Characterising Shifts in the Resistome and Microbial Community Structure of Cattle Slurry Amended Agricultural Soil

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International and UK government reports have cited antibiotic use as a significant driver of antibiotic resistance (AR) in agricultural environments at the national and global scale. Unmetabolised antibiotics excreted in faeces and urine from livestock receiving antibiotic treatment are frequently highlighted as a selection pressure for resistant bacteria in slurry tanks and fields fertilised with animal husbandry waste. In this way, the application of animal waste on agricultural land represents a perturbation of the soil microbiome. From a human health perspective, crops destined for human consumption could also become contaminated with antibiotic residues and/or with bacteria carrying AR genes. However, assessing the flow of antibiotic resistance within farm environments is challenging due to their complex, multi-compartmental nature. As a result, the resilience of soil microbial communities and the response of the soil resistome to slurry application remain poorly understood.

Key aims are to quantify AR within cattle slurry amended soils and to characterise factors which govern AR at the University of Nottingham (UoN) Dairy Farm site over two seasons of slurry application (2017/18). Specific objectives were to determine how antibiotic resistance profiles and community structure of soil bacteria respond to successive slurry applications, to establish a baseline for unamended soils in the same geographical area and to use the real-world data gathered to generate statistical models of AR in slurry amended field soils. By using a combination of classical culture and molecular techniques at the field scale we sought to negate common issues of methodology bias. Over 350 isolates were tested for phenotypic resistance to a range of antibiotics over the study period. Approximately 11% of these isolates were multi-drug resistant, with sub-sets of these isolates displaying resistance to select penicillins, 1st and 3rd generation cephalosporins, phenicols, nitrofurans, and synthetic quinolones. Soil samples were subject to DNA extraction and metagenomic analysis to elucidate microbial community composition and the resistome. Data will be discussed and contextualised within the current understanding of AR in the environment and farm management practices.