

**P131****Farm-scale differentiation of active microbial colonizers**Sarah Richards<sup>1</sup>, William King<sup>2</sup>, Terrence Bell<sup>1</sup><sup>1</sup>Penn State, State College, PA, USA. <sup>2</sup>Cornell University, Ithica, NY, USA**Abstract**

Microbial movement is important for replenishing lost soil microbial biodiversity and driving plant root colonization, particularly in managed agricultural soils, where microbial diversity and composition can be disrupted. Despite abundant survey-type microbiome data in soils, which are obscured by legacy DNA and microbial dormancy, we do not know how active microbial pools are shaped by local soil properties, agricultural management, and at differing spatial scales. To determine how active microbial colonizers are shaped by spatial scale and environmental conditions, we buried microbial traps (i.e., sterile soil enclosed by permeable mesh membranes) across transects of a forest-adjacent farm and under 16 cover crop treatments in a randomized block design within an organically managed agricultural research farm. Bulk soil and deployed traps were collected for 16S rRNA gene and fungal ITS amplicon sequencing at two time-points to identify early re-colonization and community development. We hypothesized that 1) different cover crop mixtures, either single- or multi-species, would stimulate different portions of the soil microbial pool, and 2) at finer spatial scales, the active (soil-recolonized) microbial pool would be different relative to surrounding bulk soil. We found that bacteria had greater colonization consistency (within-group similarity) among replicate communities. Relative to bacterial colonizers, fungal colonizers shared a greater compositional overlap to sequences from the surrounding local bulk, suggesting that these groups respond to distinct environmental constraints. Understanding how environmental constraints and spatial scales impact microbial recolonization dynamics and community assembly are essential for identifying how farm management can be used to intentionally shape agricultural microbiomes.

