Web Ecol., 26, 119–155, 2026
https://doi.org/10.5194/we-26-119-2026

eef Web Ecology Open Access

Forb species benefit more than grasses from a diverse arbuscular mycorrhizal fungal community in semi-arid grasslands

Yelyzaveta Shpilkina[1,10,11], Martti Vasar[2], Sergio Asensio[1,8], Victoria Ochoa[9], Beatriz Gozalo[1], Kolja Enste[3], Martin Zobel[2], Francesco de Bello[5], Marcel van der Heijden[6], Fernando T. Maestre[7], and Lena Neuenkamp[1,3,4]

[1]Instituto Multidisciplinar Para el Estudio del Medio "Ramón Margalef", Universidad de Alicante, Carretera de San Vicente del Raspeig s/n, 03690 San Vicente del Raspeig, Spain
[2]Department of Botany, Institute of Ecology and Earth Sciences, University of Tartu, J. Liivi tn. 2, 50409 Tartu, Estonia
[3]Faculty of Biology, University of Bielefeld, Universitätsstr. 25, 33615 Bielefeld, Germany
[4]Joint Institute for Individualisation in a Changing Environment (JICE), University of Münster and Bielefeld University, Münster and Bielefeld, Germany
[5]Desertification Research Centre (CIDE), Carretera. Moncada-Náquera, Km 4,5. 46113 Valencia, Spain
[6]Agroscope, Reckenholzstrasse 191, 8046 Zürich, Switzerland
[7]Environmental Sciences and Engineering, Biological and Environmental Science and Engineering Division, King Abdullah University of Science and Technology, Thuwal, 23955-6900, Kingdom of Saudi Arabia
[8]Grupo de Ecoloxía Animal (GEA), Universidad de Vigo, 36310 Vigo, Spain
[9]Instituto Universitario de Investigación en el Olivar y Aceites de Oliva-INUO, Universidad de Jaén, 23071 Jaén, Spain
[10]ICREA-Complex Systems Lab, University Pompeu Fabra, Dr. Aiguader 80, Barcelona 08003, Spain
[11]Institut de Biologia Evolutiva, Pg. Maritim de la Barceloneta 37, Barcelona 08003, Spain

Correspondence: Yelyzaveta Shpilkina (liza.shpilkina@gmail.com)

Received: 2 December 2025 – Revised: 30 June 2026 – Accepted: 3 July 2026 – Published: 29 July 2026

Abstract. In exchange for the carbon assimilated by plants, mycorrhizal fungi increase plant nutrient supply, protect them against pathogens and drought, and influence soil formation and aggregation, among other benefits. These processes, in turn, affect the diversity of vegetation and various ecosystem functions, including biomass production. While plant functional diversity is known to mediate mycorrhizal effects on dryland diversity and functioning, experimental tests of such effects are scarce. We conducted an experiment using simplified grassland communities with forbs and grasses to evaluate the effect of arbuscular mycorrhizal fungi (AMF) and their diversity on plant biomass production. At the community level, the impact of AMF richness on plant biomass production was negative, with shoot and root production consistently decreasing with higher AMF richness. However, the biomass response was somewhat mediated by plant functional group identity, revealing that forb species benefit more than grasses from a diverse AMF community. Specifically, leaf production was controlled by grass dominance, leading to grass-dominant communities with low-diversity AMF inoculum producing the most shoot biomass. This research suggests that a full understanding of AMF–plant interactions requires accounting for the complexities of nutrient economy mechanisms, and joint assessment of AMF community diversity and plant functional traits or groups enables us to disentangle these mechanisms in semi-arid grasslands.

Published by Copernicus Publications on behalf of the European Ecological Federation (EEF).

1 Introduction

It is well known that the current plant biodiversity crisis caused by global environmental change compromises ecosystem functioning, reducing the provision of essential ecosystem services (Millennium Ecosystem Assessment, 2005; Díaz and Cabido, 2001; Eisenhauer et al., 2012). While plant biomass production is a crucial ecosystem function and often benefits from plant diversity (Millennium Ecosystem Assessment, 2005; Schnitzer et al., 2011), an increasing body of research has also highlighted the key contribution of soil organisms and their biodiversity to biomass production (van Ruijven et al., 2020; Delgado-Baquerizo et al., 2016). For instance, while some studies have shown that host-specific soil microbes can significantly influence the diversity–productivity relationship (Schnitzer et al., 2011), the specific role of widespread symbiotic partners like arbuscular mycorrhizal fungi (AMF) remains less clear.

Understanding the role of microbial interactions, particularly the symbiosis between plants and arbuscular mycorrhizal fungi (AMF), is of special interest to understand the functioning of natural plant communities and their response to biodiversity loss, as AMF form mutualistic relationships with the majority of land plants (Smith and Read, 2008). Their extensive hyphal network enhance plant nutrient acquisition (Jansa et al., 2011; Smith and Smith, 2011), protect against pathogens and plant diseases (Jung et al., 2012), improve water relations and drought tolerance, and influence soil formation and aggregation, among other benefits (van der Heijden, 2002; Pozo et al., 2015; Augé et al., 2016). Thereby AMF influence the growth of many plant species (Hoeksema et al., 2010). In return, plants supply AMF with carbon compounds, which they cannot synthesize independently (Smith and Read, 2008). Beyond these direct effects, AMF interact with a wide range of organisms – including herbivores, soil invertebrates, saprotrophs, bacteria, and other mutualists (van der Heijden, 2002; Yang et al., 2014; Paudel et al., 2016; Heinen et al., 2018) – in ways that shape plant diversity, alter species composition, and contribute to multiple ecosystem functions (van der Heijden et al., 1998; van der Heijden et al., 2002; van der Heijden et al., 2008; Wagg et al., 2015; Neuenkamp et al., 2018). Although AMF are well known to enhance plant biomass and diversity, a key open question is how they mediate the relationship between plant diversity and productivity – an issue central to elucidating the mechanisms through which biotic interactions affect ecosystem functioning and to predicting ecosystem responses to global change.

A potential modulator of AMF effects on the plant diversity–productivity relationship is the plant resource economy. The benefits derived from the AMF–plant symbiosis depend on the plant's demand for additional nutrients and the associated carbon costs of supporting fungal partners (Johnson et al., 2003). Plant functional traits and types have been shown to influence these benefits (Hoeksema et al., 2010; Neuenkamp et al., 2019). For instance, Hoeksema et al. (2010) reported stronger growth responses to AMF inoculation in non-N-fixing forbs compared to N-fixing species, likely because many studies were conducted on phosphorus-rich soils that may have precluded a net benefit from AMF symbiosis in N-fixing plants and because the higher carbon costs of maintaining both fungal and bacterial symbionts may lead to antagonistic interactions between the two symbioses. In contrast, C4 grasses with thick roots often profit from AMF associations due to their limited capacity to acquire nutrients such as nitrogen and phosphorus. These differences in benefits, often termed AMF dependency (van der Heijden, 2002; Romero et al., 2023), can alter plant competitiveness, coexistence, and ultimately community diversity and productivity (van der Heijden et al., 2002; Neuenkamp et al., 2019). AMF effects on plant coexistence are thought to operate through equalizing mechanisms (Tedersoo et al., 2020) whereby both AMF-dependent and less-dependent species gain more equal access to nutrients. This mechanism can promote productivity by reducing competitive asymmetries (Neuenkamp et al., 2019). Consequently, positive AMF effects on coexistence, diversity, and productivity are expected to be strongest in communities with contrasting resource economies, such as mixtures of different functional types (e.g., grasses and forbs). Yet these assumptions remain largely untested.

At the same time, commercial AMF inoculants are gaining attention in agriculture as potential "biofertilizers" designed to boost AMF spore density and enhance crop yields (Elliott et al., 2020). Unlike diverse natural AMF communities, which comprise taxa with distinct ecological strategies, commercial inocula usually consist of only a few, often widespread species (Brito et al., 2021; Godoy et al., 2023). Because soil microbial diversity generally is linked to ecosystem multifunctionality (Wagg et al., 2014; Jing et al., 2015; Delgado-Baquerizo et al., 2016), AMF diversity is also expected to influence both plant productivity and interspecific interactions (Vogelsang et al., 2006; Mariotte et al., 2012). Although commercial AMF inoculants can increase crop productivity (George and Ray, 2023; Hussain et al., 2021), the current consensus is that intact resident AMF communities are typically more effective and beneficial (Brito et al., 2021). Inconsistencies across studies (Elliot et al., 2020) highlight that the relationship between AMF diversity and plant functional diversity remains poorly understood. Integrating plant functional diversity into AMF research could provide key insights into how fungal diversity regulates ecosystem processes and help explain variation in inoculation outcomes.

To address these gaps, we conducted a greenhouse experiment testing how AMF influence biomass production across plant communities differing in functional diversity, represented by two distinct functional types: grasses and forbs. We assembled four-species communities spanning a gradient in functional diversity (0 %–100 % grasses). While trait-based

metrics such as specific leaf area or specific root area provide finer resolution (Weigelt et al., 2021), functional-type proportions serve as a coarser but informative measure of resource-economy diversity (Díaz and Cabido, 2001). Productivity was measured as plant biomass production over the duration of the experiment in communities with and without AMF, and we further examined the relationship between AMF diversity – measured as AMF richness – and plant biomass production. For inoculation, we used four AMF taxa commonly occurring in European grasslands. Specifically, we hypothesized the following.

H1 The positive effect of plant functional diversity on plant community biomass production increases in the presence of AMF. This is expected because AMF not only enhance resource uptake but also promote resource sharing among plants (Hart et al., 2003; Neuenkamp et al., 2019). If AMF sustain more balanced species representation within communities, greater functional diversity (here, mixtures of grasses and forbs) should enhance ecosystem functioning (Tilman et al., 1997; Cadotte et al., 2011).

H2 The positive effect of plant functional diversity on plant community biomass production increases with AMF richness. AMF richness is hypothesized to promote biomass production through complementarity among fungal species or via sampling effects, where influential taxa are more likely to be present (Wagg et al., 2011; Powell and Rillig, 2018). In communities differing in resource-use strategies, higher AMF richness should increase the likelihood of niche differentiation and complementary interactions (Powell and Rillig, 2018).

2 Methods

2.1 Soil inoculum

We conducted a greenhouse experiment using experimental grasslands as a model system in the greenhouse facilities of the University of Alicante (SE Spain, 38.37978, −0.52732). Grasslands are widely distributed globally and most of their plant species are colonized by AMF, which are essential for their functioning and capacity to deliver ecosystem services (Kojima et al., 2014). In addition, grasslands are frequently used as a model system to study the consequences of biodiversity loss, since grassland species complete their life cycle within a few months and are thus easy to study using manipulative experiments (Tilman et al., 1996; Roscher et al., 2004; Maestre and Reynolds, 2006; Maestre et al., 2006; Eisenhauer et al., 2016).

To test the effect of AMF on the experimental grassland communities, half of them (AMF treatment, labelled as M) received 100 g of living inoculum consisting of substrate and root fragments from four AMF single-spore cultures, while the other half (non-AMF treatment, labeled NM) received the same inoculum after sterilization by autoclaving (121 °C, 90 min). The AMF treatment inoculum comprised four species commonly occurring in European grasslands (Oehl et al., 2010): *Claroideoglomus claroideum* (isolate number, 0913E), *Funneliformis mosseae* (1113B), *Glomus diaphanum* (1013A), and *Rhizoglomus irregularis* (0813B). These species were cultivated in a greenhouse using *Plantago lanceolata* as the host plant in an autoclaved substrate composed of 15 % grassland soil and 85 % sand. Following cultivation, the inoculum contained both the AMF species and their associated microbial communities. Preparation of living and sterile inocula followed Jia et al. (2021), using cultures from the Swiss Collection of AMF (https://www.agroscope.admin.ch/en/swiss-collection-of-arbuscular-mycorrhizal-fungi-saf, last access: 23 July 2026). To ensure that the soil substrate of the experimental plant communities contained the same soil communities and only differed in the presence of the selected AMF species, we followed the three steps below.

1. Each plant community was grown in 3 L pots filled with a 50 %/50 % mixture of gamma-radiated (25 Gky), sterile substrate containing 50 % local sand and 50 % local soil from a nearby field site (provided by Charco Orgánicos Alicantinos S.L.; Alicante, Spain; https://charco.org/, last access: 23 July 2026). The sterilization process for the substrate followed the standard procedure employed by the company Aragogamma S.L. (Barcelona, Spain; https://aragogamma.com/, last access: 23 July 2026), with the substrate being gamma-radiated in smaller sections of 5–6 kg each, ensuring that the height of each block did not exceed 10 cm.

2. 100 g of living or sterilized inoculum was added to each pot.

3. To correct for potential differences in non-AMF soil microbial communities among treatments, all pots received 50 mL of the same microbial filtrate, following Neuenkamp et al. (2019). The microbial wash was prepared by wet-sieving 7 kg of living inoculum through a 25 µm sieve with 14 L of deionized water.

2.2 Greenhouse experiment

To test whether AMF modulate the effect of plant functional diversity on ecosystem functioning, we established a greenhouse experiment with 256 pots containing plant communities spanning a functional diversity gradient. In total, 16 common grassland species of two functional types were selected: grasses (*Agrostis capillaris, Brachypodium retusum, Dactylis glomerata, Deschampsia cespitosa, Festuca rubra, Lolium perenne, Phleum pratensis, and Poa pratensis*) and forbs (*Achillea millefolium, Bellis perennis, Plantago albicans, Prunella vulgaris, Rumex acetosa, Sanguisorba minor, Silene vulgaris,* and *Taraxacum officinalis*), commonly found

across European grasslands. These species vary in leaf and root resource strategies along the acquisitive–conservative spectrum (Weigelt et al., 2021). Four-species communities were assembled to represent a gradient in functional diversity, defined by varying proportions of grasses and forbs (0 %–100 % grasses). While trait-based metrics such as specific leaf area or specific root area provide finer resolution (Weigelt et al., 2021), functional-type proportions offer a coarser but informative proxy for functional diversity (Díaz and Cabido, 2001), which we used here.

Seeds were obtained from a regional producer (Semillas Cantueso S.L.; Villarrubia, Spain), surface-sterilized in 1.25 % sodium hypochlorite, and germinated for 5 weeks (March 2022) in autoclaved sand (121 °C, 90 min). Ten individuals per species were measured for traits including height, diameter, and aboveground and belowground biomass. Seedlings were then transplanted into pots: each community pot contained four individuals (see species combinations in Table A1 in the Appendix). For each species, three monocultures (four seedlings of the same species) were also established. In total, we created 128 communities (80 mixtures and 48 monocultures), each planted both with living AMF inoculum (M) and sterilized inoculum (NM), resulting in 256 pots. To prevent cross-contamination, all tools were sterilized with 90 % ethanol between uses.

Our target variable was community growth rate, measured as biomass production over the experimental period. Plant height (ground to uppermost leaf collar) and stem diameter (two orthogonal measures) were recorded for each individual immediately after planting and again 3 months later. Biomass production was estimated as the difference between initial and final dry biomass, derived from species-specific allometric regressions. For calibration, we measured height, diameter, and root and shoot dry mass (dried at 55 °C for 48 h) of non-transplanted seedlings and tested several geometric proxies for plant volume (e.g., cone, cylinder, cover). The best-fitting geometric variable was then used in linear regressions to predict individual biomass from height and diameter (see Sect. 5 for details).

During the 15-week growth period, pots were randomly arranged on greenhouse benches under a 16 h light: 8 h dark cycle and watered regularly. The duration of the experiment was established accordingly with other greenhouse-based experiments concerning plant–AMF interaction studies (Neuenkamp et al., 2019; Conti et al., 2025; Qin et al., 2022) to ensure advanced AMF colonization and the establishment of adult plant communities. Dead seedlings were replaced during the first 3 weeks, with height and diameter measures updated accordingly. To prevent fungal or bacterial diseases, a potassium–soap solution was applied to all shoots. At harvest (June 2022), all plants were collected, separated into roots and shoots, cleaned, and dried at 55 °C for 48 h. We determined shoot biomass for each individual and root biomass at the community level. To also be able to control for potential shifts in nutrient availability and AM fungal community structure and diversity in the soil, we also collected soil samples from each pot upon harvesting and stored one part at −20 °C for AM fungal community analysis and let the other part dry at air temperature for soil nutrient analysis.

2.3 Assessment of AMF colonization and communities

2.3.1 AMF root colonization

To assess inoculation success, percentage colonization by AM fungi of the roots of the plant individuals in experimental plant communities was estimated from a subset of samples for every treatment combination ($n = 5 \times 3 \times 2 =$ 30 individual samples). We stained the roots with blue ink, mounted them on microscope slides, and estimated colonization using the magnified grid–line intersection method (McGonigle et al., 1990). In each sample, presence and absence of AMF structures (hyphae, vesicles, arbuscules, and coils) were scored for at least 50 intersections of the root and the vertical crosshair using a light microscope at 400× magnification. An intersection was considered mycorrhizal if the vertical crosshair intersected any AMF structure. We found root colonization for inoculated and control samples, and thus present colonization and subsequent effects on plant performance results not only from soil inoculum but also from airborne spores and AMF present in the potting substrate.

2.3.2 AMF community sequencing, quality control, and identification

We assessed whether inoculation effects on plant performance were driven not only by changes in overall AMF abundance but also by shifts in AMF community composition and diversity. Therefore, we analyzed AMF community structure in a subset of samples ($n = 96$) using DNA-based AMF species richness of experimental soils.

DNA was extracted from 0.5 g of frozen soil with the DNeasy PowerSoil Pro Kit (Qiagen) following the company's instructions. AMF sequences were amplified from soil DNA extracts using the fungal-specific primers for the second internal transcribed spacer (ITS2) ribosomal RNA marker region: forward primer – fITS7 (5′ GTGARTCATCGAATCTTTG 3′) (Ihrmark et al., 2012); reverse primer – ITS4 (5′ TCCTCCGCTTATTGATATGC 3′) (White et al., 1990). These primers also included the primer sequences attached to their 5' ends for Illumina sequencing. The ITS7-ITS4 primer pair amplifies the fungal ITS2 region and targets the broader fungal community rather than AMF specifically. Consequently, AMF sequences typically represent a relatively small proportion of the total reads obtained with this primer set. Nevertheless, previous studies have shown that ITS-based approaches can still capture AMF diversity and produce comparable ecological patterns when AMF reads are extracted from the broader fungal dataset (Kohout et al., 2013; Lekberg et al., 2018). The high sequencing depth in our study therefore allowed detection of AMF taxa despite

their relatively low representation in the total fungal community.

In the first amplification step, PCRs were carried out in a final volume of 12.5 µL, containing 4.5 µL of template DNA, 0.5 µM of the primers, 7.81 µL of Supreme NZYTaq 2x Green Master Mix (NZYTech), and ultrapure water up to 12.5 µL. The reaction mixture was incubated as follows: an initial denaturation step at 95 °C for 5 min, followed by 35 cycles of 95 °C for 30 s, 47 °C for 45 s, 72 °C for 45 s, and a final extension step at 72 °C for 7 min.

Symmetric dual-indexing oligonucleotides (eight base pairs) required for multiplexing samples within the same sequencing pool were added in a second PCR step, using identical conditions but with only five cycles and an annealing temperature of 60 °C. For a schematic overview of the library preparation process, please see Fig. 1 in Vierna et al. (2017).

Library size was verified by running the libraries on 2 % agarose gels stained with GreenSafe (NZYTech) and imaging them under UV light. Then, libraries were purified using the Mag-Bind RXNPure Plus magnetic beads (Omega Bio-tek), following the instructions provided by the manufacturer. Finished libraries were pooled in equimolar quantities according to the results of a Qubit dsDNA HS Assay (Thermo Fisher Scientific) quantification. The pool was sequenced using Illumina sequencing in a fraction of a NovaSeq 6000 PE250 flow cell (Illumina) with a 2×250 base pair (bp) chemistry, targeting a total output of 8 gigabases (Gb).

General fungal sequences (ITS) were analysed using the gDAT pipeline (Vasar et al., 2021). Reads were demultiplexed by sample using double barcodes, allowing one mismatch per read. Primer sequences were verified with the same mismatch tolerance. Only paired-end reads with an average quality score > 30 for both reads were retained, and barcode and primer sequences were subsequently removed. Sequences were trimmed at 220 bases for forward and 180 bases for reverse reads to improve the combination rate following Sepp et al. (2021). Paired-end reads were combined with FLASh (v1.2.10, Magoč and Salzberg, 2011), using the default thresholds: overlap between 10 bp and 300 bp and overlap identity at least 75 %; orphaned reads were removed. Combined sequences were clustered with 97 % identity using vsearch (v2.14.1, Rognes et al., 2016) into operational taxonomic units (OTUs), used here as a proxy for putative species-level diversity and a threshold commonly applied in fungal community studies to enable comparison across datasets (Schreiner et al., 2026). Putative chimeric sequences were identified and removed using vsearch in reference mode using the UNITE database (status April 2024; Nilsson et al., 2018).

General fungal sequences (ITS) were assigned to taxa in the UNITE database (status April 2024; Nilsson et al., 2018) with 80 % alignment and 90 %, 95 %, and 97 % alignments for identification up to family, genus, and species level, respectively. To extract the AMF taxa from the general fungal taxa, only those taxa were selected and assigned to the phylum Glomeromycota and the functional group AMF based on the FungalTraits database (Põlme et al., 2020). Only FungalTraits assignments with confidence levels of probable and highly probable were retained, whereas the remaining fungal taxa were considered undefined fungi.

Illumina 2×250 bp sequencing produced a total of $2 \times 6\,003\,112$ raw paired-end reads for the fungal ITS marker region. After quality control, combining the paired-end reads and the removal of chimeric sequences, 5 688 263 final reads remained for downstream analysis. Singleton reads (i.e., those occurring only once in the dataset) were removed prior to read pairing. Amplicon sequencing of 96 soil samples yielded 6355 fungal OTUs (ITS region), of which 233 were assigned to AMF. AMF diversity was quantified as species richness, defined as the number of OTUs belonging to AMF. To account for differences in sequencing depth among samples, richness was rarefied to the minimum number of sequences per sample using the rarefy function in the vegan package (Oksanen et al., 2024) within R (ver. 4.2.2) and RStudio (ver. 2022.12.0). Representative sequences for treatment combinations are accessible from the European Nucleotide Archive under BioProject ID PRJNA1345342.

2.4 Soil nutrient analysis

Plant-available nitrogen (nitrate and ammonium) and phosphorus (phosphate) were measured in dried soil samples as those nutrients are known to potentially interact with plant–AMF interactions (Hoeksema et al., 2010). Ammonium and nitrate were extracted with 0.5 M K_2SO_4 at a 1 : 5 soil : extractant ratio, following Maestre et al. (2022). Soil suspensions were shaken for 1 h at 200 rpm and 20 °C, and then filtered through 0.45 µm Millipore filters. Plant-available P (P Olsen; PO_4^{3-}–P) was extracted from 0.5 g of soil with 30 mL of 0.5 M $NaHCO_3$ (pH 8.5), by shaking for 16 h at 200 rpm and 20 °C, and then filtered through 0.45 µm Millipore filters. K_2SO_4 and $NaHCO_3$ filtrates were stored at 4 °C and analyzed colorimetrically within 24 h of extraction. Ammonium concentration was determined directly using the indophenol blue method and expressed as µg N-NH_4^+ g^{-1} soil (Sims et al., 1995). Nitrate was first reduced to NH_4^+-N with Devarda's alloy, quantified using the same method and expressed as µg N-NO_3^- g^{-1} soil. Phosphorus concentration was determined colorimetrically at 660 nm following the malachite green method (Fernández et al., 1985) and expressed as µg P-PO_4 g^{-1} soil.

2.5 Initial biomass estimation via allometries

We used community biomass production as a proxy for ecosystem functioning (Millennium Ecosystem Assessment, 2005; Schnitzer et al., 2011). To calculate the growth rate of plants, we needed data for the final biomass production (June 2022) and the initial biomass production (March 2022),

which we lacked. To estimate initial biomass production, we used allometric models, which are a common and time-efficient way to estimate plant biomass production without destructive plant harvest by establishing the relationship between plant size and biomass production (Sala and Austin, 2000). Allometric models are commonly used to estimate the biomass of trees and shrubs (Northup et al., 2005; Ali et al., 2015; Huff et al., 2017), but fewer studies have been conducted with grasses and forbs (Sanaei et al., 2018).

We analyzed the relationships between seedling biomass (aboveground and belowground) and morphological traits (height and diameter). Height was measured as the vertical distance from the tallest vegetative part to the soil surface, and diameter was determined from two orthogonal measurements of plant spread taken from above. These traits were then incorporated into geometric formulas representing canopy size and plant volume: (1) cone volume, (2) cylinder volume, and (3) plant coverage area:

$$V_{\text{cone}} = \frac{1}{3} \times \pi \times r^2 \times h, \quad (1)$$

$$V_{\text{cylinder}} = \pi \times r^2 \times h, \quad (2)$$

$$V_{\text{coverage}} = \pi \times r^2, \quad (3)$$

where r refers to the radius of the plant (calculated from the diameter measure) and h is its height.

For each plant species, we used correlation analysis between biomass and geometric measures. We identified the geometric variable best related to seedling biomass based on correlation analyses, using goodness-of-fit measures (p values and coefficients of determination, R^2; Tables A2 and A3 in the Appendix) and visual inspection of correlation plots (Figs. A1 and A2 in the Appendix). Because biomass can exhibit logarithmic relationships with geometric measures, log-transformed variables were also included in the analysis. Outliers were identified visually following the recommendations of Zuur et al. (2010). Species-specific models were used instead of a pooled model because species differ markedly in morphology and resource-use strategies, making separate allometric relationships more accurate for biomass estimation and ecologically meaningful (Shipley et al., 2006; Poorter et al., 2011; Mulatu et al., 2024).

Correlation plots were generated using the ggplot function from the ggplot2 package (Wickham, 2016), and correlation analyses were performed with the corr.test function from the psych package (Revelle, 2023). To facilitate data management, the melt function from the reshape2 package (Wickham, 2007) was used to transform the data from wide to long format, in which variable names and their corresponding values are stored in separate columns. The complete R code, as well as dataset (Neuenkamp and Shpilkina, 2026), for this part of analysis is available via Zenodo (Neuenkamp, 2026).

The estimated initial aboveground and belowground biomass from the calculated allometric coefficient for each plant community is summarized in Table A4 in the Appendix. The corresponding growth rate measurement obtained by subtracting final from the initial biomass for each experimental community and grass dominance percentages is represented in Table A5 in the Appendix.

2.6 Statistical analysis

To test the effects of AMF presence, AMF diversity, and grass dominance on plant biomass production, we performed two-way analyses of variance (ANOVA). For the AMF presence treatment, the independent variables were (1) AMF treatment (M vs. NM) and (2) grass dominance percentage, with five levels (0 %, 25 %, 50 %, 75 %, and 100 %, depending on the proportion of grasses in the community). For the AMF diversity analysis, the independent variables were (1) rarefied AMF richness and (2) grass dominance percentage, again with five levels.

Analyses followed a stepwise procedure: average AMF and grass-dominance effects were estimated using linear regression models (lm function, base R; Zuur et al., 2009). Model residuals were visually inspected to verify assumptions of homogeneity of variances and normality. When assumptions were not met, response variables were log-transformed to stabilize residual variances (Zuur et al., 2010). Model estimates were then tested for significance using ANOVA (Anova function, car package; Fox et al., 2019). Both additive and interactive effects of predictors were initially included; however, when interaction terms were non-significant, only additive effects were retained to maximize statistical power and model parsimony (Zuur et al., 2010). As some variation in plant-available soil nutrients (nitrate, ammonium, phosphate) was visible among independent variable combinations (Figs. A3 and A4 in the Appendix), such variation was accounted for in all models by adding the first principal component axis (soil PC1) as an additional additive independent variable (prcomp function, stats package; R Core Team, 2025). All statistical analyses were carried out in R (ver. 4.2.2) in the RSTUDIO environment (ver. 2022.12.0). Data visualization was performed using functions from base R, the ggplot2 package (Wickham, 2016), and the patchwork package (Pedersen, 2024). Database management was performed using Microsoft Excel software. The complete R code, as well as dataset (Neuenkamp and Shpilkina, 2026), for this part of analysis is available via Zenodo (Neuenkamp, 2026).

3 Results

3.1 AMF inoculation success

Root colonization was detected in both inoculated and control samples (mean ± SE: control = 53 % ± 27 %; inoculated = 61 % ± 29 %), with a similar proportion of AMF sequences among all fungal DNA reads (≈ 0.03 % in both treatments). These findings indicate that control soils were not en-

tirely AMF-free, and inoculation effects cannot be attributed simply to AMF presence or abundance. However, molecular analyses of soil DNA revealed that inoculation significantly altered AMF community structure and diversity. Specifically, AMF diversity was reduced in inoculated samples (Fig. 1, Table 1), likely because the inoculum concentrated community composition around the four introduced strains, whereas control treatments supported a broader range of fungal taxa. Therefore, we focus our further analysis on the effect of AMF diversity in interaction with plant community structure on biomass production, moving beyond the initial presence-absence approach.

3.2 AMF diversity and plant functional diversity effects on plant biomass production

Plant biomass production over the course of the experiment, measured as plant growth rates, decreased with AMF diversity (Fig. 2). For leaf biomass production, the degree of decrease depended on the proportion of grasses with negative responses to AMF richness increasing with proportion of grasses ($F = 3.564$, $p = 0.063$; Fig. 2A). Due to the experimental communities with very high AMF richness (> 40 taxa) this grass-proportion-mediated AMF richness effect was weak and only marginally significant ($p < 0.1$). Root biomass production showed a clear decline with increasing AMF richness independently of grass proportion in experimental communities ($F = 8.810$, $p = 0.004$; Fig. 2B). Grass dominance showed significant effects on aboveground (Fig. 2A) but not on belowground biomass production (Fig. 2B).

4 Discussion

4.1 Focus shift: from AMF presence to AMF diversity effects

The effect of AMF on ecosystem functioning is a developing area of plant-mycorrhizal research (van der Heijden et al., 2015; Klironomos et al., 2010). However, the contribution of AMF biodiversity to ecosystem functioning remains yet understudied (Powell and Rillig, 2018), while being crucial to understand soil functioning and plant community dynamics. Our first hypothesis explicitly addressed the effect of the presence of AMF and their interaction with plant functional diversity on biomass production. However, as stated in Sect. 3.1, both treatments, inoculated with living AMF and control inoculum, showed a similar degree of AMF colonization. This suggests that our initial focus on AMF presence-versus-absence effect was no longer relevant, and we shifted the focus of our analysis to the influence of AMF richness and plant functional diversity on biomass production, as discussed in detail in Sect. 4.2. This shift aligns more closely with natural and agricultural systems, where soils are rarely AMF-free and where plant responses occur in the presence of naturally occurring AMF communities rather than sterile controls (e.g., Wubs et al., 2016; Neuenkamp et al., 2019). Although unexpected, this outcome gave us the opportunity to discuss the possible impact of commercial AMF inocula, resulting in higher plant biomass production but at the price of naturally occurring AMF diversity.

Regarding the possible pathways of the AMF contamination of control pots, three different pathways are most likely. First, although the soil irradiation was carried out by an external facility following standard procedures as described in the Methods section, incomplete sterilization cannot be entirely ruled out. Second, AMF spores may disperse via air and dust (Chaudhary et al., 2020), particularly under greenhouse conditions with high humidity and open ventilation. This was the case in our experiment at the beginning due to high outside humidity after spring rainfalls. In this case, the contamination should have affected both pots, inoculated with fungal and control inoculum. However, it is likely that the already established, highly competitive inoculated AMF occupied the available root and soil niches, limiting the establishment of external background taxa through competitive exclusion. Finally, seeds themselves may represent a potential source of AMF propagules even after their sterilization as described in the Methods section and as demonstrated for Glomeromycota DNA in surface-sterilized seeds of grass species (Guo et al., 2020).

4.2 Effects of AMF richness and plant functional composition on biomass production

Contrary to the expectation that greater AMF and plant functional diversity enhances ecosystem functioning, we observed that increased AMF richness negatively affected plant biomass production, with this effect being either independent of or decreasing with functional diversity (hypothesis 2). Analysis of AMF root colonization and AMF community composition showed that inoculation effects were mostly driven by shifts in AMF richness and not AMF abundance. These results support earlier studies showing clear effects of AMF composition on plant competition and ultimately community assembly (Neuenkamp et al., 2019). Theory predicts stronger functioning of diverse communities due to complementary resource use (Wagg et al., 2011; Powell and Rillig, 2018), and one should thus expect stronger promotion of plant biomass production by diverse AMF communities (Maherali and Klironomos, 2007; Wagg et al., 2014). Our results contradict this assumption as biomass production decreased with AMF richness, suggesting that dominance of a few well-functioning AMF taxa was the more relevant driver of biomass production.

Indeed, differences in AMF functionality, such as promotion of plant growth, exist (Maherali and Klironomos, 2007), with the inoculated taxa being among those known for their functionality and competitiveness (e.g., *Rhizoglomus intraradices, Glomus claroideum)* (Janoušková et al.,

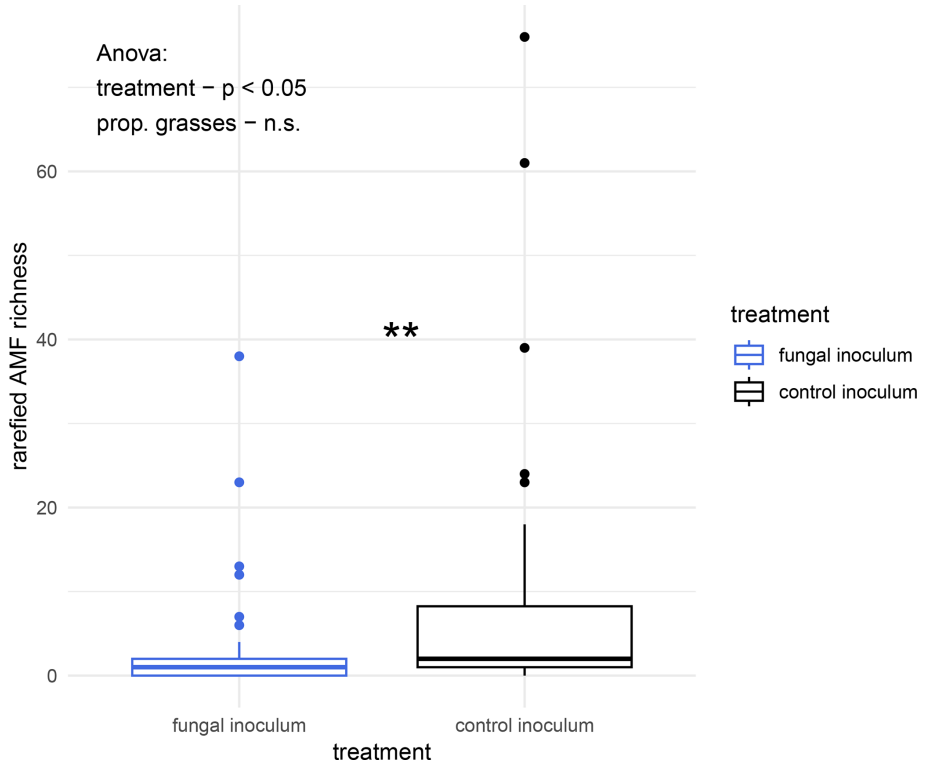

Figure 1. Differences in arbuscular mycorrhizal fungal (AMF) richness in samples with living AMF inoculum (mycorrhizal) and sterilized inoculum (non-mycorrhizal). Boxplots represent the rarefied number of AMF taxa for non-mycorrhizal (NM) and mycorrhizal (M) treatments. AMF richness was significantly lower in mycorrhizal treatments compared to non-mycorrhizal treatments. The proportion of grasses had no significant effect on AMF richness. ** indicates $p < 0.01$.

Table 1. Summary of statistical results from linear models of leaf growth rate, root growth rate, and rarefied arbuscular mycorrhizal fungal (AMF) richness. Shown are effect estimates and their standard errors (SE) retrieved from linear models, as well as the sum of squares (Sum Sq), degrees of freedom (Df), test statistic (F value), and significance (p value) for all explanatory variables from ANOVAs. All response variables were log transformed to conform with parametric modeling assumptions.

Response	Explanatory variables	Estimate	SE estimate	Sum Sq	Df	F value	p value
Leaf growthratelog	AMF richnessrarefied, log	0.0013	0.0436	0.000	1	0.001	0.977
	Proportion of grasses (%)	0.0026	0.0012	0.269	1	4.595	0.035
	Soil PC1	−0.0409	0.0142	0.489	1	8.342	0.005
	AMF richness*proportion of grasses (%)	−0.0012	0.0007	0.173	1	2.960	0.089
Root growthratelog	AMF richnessrarefied, log	−0.0875	0.0293	0.747	1	8.929	0.004
	Proportion of grasses (%)	0.0005	0.0010	0.026	1	0.312	0.578
	Soil PC1	−0.0263	0.0169	0.203	1	2.421	0.124
AMF richnessrarefied, log	Treatment	0.6932	0.2486	9.054	1	7.778	0.007
	Proportion of grasses (%)	−0.0041	0.0036	1.495	1	1.284	0.261
	Soil PC1	0.0462	0.0649	0.591	1	0.508	0.278

2013). Supporting this assumption, inoculation coincided in our experiment with higher biomass production and lower AMF richness, thereby indicating that inoculation steered AMF communities to the dominance of the four inoculated AMF taxa (Janoušková et al., 2017; Islam et al., 2021). AMF richness diversity was consequently higher in control than inoculated plant communities, showing an unsuccessful AMF-free control treatment, which was underlined by equal AMF root colonization across treatments. Nevertheless, DNA-based assessment of AMF richness allowed us

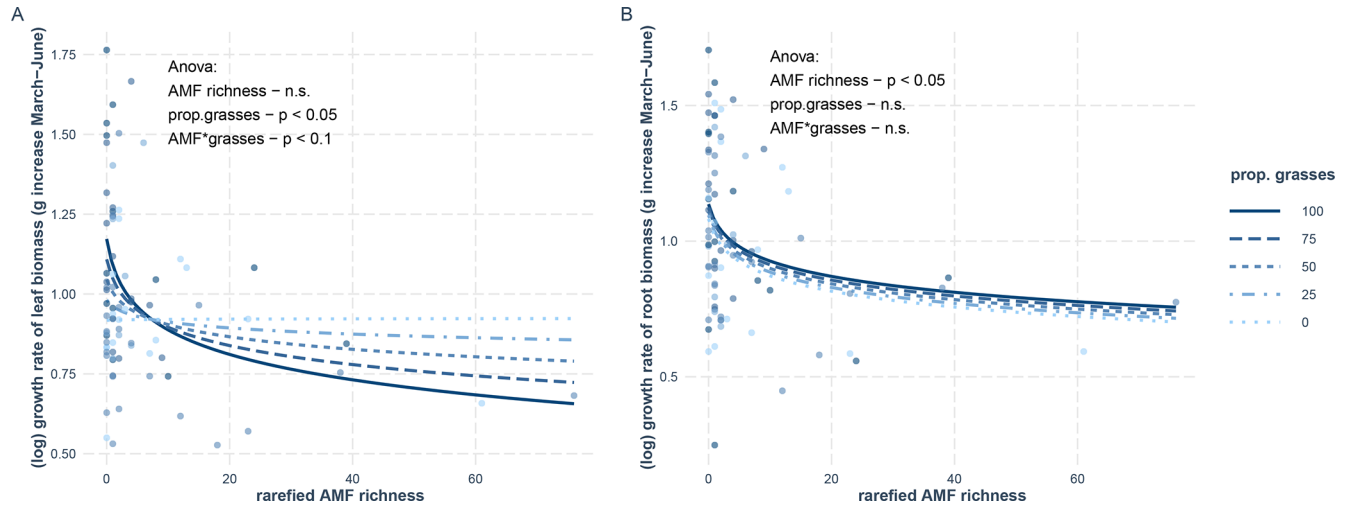

Figure 2. Effects of arbuscular mycorrhizal fungal (AMF) richness and grass proportion (prop. grasses, %) on the growth rate of leaf **(A)** and root **(B)** biomass. Growth responses to AMF richness are shown for different degrees of grass proportion. Rarefied AMF richness was used as a response variable.

to detect an inoculation-generated gradient of AMF richness with subsequent effects on plant biomass production, highlighting the relevance of qualitative AMF community aspects like composition beyond purely presence/absence when assessing AMF effects.

Finally, the observed dependency of aboveground biomass responses to AMF richness on plant functional diversity (i.e. grass dominance) in our experimental communities support the idea of coupling between plant and AMF functional composition (Neuenkamp et al., 2019; Tedersoo et al., 2020). It was expected that where AMF facilitate resource sharing, this effect should become stronger with increasing AMF and plant functional diversity through diversified resource uptake strategies including AM symbiosis, leading to synergistic effects that boost ecosystem functioning (Tilman et al., 1997; Cadotte et al., 2011). Such synergy implies that higher plant functional diversity should enable stronger AMF effects by enhancing the chance of effective matches between plant and AMF individuals based on their host preferences. However, growth rate dynamics observed in our experiment contradict the assumed positive relationship between AMF and plant diversity (Hiiesalu et al., 2014), as biomass production in grass-dominated plant communities profited not from high AMF diversity but from the engineered low-diversity inoculum. In contrast, plant communities predominantly composed of forb species benefited more from the presence of a diverse AMF community. As previously mentioned, these observations could be related to agricultural soils, where competitive AMF strains can be used to enhance crop production (George and Ray, 2023; Hussain et al., 2021) but at the cost of sacrificing soil mycorrhizal diversity (Neuenkamp et al., 2024).

4.3 Relevance of AMF and plant functional composition on ecosystem functioning

Our hypotheses focused on the mediation of AMF effects on biomass production by plant functional composition, whose results we discussed above. While we found little evidence for interactive effects, our study showed that plant aboveground and belowground biomass production was mediated primarily by different drivers.

Plant functional composition was the primary driver of grassland aboveground biomass production, while AMF diversity was the primary driver of grassland belowground biomass. Contrary to our expectations, and similar to the AMF richness effects, aboveground biomass was highest in communities dominated by grasses, while a mix of functional types (grasses and forbs) did not increase biomass production. We observed no effect of functional composition on belowground biomass production, which is surprising since one proposed mechanism by which ecosystem functioning might be regulated is plant functional diversity (Gross et al., 2017; Cadotte et al., 2011; Le Bagousse-Pinguet et al., 2021). Grasses and forbs often have different root systems and strategies for resource acquisition (Neuenkamp et al., 2019; Hoeksema et al., 2010), which should allow them to acquire nutrients more efficiently, thus enhancing overall biomass production in the community. However, our result indicates that the presence and influence of dominant grass species play a significant role in driving aboveground biomass production in experimental grassland ecosystems. Grasses are known for their high growth rates and efficient resource acquisition strategies (Da Silveira Pontes et al., 2015). Additionally, functional traits of dominant types can have an important impact on ecosystem functions because dominant species contribute more to community-level properties than

other species (Cheng et al., 2021; Lisner et al., 2023). Indeed, previous studies highlighted that the identification of relevant functional traits of dominant species are essential to understanding the role of plant diversity in such ecosystem processes as aboveground biomass production (Roscher et al., 2012; Cadotte et al., 2009; Lisner et al., 2023). Given that belowground biomass production lacked such a pronounced effect of functional composition (i.e., grass dominance), maybe competition for light in communities was a relevant driver of aboveground biomass (Weiner, 1990). Grasses due to their upright growth can avoid light competition better compared to forbs with larger, more horizontally positioned leaves. Nevertheless, as the observed context-dependency of AMF diversity effects with grass dominance were statistically weak ($p < 0.1$), more experiments are needed to further investigate the nature and relevance of this context-dependency.

Consistent with our expectations, biomass production responded to differences in AMF community structure, although belowground biomass showed a stronger response than aboveground biomass. The relatively stronger effect of AMF richness on belowground compared to aboveground biomass production may be attributed to the resource exchange dynamics between plant species and AMF. Certain plant species may prioritize allocating nutrients to AMF or to belowground biomass rather than allocating them towards aboveground biomass production. Indeed, many grassland species are known to concentrate their biomass belowground (de Miranda et al., 2014). A recent large-scale study demonstrated that mycorrhizal symbiosis enhances soil carbon storage by elevating biomass allocation to belowground (Zhang et al., 2025). Additionally, due to this belowground investment, the hyphal network is expected to be enhanced, improving soil structure and potentially leading to increased water and nutrient uptake and availability for other plant species in the community, affecting plant composition and even promoting plant diversity, as also observed in Zhang et al. (2025).

5 Conclusions

Our results show that AMF richness and grass dominance independently influenced plant biomass production. Grass dominance increased aboveground biomass, likely reflecting the advantageous morphological and functional traits of grass species. In contrast, AMF richness had a stronger effect on belowground biomass, with only a weak influence on aboveground productivity, suggesting that AMF primarily enhance root-mediated resource acquisition and allocation. However, inoculation also reduced overall AMF richness, likely due to the dominance of the competitive strains included in the inoculum. This finding has implications for sustainable agriculture, where AMF are often promoted as a "green" alternative to chemical fertilizers (George and Ray, 2023), but their consequences on local soil biodiversity, biotic interactions, and ecosystem functioning are poorly understood (Neuenkamp et al., 2024). Thus, a next step would be to assess the coupling of AMF and plant functional diversity effects on ecosystem processes such as nutrient cycling, especially as our models revealed some treatment-dependent variation in soil nutrient availability.

Appendix A

Table A1. Full list of the experimental plant communities' composition; each community contains four individuals. Communities labelled as "M" contain living AMF inoculum, the ones labelled as "NM" contain sterile AMF inoculum.

Ordered ID	Label	Species 1	Species 2	Species 3	Species 4
1	M_SM1	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*
2	M_SM2	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*
3	M_SM3	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*
4	M_AM1	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*
5	M_AM2	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*
6	M_AM3	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*
7	M_BP1	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*
8	M_BP2	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*
9	M_BP3	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*
10	M_TO1	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*
11	M_TO2	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*
12	M_TO3	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*
13	M_PA1	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*
14	M_PA2	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*
15	M_PA3	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*
16	M_PV1	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*
17	M_PV2	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*
18	M_PV3	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*
19	M_RA1	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*
20	M_RA2	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*
21	M_RA3	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*
22	M_SV1	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*
23	M_SV2	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*
24	M_SV3	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*
25	M_BR1	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*
26	M_BR2	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*
27	M_BR3	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*
28	M_DG1	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*
29	M_DG2	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*
30	M_DG3	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*
31	M_FR1	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*
32	M_FR2	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*
33	M_FR3	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*
34	M_LP1	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*
35	M_LP2	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*
36	M_LP3	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*
37	M_PHP1	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*
38	M_PHP2	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*
39	M_PHP3	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*
40	M_PP1	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*
41	M_PP2	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*
42	M_PP3	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*
43	M_AC1	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*
44	M_AC2	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*
45	M_AC3	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*
46	M_DC1	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*
47	M_DC2	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*
48	M_DC3	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*
49	M_G1	*Brachypodium retusum*	*Dactylis glomerata*	*Festuca rubra*	*Phleum pratensis*
50	M_G2	*Dactylis glomerata*	*Festuca rubra*	*Phleum pratensis*	*Agrostis capillaris*

Table A1. Continued.

Ordered ID	Label	Species 1	Species 2	Species 3	Species 4
51	M_G3	*Brachypodium retusum*	*Dactylis glomerata*	*Phleum pratensis*	*Poa pratensis*
52	M_G4	*Festuca rubra*	*Phleum pratensis*	*Poa pratensis*	*Deschampsia cespitosa*
53	M_G5	*Brachypodium retusum*	*Dactylis glomerata*	*Lolium perenne*	*Phleum pratensis*
54	M_G6	*Dactylis glomerata*	*Lolium perenne*	*Phleum pratensis*	*Agrostis capillaris*
55	M_G7	*Dactylis glomerata*	*Phleum pratensis*	*Deschampsia cespitosa*	*Agrostis capillaris*
56	M_G8	*Brachypodium retusum*	*Festuca rubra*	*Poa pratensis*	*Deschampsia cespitosa*
57	M_G9	*Brachypodium retusum*	*Lolium perenne*	*Deschampsia cespitosa*	*Agrostis capillaris*
58	M_G10	*Festuca rubra*	*Phleum pratensis*	*Deschampsia cespitosa*	*Agrostis capillaris*
59	M_G11	*Festuca rubra*	*Lolium perenne*	*Phleum pratensis*	*Poa pratensis*
60	M_G12	*Brachypodium retusum*	*Festuca rubra*	*Phleum pratensis*	*Agrostis capillaris*
61	M_G13	*Dactylis glomerata*	*Lolium perenne*	*Poa pratensis*	*Deschampsia cespitosa*
62	M_G14	*Dactylis glomerata*	*Festuca rubra*	*Phleum pratensis*	*Deschampsia cespitosa*
63	M_G15	*Phleum pratensis*	*Poa pratensis*	*Deschampsia cespitosa*	*Agrostis capillaris*
64	M_G16	*Brachypodium retusum*	*Phleum pratensis*	*Deschampsia cespitosa*	*Agrostis capillaris*
65	M_F1	*Achillea millefolium*	*Bellis perennis*	*Prunella vulgaris*	*Rumex acetosa*
66	M_F2	*Taraxacum officinale*	*Prunella vulgaris*	*Rumex acetosa*	*Silene vulgaris*
67	M_F3	*Sanguisorba minor*	*Taraxacum officinale*	*Prunella vulgaris*	*Silene vulgaris*
68	M_F4	*Sanguisorba minor*	*Bellis perennis*	*Prunella vulgaris*	*Rumex acetosa*
69	M_F5	*Sanguisorba minor*	*Achillea millefolium*	*Bellis perennis*	*Rumex acetosa*
70	M_F6	*Achillea millefolium*	*Taraxacum officinale*	*Plantago albicans*	*Rumex acetosa*
71	M_F7	*Sanguisorba minor*	*Achillea millefolium*	*Plantago albicans*	*Prunella vulgaris*
72	M_F8	*Sanguisorba minor*	*Achillea millefolium*	*Taraxacum officinale*	*Prunella vulgaris*
73	M_F9	*Achillea millefolium*	*Bellis perennis*	*Taraxacum officinale*	*Silene vulgaris*
74	M_F10	*Achillea millefolium*	*Plantago albicans*	*Prunella vulgaris*	*Silene vulgaris*
75	M_F11	*Achillea millefolium*	*Bellis perennis*	*Plantago albicans*	*Silene vulgaris*
76	M_F12	*Bellis perennis*	*Taraxacum officinale*	*Prunella vulgaris*	*Silene vulgaris*
77	M_F13	*Sanguisorba minor*	*Taraxacum officinale*	*Rumex acetosa*	*Silene vulgaris*
78	M_F14	*Sanguisorba minor*	*Plantago albicans*	*Rumex acetosa*	*Silene vulgaris*
79	M_F15	*Sanguisorba minor*	*Bellis perennis*	*Plantago albicans*	*Prunella vulgaris*
80	M_F16	*Sanguisorba minor*	*Achillea millefolium*	*Plantago albicans*	*Rumex acetosa*
81	M_GF1	*Bellis perennis*	*Festuca rubra*	*Lolium perenne*	*Phleum pratensis*
82	M_GF2	*Taraxacum officinale*	*Plantago albicans*	*Prunella vulgaris*	*Festuca rubra*
83	M_GF3	*Taraxacum officinale*	*Dactylis glomerata*	*Phleum pratensis*	*Agrostis capillaris*
84	M_GF4	*Achillea millefolium*	*Plantago albicans*	*Dactylis glomerata*	*Lolium perenne*
85	M_GF5	*Sanguisorba minor*	*Plantago albicans*	*Silene vulgaris*	*Festuca rubra*
86	M_GF6	*Bellis perennis*	*Silene vulgaris*	*Festuca rubra*	*Deschampsia cespitosa*
87	M_GF7	*Taraxacum officinale*	*Brachypodium retusum*	*Festuca rubra*	*Phleum pratensis*
88	M_GF8	*Taraxacum officinale*	*Plantago albicans*	*Dactylis glomerata*	*Lolium perenne*
89	M_GF9	*Prunella vulgaris*	*Rumex acetosa*	*Poa pratensis*	*Deschampsia cespitosa*
90	M_GF10	*Sanguisorba minor*	*Dactylis glomerata*	*Lolium perenne*	*Poa pratensis*
91	M_GF11	*Achillea millefolium*	*Taraxacum officinale*	*Prunella vulgaris*	*Lolium perenne*
92	M_GF12	*Sanguisorba minor*	*Prunella vulgaris*	*Brachypodium retusum*	*Festuca rubra*
93	M_GF13	*Sanguisorba minor*	*Festuca rubra*	*Lolium perenne*	*Poa pratensis*
94	M_GF14	*Achillea millefolium*	*Taraxacum officinale*	*Rumex acetosa*	*Agrostis capillaris*
95	M_GF15	*Bellis perennis*	*Prunella vulgaris*	*Festuca rubra*	*Deschampsia cespitosa*
96	M_GF16	*Prunella vulgaris*	*Rumex acetosa*	*Brachypodium retusum*	*Agrostis capillaris*
97	M_GF17	*Achillea millefolium*	*Rumex acetosa*	*Brachypodium retusum*	*Deschampsia cespitosa*
98	M_GF18	*Rumex acetosa*	*Brachypodium retusum*	*Poa pratensis*	*Agrostis capillaris*
99	M_GF19	*Sanguisorba minor*	*Achillea millefolium*	*Poa pratensis*	*Agrostis capillaris*
100	M_GF20	*Achillea millefolium*	*Bellis perennis*	*Brachypodium retusum*	*Poa_pratensis*
101	M_GF21	*Plantago albicans*	*Festuca rubra*	*Lolium perenne*	*Agrostis capillaris*
102	M_GF22	*Rumex acetosa*	*Phleum pratensis*	*Poa pratensis*	*Deschampsia cespitosa*
103	M_GF23	*Plantago albicans*	*Silene vulgaris*	*Brachypodium retusum*	*Festuca rubra*
104	M_GF24	*Taraxacum officinale*	*Prunella vulgaris*	*Rumex acetosa*	*Brachypodium retusum*
105	M_GF25	*Taraxacum officinale*	*Rumex acetosa*	*Silene vulgaris*	*Brachypodium retusum*

Table A1. Continued.

Ordered ID	Label	Species 1	Species 2	Species 3	Species 4
106	M_GF26	*Sanguisorba minor*	*Brachypodium retusum*	*Dactylis glomerata*	*Deschampsia cespitosa*
107	M_GF27	*Bellis perennis*	*Prunella vulgaris*	*Dactylis glomerata*	*Festuca rubra*
108	M_GF28	*Achillea millefolium*	*Taraxacum officinale*	*Plantago albicans*	*Poa pratensis*
109	M_GF29	*Taraxacum officinale*	*Prunella vulgaris*	*Festuca rubra*	*Lolium perenne*
110	M_GF30	*Sanguisorba minor*	*Taraxacum officinale*	*Rumex acetosa*	*Lolium perenne*
111	M_GF31	*Sanguisorba minor*	*Achillea millefolium*	*Phleum pratensis*	*Deschampsia cespitosa*
112	M_GF32	*Sanguisorba minor*	*Bellis perennis*	*Lolium perenne*	*Phleum pratensis*
113	M_GF33	*Bellis perennis*	*Taraxacum officinale*	*Lolium perenne*	*Phleum pratensis*
114	M_GF34	*Silene vulgaris*	*Dactylis glomerata*	*Festuca rubra*	*Deschampsia cespitosa*
115	M_GF35	*Achillea millefolium*	*Plantago albicans*	*Phleum pratensis*	*Agrostis capillaris*
116	M_GF36	*Taraxacum officinale*	*Brachypodium retusum*	*Festuca rubra*	*Agrostis capillaris*
117	M_GF37	*Plantago albicans*	*Silene vulgaris*	*Brachypodium retusum*	*Dactylis glomerata*
118	M_GF38	*Sanguisorba minor*	*Bellis perennis*	*Festuca rubra*	*Agrostis capillaris*
119	M_GF39	*Plantago albicans*	*Prunella vulgaris*	*Silene vulgaris*	*Dactylis glomerata*
120	M_GF40	*Rumex acetosa*	*Silene vulgaris*	*Festuca rubra*	*Phleum pratensis*
121	M_GF41	*Plantago albicans*	*Lolium perenne*	*Phleum pratensis*	*Agrostis capillaris*
122	M_GF42	*Taraxacum officinale*	*Silene vulgaris*	*Lolium perenne*	*Phleum pratensis*
123	M_GF43	*Taraxacum officinale*	*Dactylis glomerata*	*Festuca rubra*	*Phleum pratensis*
124	M_GF44	*Bellis perennis*	*Rumex acetosa*	*Brachypodium retusum*	*Deschampsia cespitosa*
125	M_GF45	*Rumex acetosa*	*Lolium perenne*	*Poa pratensis*	*Agrostis capillaris*
126	M_GF46	*Bellis perennis*	*Rumex acetosa*	*Dactylis glomerata*	*Festuca rubra*
127	M_GF47	*Achillea millefolium*	*Bellis perennis*	*Poa pratensis*	*Agrostis capillaris*
128	M_GF48	*Achillea millefolium*	*Silene vulgaris*	*Brachypodium retusum*	*Deschampsia cespitosa*
129	NM_SM1	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*
130	NM_SM2	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*
131	NM_SM3	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*	*Sanguisorba minor*
132	NM_AM1	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*
133	NM_AM2	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*
134	NM_AM3	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*	*Achillea millefolium*
135	NM_BP1	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*
136	NM_BP2	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*
137	NM_BP3	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*	*Bellis perennis*
138	NM_TO1	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*
139	NM_TO2	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*
140	NM_TO3	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*	*Taraxacum officinale*
141	NM_PA1	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*
142	NM_PA2	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*
143	NM_PA3	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*	*Plantago albicans*
144	NM_PV1	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*
145	NM_PV2	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*
146	NM_PV3	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*	*Prunella vulgaris*
147	NM_RA1	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*
148	NM_RA2	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*
149	NM_RA3	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*	*Rumex acetosa*
150	NM_SV1	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*
151	NM_SV2	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*
152	NM_SV3	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*	*Silene vulgaris*
153	NM_BR1	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*
154	NM_BR2	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*
155	NM_BR3	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*	*Brachypodium retusum*
156	NM_DG1	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*
157	NM_DG2	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*
158	NM_DG3	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*	*Dactylis glomerata*
159	NM_FR1	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*
160	NM_FR2	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*

Table A1. Continued.

Ordered ID	Label	Species 1	Species 2	Species 3	Species 4
161	NM_FR3	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*	*Festuca rubra*
162	NM_LP1	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*
163	NM_LP2	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*
164	NM_LP3	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*	*Lolium perenne*
165	NM_PHP1	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*
166	NM_PHP2	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*
167	NM_PHP3	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*	*Phleum pratensis*
168	NM_PP1	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*
169	NM_PP2	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*
170	NM_PP3	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*	*Poa pratensis*
171	NM_AC1	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*
172	NM_AC2	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*
173	NM_AC3	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*	*Agrostis capillaris*
174	NM_DC1	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*
175	NM_DC2	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*
176	NM_DC3	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*	*Deschampsia cespitosa*
177	NM_G1	*Brachypodium retusum*	*Dactylis glomerata*	*Festuca rubra*	*Phleum pratensis*
178	NM_G2	*Dactylis glomerata*	*Festuca rubra*	*Phleum pratensis*	*Agrostis capillaris*
179	NM_G3	*Brachypodium retusum*	*Dactylis glomerata*	*Phleum pratensis*	*Poa pratensis*
180	NM_G4	*Festuca rubra*	*Phleum pratensis*	*Poa pratensis*	*Deschampsia cespitosa*
181	NM_G5	*Brachypodium retusum*	*Dactylis glomerata*	*Lolium perenne*	*Phleum pratensis*
182	NM_G6	*Dactylis glomerata*	*Lolium perenne*	*Phleum pratensis*	*Agrostis capillaris*
183	NM_G7	*Dactylis glomerata*	*Phleum pratensis*	*Deschampsia cespitosa*	*Agrostis capillaris*
184	NM_G8	*Brachypodium retusum*	*Festuca rubra*	*Poa pratensis*	*Deschampsia cespitosa*
185	NM_G9	*Brachypodium retusum*	*Lolium perenne*	*Deschampsia cespitosa*	*Agrostis capillaris*
186	NM_G10	*Festuca rubra*	*Phleum pratensis*	*Deschampsia cespitosa*	*Agrostis capillaris*
187	NM_G11	*Festuca rubra*	*Lolium perenne*	*Phleum pratensis*	*Poa pratensis*
188	NM_G12	*Brachypodium retusum*	*Festuca rubra*	*Phleum pratensis*	*Agrostis capillaris*
189	NM_G13	*Dactylis glomerata*	*Lolium perenne*	*Poa pratensis*	*Deschampsia cespitosa*
190	NM_G14	*Dactylis glomerata*	*Festuca rubra*	*Phleum pratensis*	*Deschampsia cespitosa*
191	NM_G15	*Phleum pratensis*	*Poa pratensis*	*Deschampsia cespitosa*	*Agrostis capillaris*
192	NM_G16	*Brachypodium retusum*	*Phleum pratensis*	*Deschampsia cespitosa*	*Agrostis capillaris*
193	NM_F1	*Achillea millefolium*	*Bellis perennis*	*Prunella vulgaris*	*Rumex acetosa*
194	NM_F2	*Taraxacum officinale*	*Prunella vulgaris*	*Rumex acetosa*	*Silene vulgaris*
195	NM_F3	*Sanguisorba minor*	*Taraxacum officinale*	*Prunella vulgaris*	*Silene vulgaris*
196	NM_F4	*Sanguisorba minor*	*Bellis perennis*	*Prunella vulgaris*	*Rumex acetosa*
197	NM_F5	*Sanguisorba minor*	*Achillea millefolium*	*Bellis perennis*	*Rumex acetosa*
198	NM_F6	*Achillea millefolium*	*Taraxacum officinale*	*Plantago albicans*	*Rumex acetosa*
199	NM_F7	*Sanguisorba minor*	*Achillea millefolium*	*Plantago albicans*	*Prunella vulgaris*
200	NM_F8	*Sanguisorba minor*	*Achillea millefolium*	*Taraxacum officinale*	*Prunella vulgaris*
201	NM_F9	*Achillea millefolium*	*Bellis perennis*	*Taraxacum officinale*	*Silene vulgaris*
202	NM_F10	*Achillea millefolium*	*Plantago albicans*	*Prunella vulgaris*	*Silene vulgaris*
203	NM_F11	*Achillea millefolium*	*Bellis perennis*	*Plantago albicans*	*Silene vulgaris*
204	NM_F12	*Bellis perennis*	*Taraxacum officinale*	*Prunella vulgaris*	*Silene vulgaris*
205	NM_F13	*Sanguisorba minor*	*Taraxacum officinale*	*Rumex acetosa*	*Silene vulgaris*
206	NM_F14	*Sanguisorba minor*	*Plantago albicans*	*Rumex acetosa*	*Silene vulgaris*
207	NM_F15	*Sanguisorba minor*	*Bellis perennis*	*Plantago albicans*	*Prunella vulgaris*
208	NM_F16	*Sanguisorba minor*	*Achillea millefolium*	*Plantago albicans*	*Rumex acetosa*
209	NM_GF1	*Bellis perennis*	*Festuca rubra*	*Lolium perenne*	*Phleum pratensis*
210	NM_GF2	*Taraxacum officinale*	*Plantago albicans*	*Prunella vulgaris*	*Festuca rubra*
211	NM_GF3	*Taraxacum officinale*	*Dactylis glomerata*	*Phleum pratensis*	*Agrostis capillaris*
212	NM_GF4	*Achillea millefolium*	*Plantago albicans*	*Dactylis glomerata*	*Lolium perenne*
213	NM_GF5	*Sanguisorba minor*	*Plantago albicans*	*Silene vulgaris*	*Festuca rubra*
214	NM_GF6	*Bellis perennis*	*Silene vulgaris*	*Festuca rubra*	*Deschampsia cespitosa*
215	NM_GF7	*Taraxacum officinale*	*Brachypodium retusum*	*Festuca rubra*	*Phleum pratensis*

Table A1. Continued.

Ordered ID	Label	Species 1	Species 2	Species 3	Species 4
216	NM_GF8	*Taraxacum officinale*	*Plantago albicans*	*Dactylis glomerata*	*Lolium perenne*
217	NM_GF9	*Prunella vulgaris*	*Rumex acetosa*	*Poa pratensis*	*Deschampsia cespitosa*
218	NM_GF10	*Sanguisorba minor*	*Dactylis glomerata*	*Lolium perenne*	*Poa pratensis*
219	NM_GF11	*Achillea millefolium*	*Taraxacum officinale*	*Prunella vulgaris*	*Lolium perenne*
220	NM_GF12	*Sanguisorba minor*	*Prunella vulgaris*	*Brachypodium retusum*	*Festuca rubra*
221	NM_GF13	*Sanguisorba minor*	*Festuca rubra*	*Lolium perenne*	*Poa pratensis*
222	NM_GF14	*Achillea millefolium*	*Taraxacum officinale*	*Rumex acetosa*	*Agrostis capillaris*
223	NM_GF15	*Bellis perennis*	*Prunella vulgaris*	*Festuca rubra*	*Deschampsia cespitosa*
224	NM_GF16	*Prunella vulgaris*	*Rumex acetosa*	*Brachypodium retusum*	*Agrostis capillaris*
225	NM_GF17	*Achillea millefolium*	*Rumex acetosa*	*Brachypodium retusum*	*Deschampsia cespitosa*
226	NM_GF18	*Rumex acetosa*	*Brachypodium retusum*	*Poa pratensis*	*Agrostis capillaris*
227	NM_GF19	*Sanguisorba minor*	*Achillea millefolium*	*Poa pratensis*	*Agrostis capillaris*
228	NM_GF20	*Achillea millefolium*	*Bellis perennis*	*Brachypodium retusum*	*Poa_pratensis*
229	NM_GF21	*Plantago albicans*	*Festuca rubra*	*Lolium perenne*	*Agrostis capillaris*
230	NM_GF22	*Rumex acetosa*	*Phleum pratensis*	*Poa pratensis*	*Deschampsia cespitosa*
231	NM_GF23	*Plantago albicans*	*Silene vulgaris*	*Brachypodium retusum*	*Festuca rubra*
232	NM_GF24	*Taraxacum officinale*	*Prunella vulgaris*	*Rumex acetosa*	*Brachypodium retusum*
233	NM_GF25	*Taraxacum officinale*	*Rumex acetosa*	*Silene vulgaris*	*Brachypodium retusum*
234	NM_GF26	*Sanguisorba minor*	*Brachypodium retusum*	*Dactylis glomerata*	*Deschampsia cespitosa*
235	NM_GF27	*Bellis perennis*	*Prunella vulgaris*	*Dactylis glomerata*	*Festuca rubra*
236	NM_GF28	*Achillea millefolium*	*Taraxacum officinale*	*Plantago albicans*	*Poa pratensis*
237	NM_GF29	*Taraxacum officinale*	*Prunella vulgaris*	*Festuca rubra*	*Lolium perenne*
238	NM_GF30	*Sanguisorba minor*	*Taraxacum officinale*	*Rumex acetosa*	*Lolium perenne*
239	NM_GF31	*Sanguisorba minor*	*Achillea millefolium*	*Phleum pratensis*	*Deschampsia cespitosa*
240	NM_GF32	*Sanguisorba minor*	*Bellis perennis*	*Lolium perenne*	*Phleum pratensis*
241	NM_GF33	*Bellis perennis*	*Taraxacum officinale*	*Lolium perenne*	*Phleum pratensis*
242	NM_GF34	*Silene vulgaris*	*Dactylis glomerata*	*Festuca rubra*	*Deschampsia cespitosa*
243	NM_GF35	*Achillea millefolium*	*Plantago albicans*	*Phleum pratensis*	*Agrostis capillaris*
244	NM_GF36	*Taraxacum officinale*	*Brachypodium retusum*	*Festuca rubra*	*Agrostis capillaris*
245	NM_GF37	*Plantago albicans*	*Silene vulgaris*	*Brachypodium retusum*	*Dactylis glomerata*
246	NM_GF38	*Sanguisorba minor*	*Bellis perennis*	*Festuca rubra*	*Agrostis capillaris*
247	NM_GF39	*Plantago albicans*	*Prunella vulgaris*	*Silene vulgaris*	*Dactylis glomerata*
248	NM_GF40	*Rumex acetosa*	*Silene vulgaris*	*Festuca rubra*	*Phleum pratensis*
249	NM_GF41	*Plantago albicans*	*Lolium perenne*	*Phleum pratensis*	*Agrostis capillaris*
250	NM_GF42	*Taraxacum officinale*	*Silene vulgaris*	*Lolium perenne*	*Phleum pratensis*
251	NM_GF43	*Taraxacum officinale*	*Dactylis glomerata*	*Festuca rubra*	*Phleum pratensis*
252	NM_GF44	*Bellis perennis*	*Rumex acetosa*	*Brachypodium retusum*	*Deschampsia cespitosa*
253	NM_GF45	*Rumex acetosa*	*Lolium perenne*	*Poa pratensis*	*Agrostis capillaris*
254	NM_GF46	*Bellis perennis*	*Rumex acetosa*	*Dactylis glomerata*	*Festuca rubra*
255	NM_GF47	*Achillea millefolium*	*Bellis perennis*	*Poa pratensis*	*Agrostis capillaris*
256	NM_GF48	*Achillea millefolium*	*Silene vulgaris*	*Brachypodium retusum*	*Deschampsia cespitosa*

Table A2. Best selected allometric relationships for aboveground biomass for each experimental plant species. The R^2 of Spearman rank correlation tests are shown with their corresponding p values (in brackets).

Species	Shoot biomass (g) – coverage (cm^2)	Shoot biomass (g) – (log) coverage (cm^2)	Shoot biomass (g) – cylinder (cm^3)	Shoot biomass (g) – log(cylinder) (cm^3)	Shoot biomass (g) – height (cm)
Achillea millefolium				0.94 ($p = 0.00$)	
Agrostis capillaris				0.86 ($p = 0.00$)	
Bellis perennis				0.86 ($p = 0.00$)	
Brachypodium retusum	0.94 ($p = 0.00$)				
Dactylis glomerata					0.93 ($p = 0.00$)
Deschampsia cespitosa				0.83 ($p = 0.01$)	
Festuca rubra	0.61 ($p = 0.06$)				
Lolium perenne		0.85 ($p = 0.00$)			
Phleum pratensis				0.79 ($p = 0.01$)	
Plantago albicans			0.92 ($p = 0.00$)		
Poa pratensis					0.83 ($p = 0.01$)
Prunella vulgaris				0.91 ($p = 0.00$)	
Rumex acetosa				0.92 ($p = 0.00$)	
Sanguisorba minor		0.76 ($p = 0.02$)			
Silene vulgaris	0.97 ($p = 0.00$)				
Taraxacum officinalis	0.78 ($p = 0.01$)				

Table A3. Best selected allometric relationships for belowground biomass for each experimental plant species. The R^2 of Spearman rank correlation tests are shown with their corresponding p values (in brackets).

Species	Root biomass (g) – coverage (cm^2)	Root biomass (g) – cylinder (cm^3)	Root biomass (g) – log (cylinder) (cm^3)	Root biomass (g) – height (cm)	Root biomass (g) – shoot biomass (g)	Log(root biomass) (g) – log(shoot biomass) (g)
Achillea millefolium						0.74 ($p = 0.01$)
Agrostis capillaris	0.86 ($p = 0.00$)					
Bellis perennis						0.77 ($p = 0.01$)
Brachypodium retusum		0.93 ($p = 0.00$)				
Dactylis glomerata						0.72 ($p = 0.02$)
Deschampsia cespitosa						0.85 ($p = 0.00$)
Festuca rubra						0.81 ($p = 0.00$)
Lolium perenne						0.97 ($p = 0.00$)
Phleum pratensis						0.82 ($p = 0.00$)
Plantago albicans						0.25 ($p = 0.49$)
Poa pratensis					−0.4 (0.28)	
Prunella vulgaris	0.65 ($p = 0.06$)					
Rumex acetosa				0.27 ($p = 0.52$)		
Sanguisorba minor					0.45 ($p = 0.22$)	
Silene vulgaris			0.82 ($p = 0.00$)			
Taraxacum officinalis					0.9 ($p = 0.00$)	

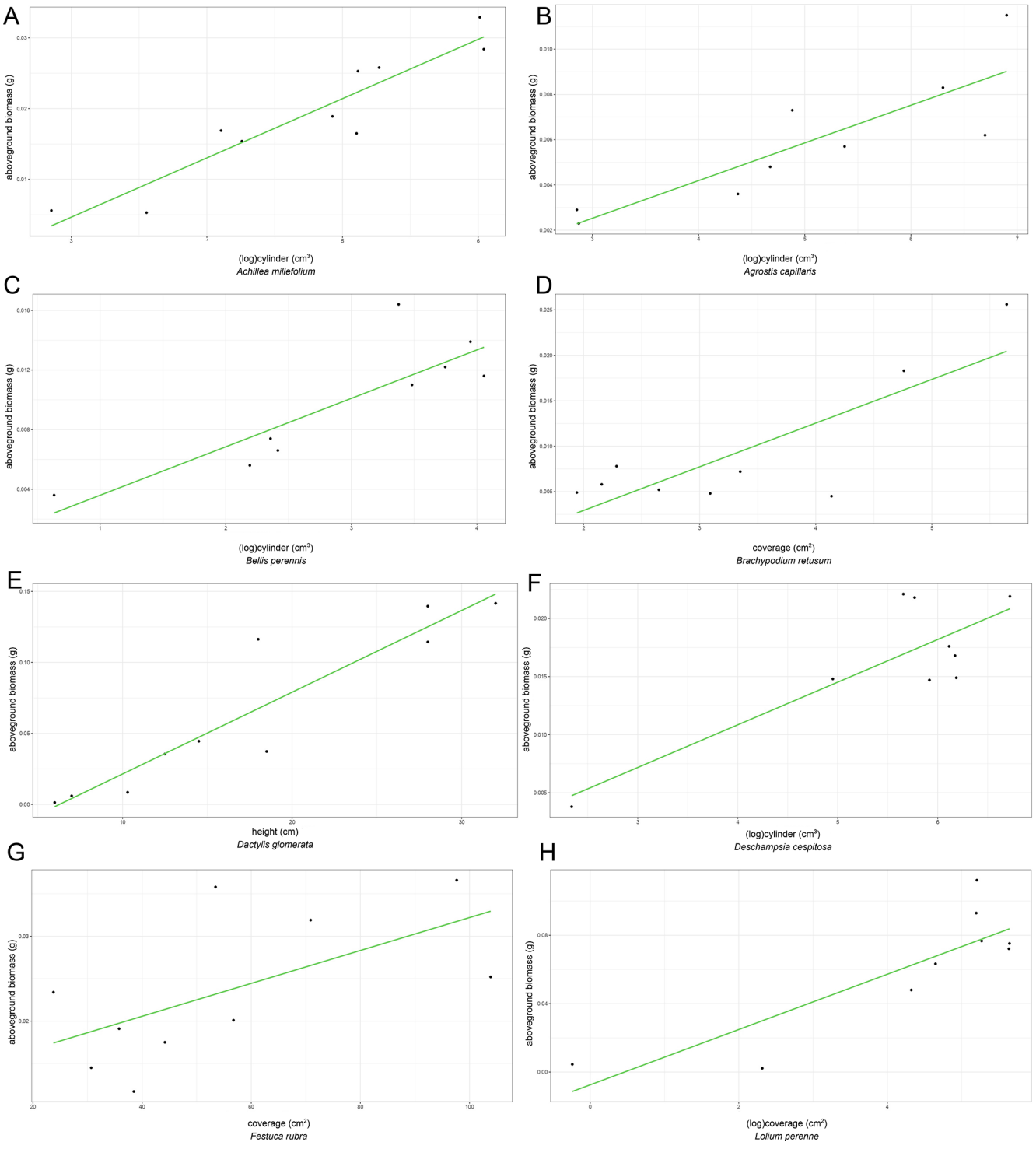
A
aboveground biomass (g)
(log)cylinder (cm³)
Achillea millefolium
B
aboveground biomass (g)
(log)cylinder (cm³)
Agrostis capillaris
C
aboveground biomass (g)
(log)cylinder (cm³)
Bellis perennis
D
aboveground biomass (g)
coverage (cm²)
Brachypodium retusum
E
aboveground biomass (g)
height (cm)
Dactylis glomerata
F
aboveground biomass (g)
(log)cylinder (cm³)
Deschampsia cespitosa
G
aboveground biomass (g)
coverage (cm²)
Festuca rubra
H
aboveground biomass (g)
(log)coverage (cm²)
Lolium perenne

Figure A1.

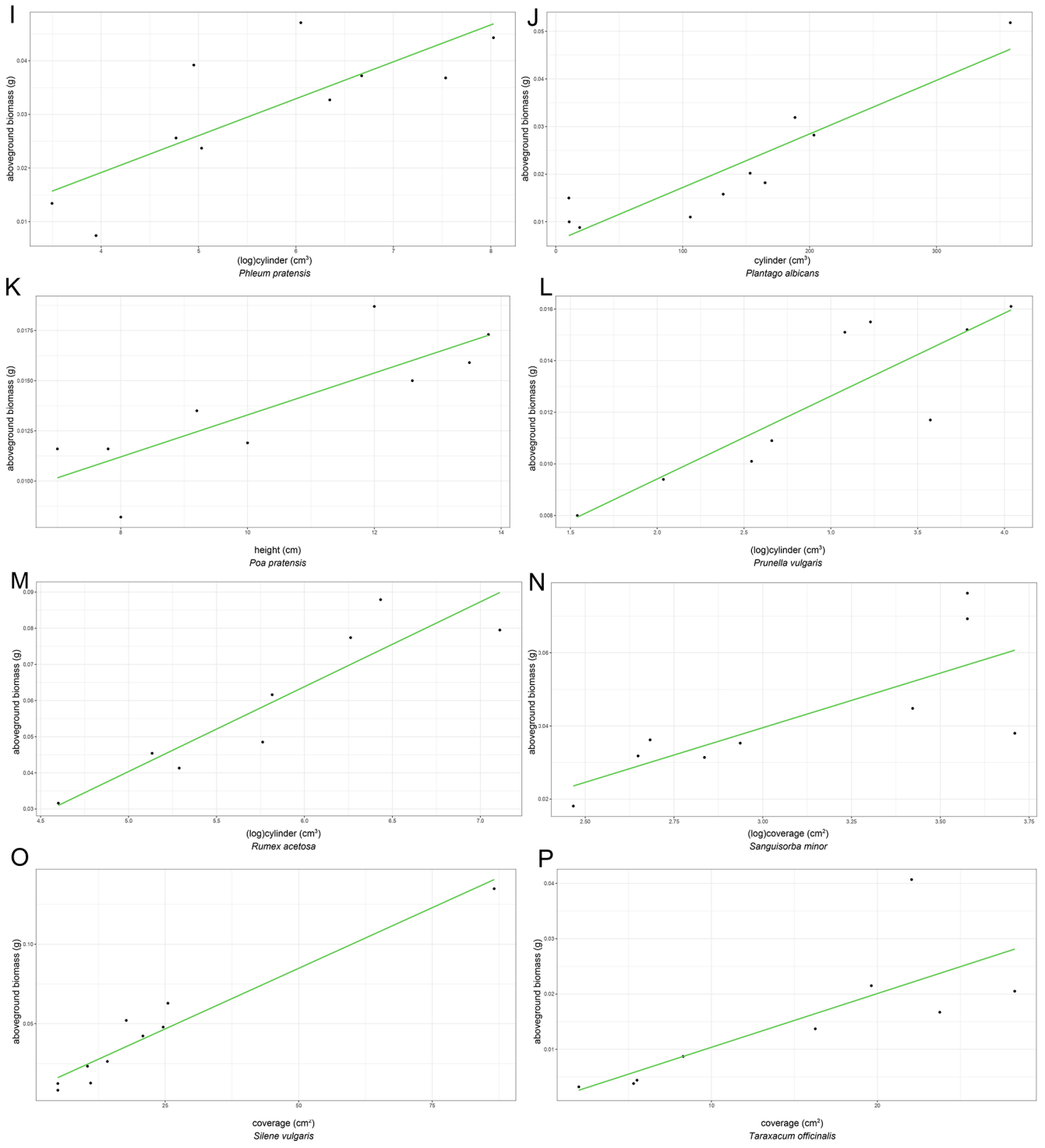

Figure A1. Correlation plots **(A–P)** showing the relationships between different variables and aboveground biomass for all 16 selected species, represented in the alphabetic order. The plots illustrate the correlations between height, cylinder volume, (log)cylinder volume, coverage, log(coverage), and other relevant variables used in estimating aboveground biomass.

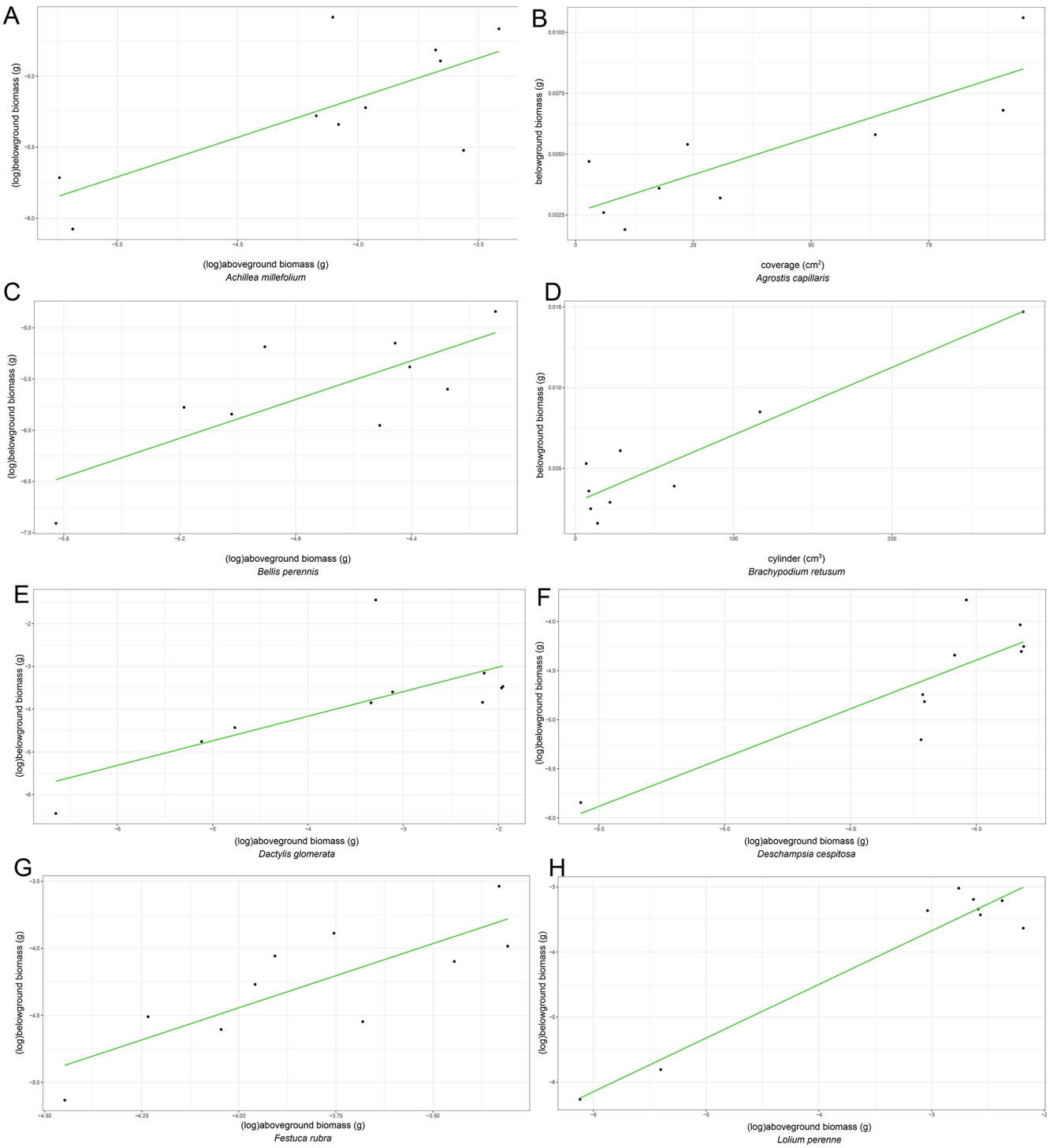
A
(log)belowground biomass (g)
(log)aboveground biomass (g)
Achillea millefolium
B
belowground biomass (g)
coverage (cm²)
Agrostis capillaris
C
(log)belowground biomass (g)
(log)aboveground biomass (g)
Bellis perennis
D
belowground biomass (g)
cylinder (cm³)
Brachypodium retusum
E
(log)belowground biomass (g)
(log)aboveground biomass (g)
Dactylis glomerata
F
(log)belowground biomass (g)
(log)aboveground biomass (g)
Deschampsia cespitosa
G
(log)belowground biomass (g)
(log)aboveground biomass (g)
Festuca rubra
H
(log)belowground biomass (g)
(log)aboveground biomass (g)
Lolium perenne

Figure A2.

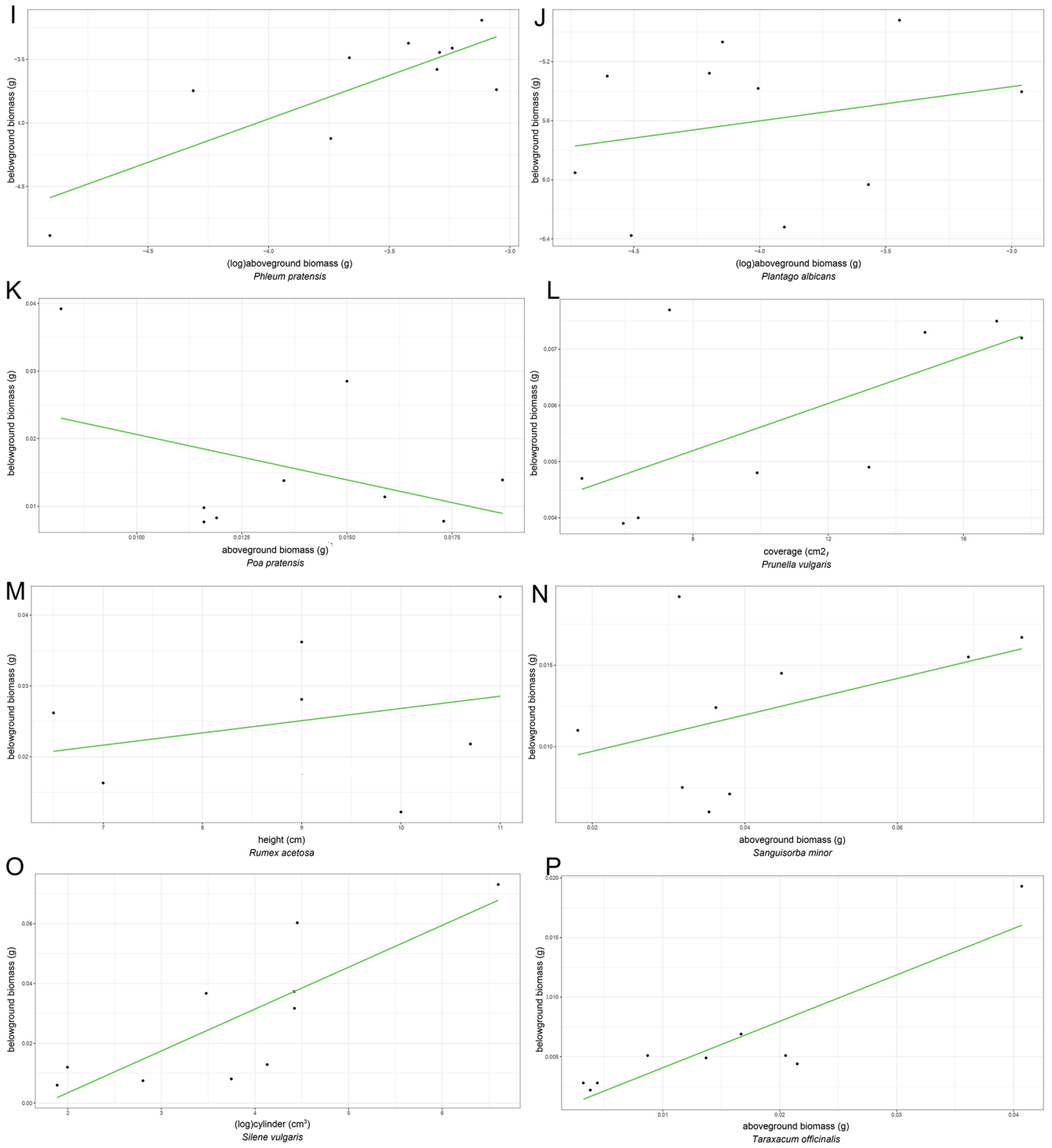

Figure A2. Correlation plots **(A–P)** showing the relationships between different variables and belowground biomass for all 16 selected species, represented in the alphabetic order. The plots illustrate the correlations between height, cylinder volume, (log)cylinder volume, coverage, log(coverage), aboveground biomass, and other relevant variables used in estimating belowground biomass.

Table A4. Complete table for estimated biomasses of the experimental plant communities.

Community no.	Label	Aboveground biomass (g)	Belowground biomass (g)
1	M_SM1	0.141283334	0.037033385
2	M_SM2	0.12922228	0.033871925
3	M_SM3	0.163921763	0.042967402
4	M_AM1	0.060254685	0.020930385
5	M_AM2	0.064774058	0.022956505
6	M_AM3	0.066024028	0.023305916
7	M_BP1	0.022893503	0.00947561
8	M_BP2	0.021244397	0.008046746
9	M_BP3	0.035511084	0.015009607
10	M_TO1	0.063755478	0.025316757
11	M_TO2	0.084462936	0.033539512
12	M_TO3	0.045252311	0.017969307
13	M_PA1	0.042445947	0.010107123
14	M_PA2	0.007154742	0.000735584
15	M_PA3	0.011906903	0.001629703
16	M_PV1	0.045616848	0.017213971
17	M_PV2	0.035693929	0.010081383
18	M_PV3	0.048865171	0.018965768
19	M_RA1	0.113819333	0.046863589
20	M_RA2	0.129218419	0.053203957
21	M_RA3	0.121853639	0.050171607
22	M_SV1	0.072602148	0.104461963
23	M_SV2	0.100614533	0.113235448
24	M_SV3	0.133214454	0.131487254
25	M_BR1	0.044324709	0.009918737
26	M_BR2	0.022706438	0.006724251
27	M_BR3	0.041023933	0.017662021
28	M_DG1	0.194850282	0.178955459
29	M_DG2	0.193619649	0.177443008
30	M_DG3	0.184595004	0.169094816
31	M_FR1	0.126912172	0.084963209
32	M_FR2	0.075424228	0.047612636
33	M_FR3	0.079320108	0.051972336
34	M_LP1	0.19610018	0.131547381
35	M_LP2	0.222396125	0.152091125
36	M_LP3	0.319181146	0.226085344
37	M_PHP1	0.105545886	0.098994431
38	M_PHP2	0.140535611	0.132474679
39	M_PHP3	0.142460049	0.13430834
40	M_PP1	0.04300089	0.043629657
41	M_PP2	0.037397744	0.03794458
42	M_PP3	0.046258533	0.046934934
43	M_AC1	0.027367662	0.018748357
44	M_AC2	0.018426052	0.005432024
45	M_AC3	0.017061045	0.007603473
46	M_DC1	0.054882129	0.037337871
47	M_DC2	0.069853443	0.048173504
48	M_DC3	0.067263379	0.04627788
49	M_G1	0.111431062	0.089643537
50	M_G2	0.104563053	0.086215688
51	M_G3	0.097107282	0.087755154
52	M_G4	0.087257211	0.073231591
53	M_G5	0.168154698	0.137418741

Table A4. Continued.

Community no.	Label	Aboveground biomass (g)	Belowground biomass (g)
54	M_G6	0.146534663	0.131728189
55	M_G7	0.1150161	0.100427354
56	M_G8	0.03992032	0.027869384
57	M_G9	0.105790688	0.071716842
58	M_G10	0.074272385	0.055583631
59	M_G11	0.086555986	0.066900466
60	M_G12	0.075649112	0.054058427
61	M_G13	0.116371769	0.090932221
62	M_G14	0.107462678	0.089807981
63	M_G15	0.067856627	0.061628414
64	M_G16	0.056793913	0.04502239
65	M_F1	0.05804158	0.021570632
66	M_F2	0.09633789	0.06023017
67	M_F3	0.066998102	0.040011008
68	M_F4	0.078191544	0.025496273
69	M_F5	0.116511286	0.026879425
70	M_F6	0.05972076	0.023027104
71	M_F7	0.068718839	0.019623534
72	M_F8	0.078221729	0.023982039
73	M_F9	0.077052697	0.04807603
74	M_F10	0.042491294	0.039032689
75	M_F11	0.095884823	0.04180929
76	M_F12	0.089100878	5.34E-02
77	M_F13	0.130168824	0.064587861
78	M_F14	0.125587662	0.06108814
79	M_F15	0.044839479	0.014298807
80	M_F16	0.101580173	0.032050591
81	M_GF1	0.140261204	0.103021029
82	M_GF2	0.056994564	0.029625495
83	M_GF3	0.085822323	0.065974629
84	M_GF4	0.172120068	0.124470825
85	M_GF5	0.112224564	0.063298417
86	M_GF6	0.065632962	0.053637275
87	M_GF7	0.096355863	0.065743625
88	M_GF8	0.1203144	0.084467183
89	M_GF9	0.053638218	0.031468462
90	M_GF10	0.192178077	0.128173105
91	M_GF11	0.113566969	0.068948984
92	M_GF12	0.153940806	0.086700599
93	M_GF13	0.164797908	0.1011348
94	M_GF14	0.096556927	0.039551102
95	M_GF15	0.043436378	0.022021716
96	M_GF16	0.142167006	0.052859435
97	M_GF17	0.072029268	0.033098739
98	M_GF18	0.038803369	0.024298644
99	M_GF19	0.082810016	0.044958662
100	M_GF20	0.039875233	0.024693009
101	M_GF21	0.097265786	0.063681303
102	M_GF22	0.080276966	0.058858913
103	M_GF23	0.071133692	0.04379506
104	M_GF24	0.085001097	0.035494922
105	M_GF25	0.076917835	0.053320519
106	M_GF26	0.114318093	0.090063882
107	M_GF27	0.101734421	0.081204515

Table A4. Continued.

Community no.	Label	Aboveground biomass (g)	Belowground biomass (g)
108	M_GF28	0.028294805	0.016336088
109	M_GF29	0.121301916	0.077240837
110	M_GF30	0.147361482	0.069903469
111	M_GF31	0.089596124	0.040716841
112	M_GF32	0.145230448	0.091315434
113	M_GF33	0.117025812	0.076267355
114	M_GF34	0.159025664	0.12910929
115	M_GF35	0.059718396	0.041606803
116	M_GF36	0.067291687	0.028457317
117	M_GF37	0.081573252	0.076726141
118	M_GF38	0.086137442	0.032900465
119	M_GF39	0.07395568	0.069773171
120	M_GF40	0.147365828	0.110773694
121	M_GF41	0.131508497	8.89E-02
122	M_GF42	0.135994077	0.106415664
123	M_GF43	0.125806843	0.106177758
124	M_GF44	0.051847667	0.024672593
125	M_GF45	0.122509981	0.083442261
126	M_GF46	0.088252639	0.061557484
127	M_GF47	0.047076969	0.028666183
128	M_GF48	0.064839853	0.048551282
129	NM_SM1	0.133254707	0.03492891
130	NM_SM2	0.164325742	0.043073293
131	NM_SM3	0.161358195	0.042295436
132	NM_AM1	0.064789243	0.022809164
133	NM_AM2	0.05277629	0.017959403
134	NM_AM3	0.077109974	0.028307411
135	NM_BP1	0.022596229	0.009731462
136	NM_BP2	0.033554658	0.013765569
137	NM_BP3	0.034070927	0.013889703
138	NM_TO1	0.0250195	0.00993503
139	NM_TO2	0.025663088	0.010190594
140	NM_TO3	0.064399067	0.025572321
141	NM_PA1	0.02985338	0.006042393
142	NM_PA2	0.017732276	0.002641924
143	NM_PA3	0.01213877	0.001679207
144	NM_PV1	0.047746591	0.01736597
145	NM_PV2	0.030701022	0.009408784
146	NM_PV3	0.021194978	0.006516989
147	NM_RA1	0.121184113	0.049895939
148	NM_RA2	0.134574623	0.055409302
149	NM_RA3	0.093733568	0.038593544
150	NM_SV1	0.132619022	0.119377665
151	NM_SV2	0.184908808	0.132034433
152	NM_SV3	0.148046133	0.130007952
153	NM_BR1	0.133547228	0.062614605
154	NM_BR2	0.049765549	0.019736936
155	NM_BR3	0.021574744	0.008963761
156	NM_DG1	0.223154849	0.205424382
157	NM_DG2	0.252279839	0.233002785
158	NM_DG3	0.20510556	0.188513461
159	NM_FR1	0.159497309	0.11010335
160	NM_FR2	0.087591839	0.056113194
161	NM_FR3	0.128345856	0.085976921

Table A4. Continued.

Community no.	Label	Aboveground biomass (g)	Belowground biomass (g)
162	NM_LP1	0.208549649	0.1401776
163	NM_LP2	0.306344401	0.215720098
164	NM_LP3	0.267397023	0.185014015
165	NM_PHP1	0.129752185	0.12208923
166	NM_PHP2	0.086350598	0.081032894
167	NM_PHP3	0.133259404	0.1254514
168	NM_PP1	0.046910062	0.047595989
169	NM_PP2	0.037137132	0.037680158
170	NM_PP3	0.046910062	0.047595989
171	NM_AC1	0.017808821	0.00296224
172	NM_AC2	0.025550059	0.019060829
173	NM_AC3	0.024091479	0.016744366
174	NM_DC1	0.065131533	0.044639947
175	NM_DC2	0.050199832	0.033668686
176	NM_DC3	0.050712637	0.034001172
177	NM_G1	0.157258401	0.132471193
178	NM_G2	0.079781692	0.068941576
179	NM_G3	0.093683781	0.086370938
180	NM_G4	0.09093209	0.074586619
181	NM_G5	0.246534062	0.200453559
182	NM_G6	0.176924664	0.141717981
183	NM_G7	0.101601166	0.086674076
184	NM_G8	0.056274154	0.042713365
185	NM_G9	0.105566038	0.072692402
186	NM_G10	0.055894084	0.038595025
187	NM_G11	0.104605086	0.079032333
188	NM_G12	0.057615812	0.047730584
189	NM_G13	0.187971005	0.153131997
190	NM_G14	0.127610674	0.105840432
191	NM_G15	0.058029118	0.047498208
192	NM_G16	0.040461852	0.029479612
193	NM_F1	0.084735299	0.037895789
194	NM_F2	0.125385589	0.071484811
195	NM_F3	0.092105533	0.049502224
196	NM_F4	0.079699987	0.027339498
197	NM_F5	0.092410024	0.032135594
198	NM_F6	0.078727017	0.029932469
199	NM_F7	0.138632931	0.044707316
200	NM_F8	0.085176032	0.028758061
201	NM_F9	0.06394407	0.045968769
202	NM_F10	0.068207694	0.0404798
203	NM_F11	0.036028434	0.025058898
204	NM_F12	0.099203451	0.053503568
205	NM_F13	0.152360312	0.070532583
206	NM_F14	0.096827874	0.054177809
207	NM_F15	0.046012829	0.016205985
208	NM_F16	0.075368236	0.025709551
209	NM_GF1	0.149116454	0.109847553
210	NM_GF2	0.053190696	0.017906952
211	NM_GF3	0.105675909	0.091018094
212	NM_GF4	0.192453579	0.129693076
213	NM_GF5	0.128386053	0.064898272
214	NM_GF6	0.075936198	0.06090138

Table A4. Continued.

Community no.	Label	Aboveground biomass (g)	Belowground biomass (g)
215	NM_GF7	0.08159655	0.055600492
216	NM_GF8	0.138917993	0.107617275
217	NM_GF9	0.058047037	3.78E-02
218	NM_GF10	0.195437113	0.134918912
219	NM_GF11	0.095348134	0.054293817
220	NM_GF12	0.075846747	3.24E-02
221	NM_GF13	0.155555092	0.088502823
222	NM_GF14	0.081881869	0.03111114
223	NM_GF15	0.043946663	0.023996528
224	NM_GF16	0.077048336	0.032733401
225	NM_GF17	0.134334976	0.068423066
226	NM_GF18	0.027519818	0.013561062
227	NM_GF19	0.054828679	0.023433309
228	NM_GF20	0.054178952	0.026774774
229	NM_GF21	0.10452825	0.076013928
230	NM_GF22	0.092692818	6.84E-02
231	NM_GF23	0.081474332	0.048339387
232	NM_GF24	0.068530096	0.029687692
233	NM_GF25	0.25496102	0.120593099
234	NM_GF26	0.148880807	0.094834962
235	NM_GF27	0.080624836	0.055086531
236	NM_GF28	0.033219184	0.016884174
237	NM_GF29	0.17308584	9.93E-02
238	NM_GF30	0.169753634	0.08662966
239	NM_GF31	0.10872861	0.065798743
240	NM_GF32	0.150984354	0.099442182
241	NM_GF33	0.098180013	0.070443877
242	NM_GF34	0.13907394	0.105880111
243	NM_GF35	0.051183459	0.034048066
244	NM_GF36	0.039006605	0.018289489
245	NM_GF37	0.106705377	0.096108514
246	NM_GF38	0.089124156	0.040719556
247	NM_GF39	0.114139985	0.077114959
248	NM_GF40	0.122828175	0.101321975
249	NM_GF41	0.137316408	0.112600806
250	NM_GF42	0.137485806	0.11231969
251	NM_GF43	0.118714425	0.095059633
252	NM_GF44	0.058580821	0.030392313
253	NM_GF45	0.143556732	0.09802755
254	NM_GF46	0.103606109	8.08E-02
255	NM_GF47	0.046203519	0.025543903
256	NM_GF48	0.088601911	0.051817267

Table A5. Complete table for growth rate, i.e., biomass production, of each experimental plant community and the percentage of their grass dominancy.

Community no.	Label	Shoot growth rate (g)	Root growth rate (g)	Grass dominance (%)
1	M_SM1	1.538	0.473	0
2	M_SM2	0.850	0.552	0
3	M_SM3	1.255	1.263	0
4	M_AM1	1.259	0.549	0
5	M_AM2	1.134	0.547	0
6	M_AM3	1.593	1.187	0
7	M_BP1	1.556	1.241	0
8	M_BP2	1.858	1.162	0
9	M_BP3	1.633	0.895	0
10	M_TO1	1.175	1.225	0
11	M_TO2	0.854	1.397	0
12	M_TO3	0.604	1.348	0
13	M_PA1	1.156	0.740	0
14	M_PA2	1.162	0.225	0
15	M_PA3	1.427	0.949	0
16	M_PV1	0.783	1.033	0
17	M_PV2	1.983	1.336	0
18	M_PV3	1.720	0.971	0
19	M_RA1	1.905	2.088	0
20	M_RA2	1.220	3.052	0
21	M_RA3	2.587	6.745	0
22	M_SV1	1.097	0.986	0
23	M_SV2	1.398	2.077	0
24	M_SV3	0.806	1.634	0
25	M_BR1	1.004	0.940	100
26	M_BR2	0.966	0.839	100
27	M_BR3	1.698	0.953	100
28	M_DG1	6.494	5.636	100
29	M_DG2	2.876	2.497	100
30	M_DG3	2.094	1.426	100
31	M_FR1	1.293	1.410	100
32	M_FR2	2.524	2.107	100
33	M_FR3	1.879	1.243	100
34	M_LP1	4.663	3.043	100
35	M_LP2	1.866	1.403	100
36	M_LP3	1.610	1.569	100
37	M_PHP1	1.173	1.567	100
38	M_PHP2	1.168	1.362	100
39	M_PHP3	1.446	2.340	100
40	M_PP1	0.661	1.391	100
41	M_PP2	0.851	1.408	100
42	M_PP3	1.643	1.393	100
43	M_AC1	3.051	1.272	100
44	M_AC2	2.220	0.685	100
45	M_AC3	3.442	1.143	100
46	M_DC1	1.454	0.933	100
47	M_DC2	1.819	1.867	100
48	M_DC3	2.652	2.268	100
49	M_G1	3.917	3.875	100
50	M_G2	5.464	4.748	100
51	M_G3	2.522	3.317	100
52	M_G4	2.967	3.181	100
53	M_G5	4.836	4.497	100

Table A5. Continued.

Community no.	Label	Shoot growth rate (g)	Root growth rate (g)	Grass dominance (%)
54	M_G6	1.952	1.179	100
55	M_G7	1.639	2.174	100
56	M_G8	1.944	2.351	100
57	M_G9	1.389	0.963	100
58	M_G10	0.935	0.870	100
59	M_G11	1.658	2.268	100
60	M_G12	1.774	1.421	100
61	M_G13	1.212	1.524	100
62	M_G14	1.071	0.900	100
63	M_G15	1.601	1.713	100
64	M_G16	1.512	1.345	100
65	M_F1	1.301	2.189	0
66	M_F2	2.262	4.010	0
67	M_F3	1.952	2.266	0
68	M_F4	1.571	1.465	0
69	M_F5	0.733	1.403	0
70	M_F6	1.229	1.387	0
71	M_F7	1.300	0.811	0
72	M_F8	0.761	1.162	0
73	M_F9	2.442	2.922	0
74	M_F10	1.426	0.647	0
75	M_F11	2.033	2.568	0
76	M_F12	0.910	1.277	0
77	M_F13	1.509	1.466	0
78	M_F14	1.223	1.994	0
79	M_F15	1.514	0.796	0
80	M_F16	1.657	2.638	0
81	M_GF1	1.679	1.727	75
82	M_GF2	1.782	1.401	25
83	M_GF3	2.733	3.364	75
84	M_GF4	1.862	2.050	50
85	M_GF5	1.407	1.667	25
86	M_GF6	2.343	1.652	50
87	M_GF7	2.562	3.319	75
88	M_GF8	1.974	2.610	50
89	M_GF9	0.875	1.479	50
90	M_GF10	1.557	1.362	75
91	M_GF11	3.365	2.721	25
92	M_GF12	0.665	1.088	50
93	M_GF13	2.060	1.134	75
94	M_GF14	0.992	1.051	25
95	M_GF15	1.125	1.288	50
96	M_GF16	3.307	2.702	50
97	M_GF17	0.897	1.057	50
98	M_GF18	1.850	2.710	75
99	M_GF19	1.337	1.470	50
100	M_GF20	0.959	1.406	50
101	M_GF21	2.467	2.231	75
102	M_GF22	1.859	2.291	75
103	M_GF23	1.418	1.827	50
104	M_GF24	1.674	2.639	25
105	M_GF25	1.222	1.212	25
106	M_GF26	1.024	0.780	75
107	M_GF27	3.497	2.993	50

Table A5. Continued.

Community no.	Label	Shoot growth rate (g)	Root growth rate (g)	Grass dominance (%)
108	M_GF28	1.021	1.614	25
109	M_GF29	1.607	1.033	50
110	M_GF30	1.221	1.260	25
111	M_GF31	2.479	2.494	50
112	M_GF32	3.044	3.383	50
113	M_GF33	1.242	1.034	50
114	M_GF34	2.300	3.186	75
115	M_GF35	1.540	2.773	50
116	M_GF36	0.927	1.882	75
117	M_GF37	1.103	1.518	50
118	M_GF38	1.044	1.177	50
119	M_GF39	1.876	1.685	25
120	M_GF40	3.656	4.684	50
121	M_GF41	1.223	1.626	75
122	M_GF42	0.758	1.688	50
123	M_GF43	1.824	2.049	75
124	M_GF44	1.129	1.701	50
125	M_GF45	3.366	3.671	75
126	M_GF46	1.272	1.573	50
127	M_GF47	1.774	2.286	50
128	M_GF48	1.585	1.726	50
129	NM_SM1	1.286	0.555	0
130	NM_SM2	0.684	0.623	0
131	NM_SM3	0.917	1.183	0
132	NM_AM1	1.354	0.307	0
133	NM_AM2	1.086	0.312	0
134	NM_AM3	0.732	0.642	0
135	NM_BP1	1.576	0.641	0
136	NM_BP2	1.275	0.777	0
137	NM_BP3	1.485	0.536	0
138	NM_TO1	0.376	0.696	0
139	NM_TO2	0.563	1.200	0
140	NM_TO3	0.714	1.480	0
141	NM_PA1	0.710	0.144	0
142	NM_PA2	1.241	0.443	0
143	NM_PA3	0.627	0.409	0
144	NM_PV1	0.861	0.893	0
145	NM_PV2	1.318	0.516	0
146	NM_PV3	1.428	0.804	0
147	NM_RA1	2.608	4.435	0
148	NM_RA2	0.924	1.270	0
149	NM_RA3	0.905	1.772	0
150	NM_SV1	0.626	1.111	0
151	NM_SV2	0.964	1.438	0
152	NM_SV3	1.651	2.525	0
153	NM_BR1	0.735	0.748	100
154	NM_BR2	0.629	0.646	100
155	NM_BR3	1.567	0.786	100
156	NM_DG1	1.476	1.269	100
157	NM_DG2	5.782	3.682	100
158	NM_DG3	1.704	1.106	100
159	NM_FR1	1.439	0.885	100
160	NM_FR2	1.547	1.299	100
161	NM_FR3	2.130	1.583	100

Table A5. Continued.

Community no.	Label	Shoot growth rate (g)	Root growth rate (g)	Grass dominance (%)
162	NM_LP1	4.770	4.925	100
163	NM_LP2	1.632	1.359	100
164	NM_LP3	4.321	5.050	100
165	NM_PHP1	1.129	1.224	100
166	NM_PHP2	1.172	1.485	100
167	NM_PHP3	3.426	5.249	100
168	NM_PP1	0.703	1.447	100
169	NM_PP2	0.572	1.313	100
170	NM_PP3	0.732	1.478	100
171	NM_AC1	1.861	0.527	100
172	NM_AC2	3.983	2.236	100
173	NM_AC3	2.235	0.754	100
174	NM_DC1	2.474	1.666	100
175	NM_DC2	1.099	1.032	100
176	NM_DC3	1.918	1.441	100
177	NM_G1	3.642	3.038	100
178	NM_G2	1.599	1.141	100
179	NM_G3	3.465	3.064	100
180	NM_G4	1.073	2.360	100
181	NM_G5	1.328	1.374	100
182	NM_G6	2.003	1.593	100
183	NM_G7	1.953	0.748	100
184	NM_G8	1.428	1.751	100
185	NM_G9	1.519	0.282	100
186	NM_G10	1.194	1.276	100
187	NM_G11	1.844	1.351	100
188	NM_G12	2.182	1.267	100
189	NM_G13	1.901	1.682	100
190	NM_G14	1.801	1.429	100
191	NM_G15	1.101	1.267	100
192	NM_G16	1.168	1.241	100
193	NM_F1	1.554	1.912	0
194	NM_F2	1.823	2.519	0
195	NM_F3	1.257	0.941	0
196	NM_F4	1.579	2.343	0
197	NM_F5	1.892	3.523	0
198	NM_F6	1.360	1.800	0
199	NM_F7	0.931	0.810	0
200	NM_F8	0.404	0.597	0
201	NM_F9	1.335	0.844	0
202	NM_F10	1.046	1.045	0
203	NM_F11	1.593	1.040	0
204	NM_F12	2.300	1.437	0
205	NM_F13	2.536	3.420	0
206	NM_F14	0.640	1.411	0
207	NM_F15	1.353	1.634	0
208	NM_F16	0.703	0.485	0
209	NM_GF1	1.650	1.200	75
210	NM_GF2	1.376	1.292	25
211	NM_GF3	2.393	2.359	75
212	NM_GF4	3.366	3.715	50
213	NM_GF5	1.390	0.985	25
214	NM_GF6	2.203	1.569	50

Table A5. Continued.

Community no.	Label	Shoot growth rate (g)	Root growth rate (g)	Grass dominance (%)
215	NM_GF7	1.267	1.115	75
216	NM_GF8	1.470	1.083	50
217	NM_GF9	0.701	1.493	50
218	NM_GF10	2.489	1.015	75
219	NM_GF11	2.439	1.096	25
220	NM_GF12	1.451	1.753	50
221	NM_GF13	1.754	2.806	75
222	NM_GF14	0.818	1.579	25
223	NM_GF15	0.855	0.566	50
224	NM_GF16	2.342	2.838	50
225	NM_GF17	1.514	2.726	50
226	NM_GF18	1.261	1.157	75
227	NM_GF19	0.694	0.787	50
228	NM_GF20	0.481	0.624	50
229	NM_GF21	1.105	1.459	75
230	NM_GF22	2.816	4.506	75
231	NM_GF23	1.777	1.322	50
232	NM_GF24	0.810	1.345	25
233	NM_GF25	1.314	1.785	25
234	NM_GF26	1.030	0.575	75
235	NM_GF27	0.978	1.171	50
236	NM_GF28	0.406	0.713	25
237	NM_GF29	1.436	1.031	50
238	NM_GF30	1.229	2.368	25
239	NM_GF31	1.100	1.309	50
240	NM_GF32	1.318	1.295	50
241	NM_GF33	1.331	1.580	50
242	NM_GF34	1.260	1.609	75
243	NM_GF35	0.769	1.241	50
244	NM_GF36	0.965	0.912	75
245	NM_GF37	1.268	1.759	50
246	NM_GF38	1.681	1.774	50
247	NM_GF39	3.066	3.138	25
248	NM_GF40	1.556	1.969	50
249	NM_GF41	1.227	2.818	75
250	NM_GF42	1.531	1.682	50
251	NM_GF43	4.291	3.580	75
252	NM_GF44	1.192	1.864	50
253	NM_GF45	1.625	1.617	75
254	NM_GF46	1.206	1.714	50
255	NM_GF47	1.625	1.749	50
256	NM_GF48	2.661	2.603	50

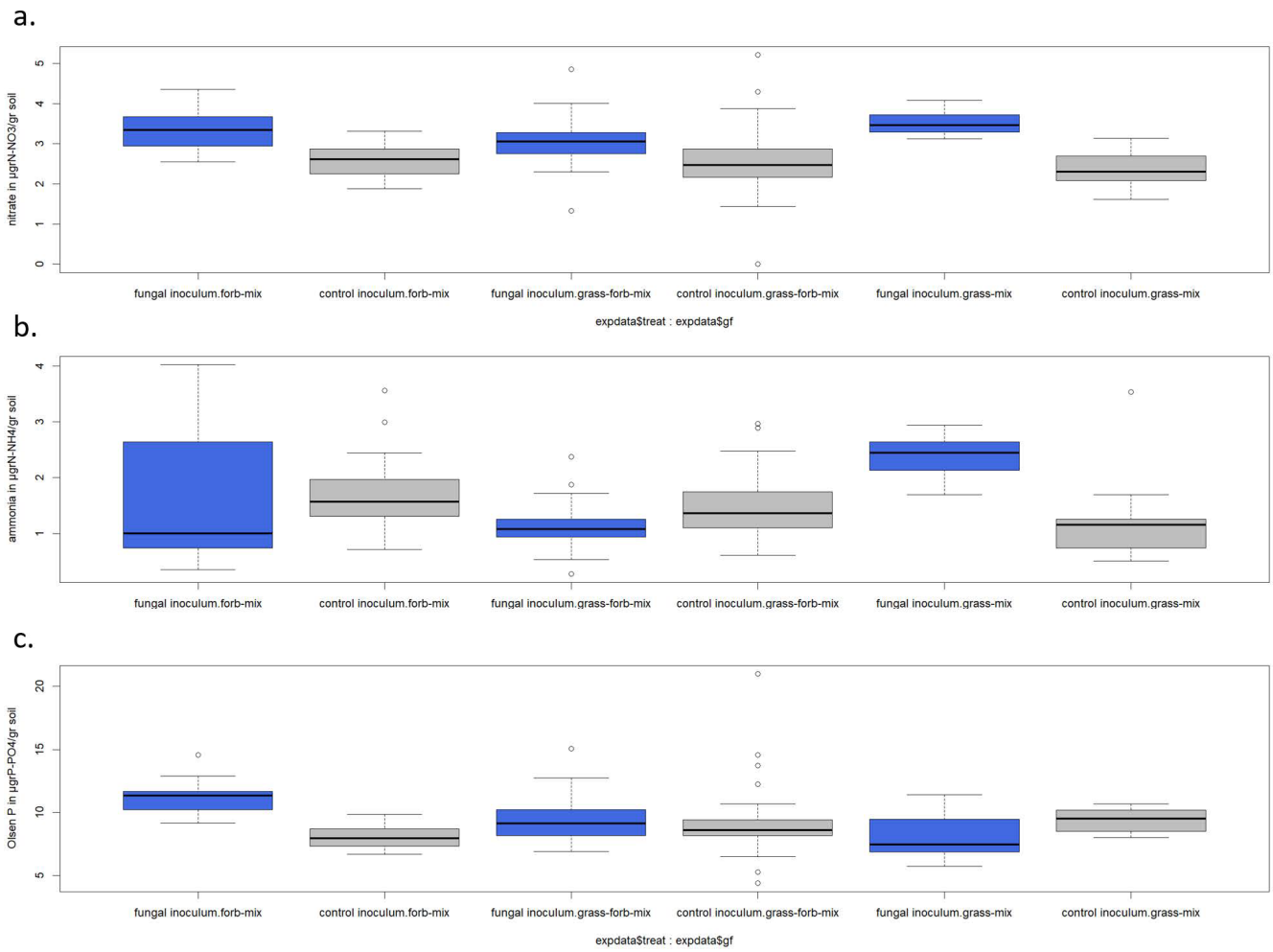

Figure A3. Boxplots showing the variation in plant-available nitrate **(a)**, ammonium **(b)**, and phosphate **(c)** among treatment and experimental plant composition for all plots ($n = 160$).

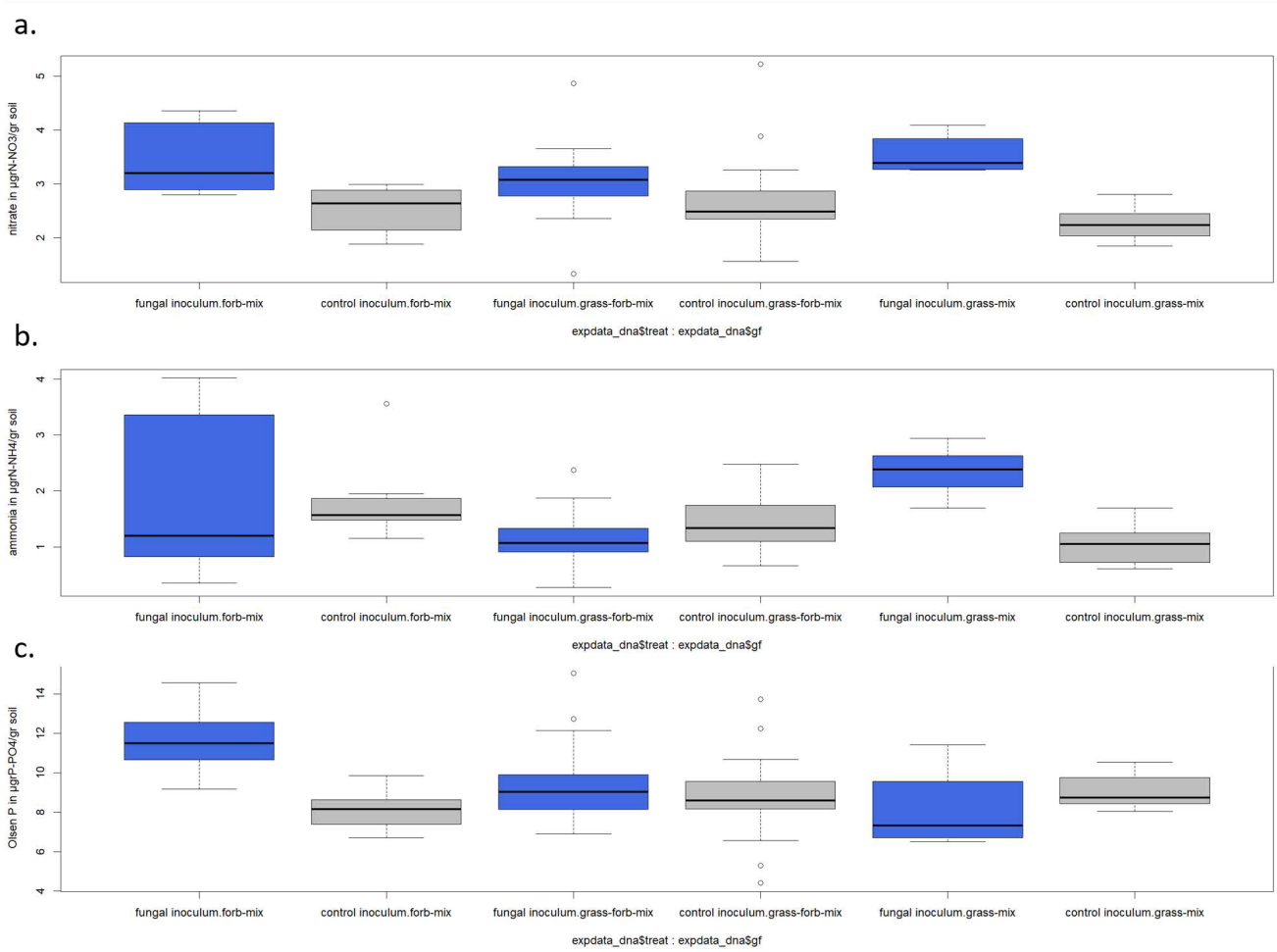

Figure A4. Boxplots showing the variation in plant-available nitrate **(a)**, ammonium **(b)**, and phosphate **(c)** among treatment and experimental plant composition for only the plots where soil DNA was also analysed ($n = 80$).

Code availability. RCode used for data preparation and analysis is publicly available via our GiHub repository, linked with doi via Zenodo (https://doi.org/10.5281/zenodo.20957440, Neuenkamp, 2026).

Data availability. Representative sequences for AMF treatment combinations are accessible from the European Nucleotide Archive under BioProject ID PRJNA1345342. All analysed data are publicly available via our Zenodo repository (https://doi.org/10.5281/zenodo.18924702, Neuenkamp and Shpilkina, 2026).

Author contributions. LN conceived the study. The greenhouse experiment was designed by LN, with MvdH, FTM, FdB, MZ, BG, VO, and SA contributing to the finalisation of the design. MvdH contributed the fungal inoculum. The greenhouse experiment was carried out primarily by LN, YS, and SA. BG and VO assisted with setting up and harvesting the experiment. Laboratory analyses were performed by YS, VO, BG, LN, MV, and SA. Data processing and statistical analyses were conducted by YS, LN, and MV, with additional support for analytical decisions and interpretation from all co-authors. YS and LN wrote the first draft of the article. All authors contributed to discussions on experimental design, provided input on data analysis, reviewed the article, and approved the final version. LN coordinated the project and managed funding.

Competing interests. The contact author has declared that none of the authors has any competing interests.

Acknowledgements. MV and MZ were funded by the Estonian Research Council (PRG 1836) and by the Estonian Ministry of Education and Research (Centre of Excellence AgroCropFuture "Agroecology and new crops in future climates", TK200). LN was funded by the European Union under EXCELLENT SCIENCE – Marie Skłodowska-Curie Actions (MYFUN, 835472). We thank the entire Dryland Ecology and Global Change Lab for helping with the set up and harvest of the experiment. FTM acknowledges support from the King Abdullah University of Science and Technology (KAUST). YS was supported through a research technician contract funded by the Ajuntament de Barcelona and "la Caixa" Foundation.

Financial support. This research has been supported by the EU H2020 Marie Skłodowska-Curie Actions (grant no. 835472) and the Haridus-ja Teadusministeerium (grant no. TK200).

Review statement. This paper was edited by Daniel Montesinos and reviewed by Celestino Quintela-Sabarís and three anonymous referees.

References

Ali, A., Xu, M.-S., Zhao, Y.-T., Zhang, Q.-Q., Zhou, L.-L., Yang, X.-D., and Yan, E.-R.: Allometric biomass equations for shrub and small tree species in subtropical China, Silva Fenn., 49, https://doi.org/10.14214/sf.1275, 2015.

Augé, R. M., Toler, H. D., and Saxton, A. M.: Mycorrhizal Stimulation of Leaf Gas Exchange in Relation to Root Colonization, Shoot Size, Leaf Phosphorus and Nitrogen: A Quantitative Analysis of the Literature Using Meta-Regression, Front. Plant Sci., 7, https://doi.org/10.3389/fpls.2016.01084, 2016.

Brito, I., Carvalho, M., and Goss, M. J.: Managing the functional diversity of arbuscular mycorrhizal fungi for the sustainable intensification of crop production, Plants, People, Planet, 3, 491–505, https://doi.org/10.1002/ppp3.10212, 2021.

Cadotte, M. W., Cavender-Bares, J., Tilman, D., and Oakley, T. H.: Using Phylogenetic, Functional and Trait Diversity to Understand Patterns of Plant Community Productivity, PLoS One, 4, e5695, https://doi.org/10.1371/journal.pone.0005695, 2009.

Cadotte, M. W., Carscadden, K., and Mirotchnick, N.: Beyond species: functional diversity and the maintenance of ecological processes and services, J. Appl. Ecol., 48, 1079–1087, https://doi.org/10.1111/j.1365-2664.2011.02048.x, 2011.

Chaudhary, V. B., Nolimal, S., Sosa-Hernández, M. A., Egan, C., and Kastens, J.: Trait-based aerial dispersal of arbuscular mycorrhizal fungi, New Phytol., 228, 238–252, https://doi.org/10.1111/nph.16667, 2020.

Cheng, Z., Cui, Z., Shi, J., Liu, Y., La Pierre, K. J., and Wu, G.-L.: Plant functional types drive differential responses of grassland ecosystem functions along a precipitation gradient, Ecol. Indic., 133, 108433, https://doi.org/10.1016/j.ecolind.2021.108433, 2021.

Conti, G., Urcelay, C., Gundel, P. E., and Piñeiro, G.: The potential of arbuscular mycorrhizal fungi to improve soil organic carbon in agricultural ecosystems: A meta-analytical approach, Funct. Ecol., 39, 1016–1030, https://doi.org/10.1111/1365-2435.14753, 2025.

Da Silveira Pontes, L., Maire, V., Schellberg, J., and Louault, F.: Grass strategies and grassland community responses to environmental drivers: a review, Agron. Sustain. Dev., 35, 1297–1318, https://doi.org/10.1007/s13593-015-0314-1, 2015.

De Miranda, S. D. C., Bustamante, M., Palace, M., Hagen, S., Keller, M., and Ferreira, L. G.: Regional Variations in Biomass Distribution in Brazilian Savanna Woodland, Biotropica, 46, 125–138, https://doi.org/10.1111/btp.12095, 2014.

Delgado-Baquerizo, M., Maestre, F. T., Reich, P. B., Jeffries, T. C., Gaitan, J. J., Encinar, D., Berdugo, M., Campbell, C. D., and Singh, B. K.: Microbial diversity drives multifunctionality in terrestrial ecosystems, Nat. Commun., 7, 10541, https://doi.org/10.1038/ncomms10541, 2016.

Díaz, S. and Cabido, M.: Vive la différence: plant functional diversity matters to ecosystem processes, Trends Ecol. Evol., 16, 646–655, https://doi.org/10.1016/S0169-5347(01)02283-2, 2001.

Eisenhauer, N., Reich, P. B., and Scheu, S.: Increasing plant diversity effects on productivity with time due to delayed soil biota effects on plants, Basic Appl. Ecol., 13, 571–578, https://doi.org/10.1016/j.baae.2012.09.002, 2012.

Eisenhauer, N., Barnes, A. D., Cesarz, S., Craven, D., Ferlian, O., Gottschall, F., Hines, J., Sendek, A., Siebert, J., Thakur, M. P., and Türke, M.: Biodiversity–ecosystem function experiments reveal the mechanisms underlying the consequences of biodiversity change in real world ecosystems, J. Veg. Sci., 27, 1061–1070, https://doi.org/10.1111/jvs.12435, 2016.

Elliott, A. J., Daniell, T. J., Cameron, D. D., and Field, K. J.: A commercial arbuscular mycorrhizal inoculum increases root colonization across wheat cultivars but does not increase assimilation of mycorrhiza-acquired nutrients, Plants, People, Planet, 3, 588–599, https://doi.org/10.1002/ppp3.10094, 2020.

Fernández, J. A., Niell, F. X., and Lucena, J.: A rapid and sensitive automated determination of phosphate in natural waters1, Limnol. Oceanogr., 30, 227–230, https://doi.org/10.4319/lo.1985.30.1.0227, 1985.

Fox, J., Weisberg, S., Price, B., Adler, D., Bates, D., Baud-Bovy, G., Bolker, B., Ellison, S., Firth, D., Friendly, M., Gorjanc, G., Graves, S., Heiberger, R., Krivitsky, P., Laboissiere, R., Maechler, M., Monette, G., Murdoch, D., Nilsson, H., Ogle, D., Proctor, I., Ripley, B., Short, T., Venables, W., Walker, S., Winsemius, D., Zeileis, A., and R-Core: car: Companion to Applied Regression, https://doi.org/10.32614/CRAN.package.car, 2019.

George, N. P. and Ray, J. G.: The inevitability of arbuscular mycorrhiza for sustainability in organic agriculture – A critical review, Front. Sustain. Food Syst., 7, 1124688, https://doi.org/10.3389/fsufs.2023.1124688, 2023.

Godoy, R., Acuña, L., Silva-Flores, P., Aguilera, P., and Marín, C.: Native Arbuscular Mycorrhizal Fungi Improved Araucaria araucana Growth over Commercial Inoculum Under Greenhouse

and Field Conditions, J. Soil Sci. Plant Nut., 23, 6459–6468, https://doi.org/10.1007/s42729-023-01501-2, 2023.

Gross, N., Bagousse-Pinguet, Y. L., Liancourt, P., Berdugo, M., Gotelli, N. J., and Maestre, F. T.: Functional trait diversity maximizes ecosystem multifunctionality, Nat. Ecol. Evol., 1, 0132, https://doi.org/10.1038/s41559-017-0132, 2017.

Guo, J., Bowatte, S., and Hou, F.: Diversity of endophytic bacteria and fungi in seeds of Elymus nutans growing in four locations of Qinghai Tibet Plateau, China, Plant Soil, 459, 49–63, https://doi.org/10.1007/s11104-020-04608-y, 2020.

Hart, M. M., Reader, R. J., and Klironomos, J. N.: Plant coexistence mediated by arbuscular mycorrhizal fungi, Trends Ecol. Evol., 18, 418–423, https://doi.org/10.1016/S0169-5347(03)00127-7, 2003.

Heinen, R., Biere, A., Harvey, J. A., and Bezemer, T. M.: Effects of Soil Organisms on Aboveground Plant-Insect Interactions in the Field: Patterns, Mechanisms and the Role of Methodology, Front. Ecol. Evol., 6, https://doi.org/10.3389/fevo.2018.00106, 2018.

Hiiesalu, I., Pärtel, M., Davison, J., Gerhold, P., Metsis, M., Moora, M., Öpik, M., Vasar, M., Zobel, M., and Wilson, S. D.: Species richness of arbuscular mycorrhizal fungi: associations with grassland plant richness and biomass, New Phytol., 203, 233–244, https://doi.org/10.1111/nph.12765, 2014.

Hoeksema, J. D., Chaudhary, V. B., Gehring, C. A., Johnson, N. C., Karst, J., Koide, R. T., Pringle, A., Zabinski, C., Bever, J. D., Moore, J. C., Wilson, G. W. T., Klironomos, J. N., and Umbanhowar, J.: A meta-analysis of context-dependency in plant response to inoculation with mycorrhizal fungi, Ecol. Lett., 13, 394–407, https://doi.org/10.1111/j.1461-0248.2009.01430.x, 2010.

Huff, S., Ritchie, M., and Temesgen, H.: Allometric equations for estimating aboveground biomass for common shrubs in northeastern California, Forest Ecol. Manag., 398, 48–63, https://doi.org/10.1016/j.foreco.2017.04.027, 2017.

Hussain, S., Sharif, M., and Ahmad, W.: Selection of efficient phosphorus solubilizing bacteria strains and mycorrhizea for enhanced cereal growth, root microbe status and N and P uptake in alkaline calcareous soil, Soil Sci. Plant Nutr., 67, 259–268, https://doi.org/10.1080/00380768.2021.1904793, 2021.

Ihrmark, K., Bödeker, I. T. M., Cruz-Martinez, K., Friberg, H., Kubartova, A., Schenck, J., Strid, Y., Stenlid, J., Brandström-Durling, M., Clemmensen, K. E., and Lindahl, B. D.: New primers to amplify the fungal ITS2 region – evaluation by 454-sequencing of artificial and natural communities, FEMS Microbiol. Ecol., 82, 666–677, https://doi.org/10.1111/j.1574-6941.2012.01437.x, 2012.

Islam, M. N., Germida, J. J., and Walley, F. L.: Survival of a commercial AM fungal inoculant and its impact on indigenous AM fungal communities in field soils, Appl. Soil Ecol., 166, 103979, https://doi.org/10.1016/j.apsoil.2021.103979, 2021.

Janoušková, M., Krak, K., Wagg, C., Štorchová, H., Caklová, P., and Vosátka, M.: Effects of Inoculum Additions in the Presence of a Preestablished Arbuscular Mycorrhizal Fungal Community, Appl. Environ. Microb., 79, 6507–6515, https://doi.org/10.1128/AEM.02135-13, 2013.

Janoušková, M., Krak, K., Vosátka, M., Püschel, D., and Štorchová, H.: Inoculation effects on root-colonizing arbuscular mycorrhizal fungal communities spread beyond directly inoculated plants, PLoS One, 12, e0181525, https://doi.org/10.1371/journal.pone.0181525, 2017.

Jansa, J., Finlay, R., Wallander, H., Smith, F. A., and Smith, S. E.: Role of Mycorrhizal Symbioses in Phosphorus Cycling, in: Phosphorus in Action: Biological Processes in Soil Phosphorus Cycling, edited by: Bünemann, E., Oberson, A., and Frossard, E., Springer, Berlin, Heidelberg, 137–168, https://doi.org/10.1007/978-3-642-15271-9_6, 2011.

Jia, Y., van der Heijden, M. G. A., Wagg, C., Feng, G., and Walder, F.: Symbiotic soil fungi enhance resistance and resilience of an experimental grassland to drought and nitrogen deposition, J. Ecol., 109, 3171–3181, https://doi.org/10.1111/1365-2745.13521, 2021.

Jing, X., Sanders, N. J., Shi, Y., Chu, H., Classen, A. T., Zhao, K., Chen, L., Shi, Y., Jiang, Y., and He, J.-S.: The links between ecosystem multifunctionality and above- and belowground biodiversity are mediated by climate, Nat. Commun., 6, 8159, https://doi.org/10.1038/ncomms9159, 2015.

Johnson, D., Vandenkoornhuyse, P. J., Leake, J. R., Gilbert, L., Booth, R. E., Grime, J. P., Young, J. P. W., and Read, D. J.: Plant communities affect arbuscular mycorrhizal fungal diversity and community composition in grassland microcosms, New Phytol., 161, 503–515, https://doi.org/10.1046/j.1469-8137.2003.00938.x, 2003.

Jung, S. C., Martinez-Medina, A., Lopez-Raez, J. A., and Pozo, M. J.: Mycorrhiza-Induced Resistance and Priming of Plant Defenses, J. Chem. Ecol., 38, 651–664, https://doi.org/10.1007/s10886-012-0134-6, 2012.

Klironomos, J., Zobel, M., Tibbett, M., Stock, W. D., Rillig, M. C., Parrent, J. L., Moora, M., Koch, A. M., Facelli, J. M., Facelli, E., Dickie, I. A., and Bever, J. D.: Forces that structure plant communities: quantifying the importance of the mycorrhizal symbiosis, New Phytol., 189, 366–370, https://doi.org/10.1111/j.1469-8137.2010.03550.x, 2010.

Kohout, P., Sudová, R., Janoušková, M., Čtvrtlíková, M., Hejda, M., Pánková, H., Slavíková, R., Štajerová, K., Vosátka, M., and Sýkorová, Z.: Comparison of commonly used primer sets for evaluating arbuscular mycorrhizal fungal communities: Is there a universal solution?, Soil Biol. Biochem., 68, 482–493, https://doi.org/10.1016/j.soilbio.2013.08.027, 2013.

Kojima, T., Jenkins, S., Weerasekara, A., and Fan, J.-W.: Arbuscular Mycorrhizal Diversity and Function in Grassland Ecosystems, in: Mycorrhizal Fungi: Use in Sustainable Agriculture and Land Restoration, edited by: Solaiman, Z. M., Abbott, L. K., and Varma, A., Springer, Berlin, Heidelberg, 149–169, https://doi.org/10.1007/978-3-662-45370-4_9, 2014.

Le Bagousse-Pinguet, Y., Gross, N., Saiz, H., Maestre, F. T., Ruiz, S., Dacal, M., Asensio, S., Ochoa, V., Gozalo, B., Cornelissen, J. H. C., Deschamps, L., García, C., Maire, V., Milla, R., Salinas, N., Wang, J., Singh, B. K., and García-Palacios, P.: Functional rarity and evenness are key facets of biodiversity to boost multifunctionality, P. Natl. Acad. Sci. USA, 118, e2019355118, https://doi.org/10.1073/pnas.2019355118, 2021.

Lekberg, Y., Vasar, M., Bullington, L. S., Sepp, S., Antunes, P. M., Bunn, R., Larkin, B. G., and Öpik, M.: More bang for the buck? Can arbuscular mycorrhizal fungal communities be characterized adequately alongside other fungi using general fungal primers?, New Phytol., 220, 971–976, https://doi.org/10.1111/nph.15035, 2018.

Lisner, A., Konečná, M., Blažek, P., and Lepš, J.: Community biomass is driven by dominants and their characteristics – The insight from a field biodiversity experiment with realistic species loss scenario, J. Ecol., 111, 240–250, https://doi.org/10.1111/1365-2745.14029, 2023.

Maestre, F. T. and Reynolds, J. F.: Nutrient Availability and Atmospheric CO_2 Partial Pressure Modulate the Effects of Nutrient Heterogeneity on the Size Structure of Populations in Grassland Species, Ann. Bot., 98, 227–235, https://doi.org/10.1093/aob/mcl093, 2006.

Maestre, F. T., Bradford, M. A., and Reynolds, J. F.: Soil heterogeneity and community composition jointly influence grassland biomass, J. Veg. Sci., 17, 261–270, https://doi.org/10.1111/j.1654-1103.2006.tb02445.x, 2006.

Maestre, F. T., Bagousse-Pinguet, Y. L., Delgado-Baquerizo, M., Eldridge, D. J., Saiz, H., Berdugo, M., Gozalo, B., Ochoa, V., Guirado, E., García-Gómez, M., Valencia, E., Gaitán, J. J., Asensio, S., Mendoza, B. J., Plaza, C., Díaz-Martínez, P., Rey, A., Hu, H.-W., He, J.-Z., Wang, J.-T., Lehmann, A., Rillig, M. C., Cesarz, S., Eisenhauer, N., Martínez-Valderrama, J., Moreno-Jiménez, E., Sala, O., Abedi, M., Ahmadian, N., Alados, C. L., Aramayo, V., Amghar, F., Arredondo, T., Ahumada, R. J., Bahalkeh, K., Salem, F. B., Blaum, N., Boldgiv, B., Bowker, M. A., Bran, D., Bu, C., Canessa, R., Castillo-Monroy, A. P., Castro, H., Castro, I., Castro-Quezada, P., Chibani, R., Conceição, A. A., Currier, C. M., Darrouzet-Nardi, A., Deák, B., Donoso, D. A., Dougill, A. J., Durán, J., Erdenetsetseg, B., Espinosa, C. I., Fajardo, A., Farzam, M., Ferrante, D., Frank, A. S. K., Fraser, L. H., Gherardi, L. A., Greenville, A. C., Guerra, C. A., Gusmán-Montalvan, E., Hernández-Hernández, R. M., Hölzel, N., Huber-Sannwald, E., Hughes, F. M., Jadán-Maza, O., Jeltsch, F., Jentsch, A., Kaseke, K. F., Köbel, M., Koopman, J. E., Leder, C. V., Linstädter, A., Roux, P. C. L., Li, X., Liancourt, P., Liu, J., Louw, M. A., Maggs-Kölling, G., Makhalanyane, T. P., Issa, O. M., Manzaneda, A. J., Marais, E., Mora, J. P., Moreno, G., Munson, S. M., Nunes, A., Oliva, G., Oñatibia, G. R., Peter, G., Pivari, M. O. D., Pueyo, Y., Quiroga, R. E., Rahmanian, S., Reed, S. C., et al.: Grazing and ecosystem service delivery in global drylands, Science, 378, 915–920, https://doi.org/10.1126/science.abq4062, 2022.

Magoč, T. and Salzberg, S. L.: FLASH: fast length adjustment of short reads to improve genome assemblies, Bioinformatics, 27, 2957–2963, https://doi.org/10.1093/bioinformatics/btr507, 2011.

Maherali, H. and Klironomos, J. N.: Influence of phylogeny on fungal community assembly and ecosystem functioning, Science, 316, 1746–1748, https://doi.org/10.1126/science.1143082, 2007.

Mariotte, P., Meugnier, C., Johnson, D., Thébault, A., Spiegelberger, T., and Buttler, A.: Arbuscular mycorrhizal fungi reduce the differences in competitiveness between dominant and subordinate plant species, Mycorrhiza, 23, 267–277, https://doi.org/10.1007/s00572-012-0465-8, 2012.

McGonigle, T. P., Miller, M. H., Evans, D. G., Fairchild, G. L., and Swan, J. A.: A new method which gives an objective measure of colonization of roots by vesicular – arbuscular mycorrhizal fungi, New Phytol., 115, 495–501, https://doi.org/10.1111/j.1469-8137.1990.tb00476.x, 1990.

Millennium Ecosystem Assessment (Program) (Ed.): Ecosystems and human well-being: synthesis, Island Press, Washington, DC, 137 pp., ISBN: 1-59726-040-1, 2005.

Mulatu, A., Negash, M., and Asrat, Z.: Species-specific allometric models for reducing uncertainty in estimating above ground biomass at Moist Evergreen Afromontane Forest of Ethiopia, Sci. Rep.-UK, 14, 1147, https://doi.org/10.1038/s41598-023-51002-6, 2024.

Neuenkamp, L.: LoopingLena/MYFUN_experiment-paper_growthrate_grassdominance: v.1.2. RCode to MYFUN_experimental_paper1_grassdominance (MYFUN_experiment_RCode_paper1_v1.2), Zenodo [code], https://doi.org/10.5281/zenodo.20957440, 2026.

Neuenkamp, L. and Shpilkina, Y.: Dataset for "Effects of mycorrhizal fungi and the functional diversity of plants on ecosystem functioning: an experimental approach", Zenodo [data set], https://doi.org/10.5281/zenodo.18924702, 2026.

Neuenkamp, L., Moora, M., Öpik, M., Davison, J., Gerz, M., Männistö, M., Jairus, T., Vasar, M., and Zobel, M.: The role of plant mycorrhizal type and status in modulating the relationship between plant and arbuscular mycorrhizal fungal communities, New Phytol., 220, 1236–1247, https://doi.org/10.1111/nph.14995, 2018.

Neuenkamp, L., Zobel, M., Lind, E., Gerz, M., and Moora, M.: Arbuscular mycorrhizal fungal community composition determines the competitive response of two grassland forbs, PLoS One, 14, e0219527, https://doi.org/10.1371/journal.pone.0219527, 2019.

Neuenkamp, L., García de León, D., Hamer, U., Hölzel, N., McGale, E., and Hannula, S. E.: Comprehensive tools for ecological restoration of soils foster sustainable use and resilience of agricultural land, Commun. Biol., 7, 1577, https://doi.org/10.1038/s42003-024-07275-2, 2024.

Nilsson, R. H., Larsson, K.-H., Taylor, A. F. S., Bengtsson-Palme, J., Jeppesen, T. S., Schigel, D., Kennedy, P., Picard, K., Glöckner, F. O., Tedersoo, L., Saar, I., Kõljalg, U., and Abarenkov, K.: The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications, Nucleic Acids Res., 47, D259–D264, https://doi.org/10.1093/nar/gky1022, 2018.

Northup, B. K., Zitzer, S. F., Archer, S., McMurtry, C. R., and Boutton, T. W.: Above-ground biomass and carbon and nitrogen content of woody species in a subtropical thornscrub parkland, J. Arid Environ., 62, 23–43, https://doi.org/10.1016/j.jaridenv.2004.09.019, 2005.

Oehl, F., Laczko, E., Bogenrieder, A., Stahr, K., Bösch, R., van der Heijden, M., and Sieverding, E.: Soil type and land use intensity determine the composition of arbuscular mycorrhizal fungal communities, Soil Biol. Biochem., 42, 724–738, https://doi.org/10.1016/j.soilbio.2010.01.006, 2010.

Oksanen, J., Simpson, G. L., Blanchet, F. G., Kindt, R., Legendre, P., Minchin, P. R., O'Hara, R. B., Solymos, P., Stevens, M. H. H., Szoecs, E., Wagner, H., Barbour, M., Bedward, M., Bolker, B., Borcard, D., Borman, T., Carvalho, G., Chirico, M., Caceres, M. D., Durand, S., Evangelista, H. B. A., FitzJohn, R., Friendly, M., Furneaux, B., Hannigan, G., Hill, M. O., Lahti, L., Martino, C., McGlinn, D., Ouellette, M.-H., Cunha, E. R., Smith, T., Stier, A., Braak, C. J. F. T., and Weedon, J.: vegan: Community Ecology Package, https://doi.org/10.32614/CRAN.package.vegan, 2024.

Paudel, S., Longcore, T., MacDonald, B., McCormick, M. K., Szlavecz, K., Wilson, G. W. T., and Loss, S. R.: Belowground interactions with aboveground consequences: Invasive earth-

worms and arbuscular mycorrhizal fungi, Ecology, 97, 605–614, https://doi.org/10.1890/15-1085, 2016.

Pedersen, T. L.: patchwork: The Composer of Plots, https://doi.org/10.32614/CRAN.package.patchwork, 2024.

Põlme, S., Abarenkov, K., Nilsson, R. H., Lindahl, B. D., Clemmensen, K. E., Kauserud, H., Nguyen, N., Kjøller, R., Bates, S. T., Baldrian, P., Frøslev, T. G., Adojaan, K., Vizzini, A., Suija, A., Pfister, D., Baral, H.-O., Järv, H., Madrid, H., Nordén, J., Liu, J.-K., Pawlowska, J., Põldmaa, K., Pärtel, K., Runnel, K., Hansen, K., Larsson, K.-H., Hyde, K. D., Sandoval-Denis, M., Smith, M. E., Toome-Heller, M., Wijayawardene, N. N., Menolli, N., Reynolds, N. K., Drenkhan, R., Maharachchikumbura, S. S. N., Gibertoni, T. B., Læssøe, T., Davis, W., Tokarev, Y., Corrales, A., Soares, A. M., Agan, A., Machado, A. R., Argüelles-Moyao, A., Detheridge, A., De Meiras-Ottoni, A., Verbeken, A., Dutta, A. K., Cui, B.-K., Pradeep, C. K., Marín, C., Stanton, D., Gohar, D., Wanasinghe, D. N., Otsing, E., Aslani, F., Griffith, G. W., Lumbsch, T. H., Grossart, H.-P., Masigol, H., Timling, I., Hiiesalu, I., Oja, J., Kupagme, J. Y., Geml, J., Alvarez-Manjarrez, J., Ilves, K., Loit, K., Adamson, K., Nara, K., Küngas, K., Rojas-Jimenez, K., Bitenieks, K., Irinyi, L., Nagy, L. G., Soonvald, L., Zhou, L.-W., Wagner, L., Aime, M. C., Öpik, M., Mujica, M. I., Metsoja, M., Ryberg, M., Vasar, M., Murata, M., Nelsen, M. P., Cleary, M., Samarakoon, M. C., Doilom, M., Bahram, M., Hagh-Doust, N., Dulya, O., Johnston, P., Kohout, P., Chen, Q., Tian, Q., Nandi, R., Amiri, R., Perera, R. H., et al.: FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles, Fungal Divers., 105, 1–16, https://doi.org/10.1007/s13225-020-00466-2, 2020.

Poorter, H., Niklas, K. J., Reich, P. B., Oleksyn, J., Poot, P., and Mommer, L.: Biomass allocation to leaves, stems and roots: meta-analyses of interspecific variation and environmental control, New Phytol., 193, 30–50, https://doi.org/10.1111/j.1469-8137.2011.03952.x, 2011.

Powell, J. R. and Rillig, M. C.: Biodiversity of arbuscular mycorrhizal fungi and ecosystem function, New Phytol., 220, 1059–1075, https://doi.org/10.1111/nph.15119, 2018.

Pozo, M. J., López-Ráez, J. A., Azcón-Aguilar, C., and García-Garrido, J. M.: Phytohormones as integrators of environmental signals in the regulation of mycorrhizal symbioses, New Phytol., 205, 1431–1436, https://doi.org/10.1111/nph.13252, 2015.

Qin, M., Li, L., Miranda, J.-P., Tang, Y., Song, B., Oosthuizen, M. K., and Wei, W.: Experimental duration determines the effect of arbuscular mycorrhizal fungi on plant biomass in pot experiments: A meta-analysis, Front. Plant Sci., 13, https://doi.org/10.3389/fpls.2022.1024874, 2022.

R Core Team: R: A Language and Environment for Statistical Computing, R Foundation for Statistical Computing, Vienna, Austria, https://www.R-project.org/ (last access: 15 June 2026), 2025.

Revelle, W.: psych: Procedures for Psychological, Psychometric, and Personality Research, https://doi.org/10.32614/CRAN.package.psych, 2023.

Rognes, T., Flouri, T., Nichols, B., Quince, C., and Mahé, F.: VSEARCH: a versatile open source tool for metagenomics, PeerJ, 4, e2584, https://doi.org/10.7717/peerj.2584, 2016.

Romero, F., Argüello, A., de Bruin, S., and van der Heijden, M. G. A.: The plant–mycorrhizal fungi collaboration gradient depends on plant functional group, Funct. Ecol., 37, 2386–2398, https://doi.org/10.1111/1365-2435.14395, 2023.

Roscher, C., Schumacher, J., Baade, J., Wilcke, W., Gleixner, G., Weisser, W. W., Schmid, B., and Schulze, E.-D.: The role of biodiversity for element cycling and trophic interactions: an experimental approach in a grassland community, Basic Appl. Ecol., 5, 107–121, https://doi.org/10.1078/1439-1791-00216, 2004.

Roscher, C., Schumacher, J., Gubsch, M., Lipowsky, A., Weigelt, A., Buchmann, N., Schmid, B., and Schulze, E.-D.: Using plant functional traits to explain Diversity–Productivity relationships, PLoS ONE, 7, e36760, https://doi.org/10.1371/journal.pone.0036760, 2012.

Sala, O. E. and Austin, A. T.: Methods of Estimating Aboveground Net Primary Productivity, in: Methods in Ecosystem Science, edited by: Sala, O. E., Jackson, R. B., Mooney, H. A., and Howarth, R. W., Springer New York, New York, NY, 31–43, https://doi.org/10.1007/978-1-4612-1224-9_3, 2000.

Sanaei, A., Ali, A., Ahmadaali, K., and Jahantab, E.: Generalized and species-specific prediction models for aboveground biomass in semi-steppe rangelands, J. Plant Ecol., 12, 428–437, https://doi.org/10.1093/jpe/rty037, 2018.

Schnitzer, S. A., Klironomos, J. N., Hille Ris Lambers, J., Kinkel, L. L., Reich, P. B., Xiao, K., Rillig, M. C., Sikes, B. A., Callaway, R. M., Mangan, S. A., Van Nes, E. H., and Scheffer, M.: Soil microbes drive the classic plant diversity–productivity pattern, Ecology, 92, 296–303, https://doi.org/10.1890/10-0773.1, 2011.

Schreiner, F.-R., Hölzel, N., Hamer, U., Hinderling, J., Irmscher, V., Paeenroudposhti, N. R., Prada-Salcedo, L. D., Prati, D., Vieira, S., and Neuenkamp, L.: Slow and context-dependent: Responses to grassland extensification across a comprehensive set of ecosystem attributes, Agr. Ecosyst. Environ., 401, 110277, https://doi.org/10.1016/j.agee.2026.110277, 2026.

Sepp, S.-K., Davison, J., Moora, M., Neuenkamp, L., Oja, J., Roslin, T., Vasar, M., Öpik, M., and Zobel, M.: Woody encroachment in grassland elicits complex changes in the functional structure of above- and belowground biota, Ecosphere, 12, e03512, https://doi.org/10.1002/ecs2.3512, 2021.

Shipley, B., Lechowicz, M. J., Wright, I., and Reich, P. B.: Fundamental Trade-Offs Generating the Worldwide Leaf Economics Spectrum, Ecology, 87, 535–541, https://doi.org/10.1890/05-1051, 2006.

Sims, G. K., Ellsworth, T. R., and Mulvaney, R. L.: Microscale determination of inorganic nitrogen in water and soil extracts, Commun. Soil Sci. Plan., 26, 303–316, https://doi.org/10.1080/00103629509369298, 1995.

Smith, S. E. and Read, D. J.: Mycorrhizal symbiosis, 3rd edn., Academic Press, Amsterdam Boston, ISBN 9780080559346, 2008.

Smith, S. E. and Smith, F. A.: Roles of Arbuscular Mycorrhizas in Plant Nutrition and Growth: New Paradigms from Cellular to Ecosystem Scales, Annu. Rev. Plant Biol., 62, 227–250, https://doi.org/10.1146/annurev-arplant-042110-103846, 2011.

Tedersoo, L., Bahram, M., and Zobel, M.: How mycorrhizal associations drive plant population and community biology, Science, 367, eaba1223, https://doi.org/10.1126/science.aba1223, 2020.

Tilman, D., Wedin, D., and Knops, J.: Productivity and sustainability influenced by biodiversity in grassland ecosystems, Nature, 379, 718–720, https://doi.org/10.1038/379718a0, 1996.

Tilman, D., Knops, J., Wedin, D., Reich, P., Ritchie, M., and Siemann, E.: The Influence of Functional Diversity and Composition on Ecosystem Processes, Science, 277, 1300–1302, https://doi.org/10.1126/science.277.5330.1300, 1997.

Van Der Heijden, M. G. A.: Arbuscular Mycorrhizal Fungi as a Determinant of Plant Diversity: in Search of Underlying Mechanisms and General Principles, in: Mycorrhizal Ecology, vol. 157, edited by: Van Der Heijden, M. G. A. and Sanders, I. R., Springer Berlin Heidelberg, Berlin, Heidelberg, 243–265, https://doi.org/10.1007/978-3-540-38364-2_10, 2002.

Van Der Heijden, M. G. A., Klironomos, J. N., Ursic, M., Moutoglis, P., Streitwolf-Engel, R., Boller, T., Wiemken, A., and Sanders, I. R.: Mycorrhizal fungal diversity determines plant biodiversity, ecosystem variability and productivity, Nature, 396, 69–72, https://doi.org/10.1038/23932, 1998.

Van Der Heijden, M. G. A., Bardgett, R. D., and Van Straalen, N. M.: The unseen majority: soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems, Ecol. Lett., 11, 296–310, https://doi.org/10.1111/j.1461-0248.2007.01139.x, 2008.

Van Der Heijden, M. G. A., Martin, F. M., Selosse, M., and Sanders, I. R.: Mycorrhizal ecology and evolution: the past, the present, and the future, New Phytol., 205, 1406–1423, https://doi.org/10.1111/nph.13288, 2015.

van Ruijven, J., Ampt, E., Francioli, D., and Mommer, L.: Do soil-borne fungal pathogens mediate plant diversity–productivity relationships? Evidence and future opportunities, J. Ecol., 108, 1810–1821, https://doi.org/10.1111/1365-2745.13388, 2020.

Vasar, M., Davison, J., Neuenkamp, L., Sepp, S.-K., Young, J. P. W., Moora, M., and Öpik, M.: User-friendly bioinformatics pipeline gDAT (graphical downstream analysis tool) for analysing rDNA sequences, Mol. Ecol. Resour., 21, 1380–1392, https://doi.org/10.1111/1755-0998.13340, 2021.

Vierna, J., Doña, J., Vizcaíno, A., Serrano, D., and Jovani, R.: PCR cycles above routine numbers do not compromise high-throughput DNA barcoding results, Genome, 60, 868–873, https://doi.org/10.1139/gen-2017-0081, 2017.

Vogelsang, K. M., Reynolds, H. L., and Bever, J. D.: Mycorrhizal fungal identity and richness determine the diversity and productivity of a tallgrass prairie system, New Phytol., 172, 554–562, https://doi.org/10.1111/j.1469-8137.2006.01854.x, 2006.

Wagg, C., Jansa, J., Schmid, B., and van der Heijden, M. G. A.: Belowground biodiversity effects of plant symbionts support aboveground productivity, Ecol. Lett., 14, 1001–1009, https://doi.org/10.1111/j.1461-0248.2011.01666.x, 2011.

Wagg, C., Bender, S. F., Widmer, F., and Van Der Heijden, M. G. A.: Soil biodiversity and soil community composition determine ecosystem multifunctionality, P. Natl. Acad. Sci. USA, 111, 5266–5270, https://doi.org/10.1073/pnas.1320054111, 2014.

Wagg, C., Veiga, R., and Van Der Heijden, M. G. A.: Facilitation and Antagonism in Mycorrhizal Networks, in: Mycorrhizal Networks, vol. 224, edited by: Horton, T. R., Springer Netherlands, Dordrecht, 203–226, https://doi.org/10.1007/978-94-017-7395-9_7, 2015.

Weigelt, A., Mommer, L., Andraczek, K., Iversen, C. M., Bergmann, J., Bruelheide, H., Fan, Y., Freschet, G. T., Guerrero-Ramírez, N. R., Kattge, J., Kuyper, T. W., Laughlin, D. C., Meier, I. C., van der Plas, F., Poorter, H., Roumet, C., van Ruijven, J., Sabatini, F. M., Semchenko, M., Sweeney, C. J., Valverde-Barrantes, O. J., York, L. M., and McCormack, M. L.: An integrated framework of plant form and function: the belowground perspective, New Phytol., 232, 42–59, https://doi.org/10.1111/nph.17590, 2021.

Weiner, J.: Asymmetric competition in plant populations, Trends Ecol. Evol., 5, 360–364, https://doi.org/10.1016/0169-5347(90)90095-U, 1990.

White, T. J., Bruns, T., Lee, S., and Taylor, J.: Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics, in: PCR Protocols, edited by: Innis, M. A., Gelfand, D. H., Sninsky, J. J., and White, T. J., Academic Press, San Diego, 315–322, https://doi.org/10.1016/B978-0-12-372180-8.50042-1, 1990.

Wickham, H.: ggplot2: Elegant Graphics for Data Analysis, Springer-Verlag New York, ISBN 978-3-319-24277-4, 2016.

Wickham, H.: Reshaping data with the reshape package, J. Stat. Softw., 21, 1–20, https://www.jstatsoft.org/v21/i12/ (last access: 23 July 2026), 2007.

Wickham, H., Chang, W., Henry, L., Pedersen, T. L., Takahashi, K., Wilke, C., Woo, K., Yutani, H., Dunnington, D., van den Brand, T., Posit, and PBC: ggplot2: Create Elegant Data Visualisations Using the Grammar of Graphics, https://doi.org/10.32614/CRAN.package.ggplot2, 2025.

Wubs, E. R. J., Van Der Putten, W. H., Bosch, M., and Bezemer, T. M.: Soil inoculation steers restoration of terrestrial ecosystems, Nat. Plants, 2, 16107, https://doi.org/10.1038/nplants.2016.107, 2016.

Yang, H., Dai, Y., Wang, X., Zhang, Q., Zhu, L., and Bian, X.: Meta-Analysis of Interactions between Arbuscular Mycorrhizal Fungi and Biotic Stressors of Plants, Sci. World J., 2014, 746506, https://doi.org/10.1155/2014/746506, 2014.

Zhang, E., Wang, Y., Crowther, T. W., Sun, W., Chen, S., Zhou, D., Shangguan, Z., Huang, J., He, J.-S., Wang, Y., Sheng, J., Tang, L., Li, X., Dong, M., Wu, Y., Hu, S., Bai, Y., and Yu, G.: Mycorrhiza increases plant diversity and soil carbon storage in grasslands, P. Natl. Acad. Sci. USA, 122, e2412556122, https://doi.org/10.1073/pnas.2412556122, 2025.

Zuur, A., Ieno, E. N., Walker, N., Saveliev, A. A., and Smith, G. M.: Mixed Effects Models and Extensions in Ecology with R, Springer Science & Business Media, 579 pp., https://doi.org/10.1007/978-0-387-87458-6, 2009.

Zuur, A. F., Ieno, E. N., and Elphick, C. S.: A protocol for data exploration to avoid common statistical problems: *Data exploration*, Methods Ecol. Evol., 1, 3–14, https://doi.org/10.1111/j.2041-210X.2009.00001.x, 2010.