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Belowground dynamics and plant growth effects of fungal pathogens in a grassland biodiversity experiment

Abstract

Soil-borne fungal pathogens play key roles in shaping plant communities. They promote plant diversity by controlling the overgrowth of dominant plant species, but may also reduce overall productivity in less diverse communities where susceptible hosts abound. Understanding pathogen dynamics can therefore provide insights for managing both natural and agricultural ecosystems, to maintain biodiversity and improve productivity and resilience to a changing environment.

However, we lack understanding on the diversity and function of soil-borne fungal pathogens in natural communities, such as which fungal species affect specific plants, how pathogens are transmitted between neighboring plants, and how their abundance and disease are influenced by the diversity and composition of plant stands.

We addressed these knowledge gaps using a grassland biodiversity experiment encompassing experimental plant communities varying in species richness and composition (Fig. 1a). In each of these communities, we planted seedlings of a forb (*Leucanthemum vulgare*, family Asteraceae) and a grass (*Arrhenatherum elatius*, family Poaceae) species to monitor their infection loads by fungal pathogens under different plant community contexts and compare these with changes in their growth. After three months, we investigated fungal communities in roots and soil of all plants using environmental sequencing techniques and measured aboveground plant biomass.

We found that the composition of fungal communities in roots and soil was determined by the composition of plant communities, enabling us to detect fungi with preferences for specific plant lineages. Focusing on fungal taxa with known pathogenic lifestyles, we found that the forb *L. vulgare* showed a greater degree of infection by specific pathogens when surrounded by closely related plant species, and that these pathogens were transmitted via soil rather than direct contacts between roots (Fig. 1b). However, pathogen infection of the grass *A. elatius* was unaffected by the surrounding vegetation, and we also did not detect any relationship between pathogen infection and reductions in growth for any of the seedling species (Fig. 1b).

Our study shows that the belowground transmission of specific fungal pathogens can be amplified in the vicinity of related plant taxa, suggesting a densitydependent contagion between susceptible hosts. However, the distinct transmission patterns observed in *A. elatius*, and the lack of a clear link between pathogen infection and seedling growth, highlight the complex interplay between plant and fungal communities, alongside factors related to their phenological and/or physiological status, in shaping the epidemiology of soil-borne diseases in biodiverse communities.





Figure 1. Overview of the grassland biodiversity experiment (*a*) and the results of this study (*b*). *a*: The biodiversity experiment included plots with experimental grasslands varying in plant diversity and composition. Three plots are delineated in white. *b*: We observed an increased transmission of specific soil-borne pathogens in Leucanthemum vulgare roots when the seedlings were surrounded by closely related forb species. However, this was not observed in the grass Arrhenatherum elatius when surrounded by other grasswes. The abundance of specific pathogens in roots showed no correlation with plant growth in both plant species. Empty arrows indicate non-significant relationships.