IMS Newsletter
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International Mycorrhiza Society

The International Mycorrhiza Society quarterly e-newsletter

Photo: *Russula* sp. ("Funga UV"), by Francisco Sánchez Poblete
1st place at the 10 Valdivia FungiFest photo contest 2024

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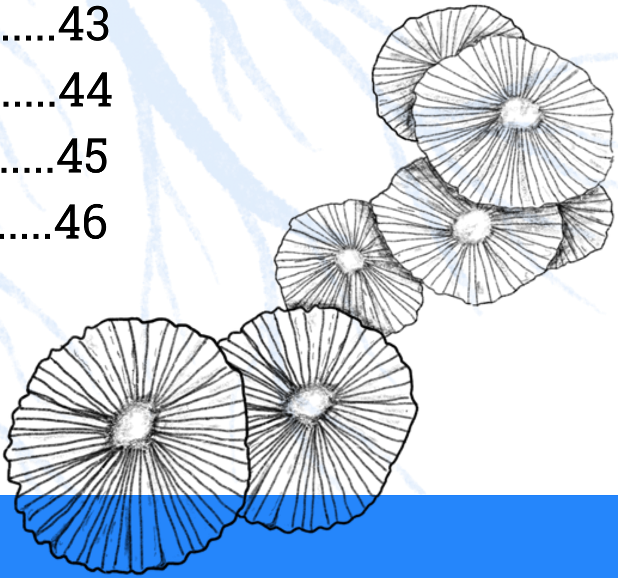

Editorial: New Presidency of the IMS

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A message from the new IMS President: Justine Karst

Hello International Mycorrhiza Society (IMS) members! My name is Justine Karst and I am the new President of our society as of August 9, 2024. First, I would like to thank Marcel G. A. van der Heijden for his service as President (2020–2024), and Ian Dickie and Jonthan Plett for their roles as Board Directors (2020–2024). Please welcome Jan Jansa as our new Vice-President, Pedro M. Antunes as a new Board Director, and Jonathan Plett as the lead organizer of ICOM13. I am grateful and excited to have such a wonderful team to work with. I joined the IMS Board of Directors in 2019 and was elected Vice-President in 2022. I lead a small small lab at the University of Alberta, Canada, and we study the mycorrhizal ecology of the boreal forest. We are interested in the role ectomycorrhizal fungi play in how these forests function. I am thrilled that mycorrhizal ecology has (finally!) reached the public, but I am concerned that some popular ideas are far ahead of the science. As a scientific society, I believe it's important that we not only advance research on mycorrhizas but also inform the public and land managers on the nature and extent of evidence underpinning our knowledge.There is much promise and uncertainty in what we do; both must be conveyed.

Over the next two years, we will be supporting Jonathan Plett and his team to make ICOM13 (13th International Conference on Mycorrhiza) informative, engaging, fun, and inclusive. ICOM is our flagship event and as always, IMS puts a high priority on making this conference a success for our members. We also hope to build a new website and continue growing our communications with members and beyond.

As an international society, most of us live and work far from other members. If you have already met me, you will know how much I enjoy thoughtful discussions, especially over nice food and wine. While this might not always be possible (until ICOM13!), please know that I am always happy to have a zoom or email conversation about the IMS (or mycorrhizas) with you. In this way, we can make our worlds a little more connected. Please stay tuned for more updates from the IMS Board. Thank you very much for your membership with the IMS.

Call for Secretary

The IMS Board is looking for a secretary. This is a non-voting position, so this person does not need to be an IMS member. The duration of the position would ideally be for four years. Tasks involved: setting up meetings, taking minutes of meetings, emailing minutes and action items following from meetings, and keeping records of IMS documents. The start date is as soon as possible. Please email IMS President, Justine Karst for inquiries: (karst@ualberta.ca)

Call for Ecology Topic Editor for the IMS Newsletter

The IMS Newsletter Editorial Board is looking for a new topic editor in the area of ecology. Tasks involved: once yearly invite researchers to showcase their published or unpublished research in the newsletter. This involves contacting researchers and working with them to develop a ~800 word 'behind-the-scenes' look at their research in any area of ecology. The start date is February 2025. Please email César Marín, Editor-in-Chief for inquiries: (cmarind@santotomas.cl).

Early Career Researchers are welcome!

In this issue…

As always, please find on page 8 the Top 10 mycorrhizal research papers of the last four months (papers published between May and August, 2024). The first place article was published by Sir David Read and co-authors in *New Phytologist,* showing direct photosynthate transfer from an autotrophic orchid to conspecific heterotrophic protocorms through a common mycorrhizal network. The second place article was published by Jordana Oliveira and co-authors on *Annual Review of Microbiology*, where they examine the impact of genomic technologies on our view of arbuscular mycorrhizal fungi (AMF) genetics and evolution. An article published in *New Phytologist* by Laura M. Bogar, was ranked third. She proposes that source–sink dynamics are "an essential basic model to explain the movement of plant and fungal resources".

This 15th issue of the IMS Newsletter includes one meeting report, two short articles, and three YouTube interviews.

The meeting report led by Valentina Borda and co-authors details the topics, advances, concerns, research gaps (particularly Global North-South gaps), and societal implications of plant and fungal invasions, all aspects discussed during the 45th New Phytologist Symposium "Ecological and evolutionary consequences of plant-fungal invasions", which took place from June 26 to 29, 2024, at the University of Campinas, Brazil. This Meeting report reflects equal contributions from a combination of early career and senior researchers whose research crosses a variety of disciplines.

Please also find a short article by Olga A. Lastovetsky from University College Dublin, about her discovery of a high diversity of endobacteria (up to 227 Operational Taxonomic Units in one particular spore) living inside 87 AMF spores, in two contrasting sites in Ireland. Most functions of such bacteria are unknown, albeit some might be parasitic and some might be conditional mutualists. Head over to YouTube to watch Olga's interview.

Photos of the SPUN expedition to the Atacama by Mateo Barrenengoa & Diego Fuentes - read more about it here.

A second short article was co-written by three Indigenous environmental leaders of the Council of Atacameños Peoples (“Consejo de Pueblos Atacameños”) from the Atacama Desert in Chile, two ecologists, and one social scientist. The article is about a SPUN-funded survey across the Atacama desert, where the Indigenous communities selected the 41 sampling sites according to their knowledge and interests. So far, even in the driest place on Earth, the authors are finding a very high AMF biodiversity!

The three new YouTube interviews include one with Juan Díaz-Colunga (Ramón y Cajal Researcher in Spain) by César Marín, on how concepts developed in quantitative genetics (epistasis in particular) can be applied to predict functions of microbial communities based on species absence/presence data alone (without abundance information).

In the second, Maria Alice Neves interviews Julieta Alvarez-Manjarrez (Universidad Nacional Autónoma de México, México) on how a hurricane affected mycorrhizal co-occurrence networks in Mexico one and two years after the disturbance. The hurricane was of course, unexpected, and damaged the sampling sites of an on-going project by Julieta and her team...

What a way to make lemonade!

And finally, Rebecca A. Bunn (Western Washington University, United States) and Ana Corrêa (Universidade de Lisboa, Portugal) are interviewed by César Marín (Universidad Santo Tomás, Chile) and Pedro M. Antunes (Algoma University, Canada) about the recent Tansely review they led in New Phytologist on contrasting mechanisms explaining the transfer of carbon from plants to mycorrhizal fungi: 'Surplus C' hypotheses and Biological Market Models.

As always, please find our sections like IMS Seminars, Tools, and Events.

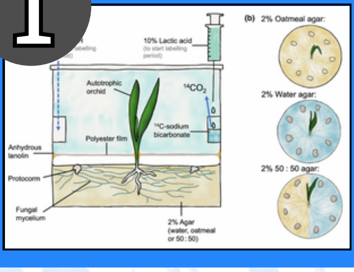
Finally, a big thanks to Melissa Davie and Rosario Iacono for updating the design of our newsletter. We hope you enjoy!

Illustrations created by Melissa Davie.

TOP 10 Mycorrhizal Research Papers*

Images from study figures

1



Read DJ, Haggar J, Magkourilou E, Durant E, Johnson D, Leake JR, Field KJ. 2024. **Photosynthate transfer from an autotrophic orchid to conspecific heterotrophic protocorms through a common mycorrhizal network**. *New Phytol* 243: 398-406. https://doi.org/10.1111/nph.19810

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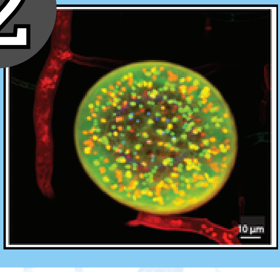

Oliveira J, Yildirir G, Corradi N. 2024. **From chaos comes order: genetics and genome biology of arbuscular mycorrhizal fungi**. *Annu Rev Microbiol* 78. https://doi.org/10.1146/annurev-micro-041522-105143

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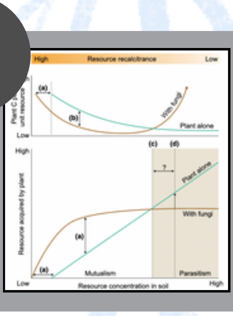

Bogar LM. 2024. **Modified source–sink dynamics govern resource exchange in ectomycorrhizal symbiosis**. *New Phytol* 242:1523-1528. https://doi.org/10.1111/nph.19259

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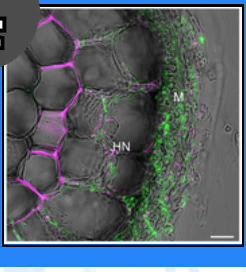

Li H, Ge Y, Zhang Z, *et al.* (2024). **Arbuscular mycorrhizal conserved genes are recruited for ectomycorrhizal symbiosis**. *New Phytol* 242:1860-1864. https://doi.org/10.1111/nph.19259

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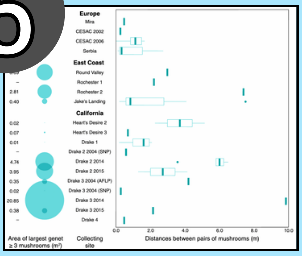

Golan J, Wang YW, Adams CA, *et al.* 2024. **Death caps (*Amanita phalloides*) frequently establish from sexual spores, but individuals can grow large and live for more than a decade in invaded forests.** *New Phytol* 242: 1753-1770. https://doi.org/10.1111/nph.19483

TOP 10

6

Lekberg Y, Jansa J, McLeod M, *et al*. 2024. **Carbon and phosphorus exchange rates in arbuscular mycorrhizas depend on environmental context and differ among co-occurring plants**. *New Phytol* 242:1576-1588. https://doi.org/10.1111/nph.19501

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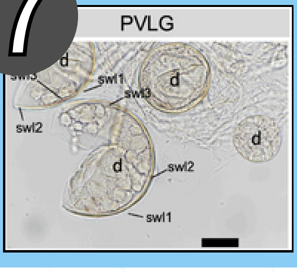

Kokkoris V, Banchini C, Paré L, *et al*. 2024. ***Rhizophagus irregularis*, the model fungus in arbuscular mycorrhiza research, forms dimorphic spores**. *New Phytol* 242:1771-1784. https://doi.org/10.1111/nph.19121

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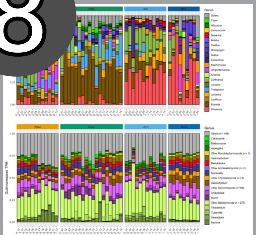

Auer L, Buée M, Fauchery L, *et al*. 2024. **Metatranscriptomics sheds light on the links between the functional traits of fungal guilds and ecological processes in forest soil ecosystems**. *New Phytol* 242: 1676-1690. https://doi.org/10.1111/nph.19471

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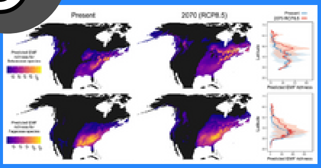

Van Nuland ME, Qin C, Pellitier PT, Zhu K, Peay KG. 2024. **Climate mismatches with ectomycorrhizal fungi contribute to migration lag in North American tree range shifts**. *Proc Natl Acad Sci USA* 121:e2308811121. https://doi.org/10.1073/pnas.2308811121

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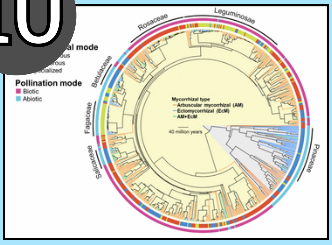

10. Yamawo A, Ohno M. 2024. **Joint evolution of mutualistic interactions, pollination, seed dispersal mutualism, and mycorrhizal symbiosis in trees**. *New Phytol* 243:1586-1599. https://doi.org/10.1111/nph.19783

* Selected from 202 Web of Science articles published between May and August, 2024 by: Pedro M. Antunes, Francis M. Martin, Ido Rog, Jason Hoeksema, Joseph Birch, Jan Jansa, Judith Lundberg-Felten, Annegret Kohler, Jeff Powell, Camille Truong, Junling Zhang, and César Marín

MEETING REPORT

Ecological and evolutionary consequences of plant-fungal invasions

Summary on the 45th New Phytologist Symposium | 26–29 June 2024 | University of Campinas, Brazil

Valentina Borda[1], Eduardo Choreño-Parra[2], Li Yan[3], Cecelia Stokes[4], Anna Schertler[5], Pedro M. Antunes[6]*

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The 45th New Phytologist Symposium organized by Erika Buscardo, Jason Hoeksema, László Nagy, and Miranda Hart, provided diverse and timely insights into plant-fungal invasion science - defined here as is the study of how non-native invasive fungal species interact with native and/or non-native plants and impact communities and ecosystems. Topics included conservation, ecological restoration, social aspects and fungal applications, with a focus on functional ecology across various guilds - including mycorrhiza, endophytes, pathogens, and saprotrophs - and spanning forests and grassland ecosystems (Fig. 1). Importantly, the event demonstrated the major service of scientific foundations such as the New Phytologist Foundation (kudos to Christine Phillips and the entire New Phytologist team) in promoting diversity and inclusion while advancing our field of scientific endeavour. The Symposium hosted 91 participants (Fig. 2)

Figure 2. Symposium participants at the Unicamp auditorium, State University of Campinas, Campinas, SP, Brazil. Credit: Christine Phillips

from 24 countries, including 28 speakers and 23 poster presenters (11 of them giving additional flash talks). Participants were 42% male, 57% female, and 1% non-binary. Among them, 34% were established researchers and faculty members, including editors of the New Phytologist's Foundation journals, 19% post-doctoral researchers, 29% Ph.D. students, and 15% Masters/Undergraduate students. Additionally, 16 delegates received travel and accommodation support from the New Phytologist Foundation to attend.

The meeting bridged the gap between the Global North and South and brought together a diverse community to assess the current knowledge of plant-fungal invasions and establish key research directions for addressing ecological challenges. The Symposium provided a unique opportunity to exchange knowledge and build long-term collaborative relationships spanning multiple career stages and parts of the world.

Major takeaways from the symposium:

The importance of a critical stance towards existing paradigms and the need for a more predictive science.

Recent investigations of popular ecological concepts (e.g., Karst et al., 2023, Bunn et al., 2024), urge us to constantly evaluate evidence and adapt our understanding accordingly. Robust theory and manipulative experiments are essential for advancing our knowledge of ecological processes and drawing broader conclusions that minimize context dependencies However, plant-fungal invasions research has not adequately provided clear science-based directions for stakeholder decision-making, which may partly explain challenges in policy and guideline implementation related to ecological applications. In this context, despite how challenging it may be (see Raerinne, 2024), developing a more predictive ecology becomes an important goal when addressing global change phenomena such as biological invasions.

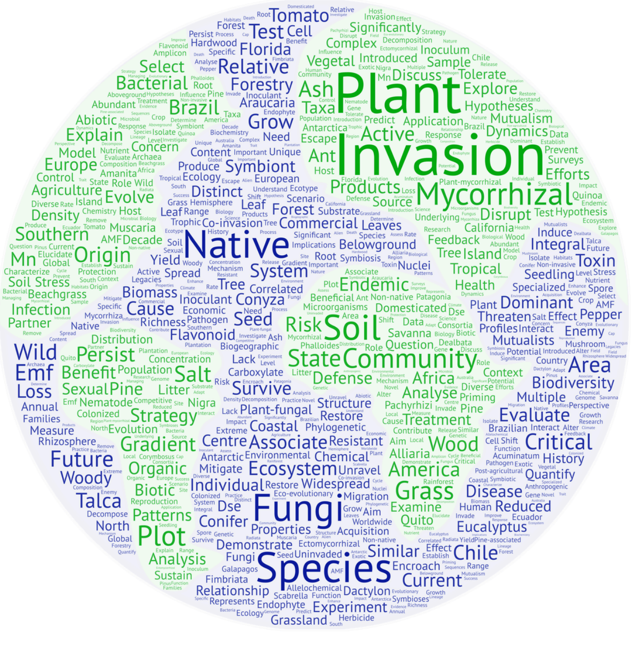

Figure 1. Word cloud featuring at least five key recurring terms from the complete conference program. Made with WordArt.com

The symposium started with a keynote on the ‘emerging science of linked plant-fungal invasions’ (Dickie et al., 2017), highlighting the plethora of interactions that arise during this process and challenging ‘mutualism limitation’ (Janzen, 1966) and ‘enemy release’ (Elton, 1958) hypotheses. Notably, plant communities have higher pathogen richness in managed systems (Makiola et al., 2019, 2022), suggesting that pathogen spillover from non-native to native plants may be an important mechanism in invasion processes (Waller et al., 2020).

In the context of novel plant-fungal interactions and rapid evolution, the ‘degraded mutualisms’ hypothesis, suggesting mutualistic relationships can deteriorate due to environmental filtering, was contrasted with the ‘enhanced mutualisms’ hypothesis, arguing stronger mutualisms in non-native ranges can promote invasion success (Sheng et al., 2022). Although biogeographical comparisons of microbial communities spanning wide geographic coverage in both introduced and native ranges are rarely made, new data from 17 populations of *Conyza canadensis* across their native and introduced range indicated an association with a richer and closely related community of arbuscular mycorrhizal (AM) fungi in the introduced range, predominantly involving Glomeraceae. This finding, which supports the “enhanced mutualisms” hypothesis, raises important questions about predicting which invasive mechanisms are most significant for individual plant species.

Further evidence for ‘enhanced mutualisms’ was reported in different invasive plants and ecosystems. For instance, the interaction between endophytic fungi and an invasive grass confers herbivore protection, thereby emphasizing the need of studying multi-trophic interactions (Omacini et al., 2001). In addition, beneficial fungal endophytes may drive the invasiveness of the grass Poa annua in Antarctica, one of the most remote places on Earth (Ballesteros et al., 2022; Molina-Montenegro et al., 2023).

The importance of metabolite production influencing invasion processes was highlighted (Borda et al., 2022). The ‘novel weapons’ hypothesis, which proposes that a defensive trait new to the resident community results in a competitive advantage (Callaway and Ridenour, 2004), is often invoked to explain the success of invasive plants. Plant secondary metabolites can protect against herbivory (Mithöfer and Boland, 2012), acting as an important mechanism in competition when encountering resident species (Kalisz et al., 2021). However, there are concerns regarding citation biases, spatial autocorrelation and other methodological limitations in studies suggesting that mutualist disruption via allelopathy is an important ecological mechanism in plant invasions (Colautti, unpublished).

Overall, the research presented suggest we are still uncovering patterns and establishing a consistent framework, with plant-based models serving as a reference. However, as research increasingly highlights the role of fungi on the ecology of invasions, expanding our focus to myco-centric and symbio-centric views of plant-fungal associations will improve our understanding of invasion biology and lead to a more informed and predictive science.

The disconnection between ecological evidence and societal views on the practice of commercial fungal applications.

This discrepancy calls for more comprehensive research, data collection, and communication with relevant stakeholders. Many uncertainties persist, particularly regarding the use of commercial inocula and the introduction of non-native edible fungi; e.g., golden oyster mushroom, (*Pleurotus citrinopileatus*) in North America, which is associated with significantly lower native fungal richness (Veerabahu, unpublished; Bruce, 2018). A deeper understanding of the geographic origins of strains/species and their ecological roles is essential for assessing potential impacts from applications.

The concept of “everything is everywhere” is not true for global microbial distributions (O’Malley, 2007) and the prolific use of fungal inoculants and their impacts on native communities is a crucial issue to consider (Hart et al., 2018). AM fungi have high intraspecific genotypic variation (up to 50%), questioning the conventional concept of species (Oliveira et al., 2024), and highlighting concerns about introducing foreign AM fungal inocula without considering cryptic taxa. These findings may explain the high functional variability present within the same AM fungal species. Gene expression and nuclear dynamics in spores can also greatly vary with regard to the plant host (Kokkoris et al., 2021; Oliveira & Corradi, 2024). It is thus evident why missing or inadequate legal regulation of fungal inoculants worldwide promotes interregional biological exchange, with unforeseen consequences.

Native fungi can effectively improve crop growth compared to commercial inocula (e.g., Koziol et al., 2024; Godoy et al., 2023). Furthermore, rare AM fungal species may be important for restoration of significant and unique ecosystems, indicating that inoculants may still aid conservation (Kajihara et al., 2022). Soil augmentation or taking advantage of soil microbial legacies and feedbacks to optimize crop rotation sequences (Koyama et al., 2022) are alternative strategies for managing local AM fungi (Johnson and Gibson, 2021). In addition, there is evidence of environmentally driven selection for highly efficient native AM fungi (Pellegrino et al., 2022). Altogether, these studies highlight the promise of using native fungal inoculants instead of commercial inoculants (e.g., see Silva-Flores et al., 2021). As the commercialization of fungi and their application increases, the need to promote the use of native organisms and local products is critical to prevent invasions and create effective management techniques.

The global emergence of fungal invasions necessitates the establishment of baseline data to advance the knowledge of plant-fungal invasions.

Fungal and plant-fungal invasions are occurring worldwide with pervasive consequences. Significant gaps in data and knowledge baselines remain; for example, delineating cryptic species, fungal biogeography, and differences in ecology in native and introduced ranges. Mutualistic fungi have only recently been included in the invasion science conversation and the mechanisms and traits contributing to their success are not fully understood. The flexible reproductive traits of some ectomycorrhizal fungi may explain their invasion success (Wang et al., 2023). The ability of Sulloid fungi to disperse long distances by biotic and abiotic vectors, as well as establish resistant and pervasive spore banks may partially explain the invasiveness of pines (Policelli et al., 2019). In addition, applying common concepts in plant and animal invasion biology, for example ‘enemy release’ (Keane & Crawley, 2002) and ‘novel weapons’ hypotheses, may elucidate other patterns of invasive, mutualistic fungi. Incorporating fungal traits into management plans could potentially mitigate the escape of trees outside of plantation and help efforts to assist migration of plant species impacted by climate change (Argüelles-Moyao & Galicia, 2024).

Disentangling fungal biogeography and thus identifying native and non-native members of fungal communities is important for minimizing invasion risk. An attempt to quantify such novel associations of plant pathogens on a global scale, revealed that those were especially common among widespread generalist species (Schertler et al, unpublished). A significant portion of recorded associations cannot be clearly classified as invasive due to insufficient knowledge of fungal native and introduced ranges. The commercial use of non-invasive fungal inocula was suggested as a potential strategy to reduce fungal-plant co-invasion risk (Hayward et al., 2015).

Challenges remain, particularly for taxa with ambiguous species boundaries, as exemplified by research on the pathogenic Ceratocystis fimbriata sensu lato complex (Fourie et al., 2020). Cryptic speciation, when unknown, can obscure our understanding of fungal ecology, host range, and distribution. A deeper understanding of fungal basic biology and ecology is crucial to understand the drivers and mechanisms of the invasion process and assess their potential impacts post introduction.

There is a need for holistic approaches to restoration and management practices that consider the below-ground dynamics of mycorrhizae.

Plant-focused rehabilitation often overlooks native fungal biodiversity, as non-native plant removal can leave behind mycorrhizal symbionts (Sapsford et al., 2021). Therefore, managing mycorrhizal communities is essential for establishing and restoring target native plants by addressing native mycorrhizal degradation and integrating host-specific interactions, site conditions, and fungal inoculum origins into restoration efforts.

Considering the impacts of restoration campaigns on soil fungal communities is crucial since plant-focused rehabilitation efforts alone are often insufficient (Godefroid et al., 2011). In addition, invasions by non-mycorrhizal plant hosts can change mycorrhizal abundance (Maltz et al., 2016). However, challenges in restoring native mycorrhizal communities are significant (Wall et al., 2020; Roche et al., 2021). For example, in Brazil's native savannas (Cerrado), mycorrhizal communities did not recover after three years of seeding with native plants (Abrahão unpublished). Similarly, research has underscored the difficulty of re-establishing late successional species, raising the question of whether plants should be transported with their mycorrhizas for more effective restoration (Koziol et al., 2022). Finally, there is a critical need to restore belowground processes in tandem with aboveground ones, taking in consideration that non-native fungi might prime environments for further invasions (Policelli et al., 2019, Sapsford et al., 2021). These studies demonstrate the need to fully integrate fungi in ecological restoration science.

The consequences of plant-fungal invasions for ecosystem functioning need to be addressed.

When plants and fungi are introduced to new environments, their traits can modify broad ecological processes such as productivity, carbon storage, and nutrient cycling (Hoeksema et al., 2020). However, unlike plants, the specific role of fungi in invaded ecosystems has been scarcely tested. Research has shown that invasive beachgrass (*Ammophila arenaria*) can enhance litter decomposition by modifying the relative abundance of key microbial decomposers (Fuqua, unpublished). Similarly, studies indicate that saprotrophic fungal communities decompose wood from non-native pines at lower rates, though this effect is ecosystem-dependent (Wijas et al., 2024b,a). In pine-invaded systems, shifts in bacterial and fungal community composition are being documented, along with changes in soil physicochemical properties (Siggers et al., unpublished).

Mycorrhizal fungi may have a role in priming organic matter decay and influencing soil carbon storage (Horsch et al., 2023). Additional evidence suggests that mycorrhizal fungi may prime decomposition in invaded systems depending on the quality of organic matter produced by non-native plants (Choreño-Parra and Treseder, 2024). Further studies have emphasized the influence of fungi on nutrient cycling. Ectomycorrhizal fungi, for example, were shown to alter nutrient cycling by mining soil nitrogen, enabling fast-growing pines to meet their nutrient demands (Vietorisz, unpublished). In phosphorus-impoverished habitats of south-western Australia, certain plant species have successfully invaded by associating with local AM fungi, which release root carboxylates to facilitate phosphorus acquisition

(Tang, Yan, and Lambers, unpublished). These findings collectively highlight the critical role of fungal communities and their interactions with invasive plants in altering ecosystem processes, potentially promoting the invasion process (Zhang et al., 2019).

Conclusions

The 45th New Phytologist Symposium provided a diverse platform for discussing the complexities of plant-fungal co-invasions, underscoring that the scientific scope of this field is broader than initially suggested. The sessions and discussions revealed that while significant progress has been made in understanding the ecological and evolutionary dynamics of these interactions, several critical aspects require further exploration. Current research on plant-fungal invasions ranges from the rapid evolution of mycorrhizal responses (Delavaux & Bever, 2022) to the ecological repercussions of invasions (Dickie et al., 2017). However, a significant imbalance was evident, with evolutionary dynamics receiving comparatively less attention. Moreover, several critical questions remain unanswered. Notably, the broader ecological consequences of fungal invasions are still relatively underexplored (Hoeksema et al., 2020). Furthermore, specific mechanisms through which fungi contribute to or are influenced by plant invasions remain unclear.

A recurrent discussion topic was the necessity of better integrating fungi into the wider field of invasion science. Unlike well-established research of plant invasions, the focus on plant-fungal invasions is relatively new and often disconnected from disciplines like plant pathology, which could significantly inform ecological research. Both interdisciplinary and multi-scale research approaches are essential to understand the impacts of non-native fungi in diverse ecological contexts. Additionally, engaging a broader spectrum of stakeholders is key to ensure that scientific discoveries are translated into actionable policies and increased public awareness. As public interest in “beneficial” fungi continues to grow, there is a pressing need to effectively communicate the potential ecological risks posed by fungal invasions. A narrative grounded in robust scientific evidence is crucial to counteract misconceptions and to guide responsible practices in the use of fungi in agriculture, forestry, ecological restoration, and other sectors.

Future Research Directions

1) Microbial Community Impacts: What aspects (e.g., traits, strains, species, guilds) of microbial communities have the most significant impacts on ecosystems and global processes?

2) Identifying Native Fungi: How can we accurately determine which fungi are native, and what implications does this have for managing plant-fungal invasions?

3) Evolutionary Dynamics: What are the evolutionary dynamics of plant-fungal co-invasions, and how do they affect the trajectory of invasiveness in different ecosystems?

3) Evolutionary Dynamics: What are the evolutionary dynamics of plant-fungal co-invasions, and how do they affect the trajectory of invasiveness in different ecosystems?

4) Soil Biota Interactions: How do non-native fungi interact with native soil biota, and what are the consequences for ecosystem health and biodiversity?

5) Tree-Fungal vs. Grass/Fern-Fungal Invasions: How do tree-fungal invasions compare to those affecting grasses and ferns, and why might the latter be more challenging to restore in some ecosystems?

6) Role in Facilitating/Hindering Other Invasions: What roles do fungi play in facilitating or hindering the invasions of other organisms, including plants, animals, and other microbes?

7) Predicting and Mitigating Impacts: How can we predict and mitigate the impacts of plant-fungal invasions across various climatic and environmental contexts, particularly in the face of global change, while also understanding their influence on key ecological processes (e.g., carbon storage). How can global monitoring and research efforts be coordinated to address these challenges?

8) Ecosystem Services and restoration: What are the implications of plant-fungal invasions for ecosystem functions and services, and how can management strategies be developed to ensure key services are preserved?

9) Interdisciplinary Approaches: How can interdisciplinary approaches, including the integration of genetics, plant pathology, invasion biology, and ecology, improve our understanding and management of fungal and plant-fungal invasions?

10) Commercialization and Risks: What are the potential risks associated with the commercialization of fungi, and how can policies be developed to prevent the spread of invasive species through trade and agriculture?

11) Engaging Stakeholders: How can we best engage stakeholders, including policymakers, land managers, indigenous peoples, public and private sector and the society, in the development and implementation of evidence-based strategies to manage and mitigate plant-fungal invasions?

12) Global Collaboration: How can we harmonize global databases, protocols, and research frameworks to foster a more cohesive and collaborative approach to studying and managing plant-fungal invasions?

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Spores of arbuscular mycorrhizal fungi host surprisingly diverse communities of endobacteria

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How many different bacteria can live inside a fungus? Bacteria living inside fungi have gone largely unnoticed until the late 1990s/early 2000s, when intracellular bacteria were first described in arbuscular mycorrhizal fungi (AMF) (Bianciotto et al., 1996) and inside spores and hyphae of Rhizopus microsporus (Partida-Martinez & Hertweck, 2005). Initially, fungal endobacteria were considered biological oddities, however, research on bacterial-fungal interactions has gained considerable momentum in recent years as we are starting to realize that many different types of fungi, particularly within the early diverging fungal groups (Mucoromycotina, Glomeromycotina, Mortierellomycotina) can host bacteria inside their cells (Pawlowska et al., 2018). These intracellular bacteria, termed "endobacteria" live inside fungal hyphae and can be vertically transmitted from one host generation to the next in spores. Endobacteria often play important roles in fungal biology including metabolism (Lastovetsky et al., 2016; Uehling et al., 2019), reproduction (Partida-Martinez et al., 2007; Mondo et al., 2017), pathogenicity (Itabangi et al., 2022), and protection from soil predators (Richter et al., 2022). As a result, endobacteria are of rising interest in fungal biology as important modulators of host function and interaction with other organisms and the environment. Despite managing to fly under the radar for so long, endobacteria in AMF were actually noted many decades ago, with evidence of bacteria-like-organelles first detected in the 1970s (Mosse, 1970). Since then, two different endobacteria were described in AMF: Candidatus *Glomeribacter gigasporarum* (Bianciotto et al., 2003) (CaGg) and Candidatus *Moeniiplasma glomeromycotorum* (Naito et al., 2017) (CaMg). CaGg are the better studied endosymbionts and have been shown to provide benefits to their AMF host. For example, AMF with CaGg had higher sporulation success and formed longer presymbiotic hyphae than AMF without CaGg (Lumini et al., 2007; Salvioli et al., 2016). On the other hand, the role of CaMg endobacteria in AMF biology remains experimentally untested, but they have been hypothesized to be parasites (Toomer et al., 2015). However, most of what we know about the AMF-endobacteria relationship has come from studies of AMF derived from culture collections, with limited knowledge about the prevalence and distribution of endobacteria in nature.

In this work we set out to assess the *entire* diversity of endobacteria associated with spores of AMF isolated directly from the field. We collected rhizosphere soil from two sites: a natural dune ecosystem located on the east coast of Ireland and a nearby agricultural grassland. From these soil samples, we extracted hundreds of AMF spores, and surface-sterilized them. Each spore was then individually genotyped and surveyed for the presence of *Ca*Mg, *Ca*Gg, and any other endobacteria using PCR with specific as well as universal bacterial primers.

Assessment of endobacterial prevalence revealed that the two known endobacteria differed dramatically in their distribution: GaGg were extremely rare, being detected in only 1% of the spores, whereas CaMg were very common, being found in 80% of spores. This distribution pattern did not differ between dune and agricultural grassland environments and was almost identical to what was found in the only other study of AMF endobacteria in nature, located thousands of miles away in Cape Cod, Massachusetts, United States (Lastovetsky et al., 2018).

Therefore, this low/high (CaGg/CaMg) endobacteria distribution pattern in nature is likely meaningful and perhaps related to their function in AMF; however, without direct experimental evidence it is hard to speculate as to what it means just yet.

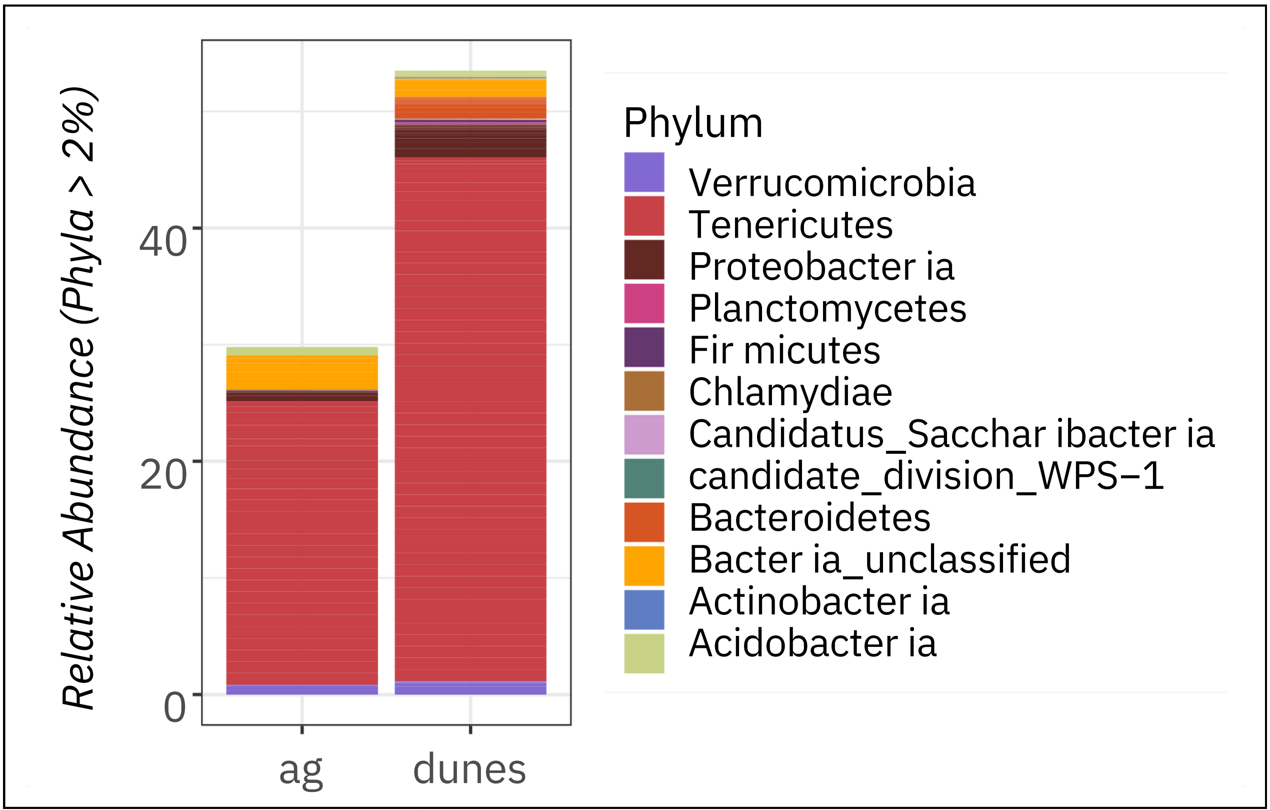

Figure 1. Relative Abundance of endobacteria at Phylum level in AMF spores. The bars are of uneven heights due to less spores recovered from the agricultural grassland site. CaMg belong to the Tenericutes phylum.

We then took the 84 spores which harboured endobacteria according to our PCR-based screen and subjected them to total bacterial community profiling using amplicon sequencing of the 16S rRNA gene on the Illumina MiSeq platform. The data that we got back was quite unexpected. We found that CaMg and CaGg were by far not the only endosymbionts in AMF spores, with bacteria belonging to 10 other Phyla detected in our data set (Fig. 1). Remarkably, individual AMF spores could be home to as many as 277 different bacterial "species" (i.e. operational taxonomic units, or OTUs), which were not CaGg or CaMg, and were previously unknown to have an endofungal lifestyle. These bacteria instead were mostly known as free-living in terrestrial and aquatic environments. What are they doing in AMF spores?

According to recent work by Venkatesh et al. (2022), *Aspergillus flavus* chlamydospores (environmentally resilient survival structures formed by some fungi) could be invaded by free-living bacteria. In these chlamydospores, bacteria had higher chances of survival under stressful conditions such as low temperature and low nutrient availability. These bacteria were termed "hitchhikers", and it was proposed that being able to utilize chlamydospores for housing might be an intriguing new survival strategy for certain bacteria under the stress of winter cold and in times of nutrient scarcity (Arnold, 2022). This led us to hypothesize that perhaps the diverse bacterial communities that we found inside AMF spores were in fact bacterial hitchhikers. After all, AMF spores are packed full of nutritious glycogen and lipids and their thick walls could protect from unfavorable environmental conditions.

Despite this plethora of bacterial hitchhikers, CaMg endobacteria were still the most frequently found across AMF and also had the highest relative abundance inside individual spores (Fig. 1).

Now, CaMg are unusual in that their populations are typically diverse even within the same AMF individual, with as many as 3 OTUs previously detected within a single spore (Toomer et al., 2015; Lastovetsky et al., 2018). Using our methods, we found that individual AMF spores can host as many as 50 (!) CaMg OTUs, with the average of 22 OTUs found per spore.

Such high intra-host diversity of endosymbionts is considered to be a hallmark of parasites, as diversity is expected to increase competition dynamics among symbionts at a cost to the host (Frank, 1996). In fact, this high intra-host diversity of CaMg populations is one of the reasons they were hypothesized to be parasites in the first place (Toomer et al., 2015). But CaMg are extremely common in field AMF! (see above). Therefore, it is very unlikely that they would be maintained to such high levels in natural AMF populations if they do not provide any benefit to their host, as it is expected for selection to remove such parasites from host populations. We therefore propose that CaMg might actually act as conditional mutualists of AMF. In a conditional mutualism, symbionts improve host fitness under specific conditions, and in the realm of bacterial-fungal interactions there is evidence that bacterial endosymbionts can provide a conditional benefit to their fungal host in the presence of predators. For example, Mycetohabitans sp. endobacteria of Rhizopus microsporus produce a toxin that protects the fungus from soil micropredators (Richter et al., 2022). Analogously, Mycoavidus endobacteria protect their Mortierella fungal host from predation by nematodes (Büttner et al., 2021). These endobacteria are therefore acting as defensive mutualists of fungi.

In our paper, we hypothesize that CaMg might analogously act as defensive mutualists of AMF. This hypothesis is based on our observation that AMF spores harbouring higher diversity of CaMg populations harboured less diverse population of all other (potentially hitchhiker) endobacteria (Fig. 2). In this way, by maintaining high population

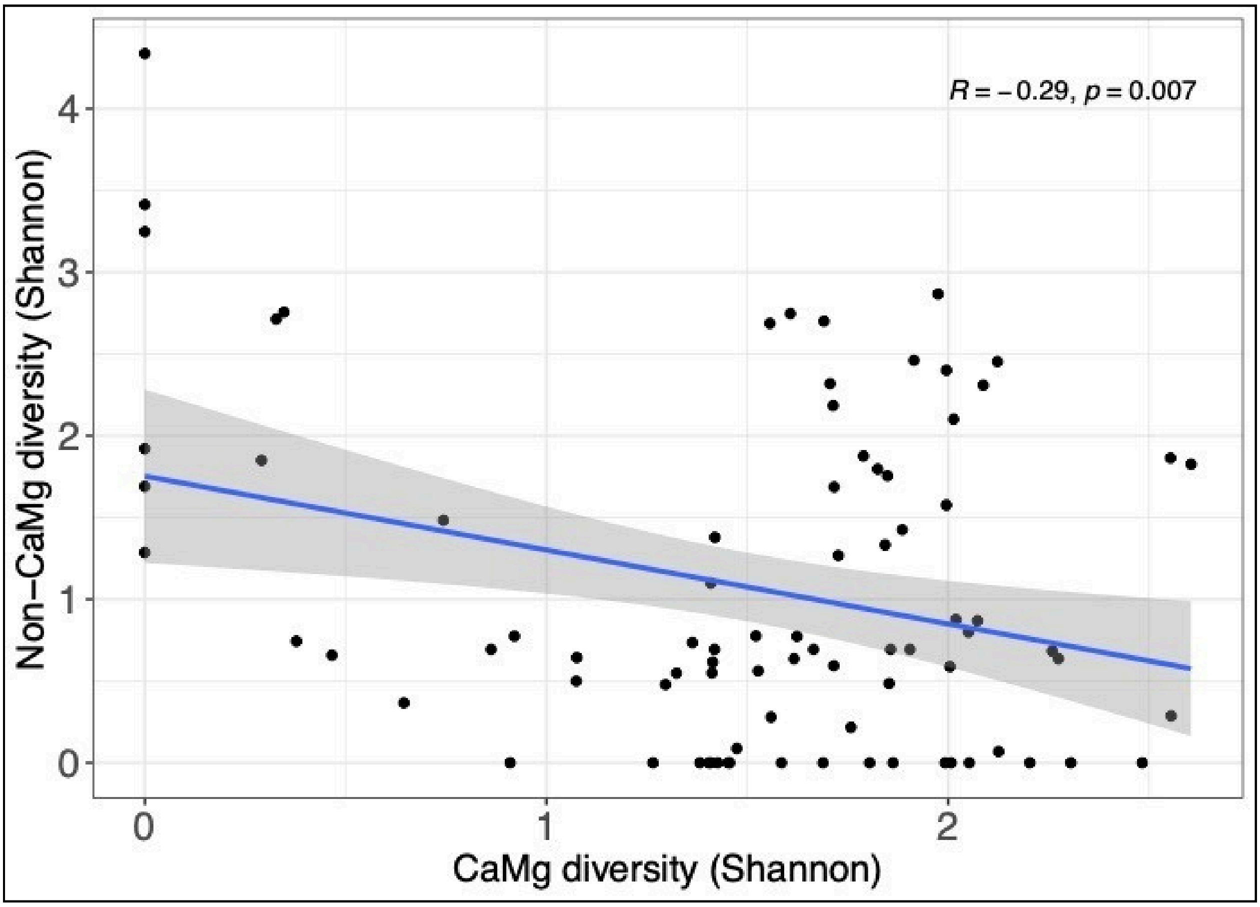

Figure 2. Significant correlation between CaMg and non-CaMg Shannon diversity. Pearson correlation coefficient and P value were calculated by the stat_cor function in R, grey area represents 95% confidence interval.

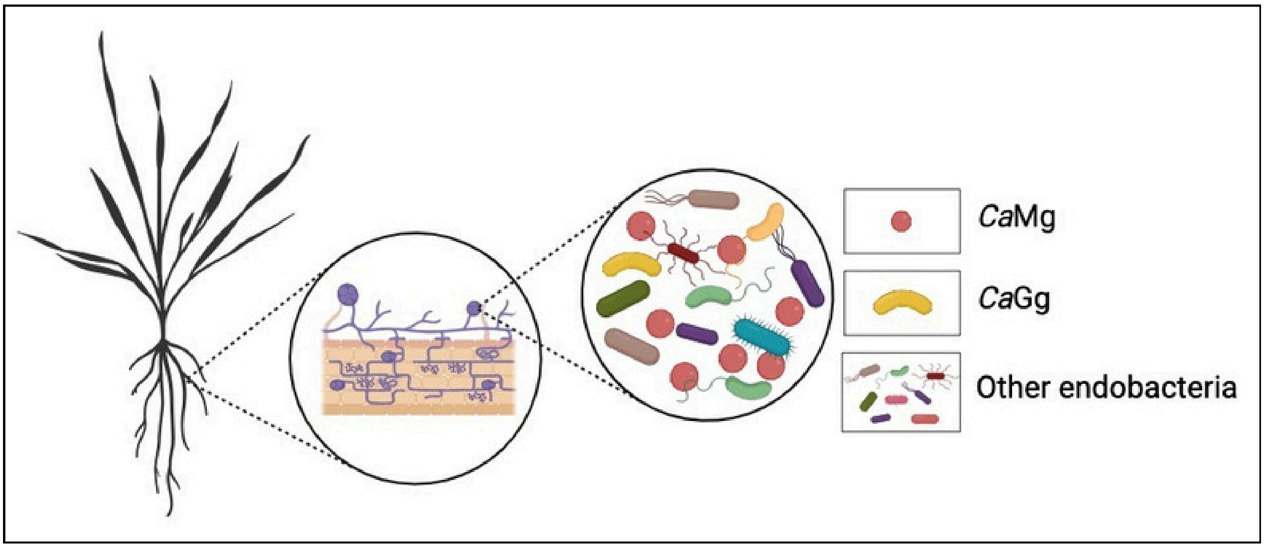

Figure 3. Schematic representation of the diversity of endobacteria in spores of arbuscular mycorrhizal fungi. Created with Biorender.com.

diversity within AMF, CaMg are likely more effective at outcompeting all other endobacteria, which might otherwise be detrimental to AMF. Of course, this hypothesis requires experimental testing.

Collectively, our study emphasizes a previously unknown level of complexity of endobacteria associated with AMF and highlights the need to understand their function in the biology of these widespread symbionts of plants.

So, to answer the question posed at the beginning: How many different bacteria can live inside a fungus? – it turns out that the answer is: many more than we thought possible (Fig.3). But what are they all doing in there? We don't know yet, but I think it's time to find out.

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Efforts towards a more collaborative and anti-colonial research, co-constructing mycorrhizal research in the Atacama Desert

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In December 2023 we set out on a joint expedition between the Society for the Protection of Underground Networks (SPUN) and the Environment Unit of the Council of Atacameños Peoples. SPUN is an international nonprofit scientific organization dedicated to the study and conservation of mycorrhizal fungi. The Indigenous Association Council of Atacama Peoples (CPA) is an organization of traditional authorities and leaders from the 18 communities of the “Atacama La Grande” territory in the Salar de Atacama basin (in northern Chile). Currently, the CPA has an Environment Unit which is constituted of environmental representatives from the same communities and professionals, mostly from the Lickanantay community, who ensure the protection of the water and ecosystems of the Lickanantay territory in the Salar de Atacama basin and in the highlands of the Andes Mountain Range. For more than 30 years, this Indigenous organization has been the entity that has ensured the defense and interests of the territory, and particularly since 2015 the work expanded to fulfill environmental compromises to support the communities that are part of it.

This expedition was neither the beginning nor the end of the joint work: it was the meeting space to

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better understand the diversity of mycorrhizal fungi in the Lickanantay territory, in what today is deemed as "the Antofagasta Region of Chile". This territory is part of the Lickanantay peoples ancient lands, way before Chile existed as an State. For this purpose, a transdisciplinary team was brought together to share expert knowledge from the Lickanantay and Western scientific perspectives at the anthropological, mythological, ecological, and local knowledge levels.

The collaboration began in March 2023 after defining the common interest in exploring mycorrhizal fungal biodiversity of the middle zone of the Atacama Desert, about which very little or practically nothing is known in terms of the biodiversity and functioning of mycorrhizal fungi (Marín et al. 2022). The information gap and the need to better grasp the role of this group of fungi in these ecosystems gave rise to a project that involved several phases. Regarding agricultural systems, the CPA's Environment Unit was interested in better understanding the effect of traditional flood irrigation on the soil when compared to newer technical irrigation methods. As drought becomes an increasingly menacing problem, particularly in this region, new irrigation technologies can serve to maintain higher levels of yield production. This is particularly important since arbuscular mycorrhizal fungi have been shown to increase grain yield at a global scale (Zhang et al. 2019) and drought tolerance in crops (Mathimaran et al. 2017).

This collaboration is part of a series of efforts to move beyond dominant ways of doing extractive and colonial science and instead co-construct science. As Whitt (2009), Kimmerer, (2020), Trisos et al. (2021), Ferdinand and Smith (2022), and Hirschfeld et al. (2023), have already highlighted,

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the scientific practice of ecology is embedded in deeply colonial roots. This practice is particularly strong in global soil research, “where scientists from wealthier nations collect soil samples from less-developed countries, take the samples back to their country for analysis and publish the results with little involvement of local researchers” (Minasny et al. 2020). Thus, it is urgent to decolonize what we consider “expert knowledge”, the very access to science –today highly concentrated in white male scientists from the Global North (Crisos et al., 2021)– and the motivations and methods to carry out research and scientific expeditions.

To begin the dialogue, the first phase consisted of workshops where we explored how the biological sciences understand soil, its components, and its relationship, effects, and interactions with the Fungi kingdom. In turn, these spaces allowed the exchange of ancestral knowledge about these concepts and Atacama Desert ecosystems, where the need to challenge the dominant references of what constitutes “poor” ecosystems and soils, and the quantitative bias of approaches to “biodiversity” became evident. For the people of the desert, these are not “poor” ecosystems, but rather the expression of sacredness and abundance, where they have lived and thrived for thousands of years. As such, it was vital to re-frame Western science terms so that they could adapt to understanding each territory in its context, and thus encourage respectful dialogue between different knowledge systems.

In this way, the expedition carried out had several different characteristics associated with the recognition of what it means to carry out scientific work in ancestral indigenous territories. We consider it essential to connect with the Indigenous organizations of the territories and follow their protocols. The Environment Unit of the CPA works with several protocols according to what each community has defined for entering their specific territories, along with the ways in which research should be carried out and information should be safeguarded. Thus, for all sampling points, there was previous work done by the Environment Unit of the CPA; this previous work allowed us to contextualize the communities about the research to be carried out and the samples and protocols to implement (that is: what, why, and how to research before sampling in their territories). Similarly, we worked together to define when the sampling could be carried out, and who would attend from the Environment Unit of the CPA, SPUN, and members of each community.

The sampling sites were defined primarily by the Environment Unit of the CPA and consulted by the environmental representatives of the communities involved, given the work that they already carry out in the territory and the existing sampling points that the Unit constantly monitors, regarding water and biodiversity, among others. This not only points out local places of interest but also

Photos of the SPUN expedition to the Atacama by Mateo Barrenengoa & Diego Fuentes - read more about it here.

provides consistent information with a greater temporal scope. When carrying out the expedition, this not only allowed us to interact on the basis of respect for the ancestral practices and their relationship with the territory, but also allowed us to have local experts who not only knew the species of fauna and flora that were present in each site, but also had knowledge regarding the social, climatic, and ecological changes and challenges that had affected those areas over time (Soto Hernández, 2023).

Considering that for the Lickanantay – Atacameños, the relationship they have with their environment is important, respecting Puri (water), the tutelary hills, and the Patta Hoiri (Mother Earth) was key in the sampling process itself. As such, we followed protocols to better relate with the non-human beings, asking permission from Mother Earth to take samples and therefore, ensuring the health of the human group and the non-human beings in each site, alongside the effectiveness of our expedition. Part of the protocols involved the accompaniment of local community members of the different places where the samples were taken, with the involvement of those who know their territory best, and with the commitment to return the information to the communities.

At the moment, we are processing the samples. So far, we can say that 35 out the 41 soil samples collected showed high DNA concentration – something very good and surprising for the driest place on Earth! Subsequently, the scientific analysis work will give way to meetings with the Environment Unit of the CPA to define what results are of interest to them and how to communicate them in ways that are accessible and relevant to the CPA communities. Thus, this experience constitutes a blueprint and an invitation to the scientific community to retrace the colonial practices of the scientific disciplines and build new ways to engage with the local communities that have ancestrally inhabited territories of scientific interest. It is possible that, in this new ecology of knowledge, we will learn much more about the ecology that we seek to expand.

ACKNOWLEDGEMENTS
We are very grateful for the financial support received from SPUN and the CPA to carry out this expedition and research. We are also sincerely thankful to the communities of Socaire, Toconao, Cucuter, Solor, Machuca and Catarpe for their support during the expedition, the knowledge shared, and commitment to the sampling process: nothing would have been possible without you.
Many and special thanks to documentalists Mateo Barrenengoa and Diego Fuentes for a wonderful documentation of this expedition.

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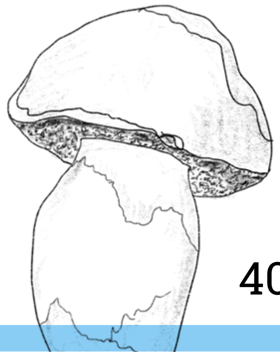


Global epistasis & emergence of function in microbial consortia - Juan Díaz-Colunga

César Marín (Full Professor, Universidad Santo Tomás, Chile) interviews **Juan Díaz-Colunga, Ramón y Cajal** Researcher in Spain, about how simple statistical models predict a species' effect on a community-level function. Such global ecological epistasis mirrors patterns reported in genetics.

WATCH NOW

Interview: https://southmycorrhizas.org/reading/july-2024/ - **[Spanish subtitles]**
Study: Diaz-Colunga J, Skwara A, Vila JC, Bajic D, Sanchez A. 2024. Global epistasis and the emergence of function in microbial consortia. Cell 187: 3108-3119. https://doi.org/10.1016/j.cell.2024.04.016

How hurricanes affect mycorrhizas - Julieta Alvarez Manjarrez

Prof. Maria Alice Neves (Federal University of Santa Catarina, Brazil) interviews **Prof. Julieta Alvarez Manjarrez** (UNAM, México) about how a hurricane affected mycorrhizal co-occurence networks in Mexico after one and two years.

WATCH NOW

Interview: https://southmycorrhizas.org/reading/august-2024/ - **[English subtitles]**
Study: Alvarez-Manjarrez J, Bahram M, Polme S, Garibay-Orijel R. 2024. Impact of hurricane disturbance on mycorrhizal co-occurrence networks: Resilience and community dynamics in the Neotropics. Fungal Ecology 70: 101354. https://doi.org/10.1016/j.funeco.2024.101354

What determines the transfer of carbon from plants to mycorrhizal fungi? - Rebecca A. Bunn and Ana Corrêa

Prof. César Marín (Universidad Santo Tomás, Chile) and Prof. Pedro M. Antunes (Algoma University, Canada), interview **Prof. Rebecca A. Bunn** (Western Washington University, United States) **and Ana Corrêa** (Universidade de Lisboa, Portugal) about their (and co-authors) recent Tansely review about contrasting mechanisms explaining the transfer of carbon from plants to mycorrhizal fungi: ‘Surplus C’ hypotheses and Biological Market Models.

WATCH NOW

Interview: https://southmycorrhizas.org/reading/october-2024/
Study: Bunn RA, Corrêa A, Joshi J, et al. 2024. What determines transfer of carbon from plants to mycorrhizal fungi?. New Phytologist 244: 1199-1215. https://doi.org/10.1111/nph.20145

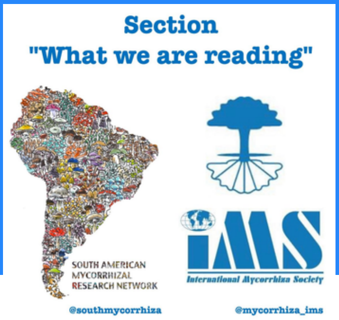
Interested in being interviewed or know someone who would be? We would love to hear from you!

Contact Prof. César Marín for more information

SUBSCRIBE

Thanks for watching!

Subtitles and Spanish/English translations by Melissa Davie

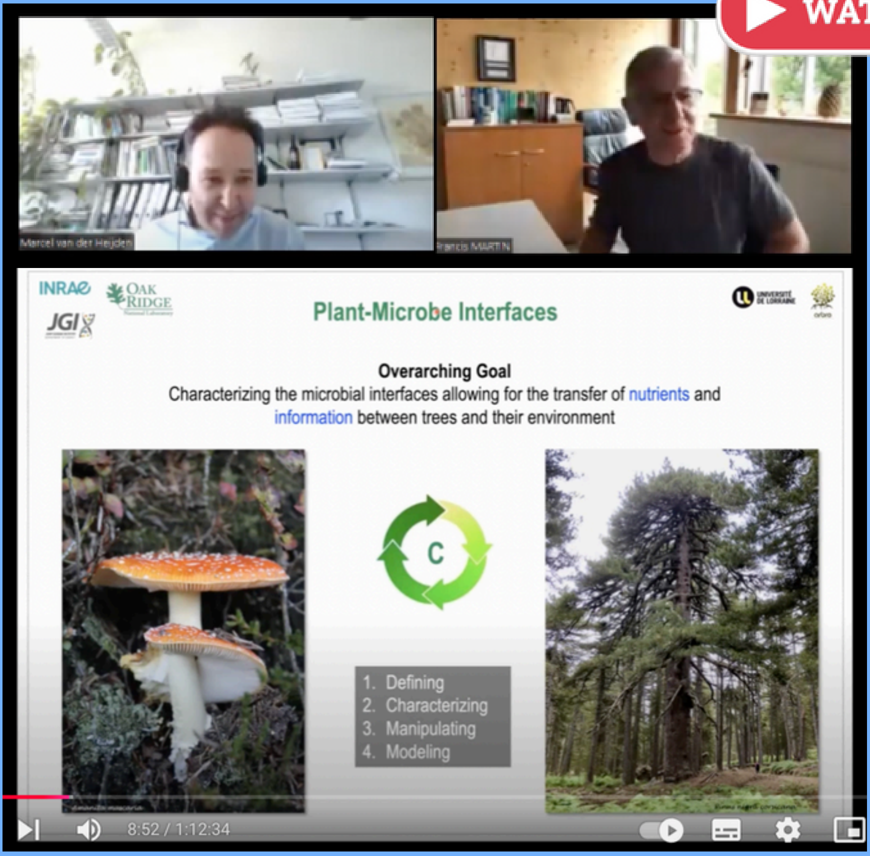


A welcome to the IMS Virtual Seminar Series

From molecular ecology to environmental genomics - Francis Martin

The IMS Seminar series consists of talks by mycorrhizal researchers from around the world at all career stages. The first seminar was presented by Dr. Francis Martin, Past President of the IMS and awardee of as Eminent Mycorrhizal Researcher at ICOM11 (2022).

WATCH NOW

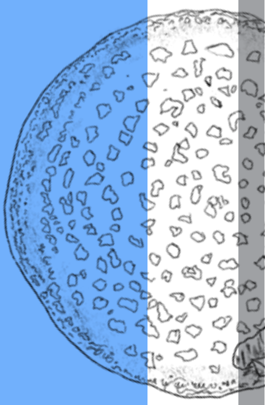


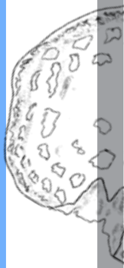
Plant-Microbe Interfaces

Overarching Goal
Characterizing the microbial interfaces allowing for the transfer of nutrients and information between trees and their environment

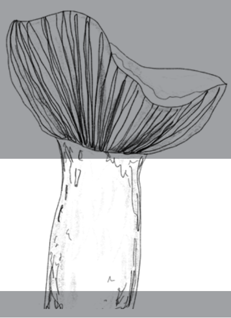
C

1. Defining
2. Characterizing
3. Manipulating
4. Modeling





Stay up to date with our Seminar Series by following our **YouTube channel** and **social media accounts**!



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Updated LSU database for arbuscular mycorrhizal fungi (AMF)

Delavaux et al. (2024) present their updated database and pipeline with an expanded backbone tree to include four newly described AMF genera and changes to improve ease and consistency of implementation of the bioinformatic pipeline.

Study: Delavaux CS, Ramos RJ, Stürmer SL, Bever JD. 2024. An updated LSU database and pipeline for environmental DNA identification of arbuscular mycorrhizal fungi. Mycorrhiza 34:369-373. https://doi.org/10.1007/s00572-024-01159-3

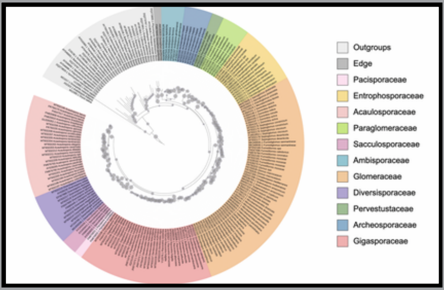
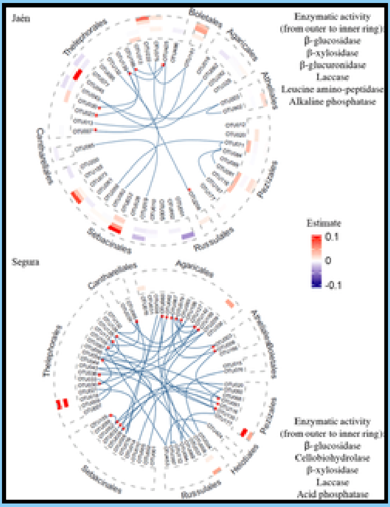


Image from study:
An updated AMF LSU backbone tree.

Relating community network complexity with multi-enzymatic activity



Prieto-Rubio et al. (2024) relate different topological metrics of the networks formed by ectomycorrhizal fungal communities of two host Mediterranean species, with the multi-enzymatic activity of those forest soils. This constitutes a pioneer way to relate emergent properties of microbial communities with ecosystem functions.

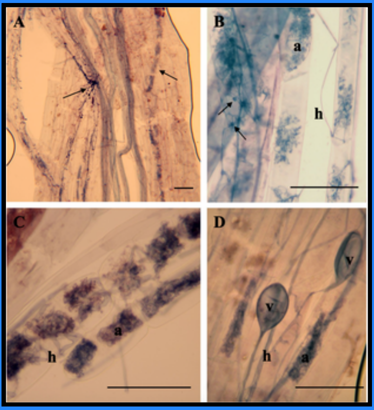
Study: Prieto-Rubio J, Garrido JL, Alcántara JM, Azcón-Aguilar C, Rincón A, López-García Á. 2024. Ectomycorrhizal fungal network complexity determines soil multi-enzymatic activity. Soil 10:425-439. https://doi.org/10.5194/egusphere-2024-119

Image from study: Co-occurence ECM fungal networks and contributions of fungal OTU's to soil extracellular enzymatic activity.

New primers for Mucoromycotinian AMF

Seeliger et al. (2024) modified 'AM' 18S rRNA primers which co-amplify Glomeromycotina-AMF and Mucoromycotina-AMF to reduce bias against Mucoromycotina, and compared against a new fine root endophyte primer set which selectively amplifies Mucoromycotina.

Study: Seeliger M, Hilton S, Muscatt G, et al. 2024. New fungal primers reveal the diversity of Mucoromycotinian arbuscular mycorrhizal fungi and their response to nitrogen application. Environ Microbiome 19:71. https://doi.org/10.1186/s40793-024-00617-x



Microscopy images from study.

ishpssb international society for the history, philosophy and social studies of biology

Biennial meeting of the International Society for the History, Philosophy and Social Studies of Biology - ISHPSSB 2025

Place: Porto, Portugal
Date: 20-25 July, 2025
Organizers: University of Porto
Website: https://ishpssb2025.icbas.up.pt/

4° Congreso Latinoamericano de Ecología Microbiana #ISMELAT2025

Place: Mérida, México
Date: 4-9 August, 2025
Organizers: ISME Latinoamérica & Universidad Nacional Autónoma de México
Website: https://ismelat2025.org/

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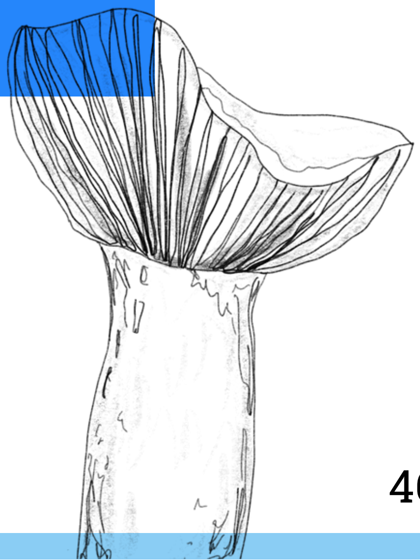

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