

Antibiotics promote resistance on experimental croplands

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June 16, 2017 - Canadian researchers have generated both novel and existing antibiotic resistance mechanisms on experimental farmland, by exposing the soil to specific antibiotics. The research is published in

Applied and Environmental Microbiology, a journal of the American Society for Microbiology.

"Antimicrobial resistance is a global threat to human and animal health with bacteria now resistant to the last-resort [antibiotics](#), including carbapenems and polymyxins," said corresponding author Ed Topp, PhD, Principal Research Scientist at Agriculture and Agri-Food, Canada, London, Ontario, describing the motivation for the research.

Antibiotics have been getting into crop production systems via application of manures from livestock, which are given antibiotics to maintain health under crowded production conditions. Antibiotics also get into croplands when human waste is applied as fertilizer, and directly from livestock on pasture. (Certain different antibiotics used to be given to livestock to promote faster growth, but Topp said that in both Canada and the US, the regulations now prohibit that, and his experiments did not include those antibiotics.)

In the study, Topp and his collaborators, including first author Calvin Lau, PhD, a Visiting Fellow at Agriculture and Agri-Food, Canada, exposed farm plots to antibiotics, over periods of up to 16 years.

Topp's research team ultimately sampled soil from the plots, extracting DNA, and cloning large fragments of that DNA into a strain of *E. coli* that is sensitive to most antibiotics. They then plated large numbers of *E. coli* onto a medium that contained one of several antibiotics, including from the classes of macrolides, β -lactams, and sulfonamides.

"Any colonies that grew would presumptively contain a cloned fragment that conferred resistance," said Topp. "We obtained a total of 36 [antibiotic resistance genes](#) from the antibiotic-resistant *E. coli*."

The investigators compared the resistance genes with currently known

resistance genes. Some of those obtained were not new. Others were similar to existing [resistance genes](#), but not precisely the same. Some coded for multi-drug efflux pumps, which are multi-drug resistance mechanisms embedded in the bacterial membrane that pump specific antibiotics out of the bacteria. And "In a few cases the DNA sequences [in the [genes](#)] were unlike any known," said Topp.

In one instance, the investigators discovered a novel gene conferring resistance to the [macrolide antibiotics](#), which was a small 61 residue proline-rich peptide, said Topp. The resistance mechanism has yet to be determined.

"Results from these studies will establish the risk of crop contamination, potential enrichment of [antimicrobial resistance](#) in environmental bacteria, and effects of antibiotics on non-target micro-organisms that underpin many of the services provided by ecosystems," said Topp. For example, if the evidence shows that effluents from municipal water treatment, from animal manure, or from pharmaceutical manufacturing plants are selecting for antibiotic resistant bacteria in the environment, that may justify treatment of such waste streams prior to application on croplands.

Provided by American Society for Microbiology

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