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Of Microbes & Manure: Investigating Soil Community Assembly in Response to Manure Amendment

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Injection of liquid dairy manure near Morris, MN.

The value of animal manure as a soil amendment has been recognized since the Neolithic era, where it is thought that the early farmers applied manure as a long-term investment in the productivity of their land. Today, we know that in addition to supplying necessary plant nutrients (e.g., N, P, K, Ca, Mg, S), manure amendments can have lasting benefits for many physical, chemical, and biological aspects of soil health. Most notably, manure amendments can reduce soil bulk density, increase water infiltration, buffer soil pH, and increase soil organic matter (SOM). Moreover, mineralization of SOM by soil microbes (bacteria, fungi, protozoa, and viruses, collectively the 'microbiome') makes organic nutrients available to plants, acting as a slow-release fertilizer. The many benefits of applying manure to agricultural fields make the practice an important means for combatting land degradation due to excessive tillage and erosion. However, manure amendments also pose challenges for land managers with regards to nutrient losses due to runoff or leaching and greenhouse gas emissions (e.g., N_2O, methane). Additionally, antibiotic resistance elements from animal gut microbiomes, which are thought to be linked with the use of antibiotics in animal production systems, may pose a significant threat to human health.

Soil microbial communities are central to many of the benefits and potential risks of applying manure to fields. Despite their importance, soil communities are arguably among the most difficult-to-study and least-understood components of agricultural systems. Common soil health assessments typically use measures of microbial respiration or biomass. However, these measures lack the ability to evaluate the composition or diversity of microbial communities. Advances in DNA sequencing technologies in the last decade have revolutionized microbiome research and promise exciting new insights into relationships between agricultural management practices (e.g., manure amendments, soil microbial communities, soil health). Leveraging these and other 'meta-omic' tools, researchers are now able to decipher composition, diversity, and function of soil communities with unprecedented detail. Studies have shown manure amendments can fundamentally restructure soil microbial communities with significant impacts on nutrient cycling and suppression of plant diseases. However, attempts to deliberately manage soil microbial communities using manure or other organic amendments often yield unpredictable results, due in part to the incredible diversity of soil organisms and the enormous variability in microbial communities across space, soil types, and cropping systems.

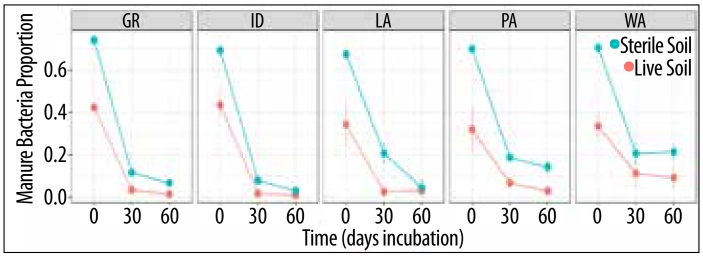
A multidisciplinary researcher team at the USDA Plant Science Research Unit and the University of Minnesota, encompassing expertise in soil microbiology, agronomy, and manure management, is investigating fundamental questions regarding how dairy manure amendments impact soil microbiome assembly and the fate of manure-borne microorganisms in soils. Research has initially focused on determining if there are consistent impacts of manure on soil microbes and identifying the primary forces that drive microbial community assembly in soil. Manure harbors an abundance of microbes, largely derived from the animal gut, that are introduced to soils. However, because soil microbiomes are incredibly diverse and well-adapted to the soil environment that they inhabit, indigenous microbial populations may quickly outcompete microbes introduced along with manure. Moreover, the soil physical and chemical environment is distinct from that experienced by microbes inhabiting the animal gut or manure, and may present a strong barrier to the establishment of introduced microbes. Finally, manure amendments are likely to impact indigenous soil microbes by providing a rich source of nutrients to support their growth, or through their effects on other physical or chemical aspects of soils such as pH.

To investigate the relative importance of these possibilities on microbiome assembly in a controlled setting, diverse soils were collected from locations in Minnesota, Pennsylvania, and Idaho. Small soil ecosystems were set up in a laboratory and were amended with raw dairy manure slurry at typical field rates. Soil samples were collected at 0, 30, and 60 days after incorporation of manure, and microbiomes were characterized from each sample using high-throughput DNA sequencing of marker genes.

Contrasts between manure-amended and non-amended soils identified numerous bacteria that increased significantly in relative abundance in response to manure over time. However, there was little overlap in the identity of bacteria responding to manure amendments among the different soils, consistent with location-specific differences in how soil communities respond to manure amendments. Despite the soil-specific responses there was some similarity in ecological strategy. For example, a number of bacteria commonly responded to manure amendment that are often observed in association with plant roots and have biocontrol activity against a wide range of soil-borne plant pathogens. Together, this suggests that responses may be more predictable using microbial ecological strategy- or trait-based frameworks. Intriguingly, these results also suggest that changes in soil microbial communities due to manure amendments have the potential to impact the composition and function of plant-associated microbial communities.

Manure-associated microbes were identified by comparing manure-amended and control communities and tracked over time. These bacteria declined rapidly in relative abundance after 30 days even in sterilized soil (Figure 1), indicating soil environment presents a strong filter against establishment of bacteria from manure. Further, presence of indigenous communities provided an additional barrier to invasion, suggesting abiotic and biotic factors contribute to soil community resilience in the face of introduced microbes. Indigenous microbial communities responded to carbon/nutrient inputs or physiochemical changes elicited by manure amendments, rather than by manure microbes.

Figure 1. Bacteria associated with manure decline rapidly after introduction to both live and killed soils from different locations in Minnesota (GR, LA, WA), Pennsylvania (PA), and Idaho (ID).



This research sheds light on how manure amendments drive changes in soil microbial communities. Although soils appear to be quite resilient to manure-borne microbe invasion, due to abiotic and biotic barriers, manure stimulates growth of potentially beneficial indigenous soil bacteria. Further work is being conducted at University of Minnesota Long-term Agricultural Research fields investigating manure and synthetic fertilizer impacts on soil microbiomes and agronomic factors in a corn-alfalfa system to better understand benefits of manure amendments and alfalfa in crop rotations.