



International Mycorrhiza Society

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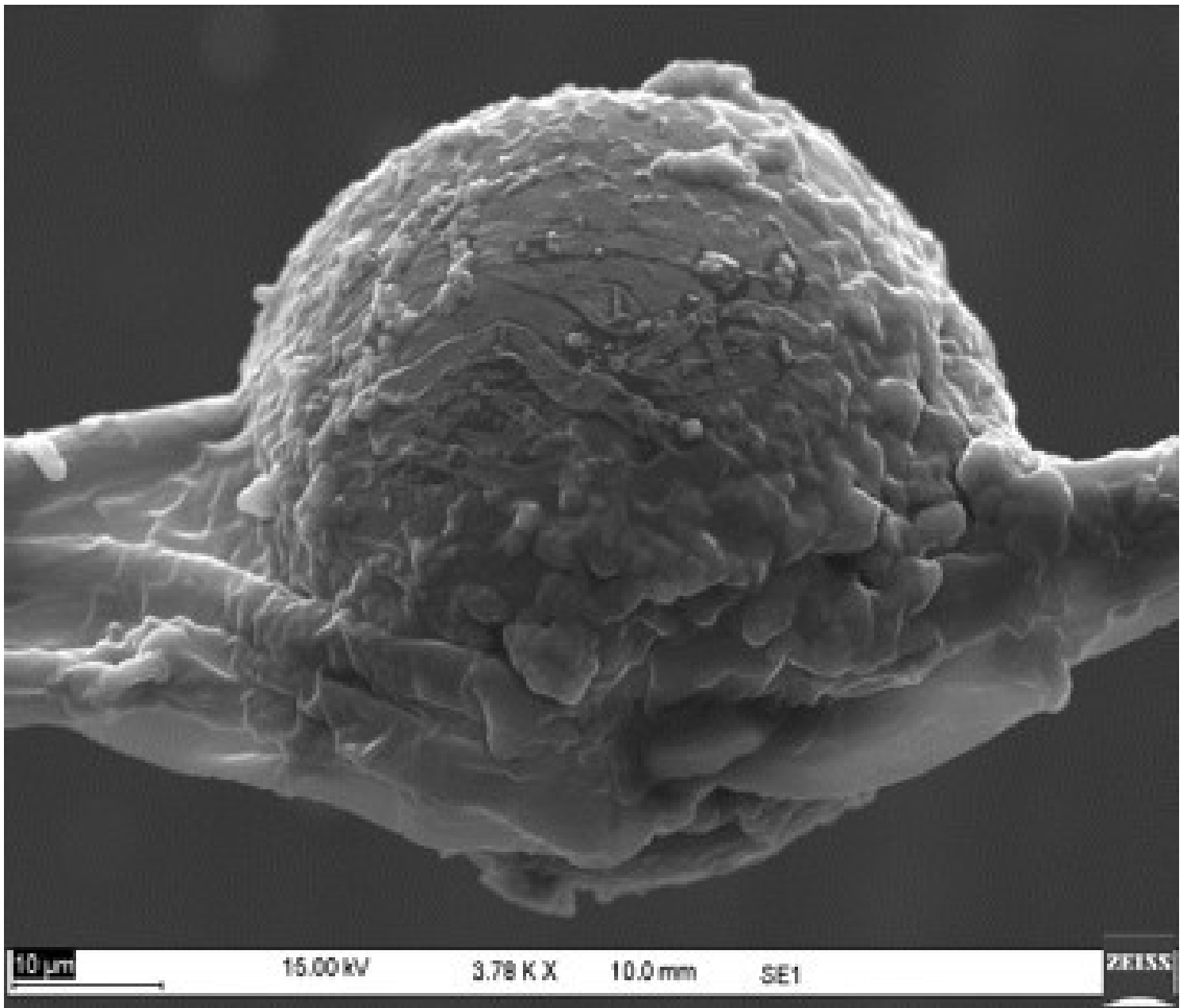
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IMS Newsletter

Indexed in Latindex

The International Mycorrhiza Society quarterly e-newsletter



Rhizophagus irregularis, by Aditi Pandit

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Editorial: ICOM12

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The 12th International Conference on Mycorrhiza (ICOM12) will take place in Manchester, United Kingdom, 4-9 August 2024. After ICOM12, the current Vice President of the International Mycorrhiza Society (IMS), Justine Karst will become the new President of the IMS and Marcel van der Heijden will move to Past President. As such, this is the last Newsletter that Marcel contributes as President of the IMS. I (César Marín) am very, very thankful to Marcel for the idea of creating the IMS Newsletter back in 2019, probably after talking at the Wines of the World night during ICOM10 in Mérida, México. It has been a transformative experience, which I truly enjoy. Although it takes some time and dedication -several dozen hours of work every four months, in addition to constantly check the mycorrhizal literature and constantly coordinate/email editors, authors, interviewees- for me it has been a wonderful experience. It keeps me very much up to date with the mycorrhizal literature, something very good when writing my own papers and grant applications, and when reviewing others. I also appreciate a lot the messages of encouragement of the mycorrhizal researcher community, the enthusiasm, and the quality of the material published. I am very happy as Editor-in-Chief of the Newsletter, and currently we are working on improving it (see details below). It was Marcel and the IMS Board who had the enlighten idea of having the Newsletter (starting in 2020) and then, to have the elected position

(2022) of IMS Communications Director (Patricia Silva-Flores). Please find on page 9 an interview with Marcel about his time presiding over the IMS, his views on science, science leadership, mycorrhizal applications, on how to lead scientists and students, and overall on his illustrious career – which I think the whole mycorrhizal research community is thankful for. Nevertheless, as Past President, Marcel will keep being deeply involved at the IMS.

It has been a great pleasure to act as president of IMS (Marcel G.A. van der Heijden). Mycorrhizal research fascinates me already for over 30 years and every year appealing new discoveries are being made – the speed of discovery is not slowing down! Also, mycorrhizal researchers and the research community as a whole is very cooperative (not a surprise when studying symbiosis!) and this is highly motivating. I have still many years to come so I very much look forward to see mycorrhizal research and the IMS develop. At this place, I would thank my colleagues, students, many scientists who contributed to mycorrhizal research, those who helped someone else moving on, those who inspired me, advised me, or made me laugh, and to the IMS!

ICOM12 News.

Early Bird Registration is closed, but Late Registration still possible

Please visit the ICOM12 information for full information: <https://icom12.org/>

ICOM12 is being organized by Prof. David

Johnson and his team. The ICOM12 Plenary Speakers are: Bala Chaudhary (Dartmouth College, United States), Giles Oldroyd (University of Cambridge, United Kingdom), Lingli Liu (Institute of Botany, Chinese Academy of Sciences, China), and Uta Paszkowski (University of Cambridge, United Kingdom).

Please find the full list of speakers by theme, including plenary talks, keynote speakers, and rising stars here: <https://icom12.org/invited-speakers/>

The complete ICOM12 program can be found here: <https://icom12.org/scientific-programme/>

ICOM12 includes many topics: Mycorrhizas as Drivers of Interaction Networks, Managing Mycorrhizas for Sustainability & Food Security, Regulation and Transport in Mycorrhizal Networks, Functional Consequences of Mycorrhizal Diversity, Ecosystem Functioning, Omics and Ecology, Environmental Change, Physiology, Evolution & Taxonomy, and Management & Applications.

ICOM12 also has a total of seven workshops on a myriad of topics, including: “Common mycorrhizal networks- Who’s the boss?” (Chairs: Joanna Weremijewicz, United States and Nils Henriksson, Sweden); “Advances in Macroecology and Biogeography of Mycorrhizal Fungi” (Chairs: Adriana Corrales, Colombia and Clara Qin, United States); “Current and Future Approaches towards the Molecular Ecology of Arbuscular Mycorrhizal Fungi” (Chairs: Cameron Egan, United States & Bethan Manley, United Kingdom); “Refining Arbuscular Mycorrhizal Fungal Traits for Enhanced Ecological Predictability” (Chairs: Pedro Madeira Antunes, Canada and Sidney Stürmer, Brazil); In-situ studies of mycorrhizal function: Is our toolbox expanding? (Chairs: Ylva Lekberg, United States & Björn Lindahl, Sweden); “The ‘other’ endomycorrhizas: ecology, diversity, molecular biology, and methods for study” (Chairs: Alan Wanke, United

Kingdom; Camille S. Delavaux, Switzerland; Laura van Galen, Switzerland; and Silvia Pressel, United Kingdom); and “Natural selection in arbuscular mycorrhizal symbioses” (Chairs: César Marín, Chile and Nancy Collins Johnson, United States). The full details of the seven workshops are available here:

<https://icom12.org/workshop-details/>

Call for award nominations to be given during ICOM12.

The International Mycorrhiza Society offers four prestigious awards at the next meeting in Manchester, United Kingdom. These are the: 1) Best Student Award, 2) the Early Career Award, 3) the Mid-Career Award, and 4) the Eminent Researcher Award. If you know a person which you feel deserves an award or if you like to nominate yourself because you feel you made a ground breaking discover, please check out the terms of reference here: <https://mycorrhizas.org/icom/icom-12/>

The deadline for nomination is 30 June 2024.

IMS News.

Two elected board positions to be filled:

After four years of service, Ian Dickie will leave the Board of Directors – we are very thankful to Ian for his great contributions to our Society. As such, at ICOM12 two positions need to be filled:

- New Vice President of the IMS (it can be someone from the current Board or from outside).

- New member of the Board of Directors.

If you are interested in filling/apply to any of these positions, please send your picture and a short bio-sketch to Justine Karst, IMS Vice President (karst@ualberta.ca), until 30 June of 2024.

The IMS members can vote for the Board of Directors and the Vice President electronically until the 7th of August The New Vice President and the new Board Members will be announced on the last day of ICOM12 in Manchester, United Kingdom.

IMS Seminars.

We are proud to announce that IMS has initiated a new online seminar series. The first IMS Seminar was presented by IMS Past President and Eminent Mycorrhiza Researcher Awardee, Francis M. Martin, Research Director Emeritus at the National Research Institute for Agriculture, Food and Environment (INRAE) in Nancy, France. Francis gave a beautiful overview on the “evolution” of research on mycorrhizas, especially environmental genomics. The seminar, entitled “Reflections on a Journey through Mycorrhizal Research: Transitioning from Molecular Ecology to Environmental Genomics” is available at the newly created YouTube channel of the IMS ([@mycorrhiza_ims](https://www.youtube.com/@mycorrhiza_ims)).

Link:

https://youtu.be/6_XwWqu958U?si=j_MYsosljg74Nw4k

Special thanks to Patricia Silva-Flores (IMS Communications Director) and Ana I. Bermúdez-Contreras (PhD student at the Karst Lab, University of Alberta, Canada) for organizing the IMS Seminars. The next IMS Seminars will be given by Matthias Rillig and Vasilis Kokkoris on June 24, 2024, at 15:00 CET. Please follow the IMS social media (Twitter/Instagram: [@mycorrhiza_ims](https://www.instagram.com/mycorrhiza_ims)) for further information on the IMS Seminars, which will occur monthly (with exceptions for holiday and ICOM12 months). Check on page 27 for further information.

Call for ICOM14 proposals in 2028.

If you are interested in organizing ICOM14 in 2028, please write to Katarina Zachariasova (zachariasova@associationhouse.cz), IMS President Marcel van der Heijden (marcel.vanderheijden@agroscope.admin.ch), and IMS Vice-President Justine Karst (karst@ualberta.ca), so your proposal can be presented during ICOM12 in Manchester, United Kingdom. Please do so until 30 June of 2024. For the terms of reference, see the following link: <https://mycorrhizas.org/wp-content/uploads/2024/02/ICOM14-bid.pdf>. If more than two proposals are submitted, the IMS Board will select the two best

ones and these two proposals have the opportunity to be presented at the IMS members meeting during ICOM12 (9 August, 2024; 13:30 to 15:30). The IMS members can vote for the preferred location. Remember that the 13th International Conference on Mycorrhiza (ICOM13), will take place in Cairns, Australia, in 2026.

IMS Newsletter news.

Articles/interviews welcomed

If you want to highlight your recent mycorrhizal research/publications formally or informally, to give your expert opinion on any mycorrhizal topic of interest, or to present the 'behind-the-scenes' stories often not shown in publications, please reach out to us. There are two ways you can do this. First, you can write a short article (800-1200 words), which our Editorial Team will review. Check all the articles over the last four years here: <https://southmycorrhizas.org/ims-newsletter/>. Second, we can program a YouTube interview through the South American Mycorrhizal Research Network channel (see our interviews here: <https://www.youtube.com/@whatwearereading6719/videos>). Please get in touch with IMS Newsletter Editor-in-Chief César Marín (cmarind@santotomas.cl) if interested!

We are happy to announce two new editorial board members of the IMS Newsletter.

As our Newsletter keeps growing, so does the amount of work required to handle it. As such, we welcome new members to our Editorial Board:

- **Managing Editor:** Dr. Rosario Iacono, Postdoctoral researcher at the Helmholtz Centre for Environmental Research (UFZ), Germany.

- **Editorial Assistant:** MPhil Melissa Davie.

Both Rosario and Melissa will help the Editor-in-Chief regarding the IMS Newsletter presentation, graphic design, social media and online presence, among others. Welcome!



Rosario Iacono



Melissa Davie

In this issue...

The Top 10 mycorrhizal research papers of the last four months (papers published between January and April, 2024) include an article by Adam Frew and co-authors (Rank 1). This *ISME Journal* article presents what the authors deem as “the defence-directed hypothesis” for explaining arbuscular mycorrhizal (AM) fungi assembly. This hypothesis “proposes that stressed plants selectively recruit AM fungi from the local pool of taxa with traits that enhance their defence mechanisms against herbivores and/or pathogens” (Frew *et al.* 2024). Please also find a YouTube interview to Adam by PhD student Luke Florence. The second-best paper was by Edith C. Hammer and co-authors (*Fungal Ecology*), who developed microengineered soil chips to assess hyphal exploration strategies and habitat modification by an AM fungi. The third rank was a *Nature Communications* paper by C. A. Bell and co-authors, who show that host potato plants selectively allocate carbon to tissues interacting with AM fungi rather than to tissues interacting with phytophagous parasites.

This 14th IMS Newsletter issue includes one written interview (with the departing IMS President, Marcel G.A. van der Heijden), two short articles, and four YouTube interviews. A first short article, by Francis M. Martin and co-authors present the aims, methods, challenges, and preliminary results of their project entitled “*Metatranscriptomics of the Forest Soil Ecosystems*”, a project funded

by the United States Department of Energy – Joint Genome Institute (JGI). Among the most interesting results, they have found that gene expression encoding enzymes responsible for the degradation of plant cell walls is higher in saprotrophic fungi than in ectomycorrhizal and pathogenic fungi. A second short article, by Bruno Tomio Goto and co-authors elaborates in great detail on the history and state of the art of AM fungi (Phylum Glomeromycota) taxonomy. Although these fungi were first described by the mid XIX century, it was only about 50 years ago that the taxonomic description of new species really took off. Despite this, the authors claim -and we agree- that very few new AM fungi species are described every year, because, sadly, there are still very few AM fungal taxonomists. As an example of this issue, the five authors of this article have described 100 AMF species, about 27% of the known species of the phylum.

In addition, four YouTube interviews occurred, which include several topics, such as AM fungi community assembly and plant defence (Adam Frew; above-mentioned), AMF endobacteria (Olga A. Lastovetsky), a phylogenetic analysis of plant adaptation to drought given by mycorrhizas (Marco Cosme), and the relationships between mycorrhizal fungi and decomposition (Eduardo M. Choreño-Parra). Olga A. Lastovetsky (University College Dublin, Ireland) was interviewed by César Marín (Universidad Santo Tomás, Chile) on her remarkable *New Phytologist* article where the endobacteria living in 84 AMF spores, were sequencing, obtaining in average 184 bacterial Operational Taxonomic Units (OTUs) per spore – one spore had 227 OTUs! Jason D. Hoeksema (University of Mississippi, United States), interviewed Marco Cosme (Université de Picardie Jules Verne, France), about his recent *Communications Biology* paper entitled: “Mycorrhizas drive the evolution of plant adaptation to drought”. Finally, Eduardo M. Choreño-Parra (PhD Student, University of California, Irvine, United

States) was interviewed by Nahuel Policelli (CONICET, Argentina) about his recent *New Phytologist* article entitled: "Mycorrhizal fungi modify decomposition: a meta-analysis". As a novelty, and in an effort to promote language inclusivity in mycorrhizal research, this interview was conducted in Spanish and is subtitled in English. We thank Nahuel for taking the time doing the inclusive task of editing and adding English subtitles! Please also find our new IMS Newsletter section: IMS Seminars, on page 27. Please also find on page 32, a call for collaboration by Lena Neuenkamp and Erica McGale, based on their *Plants, People, Planet* opinion article (<https://doi.org/10.1002/ppp3.10390>). As always, please find our Tools and Events sections at the end of our Newsletter.

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<https://doi.org/10.1093/ismejo/wrae007>



Top 10 papers on mycorrhizal research*

- 1.** Frew A, Weinberger N, Powell JR, Watts-Williams SJ, Aguilar-Trigueros CA. 2024. Community assembly of root-colonizing arbuscular mycorrhizal fungi: beyond carbon and into defence? *ISME J* 18: wrae007. <https://doi.org/10.1093/ismejo/wrae007>
- 2.** Hammer EC, Arellano-Caicedo C, Mafla-Endara PM, *et al.* 2024. Hyphal exploration strategies and habitat modification of an arbuscular mycorrhizal fungus in microengineered soil chips. *Fungal Ecol* 67: 101302. <https://doi.org/10.1016/j.funeco.2023.101302>
- 3.** Bell CA, Magkourilou E, Ault JR, Urwin PE, Field KJ. 2024. Phytophagy impacts the quality and quantity of plant carbon resources acquired by mutualistic arbuscular mycorrhizal fungi. *Nat Commun* 15: 801. <https://doi.org/10.1038/s41467-024-45026-3>
- 4.** Netherway T, Bengtsson J, Buegger F, *et al.* 2024. Pervasive associations between dark septate endophytic fungi with tree root and soil microbiomes across Europe. *Nat Commun* 15: 159. <https://doi.org/10.1038/s41467-023-44172-4>
- 5.** Sato H. 2024. The evolution of ectomycorrhizal symbiosis in the Late Cretaceous is a key driver of explosive diversification in Agaricomycetes. *New Phytol* 241: 444-460. <https://doi.org/10.1111/nph.19055>
- 6.** Zhang C, van der Heijden MG, Dodds BK, *et al.* 2024. A tripartite bacterial-fungal-plant symbiosis in the mycorrhiza-shaped microbiome drives plant growth and mycorrhization. *Microbiome* 12: 13. <https://doi.org/10.1186/s40168-023-01726-4>
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- 8.** Hobbie EA, Keel SG, Klein T, *et al.* 2024. Tracing the spatial extent and lag time of carbon transfer from *Picea abies* to ectomycorrhizal fungi differing in host type, taxonomy, or hyphal development. *Fungal Ecol* 68: 101315. <https://doi.org/10.1016/j.funeco.2023.101315>
- 9.** Mei Y, Zhang M, Cao G, *et al.* 2024. Endofungal bacteria and ectomycorrhizal fungi synergistically promote the absorption of organic phosphorus in *Pinus massoniana*. *Plant Cell Environ* 47: 600-610. <https://doi.org/10.1111/pce.14742>
- 10.** García-Montero LG, Monleón VJ, Valverde-Asenjo I, *et al.* 2024. Niche construction by two ectomycorrhizal truffle species (*Tuber aestivum* and *T. melanosporum*). *Soil Biol Biochem* 189: 109276. <https://doi.org/10.1016/j.SOILBIO.2023.109276>

*Selected from 193 Web of Science articles published between *January – April*, 2024 by: Bala Chaudhary, Jan Jansa, Justine Karst, Junling Zhang, Annegret Kohler, Judith Lundberg-Felten, Jeff Powell, Ido Rog, Mark Anthony, Camille Truong, Liangdong Guo, and César Marín.

Marcel G.A. van der Heijden interview: mycorrhizal biodiversity and functioning, applications, and IMS future

By: César Marín^{1, 2*}

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The 12th International Conference on Mycorrhiza (ICOM12) will occur in Manchester, United Kingdom, on 4-9 August 2024. After ICOM12, the current Vice President of the International Mycorrhiza Society (IMS), Justine Karst, will become the new President of the IMS, and Marcel G.A. van der Heijden will move to Past President. At the IMS, we are very thankful to Marcel for the immense work done these past four years. His vision, kindness, and strong work ethics has undoubtedly contributed significantly to our Society. And, of course, I think many worldwide mycorrhizal communities are very grateful to Marcel for his outstanding contributions to mycorrhizal ecology.

Prof. Dr. Marcel G.A. van der Heijden is Professor at the Department of Plant and Microbial Biology at the University of Zürich, Switzerland, he heads the Plant-Soil-Interactions Research Group at Agroscope, Switzerland and he is Professor of Mycorrhizal Ecology at Utrecht University, the Netherlands. Marcel obtained his PhD at the University of Basel in Switzerland in 1999 under the supervision of Ian R. Sanders, Andres Wiemken, and Thomas Boller. Marcel has supervised 19 PhD students (currently 6) and 22 postdocs since 2000. Eight of his postdocs are now Professors. He has been the Principal Investigator of 19 projects that amount a total of > €7.5 millions. His productivity is impressive, with more than 185 peer-reviewed publications. At the moment of writing this interview, in his



Google Scholar profile Marcel had 76 publications cited more than 100 times, and 10 cited more than 1000 times! In addition, Marcel has strong collaborations in over 20 countries, with a wide range of researchers.

I think his early (1998) contribution, together with John Klironomos, has been fundamental for soil ecology and the whole field of community and ecosystem ecology in general. It showed, using experimental microcosms, the causal relationships between mycorrhizal fungal biodiversity, plant biodiversity, and ecosystem productivity. I teach community and ecosystem ecology to PhD students in

Chile, and Marcel's work is very often used and discussed in my classes. I find two further studies fascinating and helpful for teaching. One was published in *Nature Communications* in 2019 with Cameron Wagg as the first author; the other was published in *Science of The Total Environment* in 2023 with Ferran Romero as the first author and Marcel as the senior author in both cases. In addition to worldwide measurements of soil biodiversity and ecosystem functioning (by people like Manuel Delgado-Baquerizo), these studies showed a positive relationship between soil biodiversity and ecosystem functions and services. His many highly cited contributions on this topic testify to Marcel's colossal impact. He also has dabbled in mycorrhizal applications over the last decades, with a recent study published in *Nature Microbiology* (first author: Stefanie Lutz) showing that the main predictor of mycorrhizal inoculation success is the abundance of pathogenic fungi in the soil before the inoculation. Although more research is needed (i.e., more crops, climates, consortia, or species of mycorrhizal fungi used), this finding, of course, can have significant implications for (an intelligent) agricultural management based on the application of arbuscular mycorrhizal fungi (AMF) bioinoculants.

I am thrilled to present this interview with Marcel to our readers.

When did you start to study mycorrhizas?

I did my Master thesis (1994) at Utrecht University on mycorrhizal fungi, specifically testing whether mycorrhizal fungi alter competitive relationships between two plants.

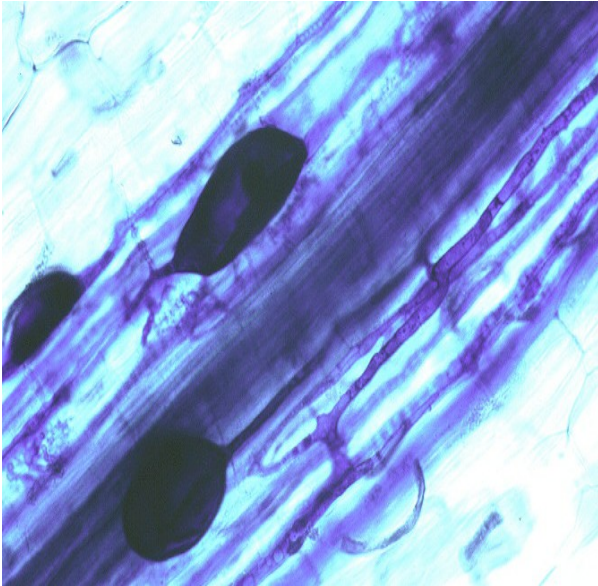
What do you think is your biggest contribution to mycorrhizal research, or more broadly, to soil ecology?

That is a difficult question. In my PhD we investigated the impact of arbuscular

mycorrhizal fungi (AMF) and AMF diversity on plant productivity and ecosystem functioning. This work, together with John Klironomos and others was published in *Nature* (1998) and got a lot of attention. I also very much like the work done by Cameron Wagg, for sure one of my very best PhD students, demonstrating the link between soil biodiversity and ecosystem multifunctionality (Wagg *et al.* 2014, PNAS). This work not only included AMF, but the whole soil community. I also really like our recent work demonstrating that inoculation with mycorrhizal fungi can promote crop yield. This possibly will have the biggest impact, as it provides a tool to make agriculture more sustainable and help plants grow (or protect themselves) (Lutz *et al.* 2023, *Nature Microbiology*). With our team we move on in this research field and I look forward to see how this develops. Finally, I have been writing a number of reviews on mycorrhizas and soil microbes with Sam Banerjee, Francis Martin and others, and that has been fun (e.g. Banerjee *et al.* 2018, *Nature Reviews Microbiology*; Banerjee & van der Heijden. 2023, *Nature Microbiology*; Martin and van der Heijden 2024, *New Phytologist*).

How much have we advanced in our understanding of the correlational and causal relationships between soil biodiversity and ecosystem functioning? What are the knowledge gaps on this subject?

An increasing number of studies shows that soil biodiversity is linked to ecosystem functioning. However, experimental evidence, especially from the field is still poor, and there is still a large knowledge gap. It is obvious that soil life plays a key role in ecosystems. The question is to which extent can we influence this to promote plant yield, soil health or ecosystem sustainability. I am very happy that there is so much interest for soil health (among farmers, land managers, policy makers, etc.), and I do hope that we manage to make agriculture more



Clover (*Trifolium pratense*) root colonized by arbuscular mycorrhizal fungi (in blue). Hyphae and vesicles (blue black balloons) are shown. **Photo:** Marcel G.A. van der Heijden.

sustainable, e.g. through field inoculations with beneficial microbes or by enhancing crop cover, crop rotation or reducing soil disturbance.

What attracted you in the first place to the study of the relationship between soil biodiversity and ecosystem functioning?

I have always been fascinated by the interaction between soil biota and plants. Mycorrhizas obviously play a key role and I have been intrigued by them since my Biology study in Wageningen, the Netherlands.

How do you define “success” and “happiness” in science?

Difficult question. Happiness in science is about joy, fun, exciting results, teamwork, nice exchange with others. Success is difficult to measure. Obviously, well cited and novel scientific discoveries are, in my opinion, a strong indicator for scientific success. The application of scientific discoveries to the real world is very useful as an indicator for success (including the path to development). Success is usually team-work; for sure in my case as I had

the luck to work together with many gifted people, who complemented me in an excellent way. Also, the importance of teaching should not be underestimated. For me personally, it is fun to give lectures and talks and motivate people for research, especially on mycorrhizas, microbes, soils and sustainable agriculture.

Which is your favorite conference to attend and why?

There are many nice conferences and I often like the smaller ones where there is the opportunity to exchange with many/most of participants. Since 1998 (Uppsala, Sweden), I went to almost all (except one I believe) international conferences on mycorrhiza (ICOM).

Who were your most influential mentors?

The work by David Read has been very influential to me. Also, I had various mentors at a management level (or science management), such as Bernhard Schmid or Willy Kessler. There are obviously many other people who have been very important for my scientific career, fun in the lab and the daily work, including friends and family.

What is your favorite fungi?

Rhizoglyphus irregularis, the AMF we use for our field experiments.

Your research has shown that many AMF-based bioinoculants do not work. How do you see the past, present, and future of AMF bioinoculants? Was there too much hype in the past (ie., when you started)? How is it now? Is there hope for the future?

Yes, of course there is hope for the future. There are some good products on the market and I assume that over time the bad products will disappear. Also, regulations are improving. I recommend every producer to test that their



Marcel in the Colombian Amazonas, 2023.

mycorrhizal product actively colonizes plant roots. With such a test, bad products will be selected out automatically, and for the long-term persistence and economic benefit of companies this is a must. So if you are an AMF bio-inoculant producer reading this, and you do not yet do this, please consider it! The field of biostimulants and biologicals is developing rapidly and I hope that broad-scale application of mycorrhizal fungi and other beneficial microbes to agriculture will be widely practiced in the future.

What would you recommend to PhD students in general?

Motivation, enthusiasm, hard work, and drive for research is most important. That is something that comes from inside. Make sure your experimental design and the research questions you tackle are good and have novel aspects. Talk with other people about questions you have related to your research or career. Many scientists are very open minded and give their opinion for “free”. Also, it is beneficial and rewarding to cooperate with others! Ask

good questions on how to solve scientific or other problems. I have a (long) list of ideas and potential experiments I like to do. It is always useful to have such a list. Be patient and be persistent. If you are a non-native speaker – read good scientific literature and analyze how others write good papers. For scientific success, it is not only important to make that unique discovery, but also ensure that your study is appealing when people read it or listen to your talk (science is also about marketing). During my PhD, I always read papers from David Read because they are so beautiful written (my English was terrible when I started my PhD). It helped a lot.

You are obviously very productive in terms of publishing articles. Can you give us some general tips on how to increase or sustain writing productivity?

I collaborate with many people, we have an excellent and collaborative research team, I have many ideas for papers and projects and we have an excellent infrastructure at my research institutes.

How do you see the near and not-so-near future of mycorrhizal research in general, and specifically of mycorrhizal ecology? Which topics need to be addressed?

There are a number of key areas including mycorrhizal genomics, interactions with other microbes (mycorrhiza helper bacteria, food webs), use of mycorrhizas for sustainable agricultural and forestry. It is always appealing to explore global patterns and search for general mechanisms including recognition and molecular cross-talk and exchange of plants with mycorrhizal fungi.

And what about the future of the International Mycorrhiza Society (IMS)?

Mycorrhizal research is vibrant, appealing and every year novel discoveries are being made. So I foresee a successful future. I would be pleased if researchers within the different research directions (e.g. ecology, agriculture, molecular biology, taxonomy, etc.) are united and actively exchange and support each other within the Society. I really like the IMS Newsletter and also the new IMS Seminars, and hope we manage to further engage and activate people from the different research fields to join the Society and contribute actively.



Arbuscular Mycorrhizal Fungi collection.

Photo: Fritz Oehl.

Research commentaries

Linking genes to ecological traits in fungal communities of forest soils

Francis M. Martin^{1*}, Lucas Auer¹, Annegret Kohler¹ and Marc Buée¹

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Forest soil microbial communities, including those inhabiting plant roots, litter, humus, and coarse woody debris, are vital for forest biogeochemical cycles and tree biology. Fungi are a significant component of these microbial communities and can be classified into several ecological guilds including leaf litter decomposers, humus saprobes, white- and brown-rot wood decayers, plant/animal/fungal parasites, and mycorrhizal symbionts. The challenge for ecologists is to understand the factors that contribute to the functional diversity of natural fungal communities at different spatial and temporal scales. Furthermore, the functional properties of the individual species and their synergistic effects are often unknown.

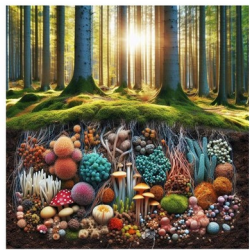
Our project "*Metatranscriptomics of the Forest Soil Ecosystems*" funded by the United States Department of Energy – Joint Genome Institute (JGI) was designed to connect genes to ecological traits and gain a deeper understanding of the influence of forest associations on the composition and functioning of soil fungal communities. The ultimate goal was to provide an explanation for the mechanisms underlying the microbial exploitation of soil resources in boreal, temperate, Mediterranean, and tropical forests. Specifically, we sought to clarify the physiological processes that occur along the "saprotrophism-mutualism" continuum, encompassing decaying wood, litter, and humus saprobes as well as the mycelial networks of mycorrhizal partners,

and to identify the key genes and metabolic pathways involved in these ecological interactions. In this study, several technological challenges had to be overcome.

Technical challenges

Functional molecular studies of soil fungi have been hampered by several technical challenges, including (i) inadequate methodologies for extracting fungal mRNA from soils, (ii) a limited number of reference genomes for fungi to map soil RNAs, and (iii) the absence of dedicated bioinformatics tools to exploit the massive datasets generated by high-throughput sequencing of metatranscriptomes. Our international consortium of scientists and the JGI has developed new approaches for quantifying gene expression in soil fungal communities.

Using high-throughput RNA profiling of soil hyphae, we assessed whether multiple saprotrophic and symbiotic species can coexist beneath the same host tree by utilizing the same resources and performing identical ecological functions (i.e., exhibiting high functional similarity) or by utilizing different resources and providing distinct or complementary functions (i.e., exhibiting limited functional similarity). Our toolkit (**Fig. 1**) was used to explore the taxonomic and functional diversity of fungi in several types of forest ecosystems, from boreal forests in Quebec and Sweden to temperate forests in France and Spain and tropical



Forest soil is an extremely **complex** and **diverse** environment

RNA extraction issues → low coverage → incomplete genes
low comparability

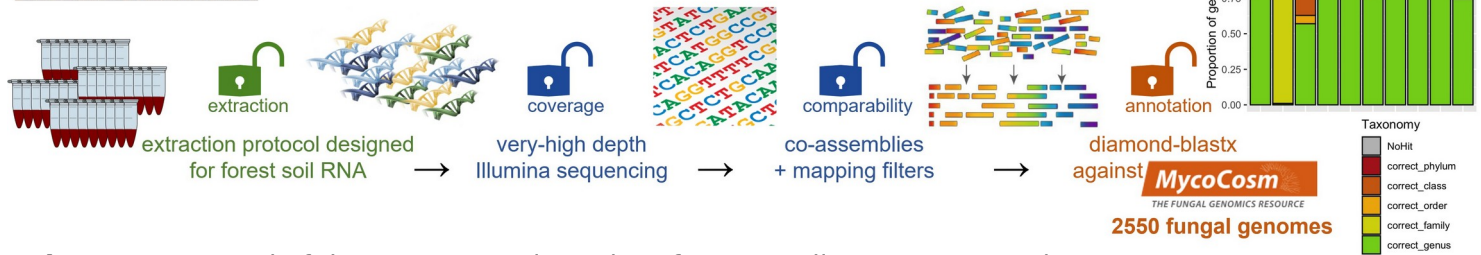


Figure 1. Protocol of the *Metatranscriptomics of Forest Soil Ecosystems* project.

old-growth forests in Yunnan, China (Auer *et al.*, 2024; Zeng *et al.*, 2023).

Approximately two grams of sieved soil samples was collected from 51 soil cores, snap-frozen, and total RNA was extracted using the Qiagen RNeasy PowerSoil Total RNA kit.

Eukaryotic poly-A RNA was linearly amplified from the extracted total RNA using the Invitrogen Message AmpII kit. The linearly amplified RNA was reverse-transcribed into cDNAs (Novogene). The cDNAs were subsequently sequenced on an Illumina NovaSeq sequencer using the HiSeq platform (250 bp paired-end reads). RNA reads from each site were assembled into cDNA contigs using the MEGAHIT software (Li *et al.*, 2015) (Figure 1). For each sample, filtered reads were mapped onto the corresponding *de novo* metatranscriptome assemblies using *Bowtie2* software (Langmead *et al.*, 2009). These contigs were annotated using the *DIAMOND* software (Buchfink *et al.*, 2015) and two different databases: GenBank non-redundant and JGI MycoCosm (Grigoriev *et al.*, 2014) Because of the increasing number of available fungal genomes (>2550) from ecologically relevant species in the JGI MycoCosm database, it was possible to map up to 38% of the reads to the reference fungal gene repertoires, including genes responsible for nutrient scavenging (e.g.,

proteases and lipases) and soil organic matter (SOM) decomposition (e.g., carbohydrate active enzymes).

High functional diversity despite diverse taxonomic compositions

As reported in studies using environmental rDNA metabarcoding (Beugnon *et al.*, 2021; Asplund *et al.*, 2019), data obtained from fungal transcripts indicated that forest type had a considerable impact on both the taxonomic diversity and composition of active fungal communities. Although the assortment of saprotrophic, pathogenic, and symbiotic fungi can fluctuate strikingly among forest types, these soil microorganisms commonly possess remarkably similar functions, such as those involved in central metabolism and developmental pathways. This finding indicates an unexpectedly high degree of ecological redundancy in growth-related functions among the fungal guilds.

Soil organic matter decomposition

However, our analysis also revealed that the expression profiles of genes involved in polysaccharide and protein degradation as well as nutrient scavenging differed between and within fungal guilds (e.g., saprotrophic vs. ectomycorrhizal species), suggesting that these organisms have adapted to specific niches. The expression of genes encoding enzymes responsible for the degradation of plant cell walls, such as cellulases and hemicellulases, was

higher in saprotrophic fungi than that in ectomycorrhizal and pathogenic fungi. However, ectomycorrhizal and pathogenic fungi showed slightly higher gene expression levels than saprotrophic fungi for enzymes involved in fungal cell wall degradation such as chitinase. Moreover, transcripts for N-related transporters were more abundant in ectomycorrhizal fungi than in other groups. These findings suggest that ectomycorrhizal and saprotrophic fungi compete for N in SOM, potentially modulating the carbon cycling.

Conclusions and future research

The present study yielded a set of tools that facilitated the integration of genetic and functional data for soil fungi, thereby enabling extensive research on the interactions between fungal communities, soil properties, and environmental variables in diverse forest ecosystems. However, several challenges continue to impede the widespread application of metatranscriptomics. For instance, RNA is more labile than DNA and is generally more difficult to extract from certain types of soils such as sandy soils. RNA analysis requires the snap-freezing of samples in liquid nitrogen or dry ice, which can be challenging in remote locations. Moreover, although the current collection of sequenced fungal genomes is substantial (> 4500 species), it represents only a small fraction (~ 1%) of the known species. As a result, less than half of the sequenced RNA reads could be mapped to available reference genomes. Thousands of additional genomes must be sequenced to fully understand the genetic and functional diversity of the fungal communities. Finally, the high cost of transcriptome profiling (>\$200 per sample) limits the number of soil samples that can be processed to generate the global environmental transcriptome atlas.

Future research should focus on developing comprehensive techniques that integrate rRNA metabarcoding to analyze operational taxonomic unit distribution, estimate fungal genotype size through multi-locus eDNA population

genomics, and employ metatranscriptomics, metaproteomics, and metabolic flux measurements across various components of forest or grassland plots. This holistic approach, which encompasses the genome to ecosystem level, is crucial for understanding the role of fungal communities in intricate terrestrial ecosystems.

Additionally, these methodologies can be used to evaluate the impact of global phenomena such as climate change and deforestation on the functional ecology of soil microorganisms.

Acknowledgements

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How far have we progressed in Glomeromycota taxonomy and systematics?

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Taxonomy is the discipline that names, organizes, and defines species, the fundamental units of biological classification. In recent decades we have experienced significant advances in the descriptions of fungal taxa and classification revisions, reflecting new data obtained mainly from studies using genetic tools. On average, more than 2,000 fungal species are described per year, resulting from intense work by taxonomists who recently came together to create an international consortium to discuss, organize, and establish a broad foundation for the fungal classification (Hyde *et al.* 2023). Even with these advancements, it is estimated that over 94% of fungal species have not been described yet (Antoneli *et al.* 2023). A particular challenge in fungal taxonomy is the phylum *Glomeromycota* (arbuscular mycorrhizal fungi; AMF), a group of obligate symbiont microorganisms forming arbuscular mycorrhizas in the roots of ca. 72% of vascular plants in terrestrial and aquatic environments (Meng *et al.* 2023), and with representatives (*Funneliformis* and *Rhizoglyphus*) among the 100 most cited fungal genera in the world (Bhunjun *et al.* 2024).

The *Glomeromycota* taxonomy began in

1844 with the description of the first two species, *Glomus macrocarpum* and *G. microcarpum*. The discovery of these early species was possible because their spores were formed in large sporocarps, visible to the naked eye. The recognition of the symbiotic nature of this group of fungi and their ability to enhance plant growth, the techniques for extraction of spores from the soil, and the possibility of growing them in culture resulted in an increasing interest (Koide and Mosse 2004) and the description of new taxa, including species that produced spores singly, invisible without the use of a microscope (Sportes *et al.* 2021). Gerdemann and Trappe (1974), using refined spore wall characteristics, established the foundations of the AMF taxonomy and proposed the first classification, as members of the family *Endogonaceae*. Later, significant improvements were introduced including a revision of the classification, nomenclature of the spore wall components, and subcellular organization of spores (Walker 1983; Morton 1988; Morton and Benny 1990). At this time, the most significant taxonomic

novelties were the transfer of the genera *Glomus* and *Sclerocystis* from the family *Endogonaceae* to the *Glomeraceae*, and the placement of AMF in a new order, *Glomerales*.

Exceptionally valuable changes in the taxonomy of *Glomeromycota* have been made in the last two decades, mainly due to the involvement of molecular techniques. The first descriptions of AMF including morphological and molecular characteristics date back to 2000 (Declerck *et al.* 2000). Morton and Redecker (2001) proposed the first reclassification of AMF based on the phylogenetic analysis of the 18S *nuc* rDNA gene. Also in 2001, the genus *Glomus* was indicated to be polyphyletic and AMF were placed in a newly created phylum, *Glomeromycota* (Schüßler *et al.* 2001).

The studies discussed above and subsequent phylogenetic analyses have clearly demonstrated that the use of molecular data significantly sharpens the boundaries between species and increases the reliability of their classification (Oehl *et al.* 2011; Błaszowski *et al.* 2022; Wijayawardene *et al.* 2022). Recently, phylogenomic analyses were applied to shed light on the relationship within the members of the *Glomeromycota* and their position in the fungal kingdom (Montoliu-Nerin *et al.* 2021). The taxonomic rank of this monophyletic lineage of basal fungi as Phylum or Subphylum has a long lasting debate (Spatafora *et al.* 2016; Montoliu-Nerin *et al.* 2021; Wijayawardene *et al.* 2022), but recent evidence reinforces their status as Phylum (*Glomeromycota*) and unveils their relationship with Dikarya (Wijayawardene *et al.* under review).

The difficulties in the study of *Glomeromycota* arise mainly from the following two reasons. First, numerous members of the *Glomeromycota* are missed in sampling due to infrequent or seasonal spore formation. Second, the lack of basic knowledge about the biology and life history strategies (e.g., requirements

for germination of spores, the presence of a suitable host plant, and the conditions for growing both partners), which make it impossible to fully understand the life cycle and, consequently, the morphology of the specimens found.

Glomeromycotan species identification based on spore morphology alone requires experience and access to vouchers of the type and reference materials deposited in collections (**Fig. 1**). *Glomeromycota* members produce only one reproductive structure (glomerospores) with useful phenotypic and histochemical characters (spore ontogeny, morphometrics, subcellular structure, staining in Melzer's reagent) for morphological identification. The number of diagnostic morphological features is small - mainly for species forming glomoid spores, where these characters present phenotypic and histochemical variability. Furthermore, some members of the *Glomeromycota* may produce two different spore types (dimorphism and synanomorphism), and the recognition of only one morph may lead to incorrect taxonomic conclusions (Goto *et al.* 2008; Bills and Morton 2015; Błaszowski *et al.* 2022; Kokkoris *et al.* 2024). Nevertheless, morphological characters remain important for differentiating groups at different taxonomic levels or for guiding the selection of fungi that may belong to new species (**Fig. 2**). For instance, the germinal shields (or orbs) and spore wall organization are important for distinguishing acaulosporoid, pacisporoid, scutellosporoid, and ambisporoid spores, and the morphology of the subtending hypha to discriminate glomoid spores (Oehl *et al.* 2011).

Glomeromycota have a complex genetic structure with multinucleate spores and a coenocytic mycelium, which is the cause of the high molecular variability and intragenomic polymorphism (Chen *et al.* 2018) that significantly complicate the classification of species and gene locus "sequencing" without cloning. Moreover, the genetic basis of the *Glomeromycota*

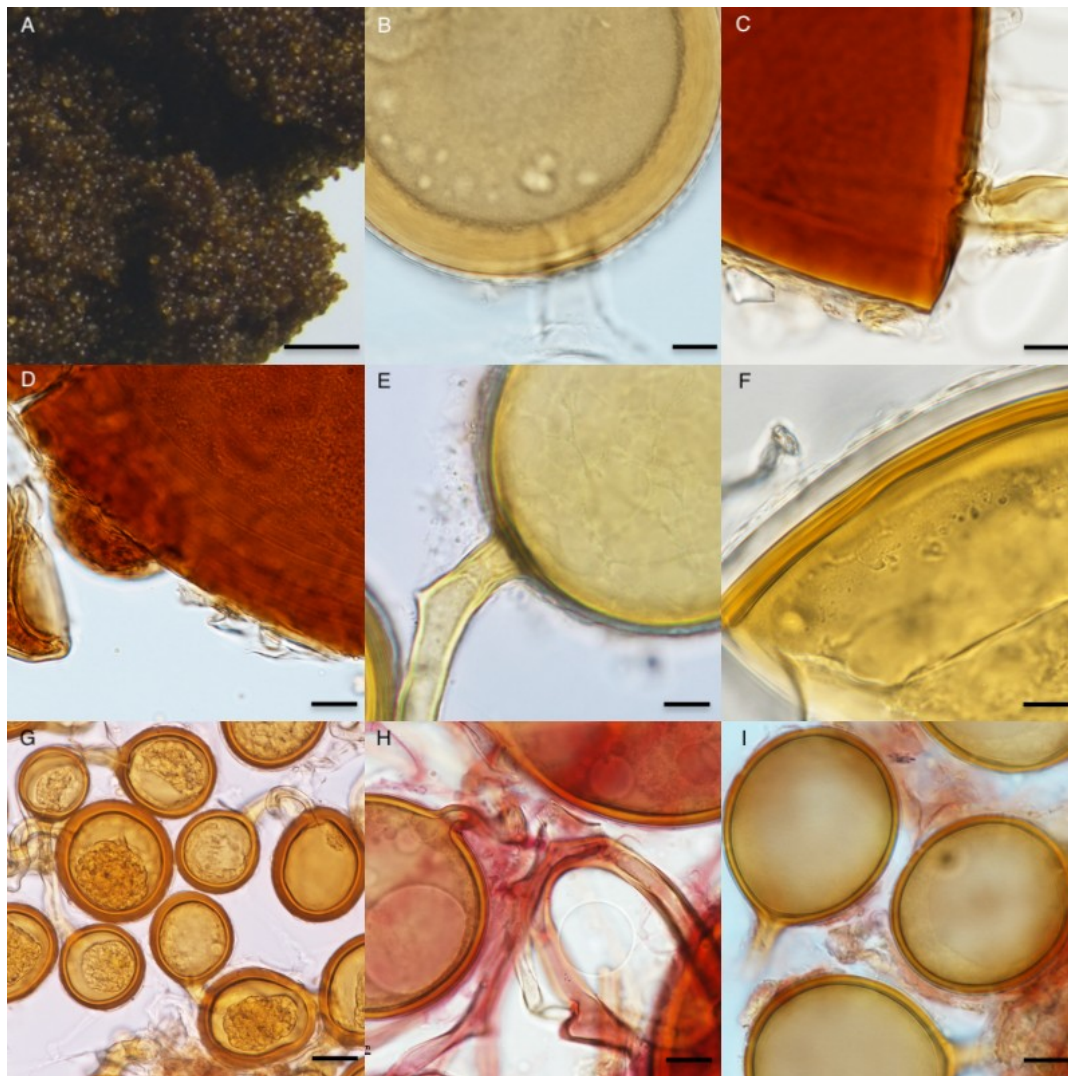


Figure 1. Diversity of glomoid spores representing different species and genera. A-B *Rhizoglomus maiae*, a glomerocarpic species described from Brazil. **C** Detail of glomerospore base of *Glomus melanosporum*, a species molecularly uncharacterized. **D** Glomerospore and aborted spores in *Corymbiglomus globiferum*. **E** Detail of spore base with subtending hypha attached in *Rhizoglomus silesianum*. **F** Spore wall of *Rhizoglomus clarum*. **G** Loose cluster of *Rhizoglomus* sp. obtained from Brazilian soil. **H** Glomerospores in clusters of *Glomus chinense*. **I** Glomerospores in *Dominikia gansuensis* from China. **B, C, D, E, F, G, I** Spores in PVLG. **H** Spores in PVLG+Melzer's reagent. Scale bars: **A** = 250 μ m, **B, C, D, E, F, H, I** = 10 μ m, **G** = 25 μ m.

reproductive system remains largely unknown. Ropars *et al.* (2016) identified putative mating-type locus, suggesting multi-allelic locus and that AMF could be heterothallic and bipolar. However, parasexual processes may also play a role in generating nuclear diversity in *Glomeromycota*. Finally, there are few mycologists in the world dealing with the morphological and molecular characterization of this commercially important group of fungi for crop production and ecological restoration. Nine collections maintain cultures of

Glomeromycota worldwide, in the American continent (**INVAM, BGIV, GINCO_CAN, CICG, Embrapa**), Europe (**BEG** and **GINCO-BEL**), India (**CMCC**), and Japan (**Naro - Maff - Japan**) among others maintained by labs. However, only three are located in the Global South (BGIV, CICG, and Embrapa). Although the use of the morphological species concept remains the rule, in recent years there have been initiatives to establish species and taxa of other ranks based on environmental sequences (Öpik *et al.* 2010; Lücking *et al.* 2021). The

environmental sequences available in databases suggest the presence of new taxa in *Glomeromycota* of different taxonomic ranks.

Despite being recognized as a basic science, the *Glomeromycota* taxonomy remains a challenge for new generations, attracting a limited number of researchers throughout history. For those uninitiated in the taxonomy of *Glomeromycota*, species identification based on morphological characters could lead to a real nightmare. The main challenge lies in the difficulty of recognizing the characteristics of the spore subcellular structure and components. Although the spores of *Glomeromycota* species are the largest compared to spores of other taxa of the fungi kingdom, they are structurally complex, these structures are difficult to detect, and their characteristics change during spore development (Goto and Maia 2006). Some proceedings have been suggested (or are required) to minimize these difficulties, such as (i) the use of pure (monosporic) cultures as a basis for describing species, ensuring single origin, and quality and reproducibility in analyses, (ii) performing ontogenetic analyses of the glomerospores to reveal the stages of differentiation of the spore subcellular components and structure throughout the development of the fungus; (iii) conducting phylogenetic analyzes to recognize the taxonomic affiliation and the positions within the *Glomeromycota* of the analyzed specimens; and (iv) learning the nature of mycorrhiza and the phenotypic and histochemical features of its structures, i.e., arbuscules, vesicles, and hyphae. All these steps are used as a "gold standardized protocol" to describe AMF species. Technical improvements are required to overcome the need of trap and single-species cultures. Obtaining high-quality complete genome sequences from single spores or nuclei, as achieved by Montoliu-Nerin *et al.* (2021), may revolutionize the description of *Glomeromycota* species.

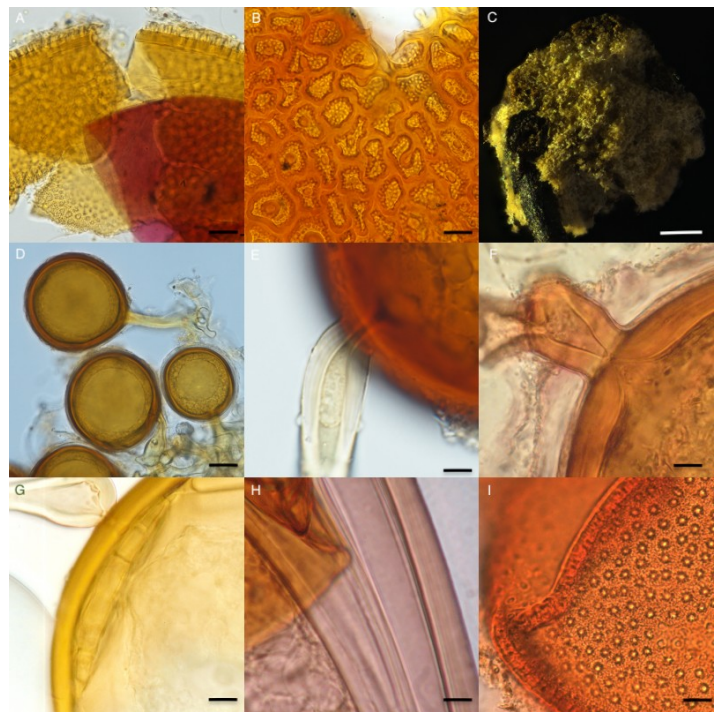


Figure 2. Diversity of glomerospores representing undescribed or described species from Brazilian soils, and species not characterized molecularly. A-B Ornamented *Acaulospora* spp. **C** Glomerocarps of *Sclerocarpum amazonicum*. **D-F** Glomoid glomerospores of new undescribed species. **G-H** Scutellosporoid glomerospores of undescribed species. **I** Ornamentation in *Racocetra minuta*, a molecularly uncharacterized AMF species. **B, D, E, G, I** Spores in PVLG. **A, F, H** Spores in PVLG+Melzer's reagent. Scale bars: **A, B, E, F, G, H, I** = 10 μ m, **C** = 1.0 mm, **D** = 50 μ m.

The rate of discovering new AMF taxa over the past two decades has been only 4.6 species per year, taking more than 200 years to describe 1,000 species, as estimated by Mueller and Schmit (2007). Analyses of environmental sequences deposited in public databases, using a 98% identity threshold, suggested a very high diversity (7,247) (Tedersoo *et al.* 2022), with new families and genera still awaiting description. In total, around 360 species have been described (**Fig. 3**) in the *Glomeromycota*, distributed in three classes, six orders, 17 families, and 49 genera (<https://biologiademycorrhizas.wixsite.com/glomeromycota>). This represents only a very small fraction (0.04%) of the estimated richness using environmental sequences, making the task of describing all *Glomeromycota* species a

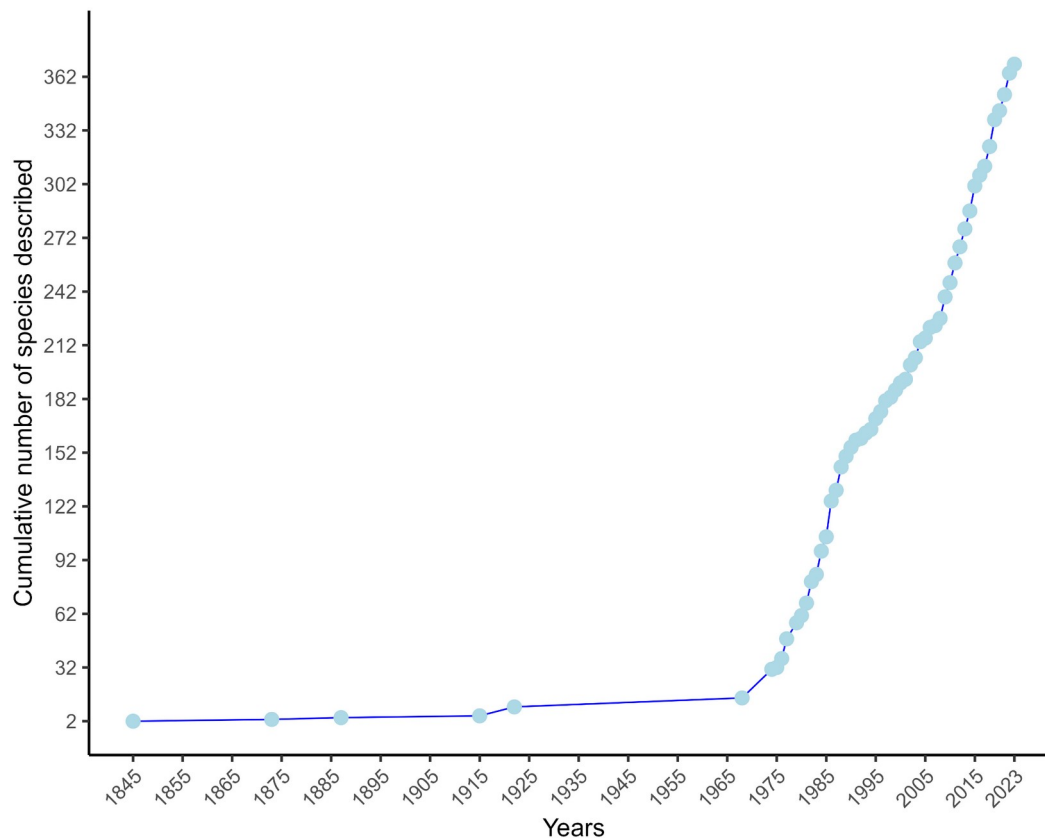


Figure 3. Evolution of glomeromycotan *sp. nov.* description through time.

“mission impossible” (more than 1,500 years), considering the current rate of descriptions (**Fig. 3**). However, in our opinion, a precise estimation is not possible at the moment since it would be largely biased by the criteria used for species boundaries and by the sampling effort.

Hyde *et al.* (2023) gathered 12 researchers linked to the *Glomeromycota* taxonomy in the Global consortium for the classification of fungi and fungus-like taxa, interestingly the majority (8) came from the Global South (Brazil and Peru). Historically, AMF taxonomists are from the Global North (England, United States, Germany, and Poland), but taxonomists from Spain and Switzerland are also involved. Unfortunately, there are no *Glomeromycota* taxonomists working in Africa, and only a few in Asia and Oceania - both hotspots of AMF biodiversity.

Only a few specialists with many years of

experience and knowledge about the morphology of AMF are able to prepare reliable descriptions of these fungi. Despite all the difficulties (financial and time resources, high expertise), this challenge is still worth it! Members of the *Glomeromycota* are wonderful organisms with enormous impacts on nature and the effects of their use by humans, so continuing to learn about AMF is of the utmost importance. This will enable, among others, (i) targeted organization of biological diversity, (ii) deeper understanding of evolution, (iii) promoting the conservation of biodiversity, (iv) more effective application of biotechnology, (v) identifying and communicating, (vi) preserving scientific heritage, and (vii) environmental education. A small group of taxonomists can be responsible for a significant scientific contribution. The authors who signed this short article participated in the description of two classes, two orders, six families, 27 genera, and 100 new species of *Glomeromycota*. This represents 66% of

the classes, 33% of the orders, 35% of the families, 55% of the genera, and 27% of the species described in the phylum. If we want to increase the quality of AMF species descriptions, we need to encourage the training of new taxonomists, develop or strengthen collaborations with taxonomists and phylogeneticists, explore new habitats and environments, and finally, fight for financial resources (as the SPUN initiative - <https://www.spun.earth/>) and permanent positions, so that these professionals can continue describing species that will be used in future applied work. Considering all the challenges awaiting at the horizon, we are wishing for a "new dawn" of AMF taxonomy, with renewed interest and effort from the members of the scientific community, in order to guarantee a promising future for this beautiful and exciting research field.

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- Wijayawardene NN, Hyde KD, Dai DQ, et al. 2022. Outline of Fungi and fungus-like taxa – 2021. *Mycosphere* 13: 53-453.
<http://dx.doi.org/10.5943/mycosphere/13/1/2>
- Walker C. 1983. Taxonomic concepts in the Endogonaceae: spore wall characteristics in species descriptions. *Mycotaxon* 18: 443-455.

YouTube interviews*

- Adam Frew on community assembly of AMF due to plant defence

Luke Florence (PhD candidate at La Trobe University, Australia) interviews Adam Frew (Lecturer at Western Sydney University) about his hypothesis paper proposing that stressed plants selectively recruit AMF from the local pool with traits that enhance their defence mechanisms against herbivores and/or pathogens.

Interview: <https://southmycorrhizas.org/reading/march-2024/>

Study: Frew A, Weinberger N, Powell JR, Watts-Williams SJ, Aguilar-Trigueros CA. 2024. Community assembly of root-colonizing arbuscular mycorrhizal fungi: beyond carbon and into defence? *ISME J* 18:wrae007.

<https://doi.org/10.1093/ismejo/wrae007>

- Olga A. Lastovetsky on AMF spores hosting surprisingly diverse communities of endobacteria

César Marín (Full Professor, Universidad Santo Tomás, Chile) interviews Olga A. Lastovetsky (Assistant Professor, University College Dublin, Ireland) about her recent recent impressive sequencing of endobacteria of almost 90 Glomeromycota spores, finding a really high biodiversity. One spore had 227 endobacterial Operational Taxonomic Units!

Interview: <https://southmycorrhizas.org/reading/what-we-are-reading-in-april-2024/>

Study: Lastovetsky OA, Caruso T, Brennan FP, Wall D, Pylni S, Doyle E. 2024. Spores of arbuscular mycorrhizal fungi host surprisingly diverse communities of endobacteria. *New Phytol* 242:1785-1797.

<https://doi.org/10.1111/nph.19605>

- Marco Cosme on how mycorrhizas drive the evolution of plant adaptation to drought

Jason D. Hoeksema (Professor at the University of Mississippi, US), interviews Marco Cosme (Professor at the Université de Picardie Jules Verne, France), about his recent article using phylogenetic comparative methods to conclude/suggest suggests that mycorrhizal associations play a facilitator role in the evolutionary processes of plant adaptation to drought.

Interview: <https://southmycorrhizas.org/reading/april-ii-2024/>

Study: Cosme M. 2023. Mycorrhizas drive the evolution of plant adaptation to drought. *Commun Biol* 6:346.

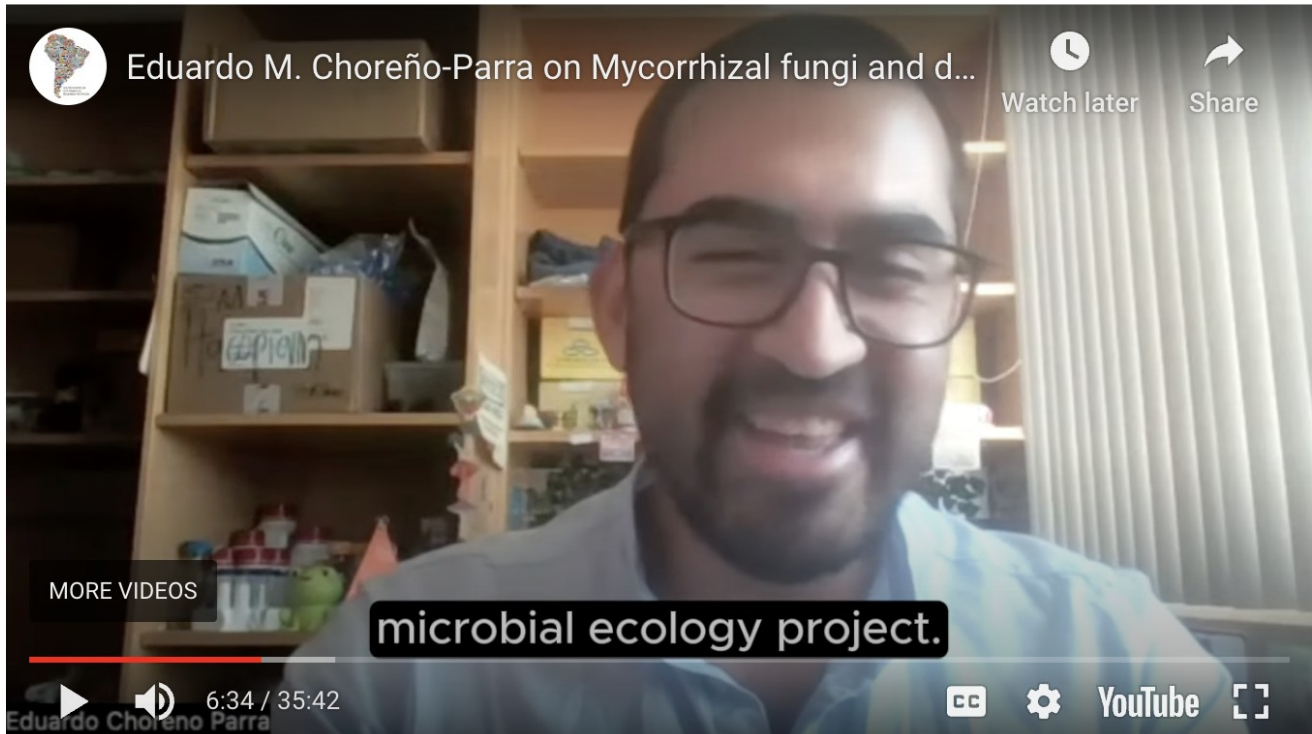
<https://doi.org/10.1038/s42003-023-04722-4>



YouTube interviews*

- Eduardo M. Choreño-Parra on mycorrhizal fungi and decomposition relationships [in Spanish; English subtitles]

Dr. Nahuel Policelli (CONICET, Argentina) interviews Eduardo M. Choreño-Parra (PhD Student, University of California, Irvine, United States) about the worldwide relationships between mycorrhizal fungi and decomposition.



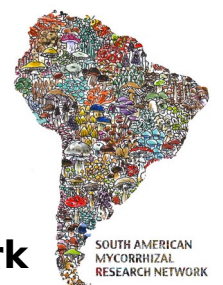
Interview: <https://southmycorrhizas.org/reading/march-2024/>

Study: Choreño-Parra EM, Treseder KK. 2024. Mycorrhizal fungi modify decomposition: a meta-analysis. *New Phytol*, 242: 2763-2774.

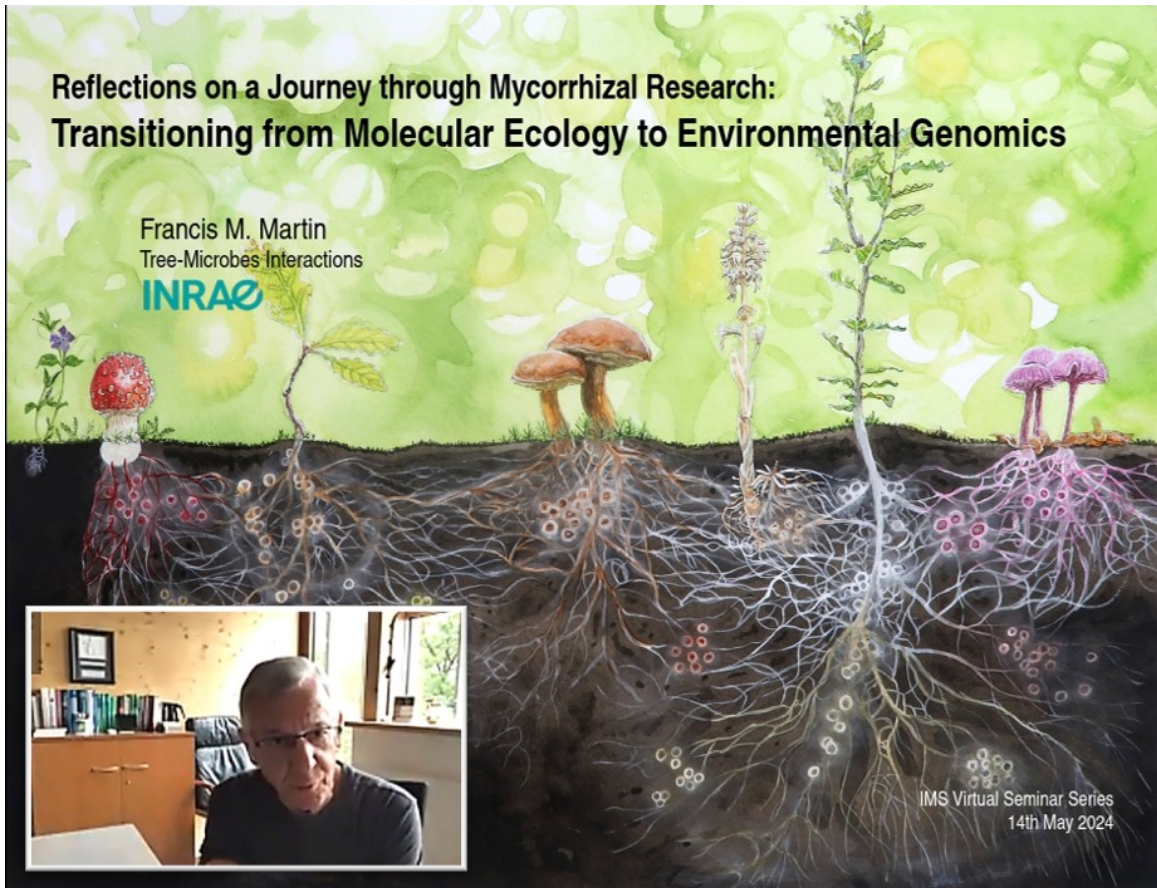
<https://doi.org/10.1111/nph.19748>

Section by: South American Mycorrhizal Research Network

Contact/Join us: <https://southmycorrhizas.org/join/>



IMS Seminars




[Watch on YouTube](#)

The first IMS Seminar was presented by IMS Past President and Eminent Mycorrhiza Researcher Awardee, Francis M. Martin, Research Director Emeritus at the National Research Institute for Agriculture, Food and Environment (INRAE) in Nancy, France. Francis gave a beautiful overview on the “evolution” of research on mycorrhizas, especially environmental genomics. The seminar, entitled “Reflections on a Journey through Mycorrhizal Research: Transitioning from Molecular Ecology to Environmental Genomics” is available at the newly created YouTube channel of the IMS ([@mycorrhiza_ims](#)).

Link: https://youtu.be/6_XwWqu958U?si=j_MYsosljg74Nw4k

Next IMS Seminars


Register here: <https://forms.gle/LmwnUu7YBX81ND6DA>



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VIRTUAL SEMINAR SERIES

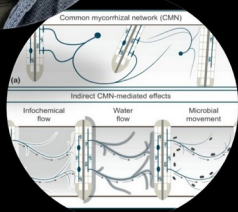
Dr. Matthias Rillig
Professor of Ecology
Freie Universität Berlin




"Clarifying the definition of common mycorrhizal networks"

June 24th 2024 at 15:00h CET

Free registration here:
<https://forms.gle/LmwnUu7YBX81ND6DA>



Picture from: Rillig, M. C., *et al* (2024). Clarifying the definition of common mycorrhizal networks. *Functional Ecology*, 00, 1–7.
<https://doi.org/10.1111/1365-2435.14545>



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VIRTUAL SEMINAR SERIES

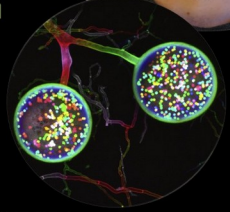
Dr. Vasilis Kokkoris
Assistant Professor
Section Systems Ecology
Amsterdam Institute for Life and Environment (A-LIFE)
Vrije Universiteit Amsterdam



"Cell and Network Dynamics in Arbuscular Mycorrhizal Fungi"

June 24th 2024 at 15:35h CET

Free registration here:
<https://forms.gle/LmwnUu7YBX81ND6DA>



Picture from: Kokkoris, V., *et al* (2021) Host identity influences nuclear dynamics in arbuscular mycorrhizal fungi. *Current Biology*
<https://doi.org/10.1016/j.cub.2021.01.035>

Tools

- **AMF-SporeChip to visualize arbuscular mycorrhizal fungi (AMF) asymbiotic fungal growth at the cellular level**

Richter *et al.* (2024) developed a microfluidic platform, the AMF-SporeChip, to visualise the foraging behaviour of germinating Rhizophagus and Gigaspora spores. This platform also allows to confront asymbiotic hyphae with physical obstacles.

Study: Richter F, Calonne-Salmon M, van der Heijden MG, Declerck S, Stanley CE. 2024. AMF-SporeChip provides new insights into arbuscular mycorrhizal fungal asymbiotic hyphal growth dynamics at the cellular level. *Lab on a Chip* 24:1930-1946. <https://doi.org/10.1039/D3LC00859B>

- **Computer vision models to predict AMF colonization using fungal morphology**

Zhang *et al.* (2024) provided a multi-scale modeling approach to predict AMF colonization, relying on a Mask Region-based Convolutional Neural Network in computer vision for pixel-wise fungal structure segmentations and mixed linear models to explore the relations of AMF colonization, root niche, and fungal structure allocation.

Study: Zhang S, Wu Y, Skaro M, *et al.* 2024. Computer vision models enable mixed linear modeling to predict arbuscular mycorrhizal fungal colonization using fungal morphology. *Sci Rep* 14:10866. <https://doi.org/10.1038/s41598-024-61181-5>

- **AMSlide for noninvasive time-lapse imaging of AMF**

McGaley *et al.* (2024) introduce AMSlide, a noninvasive, high-resolution, live-imaging system optimised for confocal microscopy of mycorrhizal roots, for analyzing whole colonization zones to subcellular structures, over timeframes from minutes to weeks.

Study: McGaley J, Schneider B, Paszkowski U. 2024. The AMSlide for noninvasive time-lapse imaging of arbuscular mycorrhizal symbiosis. *J Microsc.* Early View. <https://doi.org/10.1111/jmi.13313>

Click for previous Tools: [Vol1_I1](#) (p. 11), [Vol1_I2](#) (p. 15), [Vol1_I3](#) (p. 16), [Vol2_I1](#) (p. 19), [Vol2_I2](#) (p. 15), [Vol2_I3](#) (p. 15), [Vol3_I1](#) (p. 16), [Vol3_I2](#) (p. 17), [Vol3_I3](#) (p. 26), [Vol4_I1](#) (p. 19), [Vol4_I2](#) (p. 23), [Vol4_I3](#) (p. 34), and [Vol5_I1](#) (p. 21).

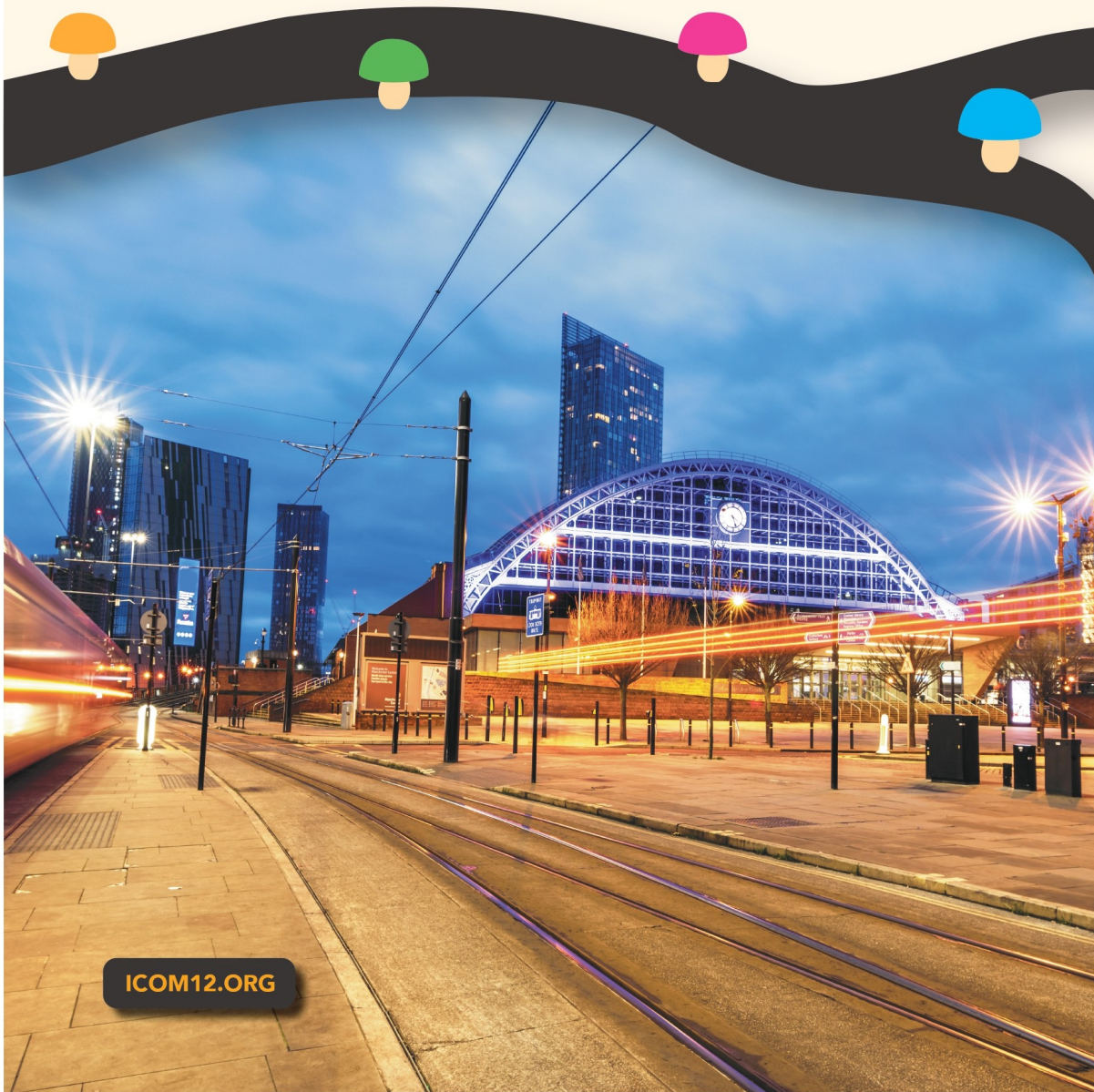
Events

ICOM12: <https://icom12.org/>



12th
INTERNATIONAL
CONFERENCE
ON MYCORRHIZA

4 - 9 August 2024
Manchester, UK



ICOM12.ORG

Events

BOTANICAL EVENTS:

IBC 2024 – XX International Botanical Congress

Website

Madrid, Spain
21 – 27 July, 2024

Organizers: SEBOT, Sociedad Botánica Española

Botanik-Tagung 2024 - International Conference of the German Society for Plant Sciences

Website

Martin Luther University Halle-Wittenberg, Germany
15 – 19 September, 2024

Organizers: Various local organizers

MYCOLOGICAL EVENTS:

45th New Phytologist Ecological and consequences of plant-fungal invasions Symposium: and evolutionary plant-fungal invasions

Website

University of Campinas, Campinas, Brazil
26 – 29 June, 2024

Organizers: New Phytologist Foundation.

12th International Mycological Congress

Website

Maastricht, Netherlands
11 – 15 August, 2024

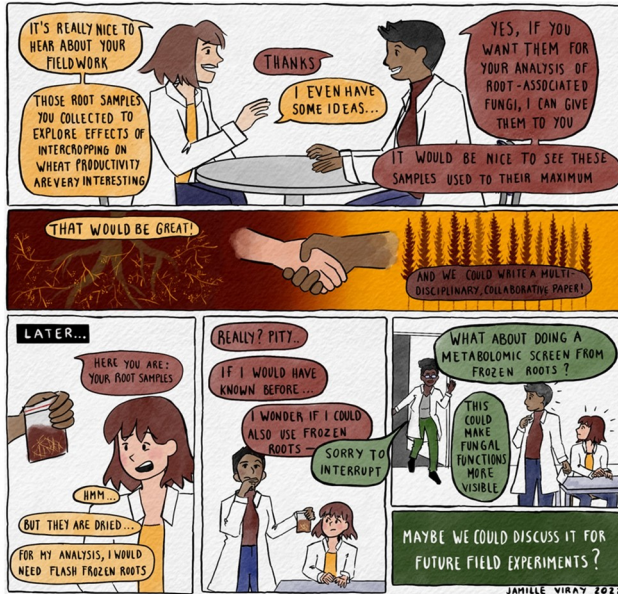
Organizers: Local & International organizers and International Mycological Association.



Call for Collaboration

Empowered through our diversity: How to bring in a new age of plant science collaboration

Neuenkamp, L. & McGale, E. - Plants, People, Planet, 2024



Who: Calling all plant-mycorrhizal scientists!

What: Sign up for a survey on roadblocks to interdisciplinary science collaborations

Why: Our paper (above) calls for your input

Where:

When: Fall 2024
(we will send the survey by email)



A big thanks from two fellow scientists,

Lena

&

Erica



Study: Neuenkamp L, McGale E. 2023. Empowered through our diversity: How to bring in a new age of plant science collaboration. *Plants People Planet* 5: 821-827. <https://doi.org/10.1002/ppp3.10390>

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- **President:** Prof. Dr. Marcel van der Heijden, Agroscope & University of Zurich, Switzerland (marcel.vanderheijden@agroscope.admin.ch).
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- Prof. Dr. Patricia Silva-Flores – Director of Communications, Catholic University of Maule, Chile (psilva@ucm.cl).

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



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