



IMS Newsletter

The International Mycorrhiza Society quarterly e-newsletter



Amanita gayana, southern Chile
Photo: Cristian Stuardo

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Editorial

Mycorrhizas & More

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We are very happy to present you the second newsletter of the International Mycorrhiza Society. The purpose of this newsletter is to provide you with information and recent highlights on one of the most ancient and abundant symbiosis on Earth, namely that between plants and mycorrhizal fungi. This symbiosis drives the growth of >80% of all land plants and it plays a key role in driving ecosystem functioning of our planet.

This newsletter includes a list of the top 10 mycorrhizal papers that a panel of experts have selected from across the different disciplines published over the last four months. We congratulate Radhakrishnan and colleagues (*Nature Plants*, 2020) with the first rank and their impressive work demonstrating that an ancestral signalling pathway is conserved in intracellular symbioses-forming plant lineages. In addition, this newsletter provides very nice research commentaries from groups around the world giving background insights into their recently published papers on fungal succession (Logan Gray and Gavin Kernaghan, Canada), the importance of rRNAs in the mycorrhizal symbiosis (Alessandro Silvestri and Luisa Lanfranco, Italy), and balancing the host immune system for beneficial mycorrhizal interactions (Erik Limpens, the Netherlands). Please also have a look



Marcel van der Heijden



Jonathan Plett

at the YouTube video interviews and a seminar with authors of recent top papers (Leho Tedersoo, Benoît Perez, Stephanie Porter, and Marc-André Selosse).

This newsletter is still under development. **If you have interest to contribute an article or act as an editor for a specific section, or if you have an excellent idea to develop something, do not hesitate to contact us.** Also, do not forget to become member of the International Mycorrhiza Society or ask your institution to become member (see: <http://mycorrhizas.org/home/join/>). This will help us to further develop the society and, if our numbers grow sufficiently, we can offer more services for the mycorrhizal community (including exchange grants, manuals, etc.). We are here to support those studying mycorrhizas and, by extension,

plant science, fungal biology, ecology, environmental research, molecular biology of plant-microbe interactions, and evolution. We believe these symbioses are the key to understanding many things, and we are happy to convince you!

As we reflect on the last four months, we cannot help but also consider the impact of the developments around the discovery, spread, and attempts to contain COVID-19. The toll this has taken have been considerable for many of us both personally and socially, and with respect to our work. Some have suffered directly from illness caused by COVID-19 or watched loved ones be afflicted. With relation to our work, many of us had to drop experiments and other obligations with little notice and transfer our work to home. Others have had to prepare (or take) online course for teaching. For post-graduate researchers, this has been especially hard as their expected career trajectory has hit a distinct bend in the road that no one could have predicted. In times like this, we must come together to support each other like in the mycorrhizal symbiosis. The rise of different video conferencing platforms has enabled us to keep in contact with each other, enabling conferences to be held online and weekly seminars, typically only held for single university departments, are now beaming worldwide (e.g. Virtual Seminars in Symbiosis hosted by Dugal Reid and colleagues). And after all this, once a vaccination is developed, we look forward to when we can meet together again in person, to share a drink, and to discuss what our new 'normal' looks like!

Beyond the health crisis, we also reflect on the increasingly visible fingerprints of

climate change: an extreme drought and bushfires in Australia this winter, high temperatures and hardly any winter in Switzerland and many parts of Europe to name but a few. This is an ongoing issue that will affect us all, especially as it appears things are changing faster than previously thought. Action is required urgently and as scientists, farmers, and environmental researchers we have the obligation to remind our policy makers what is going on. Obviously, mycorrhizal research can help; we know that mycorrhiza improve crop resistance to drought, that they promote seedling survival or enhance the resilience of the vegetation to change and that, within forest biomes, they can capture and possibly improve carbon sequestration into the soil. In order to harness this, however, we will need innovative transformative research approaches and we need to be able to implement and really change things.

We hope you enjoy this newsletter and look forward to any feedback and recommendations. In the next editorial we will consider the topic of careers in research and what we think is important for a career in mycorrhizal research and science in general.

Top 10 papers on mycorrhizal research*

1. Radhakrishnan GV, Keller J, Rich MK, *et al.* 2020. An ancestral signalling pathway is conserved in intracellular symbioses-forming plant lineages. *Nat Plants* 6: 280-289. <https://doi.org/10.1038/s41477-020-0613-7>
2. Delgado-Baquerizo M, Reich PB, Trivedi C, *et al.* 2020. Multiple elements of soil biodiversity drive ecosystem functions across biomes. *Nat Ecol Evol* 4: 210-220. <https://doi.org/10.1038/s41559-019-1084-y>
3. Teste FP, Jones MD, Dickie IA. 2020. Dual-mycorrhizal plants: their ecology and relevance. *New Phytol* 225: 1835-1851. <https://doi.org/10.1111/nph.16190>
4. Tedersoo L, Bahram M, Zobel M. 2020. How mycorrhizal associations drive plant population and community biology. *Science* 367: eaba1223. <https://doi.org/10.1126/science.aba1223>
5. Savary R, Dupuis C, Masclaux FG, Mateus ID, Rojas EC, Sanders IR. 2020. Genetic variation and evolutionary history of a mycorrhizal fungus regulate the currency of exchange in symbiosis with the food security crop cassava. *ISME J.* <https://doi.org/10.1038/s41396-020-0606-6>
6. Kang H, Chen X, Kempainen M, Pardo AG, Veneault-Fourrey C, Kohler A, Martin FM. 2020. The small secreted effector protein MiSSP7. 6 of *Laccaria bicolor* is required for the establishment of ectomycorrhizal symbiosis. *Environ Microbiol* 22: 1435-1446. <https://doi.org/10.1111/1462-2920.14959>
7. Fernandez CW, See CR, Kennedy PG. 2020. Decelerated carbon cycling by ectomycorrhizal fungi is controlled by substrate quality and community composition. *New Phytol* 226: 569-582. <https://doi.org/10.1111/nph.16269>
8. Silvestri A, Turina M, Fiorilli V, Miozzi L, Bonfante P, Lanfranco L. 2020. Different genetic sources contribute to the small RNA population in the arbuscular mycorrhizal fungus *Gigaspora margarita*. *Front Microbiol* 11: 395. <https://doi.org/10.3389/fmicb.2020.00395>
9. Venice F, Ghignone S, Salvioli di Fossalunga A, *et al.* 2020. At the nexus of three kingdoms: the genome of the mycorrhizal fungus *Gigaspora margarita* provides insights into plant, endobacterial and fungal interactions. *Environ Microbiol* 22: 122-141. <https://doi.org/10.1111/1462-2920.14827>
10. Nunes CI, Massini JLG, Escapa IH, Guido DM, Campbell K. 2020. Conifer root nodules colonized by arbuscular mycorrhizal fungi in Jurassic geothermal settings from Patagonia, Argentina. *Int J Plant Sci* 181: 196-209. <https://doi.org/10.1086/706857>

*Selected from 178 Web of Science articles *published* between January – April 2020, by: Marcel van der Heijden, Caroline Gutjahr, Jan Jansa, Jonathan Plett, Francis Martin, Justine Karst, Jason Hoeksema, Liang-Dong Guo, Judith Lundberg-Felten, and César Marín.

Research commentary

Fungal succession during the decomposition of ectomycorrhizal fine roots

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The following commentary on a recent paper (Gray and Kernaghan 2019), is the result of my M.Sc. research under Gavin Kernaghan (Saint Mary's University, Halifax), that focused on characterizing changes in fungal community structure in decomposing ectomycorrhizal (ECM) root tips.

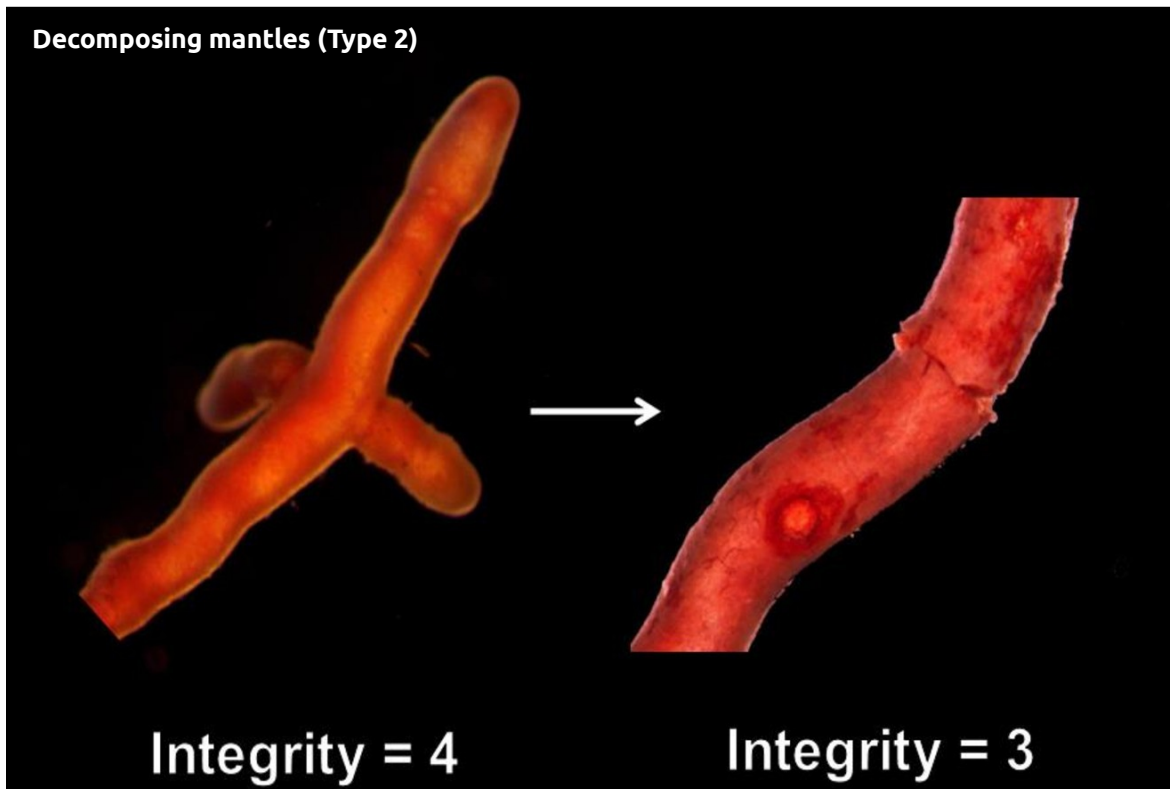
The carbon flow from plant to fungal symbiont and its subsequent deposition into surrounding soils is now recognized as an important process in soil organic matter formation and carbon storage (Clemmensen *et al.* 2013). Fixed carbon is transported directly to the ECM fungi (Högberg *et al.* 2001) and may represent up to 30% of forest net primary productivity (Allen and Kitajima 2014). As ECM fungi can comprise one third of forest belowground microbial biomass (Högberg and Högberg 2002), it is not surprising that ECM turnover can be the dominant route of carbon deposition in some forests (Godbold *et al.* 2006). Additionally, ECM tissues are nitrogen-rich due to their chitin content, with C:N ratios of ~20:1 (Wallander 2003), whereas plant litter is typically 60:1 to 90:1 (McGroddy *et al.* 2004). We therefore predicted that soil fungi would quickly access the available resources in newly senescent ECM roots. Given their intricate relationship with ECM, we also hypothesized that the first



Example of a canopy gap and "blanket" of regenerating seedlings

stages of ECM decomposition would be dominated by fungal root endophytes, as these fungi are already strategically located within fine roots.

To test this hypothesis, we needed to monitor decomposing root systems. Thankfully, given Nova Scotia's windy weather, there are plenty of windfalls in our Acadian forest, and the sudden loss of shade results in large blankets of regenerating seedlings. We chose fir and spruce seedlings at two sites, and either severed them above the root collar or left them as controls. We then left the root systems of the severed seedlings to decompose (undisturbed) in the soil, sampling monthly, while also gathering data on soil temperature, moisture, and pH. We aimed to monitor the physical integrity of the ECM during the



decomposition process and characterize changes in the associated fungal community over a 16-month period. We used cloning and direct sequencing to characterize the fungal community, gathering information on the ITS1 and ITS2 to achieve better taxonomic resolution.

We first characterized the ECM community on our sites by identifying the ECM on an initial set of unsevered seedlings using direct sequencing. As decomposing ECM would be difficult to recognize morphologically, we categorized them into very general morphotypes and monitored their physical integrity over time. We recognized four main morphotypes: Type 1 – melanized (mainly *Cenococcum*, some *Tomentella*); Type 2 – smooth, non-melanized (mainly Russulaceae); Type 3 – bright yellow, cottony (*Piloderma*); Type 4 – non-melanized, cottony (*Cortinarius* and others). As decomposition progressed, ECM were randomly

selected for DNA extraction and construction of clone libraries. Decomposition was also assessed visually and assigned an integrity score based on the remaining amount of mantle tissue: 1 = < 33%, 2 = 33–66%, 3 = 66–99%, and 4 = 100% (category 4 would be the least decomposed).

We found that the morphotypes decomposed at different rates. Type 4 mantles (white-cottony) decomposed rapidly and were lost after the first four months. Type 2 (smooth-non-melanized) and Type 3 (bright pigmented-cottony) showed intermediate rates of decomposition and were still observed after 16 months. Type 1 (melanized; mostly *Cenococcum*) did not show significant decomposition.

We found that fungal root endophyte abundance increased initially, but decreased with time. This initial increase might be due to the availability of new resources during the early stages of



mantle senescence, while their subsequent decrease appears to correlate with the loss of fungal mantles -and therefore resources- with time.

We also found that ECM sequences persisted throughout the study period, even though mantles were degraded. We hypothesize that the enduring ECM signal was the result of remaining ECM hyphae or DNA rather than viable ECM fungi. Interestingly, there was little evidence of soil/litter saprotrophic or lignocellulolytic fungi in our analysis. Since our study was limited to 16 months, it may be that these saprobes could play a larger role in root decomposition given more time.

The different decomposition rates seen among the ECM morphotypes could have important implications regarding forest soil carbon and nutrient cycling, as the rate of ECM breakdown, and therefore the rate at which ECM constituents are released to the soil, seems dependent not only on climactic factors, but also on the morphology of the individual ECM.

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Small RNAs in the arbuscular mycorrhizal symbiosis

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The discovery of small RNA (sRNAs) has represented a paradigm shift on the cellular role of RNA and, in particular, on the regulation of gene expression in eukaryotes. sRNAs are short non-coding RNA molecules that, through a complex process called RNA interference (RNAi), modulate, mainly in a negative way, the expression of target genes in a sequence-specific manner (Ghildiyal and Zamore 2009). Many biological functions are controlled by the sRNA-mediated gene silencing, such as the defense against viruses and transposable element proliferation, the regulation of developmental and physiological processes as well as the responses to biotic and abiotic stresses.

Plant sRNAs also play a regulatory role in symbiotic plant-microbe interactions, including the arbuscular mycorrhizal (AM) symbiosis. Colonization of roots by AM fungi dramatically alters the expression of various plant sRNA: some of them mediate the establishment of a functional symbiosis possibly through the regulation of genes involved in phosphate starvation response and hormone signaling (Müller and Harrison 2019), but many others remain to be characterized. Information on sRNAs and RNAi on the AM fungal partner and on their potential contribution to the AM symbiosis is even more scanty.

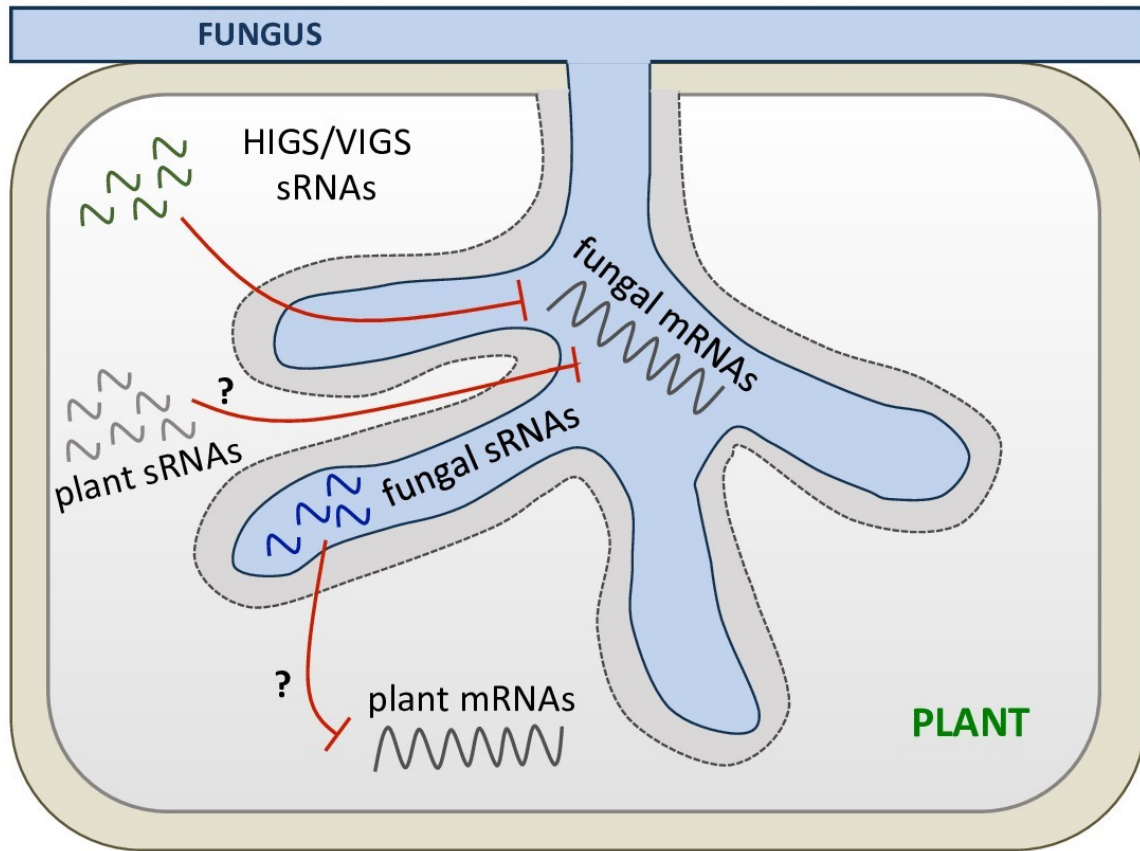
In two recent works, we investigated the sRNA populations and the RNAi-related genes of two AM fungi, *Rhizophagus*

irregularis and *Gigaspora margarita* (Silvestri *et al.* 2019, 2020). Our results pointed out that AM fungi are equipped with a complete set of RNAi-related genes that is characterized by the expansion -to an extent never observed in other organisms, of the Argonaute (AGO) and RNA-dependent RNA polymerase (RdRp) gene families. AGO and RdRp represent two core RNAi components that mediate the sRNA-target interaction and amplification of silencing signals, respectively.

Consistently with the presence of RNAi-related genes, the large scale sequencing and characterization of fungal sRNAs further support the occurrence of an active RNAi pathway in AM fungi. Indeed, in both species we detected the accumulation of sRNAs with a specific nucleotide length distribution showing an enrichment in uracil at their 5' ends, typical hallmarks of RNAi-competent fungi. With a focus on sRNAs mapping to the nuclear genome, we then identified in both species two different populations of nuclear sRNA-producing loci. This feature could indicate the existence in AM fungi of a RNAi pathway that includes two independent sRNA-generating processes.

We also pointed out that in *G. margarita*, a species hosting endobacteria and several viruses (Turina *et al.* 2018), all its metagenome -nuclear, mitochondrial, endobacterial, and viral genomes-

Putative movement of sRNAs between fungus and plant, and vice versa, in an arbuscule-containing cell



contributes to the generation of the whole sRNA population. The high level of sRNA reads mapping to viral genomes suggests that the *G. margarita* RNAi machinery is able to provide an antiviral defense. The emerging picture indicates that the sRNA world in AM fungi is extremely complex and more variegated than that normally observed in fungi. Further analyses are needed to prove how these sRNA contributes to AM fungal biology.

Interestingly, besides the endogenous regulatory functions, sRNAs are currently emerging also as important signaling molecules in different inter-species, and even inter-kingdom interactions (Huang *et al.* 2019). Indeed, sRNAs can be transferred from a “donor” to a “receiver” organism where they can regulate host gene expression by binding to the host AGO proteins, a

process known as cross-kingdom RNAi. This process is exploited in several pathogenic/parasitic interactions, in which sRNAs can behave both as “attack” and as “defense” molecules (i.e. they can be transferred from the pathogen/parasite to the host and/or vice versa). The movement of sRNA from the plant to the AM fungus is likely at the basis of the host-induced (HIGS) or viral-induced (VIGS) silencing of fungal genes which has been observed in mycorrhizal roots (Helber *et al.* 2011; Kikuchi *et al.* 2016). These findings prompted us to investigate whether the transfer of sRNA could be a natural phenomenon in the AM symbiosis.

Giving the attention to a hypothetical transfer of sRNAs from AM fungi to plants, we discovered by *in silico* analyses that some fungal sRNAs could potentially target several plant mRNA, in

some cases conserved between *R. irregularis* and *G. margarita*. These data suggest that cross-kingdom RNAi could represent a partner communication strategy in the AM symbiosis. A future challenging task will be to validate the *in silico* predictions and obtain the experimental evidence of the fungal sRNA ability to hijack the plant RNAi machinery to favor colonization. We have the feeling we are looking at the tip of an iceberg: the world of sRNA has probably a lot to say on how AM fungi successfully establish long-lasting interactions with plants, bacteria and viruses.

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Balancing the host immune system for beneficial mycorrhizal interactions

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It is becoming increasingly clear that the line between pathogenic and beneficial mycorrhizal interactions is not a sharp border but rather a fuzzy one, that is highly context dependent. Like any fungus, mycorrhizal fungi have so-called microbe-associated molecular patterns (MAMPs), such as chitin in their cell walls, that are potent triggers of host immune responses. Therefore, mycorrhizal fungi must have efficient ways to subvert the host immune system to allow a beneficial interaction with their host. They do this in strikingly similar ways as their pathogenic counterparts, in which secreted effector proteins play a key role (Plett and Martin 2015). In this commentary, I will discuss the role of lysin motif (LysM) domain containing effectors in establishing mycorrhizal interactions (Schmitz *et al.* 2019; Zeng *et al.* 2020).

The LysM domain is generally considered to bind chitin-like polysaccharides. Numerous pathogenic fungi secrete LysM domain containing effectors, consisting of one to three LysM domains, to subvert the host immune system (Rovenich *et al.* 2016). They can function in a combination of different ways. For example, they can bind to the chitinous fungal cell wall to protect against the action of plant chitinases and/or they bind chito-oligosaccharides to inhibit chitin-triggered immune responses in the plant. We recently showed that

arbuscular mycorrhizal (AM) fungi also make use of LysM effectors (Zeng *et al.* 2020). We characterized a single LysM domain containing effector from *Rhizophagus irregularis*, called RiSLM, which is highly expressed in hyphae that colonize the root (Fig. 1A). It shares both immune-suppressing functions with its pathogenic homologs and plays a positive role in symbiosis (Zeng *et al.* 2020).

However, as opposed to pathogens, AM fungi chitin-derived molecules are not only triggers of host immune responses but they are also crucial for symbiosis signaling. This touches on the important question how plants can distinguish between friend or foe. It was thought that short chain chitoooligosaccharides (such as CO4) and lipo-chitoooligosaccharides (LCO's) are produced by AM fungi to activate symbiosis signaling, while longer chain CO's (like CO8) activate immune responses. However, it has recently become apparent that plants do not discriminate between symbiosis and defense based on CO perception (Feng *et al.* 2019a). Even long-chain chitin fragments like CO8 are able to activate symbiotic responses. Furthermore, the activation of symbiosis and chitin-triggered immune signaling can require the same LysM-domain containing receptor kinase. For example, in rice or banana the LysM receptor kinase CERK1

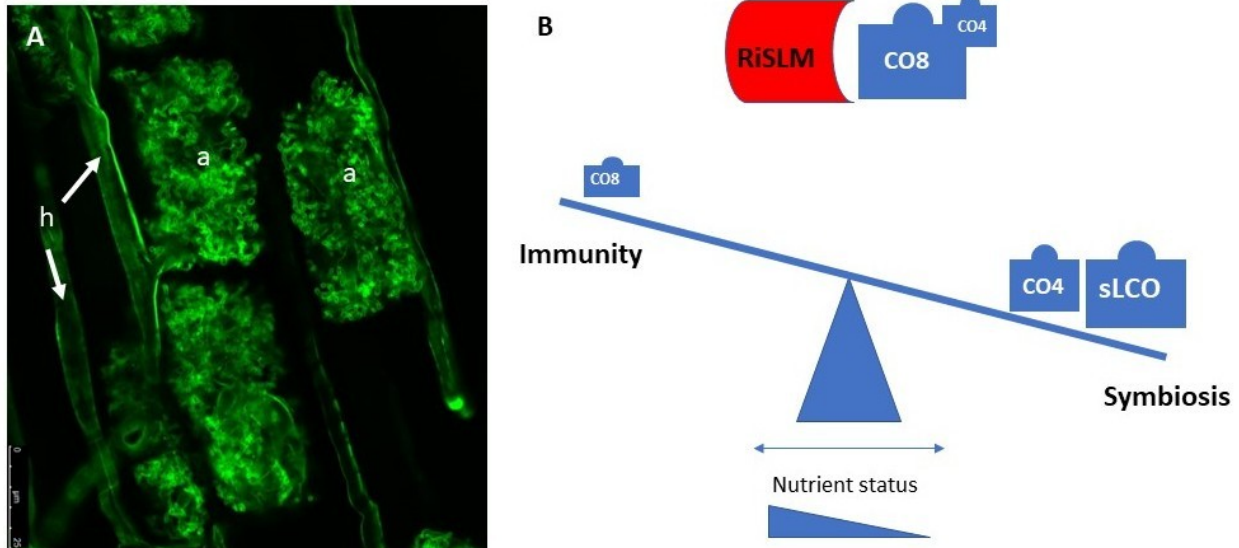


Figure 1. A. AM fungal hyphae (h) colonizing a *Medicago* root and forming arbuscules (a). **B.** RiSLM, together with the nutrient status of the plant, helps to shift the balance of immune and symbiosis signaling by chitin-like molecules to a symbiotic outcome in *Medicago*. The weight of the different chitin-like molecules (CO4, CO8, ns/sLCO's) is determined by the affinity of the corresponding LysM receptor complexes of the plant.

is required for both immunity and AM symbiosis (Miyata *et al.* 2014; Zhang *et al.* 2019). One of the current ideas is that a combination of both LCO's and CO's promotes a symbiotic outcome, while perception of CO's alone may preferentially activate defense (Feng *et al.* 2019a). So, in this context, how do AM LysM effectors fit into this picture?

We showed that RiSLM binds to both short- and long-chain CO's as well as to sulphated and non-sulphated LCO's produced by *R. irregularis*. Binding studies indicated an affinity from high to low in the order: sLCO's > nsLCO's > CO8 > CO4 (Zeng *et al.* 2020). Interestingly, RiSLM could inhibit symbiotic signaling by nsLCO's and both symbiotic and immune signaling by CO8 in *Medicago* roots, but not symbiotic signaling by sLCO's. Furthermore, it had mixed effects on CO4-induced signaling depending on its concentration. Although *in vivo* affinities may deviate from affinities determined *in vitro*, it seems reasonable that the action of RiSLM is due to competition, or

interference, with the respective receptor complexes that recognize these different chitin-like molecules. A likely scenario involves multiple LysM receptor complexes that have different affinities for the various chitin-like molecules and which may compete for shared signaling components (Feng *et al.* 2019a). The role of AM LysM effectors would be to help to tip the balance of immune and symbiosis signaling towards a symbiotic outcome (Fig. 1B).

The affinity of LysM receptor complexes for the various chitin-derived molecules differs in distinct host plants. For example, *Medicago* is highly sensitive to sLCO's, explaining why RiSLM does not affect symbiotic signaling, while rice is more responsive to CO4 (Sun *et al.* 2015). Therefore, the contribution of secreted LysM effectors may well vary in different host interactions.

In pathogenic interactions a second line of plant defense against invading microbes is present. This involves the perception of effectors, or their effect

on host proteins, and is called effector-triggered immunity. In an arms race with the plant, pathogenic fungal effectors rapidly evolve to evade recognition by the plant, leading to diversifying selection. This likely also holds for LysM effectors from pathogens as well as AM fungi. Homologs of RiSLM have been found in all currently sequenced AM genomes and they show a surprising high level of non-synonymous substitutions, even among isolates of the same species (Schmitz *et al.*, 2019; Zeng *et al.* 2020). It is tempting to speculate that the evolutionary history of the isolates, by interacting with different host plants, provided different selection pressures to evade effector-triggered immune responses. It will therefore be interesting to find out to which extent variation in LysM effectors, or any other AM fungal effector for that matter, contributes to the reported variation in mycorrhizal growth response and host-preferences observed in nature.

Another important factor in the balance of immune and symbiosis signaling that is gaining attention is the nutrient status of the plant. For example, phosphate starvation has been shown to attenuate defense responses in favor of interaction with beneficial microbes (Hacquard *et al.* 2016; Castrillo *et al.* 2017). Similarly, nutrient status has been reported to influence the recognition of chitin-derived signals from AM fungi to promote symbiosis and suppress immunity (Feng *et al.* 2019b). Whether this influence also occurs at the level of the receptors remains to be determined.

Sequencing efforts are continuing to increase the repertoire of potential effector proteins in mycorrhizal fungi, revealing both conserved as well as

species/isolate-specific effectors and host-dependent transcriptional regulation (Plett and Martin 2015; Zeng *et al.* 2018). Only a limited amount of these have so far been functionally characterized. Therefore, I expect that continuing research on effectors will prove to be a valuable avenue to further our insight into the fundamentals of symbiosis and may even lead to novel strategies to increase the application of AMF as sustainable biofertilizers.

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- Zeng T, Holmer R, Hontelez J, *et al.* 2018. Host- and stage-dependent secretome of the arbuscular mycorrhizal fungus *Rhizophagus irregularis*. *Plant J* **94**: 411-425.
- Zeng T, Rodriguez-Moreno L, Mansurkhodzhaev A, *et al.* 2020. A lysin motif effector subverts chitin-triggered immunity to facilitate arbuscular mycorrhizal symbiosis. *New Phytol* **225**: 448-460.
- Zhang L, Yuan L, Staehelin C, *et al.* 2019. The LYSIN MOTIF-CONTAINING RECEPTOR-LIKE KINASE 1 protein of banana is required for perception of pathogenic and symbiotic signals. *New Phytol* **223**: 1530-1546.

YouTube interviews*

- Leho Tedersoo on how mycorrhizae affects plant populations and communities

César Marín interviews Leho Tedersoo from the National History Museum of Estonia, on his Science paper regarding the general effects of different mycorrhizal types on different aspects of plant populations and communities.

Interview: <https://southmycorrhizas.org/reading/april-2020/>

Study: Tedersoo L, Bahram M, Zobel M. 2020. How mycorrhizal associations drive plant population and community biology. *Science* 367: eaba1223.

<https://doi.org/10.1126/science.aba1223>

- Benoît Perez on the evolution on mycoheterotrophy in arbuscular mycorrhizal associations

Daniel Acosta interviews Benoît Perez from the National Museum of Natural History in Paris, on the evolutionary history of mycoheterotrophic plants associated with arbuscular mycorrhizal fungi.

Interview: <https://southmycorrhizas.org/reading/april-ii-2020/>

Study: Perez-Lamarque B, Selosse M-A, Öpik M, Morlon H, Martos F. 2020. Cheating in arbuscular mycorrhizal mutualism: a network and phylogenetic analysis of mycoheterotrophy. *New Phytol.* <https://doi.org/10.1111/nph.16474>

- Stephanie Porter on the effect of plant domestication on microbial symbiosis

Camille Truong interviews Stephanie Porter from Washington State University about her research on plant domestication and its effect on the microbial symbiosis.

Interview: <https://southmycorrhizas.org/reading/may-2020/>

Study: Porter SS, Sachs JL. 2020. Agriculture and the Disruption of Plant–Microbial Symbiosis. *Trends Ecol Evol* 35: 426-429. <https://doi.org/10.1016/j.tree.2020.01.006>

*Section by:

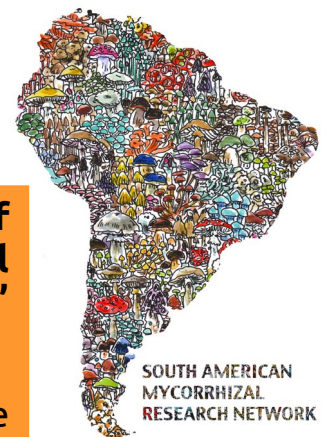
South American Mycorrhizal Research Network

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

Seminar by Marc-André Selosse from the National Museum of Natural History in Paris, entitled: “Time to re-think fungal ecological niches? Endophytic abilities in ectomycorrhizal taxa”

Link: <https://youtu.be/0qRwrp1obd8>

Organized by Camille Truong from the Biology Institute at the National Autonomous University of Mexico.



Tools

→ **Low-cost hydroponic system for studying arbuscular mycorrhiza (AM)**

Das *et al.* (2020) present a hydroponics set-up based on pipette tips and rock wool wicks for co-cultivation of AM fungi with small model plants -Falcon tubes are used for larger plants. These low-cost systems can be built with conventional and reusable lab plastic, and among other topics, can be used to study mycorrhizal signaling.

Study: Das D, Torabi S, Chapman P, Gutjahr C. 2020. A flexible, low-cost hydroponic co-cultivation system for studying arbuscular mycorrhiza symbiosis. *Front Plant Sci* 11: 63. <https://doi.org/10.3389/fpls.2020.00063>

→ **Cultivation of Matsutake**

Yamanaka *et al.* (2020) show recent advances on the cultivation of the pine-associated ectomycorrhizal fungus *Tricholoma matsutake*. This review shows studies examining bed and field cultivation of this highly-prized fungus.

Study: Yamanaka T, Yamada A, Furukawa H. 2020. Advances in the cultivation of the highly-prized ectomycorrhizal mushroom *Tricholoma matsutake*. *Mycoscience* 61: 49-57. <https://doi.org/10.1016/j.myc.2020.01.001>

→ **Mycorrhiza: phylogenetic networks for genotype assignment**

Georges-Filteau *et al.* (2020) developed *Mycorrhiza*, a machine learning approach for the genotype assignment problem. This problem consists of predicting, from the genotype of an individual, which of a known set of populations it originated from. This phylogenetic networks-based approach performed well compared to widely used mixture analysis methods as STRUCTURE and Admixture, or in datasets with a large FST or large deviation from the Hardy-Weinberg equilibrium.

Study: Georges-Filteau J, Hamelin RC, Blanchette M. 2020. *Mycorrhiza*: genotype assignment using phylogenetic networks. *Bioinformatics* 36: 212-220. <https://doi.org/10.1093/bioinformatics/btz476>

→ **PEMA and MGnify: new metabarcoding bioinformatic pipelines**

Zafeiropoulos *et al.* (2020) present PEMA, a pipeline based on the BigDataScript programming language, which allows the analyses of the of the 16S/18S rRNA, ITS, and COI marker genes from environmental DNA. Mitchell *et al.* (2020) present MGnify, a free platform ([EBI Metagenomics](#)) for the archiving, assembly, and taxonomic and functional analyses of microbiome data from different environments.

Studies: Zafeiropoulos H, Viet HQ, Vasileiadou K, *et al.* 2020. *PEMA*: a flexible Pipeline for Environmental DNA Metabarcoding Analysis of the 16S/18S ribosomal RNA, ITS, and COI marker genes. *GigaScience* 9: gaaa022. <https://doi.org/10.1093/gigascience/gaaa022>

Mitchell AL, Almeida A, Beracochea M, *et al.* 2020. *MGnify*: the microbiome analysis resource in 2020. *Nucleic Acids Res* 48: D570-D578. <https://doi.org/10.1093/nar/gkz1035>

For previous Tools: [click here](#) for the Issue 1 of the IMS Newsletter (p. 11).

IMS News

- Please register to become member of the International Mycorrhiza Society at:
<http://mycorrhizas.org/home/join/>

- **IMS working groups:**

Please contact us if you wish to organize one.

- **Diversity Statement:**

Please [click here](#) (IMS Newsletter Issue 1, p. 12) to read the **Diversity and Inclusivity Statement of the International Mycorrhiza Society**. This Statement resulted in a **Code of Conduct** that will be posted in full before the next International Conference on Mycorrhiza (ICOM)

- **Advertisement and information for the newsletter:**

Please contact César Marín (cesar.marin@uoh.cl).



<http://mycorrhizas.org/>

Events

EVENTS POSTPONED DUE TO COVID-19:

- Global Symposium on Soil Biodiversity

[Website](#)

FAO headquarters, Rome, Italy
2-4 February, 2021

Organizers: UN Food and Agriculture Organization (FAO), Global Soil Partnership (GSP), Intergovernmental Technical Panel on Soils (ITPS), UN Convention on Biological Diversity (UNCBD), Global Soil Biodiversity Initiative (GSBI).

- Soil Ecology Society Biennial Meeting 2021

[Website](#)

Discovery Hall, Richland, WA, United States
24-28 May, 2021

Organizers: Soil Ecology Society (US) and local organizers.

- Eurosoil 2020 (now 2021)

[Website](#)

Geneva, Switzerland
Second half of 2021

Organizers: European Confederation of Soil Science Societies and local organizers.

- 18th International Symposium on Microbial Ecology

[Website](#)

Cape Town, South Africa
August 2021

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.

EVENTS AS SCHEDULED:

X Latin American Mycology Congress

Website

University of Chile, Santiago, Chile,
12-14 December 2020 (may change!).

Organizers: University of Chile and local organizers.



X Congreso Latinoamericano de Micología
Chile 2020

10th International Symbiosis Society Congress

Website

Lyon, France
18-23 July 2021

Organizers: International Symbiosis Society

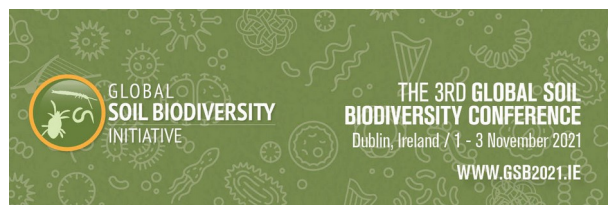


3rd Global Soil Biodiversity Conference

Website

Clayton Hotel, Dublin, Ireland
1-3 November 2021

Organizers: Global Soil Biodiversity Initiative



The **5th International Molecular Mycorrhiza Meeting** that was planned for Shanghai (July 2020) has been postponed to 2021 and specific details will be announced later.

Future ICOMs

The IMS Board of Directors is pleased to announce

ICOM11 will be held in **2021 in Beijing, China**, and organized by the Chinese Society of Mycology (Prof. Liang-Dong Guo)

and

ICOM12 will be held in **2023 in Manchester, UK**, and organized by Prof David Johnson (University of Manchester), Dr Katie Field (University of Leeds), Prof Tim Daniell (University of Sheffield), Dr Thorunn Helgason (University of York) and Dr. Uta Paszkowski (University of Cambridge)

More information at: <http://mycorrhizas.org/>