Features of the soil resistome across tundra, temperate prairie and tropical ecosystems

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Video Byte

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Abstract

Antibiotic resistance is a global threat to public health, causing an estimated 700,000 deaths each year. Soil is an important reservoir of antibiotic resistance genes (ARGs), but the potential risk of ARGs in different ecosystems and the effect of land use changes are unknown. In a recent study, researchers investigated ARG types and amounts in three native soil ecosystems: Alaskan tundra, US Midwestern prairie, and Amazon Rainforest. They found high ARG diversity and abundance in all three ecosystems. A total of 10 regulatory and 55 non-regulatory ARGs were identified that were shared by all 26 metagenomes in the three ecosystems. No significant differences were observed in ARG diversity or abundance between native prairie and agricultural soil, while conversion of Amazon rainforest to pasture increased ARG abundance. At the sequence level, the 12 most clinically relevant ARGs in the soil were distinct from those in human pathogens, and the bacterial community structure was correlated with the resistome profile, suggesting that variability in the resistome was driven by bacterial community composition. These results identify candidate background ARGs in diverse soil ecosystems, providing important insight into the factors driving antibiotic resistance in the soil that may drive further ARG emergence in the future.