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RESEARCH ARTICLE

Fungal communities driven by *Rhododendron* species correlate with pathogen protection against *Phytophthora cinnamomi*

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Abstract

Background and aims Plant interactions with soil microbial communities are critical for understanding plant health, improving horticultural and agricultural outcomes, and maintaining diverse natural communities. In some cases, disease suppressive soils enhance plant survival in the presence of pathogens. However, species-specific differences and seasonal variation complicate our understanding of the drivers of soil fungal communities and their consequences for plants. Here, we aim to describe soil fungal communities across *Rhododendron* species and seasons as well as the test for fungal indicators of *Rhododendron* species in the soil. Further, we test possible mechanisms governing disease suppressive soils to the oomycete pathogen *Phytophthora cinnamomi*. Variation in disease susceptibility to this pathogen across species and clades allows us to test for possible fungal drivers of disease suppressive soils.

Methods We conducted high throughput sequencing of the fungal communities found in soil collected under 14 *Rhododendron* species and across 2 seasons (April, October) at two sites in Ohio, USA. Phylogenetic analyses were used to ask whether fungal community composition correlated with increased plant survival with the addition of whole soil communities from a prior greenhouse experiment.

Results Effects of *Rhododendron* species ($R^2=0.13$), season ($R^2=0.01$) and their interaction on fungal communities ($R^2=0.11$) were statistically significant. Fungal community composition negatively correlated with survival following exposure to whole soil microbial communities, though this result depended on the presence of *R. minus*. Forty-five *Trichoderma* taxa were identified across our soil samples, and some *Trichoderma* were significantly associated with particular *Rhododendron* species (e.g. *Trichoderma atroviride* was associated with *R. molle*) in indicator species analyses.

Conclusion The correlation between plant responses to soil biotic communities and fungal community composition, as well as the presence of potential beneficial taxa such as *Trichoderma* and mycorrhizal fungi, are consistent with fungal-mediated survival benefits from the pathogen *Phytophthora cinnamomi*.

Keywords Disease suppressive soils · Fungal taxa · Plant-soil microbial interactions · High throughput sequencing · *Rhododendron* · Soil microbes

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Abbreviations

zOTUs	Zero-radius operational taxonomic units
lnRR.live	Soil biota responsiveness
PGLS	Phylogenetic generalized least squares)
ErMF	Ericoid mycorrhizal fungi)

Introduction

Plant interactions with soil microbes are important for understanding plant health, coexistence, and plant community composition. For example, plant species that suppress one another through plant-soil feedbacks can lead to coexistence (Bever et al. 1997) and contribute to plant community composition (Bever 2003; Van Der Putten et al. 2013; Krishna et al. 2020; Enderle et al. 2024). Experimentally, effects of plant interactions with soil microbial communities can be tested using "whole soil inocula", an approach that uses soil collected from the plant root zone to test for effects on plant performance (Pernilla Brinkman et al. 2010). These effects of the whole soil biotic community are often strong in magnitude (Crawford et al. 2019) and can increase plant survival and ability to tolerate pathogens (Liu et al. 2021). In other words, the effects of soil microbial communities can be "disease suppressive". Plants influence soil microbial communities through multiple mechanisms, including the production of root exudates (Bais et al. 2006; Rudrappa et al. 2008), leaf litter deposition (Ehrenfeld et al. 2005), and antimicrobial compounds (Berendsen et al. 2012). While it is widely thought that plant-soil feedbacks are driven by plant-species specific effects on the soil rhizosphere (Ehrenfeld et al. 2005), more work using high throughput sequencing is needed to identify microbial taxa in the soil mediating these plant-species effects (Krishna et al. 2020).

Plant species-specific effects on soil microbial community composition are an assumption of plant-soil feedback research and are commonly observed (Ushio et al. 2008; Burns et al. 2015; Krishna et al. 2020), though not found universally (reviewed in Ehrenfeld et al. 2005). Seasonal shifts in soil microbial communities could alter the effects of plant species, potentially complicating our ability to generalize from greenhouse experiments to implications in the field. Furthermore, ericoid root hairs, which house the ericoid mycorrhizal fungi (ErMF), are mostly present in the winter and spring season (Scagel et al. 2005), suggesting shifts in ErMF abundance and structure across seasons. Effects of season might also be expected because of shifts in leaf litter inputs and plant root activity (Thoms and Gleixner 2013). Leaf litter is known to influence soil pH (Finzi et al. 1998; Sayer 2005; reviews in Ehrenfeld et al. 2005), a key driver of soil microbial community composition (Fierer et al. 2012; Glassman et al. 2017). In addition, effects of season on plant species' influence of soil microbes has been found for markers of soil communities, such as microbial phospholipid fatty acids (Thoms and Gleixner 2013). Soil microbial communities may shift seasonally irrespective of their interactions with plants, such as through environmental drivers (Averill et al. 2019). Understanding the relative importance of plant species and season on soil microbial community composition might thus motivate future experiments across seasons, such as whether benefits of the soil microbial community depend on season.

Here, we focus on *Rhododendron* (Ericaceae), which are widely known for their association with ErMF (Smith and Read 2008). As a result, the diverse complement of fungal taxa in the rhizosphere in this group has been largely ignored. However, considerable research suggests that fungal species influence plant health (Miransari 2014; Schrey et al. 2014) and resistance to pathogens through induction of the plant immune system, competition with pathogens, and/or the production of antimicrobial compounds (Berendsen et al. 2012). The rhizosphere also includes many fungi such as mycorrhizae, and root endophytes (Schrey et al. 2014). For example, the symbionts involved in the remediation process of soil function and plant growth promotion have been reported from the order Deuteromycetes, including *Trichoderma* and *Gliocladium* and Sebacinales including *Piriformospora* (Waller et al. 2005; Qiang et al. 2012; Mendes et al. 2013). Some *Trichoderma* species (*Trichoderma reesei*, *Trichoderma virens,* and *Trichoderma atroviride*) play a role as a biofertilizer by producing antimicrobial compounds (Druzhinina et al. 2011) and others (*T. viride, T. harzianum, T. asperellum, T. virens,* and *T. atroviride)* may promote plant growth in horticultural crops (López-Bucio et al. 2015). Moreover, arbuscular mycorrhizal fungi (*Glomus intraradices*) and ectomycorrhizal fungi (*Pisolithus tinctonus*) are known plant mutualists that aid in nutrient acquisition for the plant (Tjamos et al. 2010; Rana et al. 2019; Medeiros et al. 2022). In

particular, *Rhododendron* has been shown to associate with arbuscular mycorrhizal fungi and ectomycorrhizal fungi, in addition to their ericoid associations (Medeiros et al. 2022). By describing the fungal community in the rhizosphere of *Rhododendron*, the current study adds to the growing body of literature on fungi that influence *Rhododendron* (Liu et al. 2024).

We use a high throughput sequencing analysis of the rhizosphere soils of 14 *Rhododendron* species across 2 sampling seasons in the field to address two goals. First, the effects of plant species and season on fungal community composition in the rhizosphere were assessed using ordination and PERMANOVA on community composition data. Significant effects of *Rhododendron* species on fungal communities were predicted based on prior studies (Medeiros et al. 2022). Further, seasonal effects on fungal communities were predicted because of differences in litter input in October compared with April. A season by *Rhododendron* species interaction was predicted because of species differences in evergreen versus deciduous leaves and seasonal variation in the hair roots (Medeiros et al. 2022). Second, we determined whether plant responses to soil biota from a separate experiment correlate with fungal community composition in that species. Prior experiments have found benefits of whole soil microbial inocula for *Rhododendron* survival in the presence of a pathogen (Liu et al. 2021). However, whether fungal communities might be implicated in this benefit is unknown. The communities described here were compared with plant responses to whole soil inocula quantified in a greenhouse study (Liu et al. 2021), to ask whether community composition correlates with plant responses. A phylogenetic generalized least squares analysis was used to test for a correlation between the benefits of soil biota and fungal community composition.

Materials and methods

Collection of soil samples

We collected rhizosphere soil samples of 14 species of *Rhododendron* (Table S1). These plants were located at Holden Arboretum (41°36′45.21″N 81°18′4.84″W) in Kirtland (Ohio, USA), and David G. Leach Center (41°49′21″N 81°31′6″W) in Madison (Ohio, USA). For each *Rhododendron* species, 8 soil samples across two seasons were collected. Whenever possible, these 8 samples were collected from 8 separate plants (see archived data at OSF). A total of 224 samples (14 species × 8 plants × 2 seasons) were collected in October (2022) and April (2023) to study the effect of season on fungal community composition. Resampling was done from the same locations in April, using GPS data and accession tags to ensure accurate resampling. Soil was sampled from the upper 5 cm because this depth contains the greatest diversity of soil microbes important to plant health (Burke and Carrino-Kyker 2021). Soils were collected using sterilized shovels, bagged, and transported on ice to the −80ºC freezer.

DNA extraction

DNA extraction was conducted on each soil sample using a phenol–chloroform method described previously (Burke et al. 2015). PCR was done using the primers 58A2F and ITS4 containing Illumina overhang adapters (as in Burke et al. 2024). These primers amplify the ITS2 region of fungal species and primer sequences are as follows: 58A2F: TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATCGATGAAGAACGCAG (Martin and Rygiewicz 2005) ITS4: GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCCTCCGCTTATTGATATGC (White 1990). Underlined portions indicate the overhang adapters. PCR conditions were as described previously (Liu et al. 2023).

High Throughput Sequencing

The amplified PCR products were sent to the Genomics Core facility at Case Western Reserve University for sequencing with a 2 × 250 bp MiSeq run. A total of 217 soil samples were successfully sequenced, which resulted in a total of 12,526,214 reads (Table S2). Reads were processed with the UNOISE3 pipeline (Edgar 2016a). For this, the forward and reverse reads were merged with the *fastq_mergepairs* command in USEARCH (version 11.0.667; Edgar 2010). After merging, a total of 9,542,977 reads were processed through the remaining pipeline. The primer sequences were removed using CutAdapt (version 2.8; Martin 2011) and the low-quality reads were filtered out with the *fastq_filter* command in USEARCH. Those reads were then clustered into zOTUs (zero-radius operational taxonomic units) using the

unoise3 command in USEARCH, which, by default, removes chimeras and zOTUs with low numbers (< 8) of sequences. The processed sequence reads (merged and with primers trimmed off) from each sample were then mapped to the zOTUs with the *otu_tab* command in USEARCH. Finally, taxonomic matches for each zOTU were made by aligning to the UNITE fungal database (version 9.0, released 2022–10-16; Abarenkov et al. 2022) using the SINTAX algorithm (Edgar 2016b). Sequence reads in the resulting zOTU table were normalized with the *estimateSizeFactors* command in the DESeq2 package (version 1.36.0) of R (version 4.2.1; R Core Team 2022). This normalization accounted for difference in sequencing depth between each sample (McMurdie and Holmes 2014).

Data analysis

Non-metric multidimensional scaling (NMDS) ordination was used to visualize changes in the fungal community structure between *Rhododendron* species and season. NMDS was conducted with the *metamds* command in the vegan package (version 2.6–4; Oksanen et al., 2022) of R and resulted in a 2-dimensional ordination with a stress value of 0.17. We used PERMANOVA first to test for effects of *Rhododendron* species, season of collection, and for a season by species interaction on fungal community composition using the *adonis2* command in the vegan package with 4999 permutation. To determine whether sampling location influenced these patterns, we also explored a PERMANOVA with species, season, location (Holden, Leach), and their interactions. Further, indicator species analysis was used in the indicspecies package (version 1.7.15; Cáceres and Legendre 2009) using the *multipatt* function with 10,000 random permutations to test for fungal taxa associated with season of sampling and *Rhododendron* species groups. Indicator species analyses was followed with a Benjamini and Hochberg (1995) correction for multiple comparisons using p.adjust in the stats package in R (Version 4.2.2; R Core Team 2022), to avoid inflated type I error.

To determine whether there was a correlation between fungal community composition and the benefits of soil biotic communities, we used the results from a prior experiment, which quantified plant benefits of whole soil inoculation in the presence of the pathogen *Phytophthora cinnamomi* (Liu et al. 2021). In brief, 14 Rhododendron species were inoculated with 5% volume conspecific field soils and then allowed that whole soil inoculum to establish for 3 weeks (Liu et al. 2021). Two-week-old *Phytophthora cinnamomi* mycelium grown on sterile rice (Liu et al. 2021) was then added to the pots. We grew three seedlings per pot then calculated the proportion survival per pot for the following analysis. The soils collected for the current study were under the same plants as those used for whole soil inoculations in Liu et al. (2021), albeit in different years. While not a direct test of mechanism, a correlation between the community structure changes measured here and plant survival in the presence of *P. cinnamomi* from Liu et al. (2021) supports the hypothesis that fungal community composition could provide protection in the presence of a pathogen. We predicted that the plant response to soil biota in the presence of the pathogen might correlate with fungal community composition. Therefore, the log response ratio in the presence of the pathogen, comparing plant survival in a live soil biota treatment with survival in a sterilized treatment, was used to calculate a metric "soil biota responsiveness."

$$\mathrm{lnRR.live} = \ln(\mathrm{Y1} + 0.01) - \ln(\mathrm{Y2} + 0.01)$$

where, Y1 and Y2 are the average plant performance (i.e. proportional survival per pot) with live soil biota (Y1) and in sterilized controls (Y2). A constant (0.01) was added to include zero values. Greater values of this metric correspond to larger improvement in survival with the addition of live soil biota.

To include a phylogeny with all 14 species sampled here, we started with the analysis from Liu et al. (2021). Because there is no existing molecular phylogeny for all of our sampled species, we synthesized the literature. For the three species added here, these taxa were manually added following the phylogenetic results of Khan et al. (2021) (Fig. 1). *Rhododendron vaseyi* (Pentanthera) was added sister to the other sampled Pentanthera with a branch length of 0.01. *Rhododendron degronianum* was added sister to a clade with *R. smirnowii* (sampled in Liu et al. 2021, but dropped from subsequent analyses here) with a branch length of 0.01. *Rhododendron catawbiense* was added sister to *R. brachycarpum* with a branch length of 0.002. The phylogeny was rooted with the outgroup *Empertrum*

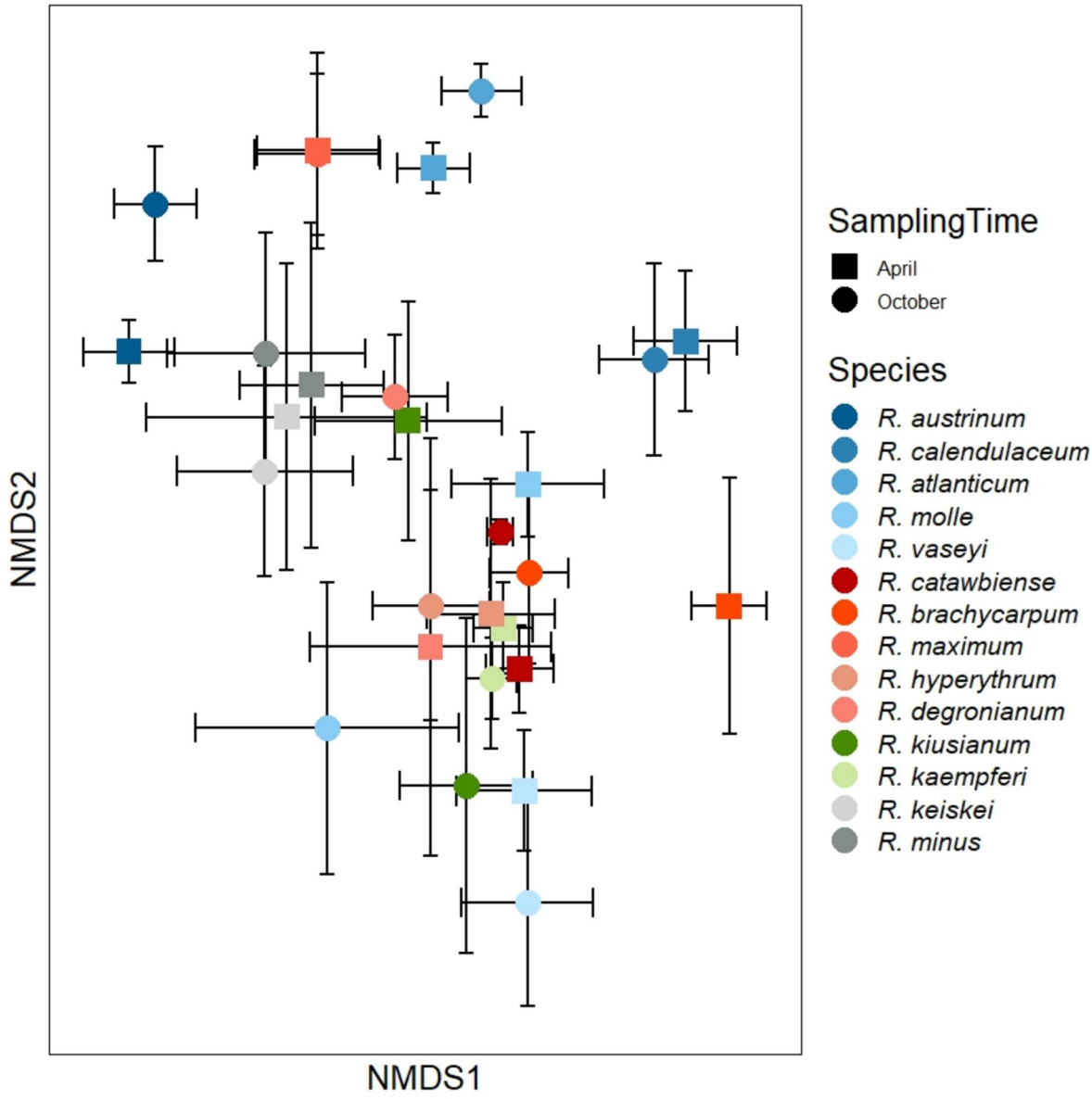

Fig. 1 The soil fungal community composition differed across 14 *Rhododendron* species sampled, as well as time of sampling (April and October) ($n = 217$). Species from Pentanthera clade such as *R. autrinum*, *R. calendulaceum*, *R. atlanticum*, *R. molle*, and *R. vaseyi* are shown in blue palette. Species belonging to Ponticum such as *R. catawbiense*, *R. brachycarpum*, *R. maximum*, *R. hyperythrum*, and *R. degronianum* are shown red color palette. Species in clade Tsutsusi including *R. kiusianum*, and *R. kaempferi* are shown in green palette. Species in *Rhododendron* clade are shown in gray color palette

nigrum and tips not in the data presented here were dropped from the phylogeny for further analysis.

To test for a correlation between fungal community composition and benefits of soil biota, a phylogenetic generalized least squares (PGLS, Martins and Hansen 1997) analysis was conducted with lnRR. live as a response variable and NMDS axis 1 and 2 as the predictor variable. We used the *pgls* function in the caper package with lambda estimated using the maximum likelihood function (Orme et al. 2023). These analyses were conducted at the species scale, using averages across the 8 soil samples per species.

Table 1 PERMANOVA results for the effects of *Rhododendron* species and sampling time and their interaction on fungal community composition ($n = 217$)

Source	DF	SS	R^2	*F*-value	*P*-value
Species	13	11.78	0.13	2.53	0.0002
Sampling Time (Oct, April)	1	1.47	0.01	1.33	0.0456
Species x Sampling Time	13	9.37	0.11	2.01	0.0002

Residual DF = 189

Separate PGLS analyses were conducted for April and October fungal community composition.

Results

Fungal community composition across two seasons

A significant season by species interaction on fungal community composition was found across the 217 sequenced samples (Table 1, Fig. 1). Plant species effects were larger than seasonal differences. Some species, such as *Rhododendron degronianum* and *R. austrinum*, had greater differences across seasons than others (Fig. 1). There were also significant species by location by sampling time differences, and the species by sampling time effects had the largest R^2 values in the model (Table S3). Differences in fungal species within the phylum Chytridiomycota largely drove seasonal differences (per indicator species analysis), though there were some seasonal differences in putative ERM in the Serendipitaceae (Vohník et al. 2016) (Table S4). There were no significant indicators of season that were in the genus *Trichoderma* (Table S4).

Rhododendrons association with *Trichoderma* species

On average, each *Rhododendron* species (8 soil samples per species), contained between 17—26 *Trichoderma* zOTUs. *Trichoderma pubescens*, *T. virens*, *T. yunnanense*, *T. harzianum*, *T. stellatum*, *T. atroviride*, *T. turrialbense*, and *T. spirale* were found in the rhizosphere soil of all *Rhododendron* species sampled. Some taxa, including *T. calamagrostidis*, *T. oligosporum*, and *T. orientale*, were found in the rhizosphere soils of only one *Rhododendron* species. *T. calamagrostidis* was found in the rhizosphere of *R. austrinum, T. oligosporum* was found in the rhizosphere of *R. molle* and *T. orientale* was found in the rhizosphere of *R. keiskei*.

The *Trichoderma* communities differed across sampled *Rhododendron*, with *T. yunnanense* more abundant than other *Trichoderma* in clade *Rhododendron* (*R. keiskei* and *R. minus*), for example (Fig. 2). Indicator species analysis found that *T. aerugineum*, *T. strictipile*, and *T. turrialbense* were significant indicators of *R. catawbiense, T. pararogersonii* was an indicator of *R. atlanticum,* and *T. atroviride* and *T. danicum* were indicators of *R. molle* (see data archiving for peer review).

Putative endophytic fungi (Lo Piccolo et al. 2015; Grunewaldt-Stöcker and von Alten 2016; Zhao et al. 2023) were also associated with particular *Rhododendron* species in indicator species analyses. For example, *Acremonium hyalinulum* and *A. persicinum* were indicators of *R. degronianum*. *A. persicinum* was also an indicator of *R. atlanticum*. Mycorrhizal fungus *Sebacina incrustans* was an indicator of *R. vaseyi*.

Benefits of soil biota correlate with fungal communities

There was a significant correlation between plant survival following pathogen inoculation from a prior experiment and soil fungal communities determined in this experiment (Table 2). These patterns were consistent between April and October fungal samples. Some species, such as *R. minus*, *R. brachycarpum*, *R. maximum*, and *R. molle* (Fig. 3) had significantly greater survival when soil biota was added compared with sterilized soils (Liu et al. 2021). When inoculated with the pathogen *Phytophthora cinnamomi*, these species exhibited higher survival when grown with soil biota, compared to without soil biota (Liu et al. 2021). This relationship was driven by *R. minus*, such that the pattern is not significant when *R. minus* was excluded from the analysis (Table S5).

Discussion

Plant-soil interactions are important for plant health and plant communities, and analyses of

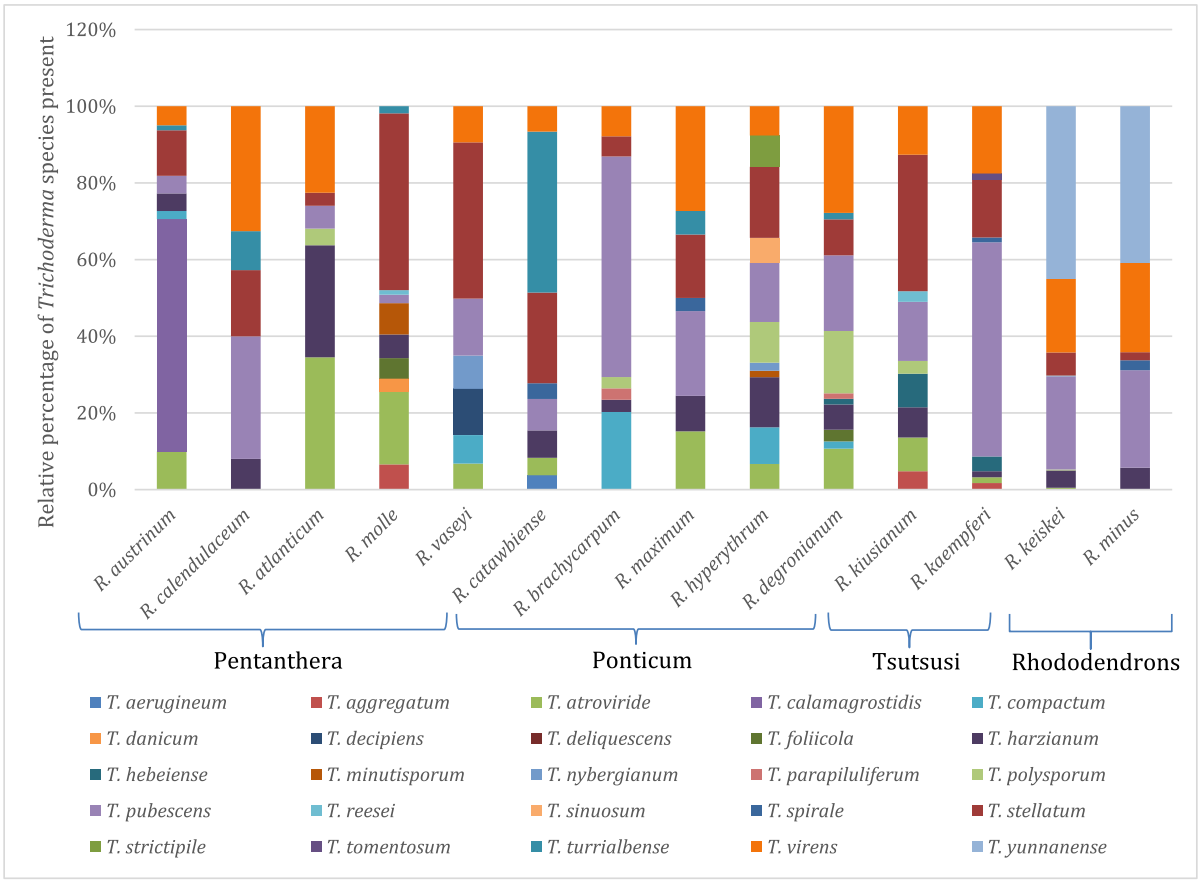

Fig. 2 Soils sampled from 14 *Rhododendron* species included 45 *Trichoderma* zOTUs. Relative abundances are shown for only samples with a relative abundance > 1 (see archived data)

Table 2 F-statistics from PGLS models showing the relationship between the fungal community in the soil and the effect size of soil biota (lnRR.live) (Liu et al. 2021) ($n = 11$)

	slope	DF	*F*-value	*P*-value
April NMDS1	−0.19	1,9	6189.6	< 0.0001
April NMDS2	0.55	1,9	5504.0	< 0.0001
Oct NMDS1	−0.27	1,9	6170.6	< 0.0001
Oct NMDS2	0.35	1,9	6546.7	< 0.0001

microbial community composition are needed to elucidate mechanisms in the soil governing plant-soil interactions (Trivedi et al. 2020). Here, the effects of plant species, season, and their interaction on *Rhododendron* fungal community composition across 14 species of *Rhododendron* are described. Caution should be used in generalizing these results beyond *Rhododendron*, as other taxa may respond differently to soil microbial interactions. There were strong effects of plant species and season on fungal community composition in the rhizosphere. Prior work found *Rhododendron* species differ greatly in their vulnerability to a common soil pathogen, *Phytophthora cinnamomi* (Liu et al. 2021). Plant survival was buffered by the presence of soil biotic communities, reducing disease-induced mortality (Liu et al. 2021). Here, the correlational evidence that components of the soil fungal community might be responsible for these survival benefits are provided. Candidate taxa include *Trichoderma* fungi, which include 17–26 zOTUs in the *Rhododendron* rhizosphere, and which are known as mycoparasites on *Phytophthora* plant pathogens (Khan et al. 2004, p. 2014; Benítez et al. 2004; Błaszczyk et al. 2014).

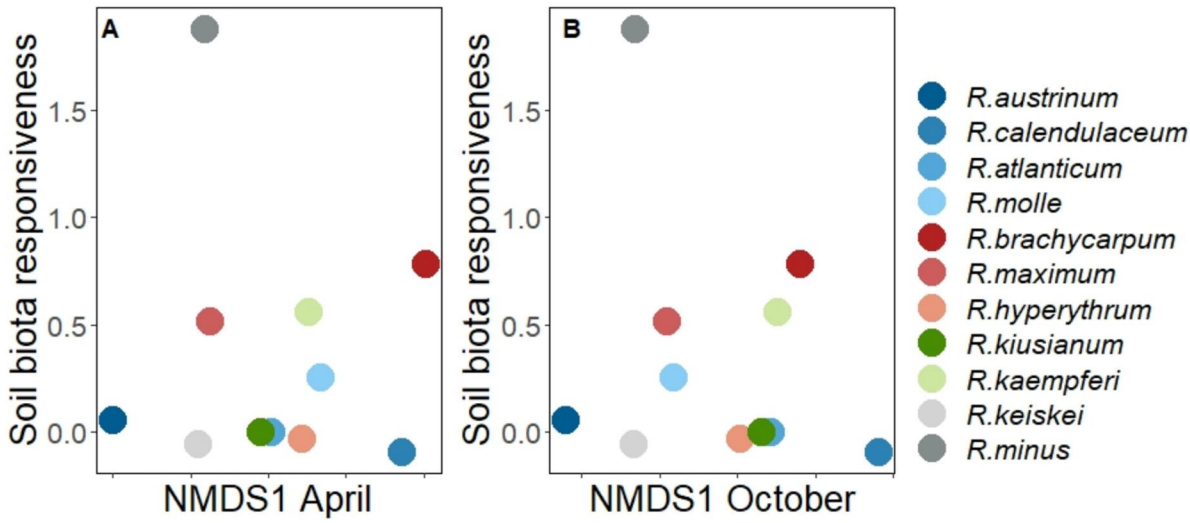

Fig. 3 Correlation between the soil biota response (relative improvement in survival when soil biota is added compared to the absence of soil biota, data from experiment in Liu et al. 2021), and the fungal community composition across 11 species of *Rhododendron* sampled in April (**A**) and October (**B**). Species from Pentanthera clade such as *R. austrinum*, *R. calendulaceum*, *R. atlanticum*, and *R. molle* are shown in blue palette. Species belonging to Ponticum such as *R. catawbiense*, *R. brachycarpum*, *R. maximum*, *R. hyperythrum*, and *R. degronianum* are shown red color palette. Species in clade Tsutsusi including *R. kiusianum*, and *R. kaempferi* are shown in green palette. Species in *Rhododendron* clade are shown in gray color palette

The statistical effect of plant species on soil microbial community composition observed here is consistent with prior literature (Ushio et al. 2008; Burns et al. 2015; Schmid et al. 2021), supporting an assumption of plant-soil feedback research. Plant species are known to have species-specific effects on soil microbial communities in the rhizosphere and surrounding soil through their effects on soil nutrient availability (Kao-Kniffin and Balser 2008), litter chemistry, pH (Ushio et al. 2008), and the production of root exudates (Bais et al. 2006; Rudrappa et al. 2008). Such plant species specific effects can influence plant-soil feedbacks (Ehrenfeld et al. 2005; Van Der Putten et al. 2016), plant community composition (Heinen et al. 2020), and ecosystem processes such as carbon sequestration (Chen et al. 2020). While plant species effects on soil microbial communities have been frequently described, our results show that particular fungal taxa, including *Trichoderma* species, were associated with individual *Rhododendron* species. This supports the hypothesis that *Trichoderma* could be a mechanism of disease suppressive soils influencing benefits to *Rhododendron*.

Mycorrhizal fungi are a possible component of the soil biota that might influence plant pathogen tolerance. Few ErMF are well-described and confirmed as mycorrhizal (Jansa and Vosátka 2000; Vohník 2020). The most well-characterized confirmed ErMF is *Hyaloscypha hepaticicola* (Vohník 2020), which was not observed in the current study. *Sebacina incrustans* was associated with *R. vaseyi*. *Sebacina incrustans* is known to form ectomycorrhizal associations with some plant species (Urban et al. 2003), and Sun et al. (2012) also found several zOTUs from the order Sebacinales in association with *R. decorum*. Several root endophytes belonging to the genus *Acremonium* were also found in the indicator species analysis including *A. hyalinulum* and *A. persicinum*. *Acremonium* species are found in association with the roots of *Rhododendron* species and their endophytic structures are similar to ericoid mycorrhizal species (Grunewaldt-Stöcker and von Alten 2016). The *Acremonium* species *A. strictum* has been reported as a protector against pathogens (Depetris et al. 2023). This species was observed as a parasite against root knot nematodes of tomato in field conditions (Lenc et al. 2015). *Acremonium* species have also been

shown to fight against *Fusarium* wilt by inducing defensive mechanisms in roots of tomato and flax species (Grunewaldt-Stöcker and von Alten 2003).

Conclusion

Prior experiments have shown that soil biotic communities can enhance survival in the presence of pathogen *Phytophthora cinnamomi* (Liu et al. 2021). The significant correlations found in the current study between biotic effect size from a greenhouse experiment and the fungal community composition measured here is consistent with the prediction that fungal taxa could play a role in the observed benefits.It should be noted that this correlation was driven by *R. minus* and does not identify mechanisms; thus, caution should be used when interpreting these community results. However, specific taxonomic groups of fungi in the rhizosphere could be important for plant survival in the presence of *P. cinnamomi*. For example, there were 45 zOTUs of *Trichoderma* representing 41 different *Trichoderma* species. *Trichoderma* are strong candidates for explaining the beneficial effect in the presence of *P. cinnamomi* (Ruiz-Gómez and Miguel-Rojas 2021) because they can act as parasites on the pathogen, upregulate the plant immune systems, and directly enhance plant growth (Brotman et al. 2010). Further, *Trichoderma* are widely considered a useful biocontrol for plant pathogens, though their context-dependent action and costs of production have limited widespread adoption (Zin and Badaluddin 2020). Further experiments are needed to confirm their effects in *Rhododendron*, but *Trichoderma* could be beneficial for this widespread nursery plant.

Author contributions Jean H. Burns, David J. Burke, and Juliana S. Medeiros conceived the ideas, developed the methodology, and acquired the funding. Jean H. Burns and Saliha Ahmad conducted the field sampling. Saliha Ahmad and Sarah R. Carrino-Kyker conducted the laboratory methodology and processed the sequencing data. Saliha Ahmad and Jean H. Burns led the data analysis and wrote the manuscript first draft. All authors contributed to manuscript writing and revision.

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Data availability Data will be archived upon publication at the open science framework. Available for peer review: https://doi.org/10.17605/OSF.IO/TMWXA.

Declarations

Competing interests The authors have no relevant financial or non-financial interests to disclose.

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