

Human, soil bacteria swap antibiotic-resistance genes: study

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Soil bacteria and bacteria that cause human diseases have recently swapped at least seven antibiotic-resistance genes, researchers at Washington University School of Medicine in St. Louis report Aug. 31 in *Science*.

According to the scientists, more studies are needed to determine how widespread this sharing is and to what extent it makes disease-causing pathogens harder to control.

"It is commonplace for antibiotics to make their way into the environment," says first author Kevin Forsberg, a graduate student. "Our results suggest that this may enhance [drug resistance](#) in soil bacteria in ways that could one day be shared with bacteria that cause human disease."

Among the questions still to be answered: Did the genes pass from soil bacteria to [human pathogens](#) or vice versa? And are the genes just the tip of a vast reservoir of shared resistance? Or did some combination of luck and a new technique for studying genes across entire bacterial communities lead the scientists to discover the shared resistance genes?

Humans only mix their genes when they produce offspring, but bacteria regularly exchange genes throughout their lifecycles. This ability is an important contributor to the rapid pace of bacterial evolution. When a [bacterial strain](#) develops a new way to beat antibiotics, it can share the strategy not only with its [descendants](#) but also with other bacteria.

Earlier studies by other scientists have identified numerous resistance genes in [strains](#) of soil bacteria. However, unlike the seven genes described in this report, the earlier genes were dissimilar to their analogs in disease-causing bacteria, implying that they had crossed between the [bacterial communities](#) a long time ago.

Most of the antibiotics used to fight illness today originated from the soil. Bacteria use the antibiotics, in part, as weapons to compete with each other for resources and survival. Scientists have long acknowledged that gives [environmental bacteria](#) an evolutionary incentive to find ways to beat antibiotics.

"We wanted to try to get a broader sense of how often and extensively antibiotic-resistance genes are shared between environmental bacteria and pathogens," says senior author Gautam Dantas, PhD, assistant professor of pathology and immunology.

The researchers isolated bacteria from soil samples taken at various U.S. locations. The bacteria's DNA was broken into small chunks and randomly inserted into a strain of *Escherichia coli* that is vulnerable to antibiotics. Scientists treated the altered *E. coli* with multiple antibiotics.

"We knew that any *E. coli* that continued to grow after these treatments had picked up a gene from the soil bacteria that was helping it fight the antibiotics," Forsberg says.

Scientists took the DNA from soil bacteria out of the surviving *E. coli* and prepared it for high-throughput sequencing. Dantas' laboratory has developed techniques that make it possible to simultaneously sequence and analyze thousands of chunks of DNA from many diverse microorganisms. The DNA can be selected for a single function, such as antibiotic resistance.

When the scientists compared antibiotic-resistance genes found in the soil bacteria to disease-causing bacteria, they were surprised to find some genes were identical not only in the sections of the genes that code for proteins but also in nearby non-coding sections that help regulate the genes' activities.

Since bacteria have such large population sizes and rapid reproduction times, their DNA normally accumulates mutations and other alterations much more quickly than the DNA of humans. The lack of changes in the resistance genes identified in the study suggests that the transfers of the genes must have occurred fairly recently, according to Dantas.

In some [soil bacteria](#), the genes are present in clusters that make the bacteria resistant to multiple classes of antibiotics, including forms of penicillin, sulfonamide and tetracycline.

"I suspect the soil is not a teeming reservoir of [resistance genes](#)," Dantas says. "But if factory farms or medical clinics continue to release [antibiotics](#) into the environment, it may enrich that reservoir, potentially making resistance [genes](#) more accessible to infectious bacteria."

More information: Forsberg KJ, Reyes A, Wang B, Selleck EM, Somer MOA, Dantas G. The shared antibiotic resistome of soil bacteria and human pathogens. *Science*, Aug. 31, 2012.

Provided by Washington University School of Medicine

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