

PUBLIC HEALTHWORKER SAFETY

Title: Occurrence and Movement of Antibiotic Resistant Bacteria and Resistance Genes in Tile-Drained Agricultural Fields Receiving Swine Manure Application - **NPB #14-015**

revised

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Scientific Abstract:

The use of tylosin at subtherapeutic levels by the swine industry provides selective pressure for antibiotic resistance in the animal gut and manure. Land application of manure from tylosin-treated swine introduces tylosin-resistant enterococci, macrolide resistant genes (*ermB*, *ermC*, *ermF*, *ermT*, and *msrA*), which confer resistance to tylosin, and other macrolide antibiotics. This study documents the occurrence and transport of tylosin-resistant enterococci, *erm* genes and tylosin in tile-drained chisel plow and no-till agricultural fields treated with liquid swine manure in alternating years from 2011-2014. In manure enterococci and tylosin resistant enterococci concentrations ranged from $>10^3$ to $>10^5$ CFUg⁻¹ manure and tylosin resistant fractions of total enterococci ranged from 70%-100%. In drainage water enterococci levels were highly variable in all four plots and no significant differences ($p>0.10$) in enterococci concentrations were detected between tillage practices or manure treatment. Tylosin-resistant enterococci were rarely detected and concentrations were not significantly different ($p>0.10$) between manure or tillage treatments. High concentrations of *ermB*, *ermC*, and *ermF* were found in manure. Averaged over four years, *ermB* concentrations were greatest (1.51×10^{12} copies g⁻¹ manure) followed by *ermF* (7.54×10^{11} copies g⁻¹ manure) and *ermC* (4.54×10^8 copies g⁻¹ manure), respectively. The highest soil concentrations for *ermB*, *ermC*, and *ermF* were detected in manure bands immediately following manure application; *msrA* and *ermT* were not found in quantities above the specified LOD. Gene concentrations in soils collected from the interband location of manured plots and control plots immediately after manure application were below detection limits for each *erm* gene. Gene concentrations in both the chisel plow and no-till soil bands the following spring were approximately an order of magnitude lower than the previous fall. *ErmB* was detected in 75% of soil samples from manure treated plots in the second year after manure application. *ErmF* was only detected in one soil sample in the second year of the crop rotation, while *ermC* was not detected. Similarly, *ermB*, *ermC*, and *ermF* were detected in tile drainage samples, while *msrA* and *ermT* were not above the limit of detection. Concentrations of *ermB* in positive samples were consistent over the four years of drainage sampling (6.36×10^2 to 5.17×10^4 copies 100 ml⁻¹), however, manured plot samples contained a significantly higher percentage of *ermB* positive samples ($p<0.10$) only in 2013 and 2014. While the first two years of study found no effect on tile drainage water quality in years of below average precipitation, higher levels of precipitation in 2013 and 2014 resulted in significant differences in resistance gene concentrations in agricultural drainage water from plots receiving manure application when compared to no-manure controls.

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