

Good news on using recycled sewage treatment plant water for irrigating crops

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A new study eases concerns that irrigating crops with water released from sewage treatment plants — an increasingly common practice in arid areas of the world — fosters emergence of the antibiotic-resistant bacteria that cause thousands of serious infections each year. The

research appears in ACS' journal *Environmental Science & Technology*.

Eddie Cytryn and colleagues explain that a large fraction of antibiotics given to people or animals pass out of the body unchanged in the urine and are transferred via sewage systems to wastewater treatment facilities. These facilities do not completely remove common antibiotics like tetracycline, erythromycin, sulfonamide and ciprofloxacin and may actually enhance the abundance of antibiotic-resistant [bacteria](#) and antibiotic-resistance genes. Previous studies have suggested that wastewater effluents can expand natural reservoirs of antibiotic resistance, which may contribute to clinically associated antibiotic resistance. Arid and semi-arid areas of the world are plagued by severe water shortages, which are expected to increase as a result of growing population and global climate change. As a result, more areas are turning to treated wastewater (TWW) to irrigate croplands. In Israel, for instance, TWW provides more than half of the water used for irrigation. The researchers wanted to find out if long-term irrigation with treated wastewater enhances antibiotic resistance in soil microbial communities, which could potentially be transferred through agricultural produce to clinically relevant bacteria.

The authors found that levels of antibiotic-resistant bacteria and genes for [antibiotic resistance](#) in fields and orchards irrigated with freshwater and TWW were essentially identical, suggesting that antibiotic-resistant bacteria that enter soil by irrigation are not able to survive or compete in that environment. The authors say there is "cause for cautious optimism" that irrigating with TWW is not increasing the prevalence of bacteria resistant to the antibiotics they studied.

More information: "Impact of Treated Wastewater Irrigation on Antibiotic Resistance in Agricultural Soils" *Environ. Sci. Technol.*, 2012, 46 (9), pp 4800–4808

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Abstract

Antibiotic resistance (AR) is a global phenomenon with severe epidemiological ramifications. Anthropogenically impacted natural aquatic and terrestrial environments can serve as reservoirs of antibiotic resistance genes (ARG), which can be horizontally transferred to human-associated bacteria through water and food webs, and thus contribute to AR proliferation. Treated-wastewater (TWW) irrigation is becoming increasingly prevalent in arid regions of the world, due to growing demand and decline in freshwater supplies. The release of residual antibiotic compounds, AR bacteria, and ARGs from wastewater effluent may result in proliferation of AR in irrigated soil microcosms. The aim of this study was to assess the impact of TWW-irrigation on soil AR bacterial and ARG reservoirs. Tetracycline, erythromycin, sulfonamide, and ciprofloxacin resistance in soil was assessed using standard culture-based isolation methods and culture-independent molecular analysis using quantitative real-time PCR (qPCR). High levels of bacterial antibiotic resistance were detected in both freshwater- and TWW-irrigated soils. Nonetheless, in most of the soils analyzed, AR bacteria and ARG levels in TWW-irrigated soils were on the whole identical (or sometimes even lower) than in the freshwater-irrigated soils, indicating that the high number of resistant bacteria that enter the soils from the TWW are not able to compete or survive in the soil environment and that they do not significantly contribute ARG to soil bacteria. This strongly suggests that the impact of the TWW-associated bacteria on the soil microbiome is on the whole negligible, and that the high levels of AR bacteria and ARGs in both the freshwater- and the TWW-irrigated soils are indicative of native AR associated with the natural soil microbiome.

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