



IMS Newsletter

The International Mycorrhiza Society quarterly e-newsletter



By: Sergio Fajardo, 2022
2nd place at the Valdivia
FungiFest photo contest

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Editorial Vol. 3 Issue 2: ICOM11 and more

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Right before ICOM11, we are happy to release the eighth version of the International Mycorrhiza Society -IMS- Newsletter. We thank all of our readers and contributors for maintaining the functioning of our Newsletter. We sincerely hope this tool contributes to the spread of mycorrhizal research and outreach around the world. Among several recent mycorrhizal news we want to highlight that the Society for the Protection of Underground Networks -SPUN- (<https://spun.earth/>), lead by Toby Kiers just made the cover of Science (DOI: 10.1126/science.add8089), regarding a recent sampling effort in northern Patagonia, Chile.

11th International Conference on Mycorrhiza (ICOM11). Online conference, July 31 to August 5, 2022

The program of ICOM11 is listed on page 18. For more information check also: <https://icom11.casconf.cn>

At ICOM11, two new positions for the IMS Board of Directors will be elected (Vice President and Director of Communications). You can vote until the 2nd of August (Midnight European Time); IMS members will receive an email and can vote. Please vote. The nominees for the Vice President position are: Justine Karst, Sidney Stürmer, Kabir Peay, and Katie Field. The nominees for Director of Communications are Patricia Silva-Flores, Camille Truong, Cameron Egan, and Vasilis Kokoris.

In this issue...

As always, please find in this issue three of our usual sections: Top 10 mycorrhizal articles, short articles/commentaries, and YouTube interviews. Regarding our Top 10 articles vote, we congratulate Johanna Wong-Bajracharya and co-authors for their first position with the *PNAS* article "The ectomycorrhizal fungus *Pisolithus microcarpus* encodes a microRNA involved in cross-kingdom gene silencing during symbiosis", which shows how *Pisolithus microcarpus* encodes a microRNA entering plant cells and stabilizing the symbiosis. The second place went to Feng Zhang and co-authors with their *New Phytologist* article "The ectomycorrhizal basidiomycete *Laccaria bicolor* releases a GH28 polygalacturonase that plays a key role in symbiosis establishment", which suggests that the pectinase LbGH28A (induced by the mycorrhizal symbiosis) is involved in the Hartig net formation and crucial for a successful symbiotic colonization. The third place went to Felipe E. Albornoz and co-authors, with their article, also published in *New Phytologist*, entitled "Agricultural land-use favours Mucoromycotinian, but not Glomeromycotinian, arbuscular mycorrhizal fungi across ten biomes", which describes how Mucoromycotinian and Glomeromycotinian arbuscular mycorrhizal fungi (AMF) are present in different albeit overlapping niches, with the former being more common in temperate agricultural regions.

Regarding our short articles, on this issue please find an article by Nguyen Thi Cuc and Katsuharu Saito about the role of polyphosphate in AMF, including an hypothetical model for P transfer at the fungus-plant interface. Also find an article by Feng Zhang and Francis M. Martin about our Top 2 voted article. In this issue you can also find links to two exciting YouTube interviews: one by Nicolás Marro about his recent work in *New Phytologist* “The effects of arbuscular mycorrhizal fungal species and taxonomic groups on stressed and unstressed plants: a global meta-analysis”, where the authors describe different functional roles of AMF genera across the world, noting that most taxa and functions are understudied. The second interview is of Prof. Dr. Caroline Gutjahr, who will soon lead a new Max Planck department, “Root Biology and Symbiosis”, at the Max Planck Institute of Molecular Plant Physiology, in Potsdam-Golm, Germany.

Finally, and as novelty on this issue, please find a written interview of Nancy Collins Johnson, Regents’ Professor at the School of Earth & Sustainability, Department of Biological Sciences, Northern Arizona University. Nancy talked with us about her impressive career, her beginnings in mycorrhizal research, achievements, her definition of happiness, lessons to students, multilevel selection, and her very influential article from 1997 on the “mutualism–parasitism continuum”.



Top 10 papers on mycorrhizal research*

1. Wong-Bajracharya J, Singan VR, Monti R, *et al.* 2022. The ectomycorrhizal fungus *Pisolithus microcarpus* encodes a microRNA involved in cross-kingdom gene silencing during symbiosis. *Proc Natl Acad Sci USA* 119:e2103527119. <https://doi.org/10.1073/pnas.2103527119>
2. Zhang F, Labourel A, Haon M, *et al.* 2022. The ectomycorrhizal basidiomycete *Laccaria bicolor* releases a GH28 polygalacturonase that plays a key role in symbiosis establishment. *New Phytol* 233:2534-2547. <https://doi.org/10.1111/nph.17940>
3. Albornoz FE, Ryan MH, Bending GD, Hilton S, Dickie IA, Gleeson DB, Standish RJ. 2022. Agricultural land-use favours Mucoromycotinian, but not Glomeromycotinian, arbuscular mycorrhizal fungi across ten biomes. *New Phytol* 233:1369-1382. <https://doi.org/10.1111/nph.17780>
4. Puy J, Carmona CP, Hiiesalu I, Öpik M, de Bello F, Moora M. 2022. Mycorrhizal symbiosis alleviates plant water deficit within and across generations via phenotypic plasticity. *J Ecol* 110:262-276. <https://doi.org/10.1111/1365-2745.13810>
5. Eagar AC, Mushinski RM, Horning AL, Smemo KA, Phillips RP, Blackwood CB. 2022. Arbuscular mycorrhizal tree communities have greater soil fungal diversity and relative abundances of saprotrophs and pathogens than ectomycorrhizal tree communities. *Appl Environ Microbiol* 88:e01782-21. <https://doi.org/10.1128/AEM.01782-21>
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8. Das D, Paries M, Hobecker K, *et al.* 2022. Phosphate starvation response transcription factors enable arbuscular mycorrhiza symbiosis. *Nat Commun* 13:477. <https://doi.org/10.1038/s41467-022-27976-8>
9. Joswig JS, Wirth C, Schuman MC, *et al.* 2022. Climatic and soil factors explain the two-dimensional spectrum of global plant trait variation. *Nat Ecol Evol* 6:36-50. <https://doi.org/10.1038/s41559-021-01616-8>
10. Looney B, Miyauchi S, Morin E, *et al.* 2022. Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyperdiverse lineage of mushroom-forming fungi. *New Phytol* 233:2294-2309. <https://doi.org/10.1111/nph.17892>

*Selected from 194 Web of Science articles published between *January – April, 2022* by: Justine Karst, Jonathan Plett, Melanie Jones, Marcel van der Heijden, Francis Martin, Jan Jansa, John Klironomos, Liang-Dong Guo, Miranda Hart, Jason Hoeksema, Judith Lundberg-Felten, Bala Chaudhary, Annegret Kohler, Joseph Cooper, Junling Zhang, and César Marín.

Research commentaries

Deciphering the function of a symbiosis-induced pectinase in ectomycorrhiza

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Ectomycorrhizal fungi establish a symbiotic mutualistic interaction with tree roots where they facilitate the acquisition of nitrogen, phosphorus, and micronutrients available in soils (van der Heijden *et al.* 2015). The development of these symbioses entails the formation of a mantle-like sheath of hyphae around the root, a fungal network called the Hartig net, growing between rhizodermal cells of the root, and an external hyphal network exploring the rhizosphere (Balestrini and Kottke 2016). The formation of the Hartig net within a host root likely relies on both the mechanical forces generated by the hydrostatic pressure at the tip of growing hyphae and on the hydrolytic activity of secreted fungal plant cell-wall-degrading enzymes (PCWDEs) (Martin *et al.* 2008; Veneault-Fourrey *et al.* 2014). Our recent genomic and transcriptomic analyses support the role of symbiosis-induced PCWDEs in plant cell wall remodeling in the establishment of the *Populus-Laccaria* symbiosis. This hypothesis is based on the observation that when fungal hyphae colonize the root apoplastic space, a set of fungal PCWDE genes, such as those coding for the expansin-like *LbEXP* and the endoglucanase *LbGH5_CBM1* acting on cellulose are upregulated. In addition, several genes belonging to the AA9 (lytic polysaccharide monooxygenases, LPMOs), and xyloglucan hydrolase GH12 families are also upregulated in symbiotic tissues

(Veneault-Fourrey *et al.* 2014; Zhang *et al.* 2018; Anasontzis *et al.* 2019; Labourel *et al.* 2020).

In our recent study (Zhang *et al.* 2022), we functionally characterized the ectomycorrhiza-induced endopolygalacturonase LbGH28A of *Laccaria bicolor* (Fig. 1). In this paper, we showed that this enzyme is involved in the Hartig net formation using a combined set of molecular and biochemical methods. First, we confirmed by qPCR that the *LbGH28A* transcripts were barely detectable in free-living mycelium, but the gene expression was significantly upregulated in ectomycorrhizal root tips. Thus, we were wondering whether this PCWDE was involved in the symbiotic development. To test this contention, we generated *L. bicolor* transformants using the *Agrobacterium*-mediated transformation RNAi method to silence the gene expression (Kempainen and Pardo 2010). Cogent with our hypothesis that *LbGH28A* was involved in Hartig net formation, we found that a series of RNAi-mutants showed a reduced ability to establish ectomycorrhizas and the Hartig net formation was aborted. Altogether our work proved that the LbGH28A enzyme played an important role in the establishment of the symbiotic interface.

We then produced the LbGH28A recombinant protein in the yeast *Pichia pastoris* in collaboration with Dr. Jean-Guy Berrin's group

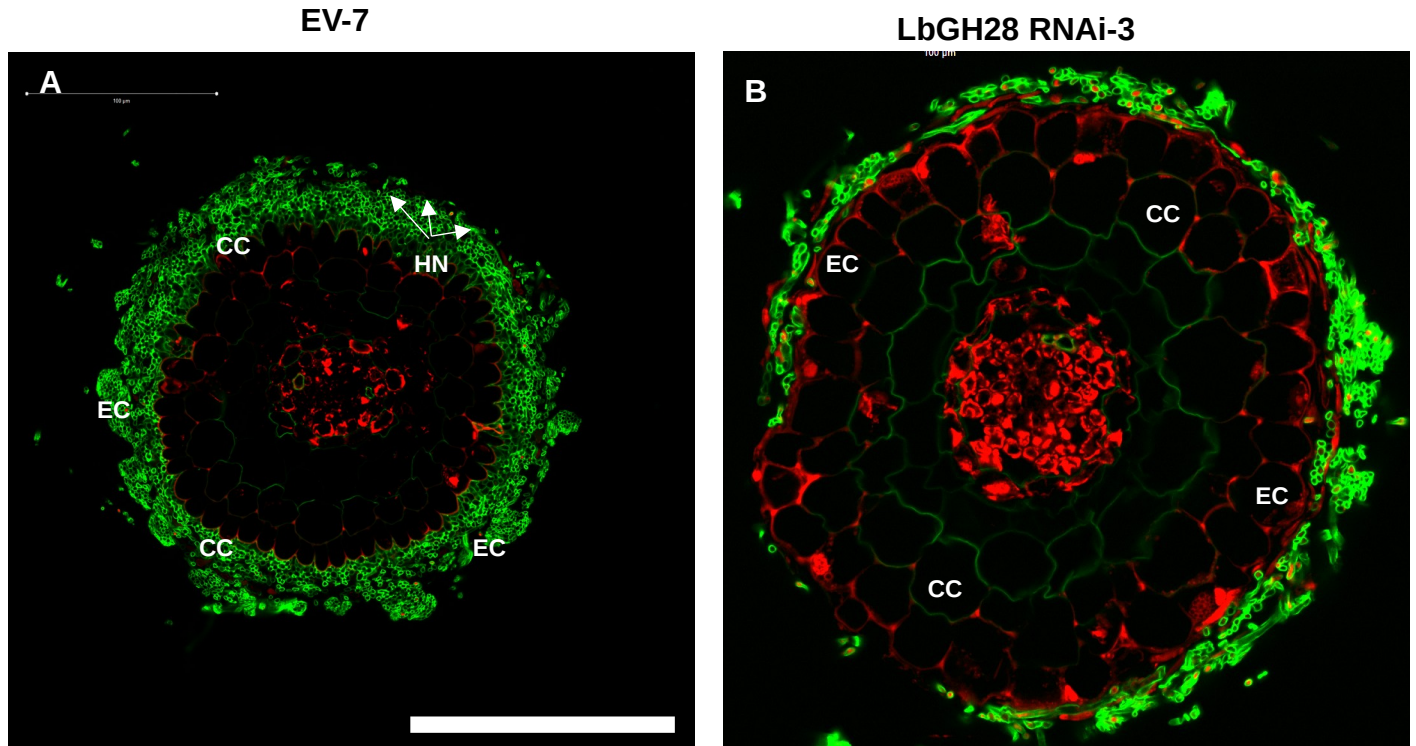


Figure 1. *LbGH28A* is required for Hartig net formation. Representative transverse cross sections of *Populus* roots colonized by (A) empty vector (EV-7) control strains or (B) RNAi-silenced (*LbGH28* RNAi-3) strains sampled three weeks after contact. Colonized roots were sectioned and stained with WGA conjugated with Alexa Fluor 488 (green) and propidium iodide (red) and imaged on a confocal laser scanning microscope. HN, Hartig net; EC, epidermal cells; CC, cortical cells. Scale bar, 100 μm Hartig net; EC, epidermal cell; CC, cortical cell.

at INRAE-Marseilles, France. The recombinant protein was used to assay the enzymic activity. In these assays, *LbGH28A* showed a high hydrolytic activity when pectin or polygalacturonic acid were used as substrates, confirming that *LbGH28A* was an endopolygalacturonase. The next challenge was to characterize the location of this secreted pectinase in ectomycorrhizal roots. We performed a series of experiments relying on indirect immunofluorescence (IIF) confocal microscopy and immunogold cytolocalization by transmission electron microscopy. The IIF assay showed that *LbGH28A* accumulated at the periphery of the hyphae forming the Hartig net and in the mantle hyphae. The immunocytolocalization study indicated that *LbGH28A* accumulated in the symbiotic interface, at the tip of the hyphae penetrating between epidermal cells. In summary, *LbGH28A* was induced by symbiotic

interaction and localized in the tip of Hartig net to potentially modify the plant cell wall during ectomycorrhizal development.

As most ectomycorrhizal fungi, *L. bicolor* lacks GH6 and GH7 cellobiohydrolases and encodes a restricted repertoire of PCWDEs. We have shown in the present study and in Zhang *et al.* (2018) that the remaining set of PCWDEs still play important roles in the symbiotic interaction. These enzymes have been recruited during the evolution of ectomycorrhizal fungi to facilitate the entrance of the hyphae in host roots. However, we are left with a number of ongoing questions including: how do these symbiosis-related PCWDEs alter the mechanical cell-wall properties during ectomycorrhiza development? How do these secreted enzymes work together to alter the polysaccharide composition at the symbiotic

interface? Do the modifications in the cell wall structures trigger the host plant immune response? If a moderate plant immune response is activated by cell wall modification, how does the colonizing fungus dampen these defense reactions? Future research will tackle these questions and also investigate the role of other symbiosis-induced PCWDEs, such as LPMOs.

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Role of polyphosphate in arbuscular mycorrhizal fungi

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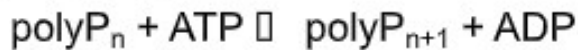
The fungus supply of phosphorus (P) to the host is a critical function of arbuscular mycorrhizal (AM) symbiosis. This function is important for plant survival and growth in ecosystems as well as for the application of AM symbiosis to sustainable agriculture. Since the discovery of the beneficial mycorrhizal effect mediated by P uptake by Baylis (1959), many researchers have studied the physiology, biochemistry, genetics, and ecology of the symbiotic P acquisition (Koide and Mosse 2004). The discovery that the mycorrhizal P uptake pathway is usually activated even in nonresponsive plant species (Smith *et al.* 2003) and that AM-specific Pi transporters in plants are required for the Pi uptake delivered by AM fungi (Javot *et al.* 2007), have greatly influenced mycorrhizal research. Nevertheless, the mechanism of the symbiotic P acquisition is not completely understood. Once the molecular and genetic aspects of this mechanism are understood, it may lead to the development of technologies that can quantitatively evaluate AM functions, as has been previously determined for nitrogen-fixing activity in root nodule symbiosis. This would be useful for research into both the ecology and agricultural applications of the AM symbiosis.

AM fungi absorb Pi from the soil via Pi transporters of the extraradical mycelium (Harrison and van Buuren 1995). Polyphosphate (polyP), a linear polymer of Pi linked by high-energy phosphoanhydride bonds, is rapidly formed from the absorbed Pi (Ezawa *et al.* 2004). PolyP accumulated in the tubular vacuoles is translocated to the intraradical mycelium and may be a major

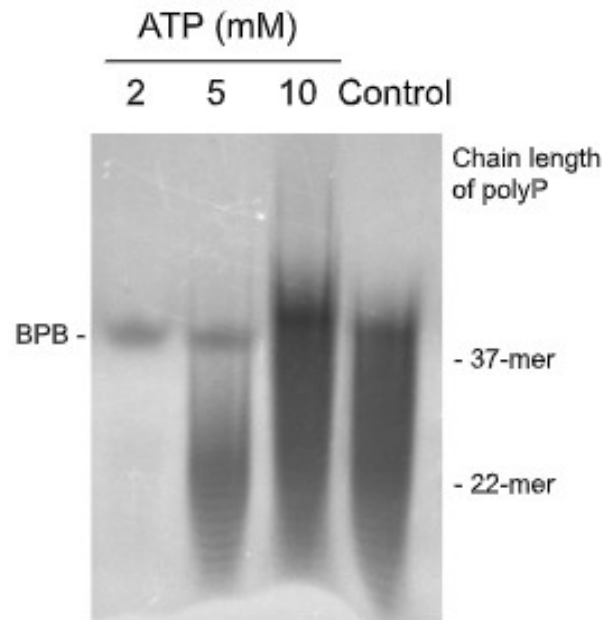
source of P eventually exported to the host. Several mechanisms for P efflux from the arbuscule have been proposed, but none are fully understood (Saito and Ezawa 2016; Ezawa and Saito 2018; Nguyen and Saito 2021; Xie *et al.* 2022). AM-specific Pi transporters localized on the periarbuscular membrane take up Pi released into the periarbuscular space (Harrison *et al.* 2002). A polyP is a crucial molecule in the symbiotic P transport system; however, research on polyP in AM symbiosis has not progressed substantially due to the difficulties of genetic and molecular analysis of AM fungi as well as the limited analytical techniques available for polyP.

For several years, no eukaryotic polyphosphate synthases had been identified; however, a yeast study revealed that the vacuolar transporter chaperone 4 (VTC4) catalyzes polyP synthesis using ATP as a substrate (Hothorn *et al.* 2009). To determine whether AM fungal VTC4 also catalyzes this reaction, we examined the biochemical properties of a recombinant catalytic domain of the *Rhizophagus irregularis* VTC4 (VTC4*) (Nguyen *et al.* 2022). VTC4* synthesized polyP using ATP as a substrate, as expected. Moreover, we investigated whether VTC4* catalyzed the reverse reaction. Interestingly, the reverse reaction occurred when polyP and high concentrations of ADP were present in the reaction solution, resulting in the depolymerization of polyP and the generation of ATP. At ATP:ADP ratios of 2:1–5:1, the reaction direction was changed. However, these findings are based on *in vitro* testing. *In*

Forward reaction



Reverse reaction



Forward and reverse reactions of VTC4. VTC4* was incubated with ATP (2, 5, 10 mM) and ADP (5 mM) in the presence of polyP. Longer polyP was synthesized at 10 mM ATP compared to control (without VTC4*), whereas polyP depolymerization was observed at 2 and 5 mM ATP.

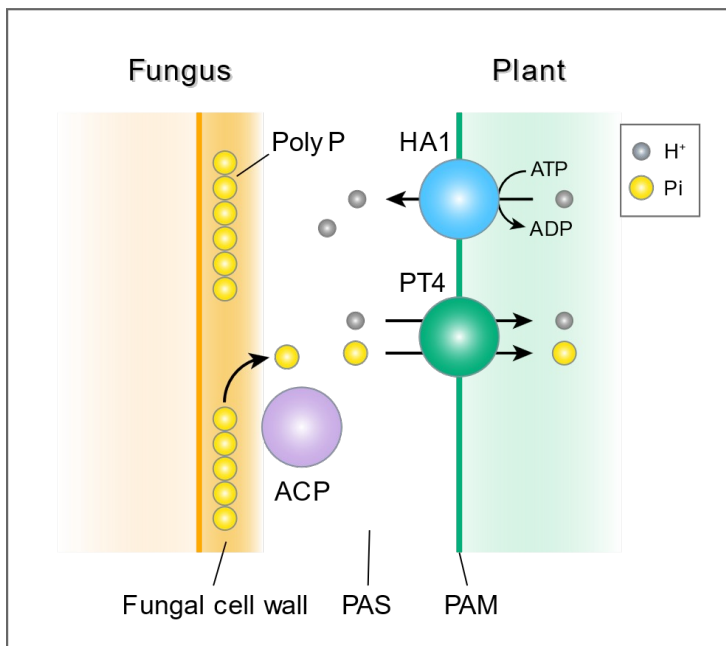
in vivo, the VTC complexes are expected to be found in the tonoplast. Future research will be required to determine whether AM fungal VTC4 catalyzes both forward and reverse reactions *in vivo*. We reasoned that a massive accumulation of polyP in vacuoles would be too energy-intensive since polyP synthesis requires a lot of ATP. Assuming that the reverse reaction occurs *in vivo*, energy would be conserved in polyP metabolism via VTC-mediated regulation of polyP accumulation and ATP regeneration. VTC4 contains an SPX domain, which acts as a sensor to regulate cellular Pi homeostasis, and the polyP polymerizing activity of VTC4 is altered by intracellular phosphate levels in yeast (Wild *et al.* 2016). VTC may be important in integrating P homeostasis with energy regulation via polyP metabolism, providing insight into the C-P exchange in the AM symbiosis.

We have also examined polyP metabolism in AM fungi histochemically (Nguyen and Saito 2021). In arbuscules of *R. irregularis* colonizing *Lotus japonicus*, polyP was mainly found in the cell walls of the trunk hyphae, but rarely in

the fine branches. However, in the *L. japonicus* H⁺-ATPase *ha1* mutant defective in symbiotic P uptake, polyP was found in the cell walls of some fine branches. The double staining revealed a contrasting distribution of polyP and acid phosphatase activity in arbuscules. The acid phosphatase activity was observed in the periarbuscular space around the fine branches. Based on our findings, we proposed a model of P transfer at the symbiotic interface in arbuscules, in which polyP secreted into the cell wall of the fine branches is hydrolyzed by acid phosphatases in periarbuscular space, and the released Pi is absorbed by plant Pi transporters. However, we do not know which acid phosphatases are active in the periarbuscular space or how polyP is incorporated into the fungal cell wall. Our model is one of several hypotheses for P release from AM fungi, and others, such as P efflux by fungal Pi transporters and the involvement of vesicle trafficking mediated by SYG protein, have recently been proposed (Ezawa and Saito 2018; Xie *et al.* 2022). Since definitive evidence for these models has yet to be obtained, it is necessary to examine the

possibility that the P efflux pathways depicted in these models exist independently or are interconnected.

Molecular genetic analysis on AM fungi is very difficult due to their obligate symbiotic nature. Myristate has recently been shown to initiate asymbiotic growth of AM fungi, indicating the viability of a pure culture of AM fungi (Sugiura *et al.* 2020). If the genetic transformation of AM fungi can be achieved using this culture technique, we may be able to gain a better understanding of the mechanism of P translocation and homeostasis in AM fungi.



Hypothetical model for P transfer at the fungus-plant interface. The model illustrates that polyP is released into the cell walls of fine branches and then subject to hydrolysis by acid phosphatase (ACP) activity located at the periarbuscular space (PAS). The liberated Pi is delivered into the plant cell by the symbiotic Pi transporter, PT4, driven by a H⁺ gradient generated across the periarbuscular membrane (PAM) by the H⁺-ATPase HA1.

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Nancy C. Johnson interview:

Mycorrhizal ecology, happiness, lessons to students, multilevel selection, and the “mutualism–parasitism continuum”

By: César Marín^{1*}

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Nancy Collins Johnson Ph.D. is a Regents' Professor at the School of Earth & Sustainability (School that she directed for four years), Northern Arizona University, where she has been working since 1997. Nancy has a B.Sc. in Biology and a Ph.D. in Ecology both from the University of Minnesota, and a M.Sc. in Botany from the University of Wisconsin, where her love for the mycorrhizal symbioses started. She has had an impressive career, which among other things, includes two Fulbright research fellowships at Lund University (Sweden) and at the Czech University of Life Sciences, an NSF postdoctoral fellowship, and a Bullard Fellowship at Harvard Forest. She advises or is a fellow of scientific societies like Society for the Protection of Underground Networks, American Association for the Advancement of Science, and Ecological Society of America, among others, and in 2018 she received the Deborah A. Neher Career Award from the Soil Ecology Section of the Ecological Society of America. Nancy usually takes many panels, mentoring, and editorial roles. Through the years she has been invited to dozen of seminars and talks around the world. Her research projects, since 1990, have targeted fundamental questions in mycorrhizal ecology: from pioneer works in the “mutualism–parasitism continuum” and the response of mycorrhizas to a changing, warmer world during the 1990s, effects (of management) and applications of mycorrhizas in agricultural settings, to a



system analysis perspective of the beneficial effects of arbuscular mycorrhizal fungi in sorghum that includes genetics, genomics, imaging, and microbiomics. Nancy’s research goes beyond mycorrhizas and Arizona, extends to fundamental and applied questions in soil ecology, and extends to the Czech Republic, the Serengeti, and around the world.

With more than 100 refereed publications and up to 18 graduate students and postdocs supervised, her impact on mycorrhizal ecology, and on how we think about mycorrhizas, is outstanding. At some point, some of her ideas could have been thought of as “out of the box”, but given their strength and continuing supporting evidence, they are now well established in mycorrhizal ecology. In particular, seeing the mycorrhizal

symbiosis as context-dependent (i.e., in soil nutrients; the “mutualism–parasitism continuum”) still feeds current debates in our area, and could even affect how we define and characterize a mycorrhiza, for example when non-nutritional mycorrhizal functions are taken into account. Nancy continues to explore new perspectives (i.e., hyphae-bacterial interactions, multilevel selection) and is very approachable, and kind, and all these excellent characteristics are reflected in the people she has supervised. In our new section at the IMS Newsletter, among other things, Nancy shares with us her beginnings in mycorrhizal research, what she considers her biggest achievements, her definition of happiness, advice to Ph.D. students, and how she sees our field in the future.

- Why and when did you start to study the mycorrhizal symbiosis?

I have been interested in soil ecology and plant symbioses since I was a child. In 1983, when I started my MS degree in Botany at the University of Wisconsin, I pondered several options for study systems (Azolla-cyanobacteria, legume-rhizobia, etc.), and when I learned about mycorrhizas, I immediately knew that I wanted to study them. I fortuitously met Tom Hunt, a graduate student in the Restoration Ecology program who had a nicely replicated experiment in a taconite mine not far from Madison. Sampling Tom’s experiment provided a wonderful opportunity to study mycorrhizal relationships in early and late successional plants as well as the responses of mycorrhizal fungi to restoration treatments. I collected soil and root samples from the experiment and tried to extract arbuscular mycorrhizal (AM) fungal spores and stain the roots to measure AM colonization based on published protocols. It was very difficult because no one at the university studied mycorrhizas, and I really

had no idea what spores and colonization should look like. It was clear that I couldn’t accomplish the measurements necessary for my research alone. My advisor Michael Adams suggested that I call Mike Miller at Argonne National Laboratory to ask for help. I’ll always remember that Mike Miller said “*you think it is hard to study mycorrhizae? We do too, and we’re experts.*” Then he invited me to his lab to learn techniques with his postdoc A-C McGraw. I also reached out to Edie and Mike Allen who were doing similar studies in Wyoming. With everyone’s help, we discovered many new things and were able to publish three papers from the taconite mine research. I was hooked on mycorrhizas and continued to study them for my PhD with Dave Tilman at the University of Minnesota, and to this day I am still intrigued by mycorrhizal symbioses.

“Successful students will be my legacy, and this work is still under construction”

- What do you consider is your biggest achievement in mycorrhizal research? How do you see your legacy? Or is this work under construction?

Successful students will be my legacy, and this work is still under construction. I have been blessed with some really smart and creative students. I continue to be impressed by their accomplishments, and it is rewarding to think that I may have helped them get started in their professional trajectories.

- Your 1997 “mutualism–parasitism continuum” paper has influenced how many of us think about mycorrhizas, how they work, and their ecology. What is the story behind it, how it came about? What is the main conclusion of that paper? After 25 years, do these conclusions still hold?

The main conclusion of that paper is that the influence of mycorrhizal symbioses on plants is context dependent, and this conclusion has survived the test of time. The International Conference on Mycorrhizas (ICOM) played a key role in that publication. In 1996, in preparation for the First ICOM at the University of California, Berkeley, Randy Molina asked Jim Graham, Andrew Smith and me to organize a session entitled: *'Can mycorrhizal associations be parasitic? Re-addressing our definition of mycorrhiza: structure vs. function.'* At that time, many people felt that by definition mycorrhizas are mutualistic, but this idea was challenged by publications by researchers like Gabe Bethlenfalvai, James Hendrix, Jim Graham, Andrew Smith and myself who had used the word 'parasitism' to describe plant growth depressions caused by mycorrhizal fungi. The workshop was very well attended, with over a hundred mycorrhizal researchers in the audience and I was completely unprepared for the fervor and contentiousness of the controversy about whether mutualistic function should be a defining characteristic of mycorrhizas. In my own work in taconite tailings and grasslands, I observed that mycorrhizal function is context dependent, the same pairs of host plants and fungi could either enhance or depress plant fitness depending on environmental conditions. Other researchers had published similar findings and I was surprised that many people in our audience so adamantly rejected the notion that in some situations, mycorrhizas can have negative effects on plants. The following week I realized that mycorrhizal science could benefit from ecological theories about species interactions, and I outlined the key points of the 1997 paper. I contacted Jim and Andrew to see if they would like to co-author a paper on this subject, and they were both very enthusiastic about the idea. At the time, I was working out

of my basement in Santa Fe New Mexico, so I got a babysitter to care for the children and went to St. John's College library to write my parts of the manuscript on a pad of yellow paper (laptops were rare back then). Working with Jim and Andrew was great, and before the end of the year we had a manuscript ready to submit to *New Phytologist*. I am happy that our publication accomplished what we had hoped. Our 1996 ICOM workshop was one of the most uncomfortable events of my life, but in hindsight it was good because it stimulated Jim, Andrew and me to build on the cost-benefit approaches of Alastair Fitter and Roger Koide and propose a theoretical framework of the conditions that are expected to generate mutualistic, commensal or even parasitic mycorrhizal symbioses. This framework has been the basis of much of my own research over the past 30 years.

- How do you define "success" and "happiness" in science? When were you happiest when doing science?

Success is when you make a discovery that advances our understanding of how the world works. My happiest times as a scientist happen when all the pieces of a puzzle line-up and new insights emerge. Major "eureka moments" follow years of work in the field, greenhouse and laboratory, but even mundane tasks - like counting and identifying mycorrhizal fungal spores using a microscope - can be enjoyable, especially if you listen to good music. Science is a systematic process for exploring the unknown - and it is fun.

- What would you recommend to PhD students in general?

When designing your graduate research program always start with a question and then figure out how to answer it using straightforward observations and experiments. Know the literature that is

relevant to your question and be sure to address new aspects that build upon what is already known. Experiments take time and effort so don't waste your time addressing inconsequential questions or questions that have already been sufficiently answered. Strive to address big questions that fit into a larger theoretical framework. Don't be shy to contact other scientists who may be able to help you. Plan a variety of different experiments and be prepared to have many of them fail. Research is the process of searching over-and-over-and-over again, that is why it is called re-search. When things don't work out as expected, learn what you can from the experience and move on. Enjoy the freedom to explore the unknown and be humble when you discover something new.

- What do you do in stressful times?

I go for a long walk in the forest or other natural area, practice some yoga and then try to get a good night sleep.

- What is your favorite conference to attend and why?

My favorite conference is ICOM because it is a small and focused meeting that allows me to travel to interesting places, make new friends and meet up with old ones. It is the only conference where everyone is a mycorrhizal geek.

- What is your favorite mycorrhizal fungal species?

Gigaspora margarita is my favorite mycorrhizal fungal species because its beautiful, big, fat, pearly white spores are so easy to see – even without a microscope!

- How to integrate bacteria and other organisms interacting with mycorrhizal hyphae into understanding the (multi)functionality of this symbiosis? How to account for those interactions? This is a great question, and something that



Gigaspora margarita. Photo by: Vasilis Kokkoris

we think about a lot in my research lab. The first step is to characterize the composition of microbial communities associated with mycorrhizal fungi and discover any patterns that may occur. The advent of high-throughput genetic analyses has made it possible to begin to elucidate the complex microbial communities associated with mycorrhizal fungi. The next step is to look for causal linkages between the structure of the mycorrhizal microbiome and the function of mycorrhizal symbiosis. This will require many creative experiments using both reductionist and holistic methods. It will also require collaborations with a diversity of researchers including bacteriologists, soil scientists, ecologists, plant physiologists, geneticists and biochemists. This is an exciting time to be a mycorrhizal researcher because new analytical and computational methods make it possible to observe and measure microbes like never before.

- A favorite topic of mine is multilevel selection (natural selection, ie. phenotypic variability, differential fitness, and heritability, occurring at least in two levels of the biological hierarchy). You have written about this regarding mycorrhizas. Do you think a multilevel selection perspective would lead to a better

understanding of the mycorrhizal symbiosis? If so, how?

Yes, I believe that the concept of multilevel selection will help generate new insights about mycorrhizas because this perspective accounts for the emergent properties that arise in mycorrhizal systems (i.e. the sum of plant-fungus-microbe-environment interactions). The traditional view of natural selection as a solely population scale phenomenon does not accommodate horizontal gene transfer, nor can it explain how mycorrhizal symbioses between plant genotypes and their associated team of microbes become adapted to local environmental conditions. In contrast, multilevel selection recognizes that variation and heritability can occur at both population and community scales and opens the possibility that groups of plants, fungi and microbes may be selected as a team based on their cumulative success in their particular environment. Group Selection Theory has been around a long time and it is finally gaining more main-stream acceptance. I believe that the next innovation in evolution science will build on group selection to develop Team Selection Theory, and mycorrhizal systems may be the perfect system to develop and test this theory.

- There are inevitable biases when studying mycorrhizas. Besides general geographical biases (ie. towards the Northern hemisphere), also more specific biases, for example, in certain regions towards the dominant mycorrhizal types (ie. arbuscular mycorrhizal fungi in the tropics), or towards the effects of mycorrhizas on plant growth and nutrition, while other functions as soil aggregation, chemical defense, and drought and disease resistance are less studied. Do you think these biases have an effect on how we understand the mycorrhizal symbiosis?

And if so, how to counteract such biases?

I agree, historical variation in scientific literature about mycorrhizas creates biases in our understanding of the symbiosis. In my opinion, the best way to counteract this problem is to increase the diversity of mycorrhizal research endeavors. One way to accomplish this goal is to encourage funding agencies to provide additional support for research in understudied parts of the world and to encourage more cross-cutting collaborations among mycorrhizal researchers and scientists in diverse applied fields such as soil science, entomology, plant pathology, agronomy and forestry as well as basic sciences such as chemistry, physics and genetics. These collaborations are likely to reveal new and exciting discoveries about the contributions of mycorrhizal symbioses to our world.

- Finally, what ecological questions do you think mycorrhizal researchers should address in the following decades? How do you see our research area developing?

Your previous question helps answer this. In my opinion, future research should strive to examine mycorrhizas in understudied ecosystems and expand the breadth of knowledge about the mechanisms that control the function of mycorrhizal symbioses in the world outside of the greenhouse and laboratory. Better understanding of the genetic mechanisms that control mycorrhizal symbiosis along with the chemical signaling among symbionts are sure to advance our field. We should expect many surprises as we expand the scope of our inferences to include the complex interactions among biotic and abiotic components of ecosystems. This expansion will meld our science with other fields of study and ultimately provide a better understanding of the world that we live in.

YouTube interviews*

- Nicolás Marro on the effects of AMF species/taxa on stressed and unstressed plants

César Marín interviews Nicolás Marro, Researcher at the Universidad Nacional de Córdoba, who discusses how different AMF species and families influence plant performance under normal conditions and also under stressful conditions (pathogens, parasites, herbivores, drought, salinity, and heavy metals).

Interview: <https://southmycorrhizas.org/reading/april-2022/>

Study: Marro N, Grilli G, Soterias F, *et al.* 2022. The effects of arbuscular mycorrhizal fungal species and taxonomic groups on stressed and unstressed plants: a global meta-analysis. *New Phytol* 235:320-332.

<https://doi.org/10.1111/nph.18102>

- Caroline Gutjahr on how arbuscular mycorrhiza goes Max Planck!

César Marín interviews Prof. Dr. Caroline Gutjahr, who talks with us about an exciting, new Max Planck department that she will lead, “Root Biology and Symbiosis”, at the Max Planck Institute of Molecular Plant Physiology, in Potsdam-Golm, Germany.

Interview: <https://southmycorrhizas.org/reading/july-2022/>

More info at:

https://www.mpimp-golm.mpg.de/2716780/news_publication_18759809_transferred

*Section by:

South American Mycorrhizal Research Network

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



Tools

→ Database and pipeline for LSU rDNA of arbuscular mycorrhizal fungi (AMF) from environmental samples

Delavaux *et al.* (2022) present an updated and improved database and bioinformatic pipeline for the phylogenetic determination of AMF, based on the large subunit (LSU) rRNA gene. Additional outgroup sequences have been included. The authors also improved their existing pipeline.

Study: Delavaux CS, Ramos RJ, Sturmer SL, Bever JD. 2022. Environmental identification of arbuscular mycorrhizal fungi using the LSU rDNA gene region: an expanded database and improved pipeline. *Mycorrhiza* 32:145-153. <https://doi.org/10.1007/s00572-022-01068-3>

→ Multiplex qPCR to distinguish AMF species from roots and soil

Heller and Carrera (2022) present novel multiplex real-time PCR to target the glomalin genes of 11 different AMF species, common to temperate agricultural soils. They were able to independently detect and measure the abundance of these fungi using DNA extracts from soil and or root tissue. This tool could give information about the specific contribution of individual (or consortia) AMF species, thus helping to design biofertilizers.

Study: Heller WP, Carrara JE. 2022. Multiplex qPCR assays to distinguish individual species of arbuscular mycorrhizal fungi from roots and soil. *Mycorrhiza* 32:155-164. <https://doi.org/10.1007/s00572-022-01069-2>

→ Synchrotron X-ray computed tomography and fluorescence/X-ray absorption to image and model P uptake by mycorrhizal hyphae

Keyes *et al.* (2022) used synchrotron X-ray computed tomography to visualize mycorrhizas in soil and synchrotron X-ray fluorescence/X-ray absorption near edge structure (XRF/XANES) elemental mapping for P, sulphur (S) and aluminium (Al) in combination with modelling.

Study: Keyes S, van Veelen A, McKay Fletcher D, *et al.* 2022. Multimodal correlative imaging and modelling of phosphorus uptake from soil by hyphae of mycorrhizal fungi. *New Phytol* 234:688-703. <https://doi.org/10.1111/nph.17980>

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), and [Vol3_I1](#) (p. 16).

ICOM11 program

TIME UTC+8:00, Beijing	Date	Aug 1st	Aug 2nd
	Topic	Mycorrhizal Omics	Mycorrhizal Diversity and Ecology
	Chairs	Francis Martin & Feng Zhang	Ian Dickie & Cheng Gao
08:00-08:50	Planery Speaker	Nicolas Corradi	Maarja Öpik
08:50-09:30	Keynote Speaker	Pierre-Marc Delaux	Kabir Peay
09:30-10:00	Coffee Break		
10:00-10:35	Keynote Speaker	Annegret Kohler	Cheng Gao
10:35-11:10	Keynote Speaker	Feng Zhang	Anne Pringle
11:10-11:45	Keynote Speaker	Sara Branco	Martin Bidartondo
11:45-12:20	Keynote Speaker	Nicole Hynson	Kitty Gehring
12:20-13:30	Break & Lunch		
13:30-15:00	Poster Session	Poster Session	Poster Session
15:00-17:30	Concurrent Session 1	Mycorrhizal Omics	Biogeography
	Chairs	Gang Wu & Tatsu Ezawa	Maarja Öpik & Colin Averill
15:00-17:30	Concurrent Session 2	Mycorrhiza & Pollution	Mycorrhizas in Restoration & Reforestation
	Chairs	Damien Blaudez & Baodong Chen	James D. Bever & Yinli Bi
15:00-17:30	Concurrent Session 3	Mycorrhizas in Ecosystems	Evolution of Mycorrhizas
	Chairs	Xubing Liu & Katie Field	Leho Tedersoo & Xiaoke Xing

TIME UTC+8:00, Beijing	Date	Aug 3rd	Aug 4th
	Topic	Mycorrhiza & Agriculture & Global Change	Cross-Talk and Trade
	Chairs	Marcel van der Heijden & Gu Feng	Jonathan Plett & Baoming Ji
08:00-08:50	Planery Speaker	Miranda Hart	Ertao Wang
08:50-09:30	Keynote Speaker	Stephanie Watts-Williams	Toby Kiers
09:30-10:00			
10:00-10:35	Keynote Speaker	Megan Ryan	Colin Averil
10:35-11:10	Keynote Speaker	Mayra Elena Gavito	Krista Plett
11:10-11:45	Keynote Speaker	Junling Zhang	Carolin Gutjahr
11:45-12:20	Keynote Speaker	Mohammad Bahram	
12:20-13:30			
13:30-15:00	Poster Session	Poster Session	Perspectives & Outlook on Mycorrhizal Research 1. Francis Martin: Genomics and Physiology of Mycorrhizae 2. Marcel van der Heijden: Ecology and Agriculture of Mycorrhizae
15:00-17:30	Concurrent Session 1	Mycorrhiza & Global Change	Molecular Biology & Physiology
	Chairs	Ian Dickie & Yong Zheng	Claire Veneault Fourrey & Feng Zhang
15:00-17:30	Concurrent Session 2	Mycorrhiza & Agriculture	Community Ecology
	Chairs	Junling Zhang & Tim Cavagnaro	Cheng Gao & Jeff Powell
15:00-17:30	Concurrent Session 3	Mycorrhizal Function	Edible Mushrooms
	Chairs	Justine Karst & David Johnson	Zhuliang Yang & Alessandra Zambonelli

Find the detailed program at: <https://icom11.casconf.cn/>

Events

MYCORRHIZAL EVENTS:

ICOM11

[Website](#)

China National Convention Center,
Beijing, China

31 July – 5 August, 2022



Organizers: Chinese Society of Mycology
and IMS
III International Symposium on
Mycorrhizal Symbiosis in South
America

[Website](#)

Instituto SINCHI, Leticia, Colombia
24 August – 2 September, 2023



Organizers: South American Mycorrhizal
Research Network and Instituto SINCHI

EVENTS POSTPONED DUE TO COVID-19:

- 18th International Symposium on Microbial Ecology

[Website](#)

Lausanne, Switzerland

13 – 19 August 2022

Organizers: International Society for Microbial Ecology

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

[Website](#)

Campinas, Brazil

Date not yet announced

Organizers: New Phytologist Trust and symposium organizers.

- 10th International Symposium on Forest Soils - ISFS 2022

[Website](#)

Zhijiang Hotel, Hangzhou, China

17 – 21 October, 2022

Organizers: Zhejiang A&F University and others



- 3rd Global Soil Biodiversity Conference

[Website](#)

Clayton Hotel, Dublin, Ireland
13 – 15 March 2023



GLOBAL
SOIL BIODIVERSITY
INITIATIVE

Organizers: Global Soil Biodiversity Initiative

EVENTS AS SCHEDULED:

10th Congress of the International
Symbiosis Society

[Website](#)

Centre des congrès, Lyon, France
25 – 29 July, 2022



Organizers: International Symbiosis
Society

22nd World Congress of Soil Science
2022

[Website](#)

Scottish Event Campus, Glasgow, UK
31 July – 5 August, 2022



Organizers: British Society of Soil Science

III Argentinian Mycology Meeting

[Website](#)

Universidad Nacional de Córdoba,
Córdoba, Argentina
17 – 21 October, 2022

Organizers: Universidad Nacional de
Córdoba & Asociación Micológica Carlos
Spegazzini



IMS Newsletter

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ICOM11 is scheduled for 31 July – 5 August, 2022 in Beijing, China. More details at: <https://icom11.casconf.cn/>

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