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Antibiotic resistance genes and residues in water and soil in close proximity to swine production facilities - molecular ecology section

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Abstract Text:

The use of antibiotics at concentrated animal feeding operations (CAFOs) for disease prevention, disease treatment, and growth promotion can contribute to the spread of antibiotic compounds, their breakdown products, and antibiotic resistant bacteria and/or the genes that confer resistance. By applying the tools of molecular biology, we have investigated the spatial and temporal distributions of antibiotic resistance genes at swine production CAFOs over a five-year period. This research has been conducted at the farm scale in order to characterize the phenomenon of antibiotic resistance in a variety of environments, including swine manure, treatment lagoons, ground and surface waters, and farm fields receiving manure amendments as fertilizer. Our results have demonstrated that leakage from waste treatment lagoons can influence the presence and persistence of tetracycline resistance genes in groundwater adjacent to swine CAFOs, and molecular phylogeny allowed us to distinguish “native” tetracycline resistance genes in control groundwater wells from manure-associated genes introduced from the lagoon. We have also been able to detect the presence of erythromycin resistance genes in CAFO surface and groundwater even though erythromycin is strictly reserved for use in humans and thus is not utilized at any of these sites. These genes are likely present because they co-confer resistance to tylosin, another macrolide antibiotic that is used at these sites. Finally, we have begun to quantify the temporal dynamics of antibiotic resistance genes in farm soils that have been fertilized with swine manure. Our work as a whole suggests that different sub-families of antibiotic resistance genes have different propensities to spread, persist, and even increase in environments that have been contaminated by swine manure.

Impact Statement:

Our research demonstrates that antibiotic use at CAFOs has the potential to influence the phenomenon of antibiotic resistance in the local environment. We can detect and distinguish this impact in spite of the presence of minor populations of native antibiotic resistant bacteria in soil and water. Ongoing research, including modeling of particle transport in groundwater, will help to determine the potential spatial and temporal extent of CAFO-derived antibiotic resistance. In addition, our group is developing high-throughput molecular approaches for the rapid detection and characterization of antibiotic resistance genes in environmental samples.