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Impacts Land Use and Climate Change on the Spread of Antibiotic Resistance in Agricultural Soils

Inhalt

Livestock manure is a primary source of antibiotic resistance in agricultural soils, with land-use type and climatic factors significantly influencing the levels and distribution of antibiotic resistance genes (ARGs). However, the combined effects of climate change and shifts in land use on the spread of antibiotic resistance from livestock manure to soil microbiomes remain largely unexplored. Within the One Health Platform, the ResistChange project addresses this knowledge gap using the Global Change Experimental Facility, which investigates the consequences of climate change on ecosystem processes across different land-use types. In this study, soils representing various agricultural management practices are amended with manure and incubated under both current and future climate scenarios based on IPCC projections. The soil resistome is analyzed via metagenomics, and the abundance of key resistance genes is quantified over time using qPCR. Preliminary results indicate that maximum water holding capacity (WHC) plays a significant role in ARG dynamics, as current soils retain more water than those projected under future climate scenarios. Metagenomic analysis of the manure revealed a predominance of vancomycin- and tetracycline-related ARGs. Our findings suggest that soil variables such as WHC, climate scenarios, and management practices influence the spread of ARGs in soil. Understanding these factors will enhance our ability to protect the health of humans, animals, and ecosystems in line with the One Health approach.

Keywords

antibiotic resistance genes, land use, climate change, resistome and mobilome

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