in using metagenomics sequencing, a modern method. That enabled the investigators to sample the entire microbiome of each student, and to sequence every resistance gene therein, rather than focusing on resistance genes in those few bacterial species that grow well on culture plates.

"Our results spotlight that to reduce antibiotic resistance we need to minimize dispersal rates from the healthcare system, and importantly, at the societal level," said Johansson. Suppressing further spread after travelers return to their home countries is crucial, and depends, he added, upon having well-informed citizens and a well-functioning public health system.

More information: The article can be found online here:
[emessaging.vertexcommunication ... 2AD1A840E5752572FD:r](https://emessaging.vertexcommunication.com/2AD1A840E5752572FD:r)

Provided by American Society for Microbiology

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