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Is the clonal plant network a pathway for horizontal transmission of endophytic fungi in the field?

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Abstract

Clonal plants form networks of ramets connected by rhizomes, which may enable not only the transport of water and assimilates but also the transport of microorganisms, including fungi that form the plant mycobiota. In this study, the following questions were asked: (1) whether the mycobiota is present in rhizomes in naturally functioning linear networks of *Maianthemum bifolium* in the field,, and (2) whether horizontal transfer of mycobiota occurs between neighbouring ramets. The presence of mycobiota was examined in ramets and rhizome internodes in 30 network fragments occurring in a pine forest. Endophytes were cultured *in vitro* on PDA medium and subcultured to obtain single colonies. A total of 256 pure isolates were obtained and molecularly identified by ITS rDNA sequence analysis (≥ 98% similarity). Altogether, 48 fungal taxa representing 32 genera were identified, mainly from *Ascomycota* and *Basidiomycota*. Some taxa were specific to ramets or internodes, while four taxa were shared, such as the biocontrol species *Meyerozyma guilliermondii*. The frequency of lateral transmission of fungi along the clone was inferred on the basis of the match in species composition between pairs of consecutive segments. Only 9 pairs (out of 31) of adjacent rhizomes and only 1 pair (out of 9) of adjacent leaves could confirm the lateral transmission of fungi. These results show that the horizontal transfer of the mycobiota in the network under natural conditions, in which plants are constantly exposed to microbial infections, is more limited than it is in networks developed under sterile and controlled laboratory conditions.

1. Introduction

A large group of clonal plants form networks in which the nodes constitute units known as ramets produced through vegetative growth from a plant mother (Klimeš et al., 1997; de Kroon et al., 2005; Oborny et al., 2012; Oborny, 2019). Ramets are interconnected by rhizomes and are capable of developing all essential structures, including leaves and roots, that are responsible for resource acquisition and assimilation. Each ramet can detach from the clonal network and live independently. In such a case, it becomes a plant mother for a new network, forming a structurally distinct clone (sensu Harper, 1977).

Rhizomes function as specific “information cables” that not only integrate the structural components of the network but also enable well-documented multidirectional transport of resources, including assimilates and water (Alpert and Stuefer, 1997; Hutchings and Wijesinghe, 1997; Stuefer, 1998). Living within a network allows ramets to acquire resources more efficiently and to share them within the clone. In heterogeneous environments, ramets may locally specialize in capturing the most abundant resource by investing biomass in the organ responsible for its acquisition. For example, under conditions of high water availability, a ramet may allocate more biomass to root development, whereas in environments with limited water but high light availability, greater investment in aboveground biomass enhances photosynthetic performance. Excess resources can then be transported to younger ramets or to those growing under less favorable conditions. This phenomenon, known as the division of labour, resulting from physiological integration, may increase clonal productivity by up to 70% (Stuefer, 1998).

Resource reallocation among ramets enhances their survival, competitiveness, invasiveness, and spatial expansion in ecosystems. A high degree of physiological integration is considered as an adaptation to the low availability of one or more key resources during the growing season (Jónsdóttir and Watson, 1997; Schwarzschild and Zieman, 2008).

Recent studies have demonstrated that clonal plants can also transmit information about environmental conditions experienced by the plant mother to daughter ramets, influencing their phenotype (Latzel and Klimešová, 2010; Verhoeven and Preite, 2013; Latzel et al., 2014; González et al., 2016; Li et al., 2018; Zhang et al., 2023). This effect results from epigenetic variations transmitted through clonal reproduction. Clonality, therefore, enables plants to occupy diverse habitats and acquire necessary resources even when their distribution varies spatially and temporally. Notably, some of the largest, oldest, and most invasive vascular plant individuals belong to clonal species (Liu et al., 2016; Lynch and Balmer, 2004; DeWoody et al., 2008).

Like most plant species studied, clonal plants also host diverse microorganisms that form a microbiome that includes bacteria, fungi, bacteriophages and other viruses. A clonal plant can thus be regarded as a metaholobiont (sensu Rosenberg et al., 2016), as the microbiome may occur in every ramet within the network as well as in rhizomes (Vannier et al., 2016). If so, an important question arises: can the microbiome, akin to water and assimilates, be transported through the clonal network between ramets? Subsequent studies by Vannier et al. (2018) demonstrated not only the transfer of bacteria and fungi between ramets but also the selective filtering of microbiota during transmission, depending on the distance between ramets. These were the first reports showing that, in addition to resource transport, the horizontal transmission of microorganisms from the plant mother to neighbouring ramets can occur within clonal networks.

In the present study, we aimed to determine whether the horizontal transfer of microorganisms—specifically endophytic fungi—also occurs under natural field conditions, where clonal networks function in heterogeneous environments. Experimental systems provide simplified models of natural conditions. In laboratory settings, environmental factors such as water, nutrients, and light can be evenly distributed and tightly controlled, potentially limiting or altering resource transport. In contrast, field conditions are inherently heterogeneous: each ramet experiences different resource availability, and transport within the network may compensate for local deficiencies. This heterogeneity may also influence microbial transmission. Moreover, under natural conditions, ramets are exposed to additional sources of endophytic fungi originating from soil, air and animals, independent of neighbouring ramets.

We addressed the following questions: (i) Is the diversity of the mycobiome higher in ramets (leaves) or in rhizomes? (ii) Are endophytic fungi present in rhizomes that connect neighbouring ramets also detected in those ramets? (iii) Does the proportion of pathogenic versus nonpathogenic endophytes change across successive generations of ramets (from youngest to oldest)?

2. Material and methods

2.1. The study species

Maianthemum bifolium belongs to the family Asparagaceae and is characterized by a wide geographical distribution. It occurs in North America, Europe, and Asia and is a common species in Poland (GBIF Secretariat, 2023). It is a perennial plant that forms a linear underground network in which ramets (i.e., offspring produced through vegetative reproduction) are interconnected by rhizomes. Within the ramet network, internodes vary in length (Łukasiewicz, 1962) (Fig. 1). In addition to being capable of asexual reproduction via vegetative growth, this species is also capable of sexual reproduction.

2.2. Material collection

We analysed 30 fragments of clonal networks, composed of 89 ramets of *M. bifolium* from three study sites (S1 = 52°00’12.9”N 17°03’16.2”E; S2 = 51°58’40.9”N 17°00’21.3”E; and S3 = 51°57’51.7”N 16°58’36.2”E) in pine forests in the Piaski Forest District (Wielkopolska region, Western Poland). Each fragment of the network, of approximately 50 cm long (up to 75 cm), after being dug from the soil, was placed in zip-lock bags and immediately transported to the laboratory of the Department of Systematic and Environmental Botany, Faculty of Biology, Adam Mickiewicz University, Poznań, Poland.

2.3. Fungal cultivation

The plant material was cut under a laminar flow hood into short fragments of approximately 3–4 cm in length. Rhizomes representing internodes between ramets, as well as leaves, were subjected to surface sterilization. They were subsequently rinsed with distilled water, immersed in 75% ethanol for 30 seconds, in 4.5% sodium hypochlorite (NaOCl) solution for 3.5 minutes, and finally in 75% ethanol for 15 seconds. After sterilization, the leaves were cut into smaller fragments, and the internodal rhizomes were split longitudinally. The prepared material was placed onto Petri dishes containing PDA supplemented with 5% chloramphenicol. In the control treatment, Petri dishes with PDA medium and chloramphenicol were flooded with the water used to rinse the leaves and internodes after sterilization. Several fragments originating from a single previously cut leaf were placed on each Petri dish. On a separate plate, a longitudinally cut fragment of an internodal rhizome excised between ramets bearing leaves was placed. The rhizomes and leaves were arranged on appropriately numbered Petri dishes to preserve the continuity of ramet growth direction within the network. This was intended to reconstruct the potential direction of fungal transfer. The material was sealed with parafilm and incubated at 25°C. Subculturing was carried out until pure fungal monocultures were obtained. A total of 256 pure fungal isolates were obtained from leaf and internode tissues in *in vitro* cultures.

2.4. Identification

Genomic DNA was extracted from the cultured isolates using the Quick-DNA Fungal/Bacterial Miniprep Kit (Zymo Research, USA) according to the manufacturer’s protocol and stored at − 20°C. Amplification of the ribosomal DNA cassette, including the SSU, ITS1, 5.8S, ITS2, and LSU rDNA regions, was performed using the primer pair ITS1F (Gardes and Bruns, 1993) and ITS4 (White et al., 1990). PCRs

were carried out in a total volume of 25 µl, containing 2.5 µl of 10× buffer, 2.5 µl of 2.5 mM dNTP mix, 0.5 µl of each primer (10 µM), 0.5 µl of Taq DNA polymerase, 13.5 µl of nuclease-free water, and 5 µl of DNA template. Amplification was conducted in a thermal cycler under the following conditions: initial denaturation at 95°C for 2 min; 37 cycles of 30 s at 95°C, 30 s at 55°C, and 60 s at 72°C; followed by a final extension at 72°C for 5 min. PCR products were submitted for sequencing to the Laboratory of Molecular Biology Techniques, Faculty of Biology, Adam Mickiewicz University in Poznań, Poland. The obtained sequences were edited with Chromas (www.technelysium.com.au) software and compared with those published in the European Molecular Biology Laboratory (EMBL) nucleotide databases and in the NCBI (www.ncbi.nlm.nih.gov) databases using BLAST (Altschul et al. 1990). Positive identification of a species was confirmed if ≥ 98% of the ITS region sequence identity was shared with the reference sequence from the databases. The obtained sequences were submitted to GenBank (Table 1).

Frequency of lateral transmission

We tested the transmission of fungi along a growing clone in *M. bifolium* tissues separately for rhizomes and leaves. This was performed by analysing the occurrence of identified fungi in pairs of two consecutive segments (either rhizomes or leaves) within the clone. We inferred lateral transmission by comparing whether a particular fungal species present in one segment was also detected in the subsequent segment. When a match between two consecutive segments in terms of at least one fungal species was encountered, we considered it a successful transfer between ramets. This category was assigned to a pair of segments regardless of whether any other species, including the non-identified ones, were also detected. When none of the fungal species present in each segment was present in the next segment, we considered it an unsuccessful transfer and treated the microbiota as originating from the outer environment, e.g., soil. However, this category comprised only pairs in which the segment contained no non-identified fungus, as the non-identified fungus could have been the transferred species. This rule has been adopted in order not to overestimate the proportion of pairs in which fungal lateral transmission did not occur.

To determine whether lateral transfer or the outer environment plays a more significant role in our study, we compared the frequency of pairs of segments that contained matching fungal species with that of pairs where the fungal species were not found in the adjacent segment. We checked if either of the two categories is statistically more frequent by performing a binomial test for a one-sample proportion on the rhizome and leaf data, assuming an expected proportion of successes in the binomial distribution equal to 0.5.

3. Results

3.1. Mycobiota diversity

A total of 52 fungal taxa were identified, including 23 species identified to the species level and 25 taxa assigned to the genus level or higher taxonomic ranks (e.g., sp., families). The identified fungi

represented 32 genera, predominantly belonging to the phylum Ascomycota and, to a lesser extent, to Basidiomycota (Table 1). Among the taxa identified to species level, the dominant species included *Meyerozyma guilliermondii*, *Colletotrichum lineola*, *Paecilomyces niveus*, *Fusarium tricinctum*, *Fusarium acuminatum*, *Alternaria alternata*, and *Neonectria radicicola*. Most of the isolated fungi belonged to genera typical of plant-associated environments, comprising both phytopathogens (e.g., *Colletotrichum*, *Fusarium*, and *Diaporthe*) as well as saprotrophic and endophytic fungi (e.g., *Clonostachys*, *Phialocephala*, *Aureobasidium*, and *Trichoderma*). Analysis of taxon distribution revealed differences in mycobiota composition between leaves and internodes, with four taxa (e.g., *Chaetomium* sp., *Meyerozyma guilliermondii*, *Colletotrichum lineola*, and *Paecilomyces niveus*) occurring in both tissue types. A total of 21 taxa were recorded in leaves, and 35 were recorded in rhizomes (Fig. 2).

Table 1
Endophytic fungal taxa isolated from the leaves and internodes of *Maianthemum bifolium* ramets, including BLAST sequence matches and GenBank accession numbers.

Fungal Taxa	Occurrence		BLAST match sequence			GenBank accession No.
	leaves	internodes	accession No.	coverage (%)	similarity (%)	
Acremonium sp.	−	+	100%	LC731836	99.3	PX563285
Alternaria alternata	−	+	100%	MZ209280	98.6	PX563238
Alternaria triticina	+	−	100%	PP157316	99.7	PX637805
Apiospora sp.	−	+	100%	MK460910	98.6	PX928760
Apodus sp.	−	+	98%	MZ380017	99.8	PX563252
Aspergillus sp.	−	+	100%	MZ380020	99.3	PX942469
Aureobasidium pullulans	+	−	100%	MT573468	99.8	PX563247
Aureobasidium sp.	+	−	100%	MW077693	99.7	PX637816
Botryotrichum domesticum	−	+	99%	MW288937	99.4	PX563277
Chaetomium globosum	+	−	100%	OQ626571	98.5	PX563248
Chaetomium rectangulare	+	−	100%	MT732798	98.6	PX563237
Chaetomium sp.	+	+	100%	MZ724867	99.8	PX637822
Clonostachys rosea	−	+	100%	MT945259	99.4	PX574302
Clonostachys sp.	+	−	100%	KU556555.1	100	PX574297
Colletotrichum acutatum	+	−	100%	AJ301906	99.0	PX942457
Colletotrichum godetiae	+	−	100%	LC206650	99.8	PX942454
Colletotrichum kakivorum	+	−	100%	LC324782	99.8	PX563233
Colletotrichum lineola	+	+	100%	MZ078530	99.5	PX563243
Colletotrichum sp.	+	−	100%	MZ078541	99.7	PX563235
Colletotrichum trifolii	+	−	100%	AJ301942	100	PX637814

Fungal Taxa	Occurrence		BLAST match sequence			GenBank accession No.
	leaves	internodes	accession No.	coverage (%)	similarity (%)	
Colletotrichum truncatum	+	–	100%	AJ301976	99.7	PX637801
Cylindrocarpon sp.	–	+	100%	KM248560	100	PX574273
Diaporthaceae sp.	–	+	100%	LT821469	99.3	PX637807
Diaporthe columnaris	–	+	100%	MN540315	99.5	PX637809
Didymella glomerata	+	–	100%	PQ453766	99.1	PX928777
Fusarium acuminatum	+	–	100%	MT428191	100	PX574268
Fusarium avenaceum	–	+	100%	MF509747	100	PX942467
Fusarium tricinctum	+	–	100%	PV351380	100	PX574283
Geomyces asperulatus	–	+	100%	MH861038	99.8	PX574284
Halenospora varia	–	+	100%	KF156329	100	PX942471
Helotiales sp.	–	+	100%	MZ078666	99.8	PX637817
Metapochonia bulbillosa	–	+	100%	KY977566	99.4	PX574276
Metapochonia sp.	–	+	99%	OQ857424	99.8	PX574275
Meyerozyma guilliermondii	+	+	100%	KF746422	100	PX574291
Meyerozyma sp.	–	+	100%	JN255506	98.1	PX563281
Nemania serpens	+	–	100%	MH931277	98.1	PX637818
Nemania sp.	–	+	100%	PP523996	98.9	PX942463
Neonectria radicicola	–	+	100%	GU934547	100	PX563259
Neonectria sp.	-	+	100%	EF601601	99	PX942453
Pichia guilliermondii	-	+	100%	EF222224	99.8	PX637825
Trichoderma harzianum	-	+	100%	PV480867	98.9	PX563273
Trichoderma sp.	-	+	100%	MH284798	98.9	PX563274

Fungal Taxa	Occurrence		BLAST match sequence			GenBank accession No.
	leaves	internodes	accession No.	coverage (%)	similarity (%)	
Didymellaceae sp.	+	-	100%	MT453292	99.3	PX637802
Rutstroemiaceae sp.	-	+	99%	OR750584	98.3	PX637808
Phomopsis sp.	-	+	100%	KT264344.	98.4	PX637810
Podospora sp.	-	+	100%	MN540307.	100	PX637812
Paecilomyces niveus	+	+	99%	OW983718	100	PX574279
Phialocephala fortinii	-	+	99%	MN947395	100	PX574271
Schizothecium inaequale	+	-	98%	AY999117	98.4	PX574289

Frequency of shared fungal taxa between adjacent segments

After excluding the pairs of segments whose fungal species identification did not allow us to unequivocally assign them to either of the two categories of microbiota origin (lateral transfer, outer environment), we obtained 31 observations for rhizomes and 9 observations for leaves. Among these, only 9 pairs of adjacent rhizomes and only 1 pair of adjacent leaves shared at least one fungal taxon, which were instances that could confirm the lateral transmission of fungi. The lack of match of fungal species between consecutive segments was statistically more frequent both for rhizomes (binomial test, $p = 0.0147$) as well as for leaves (binomial test, $p = 0.0195$) (Fig. 2).

4. Discussion

Since the discovery of the division of labour among ramets in clonal plant networks (Stuefer et al. 1996; Stuefer 1998), the biology of this group of plants has continued to be intensively studied. Today, a clonal plant is defined as a metaholobiont, that is, a network of interconnected holobionts-host organisms with their microbiota and animal symbionts (Vannier et al. 2019). The microbiota consists of bacteria, fungi, archaea and viruses, forming a dynamic system (Berg et al. 2024). The microbiota of the metaholobiont may constitute a plant resource, similar to water and assimilates. Therefore, it is expected that the microbiota may also undergo horizontal transfer from ramet to ramet, similar to other resources. This mechanism was first demonstrated under laboratory conditions in the clonal plant *Glechoma hederacea* (Vannier et al. 2018).

In the present study, we examined the diversity of fungal microbiota (mycobiota) in both ramets and rhizomes as a starting point for evaluating the prevalence of horizontal transfer under natural conditions. We found that, compared with ramet leaves, rhizome fragments, (the so-called internodes), contained more mycobiota. Under field conditions, additional sources of mycobiota acquisition occur. Ramets may

obtain the mycobiome from the air in the form of fungal spores, from the root system, and from other ramets via rhizomes; rhizomes may acquire fungi from the soil as well as from ramets. However, as underground organs, rhizomes live many years longer than the aboveground parts of ramets, allowing the accumulation of the mycobiome. Ramets, that is, the aboveground parts of *M. bifolium*, die each year after reproduction. Rhizomes, like most underground organs of clonal plants, are long lived (Łukasiewicz 1961). Therefore, the time available for acquiring the mycobiota is longer in rhizomes than in ramets. Therefore, in *M. bifolium*, compared with ramets, rhizomes harbour a larger and more diverse set of mycobiota.

The composition of the mycobiota in the rhizomes and leaves included shared fungal taxa that have been documented to have positive effects on the host plant. Three fungal species that are already used as biocontrol agents for plant protection were detected. The first species was *Meyerozyma guilliermondii*, which exhibits antibacterial and antifungal activity (Li et al. 2005; Zhang et al. 2008; Feng et al. 2010; De Marco et al. 2018; Kthiri et al. 2021). Inconsistencies in the biological classification and nomenclature of this fungus are still evident. The fungus identified molecularly in this study as *Pichia guilliermondii* is listed among more than 40 synonyms, including *M. guilliermondii* (Species Fungorum, n.d.). Both names are also assigned to members of a fungal complex that includes species such as *Candida athensensis*, *Candida carpophila*, *Candida elateridarum*, *Meyerozyma carpophila*, and *Meyerozyma caribbica* (Ghasemi et al., 2022; Herrera-Balandrano et al., 2023).

M. guilliermondii positively affects photosynthesis and transpiration and inhibits two pathogenic fungi, *Botrytis cinerea* and *Penicillium expansum* (Wisniewski et al. 1991; Zhang et al. 2025). The second fungus present in *M. bifolium* networks is *Clonostachys rosea*, which is also an antagonist of *Botrytis cinerea* (Cota et al. 2009; Hasan et al. 2022; Macarin et al. 2022). Soil inoculation with *C. rosea* positively affects the biomass and shoot length of wheat and carrot and reduces the abundance of parasitic nematode genera without affecting the diversity of non-parasitic nematodes (Iqbal et al. 2018). The third taxon was *Aureobasidium pullulans*, a well-known antagonist of *Botrytis cinerea* and *Colletotrichum acutatum* (Iqbal et al. 2023). It can therefore be expected that these three fungal species, which limit the growth of plant-pathogenic fungi, may also serve as natural protection for *M. bifolium* against such pathogens under field conditions. However, most of the identified fungal taxa forming the mycobiome of *M. bifolium* belong to groups that may act negatively on plants in many cases. These include pathogens of cultivated plants, such as *Aspergillus*, *Colletotrichum* and *Fusarium* (Dean et al. 2012; Guarnaccia et al. 2021; Guo et al. 2022).

The distribution pattern of endophytic fungi we detected suggests that the fungal communities present in ramets and rhizomes of *M. bifolium* originate from the external environmental rather than as a result of horizontal transmission. Compared with the study of Vannier et al. (2018), we observed relatively limited evidence for shared mycobiota between adjacent ramets under natural field conditions. Vannier et al. (2018) demonstrated not only the transfer of microbiota (including fungi and bacteria) between ramets but also a filtration process affecting microorganisms during transmission. In our study, pairs of adjacent rhizome and leaf segments lacking shared fungal taxa occurred significantly more frequently

than pairs sharing at least one fungal taxon. This indicates that the process of filtration of microbiota along the clonal plant network can be relatively strong. Our findings imply that, under field conditions, horizontal transmission may play a less important role in shaping the mycobiota of *M. bifolium* than acquisition from multiple external environmental sources.

Certain limitations should be taken into account when interpreting our results. First, the study was based on culture-dependent methods, which may underestimate total mycobiota diversity because only the cultivable fraction of fungal communities can be detected (Hyde and Soytong 2008). To reduce competitive exclusion during cultivation, each newly emerged fungal colony was successively transferred onto fresh media. Second, it cannot be fully excluded that some epiphytic fungi survived sterilization or that susceptible endophytes were eliminated during the procedure. However, to minimize these effects we performed surface sterilization according to commonly used and accepted protocols for endophyte isolation (Wysoczański et al. 2025). Third, ITS-based identification, although widely accepted as a fungal barcode marker (Schoch et al. 2012), does not provide strain-level resolution. Therefore, shared fungal taxa between neighbouring ramets should be interpreted as indirect evidence supporting horizontal transmission rather than definitive proof of fungal transfer.

Money et al. (2020) showed that the degree of ramet isolation in the clonal plant Brachypodium pinnatum influences ramet mycobiome diversity. However, the effect varied by fungal group. The diversity of *Basidiomycota* decreased with increasing ramet spatial isolation, whereas no such relationship was observed for *Ascomycota* and *Glomeromycotina*. It was suggested that these differences may result from the individual characteristics of fungi (traits influencing the efficiency of plant root system colonization) and from the relationship between the mycobiome and the host plant established in the previous year (Money et al. 2020). Our results also draw attention to another problem – the difference in the behaviour of biological systems under laboratory conditions and in the field, where environmental conditions have a significant impact on the research object, can be so great that the results from the laboratory cannot be replicated in the field at all (Lundberg et al. 2025). Under controlled cultivation conditions in climatic chambers in the study by Vannier et al. (2018), the mother ramet was the only potential source of mycobiota for developing clones (daughter ramets). In natural environments, however, numerous sources of mycobiota are present. Given the abundance of mycobiota sources under natural conditions, horizontal transfer may be less prevalent than demonstrated in laboratory studies. Therefore, the mycobiota of wild-growing *Maianthemum bifolium* may have been shaped primarily by other potential sources rather than by horizontal transfer.

Declarations

Ethics approval and consent to participate

Maianthemum bifolium is not a protected, endangered or rare species in Poland. Plant material was collected with permission from the Piaski Forest District (Western Poland). All field studies and plant

material collection complied with relevant institutional, national and international guidelines and legislation, including the IUCN Policy Statement on Research Involving Species at Risk of Extinction and the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES).

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no known competing financial interests or personal relationships that may have influenced the work reported in this paper.

Wojciech Wysoczański

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Author Contribution

Conceptualization and Methodology - WW, PO,MMFormal analysis - PO, WW,MWWriting - original draft - PO,WW,MLResources - WW,Supervision - MLWriting - review and editing - WW

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Data Availability

Data availabilityThe dataset supporting the findings of this study is publicly available in figshare at: https://doi.org/10.6084/m9.figshare.32163105

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Figures



Figure 1

Linear network of ramets of *M. bifolium* (May lily), with visible ramets and connections between them (rhizomes). (Photo by W. Wysoczański)

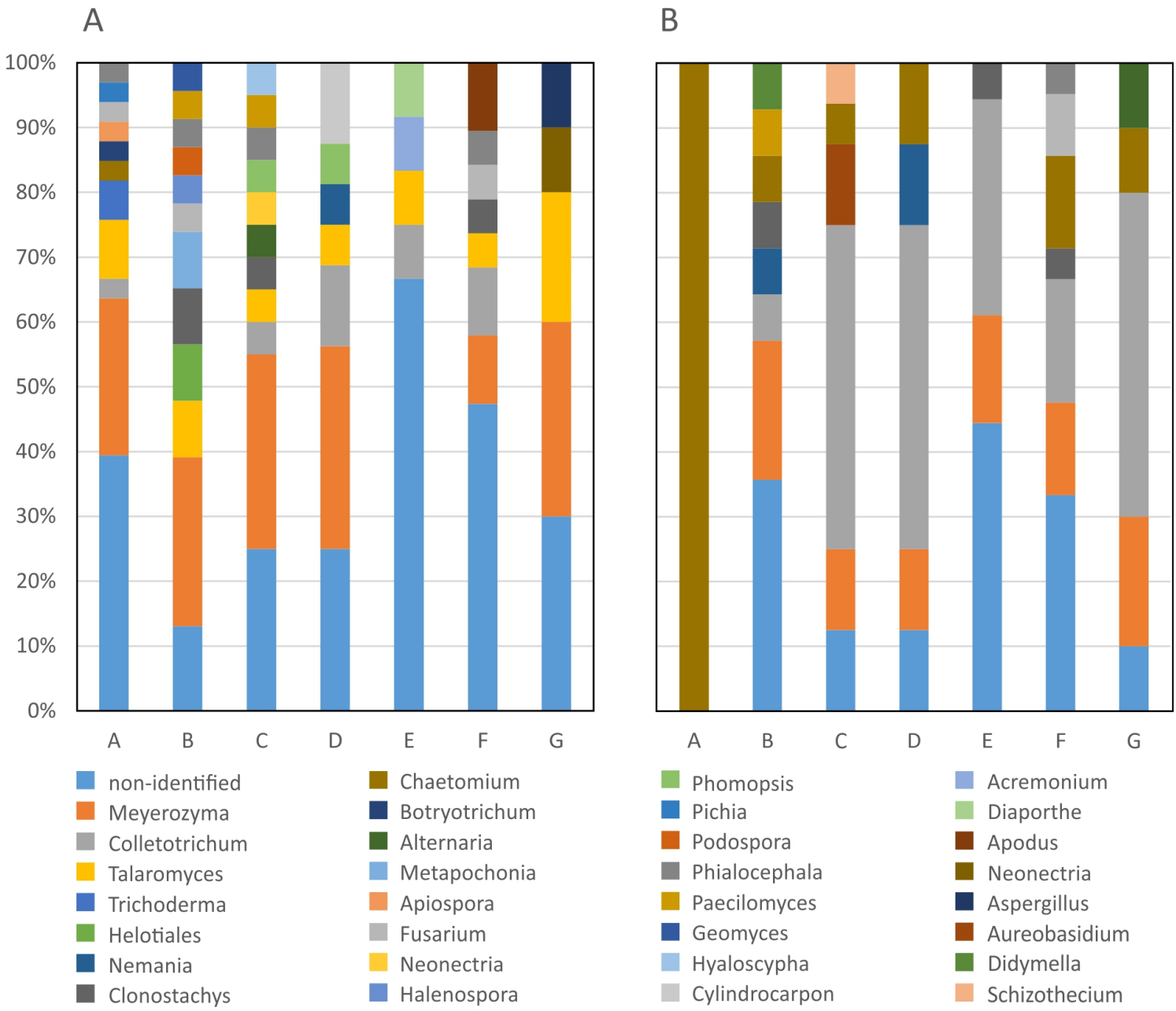


Figure 2

Species composition of endophytic fungi in consecutive segments of the analysed organs and the effectiveness of their lateral transfer. (A) Percentage of fungal taxa in adjacent rhizome segments (A–G). (B) Percentage share of fungal taxa in adjacent leaf segments (A–G). The bars represent the relative abundance of particular fungal genera and species in consecutive segments, including taxa identified to the genus level as well as the category “nonidentified”. A clear variability in mycobiota composition between successive segments is visible in both rhizomes and leaves.