

International Mycorrhiza Society

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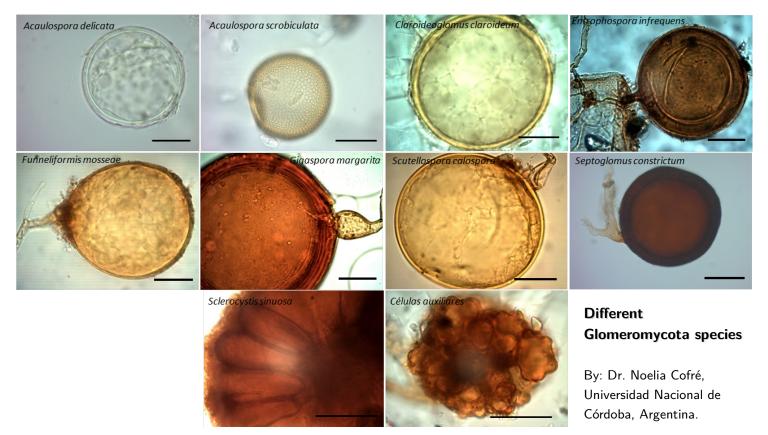
# **IMS** Newsletter

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## The International Mycorrhiza Society quarterly e-newsletter



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Ecology – Justine Karst, University of Alberta, Canada Evolution – Jason Hoeksema, University of Mississippi, US *Molecular biology* – Jonathan Plett, Western Sydney University, Australia Applications – Pedro M. Antunes, Algoma University, Canada

## The 10th IMS Newsletter - Editorial

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We are delighted to start the fourth year of the -IMS-International Mycorrhiza Society Newsletter, releasing our 10<sup>th</sup> issue (Vol. 4, Issue 1). Over the past 10 issues, the IMS Newsletter has become a space dedicated to mycorrhizal research outreach. debate. and connection. Especially, several of our editorials, short articles, and YouTube interviews express the most recent hot topics in mycorrhizal ecology, evolution, molecular biology, and applications. Topics are diverse and ranged from understanding the relationship between mycorrhizal biodiversity and functioning, ectomycorrhizal cross-talking and omics, what ecological niches are occupied by different arbuscular mycorrhizal fungal species, how fungal spores disperse, to the evolution of the ectomycorrhizal symbiosis, among many other subjects. The IMS Newsletter has also become a space to advertise our different events -namely ICOM, IMS-related news, and more. Please also follow us on Twitter: **@mycorrhiza\_ims** 

We keep encouraging worldwide mycorrhizal researchers in all stages to share their research outputs and/or ideas with us (in a short article or YouTube interview way). As Editor-in-Chief and President of the International Mycorrhiza Society, we thank all the dozens of mycorrhizal researchers who have contributed with votes, short articles, YouTube interviews, and events/jobs advertising to our Newsletter. Many thanks also to our

Executive (past and present), Board of Directors, the South American Mycorrhizal Research Network, and to the Topic Editors. We encourage further comments and suggestions to improve this space. And, in an era where sometimes it seems like all that matters is indexed articles production, we value a lot the time dedicated to our Newsletter.

## ICOM12, iMMM6, ICOM13, & South American Mycorrhizal symposium news

The 12<sup>th</sup> International Conference on Mycorrhiza (ICOM12) will take place in Manchester, United Kingdom, 6-11 August 2024. ICOM12 is organized by David Johnson, University of Manchester; Katie Field, Sheffield University; Tim Daniel, Sheffield University; Thorunn Helgason, University of York; and Uta Paszkowski, University of Cambridge.

For further news about ICOM12, follow the Twitter account: **@ICOM\_12** 

The 6<sup>th</sup> international Molecular Mycorrhiza Meeting will also take place in the United Kindgdom, in Cambridge, 25-27 September 2023. iMMM6 is organized by Sebastian Schornack and colleagues.

For further news about iMMM6, follow the Twitter account of the Sainsbury Laboratory, Cambridge University: **@slcuplants** 

At the general assembly of ICOM11 (online in China in August 2022) we also announced that applications for the organization of ICOM13 are open and interested organizations and persons were invited to send a bid before the end of December 2022. We are happy to officially announce that the board of directors has decided that the 13<sup>th</sup> International Conference on Mycorrhiza (ICOM13), will take place in Cairns, Australia, 2026. ICOM13 will be organized by Jonathan Plett, Western Sydney Anderson, Western University; lan Svdnev University; Jeff Powell. Western Sydney University; Camille Truong, Royal Botanic Gardens Victoria; Tim Cavagnaro, University of Adelaide; Stephane Watts-Fawkes, University of Adelaide, Teresa Lebel, State Herbarium of South Australia, Harley Ridgway, Plant and Food, New Zealand; Julie Deslippe, Victoria University of Wellington; Nicola Day, Victoria University of Wellington; Ian Dickie, University of Canterbury, New Zealand; and David Orlovich, University of Otago. It has been a long time since an ICOM was organized in Australia (the last one was in 2002 in Adelaide), so we are very happy to visit Australia again.

Stay tuned for further news regarding ICOM13. At the general assembly of ICOM12 in Manchester we will announce that bids for ICOM14 (e.g. in 2028) can be submitted.

Finally, we are delighted to invite you to the III International Symposium of the Mycorrhizal Symbiosis in South America, organized by the South American Mycorrhizal Research Network and the Amazon Institute for Scientific Research of Colombia (Sinchi). It will take place on 28 - 30August, 2023, in Leticia, Amazonas, Colombia. It includes courses before and after those dates. For further information please click here. For more information or sponsoring, contact Clara Peña-Venegas (cpena@sinchi.org.co) or César Marín (cmarind@santotomas.cl).

#### In this issue...

The Top 10 mycorrhizal research papers of the last four months (papers published between September and December, 2022). The first rank is for Anne Kakouridis and co-authors, for their New Phytol article entitled "Routes to roots: direct evidence of water transport by arbuscular mycorrhizal fungi to host plants". The authors used used microcosms, isotopically labeled water, and a fluorescent dye, and provided direct evidence of AM fungi directly transporting water to the plant (wild oat). Furthermore, they estimated that water transported by AM fungi across the air gap accounted for 34.6% of the water transpired by the host. The second rank is for Lingyan Zhou and co-authors, for their Nat Commun article entitled "Global systematic review with meta-analysis shows that warming effects on terrestrial plant biomass allocation are influenced by precipitation and mycorrhizal association", where, after reviewing 300 worldwide experimental warming studies, the authors found that warming-induced allocation to roots is higher in plants associated with arbuscular mycorrhizal (AM) fungi than with ectomycorrhizal (EM) fungi. A third rank was for Sara Branco and coauthors, for their New Phytol Tansley review "Mechanisms of stress tolerance and their effects on the ecology and evolution of mycorrhizal fungi".

This 10<sup>th</sup> IMS Newsletter issue includes three short articles. The first one, by Vinton Thompson (American Museum of Natural History), is about the relationships between spittlebugs, EM plants, and EM fungi mining of complex organic nitrogen (N) from soil. It is a fascinating story about an entomologist, who considered after 20 years of study to focus on the mycorrhizal symbiosis in order to understand his study system (spittlebugs). A second article by Martin Rozmoš and co-authors (Institute of Microbiology, Czech Academy of Sciences), provides evidence that chitinolytic bacteria inhabiting the AM fungi hyphosphere facilitate N acquisition by AM fungi (and its host plant) that is derived from chitin. A third short article by Kelcie Walther and coauthors, gives an overview of the scientific base, philosophy, and objectives of the Society for the Protection of Underground Networks (SPUN), Kiers lead by Toby (Vrije Universiteit Amsterdam). It also includes several ways to be involved with SPUN.

Finally, in addition to our traditional Tools and Events (with several mycological and mycorrhizal events coming up in the next few years) sections, please find interviews with Martin Ryberg about ectomycorrhizal fungi evolution. to Bala Chaudhary about fungal dispersal, and with Karst Justine and co-authors about misinformation and citation bias regarding common mycorrhizal networks in forest.



## Top 10 papers on mycorrhizal research\*

**1.** Kakouridis A, Hagen JA, Kan MP, *et al.* 2022. Routes to roots: direct evidence of water transport by arbuscular mycorrhizal fungi to host plants. *New Phytol* 236:210-221. https://doi.org/10.1111/nph.18281

**2.** Zhou L, Zhou X, He Y, *et al.* 2022. Global systematic review with meta-analysis shows that warming effects on terrestrial plant biomass allocation are influenced by precipitation and mycorrhizal association. *Nat Commun* 13:4914. https://doi.org/10.1038/s41467-022-32671-9

**3.** Branco S, Schauster A, Liao HL, Ruytinx J. 2022. Mechanisms of stress tolerance and their effects on the ecology and evolution of mycorrhizal fungi. *New Phytol* 235:2158-2175. https://doi.org/10.1111/nph.18308

**4.** Ward EB, Duguid MC, Kuebbing SE, *et al.* 2022. The functional role of ericoid mycorrhizal plants and fungi on carbon and nitrogen dynamics in forests. *New Phytol* 235:1701-1718. https://doi.org/10.1111/nph.18307

**5.** Wang F, Zhang L, Zhou J, *et al.* 2022. Exploring the secrets of hyphosphere of arbuscular mycorrhizal fungi: processes and ecological functions. *Plant Soil* 481:1-22. https://doi.org/10.1007/s11104-022-05621-z

**6.** Gomes SI, Fortuna MA, Bascompte J, Merckx VS. 2022. Mycoheterotrophic plants preferentially target arbuscular mycorrhizal fungi that are highly connected to autotrophic plants. *New Phytol* 235:2034-2045. https://doi.org/10.1111/nph.18310

**7.** Chowdhury J, Kemppainen M, Delhomme N, *et al.* 2022. *Laccaria bicolor* pectin methylesterases are involved in ectomycorrhiza development with *Populus tremula* × *Populus tremuloides*. *New Phytol* 236:639-655. https://doi.org/10.1111/nph.18358

**8.** Milani T, Hoeksema JD, Jobbágy EG, *et al.* 2022. Co-invading ectomycorrhizal fungal succession in pine-invaded mountain grasslands. *Fungal Ecol* 60:101176. https://doi.org/10.1016/j.funeco.2022.101176

**9.** Hui J, An X, Li Z, *et al.* 2022. The mycorrhiza-specific ammonium transporter ZmAMT3; 1 mediates mycorrhiza-dependent nitrogen uptake in maize roots. *Plant Cell* 34:4066-4087. https://doi.org/10.1093/plcell/koac225

**10.** Davison J, Vasar M, Sepp SK, *et al.* 2022. Dominance, diversity, and niche breadth in arbuscular mycorrhizal fungal communities. *Ecology* 103:e3761. https://doi.org/10.1002/ecy.3761

\*Selected from 131 Web of Science articles published between *September – December*, 2022 by: Justine Karst, Jonathan Plett, Melanie Jones, Francis Martin, Jan Jansa, John Klironomos, Liang-Dong Guo, Miranda Hart, Jason Hoeksema, Judith Lundberg-Felten, Bala Chaudhary, Annegret Kohler, Joseph Cooper, Junling Zhang, and César Marín.

## **Research commentaries**

## Looking for patterns in a biosphere dominated by symbioses – bugs, plants, and the microorganisms that mediate their interactions

### Vinton Thompson<sup>1\*</sup>

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The longer I work on the ecology and evolution of spittlebugs, the deeper becomes my appreciation for the pervasive importance of symbioses in the biological world. Spittlebugs are xylem sap feeding hemipteran insects, named for the foamy spit-like masses produced by their nymphs (Fig. 1). For a small, not terribly well-studied group, they have proven to offer a useful window on subtle but powerful and ubiquitous interactions among insect herbivores, plants, and symbiotic microorganisms. In a recent review of insect/plant/mycorrhizal fungus interactions (Thompson 2022), I highlight an association between spittlebugs and ectomycorrhizal (EM) plants, apparently based on the specialized abilities of EM fungi to mine nitrogen (N) from complex organic N in soil.

I got a premonition of the importance of microbial symbioses in spittlebug host plant relationships when I began exploring host plant patterns in the early 1990's. That work was stimulated by two observations. First, the abundant, widespread spittlebug *Philaenus spumarius* is an extreme polyphage, with likely more than 1,000 hosts in more than 100 plant families. Second, despite its lavishly promiscuous host associations, this spittlebug achieves highest densities as a pest of the nitrogen-fixing plant alfalfa (*Medicago sativa*). Why alfalfa, with so many hosts to choose from? The answer, it appeared, might lie in the physiology of nitrogen-fixing plants. Xylem sap is an improbable food source, dilute, and under negative pressure, requiring large insect sucking pumps and the expenditure of lots of energy to extract. Because N fixed as ammonium is too toxic to transport directly, N-fixing plants transfer N from root to shoot as amino acids. This gives xylem-feeding insects something more to eat. Not surprisingly then, a broader survey of spittlebug hosts revealed an affinity for a wide variety of Nfixing plants, including legumes, actinorhizal plants, and associative N-fixing C<sub>4</sub> grasses (Thompson 1995, 2004).

During the course of that work, I stumbled across the investigations of David Read and his colleagues (summarized in Smith and Read 2008), demonstrating and that ericoid some mobilize ectomycorrhizal fungi exploit and recalcitrant, organically complexed N in laboratory cultures. This suggested that some mycorrhizal plants might, like N-fixing plants, provide a reliable source of xylem-borne organic N for xylem feeding insects, an alluring prospect, since I already knew that there were many spittlebugs associated with pines (see Figs. 1b and 2b,c for examples).

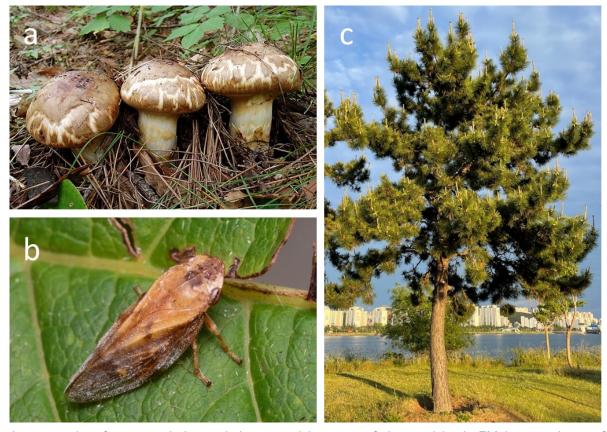
At the time, in the 1990's, the literature, including the then current editions of Smith and Read (2008), suggested that organic N might be transferred directly from mycorrhizal fungi to roots. This view has now lost currency (Hodge 2017; Nehls and Plassard 2018). There was also



**Figure 1. a.** Spittle masses of *Clastoptera obtusa* on alder. **b.** *Aphrophora canadensis* nymphs exposed in spittle mass on Monterey pine. White arrows indicate visible spittlebug nymphs within the spittles.

conflicting information about the mycorrhizal status, EM or arbuscular mycorrhizal (AM), of many plants. Because of these uncertainties (and the time pressures of a long digression into academic administration), I set aside a 2003 manuscript begun in 1997 and did not return to work on spittlebugs and mycorrhizal hosts until 2021. This had several happy consequences: 1) I did not chase the red herring of direct transfer of organic nitrogen; 2) thanks to the definitive reviews of Tedersoo and Brundrett (2017) and Brundrett and Tedersoo (2020), the risk of misclassifying AM plants as EM was averted; 3) the nature of EM versus AM nitrogen acquisition was greatly clarified, with a developing consensus EM fungi as a group (though with that tremendous variability) are especially well adapted to liberate complex organic N (Miyauchi et al. 2020); and 4) two more decades of spittlebug host plant records were available for analysis. These advances permitted me to make the case for an association between spittlebugs and EM plants (Thompson 2022).

I hope this analysis stimulates more observations on relationships between insects and mycorrhizae. There is a lot of work to be done. At the simplest observational level, I encourage mycorrhizal workers to keep an eye out for spittlebugs. I would be pleased to receive any interesting observations and provide identifications of the bugs. For example, ericoid mycorrhizae (ER) have even stronger mechanisms than EM to access tightly sequestered organic N (Smith and Read 2008; Miyauchi et al. 2020), which should make ER plants attractive to spittlebugs. Despite this, I have found records for only three spittlebugs with ER primary hosts (one in New Caledonia, of all exotic places). I suspect there are others, as well as many more spittlebugs on EM plants. At the experimental level, AM shrubs/trees and xylem feeding insects have been neglected in studies of insects-mycorrhizal fungi interactions. They deserve more attention. At the analytical level, my results support the hypothesis that EM and N-fixing plants share a phylogenetically inherited predisposition to form symbiotic relationships for



**Figure 2.** An insect-plant-fungus triad that includes a spittlebug, one of the spittlebug's EM hosts and one of the host's fungal partners. **a.** Matsutake mushrooms, fruiting bodies of *Tricholoma matsutake*, an EM associate of *Pinus densiflora*. Photo by Dr. M. Narimatsu, Iwate Prefectural Forest Technology Center, Japan. **b.** *Aphrophora flavipes*, a spittlebug pest of *P. densiflora*. Photo by WonGun Kim. **c.** *Pinus densiflora*, an EM tree of East Asia. Photo by Herman Viviers.

N-acquisition (Tedersoo and Brundrett 2017), perhaps analogous to the well-established relationship between the evolution of rhizobial Nfixation and preexisting AM pathways. It would be fascinating to tease out at the molecular level the links, if any, uniting the evolution of EM and Nfixing plants.

As an aside, I was surprised to discover that details of N transfer from fungi to plants are unresolved. It appears that both EM and AM fungi transfer N to plant roots as ammonium (Hodge 2017; Nehls and Plassard 2018). If so, mycorrhizal fungi assimilate N from soil, translocate it internally in amino acid form, and reduce it to ammonium for export to roots, only to have it immediately reconstituted in the roots as amino acids for xylem transport. Energetically, this appears to be an extravagantly wasteful

process. Many plants can take up amino acids directly from soil (Pfautsch *et al.* 2015), so why not transfer amino acids directly from fungus to root? Perhaps, as Nehls and Plassard (2018) suggest, a need to conserve fungal carbon is a factor, or perhaps, despite appearances, transfer of N to roots as ammonium is energetically more efficient than transfer as amino acids, a possibility suggested for the assimilation of soil N by mycorrhizal fungi (Pfautsch *et al.* 2015).

Lastly, I would like to call attention to two other instances of spittlebug N-nutritional interactions with symbiotic microorganisms. Behie and Bidochka (2014) review entomopathogenic fungi that live in both soil and plant tissue and convey N from dead insects to plants. One of these entomopathogens, *Metarhizium anisopliae*,

associates with sugarcane roots. It is also a major biocontrol agent for spittlebugs of sugarcane (Li et al. 2010), raising the intriguing possibility that M. anisopliae both protects sugarcane from spittlebug pests and feeds the sugarcane nitrogen from some of the bugs it kills. There is abundant evidence that sugarcane receives substantial amounts of N from N-fixing bacterial partners (Thompson 2004). Metarhizium may add bugderived N to the mix. At the other end of the xylem stream, spittlebugs and related insects have a well-defined set of bacterial and fungal symbionts that metabolize the impoverished subset of amino acids in xylem sap into a dietarily complete array (Ankrah et al. 2020). These symbionts, housed in discrete bacteriomes and offspring, passed to permit growth and reproduction on this otherwise impossibly poor food resource. As a result, from N-fixing bacteria and mycorrhizal fungi at the beginning of the xylem circuit to essential amino acid synthesizing symbionts at the other end, multiple symbioses support xylem feeding as a viable lifestyle.

I thank Jason Hoeksema for the invitation to write this commentary, WonGun Kim for permission to use his photo of *A. flavipes*, Takashi Yamanaka for arranging permission to use the photo of matsutake mushrooms from Dr. M. Narimatsu, and Herman Viviers for making his photo of *P. densiflora* available through a Creative Commons license.

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## Digging deeper into the arbuscular mycorrhizal fungal hyphosphere

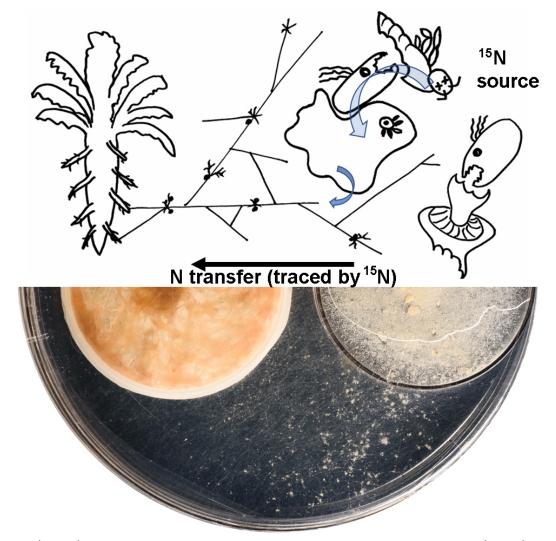
Martin Rozmoš<sup>1</sup>, Michala Kotianová<sup>1</sup>, Hana Hršelová<sup>1</sup>, Petra Bukovská<sup>1</sup>, Jan Jansa<sup>1\*</sup> <sup>1</sup>Laboratory of Fungal Biology, Institute of Microbiology, Czech Academy of Sciences, Prague, Czechia. \*E-mail: jansa@biomed.cas.cz

The arbuscular mycorrhizal (AM) fungi provide a multitude of nutritional and non-nutritional benefits to their host plants, for which they receive a share of their host photosynthetic production, besides other benefits such as access to compounds which they cannot produce themselves. e.g., fatty acids or secondary metabolites conferring protection against hyphal grazers. The role of AM fungi in soil-plant phosphorus (P) cycling is firmly established, whereas their contribution to plant nitrogen (N) acquisition from soil is actually more controversial/variable and often much less obvious than for P, particularly when looking at a whole plant nutrition level (George et al. 1995; Hodge and Storer 2015). Mycorrhizal plants sometimes show improved N status, but there also are reports available on lower rates of N acquisition by mycorrhizal plants from the soil as compared to their non-mycorrhizal counterparts, due to a competition for limited soil N resources between the fungus and the host plant (Püschel et al. 2016).

It has already been noticed since a couple of decades that AM fungi could play an important role in mineralizing soil organic matter and, consequently, (particularly organic N) affecting plant N uptake (Thirkell et al. 2016). Since AM fungi are obviously not capable of mineralizing nutrients themselves organic (Tisserant *et* al. 2013), researchers have suggested a key role in mineralization of soil organic nutrients to be played by other soil

microbes within the AM fungal hyphosphere, a soil zone under direct influence of the AM fungal hyphae (Faghihinia *et al.* 2023). Although evidence accummulated for differences in microbiome composition between the rhizosphere, AM fungal hyphosphere – and more recently also for the microbial communities tightly associated with surfaces of AM fungal hyphae, the hyphoplane, and the bulk soil (Nuccio et al. 2013; Emmett et al. 2021; Wang et al. 2023), direct proof for nutritional interplay between such soil microbes and AM fungal hyphae in exploitation of organic nutrient sources has been missing until recently.

In 2016, such direct proof of the bacterium Rahnella aquatilis facilitating release of P from phytate and thus increasing orthophosphate availability for the AM fungus, has been provided (Zhang et al. 2016). This confirmed previously assumed tight co-operation of the AM fungi with soil prokaryotes upon exploiting organic nutrient sources. And in 2022, using a similar experimental setup as in the previous study (Zhang et al. 2016), a direct proof has been published for N acquisition by the AM fungus (and its host plant) from chitin, facilitated by a chitinolytic bacterium belonging to the genus Paenibacillus (Rozmoš et al. 2022). In the latter study (Rozmoš et al. 2022), besides providing a convincing evidence that the bacterium was actually key in the utilization of organic N by the fungus, we also showed that including a bacteriovorous protist (Polysphondylium pallidum) into our experimental



**Conceptual model (above) and the compartmentalized gnotobiotic experimental system (below)** allowing to study biological processes within the arbuscular mycorrhizal fungal hyphosphere (right) connected to the host plant (*Cichorium* sp., Ri T-DNA transformed roots, left). Photo by: David Püschel. Drawing by: Martin Rozmoš.

system further increased the efficiency of N utilization by the AM fungus, most likely via speeding up release of N from the bacterial biomass. This is because within the so called "soil microbial loop" (Bonkowski 2004), where organic resources are returned to higher trophic levels via incorporation into detritovorous bacteria and then into bacteriovorous protists, a substantial part of N originally present in the substrate is released into the environment as easily bioavalable ammonium ions. This happens for stoichiometric reasons, as N actually concentrates within the protist (or other consumer) biomass due to release of part of the ingested food as  $CO_2$ . Possible involvement of protists into efficient recycling of organic N within AM fungal hyphosphere has actually been proposed years ago (Koller *et al.* 2013; Bukovská *et al.* 2018), but only now it has been experimentally and unequivocally confirmed.

Except the clear story presented above, our study also brought up some surprises. For example, chitinolytic bacteria other than *Paenibacillus* sp. (which were also included in the experimentation) did not degrade chitin in vicinity of the AM fungal hyphae, although they did so in their absence. These results indicated that some processes within the AM fungal hyphosphere only

were activated or deactivated upon close physical proximity of the partners, in agreement with some previous research (Zhang et al. 2019). The next challenge will be to start working with more complex (i.e., multispecies) microbial communities composed of several bacterial (and/or protistan) species/genotypes to decipher multisided interactions between the different microbes/trophic levels, considering a whole range interactions including of synergism and antagonism. Besides, testing various nutrient sources (e.g., proteins and nucleic acids) would possibly allow detection of compound-specific nutrient recycling pathways. Using complex organic materials (such as plant leaves or root litter) is clearly subordinate in this regard, notwithstanding their relevancy to real ecosystems, as it potentially blurs the resolution of our experimental vision focused on specific metabolic pathways. The tools to conduct such research are all currently widely available including stable isotopic labeling and tracing/probing, quantitative molecular detection assays, and high-throughput sequencing to gain insights into microbial community composition, elemental fluxes, and gene expression at both population and community levels. Maybe, the main limitation will be availability of biological models and relevant microbial cultures. This is because our capacity to isolate and culture specific microbes including whole functional guilds still represents a major bottleneck that has not changed much throughout the recent decades.

Regardless of the above-mentioned technical hurdles, the outlined programme opens fascinating perspectives that will further our understanding of the microbial interactions within the elusive AM fungal hyphosphere, tiny in size but huge in its potential importance for our sustainable future, most likely to be based fully on recycled nutrients.

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## Shifting the world's focus to underground ecosystems

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For decades, scientists have been documenting the importance of mycorrhizal fungi (Sportes et al. 2021). Research has shown that mycorrhizal interactions lay at the base of various ecosystem functions, including global nutrient cycles (Frey et al. 2019; Mo et al. 2022). Because mycorrhizal communities influence so many soil processes, the of these complex degradation ecological associations belowground can impair aboveground ecosystem functioning (Kivlin et al. 2013; Wagg et al. 2019; Powell and Rilling 2018; Duarte and Maherali 2022).

While there is a growing awareness that soils play a key role in climate regulation, much of the research on mycorrhizal interactions has been inaccessible or ignored by policy makers. This is a mistake. The FAO warns that 90% of Earth's topsoil is predicted to be at risk by 2050 (FAO 2022), and yet we still lack effective frameworks to protect soil biodiversity. A recent analysis by Guerra et al. found that more than 70% of Earth's known soil biodiversity hotspots remain unprotected by current conservation priorities (Guerra *et al.* 2022).

Urbanization, agricultural expansion, nutrient deposition, and logging are of particular concern for mycorrhizal fungi, with studies showing significant decreases in diversity and functioning under different land use changes (Rilling *et al.* 2002; Abrego *et al.* 2020; Tomao *et al.* 2020). As soils become degraded, fungal biodiversity disappears from our toolkit of climate solutions, and it becomes harder to regulate nutrient fluxes (Kivlin *et al.* 2013; Bennet and Classen 2020).

In a 'Policy Forum' letter to *Science* in 2021, researchers dubbed soil organisms as "canaries in the coal mine" because their deterioration is the first warning that ecosystems will start to underperform (Guerra *et al.* 2021). While it is largely acknowledged that the loss of soil biodiversity has the potential to induce a shocking chain reaction for the climate, underground ecosystems remain largely unprotected.

Since fungi are so often left out of conservation agendas, the scientific community lacks the tools to effectively determine priorities for fungal biodiversity conservation (Oyanedel et al. 2022). While ecological 'hotspots' were established decades ago for plants and animals, the corresponding information for soil biodiversity is absent from current national and global assessments of biodiversity, resulting in poor protection of underground ecosystems (Lofgren and Stajich 2021). In order to incorporate underground ecosystems into climate and conservation agendas, we need to systematically

map and monitor mycorrhizal biodiversity hotspots across Earth.

The Society for the Protection of Underground **Networks** (SPUN) (https://www.spun.earth/) was founded as a science-based initiative to map protect and mycorrhizal communities. In collaboration with GlobalFungi, Fungi Foundation, Global Soil Mycobiome Consortium. and the Crowther Lab, SPUN is helping map patterns of mycorrhizal biodiversity, identifying under-sampled areas, and advocating for better protection of these communities.

We do this by combining large geo-referenced fungal databases with ecological variables to generate spatial predictions of mycorrhizal diversity based on the relationships identified in a machine learning environment (van den Hoogen *et al.* 2021). This approach allows us to quantify and map the uncertainty of these model predictions, as well as characterizing undersampled ecoregions to help guide future mycorrhizal research across the globe.

## Why is it important to map mycorrhizal biodiversity?

Last fall, the International Union for the Conservation of Nature (IUCN), which maintains the global "red list" of threatened and endangered species, explicitly called for fungi to be given the same consideration as plants and animals. But the world has been slow to respond. SPUN is working to provide these data for mycorrhizal fungi. This means developing a global sampling campaign that covers all types of ecosystems: from urban green roofs (Fig. 1), to the summits of volcanoes (Fig. 2), to high-altitude wetlands, to agricultural fields that have been under intensive management for decades. In all cases, SPUN works with local researchers to develop sampling campaigns that help characterize mycorrhizal biodiversity in wide ranging ecosystems. The idea is to generate data that is useful to governments, policy makers, NGOs, and others to help diversify conservation agendas. This will require working closely with organizations, such as the IUCN, to understand what surveys and data are most useful to them.

### Call for input and collaboration Greater impact working together

Do you want to contribute to the mapping of Earth's mycorrhizal communities? Join to become a SPUN Associate here. Our goal is to build a community that enables scientists and experts to work together to map and protect mycorrhizal systems. We believe that good science can only be achieved through *transdisciplinary* approaches, and therefore we aim to work with researchers from diverse backgrounds and expertise. When you become an associate, we can help by connecting you with other researchers, students, and interns, and by bringing support and attention to your research. Our aim is to drive diverse, equitable, and inclusive research in this field.

#### Diversity of voices and knowledge

With the help of the social anthropologist Daniela Soto Hernandez, SPUN has been creating policies and guidelines to promote meaningful inclusive action in mycorrhizal research. We see these as 'living documents' that drive the way we work, and we strive to see constant improvement and input from our experiences and all the communities we work with.

We are committed to finding ways to support underrepresented groups and minorities facing structural inequalities across the globe. SPUN's sampling expeditions prioritize collaboration and consent from local community members, and we endeavor to provide resources to the most affected people and areas.



**Figure 1.** SPUN Associates get ready to sample for mycorrhizal fungi on greenroofs of the bus stops of Utrecht, Netherlands as part of a larger project on urban mycorrhizae in collaboration with Dr. Bala Chaudhary.

We acknowledge that many well-intentioned environmental initiatives end up perpetuating hegemonic power dynamics and helicopter science, due to exclusion of local communities in the processes of planning and decision-making. Therefore, we seek to ensure that our efforts build connections and networks to help the knowledge production and decision-making of those most impacted by the problems we seek to address.

#### Ways to get involved

Join us at upcoming events. SPUN will join researchers from all over the world at the Global Soil Biodiversity Conference from March 13-15 in Dublin, Ireland, and at the

III International Symposium of the Mycorrhizal Symbiosis in South America from August 24 -September 2, in Leticia, Amazonas, Colombia. Join us and share your ideas and research findings.

Work towards open data. SPUN is helping develop global maps of mycorrhizal biodiversity using fungal sequence data from (i) published studies that have been collected and curated through the GlobalFungi database, and (ii) with the collection of new data in under-sampled areas. The use of published datasets from all over the world guides global-scale estimates of mycorrhizal diversity distribution and hotspots. The use of specific models can help account for noise in data that arise from differences in protocols and the production of data from many researchers and laboratories. We recognize that a decentralized approach can lead to some tradeoffs in data consistency, and when possible, we promote standardized data collection protocols by offering

advice through all stages of mycorrhizal data collection to our associated scientists. To discuss these ideas further, we will be holding community protocol sessions with our science associates to get further input from the scientific community.

Activate journalists. We need the general public to learn more about mycorrhizal fungi – their importance for food production, healthy ecosystems, and the enormous risk of biodiversity loss that they are facing. Need help promoting your mycorrhizal research and publication? Contact our communications lead, Kelcie Walther (kelcie@spun.earth), for tips.

Activate the Youth. The education of youth will ensure future generations will know about the importance of mycorrhizal fungi and care about their conservation. Scientists are needed to produce rigorous, easy to read materials for youth and young kids. Here is one really good resource by Silva-Flores *et al.* (2021), and a collection from *Frontiers in Young Minds.* 

Join 3Fs initiative. Our partners at FungiFoundation have put together an initiative, Flora, Fauna, Funga (FFF) that seeks to "write this neglected kingdom of life into conservation and agricultural policy frameworks, protect it under international and domestic law, and unlock crucial funding for mycological research." Over 1000 scientists have signed so far. You can sign the initiative and learn more about it here.

Become a SPUN Underground Explorer. SPUN aims to fuel, motivate, and support high-quality research initiatives to sample mycorrhizal fungal diversity around the world. We just awarded our first 11 grants to researchers to sample in underexplored underground ecosystems on Earth. In addition to funds for sampling, we want to support and empower these local mycorrhizal and soil scientists not only to pursue their own independent questions, but also to share their results broadly. Watch for the next round of Underground Explorers in the coming months.

**Share your ideas.** How can we help spread the findings of your work? What milestones should we strive for? How can we collectively set the agenda for mycorrhizal research in the next five years? Email your ideas at hello@spun.earth and sign up for the newsletter.



**Figure 2.** SPUN worked with Dario Ramirez at Universidad San Francisco de Quito in Ecuador to sample high elevation soils in the Andes. Here a soil core is being collected by Justin Stewart at 4000 meters elevation from Chimborazo, one of the highest volcanoes in the world. The data generated from this collaboration will uncover fungal biodiversity in the under-sampled Andean region.

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## YouTube interviews\*

## - Martin Ryberg on the evolution of ectomycorrhizal fungi

Savannah Draud, PhD candidate at the University of Mississippi interviews Dr. Martin Ryberg, from Uppsala University, about trends in ectomycorrhizal fungal evolution.

Interview: https://southmycorrhizas.org/reading/january-2023/

<u>Study:</u> Ryberg M, Kalsoom F, Sanchez-Garcia M. 2022. On the evolution of ectomycorrhizal fungi. *Mycosphere* 13(2):1-12. https://10.5943/mycosphere/si/1f/1

## - Bala Chaudhary on fungal dispersal

Camille Truong interviews Bala Chaudhary, Associate Professor of Environmental Studies at Dartmouth College, United States, about fungal dispersion across different scales.

## Interview: https://southmycorrhizas.org/reading/february-2023/

<u>Study:</u> Chaudhary VB, Aguilar-Trigueros CA, Mansour I, Rillig MC. 2022. Fungal dispersal across spatial scales. *Annu Rev Ecol Evol Syst* 53:69-85. https://doi.org/10.1146/annurev-ecolsys-012622-021604

# - Justine Karst/M. Jones/J. Hoeksema on misinformation on common mycorrhizal networks in forests

César Marín and Guillermo Bueno interview Justine Karst (U. Alberta), Melanie Jones (U. British Columbia), and Jason Hoeksema (U. Mississipi) about misinformation, positive citation bias, and overinterpreted results regarding common mycorrhizal networks in forests.

## Interview: https://southmycorrhizas.org/reading/february-ii-2023/

<u>Study:</u> Karst J, Jones MD, Hoeksema JD. 2023. Positive citation bias and overinterpreted results lead to misinformation on common mycorrhizal networks in forests. *Nat Ecol Evol.* Early View. https://doi.org/10.1038/s41559-023-01986-1



## Tools

### $\rightarrow$ An R package to manage multiomic data

Combes *et al.* (2022) provide the *plasma* R package (version 0.9.21), which allows for varied and supervised analyses of incomplete, overlapping multiomics datasets. It also uses partial least squares in multiple steps to find models that predict survival outcomes.

<u>Study:</u> Coombes KR, Yamaguchi K, Abdelbaky S. 2022. *plasma*: Partial LeAst Squares for Multiomic Analysis. R package, version 0.9.21. URL: https://CRAN.R-project.org/package=plasma

### $\rightarrow$ Rubidium to trace mycorrhizal K transport

Kafle *et al.* (2022) used rubidium (Rb+) for the first time, as a proxy to evaluate the movement of potassium in the arbuscular mycorrhizal symbiosis. They also suggest the existence of a mycorrhizal-mediated pathway for potassium nutrition in *Medicago truncatula*.

<u>Study:</u> Kafle A, Cooney DR, Shah G, Garcia K. 2022. Mycorrhiza-mediated potassium transport in *Medicago truncatula* can be evaluated by using rubidium as a proxy. *Plant Sci* 322:111364. https://doi.org/10.1016/j.plantsci.2022.111364

## $\rightarrow$ Transparent soil (polymer) for single-spore AMF cultures

Paré *et al.* (2022) used transparent soil based on superabsorbent polymer (SAP) to initiate auotrophic cultures, based on single-spores from seven different AMF species. Such cultures were maintained over several months and under non-sterile conditions.

<u>Study:</u> Paré L, Banchini C, Hamel C, *et al.* 2022. A simple and low-cost technique to initiate single-spore cultures of arbuscular mycorrhizal fungi using a superabsorbent polymer. *Symbiosis* 88:61-73. https://doi.org/10.1007/s13199-022-00878-5

Click for previous Tools: Vol1\_11 (p. 11), Vol1\_12 (p. 15), Vol1\_13 (p. 16), Vol2\_11 (p. 19), Vol2\_12 (p. 15), Vol2\_13 (p. 15), Vol3\_11 (p. 16), Vol3\_12 (p. 17), and Vol3\_13 (p. 26).

## **MYCORRHIZAL EVENTS:**

International Symposium on **Mycorrhizal** 111 Symbiosis in South America Website Instituto SINCHI, Leticia, Colombia 28 - 30 August, 2023 (with courses before & after)

Organizers: South American Mycorrhizal Research Network and Instituto SINCHI

- The 6<sup>th</sup> international Molecular Mycorrhiza Meeting will take place in Cambridge, United Kingdom, 25 – 27 September, 2023. Further information in Twitter: @slcuplants

- The 12<sup>th</sup> International Conference on Mycorrhiza (ICOM12) will take place in Manchester, United Kingdom, 6 – 11 August, 2024. Further information in Twitter: **@ICOM\_12** 

- The 13<sup>th</sup> International Conference on Mycorrhiza (ICOM13), will take place in Cairns, Australia, in 2026. Stay tuned for further information.

University

and

## **MYCOLOGICAL EVENTS:**

Northern

Mycological Society of America

2023 Mycological Society of America Annual

## Meeting

### Website

Organizers:

Northern Arizona University, Flagstaff, AZ, United States

Arizona

29 July - August 2, 2023





## **Events**

XI Latin American Congress of Mycology Website

Hotel El Panamá, Ciudad de Panamá, Panamá 7 - 10 August, 2023

Organizers: Local organizers and Latin American Mycology Association.

12<sup>th</sup> International Mycological Congress Website MECC, Maastricht, the Netherlands 11 - 15 August, 2024

Organizers: Local & International organizers and International Mycological Association.

## **OTHER EVENTS:**

2023 Ecological Society of America Annual Meeting Website

Portland Convention Center, Portland, OR, United States 6 - 11 August, 2023

Organizers: Ecological Society of America.

## Collective Behavior Gordon Research Conference, 13 – 18 August, 2023

## Website

Grand Summit Hotel, Newry, ME, United States

## 2023 British Ecological Society Annual Meeting

Website ICC, Belfast, United Kingdom 12 - 15 December, 2023

Organizers: British Ecological Society.









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ICOM12 will be organised in the summer of 2024 in Manchester, United Kingdom, by Prof. Dr. David Johnson (University of Manchester) and colleagues.