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Impact of organic fertilization on microbiomes along the trophic chain in grassland ecosystems

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Background: Agricultural grasslands are often managed intensively, influencing soil properties and local macro and micro- communities. The impacts of such anthropogenic changes are not limited to host diversity but can also affect diversity of host-associated microbial assemblages. These changes can have cascading effects across ecosystems, resulting in significant community alterations and challenges to health and function at different levels along the trophic chain.

Methods: This study investigates how fertilization affects microbial communities in grassland ecosystems in multiple connected trophic compartments treated with organic fertilizers, i.e. biogas digestate, cow/horse manure, and pig slurry, using high throughput 16S rRNA gene sequencing.

Results: Our results indicated shifts in microbial composition in response to fertilization, which were most pronounced in belowground trophic compartments. These changes were strongly host-dependent, with the pig slurry treatment exerting the greatest impact. The presence of overlapping bacterial genera across soil, plant, and animal compartments suggests strong interactions between trophic levels. Although pig slurry-derived microbes were detected in all compartments, their low prevalence indicates an indirect effect of fertilization, associated with changes in nutrient availability.

Conclusions: Our findings demonstrate that belowground and aboveground trophic levels respond differently to fertilization-induced microbial alterations. This highlights the importance of considering host-specific and trophic interactions when evaluating the impacts of anthropogenic disturbances on ecosystems and their implications for environmental and human health.

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