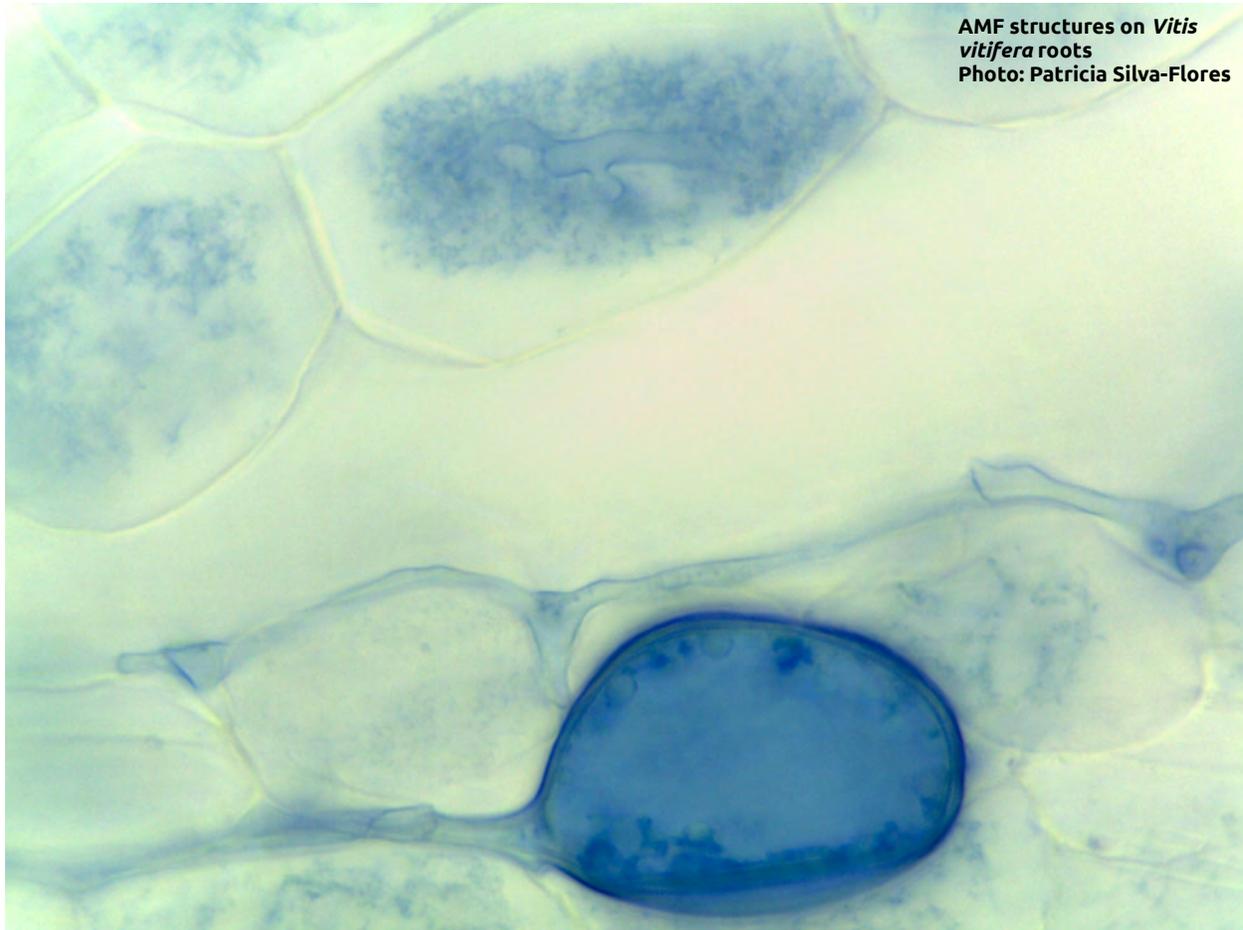




# IMS Newsletter

*The International Mycorrhiza Society quarterly e-newsletter*



AMF structures on *Vitis vitifera* roots  
Photo: Patricia Silva-Flores

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# Editorial: lets legislate on soil biodiversity!

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Global studies on soil biodiversity have significantly increased over the last decade (Marín and van der Heijden 2020). These global surveys focused on soil fungi (Tedersoos *et al.* 2014), arbuscular mycorrhizal fungi (Davison *et al.* 2015), soil bacteria (Bahram *et al.* 2018; Delgado-Baquerizo *et al.* 2018), earthworms (Philipps *et al.* 2019), protists (Oliverio *et al.* 2020), and all soil biota overall (Delgado-Baquerizo *et al.* 2020). Furthermore, recently, FAO together with other organizations published the first report on the *State of knowledge of soil biodiversity* (FAO *et al.* 2020), with contributions of more than 300 scientists worldwide. This work is a continuation of the activity started with the *Global Soil Biodiversity Atlas* (Orgiazzi *et al.* 2016). From all these important articles and reports, at least three aspects can be concluded: first, there is an increasing research capability and cooperation regarding the global study of soil biodiversity including mycorrhizal fungi. Second, the spatial, environmental, taxonomic, and functional gaps on soil ecology are large (Guerra *et al.* 2020). For instance, there are almost no examples of temporal monitoring of changes on soil biodiversity and ecosystem functions -in a changing world; although several local mycorrhizal studies have examined temporal changes (Dumbrell *et al.* 2011; Ercole *et al.* 2015), with one particular study (Averill *et al.* 2019) estimating

seasonal and intra-annual changes in soil fungal biodiversity for northern temperate latitudes. Finally, these research gaps and the lack of monitoring should urgently result in policy changes to use and consider soil biodiversity for sustainable management of ecosystems and for broader conservation targets. In line with this, mycorrhizal applications have a huge potential to make agriculture and forestry more sustainable, in supporting native flora and ecosystem restoration (Vahter *et al.* 2020), among others.

Guerra *et al.* (2020) propose a series of actions to overcome different challenges regarding the global monitoring of soil biodiversity: for legal issues related to the transport of soil samples and the data obtained from them, these actions include establishing global multilateral solutions and International Treaties, and tools aimed at knowledge transfer of the information derived from soil samples. Similarly, to overcome the sometimes scattered literature or unavailability of data on soil biodiversity, both open access partnerships and current global databases (like GBIF) should be strongly supported. Likewise, to surmount the lack of temporally explicit information on soil biodiversity and ecosystem functions, multilateral (like in the EU) funding schemes for long-term projects on soil monitoring should be proposed and pursued, also

taking advantage of existing frameworks (like the LTER sites) (Guerra *et al.* 2020). Finally, to overcome a “lack of globally distributed expertise, research funding and infrastructures”, it is suggested to promote the training and empowerment of local scientists, particularly in the developing world (Bueno *et al.* 2017, Mujica *et al.* 2019). Furthermore, it is important to establish soil health as a crucial research priority not only in farming areas but as a conservation target elsewhere (Guerra *et al.* 2020).

It is still unresolved which soil biodiversity characteristics and which ecosystem functions should be monitored at a global scale? And how to measure them? Within the framework of the global Soil Biodiversity Observation Network (Soil BON; <https://geobon.org/bons/thematic-bon/soil-bon/>), Guerra *et al.* (2021), in a Science article, suggested some specific soil biodiversity and functions measurements, deemed “essential biodiversity variables”. These include: litter decomposition, soil respiration, enzymatic activity, soil aggregation, nutrient cycling, soil biomass, intraspecific genetic diversity, population abundance, community traits of roots, habitat extent, functional diversity, and taxonomic diversity. A YouTube interview with Diana H. Wall, Scientific Chair of the Global Soil Biodiversity Initiative, and Carlos A. Guerra, who leads Soil BON, in this issue, highlight this. As mentioned by Carlos during the interview, this set of variables is specifically suited for the objectives of Soil BON -and can be limited (for example, due to international transport laws, the sampling of earthworms is almost impossible, despite being a crucial soil organism). Such framework

can also be a good base and example for other regional/continental/global soil sampling schemes with different objectives.

What are the essential biodiversity predictors for mycorrhiza? Which global knowledge gaps are there for our beloved symbiosis, at the spatial, environmental, taxonomic, and functional scales? There is no doubt these questions have occupied many mycorrhizal ecologists and physiologists over the past years and substantial progress has already been made with the global maps depicting soil fungal and mycorrhizal diversity. Hopefully this will lead to a sort-of-consensus (as that reached in Soil BON) regarding which are the gaps, and which mycorrhizal variables are “essential”, and could be used to globally monitor the biodiversity and ecosystem functions of this symbiosis.

Finally, the issue of legislation about the international transport of samples and data sharing on mycorrhiza is a bit complicated, as it encompasses three different compartments: soil, and plant and fungal tissues. While the transport of tissues is more regulated and the law on their international transport is more homogeneous, a less clear picture is presented when transporting soil across countries, especially fresh samples. This issue is important because there are concerns about the global distribution of mycorrhizal inoculum and the invasion of non-endemic mycorrhizal fungi (e.g. Schwartz *et al.* 2006; Hart *et al.* 2017). Many times, different countries have very different regulations, while in others there are clear legal gaps and unregulated aspects. This is most probably caused because until very recently, and in a majority of countries,

soil has been considered -from a policy perspective- solely from a chemical/physical perspective, or a thread perspective (eg. avoided soil erosion and pollution), but soil biodiversity has been largely been ignored. The FAO tool SoilEX (<http://www.fao.org/soils-portal/soilex/en/>) gives a detailed overview of soil legislation by each member country. Thus, we need to urgently translate into policy all these great recent advances on soil and mycorrhizal macroecological science, not solely for research needs but also for legislation and conservation purposes. As there is a significant mismatch between aboveground and belowground biodiversity hotspots (Cameron *et al.* 2019), this legislation on soil biodiversity, ultimately could lead to target priority conservation areas around the globe based on belowground biodiversity hotspots.

Note: recently, a list of online tools and resources on mycorrhizal research was developed by Patricia Silva-Flores and co-authors (*Plants, People, Planet*): <https://southmycorrhizas.org/outreach/> If you want to add an additional tool/resource, do not hesitate to write me ([cesar.marin@uoh.cl](mailto:cesar.marin@uoh.cl)).

### **In this issue...**

In this you will find the Top 10 list of mycorrhizal research articles of the last four months (January – April, 2021) selected by a panel of experts from a list of 223 articles. The Top 1 article by Feiyan Jiang and co-authors shows how arbuscular mycorrhizal hyphae increase phosphorus mineralisation from the soil by acting as vectors and hyphal highways phosphorus solubilizing bacteria (*New Phytologist*; DOI: 10.1111/nph.17081). Please also find a short article by Gu Feng and co-authors, on this amazing

discovery. The Top 2 article, in *Science* (DOI: 10.1126/science.aba6605), is authored by Pierre-Marc Delaux and Sebastian Schornack, and shows that protection against pathogens and support of symbiotic microorganisms are sustained by conserved and clade-specific plant mechanisms evolving at different speeds. The Top 3 article by Mathu Malar and co-authors (*Current Biology*; DOI: 10.1016/j.cub.2021.01.058) besides showing that the genome of *Geosiphon pyriformis* is ideal to study the emergence of the arbuscular mycorrhizal symbiosis, it also shows horizontal gene transfer between this fungus and *Nostoc*. Also in this issue find another short article by J. Marty Kranabetter and Melanie Jones, focusing on ectomycorrhizal adaptations across temperate rainforests in Canada in relation to soil phosphorus deficiencies. Also, please find our usual YouTube interviews. In this occasion, besides the aforementioned interview about Soil BON, María Isabel Mujica talks about her work on Chilean orchid mycorrhizas and their interactions with soil nutrients and fungal pathogens. Felipe Albornoz is interviewed about different mycorrhizal myths or dogmas long sustained in our mycorrhizologist community, but -in his opinion- with little base to the real World.

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## Top 10 papers on mycorrhizal research\*

1. Jiang F, Zhang L, Zhou J, *et al.* 2021. Arbuscular mycorrhizal fungi enhance mineralization of organic phosphorus (P) by carrying bacteria along their extraradical hyphae. *New Phytol* 230: 304-315. <https://doi.org/10.1111/nph.17081>
2. Delaux PM, Schornack S. 2021. Plant evolution driven by interactions with symbiotic and pathogenic microbes. *Science* 371: eaba6605. <https://doi.org/10.1126/science.aba6605>
3. Malar MC, Krüger M, Krüger C, *et al.* 2021. The genome of *Geosiphon pyriformis* reveals ancestral traits linked to the emergence of the arbuscular mycorrhizal symbiosis. *Curr Biol* 31: 1570-1577.e4. <https://doi.org/10.1016/j.cub.2021.01.058>
4. Terrer C, Phillips RP, Hungate BA, *et al.* 2021. A trade-off between plant and soil carbon storage under elevated CO<sub>2</sub>. *Nature* 591: 599-603. <https://doi.org/10.1038/s41586-021-03306-8>
5. Delavaux CS, Sturmer SL, Wagner MR, *et al.* 2021. Utility of LSU for environmental sequencing of arbuscular mycorrhizal fungi: a new reference database and pipeline. *New Phytol* 229: 3048-3052. <https://doi.org/10.1111/nph.17080>
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7. Neuenkamp L, Zobel M, Koorem K, *et al.* 2021. Light availability and light demand of plants shape the arbuscular mycorrhizal fungal communities in their roots. *Ecol Lett* 24: 426-437. <https://doi.org/10.1111/ele.13656>
8. Emmett BD, Lévesque-Tremblay V, Harrison MJ. 2021. Conserved and reproducible bacterial communities associate with extraradical hyphae of arbuscular mycorrhizal fungi. *ISME J.* <https://doi.org/10.1038/s41396-021-00920-2>
9. Abdulsalam O, Wagner K, Wirth S, *et al.* 2021. Phytohormones and volatile organic compounds, like geosmin, in the ectomycorrhiza of *Tricholoma vaccinum* and Norway spruce (*Picea abies*). *Mycorrhiza* 31: 173-188. <https://doi.org/10.1007/s00572-020-01005-2>
10. Lofgren LA, Nguyen NH, Vilgalys R, *et al.* 2020. Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. *New Phytol* 230: 774-792. <https://doi.org/10.1111/nph.17160>

\*Selected from 223 Web of Science articles published between January – April, 2021 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.

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## Research commentaries

### Phosphorus deficiencies and ectomycorrhizal adaptations in coastal temperate rainforests of British Columbia

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The Pacific coast of northwestern North America encompasses one of the largest global expanses of temperate rainforest, an area renowned for towering, conifer-dominated forests of extraordinary productivity and longevity (DellaSala *et al.* 2011). Over the past 5 years we have been investigating the ectomycorrhizal fungal communities of these unique forests to more fully understand the nutritional constraints of their soils and the corresponding adaptations provided by key symbiotic fungal species. Much of this research has taken place along the southwestern coast of Vancouver Island, where relatively high summer rainfall, cool summers, and transient snowpacks define the quintessential 'perhumid' rainforests of British Columbia. These ecosystems have strongly podzolized soils despite only emerging from glaciation approximately 12,000 years ago. High mean annual precipitation, at > 3 m per year, has contributed to rapid weathering and to Bf soil horizons enriched in Al and Fe oxides (Fig. 1a) (Sanborn *et al.* 2011). As a consequence of this intense weathering, we have found pervasive P deficiencies across this landscape, evident by very low concentrations of soil inorganic P and often very high C:P ratios of soil organic matter (Kranabetter *et al.* 2020). Despite this challenging edaphic environment we frequently see impressive productivity

for ectomycorrhizal conifers such as Douglas-fir, western hemlock, and Sitka spruce (Fig. 1b). What role do ectomycorrhizal fungi play in the adaptations of these trees to heavily podzolized, P-limited soils?

We were fortunate to have a natural edaphic gradient with a single host (Douglas-fir) across southern Vancouver Island, due to an orographic rainshadow, that provided a unique opportunity to compare native ectomycorrhizal fungal communities and their functional traits related to P constraints (Meeds *et al.* 2021). Of particular importance for P mobilization are extracellular hydrolytic enzymes (exoenzymes) that adhere to the surfaces of mantle and extramatrical hyphae of ectomycorrhizas. We quantified two types of phosphate-releasing enzyme activities, phosphomonoesterase and phosphodiesterase, on the surfaces of the ectomycorrhizae, and confirmed that these activities were negatively related to the levels of extractable inorganic P in soil. However, an even statistically stronger, 2 to 4-fold increase was found between P-releasing enzyme activities and the N:P ratio in the foliage (Fig. 2a). A similar positive response was displayed by laccase, which plays an indirect role in P acquisition by degrading cell walls in plant and fungal



**Figure 1. a.** An example of a podzolized soil with a well developed Bf horizon, and **b.** a 55 year old Sitka spruce on a productive site in the perhumid temperate rainforests of southwestern Vancouver Island.

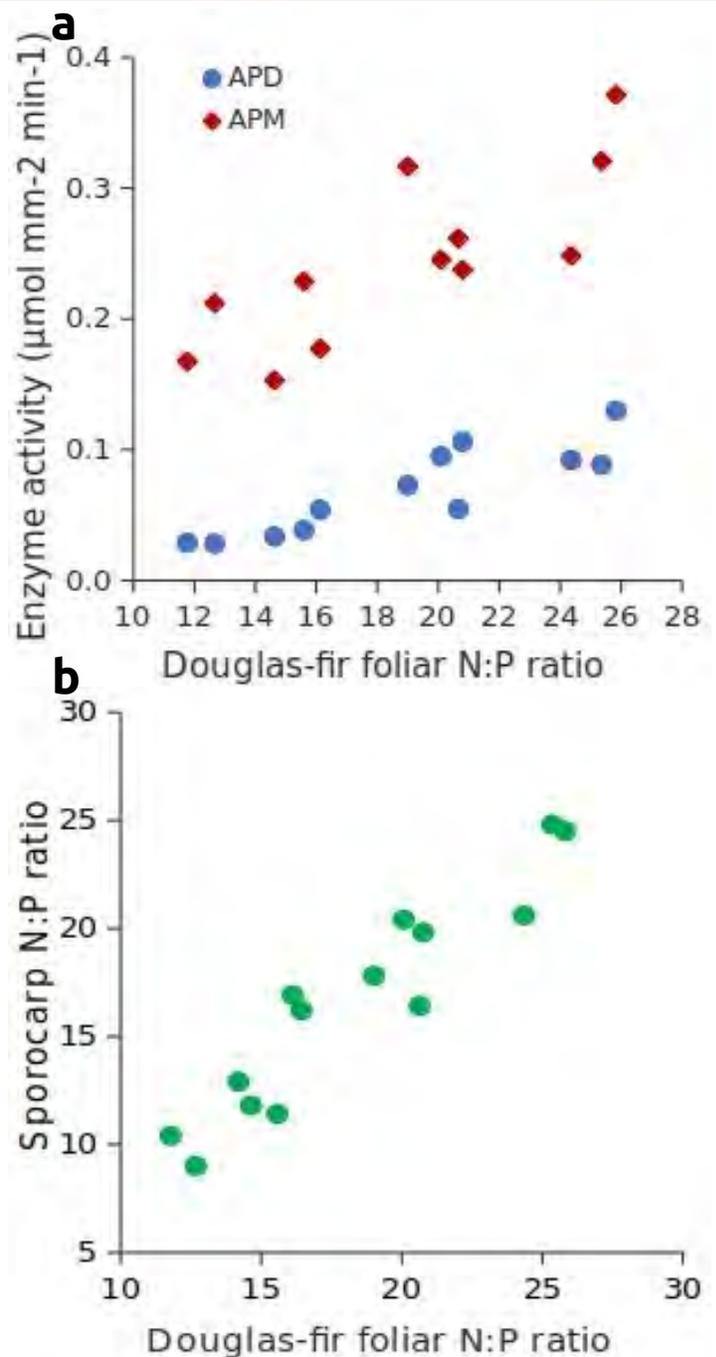
necromass. The close correlations in exoenzyme activities with host foliar N:P was an intriguing finding of the study and illustrates succinctly how mycorrhizas likely participate in an optimal allocation strategy (Johnson 2010). We suggest that the balance of P deficiencies with N constraints was a more precise predictor of enzyme allocation, rather than P alone, because both nutrients are co-limiting stand productivity and must be acquired simultaneously.

A second technique we have explored in our investigations of ectomycorrhizal fungal ecology is the analyses of N and P stoichiometry of fruiting bodies (Kranabetter *et al.* 2019). Using the same podzolization gradient with Douglas-fir,

we found sharp decreases in the P percentage of sporocarps from podzolized soils (0.47%) compared to the less weathered soils (0.67%), as well as a strong alignment with host stoichiometry (Fig. 2b). The approximately 30% decline in average sporocarp P, and elevated N:P ratios (> 15), underscores again the edaphic constraints found throughout perhumid rainforests due to a combination of limited inorganic P supplies, high microbial competition for P, and inherently poor quality of soil organic matter. In regards to forest floor horizons, for example, we found that Podzols have a larger fraction of phosphonates (as detected by <sup>31</sup>P nuclear magnetic resonance; Meeds *et al.* 2021), which are inaccessible to most

organisms because the C-P bond is generally considered very stable (Horsman and Zechel 2017). In addition, a high proportion of the phosphate monoesters on Podzols may be phytate, which is not effectively hydrolysed by the phosphomonoesterase. While these forest stands are certainly P-limited to some degree, we can only assume the productivity and nutrition of rainforest conifers would be markedly poorer under such challenging edaphic conditions without these ectomycorrhizae and their collective ability to mobilize P.

Another area of active inquiry concerning stand nutrition is the role of endemic fungi, which are the ectomycorrhizal species restricted in geographic distribution to the west coast of North America (Fig. 3). In old-growth forests of eastern Vancouver Island we determined that approximately 50% of the community were endemic species, more likely to exhibit fine-scale clustering, and greater turnover rates across local landscapes as compared to cosmopolitan species (McPolin and Kranabetter 2021). In theory, a limited dispersal pattern such as this suggests higher specialization to the local ecosystem, perhaps as a trade-off for reductions in geographic range. Some evidence for this site-based adaptation was evident across perhumid rainforests, as for example the ectomycorrhizae with the highest phosphatase activities were formed by endemic fungi found only on the podzolized soils (Meeds *et al.* 2021). The discrete distribution in species range suggests that this distinctive and largely endemic community of rainforest ectomycorrhizal fungi has metabolic attributes that greatly contribute to the ability of conifers to inhabit P-limited



**Figure 2.** As foliar N:P (molar ratio) increases, the relative constraint of P on forest productivity is expected to supersede that of N. Ectomycorrhizal fungi on Douglas-fir respond by **a.** likewise allocating increasing resources to the production of P-acquiring enzymes (APD = phosphodiesterase, APM = phosphomonoesterase), which corresponds, as seen in **b.**, to a strong alignment in ectomycorrhizal sporocarp and Douglas-fir foliar N:P (redrawn from Meeds *et al.* 2021, Kranabetter *et al.* 2019).

soils. In summary, our investigations into ectomycorrhizal fungal ecology and nutrition have highlighted the critical, specialized role of this symbiotic community in support of these extraordinary ecosystems.



**Figure 3.** An endemic ectomycorrhizal fungal species, *Ramaria sandaracina*, of the Pacific Northwest perhumid temperate rainforest.

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## Arbuscular mycorrhizal fungi enhance mineralization of organic P by carrying bacteria along their extraradical hyphae

Feiyan Jiang<sup>1</sup>, Lin Zhang<sup>1</sup>, Jiachao Zhou<sup>1</sup>, Timothy S. George<sup>2</sup> and Gu Feng<sup>1\*</sup>

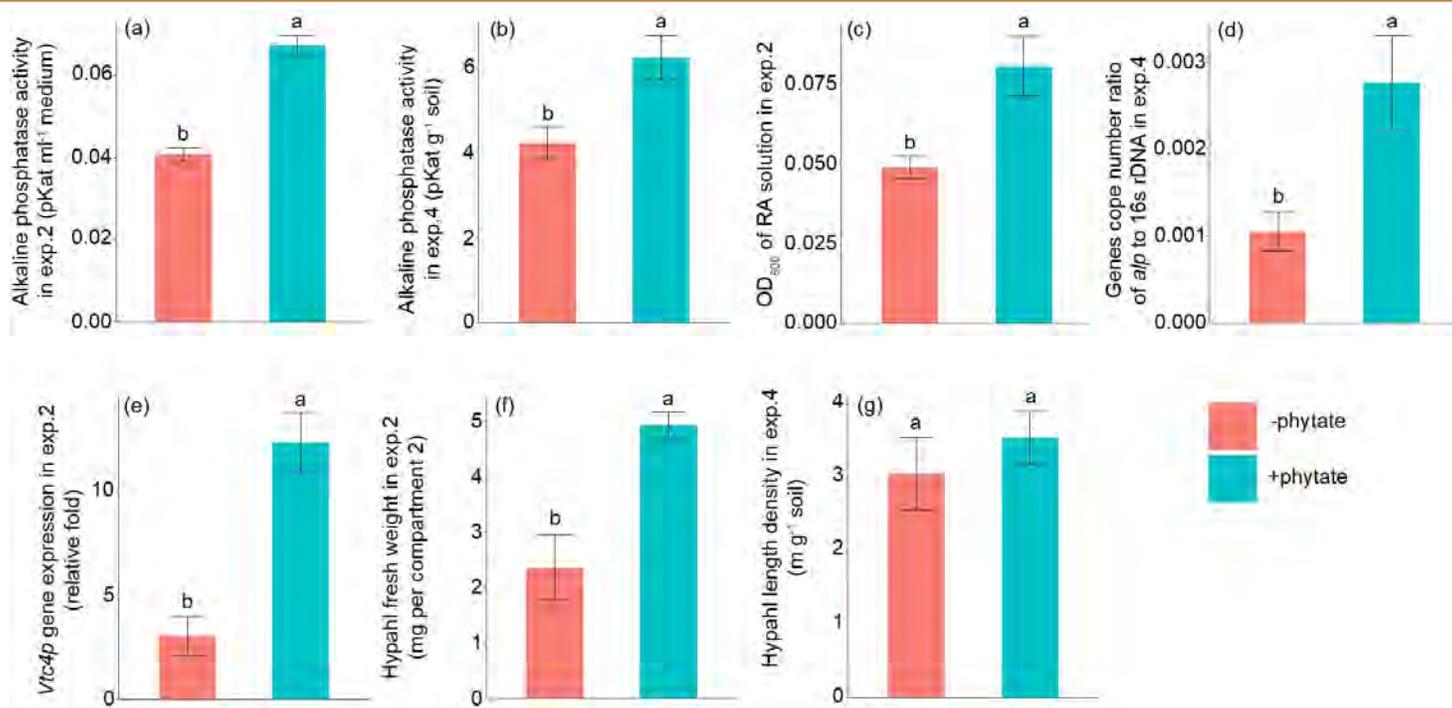
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Arbuscular mycorrhizal (AM) fungi can gain access to soil nutrient patches by producing an extensive network of fine hyphae; however, the whole genome sequence of *Rhizophagus irregularis* DAOM 197198 has revealed that this AM fungus may have limited capability to utilize organic P because of the lack of phosphatase enzyme secretion genes (Tisserant *et al.* 2013). This suggests that even when the AM fungal hyphae can reach the multitude of organic P patches in soil, they still need phosphate solubilizing bacteria (PSB) to utilize that macro-nutrient (Toljander *et al.* 2006; Zhang *et al.* 2016). Moreover, the movement of bacteria is limited to the water-filled pore space and in films of water on soil particles. The limited mobility of bacteria may reduce their ability to colonize organic P patches by chance. As such, we started to figure out if AM fungal hyphae could not only act as the habitat for bacteria, but also if the water-film on the AM fungal hyphal network can act as a highway to accelerate the bacterial movement to the nutrient patches and stimulate the utilization of organic P (Zhang *et al.* 2018a, b).

To elucidate this, four experiments, including two Petri plate experiments, one *in vitro* culture experiment (*ivCE*), and one soil culture experiment (*SCE*) with a 3D-printed microcosm, were conducted (Jiang *et al.* 2021). Our

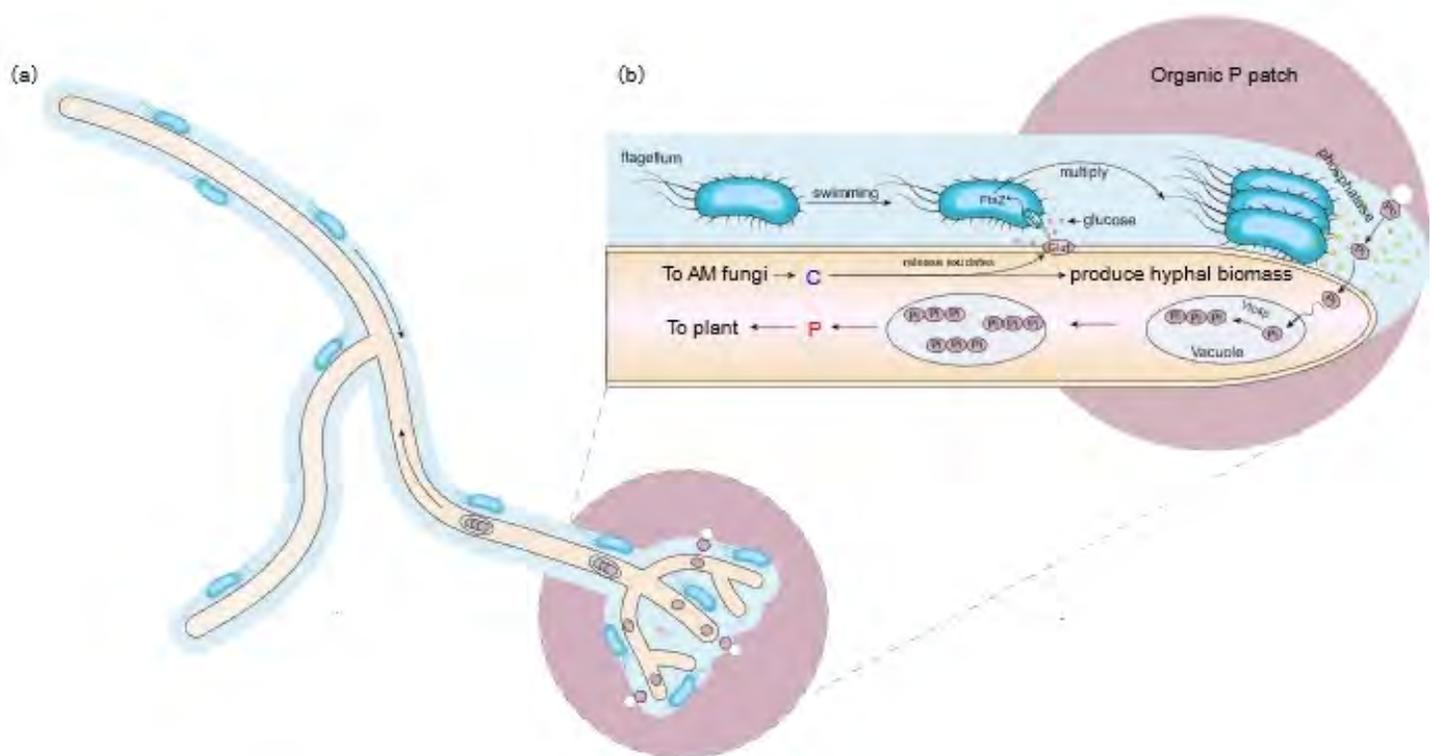
results showed that the AM extraradical hyphae were able to transport bacteria to the organic P patch both *in vitro* and *in vivo* (soil) conditions (Jiang *et al.* 2021). There were no discernible bacteria in the target compartment when plants were not inoculated with AM fungi, while more than 10<sup>7</sup> CFU g<sup>-1</sup> soil were detected in the target compartment without a significant effect of phytate addition when plants were inoculated. Furthermore, we demonstrated that bacteria could move toward organic P patches along the network of AM fungal hyphae. We found that the alkaline phosphatase activity was significantly ( $P < 0.05$ ) greater in the hyphal compartment (HC) with phytate than that in HC without phytate (Fig. 1a). The number of PSB was significantly larger in HC+phytate than in HC-phytate (Fig. 1c). The expression of a gene involved in polyP synthesis in the extraradical hyphae (*Vtc4p*) was also significantly ( $P < 0.05$ ) greater in HC+phytate compared to HC-phytate when both *R. irregularis* and PSB were present (Fig. 1e); the fresh weight of *R. irregularis* hyphae in HC+phytate was also significantly ( $P < 0.05$ ) greater than that in the HC-phytate in the presence of PSB (Fig. 1f). Likewise, the alkaline phosphatase activity in the target soil with phytate addition was significantly greater than that without phytate (Fig. 1b). The addition of phytate significantly increased the ratio of *alp* gene to 16S



**Figure 1.** **a.** Alkaline phosphatase activity in the hyphal compartment in *ivCE*. **b.** Alkaline phosphatase activity in the target soil (in the presence of AM fungi) in SCE. **c.** PSB (*Rahnella aquatilis*) numbers in HC in *ivCE*. **d.** Genes cope number ratio of *alp* to 16s rDNA of bacteria in target soil in SCE. **e.** *Vtc4p* gene expression of hyphae in the HC in *ivCE*. **f.** Hyphal fresh weight in the HC in *ivCE*. **g.** Hyphal length density of the target soil in SCE. Different letters indicate significant differences between treatments ( $P < 0.05$ ). Error bars, SE. Treatment codes are as follows: -phytate, the HC or the target soil which contained none of Na-phytate; +phytate, the HC or the target soil which contained 330  $\mu\text{M}$  in the form of Na-phytate. *alp*, the genes encoding alkaline phosphatase in the bacteria; *Vtc4p*, *polyP* synthesis gene in the extraradical hyphae of *R. irregularis*.

rDNA copy number in the target soil when *R. irregularis* hyphae were present (Fig. 1d), while the hyphal length density in the target soil was not significantly affected by phytate addition (Fig. 1g).

In conclusion, the extraradical hyphae of AM fungi can transport PSB to organic P patches and enhance organic P mineralisation both under in vitro and in vivo (soil) conditions. Bacteria move in a thick water film formed around fungal hyphae. However, the bacteria cannot be transferred to the organic P patch without an energy source in the form of hyphal exudates. Our results could be harnessed to better manage plant-microbe interactions and improve the ability of biological inocula involving AM fungi and bacteria to enhance the sustainability of agricultural crops in P limited conditions (Fig. 2).



**Figure 2.** Schematic diagram describing the postulated mechanisms of AM fungal transport of phosphate solubilizing bacteria to an organic P patch in soil and stimulation of their activity. **a.** Fungal hyphae. **b.** Deetail.

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## YouTube interviews\*

### - Isabel Mujica on orchid mycorrhizas, soil nutrients, and fungal pathogens

C. Guillermo Bueno interviews María Isabel Mujica, postdoc at Pontifical Catholic University of Chile, about the interactions between orchid mycorrhizal fungi, their plant hosts, soil nutrients, and other fungal guilds.

Interview: <https://southmycorrhizas.org/reading/march-2021/>

Study: Mujica MI, Pérez MF, Jakalski M, *et al.* 2020. Soil P reduces mycorrhizal colonization while favors fungal pathogens: observational and experimental evidence in *Bipinnula* (Orchidaceae). *FEMS Microbiol Ecol* 96: fiaa178.

<https://doi.org/10.1093/femsec/fiaa178>

### - Diana H. Wall & Carlos A. Guerra on Soil BON: global Soil Biodiversity Observation Network

César Marín interviews Diana H. Wall, Colorado State University Distinguished Professor, and Carlos A. Guerra, Researcher at the German Centre for Integrative Biodiversity Research (iDiv) about the global Soil Biodiversity Observation Network (Soil BON), an international group which objective is to “make available the soil biological and ecosystem observations needed to ensure living soil resources are sustainably conserved and managed and can support essential human needs”.

Interview: <https://southmycorrhizas.org/reading/march-ii-2021/>

Study: Guerra CA, Bardgett RD, Caon L, *et al.* 2021. Tracking, targeting, and conserving soil biodiversity. *Science* 371: 239-241.

<https://doi.org/10.1126/science.abd7926>

### - Felipe Albornoz revisiting mycorrhizal dogmas

Camille Truong interviews Felipe E. Albornoz, postdoc at CSIRO in Australia, about facts, assumptions and their consequences on mycorrhizal knowledge.

Interview: <https://southmycorrhizas.org/reading/april-2021/>

Study: Albornoz FE, Dixon KW, Lambers H. 2021. Revisiting mycorrhizal dogmas: Are mycorrhizas really functioning as they are widely believed to do? *Soil Ecol Lett* 3: 73-82. <https://doi.org/10.1007/s42832-020-0070-2>

### \*Section by:

### South American Mycorrhizal Research Network

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



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# Tools

## → LSU as a marker for AMF environmental sequencing

Delavaux *et al.* (2021) present a curated database and reference phylogenetic tree using AMF sequences from a 2012 study with sequences available at NCBI, a database of unpublished spore-derived sequences from INVAM, and additional recently described sequences from NCBI. The authors also developed a bioinformatic pipeline to work with the database, and with the hopes of “facilitate molecular work with AMF within the LSU region, leading to finer scale assessments of ecological inferences from AMF community structure”.

Study: Delavaux CS, Sturmer SL, Wagner MR, *et al.* 2021. Utility of LSU for environmental sequencing of arbuscular mycorrhizal fungi: a new reference database and pipeline. *New Phytol* 229: 3048-3052. <https://doi.org/10.1111/nph.17080>

## → Relative qPCR to quantify AMF root colonization

Bodenhausen *et al.* (2021) use a relative qPCR method to quantify AMF roots colonization, in which they normalized the AMF qPCR signal relative to a plant gene. They used the primer pair AMG1F and AM1 *in silico* showing that it covers most AMF species within plant roots without actually amplifying the plant host DNA. This method to quantify root colonization seems to be significantly less time-consuming than traditional microscopy.

Study: Bodenhausen N, Deslandes-Hérolde G, Waelchli J, *et al.* 2021. Relative qPCR to quantify colonization of plant roots by arbuscular mycorrhizal fungi. *Mycorrhiza* 31: 137-148. <https://doi.org/10.1007/s00572-020-01014-1>

## → Multilevel selection, agricultural management, and AMF

Johnson and Gibson (2021) propose a multilevel selection perspective for the agricultural management of the AMF symbiosis, looking at the effects of such perspective on the flow of matter, energy, and genetic information through mycorrhizal microbiomes in natural and agricultural ecosystems.

Study: Johnson NC, Gibson KS. 2021. Understanding multilevel selection may facilitate management of arbuscular mycorrhizae in sustainable agroecosystems. *Front Plant Sci* 11: 627345. <https://doi.org/10.3389/fpls.2020.627345>

**For previous Tools click:** [here for Issue 1](#) (p. 11), [here for Issue 2](#) (p. 15), [here for issue 3](#) (p. 16) (Vol. 1), and [here for Vol. 2, Issue 1](#) (p. 19).

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# Events

## EVENTS POSTPONED DUE TO COVID-19:

### - Ecological Society of America 2021

#### [Website](#)

Online (and some in person)  
2 – 6 August, 2021

Organizers: Ecological Society of America.

### - Eurosoil 2020 (now 2021)

#### [Website](#)

Online  
23 – 27 August, 2021

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

### - Soil Ecology Society Meeting

#### [Website](#)

Place to be defined  
May 2022

Organizers: Soil Ecology Society

### - 18<sup>th</sup> International Symposium on Microbial Ecology

#### [Website](#)

Cape Town, South Africa  
21 – 26 August 2022

Organizers: International Society for Microbial Ecology

### - 45<sup>th</sup> *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.

### 3<sup>rd</sup> Global Soil Biodiversity Conference

#### [Website](#)

Clayton Hotel, Dublin, Ireland

March 2023

Organizers: Global Soil Biodiversity Initiative



### EVENTS AS SCHEDULED:

#### 10<sup>th</sup> International Symbiosis Society Congress

#### [Website](#)

Lyon, France

18 – 23 July 2021

Organizers: International Symbiosis Society



#### II ISME Latin American Congress 2021

#### [Website](#)

Online

27 – 30 July 2021

Organizers: Universidad de Los Andes, Bogotá, Colombia.



### 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

