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Solidago canadensis and its endophytes as a self-degrading system during ex situ decomposition

Kamil Kisło

k.kislo@uw.edu.pl

Botanic Garden, Faculty of Biology, University of Warsaw https://orcid.org/0000-0002-7569-0072

Patryk Czortek

Anna Wiewiorowska

Marta Wrzosek

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Abstract

Background and Aims

Solidago canadensis is an invasive herb widespread across Eurasia and Australia, known to decompose faster than native species. However, the mechanisms driving its decomposition, particularly the role of associated microorganisms, remain poorly understood. This study aimed to assess the influence of specific components of soil biota (bacteria and fungi) from invaded and non-invaded mesic meadows on the decomposition of *S. canadensis*.

Methods

We conducted an *ex situ* decomposition experiment using shoots and leaves of *S. canadensis*. Soil solutions from invaded and non-invaded meadows were prepared and passed through syringe filters of varying pore sizes (variants A–D). We assessed primary decomposer diversity under a light microscope and analysed mass loss using generalized linear mixed models.

Results

Differences among filtration treatments were minimal, and soil solution origin (invaded vs. non-invaded meadows) had negligible effects on mass loss. Leaves and shoots decomposed at similar rates across all variants. These outcomes indicate that external microbial inputs played no detectable role in driving decomposition.

Conclusion

Our findings suggest that *S. canadensis* operates as a largely self-contained holobiont, harbouring an internal consortium of primary decomposers capable of sustaining decomposition independently of external soil communities. This highlights the functional redundancy of surrounding soil biota and may contribute to enhanced nutrient cycling in invaded ecosystems. Such a strategy aligns with invasion facilitation frameworks, including the novel weapon hypothesis, illustrating how *S. canadensis* can exploit new environments. Additionally, its consistently efficient *ex situ* decomposition suggests strong potential for valorizing harvested biomass through composting or biogas production.

Introduction

Decomposition is a crucial part of the carbon cycle, depending, among others, on the activity of the microorganisms and mesofauna. Some components of this biota can be directly responsible for mass loss through the use of their enzymes and feeding on detritus (primary decomposers), or indirectly regulate the populations of other organisms (secondary decomposers) (Hättenschwiler et al., 2005). Both of these groups contain representatives of fungi, bacteria, protists, and mesofauna. Hättenschwiler et al. (2005) suggested that bacteria and fungi are the main primary decomposers since they are the key organisms transforming detritus and regulating mesofauna's activity. Despite the high phylogenetic

heterogeneity, all of the components of decomposing biota synergistically interact with each other (i.e., commensalism, mutualism, synergistic decomposition of specific compounds), or antagonistically (i.e., competition, predation, parasitism), and the mechanisms of these interactions may vary depending on abiotic environmental factors, such as light and water availability, temperature, or type of substrate (Ferreira and Chauvet, 2010; Tylianakis et al., 2008). Decomposition, as a complex of environmental processes, remains incompletely understood despite a rapidly expanding body of literature. Its dynamics are strongly context-dependent and vary across habitats, biogeographic regions, and spatial scales. In the Anthropocene, biological invasions have emerged as an additional and still insufficiently recognised driver that can substantially alter decomposition processes.

Invasive species can disrupt ecosystem functioning, especially when they act as “environmental engineers” (Czortek et al., 2026; Xin *et al.*, 2022). By introducing novel biotic and abiotic components into the system, they contribute to the formation of novel ecosystems. As a result, they increase both functional and phylogenetic novelty (Schittko et al. 2020), which may shape decomposition processes in ways that are only beginning to be understood. Environmental engineers can influence soil moisture by modifying river and groundwater dynamics (Stromberg *et al*., 2007). They may also alter light penetration (Dyderski and Jagodziński, 2019) and shift soil nutrient processes (Ehrenfeld, 2003). In addition, they can affect litter decomposition (Castro-Díez *et al*., 2009, 2019). Their presence may further lead to novel interactions with native biota, as tissues of some invaders decompose at a similar rate across all stages of the invasion gradient (Kisło et al., 2025).

One of the invasive species belonging to the group of environmental engineers is *Solidago canadensis* (L.), a member of the Asteraceae family with a native range in North America, and indroduced range in Europe, Asia, and Australia (Ren et al., 2020; Zhang et al., 2009). It was introduced in Europe relatively recently, with the beginning of its history in the 17th century in England, with further spread in Western and Eastern Europe (Popai and Parker, 2014). Nevertheless, *S. canadensis* is considered invasive in urban and suburban environments, wetlands, forests, grasslands, and meadows, including mesic meadows protected by the Natura 2000 (Akatov et al., 2021; Kotowska et al. 2024; Tokarska-Guzik, 2005). *Solidago canadensis* is known for its engineering abilities, which include altering soil pH and the C:N ratio (Xie et al., 2023) and secreting allelopathic secondary compounds (Anžlovar et al., 2020; Deng et al., 2015). It also modifies the structure and species composition of soil biota. For example, Xu et al. (2024) showed that the dominant arbuscular mycorrhizal fungi in the rhizosphere shifted from Glomus to Paraglomus, thereby affecting interactions within soil-inhabiting communities. Nevertheless, the knowledge about the impact of these drivers on the effectiveness of primary decomposers is still limited.

Regarding the leaf litter of *S. canadensis*, different research reveals different decomposition speeds, but most of them suggest that *S. canadensis* leaf litter decomposes faster than selected species of native flora (Simon et al. 2023; Zhang et al. 2016), demonstrating, however, high context dependency of these results. This context-dependency depends strongly on the ecosystem type and accompanying environmental conditions. For example, Simon et al. (2023) investigated a lake ecosystem, whereas

Zhang et al. (2016) examined coastal grasslands. According to this context dependency, our knowledge about microorganisms involved in the *S. canadensis* decomposition process and their interactions is limited.

Since most of the decomposition experiments were conducted *in situ* (Latterini et al. 2023; Simon et al. 2023; Zhang *et al.* 2024), the authors were not able to exclude the impact of a complex of factors (i.e., weather, sunlight exposure, moisture, human activity) on the biogeochemical processes. Despite the high utility of the results of these studies, many applied ecology processes (e.g., composting or biogas production) are conducted *ex-situ* and need other gaps of knowledge to be filled for their optimisation, including microorganisms taking part in this process and even the decomposition speed. We believe that connecting the experimentally identified, normalised decomposition speed *ex-situ* with the interactions between the decomposers can be highly useful for further research on this topic.

The main goal of this study was to evaluate the impact of fungi and bacteria with different origins on *S. canadensis* shoots and leaves decomposition in the *ex situ* conditions of constant moisture and temperature. We decided to perform an *ex situ* experiment to eliminate the influence of weather conditions on decomposition. This approach also allowed us to control for spatial microheterogeneity in soil properties, including moisture, pH, and fertility. Thus, we focused specifically on the effects of different-sized organisms on the decomposition process, with particular emphasis on bacteria and fungi as the primary decomposers. We decided to collect the information about the influence of bacteria and fungi on *S. canadensis* leaves and shoots decomposition by eliminating specific components of the soil biota from the controlled experimental setup and comparing the results before and after the removal. We hypothesized that fungi and bacteria would have similar effects on the decomposition **(H1)**. We hypothesize that representatives of both microorganisms' kingdoms will act in parallel in the process of decomposition; both bacteria and fungi possess a broad pool of enzymes and can degrade hard organic material (eg, lignin; Bugg et al., 2011). Moreover, we expect them to have a positive impact on the decomposition, since Kisło et al. (2025) suggested that the taxonomic diversity of fungi was positively correlated with the mass loss. On the other hand, if there is only a slight difference between the experimental variants could show us that *S. canadensis* poses a higher than previously known threat to biodiversity since microbiota living on or inside the plant can decompose its tissues without any additional biotic components.

Materials and methods

In October 2023, we collected senescing leaves and shoots of *S. canadensis* and dried them to constant mass (60°C for 48 hours). During this period, we also collected 100 g of soil from five plots with high *S. canadensis* cover (ranging from 85% to 95%) and control plots (with less than 5% *S. canadensis* cover) located in mesic grasslands in Northeastern Poland (Central-Western Europe). The place of soil collection in the current manuscript is referred to as "soil origin", and the coordinates of these study plots are available in Supplementary Material S1. Before starting the experiment, we dried the material at 70°C for 72 hours to exclude as much epiphytic biota as possible. We prepared mesh bags containing 5g

of the material +/- 2% per each meshbag (leaves or shoots, mesh size 1mm) and soil solution with previously sampled soil and 200 ml of autoclaved distilled water. To check the impact of different fractions of soil biota on the decomposition, we prepared four variants of the experiment in sterile plastic containers. Experimental variants were as follows: A – 30 mL of unfiltered soil solution (with all of the biota fraction present), B – 30 mL of soil solution filtered through a 10 µm syringe filter, which excluded mesofauna and large protists from the soil solution, C – 30 mL of soil solution filtered through a 1.2 µm syringe filter, which excluded most of the biota from the soil solution. After that, we added 270 mL of autoclaved distilled water to each container. To check the effect of remaining endophytic biota on the decomposition, we prepared the control variant (D) with 300 mL of the autoclaved distilled water. After the preparation of all experimental variants, we put four meshbags containing leaves or shoots into each of them (containers with leaves, total n = 160, containers with shoots, total n = 160) (Fig. 1). Containers were incubated at room temperature.

We performed sampling four times per one *S. canadensis* organ variant: once every six weeks for leaves and once every twelve weeks for shoots, since shoots decompose approximately 50% slower (Anda et al., 2023). The remaining necromass from each meshbag was dried and weighed. To obtain as much biodiversity data as possible, during each sampling event, we collected five ml of suspension in which the material was immersed and five mL of water from squeezing the meshbag. These solutions were combined, and 1.5 ml of the mixture was transferred into a sterile Eppendorf tube. After centrifugation (5000 rpm, 5 min), we discarded the supernatant and resuspended the pellets in 100 µl of distilled water. We observed 25 µl of this sample under the light microscope (Nikon Eclipse Ni-U) with a gridded cover slide to count the number of bacterial cells within one field of view, and animals, fungi, and protists within 50 fields of view (microscope magnification x200). We identified the representatives of the last two groups to the genus level (Seifert *et al.*, 2011; Watanabe, 2002) and counted them. To calculate the number of bacterial cells, we placed a 100µm x 100µm square at a randomly chosen point in one randomly chosen field of view from each plot on each collection date. Despite the detection of animals and protists in several samples (Supplementary Material S2), we have decided to focus on the influence of the primary decomposers on the mass loss. To obtain the information about mass loss, we dried the material in the meshbag as at the beginning of the experiment and weighed to assess the mass loss within one sample.

Statistical analysis

We performed statistical analysis in the R Studio version. 4.3.2 (R Core Team 2025). In all of the models response variable was defined by us as a proportion of remaining mass within the sample to the initial mass (5g), hereinafter referred to as “mass loss”. We calculated taxonomic richness of fungi using the *vegan*::*specnumber*() function (Oksanen et al., 2025). We performed two-stage statistical analyses to obtain information about the influence of the fungal richness and bacterial abundance on the mass loss. At the beginning, we calculated the generalised linear mixed models using *glmmTMB*:*glmmTMB()* function (Brooks et al., 2017), and then we calculated marginal responses of each model using *ggeffects*::*ggpredict()* function (Lüdecke, 2016) and marginal means using *emmean*::*emmeans()* function

(Lenth, 2023) to model the influence of single predictor, handling other predictors at a constant (mean) level. We used the *ggplot2*::*ggplot*() function (Wickham, 2009) to visualise the marginal responses. All of the models contained a box ID (eg, S33D) nested in plot ID (eg, S33) as a random intercept. For variant D (only distilled water added), we defined “plot ID” and “soil origin” as “none”. Fragments of dark septated mycelium (DSM) and hyaline mycelium can serve as propagules in some fungal taxa and play different ecological roles (Seifert *et al.*, 2011). We decided to calculate their abundance. To perform this analysis, we used the difference between the number of hyaline mycelium fragments and the number of melanised mycelium fragments (H-DR) as a predictor. Models for leaf litter decomposition were as follows:

Eq. 1 = mass loss ~ experimental variant+soil origin+collection+experimental variant:soil origin+experimental variant:collection+collection:soil origin

Eq. 2 = mass loss ~ fungal taxonomic richness + fungal taxonomic richness:experimental variant + fungal taxonomic richness:soil origin + fungal taxonomic richness:collection

Eq. 3 = mass loss ~ H-DR + H-DR:experimental variant + H-DR:soil origin + H-DR:collection

Eq. 4 = mass loss ~ bacteria relative abundance + bacteria relative abundance:experimental variant + bacteria relative abundance:soil origin + bacteria relative abundance:collection.

Models for shoots decomposition were as follows:

Eq. 5 = experimental variant+soil origin+collection+experimental variant:soil origin+experimental variant:collection+collection:soil origin

Eq. 6 = mass loss ~ fungal taxonomic richness + fungal taxonomic richness:experimental variant + fungal taxonomic richness:soil origin + fungal taxonomic richness:collection

Eq. 7 = mass loss ~ H-DR + H-DR:experimental variant + H-DR:soil origin + H-DR:collection

Eq. 8 = mass loss ~ bacteria relative abundance + bacteria relative abundance:experimental variant + bacteria relative abundance:soil origin + bacteria relative abundance:collection

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Results

We identified 25 different fungal morphotypes. The most common morphotypes were *Fusarium* sp., *Penicillium* sp./*Aspergillus* sp., and *Cladosporium* sp., and the mean spores per sample was 31.08 with 40.38 SD. The mean number of bacterial cells per 100µm x 100µm square was 77.41 with 62.09 SD.

Leaves decomposition

After the first six weeks of the experiment, the mean mass loss was 34.67% (± 2.40% SD). After 12 weeks, it was 45.55% (± 3.41% SD), after 18 weeks, 49.78% (± 1.77% SD), and after 24 weeks, 52.31% (± 3.59% SD). Mean mass loss at the end of experiment was 52.82% (± 2.43% SD) in variant A (without filtering), 54.08% (± 3.86% SD) in variant B with filtering through a 10um filter, 52.04% (± 4.39% SD) in variant C with filtering through a 1.2um filter, and 53.64% (± 2.37% SD) in control (Fig. 2; Eq. 1).

Overall, fungal taxonomic diversity was responsible for a 10% mass loss increase (from 43% with one morphotype detected to 51% with 12 morphotypes). The addition of soil solution from invaded plots and control plots in interaction with fungal richness was responsible for 12% and 10% mass loss, respectively. After six weeks of the experiment, the fungal taxonomic diversity was responsible for a 14% decrease in the mass loss, and after 24 weeks for a 16% increase. In variant A, fungal diversity was responsible for 7% mass loss decrease, in variant B for a decrease, in variant C for 7% decrease, and in variant D for 2% increase (Fig. 3; Eq. 2).

When the abundance of DSM was higher than the abundance of hyaline mycelium decomposition ratio was also higher. Mass loss was 56% when the H-DR (hyaline minus dark ratio) was 10, and when the H-DR was 18, the mass loss ratio was 30%. There was no difference in the influence of mass loss between different soil origins in the case of the H-DR. After six weeks, the higher abundance of hyaline mycelium was responsible for a 21% decrease in the mass loss, and after 24 weeks, for a 13% decrease. In variant A, the higher abundance of hyaline mycelium was responsible for a 26% mass loss decrease, in variant B and D for a 27% mass loss decrease, and in variant C for an 18% mass loss decrease (Fig. 4; Eq. 3). Overall, bacterial relative abundance was responsible for 3% mass loss increase (from 48% with 20% of bacteria to 50% with 100% relative bacterial abundance). Bacterial relative abundance effects on the mass loss varied from negligible to weak (2% – 8%) in the interaction with other studied parameters. (Fig. 5;Eq. 4).

Shoots decomposition

Decomposition of shoots was slower than that of leaves, even with longer periods between collections. After the first 12 weeks of the experiment, the mean mass loss was 15.41% (± 2.36% SD), after 24 weeks, 18.45% (± 5.74% SD), after 36 weeks, 28.67% (± 7.39% SD), and after 48 weeks 30.66% (± 7.87% SD). Mean mass loss at the end of an experiment was 30.66% (± 7.87% SD) in variant A (without filtering), 54.08% (± 3.86% SD) in variant B with filtering through a 10um filter, 52.04% (± 4.39% SD) in variant C with filtering through 1.2um filter, and 53.64% (± 2.37% SD) in control (Fig. 2; Eq. 5).

Overall, fungal taxonomic richness was responsible for a 7% mass loss decrease (from 21% with one morphotype detected to 15% with 10 morphotypes). The addition of soil solution from invaded plots and control plots in interaction with fungal richness was responsible for a 6% and 5% mass loss decrease, respectively. After 12 weeks of the experiment, fungal taxonomic richness was responsible for a 14% decrease in the mass loss, and after 48 weeks for 18% increase. In variant A and C, fungal richness was responsible for 7% mass loss decrease, in variant B for a 10% decrease, and in variant D for 2% decrease (Fig. 3;Eq. 6).

When the abundance of dark septated mycelium (DSM) was higher than the abundance of hyaline mycelium, the decomposition ratio was also higher. Mass loss was

29% when the H-DR (hyaline minus dark ratio) was – 5, and when the H-DR was 20, the mass loss ratio was 9%. Higher abundance of hyaline mycelium was responsible for a 25% decrease in the decomposition in variants with invasive soil added, and a 20% decrease in variants with native soil added. After 12 weeks, the higher abundance of hyaline mycelium was responsible for a 21% decrease in the mass loss, and after 48 weeks for a 13% decrease. In variant A, the higher abundance of hyaline mycelium was responsible for a 21% mass loss decrease, in variant B for a 10% mass loss decrease, and in variants C and D for a 20% mass loss decrease (Fig. 4; Eq. 2).

Overall, bacterial relative abundance was responsible for a 12% mass loss decrease (from 22% with 20% of bacteria to 12% with 100% relative bacterial abundance). Soil origin had a negligible effect on the influence of the bacterial abundance on the mass loss. After 12 weeks of the experiment, bacterial relative abundance was responsible for a 13% decrease in the mass loss, and after 48 weeks for 7% increase. In all experimental variants, the abundance of bacteria had a similar negative effect (10% to 14% mass loss decrease, Fig. 5; Eq. 5).

Discussion

Mass loss within different experimental variants

In the current study, the mass loss grew faster than in earlier studies on *S. canadensis* litter decay conducted in the terrestrial environments (e.g., Zhang et al., 2016). Nevertheless, the mass loss we obtained was close to the *S. canadensis* shoot and leaf decomposition ratios reported by Anda et al. (2023) in the freshwater. This similarity was expected, as both our experiment and that of Anda *et al.* eliminated the negative effects of drought on microbial activity through their experimental setups. On the other hand, we expected more factors in our study to affect the decomposition. First of all, our expectations regarding the impact of soil origin (invaded vs. control plots) were not confirmed. We observed only negligible differences between filtration variants of soil solution and variants of suspended soil (from *Solidago* stands, and mesic meadows without *Solidago*). Moreover, our data do not show any consistent trend in these relationships. For instance, after 36 weeks, variants with soil from non-invaded plots had slightly higher mass loss than those with soil solution from invaded ones, but after another 12 weeks, their effects were relatively similar. As shown by Kisło et al. (2025), the increasing cover of *S. canadensis* on experimental plots does not affect the rate of leaf litter decomposition. Moreover, the main part of this study - different fractions of soil solutions expressed as soil solutions' filtering variants - turned out to be ineffective predictors of *S. canadensis* litter decomposition as soil solution origin (i.e., invaded and non-invaded meadows).

As regards soil origin, we observed slight differences between the decomposition speed within different filtration variants, but they are hard to interpret ecologically. They rather derive from interspecies litter quality (e.g., organs' thickness, or lignin concentration), which may exert a pronounced impact on the

decomposition (Couˆteaux *et al.*, 1995), than from ecological processes concerning the impact of saprotrophic biota. Moreover, this indicates a high degree of functional redundancy among *S. canadensis* decomposers. More specifically, when one functional group was removed or underperformed, others were able to compensate and maintain decomposition processes. For instance, the elimination of soil-borne fungi allowed bacteria to occupy more environmental niches, thus degrading more types of substrates, since the difference in mass loss between variants A, B, and C was negligible. Moreover, in our samples, we observed *Harzia* sp., a mycopathogenic fungus (Nguyen et al., 2016), which may have regulated the fungal population, and by that, the fungal impact on the decomposition, when other fungivorous organisms were missing.

Variant D (control), consisting solely of *S. canadensis* leaves/shoots and their native biota, showed a mass loss level comparable to the other variants. This allows for a cautious hypothesis that the microbiota naturally inhabiting *S. canadensis* tissues may contribute to the decomposition of its own litter. Endophyte-driven priming has already been demonstrated (Guerreiro *et al.*, 2017), and our results may indicate a similar but not yet fully confirmed mechanism. Placed in the hologenome context (Moran and Sloan, 2015), this would mean that the plant and its tissue-associated microbes form a unit capable of recycling nutrients embedded in the biomass. This link is particularly relevant for invasive species such as *S. canadensis*, which have a high nutrient demand due to their reproduction strategy based on excessive diaspore production (Hua *et al.*, 2007; Ye *et al.*, 2018). Moreover, *S. canadensis* represents a “try harder” strategy, characterized by an acquisitive pattern of resource use aimed at maximizing growth and reproductive output (Tecco et al., 2010). Because these nutrients are strongly accumulated in the leaves, conditions are favourable for the development of saprotrophs within the plant’s own tissues. This may explain both the similarity between our results and those of Anda et al. (2023) and the limited effect of soil origin or filtering. *S. canadensis* may already carry saprotrophs capable of initiating decomposition, supporting nutrient return to the plant or its offspring.

Bacteria and fungi have similar effects on the decomposition

Unexpectedly, the relative abundance of bacteria and fungal diversity showed a negative correlation with mass loss at the beginning of the experiment. Plant litter with *S. canadensis* origin may be hard to degrade due to high lignin concentration in shoots (Wiatrowska et al. 2022). Probably cuticle, as the natural barrier between inner plant tissues and the environment, needed the initial degradation process, as shown in (Logan *et al.*, 2022). Moreover, *S. canadensis* is known for producing a high diversity of secondary metabolites with different stability and potential impact on the decomposition (Zaimenko et al., 2025). Nevertheless, a high abundance of microorganisms that are not rapid decomposers may contribute to the residual mass, thereby slowing the overall rate of mass loss.

The production of secondary metabolites in the cuticule-related tissues in *S. canadensis* organs may be the reason for decreasing the impact of fungi and bacteria on the mass loss at the beginning of the experiment in both shoots and leaves. Notable inhibition by these groups’ representatives was visible after six weeks of experiment in the case of leaf litter and after 12 and 24 weeks in the case of shoots,

and we found a probable explanation for this phenomenon. Secondary metabolites of *S. canadensis* may differ between shoots and leaves, or among different organs. Anžlovar et al. (2020) showed this experimentally: extracts from different organs had varying effects on *Botrytis cinerea* growth. Studies by Reyes-Ávila et al. (2024) and Jenner et al. (2011) have shown that two of the secondary metabolites present in *S. canadensis* tissues, germacene D and limonene, have different decomposition ratios. Limonene decomposes fast, in up to seven days in the soil, and up to 40 days in the distilled water (Reyes-Ávila et al. 2024), while more than 75% of germacene D survives 63 days of biodegradation (Jenner et al. 2011). Moreover, we can expect that the substrate itself remains largely unavailable to saprotrophs, yet the aquatic environment becomes sufficiently enriched with dissolved organic compounds to stimulate bacterial cell division. Thus, bacterial abundance may increase even though the substrate is not yet undergoing intensive decomposition.

Since the current study focuses mainly on the fungal idiophase (spores), and sporulation sometimes requires specific conditions (Morton, 1961), we also checked the impact of the trophophase (vegetative mycelium) on the decomposition. Despite the knowledge that fungi with a trophophorm of hyaline mycelium have fast metabolism and are effective degraders (i.e., Basidiomycetes (Pleurotus), Mucoromycetes; Cohen *et al.*, 2002; Satari and Karimi, 2017), our results suggest the opposite dependence. Some plant-associated fungi with melanised hyphae, such as *Cladosporium* spp., show broad metabolic and functional diversity (Bensch et al., 2018; Nguyen et al., 2016). However, this factor alone does not explain why our findings differ from those of the field study by Kisło et al. (2025), in which DSM had a clearly negative effect on mass loss. One possible explanation is that under constant high humidity and optimal temperature, DSM fungi may allocate more resources to faster trophic metabolism. Another possibility is that environmental conditions select for different taxonomic groups of DSM-associated decomposers in different settings. Unfortunately, our experiment could not determine which of these two possibilities is closer to the truth.

Taken together, these patterns indicate that bacteria and fungi exert broadly similar effects on the decomposition of both leaves and shoots, regardless of soil solution origin. This consistency suggests that external microbial communities play only a minor role in shaping early and mid-term decomposition dynamics in *S. canadensis*.

Study limitations

Our experiment was conducted at room temperature, which removed the effect of varying environmental conditions but may have limited the activity of fungi requiring stratification for germination (Juge *et al.*, 2002). We also detected fungal spores and nematodes in soil-filtration variants. Because their presence on leaves and shoots was more likely than filtration errors, we treated them as components of the endophytic/epiphytic biota of *S. canadensis*. Only direct microscopy was used, as culturing would require partitioning the material and could introduce decomposition-rate biases. For the same reason, we excluded the metabarcoding approach. Using soil for experimental preparation also increased the risk of detecting dormant spores or eggs unrelated to *S. canadensis* decomposition, potentially producing false

metabarcoding signals. Moreover, the magnification used allows for a relative comparison of bacterial abundance in the sample, but without specific staining, some fraction of the bacteria may be underestimated. Moreover, some bacteria occur in colonies, and such colonies are likely to be analysed as single units.

Future experiments should therefore include two storage variants-room temperature and conditions matching the litter collection site-to avoid limiting fungal stratification. Metabarcoding should be performed before the experiment (on fresh and dried litter) to confirm the presence or absence of non-endophytic biota. Additionally, using litter from plants grown under sterile conditions would help eliminate biases introduced by endophytic communities.

Conclusions

Solidago canadensis is known for acting as an environmental engineer and changing the properties of the environment in the introduced range. When we add novel interactions with endophytic biota acting as efficient decomposers in the introduced range, as stated in Kisło et al. (2025) and in the current study, we obtain a view of a self-sufficient invader, and by that, fully adapted to modifying new areas. Our concern shall be especially important for lawmakers preparing local lists of invasive species with the highest impact on the environment and the lists of non-native species that should be eradicated from their secondary range. The second, more optimistic view of our results provides a valuable insight into the applied usage of *S. canadensis*. Since its tissues contain biota that are sufficient decomposers, the effort put into the composting of this plant seems to be relatively low, thus with a relatively low cost. In this case, our results may be part of the opportunity to fight the invasion of this plant, since mowing its shoots twice a year, according to the instructions (Gala-Czekaj et al., 2021), may be profitable for both farmers and companies selling bioproducts.

Declarations

Acknowledgments

Author Contributions

All authors contributed to the conception and design of the study. Kamil Kisło, Patryk Czortek, Anna Wiewiorowska, and Marta Wrzosek performed material preparation, data collection, and analysis. The first draft of the manuscript was written by Kamil Kisło, and all authors commented on previous versions. All authors read and approved the final manuscript.

Data Availability

The datasets generated and/or analyzed during the current study are available from the corresponding author upon reasonable request.

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Figures

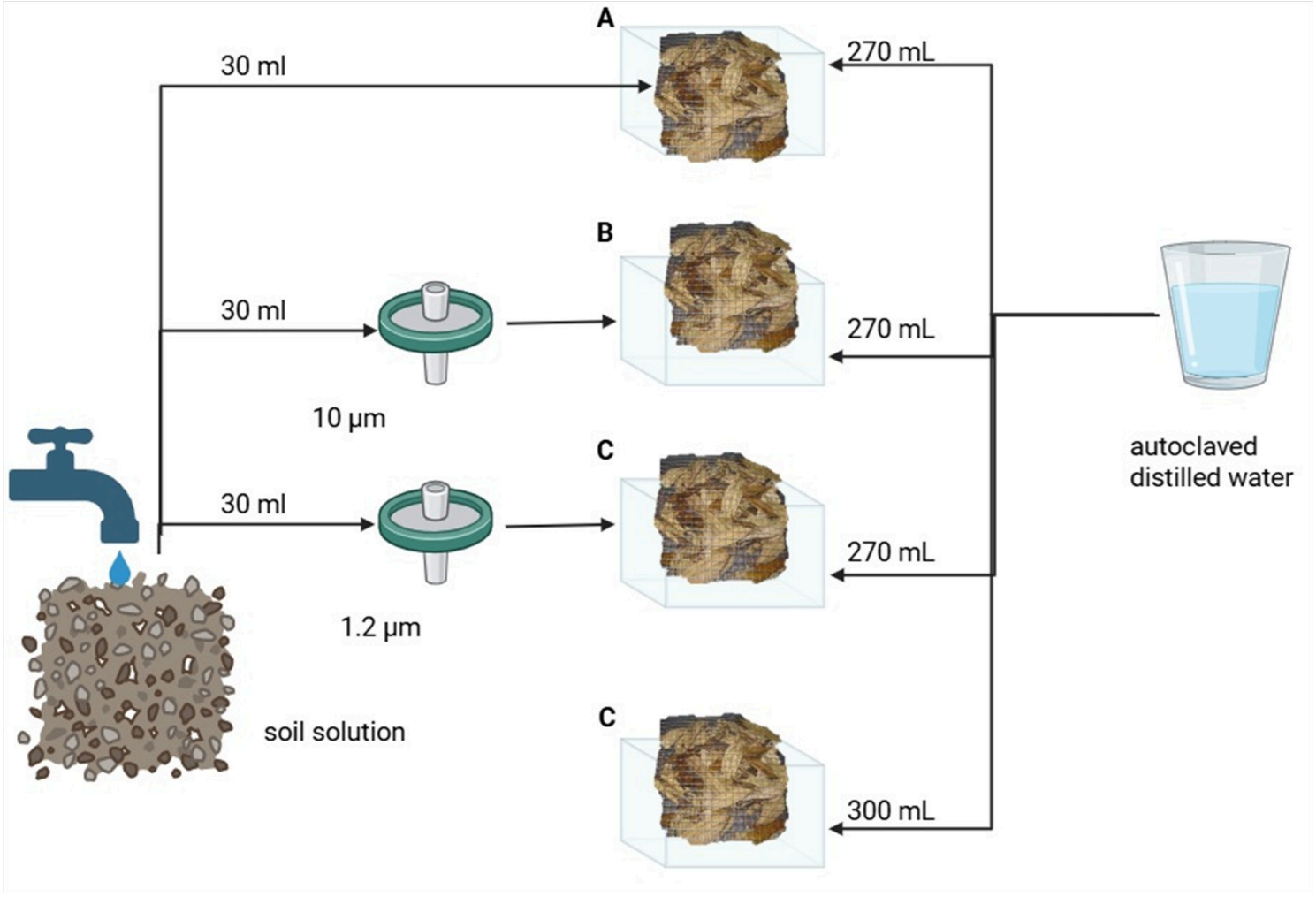

Figure 1

Experimental setup scheme. Letters in bold indicate the experimental variant (A-soil solution without filtering, B-soil solution filtered through 10µm syringe filter, C-soil solution filtered through a syringe filter with 1.2 µm pores, D-control variant with destilled water.

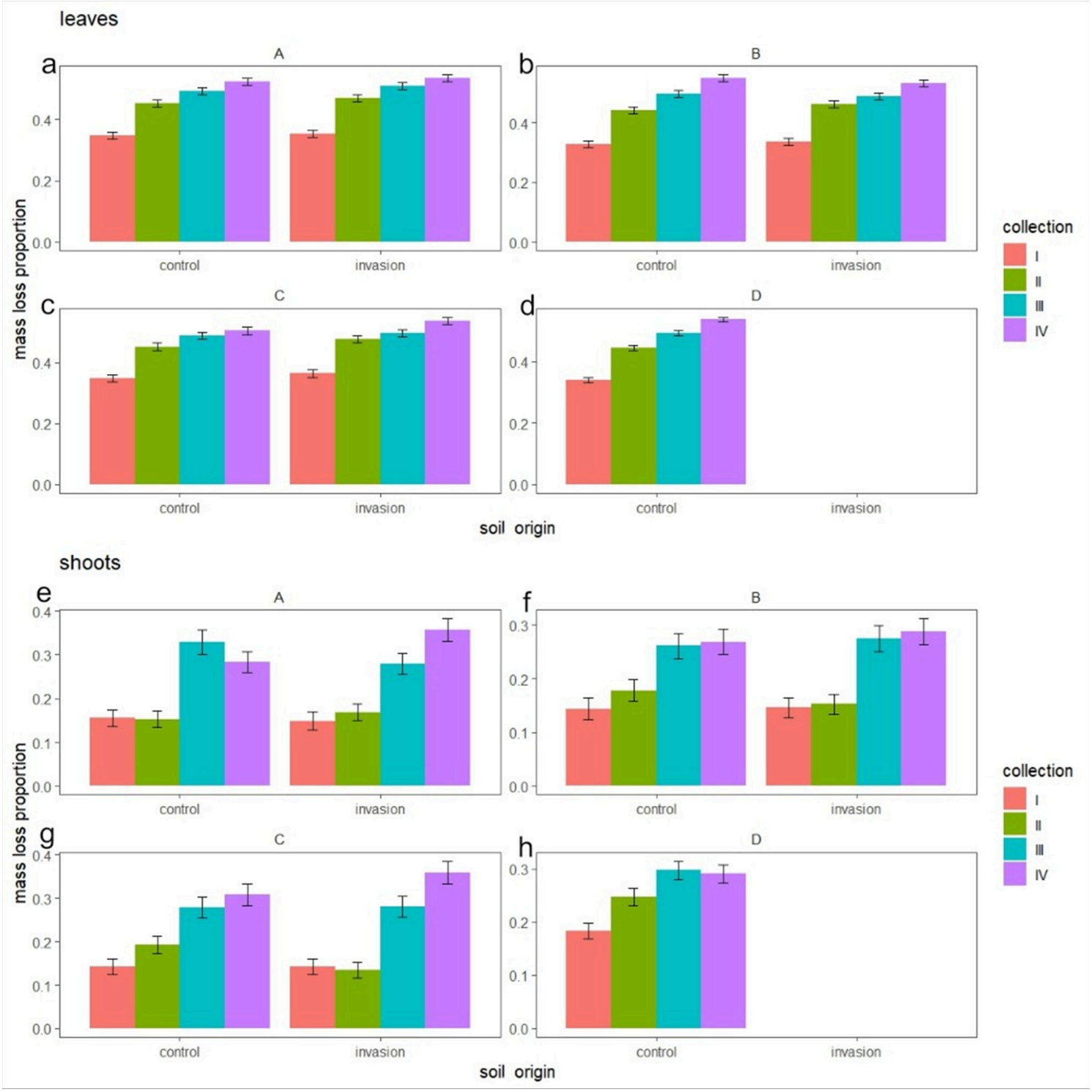

Figure 2

The influence of experimental variant and soil origin on the mass loss within different collection periods in the following parts of the experiment: a - leaves variant A, b - leaves variant B, c - leaves variant C, d - leaves variant D, e - shoots variant A, f - shoots variant B, g - shoots variant C, h - shoots variant h. Uppercase letters above each panel means: A - variant A (without filtration), B - filtration through 10 μM syringe filter, C - filtration through 1.2 μM syringe filter, D - distilled water.

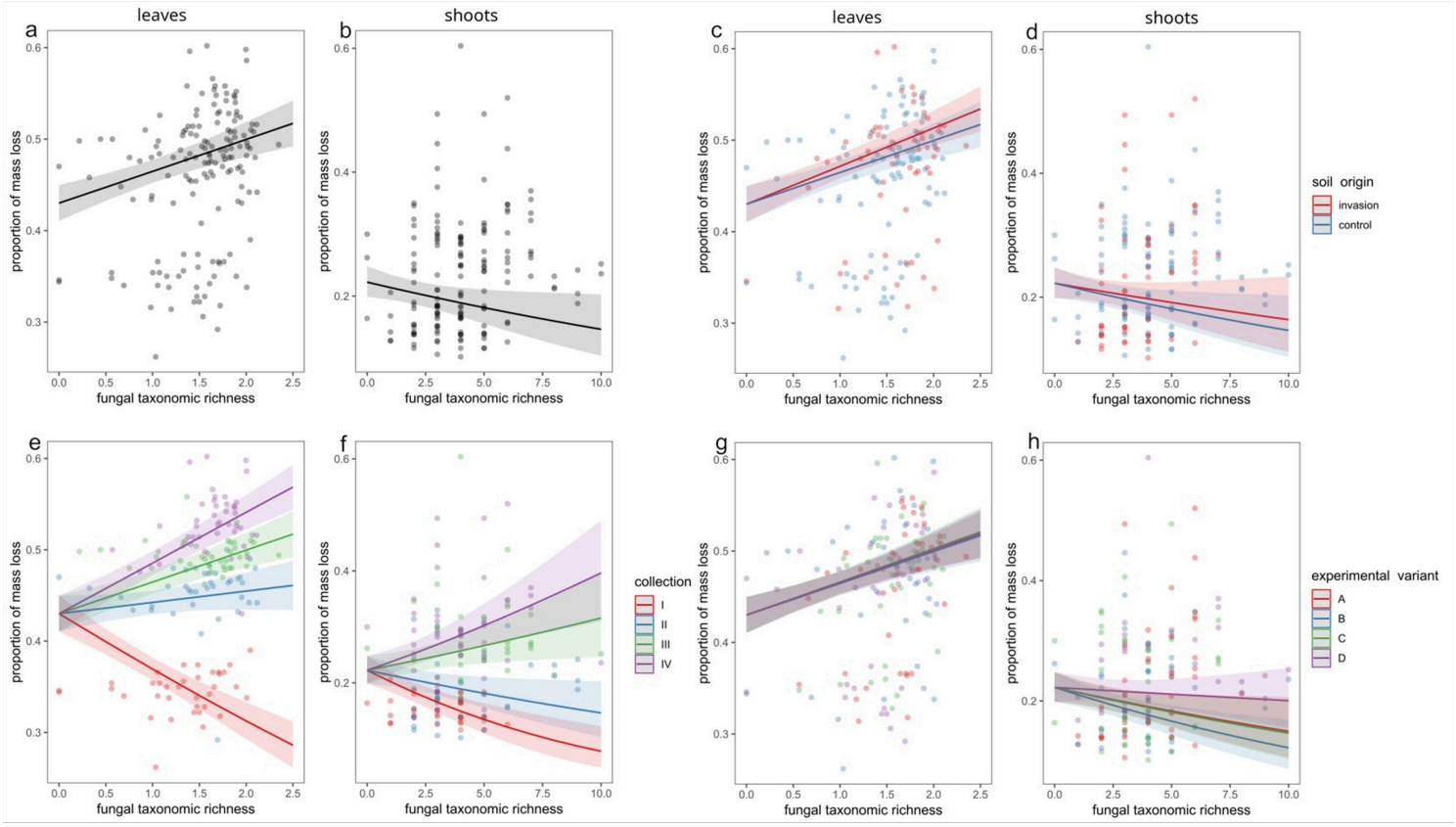

Figure 3

The influence of fungal taxonomic richness on the mass loss of leaves (a) and shoots (b), and the influence of fungal taxonomic richness in the interaction with soil origin in leaves c) and shoots (d), the influence of the fungal taxonomic richness during different collection periods in leaf (e) and shoots (f) part of the experiment, the influence of fungal taxonomic richness on the mass loss within different experimental variants in the leaves (g) and shoots (h) part of the experiment).

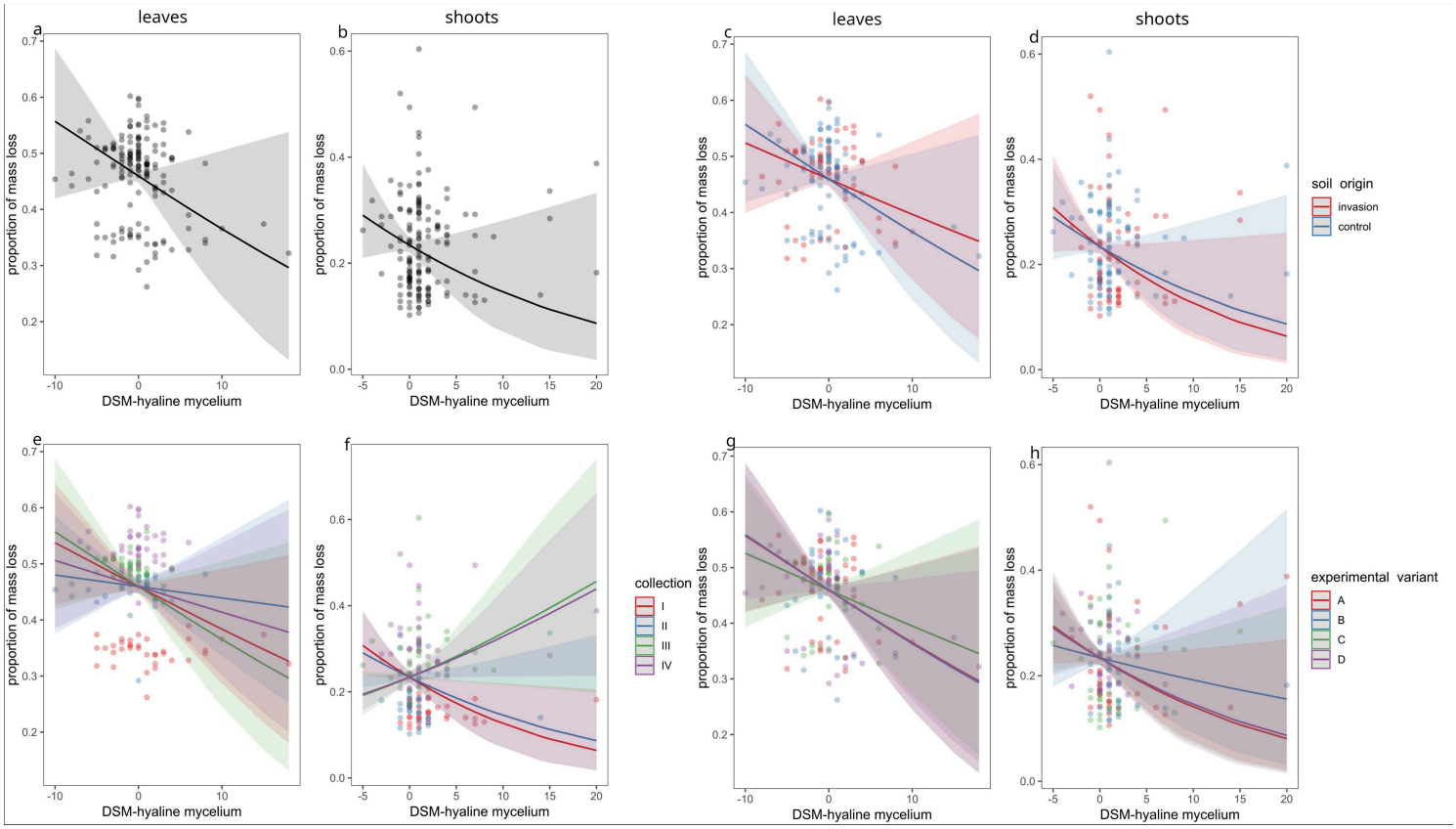

Figure 4

The influence of the difference between the number of hyaline mycelium fragments and dark septate mycelium fragments (H-DR) on the mass loss of leaves (a) and shoots (b), and the influence of H-DR in the interaction with soil origin in leaves c) and shoots (d), the influence of H-DR during different collection periods in leaf (e) and shoots (f) part of the experiment, the influence of H-DR on the mass loss within different experimental variants in the leaves (g) and shoots (h) part of the experiment.

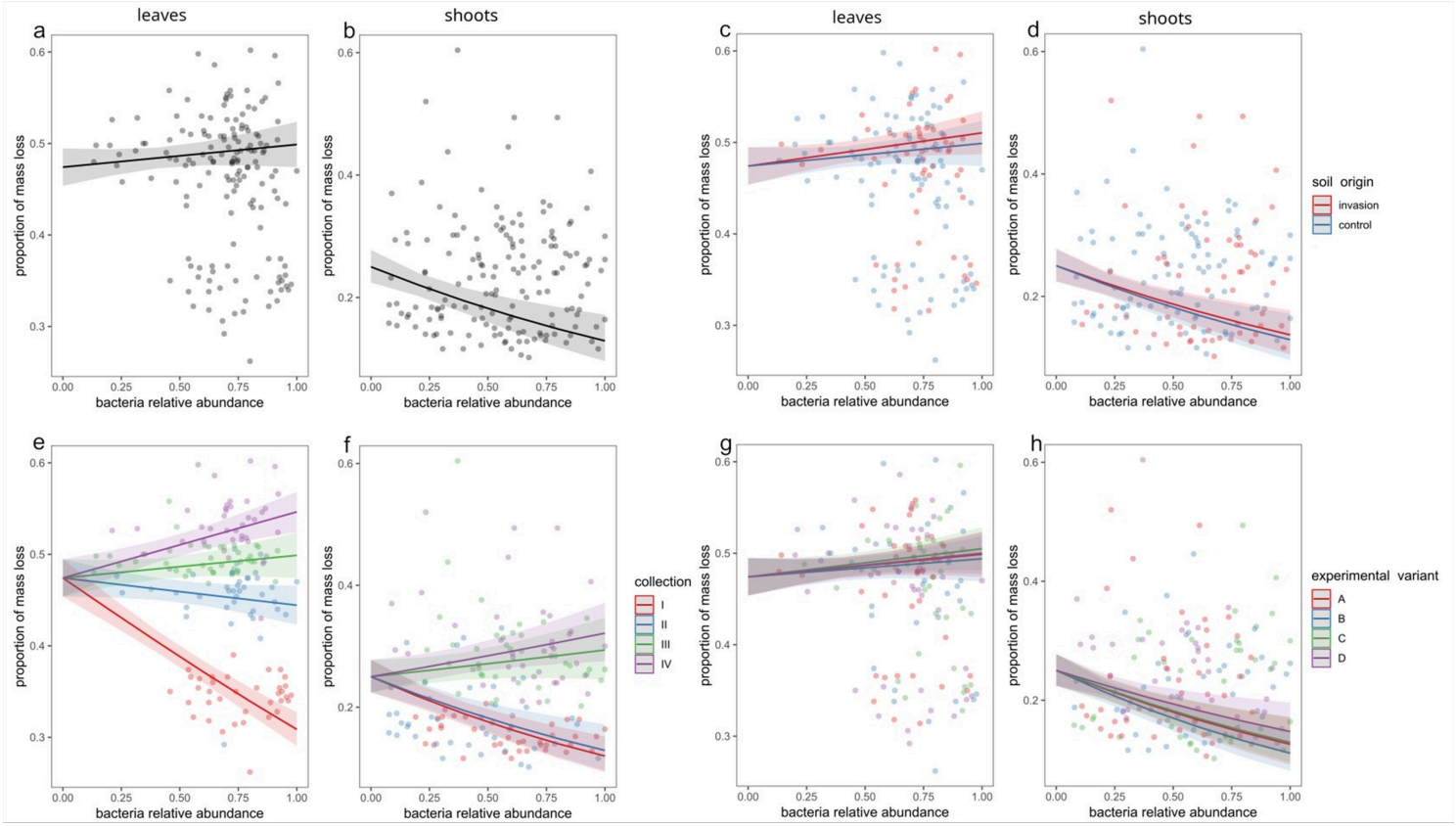

Figure 5

The influence of the bacterial relative abundance on the mass loss of leaves (a) and shoots (b), and the influence of bacterial relative abundance in the interaction with soil origin in leaves c) and shoots (d), the influence of bacterial relative abundance during different collection periods in leaf (e) and shoots (f) part of the experiment, the influence of bacterial relative abundance on the mass loss within different experimental variants in the leaves (g) and shoots (h) part of the experiment.

Supplementary Files

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