

Global South health care practices contribute to spread of antimicrobial resistance across the world, study suggests

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Research assistants setting up a stool sample collection point in Pakistan. Credit: Tamim Khawaja

Many bacteria resistant to multiple antibiotics originate in Pakistan and other parts of the Indian subcontinent. Infections caused by these

bacteria are challenging to treat; longer treatment with broad-spectrum antibiotics is required and despite this, mortality is increased in those infected with multiresistant bacteria.

A [study published](#) in *Nature Communications* sheds light on the prevalence of antimicrobial resistance in the Pakistani population. The multidisciplinary study conducted between the University of Helsinki and the Cambridge-based Wellcome Sanger Institute also investigated the short-term effects of antibiotic use on the occurrence of resistant bacteria in individual patients.

"Travelers returning from the Indian subcontinent face the highest risk of carrying multi-resistant bacteria. To understand the global emergence of resistance, it is essential to explore the [resistant strains](#) spreading in these high-risk regions," says Anu Kantele, Professor of Infectious Diseases at the University of Helsinki and Senior Medical Officer at Helsinki University Hospital.

Genes in the entire bacterial culture were identified

Researchers took rectal swab samples from roughly a thousand patients who had an appointment at a small hospital in the Lahore metropolitan area. Approximately half the patients provided control samples after a one-month monitoring period.

The researchers used the samples to explore the impact of antibiotic use on *Escherichia coli* bacteria carried by people. Samples were also collected from healthy volunteers across the Punjab, Pakistan's most populated province.

Infectious diseases physician Tamim Khawaja spent four months in Pakistan collecting samples from locals. These were cultivated on-site at a local laboratory, and the bacterial cultures were frozen and delivered to

Finland.

The DNA of the cultures was sequenced using a new deep sequencing method in cooperation with the Wellcome Sanger Institute. The analysis was conducted using new methods developed by Tommi Mäklin, Postdoctoral Researcher at the University of Helsinki, with which all information contained by DNA could be used accurately. As a result, the [research consortium](#) was able to identify diversity in E. coli bacteria, both in individuals and at the level of the population.

"Thanks to the better scalability of the latest sequencing technology and the methods developed by my team, we have opened a different perspective on research on the evolutionary dynamics of bacteria and resistance. I believe that this approach will help us achieve several breakthroughs in the next few years," says Professor Jukka Corander.

The study showed that the prevalence of the E. coli bacterial strains found in Pakistan displayed significant variation, even in samples collected from a single individual. The researchers also observed that many bacterial strains common in Europe could not compete with local strains in Pakistan, even though many can be found on both continents.

"For example, ST58, an E. coli strain common in Pakistan, has caused serious infections in countries with a high standard of living. In western countries, asymptomatic carriers of this strain are rare, but in Pakistan, ST58 was the third most common type of E. coli colonizing people. Then again, certain E. coli strains that cause [urinary tract infections](#) and are carried asymptotically by healthy people in [western countries](#) were rare in Pakistan, possibly due to the high antibiotic selective pressure," Mäklin says.

No antibiotics just in case

Some of the E. coli bacteria found in Pakistan were genetically close to strains sequenced previously in Norway.

"This is highly representative of how bacteria travel from one continent to the next as quickly as people," says Kantele.

"Reducing unnecessary antibiotic use in Western countries isn't enough; it's in everyone's best interest to help [poorer countries](#) use antibiotics more wisely. During our research, we realized that physicians often have less than a minute per patient, leading to the frequent prescription of [broad-spectrum antibiotics](#) just in case. In our health care crisis, we often forget that the crisis is far greater in poorer countries and its impact reaches us," says Khawaja.

The study is part of his doctoral dissertation.

More information: Tamim Khawaja et al, Deep sequencing of Escherichia coli exposes colonisation diversity and impact of antibiotics in Punjab, Pakistan, *Nature Communications* (2024). [DOI: 10.1038/s41467-024-49591-5](#)

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