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Soil bacteria may provide clues to curbing antibiotic resistance

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Researchers led by Gautam Dantas have found evidence that soil bacteria do not share drug resistance genes as often as infectious bacteria. Credit: Pablo Tsukayama

Drug-resistant bacteria annually sicken 2 million Americans and kill at least 23,000. A driving force behind this growing public health threat is the ability of bacteria to share genes that provide antibiotic resistance.

Bacteria that naturally live in the soil have a vast collection of genes to fight off antibiotics, but they are much less likely to share these genes, a new study by researchers at Washington University School of Medicine in St. Louis has revealed. The findings suggest that most genes from soil bacteria are not poised to contribute to antibiotic resistance in infectious bacteria.

The researchers hope that what they are learning from soil bacteria will help identify ways to reduce gene sharing among infectious bacteria, slowing the spread of drug-resistant superbugs, said senior author Gautam Dantas, PhD, assistant professor of pathology and immunology.

The results appear May 21 in *Nature*.

"Soil bacteria have strategies for fighting antibiotics that we're only just starting to learn about," Dantas said. "We need to make sure the genes that make these strategies possible aren't shared with infectious bacteria, because they could make the problem of drug-resistant infections much worse."

Most of the antibiotics used to fight illness today were devised by soil microbes, which employ them as weapons in the competition for resources and survival. Penicillin, the first successful antibiotic, came from the soil fungus Penicillium.

But widespread use of *Penicillin* and other newer antibiotics has prompted bacteria to evolve strategies for blocking, evading or otherwise resisting these drugs. Antibiotic-resistant disease now adds $20 billion to annual health-care costs and leads to 8 million additional hospital treatment days in the United States.

For the new study, the scientists analyzed bacterial DNA in 18 soil samples from agricultural and grassland sites from Minnesota and Michigan.

Using a technique they helped develop, the researchers isolated small fragments of bacterial DNA from the soils and screened those pieces for genes that confer antibiotic resistance.

Other scientists have identified sections of genetic code that make it possible for bacteria to share genes. A gene must be close to these "mobility elements" to be shared. The approximately 3,000 antibiotic resistance genes the researchers identified in soil bacteria typically were not close to such elements.

The researchers also found that the antibiotic-resistance genes in soil are linked tightly to specific bacteria, suggesting little sharing between species. In infectious bacteria, though, more frequent sharing of genes creates antibiotic-resistance portfolios that differ greatly among related bacteria.

"We suspect that one of the primary factors that drives the sharing of antibiotic resistance genes is exposure to new antibiotics," Dantas said. "Because soil bacteria need many thousands of years to develop new antibiotics, the bacteria in that community don't encounter these threats anywhere near as often as disease-causing bacteria, which we regularly treat with different antibiotics."

Dantas and his colleagues continue to study factors that affect the spread of drug resistance in bacterial communities in hospitals, the environment and the human digestive tract.

"We were happy to find that antibiotic resistance genes from soil bacteria generally aren't poised to jump suddenly into pathogens," Dantas said. "But we want to do everything we can—whether it's changing how we treat infections in medical clinics or altering the way we manage the environments where bacteria grow—to keep the odds stacked against sharing of these genes."

More information: Forsberg KJ, Patel S, Gibson MK, Lauber CL, Knight R, Fierer N, Dantas G. Bacterial phylogeny structures soil resistomes across habitats. *Nature*, May 21, 2014. [DOI: 10.1038/nature13377](http://dx.doi.org/10.1038/nature13377)

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