

Editorial

Cross-scale integration of mycorrhizal function

Introduction

Scientists working on plant symbioses have known for more than a century that mycorrhizal fungi take central stage in terrestrial ecosystems. Over the last 50 years, several leading scientists have clarified the nature of what is undoubtedly the most common, and the most important, mutualistic symbiosis in terrestrial ecosystems (Bonfante, 2018; in this issue of *New Phytologist*, pp. 982–995). Simply stated, nearly all families of land plants form root symbiotic organs, termed mycorrhizas, with soil fungi belonging to Glomeromycotina, Ascomycotina or Basidiomycotina. Within days of their emergence in the upper soil profiles, up to 95% of plant short roots are colonized by mycorrhizal fungi. The importance of this symbiosis in controlling plant nutrient status and growth, and its ecological relevance is now well established (van der Heijden *et al.*, 2015).

It is said that the relationship between mycorrhizal fungi and plants is a love story – although this metaphor is undoubtedly naive. This intimate association has its origins in an ancient and intricate relationship that allows both partners to thrive (Martin *et al.*, 2017; Field & Pressel, 2018; in this issue of *New Phytologist*, pp. 996–1011; Pither *et al.*, 2018; pp. 1148–1160; Strullu-Derrien *et al.*, 2018; pp. 1012–1030; Zobel, 2018; pp. 947–949). The long relationship between *New Phytologist* and the mycorrhizal research community has also been described as a love story, and indeed the title of a 2013 Editorial by Selosse and Martin was ‘Mycorrhizas and *New Phytologist*: une vraie histoire d’amour’. From a recent Web of Science citation analysis, it is clear that mycorrhizal research still contributes greatly to the success of the journal; the most widely cited and influential article in recent years being the Tansley review by van der Heijden *et al.* (2015), which discusses the key biological and ecological roles of the different types of mycorrhizal symbioses. This long-standing and tight association is also reflected in the organization of symposia, associated with special issues of the journal, such as the recent 33rd New Phytologist Symposium ‘*Networks of power and influence: ecology and evolution of symbioses between plants and mycorrhizal fungi*’ (Bender *et al.*, 2014). A particularly exciting aspect with mycorrhiza in the *New Phytologist*, for an Editor, but also as a reader, is the diversity of approaches covered, ranging from evolution, physiology or genomics, to molecular biology and ecology. The published papers offer the true picture of a very active research community investigating mycorrhizal symbioses in many directions and by many methods and disciplines. This paves the way for papers crossing the disciplinary borders, e.g. viewing

genomic or physiological traits as a starting point to analyze evolutionary patterns (e.g. Delaux *et al.*, 2012) or ecologically relevant questions (e.g. Bödeker *et al.*, 2014), and producing elegant, highly-cited works.

The present Editorial explores *New Phytologist*’s rich history of publishing the best research on this most fascinating and complex series of interactions, and, happily, this ‘real love story’ continues to play out. Today, with the advent of new concepts and techniques, the possibility of integration across a wide range of disciplines from genomics to molecular ecology and field ecology is becoming a reality that is much encouraged by *New Phytologist*. Since Selosse and Martin’s Editorial was published, further outstanding research in this field has appeared in the pages of the journal, including a special issue titled ‘*Ecology and evolution of mycorrhizas*’ in 2015 (see Dickie *et al.*, 2015 for an overview), and we are proud to introduce the collection presented here, which includes some of the most recent research in the area.

In this Editorial we will highlight some of the recent innovative mycorrhizal research published in the journal and look to future challenges that lie ahead. This theme is continued throughout the Forum of this issue, including Commentaries on selected papers and a series of Letters stimulated by discussions and the ideas exchanged at two conferences held in 2017, both of which the New Phytologist Trust was proud to support: the 9th International Congress on Mycorrhizas (ICOM), in Prague, Czech Republic (Waller *et al.*, 2018), and the 3rd International Molecular Mycorrhiza Meeting (iMMM3; see Plett, 2018) in Toulouse, France. The broad scope and wide range of themes covered in these meetings illustrate how diverse mycorrhizal research is. This diversity is reflected in the Editorial board of *New Phytologist*, and below we offer some insights and reflections from Editors past and present on the articles presented herein.

Arbuscular mycorrhizal symbiosis

‘Eighty percent and 400 million years’ – so starts every graduate student’s lab meeting presentations, at least if your lab works on arbuscular mycorrhiza (AM). We encourage all those graduate students (and postdocs and principal investigators) to update their knowledge of the diversity of AM in the context of all mycorrhizas by reading Brundrett & Tedersoo (2018; in this issue of *New Phytologist*, pp. 1108–1115). These authors review the global diversity of mycorrhizal and nonmycorrhizal plants and present revised estimates of mycorrhizal status based on 135 years of data, summarized in a stunning figure that also illustrates nutritional/habitat specialisations of the 8% of nonmycorrhizal plants. AM is still the most abundant type of mycorrhiza at 71%! The Tansley insight also discusses evolutionary history outlining three waves of mycorrhizal evolution, which illustrates shifts in mycorrhizal status and the fairly frequent occurrence of plant families with

multifunctional or dual ectomycorrhizal (ECM)–AM root systems. These dual systems have not yet received much attention at the physiological or molecular levels and with the availability of genomes for all partners (e.g. *Populus* / *Laccaria/Rhizophagus* and *Eucalyptus/Pisolithus/Rhizophagus* associations), these interesting multifunctional mycorrhizal roots are calling out for further investigation.

The AM status of the plant hosts is well accepted, but by contrast some aspects of AM fungal biology provoke lively debate, which simply illustrates that our knowledge of their biology is very limited. The Viewpoint by Bruns *et al.* (2018; in this issue of *New Phytologist*, pp. 963–967) summarises the thought-provoking presentations and discussions from an ICOM9 workshop on species recognition in the Glomeromycotina. Initially elevated to their own phylum (Glomeromycota) and suggested to be asexual fungi and possibly heterokaryotic, it later became clear from multi-locus analyses that AM fungi classify within the Mucoromycota. Furthermore, the current genome sequences (Tisserant *et al.*, 2013; Ropars *et al.*, 2016; Chen *et al.*, 2018; in this issue of *New Phytologist*, pp. 1161–1171) (and additional analyses) argue that these AM fungi are homokaryotic and likely sexual, even if it is a mystery as to how sex occurs. Thus, after a slight demotion, AM fungi appear somewhat more traditional than originally thought. Regardless, many aspects of their biology are still a mystery including extensive variation in their ability to promote plant growth, as pointed out in a Letter from Sanders (2018; in this issue of *New Phytologist*, pp. 968–970). One avenue to growth promotion is almost certainly via phosphate acquisition and transfer to the plant. Recent advances in phosphate metabolism, reviewed by Ezawa & Saito, 2018; in this issue of *New Phytologist*, pp. 1116–1121), report the identification of five secreted acid phosphatases expressed in the extracellular hyphae of *Rhizophagus clarus*. This is interesting because they may enable liberation of phosphate from organic sources, for which there is some biochemical evidence, but also some earlier debate (reviewed in Ezawa & Saito, 2018). Variation in genes such as these could potentially underlie variation in plant growth promotion among symbionts.

Recent advances in our knowledge of carbon transfer to the AM fungi is among the topics discussed by Lanfranco *et al.* (2018; in this issue of *New Phytologist*, pp. 1031–1046; although it should be noted that this comprehensive Tansley review covers much more). With strong evidence that the AM fungi acquire glucose from the plant, it was a surprise when the AM fungal genome and transcriptome sequences predicted that AM fungi were fatty acid auxotrophs. Subsequent studies led to the conclusion that the colonized root cells hugely increase fatty acid biosynthesis and redirect their lipid metabolism to generate an esterified-C16 fatty acid which is subsequently provided to the fungus (references can be found in Lanfranco *et al.*). Considering that AM fungi are oleaginous, and store and transport lipids throughout their mycelium, their status as fatty acid auxotrophs is a surprise – perhaps they are not so traditional after all.

Ectomycorrhizal symbiosis

Associations with ECM fungi are widespread on roots of tree species. They evolved from saprotrophic fungi with whom they still share a limited set of enzymes for degradation of organic materials such as cellulose, hemicelluloses, proteins, etc. (Martin *et al.*, 2008, 2010; Kohler *et al.*, 2015). These restricted abilities to decompose soil organic matter have been proposed to be important for their free lifestyle in absence of a host. In this special issue, Zhang *et al.* (2018; in this issue of *New Phytologist*, pp. 1309–1321) uncover a new function. They demonstrate that a distinct fungal endoglucanase (glycoside hydrolase family 5 (GH5), LbGH5-CBM1) is required for invasion of *Laccaria bicolor* into the apoplast of poplar roots, suggesting that LbGH5-CBM1 is an effector mediating fungal–host interaction. Host colonization and formation of the Hartig net were preceded by activities of this mycorrhiza-induced endocellulase. The Hartig net is the key interface for reciprocal nutrient exchange between both organisms. Here, Becquer *et al.* (2018; in this issue of *New Phytologist*, pp. 1185–1199) show that a fungal phosphate transporter (HcPT2), located in extramatrical mycelium and the Hartig net, is induced by the plant and its overexpression increases phosphate allocation to the host. When the phosphate transporter was suppressed by RNAi, root colonization was also reduced, suggesting that more beneficial fungal partners are preferred by the host plant.

Nehls & Plassard (2018; in this issue of *New Phytologist*, pp. 1047–1058) provide a comprehensive overview on the functions of ectomycorrhiza for phosphorus (P) and nitrogen (N) nutrition. Under natural conditions, trees are colonized by a multitude of different ECM fungal species, which have distinctly different abilities for N acquisition, especially under drought stress (Pena & Polle, 2014). Here, Köhler *et al.* (2018; in this issue of *New Phytologist*, pp. 1200–1210) report that higher ECM fungal species richness supports higher P uptake of the host. They further show that interaction with drought or N decreased species richness of ECM fungi and P uptake of the host plant. Complex mycorrhizal fungal communities may, thus, be advantageous to minimize the risk for nutrient imbalances.

Comprehensive ecological studies in drought-prone environments (Castaño *et al.*, 2018; in this issue of *New Phytologist*, pp. 1211–1221) and after an unusually strong flooding event (Barnes *et al.*, 2018; in this issue of *New Phytologist*, pp. 1172–1184; see also the Commentary by Johnson, 2018; in this issue of *New Phytologist*, pp. 950–951) highlight the sensitivity of ECM symbiosis to weather extremes. Climate change may therefore influence the dynamics of mycorrhizal fungal community assembly and thereby, impact biogeochemical cycles.

Mycorrhizal fungal community ecology

The fire that new methods ignited in fungal ecology (Hibbett *et al.*, 2009) has, undoubtedly, attracted a broad field of researchers to a rather narrow set of similar questions. With this special collection, understanding of the biodiversity of AM fungi gains a range of new insights with an interesting focus on grasslands (in this issue of *New Phytologist*, Jiang *et al.*, 2018, pp. 1222–1235; Neuenkamp *et al.*,

2018, pp. 1236–1247; Rasmussen *et al.*, 2018, pp. 1248–1261; Van Geel *et al.*, 2018, pp. 1262–1272). Grasslands are globally common habitats and provide important functions for humans as well as being essential parts of landscapes and biosphere. They also host diverse AM fungal communities (Pärtel *et al.*, 2017). In many areas of the world most of the grasslands have experienced and continue to experience human impact, i.e. they are semi-natural habitats. However, such habitats may harbour a substantial part of regional biodiversity and can contribute to human well-being and ecosystem functioning in a non-redundant manner. Neuenkamp *et al.* (2018, pp. 1236–1247) demonstrate that abandonment of management in Estonian seminatural calcareous grasslands brings about concurrent shifts of both plant and associating AM fungal diversities, with a change in plant community functional composition. Namely, with shrub encroaching and final forest take-over, the proportion of plants, which are less dependent on AM symbiosis (facultatively mycorrhizal plants), increased.

Drivers of AM fungal community assembly in grasslands were also explored across 46 sites in six European countries (Van Geel *et al.*, 2018, pp. 1262–1272), across different spatial scales in Åland archipelago of Finland (Rasmussen *et al.*, 2018, pp. 1248–1261) and in Tibetan alpine grasslands in China (Jiang *et al.*, 2018, pp. 1222–1235). These papers are exemplary in the field of fungal community ecology, demonstrating how apparently descriptive data are providing invaluable insights into how nature operates. These papers also illustrate how very similar questions may receive apparently contradictory answers. Here, the main drivers behind AM fungal community patterns were in some cases mostly spatial, in others mostly environmental (edaphic and/or climatic), and in others biotic (host plant or non-AM fungi-related) (Caruso, 2018; in this issue of *New Phytologist*, pp. 954–956; Hempel, 2018, pp. 952–953). It is clear that there is substantial value in these biodiversity surveys – descriptive observations of community patterns in nature – to identify which mechanisms to explore and test experimentally.

Questions around the causality behind correlations in plant–fungi–soil systems are increasingly popular, but driver–passenger relationships in mycorrhizal symbiosis remain elusive (Hempel, 2018, pp. 952–953). Often, however, there is a tendency to put the fungal symbionts in the back seat and focus on the relative importance of plants or soils as drivers. There is still a need to strengthen the ‘mycocentric perspective’ (Fitter *et al.*, 2000), because specificity in fungal–plant interactions (e.g. Lofgren *et al.*, 2018; in this issue of *New Phytologist*, pp. 1273–1284) work both ways. Although notoriously difficult to support empirically, it seems likely that mycorrhizal fungal community composition is a decisive factor during assembly of plant communities.

Causal effects of mycorrhizal fungi, either on the host (Jiang *et al.*, 2018, pp. 1222–1235; Köhler *et al.*, 2018, pp. 1200–1210) or on the soil (Storer *et al.*, 2018; in this issue of *New Phytologist*, pp. 1285–1295), are often discussed in terms of ‘functionality’ (in this issue of *New Phytologist*, Hazard & Johnson, 2018, pp. 1122–1128; Lekberg & Helgason, 2018, pp. 957–962; Powell & Rillig, 2018, pp. 1059–1075). Powell & Rillig (2018, pp. 1059–1075) provide a comprehensive review on AM fungal (functional) diversity, and in

particular, indicate research directions, questions, experiments and approaches to reach understanding on how AM fungal diversity is related to ecosystem function. They propose to consider biological stoichiometry as a conceptual framework for designing further studies disentangling diversity–function relationships. Along the same lines, Lekberg & Helgason (2018, pp. 957–962) discuss approaches to study mycorrhizal functioning in the actual field conditions, rather than in the controlled environment, and how to consider multiple mycorrhizal types simultaneously (Lekberg *et al.*, 2018, pp. 971–976). The study by Jiang *et al.* (2018, pp. 1222–1235) provides a good example by manipulating AM fungal communities in the field and testing the response of fungi to nutrient addition. However, it is important to consider that ‘functional’ interactions between mycorrhizal fungi, plants and soils in most cases will turn out to be bi-directional. Systems with bi-directional dependencies are characterized by strong feedbacks, implying that mycorrhizal interactions may act to stabilize ecosystems, if negative feedbacks prevail, or to destabilize ecosystems and propel directional changes, if positive feedbacks are common (e.g. Corrales *et al.*, 2018; in this issue of *New Phytologist*, pp. 1076–1091). The increasing realization of the importance of plant–soil feedbacks in ecosystem dynamics puts mycorrhizal symbiosis in focus of the much wider research community interested in global change and land use. Of course, the relationship between mycorrhizal symbiosis and global change is also bidirectional (Barnes *et al.*, 2018; in this issue of *New Phytologist*, pp. 1172–1184; Castaño *et al.*, 2018, pp. 1211–1221; Köhler *et al.*, 2018, pp. 1200–1210) with obvious risk scenarios of accelerating global change, but also possibilities for mitigation by well-informed land-use management.

A cross-cutting theme joining several areas of mycorrhizal research included in this special collection, is the question of what is a species, and how to delimit and recognise (identify) species to enable best research on genomics, physiology or any other field requiring that the targeted organisms are consistently named (Bruns *et al.*, 2018, pp. 963–967; Mathieu *et al.*, 2018, pp. 1129–1134; Sanders, 2018, pp. 968–970). The issue of optimal selection of approaches for detection (and identification) of fungi and mycorrhizal fungi in natural samples is further tackled by Lekberg *et al.* (2018, pp. 971–976).

An area where consistent and easy-to-communicate naming is required is the application of AM fungi. Ryan & Graham (2018; in this issue of *New Phytologist*, pp. 1092–1107) provoke the research community to take a fresh look on what is known about functional roles of AM fungi in agroecosystems and what would the crop growers need from scientists to be able to harness the potential of soil biodiversity for more environment-friendly and sustainable crop production, but also for minimizing destruction of natural habitats.

Certainly, this subject continues to receive attention from scientists, farmers, inoculum and biofertiliser producers as well as policy makers.

Rivero *et al.* (2018; in this issue of *New Phytologist*, pp. 1322–1336) examine plant metabolic plasticity in stressed tomato plants, and note that AM symbioses can help plants deal with this stress, and the Tansley insight by Sawers *et al.* (2018; in this issue of *New*

Phytologist, pp. 1135–1140) examines AM symbiosis in light of domestication and crop improvement in cereals.

A formidable challenge faced by our community is to identify the functions played by the assemblages of mycorrhizal fungi *in situ*. As a prerequisite of such large-scale functional ecology studies, we now need to accelerate the discovery of factors (e.g. gene networks) controlling the development and functioning of the various types of mycorrhizal symbioses. The fitness of the mycorrhizal symbioses is thought to be caused by interaction of hundreds of symbiosis-related genes and symbiont environment. By characterizing and manipulating patterns of gene expression, we should be able to identify the genetic hubs regulating the mycorrhizal fungal response to changing host physiology, and better understand how these interactions control ecosystem function. Critical in this endeavor will be the use of genomic information on the recently sequenced mycorrhizal fungi (Kohler *et al.*, 2015; Martino *et al.*, 2018; Chen *et al.*, 2018, pp. 1161–1171; see also Perotto *et al.*, 2018, pp. 1141–1147). The completion or impending completion of 100+ genome sequences of mycorrhizal fungi (see the Mycorrhizal Fungi page at the MycoCosm database, https://genome.jgi.doe.gov/Mycorrhizal_fungi/Mycorrhizal_fungi.info.html) provides an unprecedented opportunity to identify the key components of interspecific and organism–environment interactions (Martin *et al.*, 2017). There is no doubt that large-scale genome sequencing of mycorrhizal fungi, endophytes and related soil saprotrophs will be fertile ground for novel hypotheses about how mycorrhizal symbioses evolved in the different plant families and drive present ecosystems (van der Heijden *et al.*, 2015; Brundrett & Tedersoo, 2018, pp. 1108–1115).

Conclusions

The scientific rewards from comprehensive research programs on mycorrhizal symbioses include a greater fundamental understanding of the interactions between organisms at the community level and benefits for sustainable agriculture and forestry. A deeper understanding of the complex array of factors affecting host–fungus interactions and co-evolution could indeed ensure efficient selection of fungal symbionts for large-scale inoculation methods in forest and agricultural ecosystems, although all scientists are not so optimistic (Ryan & Graham, 2018, pp. 1092–1107). This will require a tighter collaboration with agronomists and foresters. Through the application of the advanced omics approaches at several levels – genomics, transcriptomics, proteomics and metabolomics – remarkable progress has been made in understanding the mechanisms that control the development and functioning of mycorrhizal symbioses. However, most of these studies have been carried out in simple experimental settings, such as growth chambers. Understanding how these mutualistic associations adapt and respond to changes in the biological, chemical and physical properties of agro- and natural ecosystems therefore remains a significant challenge for plant and microbial biologists. Combined community structure and function studies applying both molecular ecology and *in situ* transcriptomics and proteomics may, in the future, significantly promote our understanding of the interactions between mycorrhizal fungal species

with their hosts and with their biotic and abiotic environment. Future research on mycorrhizal symbioses would thus greatly benefit from a comprehensive approach bridging genetics, molecular biology, physiology, field ecology and agronomy. Unfortunately, the community of scientists working on mycorrhizas is partly fragmented with molecular biologists attending iMMM conferences and field ecologists gathering mainly at ICOMs. Recently, Ferlian *et al.* (2018) pointed out that ‘*this historic partitioning [iMMM / ICOM] into separate fields sometimes hinders a comprehensive understanding of how mycorrhizae function*’. In the future, we should explore ways to re-unify our community to better integrate the molecular knowledge with field ecology and provide opportunities to early career researchers to embrace all the facets of the complex mycorrhizal associations. The lack of a unified research community may lead to a lack of encouragement for students to enter into this world.

As a more optimistic note, readers in this special collection can also find two Profiles that highlight individuals who have made an enormous impact on the field of mycorrhizal research. Prof. Alastair Fitter (pp. 977–978) was a long-standing Editor of *New Phytologist*, and served on the board of the New Phytologist Trust. The second Profile features Prof. Paola Bonfante (pp. 979–981), again, another leader in the field with long-standing connections to the journal, Paola currently serves as a member of our Advisory Board. She also contributes to the collection via two articles (Bonfante, 2018, pp. 982–995; Chialva *et al.*, 2018, pp. 1296–1308), including a Tansley review which once again mines the fascinating history of mycorrhizal research. Despite this look to the past this review, and the collection as a whole, has a focus firmly on the future.

The Royal Botanic Gardens, Kew recently released a report titled *State of the World's Fungi* (Willis, 2018). This report is the first to summarize the current status of this immensely important group of organisms, and needless to say the mycorrhizal symbiosis is given great prominence. *State of the World's Fungi* highlights the importance of Fungi to life on Earth, and how it must be conserved and protected; our aim for this collection is to also highlight this importance, and to showcase the outstanding research that is contributing to our understanding of these important plant–fungal interactions.

Acknowledgements

We would like to thank the organizers of ICOM9 and iMMM3 for their outstanding service to the community. The research in FMM's lab is funded through the Laboratory of Excellence Advanced Research on the Biology of Tree and Forest Ecosystems (ANR-11-LABX 0002 01). MÖ is supported by the Estonian Research Council (IUT20-28), the European Regional Development Fund (Centre of Excellence EcolChange) and ERA-NET Cofund BiodivERsA3 (SoilMan). We would also like to thank Ian A. Dickie for his contribution to the editorial process.

Francis M. Martin^{1*}, Maria J. Harrison², Sarah Lennon³,
Björn Lindahl⁴, Maarja Öpik⁵, Andrea Polle⁶,
Natalia Requena⁷ and Marc-André Selosse^{8,9}

- ¹INRA, Université de Lorraine, UMR Interactions Arbres/Micro-Organismes, INRA-Centre Grand Est, Champenoux 54280, France;
- ²Boyce Thompson Institute, Ithaca, NY 14853, USA;
- ³New Phytologist Central Office, Bailrigg House, Lancaster University, Lancaster, LA1 4YE, UK;
- ⁴Department of Soil and Environment, Swedish University of Agricultural Sciences, Box 7014, Uppsala, SE-750 07, Sweden;
- ⁵Department of Botany, Institute of Ecology and Earth Sciences, 40 Lai St., Tartu, 51005, Estonia;
- ⁶Forest Botany and Tree Physiology, University of Goettingen, Goettingen, 37077, Germany;
- ⁷Molecular Phytopathology Department, Karlsruhe Institute of Technology, Fritz Haber-Weg 4, Geb. 30.43, 2. OG, Karlsruhe, D-76131, Germany;
- ⁸Département Systématique et Evolution, Muséum national d'Histoire naturelle, UMR 7205 ISYEB, CP 50, 45 rue Buffon, Paris, 75005, France;
- ⁹Faculty of Biology, University of Gdańsk, ul. Wita Stwosza 59, 80-308, Gdańsk, Poland
- (*Author for correspondence: tel +33 383 39 40 80; email fmartin@nancy.inra.fr)

References

- Barnes CJ, van der Gast CJ, McNamara NP, Rowe R, Bending GD. 2018. Extreme rainfall affects assembly of the root-associated fungal community. *New Phytologist* 220: 1172–1184.
- Becquer A, Garcia K, Amenc L, Rivard C, Doré J, Trives-Segura C, Szponarski W, Russet S, Baeza Y, Lassalle-Kaiser B *et al.* 2018. The *Hebeloma cylindrosporium* HcPT2 Pi transporter plays a key role in ectomycorrhizal symbiosis. *New Phytologist* 220: 1185–1199.
- Bonfante P. 2018. The future has roots in the past: the ideas and scientists that shaped mycorrhizal research. *New Phytologist* 220: 982–995.
- Brundrett MC, Tedersoo L. 2018. Evolutionary history of mycorrhizal symbioses and global host plant diversity. *New Phytologist* 220: 1108–1115.
- Bruns TD, Corradi N, Redecker D, Taylor JW, Öpik M. 2018. Glomeromycotina: what is a species and why should we care? *New Phytologist* 220: 963–967.
- Caruso T. 2018. Disentangling the factors shaping arbuscular mycorrhizal fungal communities across multiple spatial scales. *New Phytologist* 220: 954–956.
- Castaño C, Lindahl BD, Alday JG, Hagenbo A, Martínez de Aragón J, Parladé J, Pera J, Bonet JA. 2018. Soil microclimate changes affect soil fungal communities in a Mediterranean pine forest. *New Phytologist* 220: 1211–1221.
- Chen ECH, Morin E, Beaudet D, Noel J, Yildirim G, Ndikumana S, Charron P, St-Onge C, Giorgi J, Krüger M *et al.* 2018. High intraspecific genome diversity in the model arbuscular mycorrhizal symbiont *Rhizophagus irregularis*. *New Phytologist* 220: 1161–1171.
- Chialva M, Salvioli di Fossalunga A, Daghighino S, Ghignone S, Bagnaresi P, Chiappello M, Novero M, Spadaro D, Perotto S, Bonfante P. 2018. Native soils with their microbiotas elicit a state of alert in tomato plants. *New Phytologist* 220: 1296–1308.
- Corrales A, Henkel TW, Smith ME. 2018. Ectomycorrhizal associations in the tropics – biogeography, diversity patterns and ecosystem roles. *New Phytologist* 220: 1076–1091.
- Dickie IA, Alexander I, Lennon S, Öpik M, Selosse M-A, van der Heijden MGA, Martin F. 2015. Evolving insights to understanding mycorrhizas. *New Phytologist* 205: 1369–1374.
- Ezawa T, Saito K. 2018. How do arbuscular mycorrhizal fungi handle phosphate? New insight into fine-tuning of phosphate metabolism. *New Phytologist* 220: 1116–1121.
- Ferlian O, Biere A, Bonfante P, Buscot F, Eisenhauer N, Fernandez I, Hause B, Herrmann S, Krajinski-Barth F, Meier IC *et al.* 2018. Growing research networks on mycorrhizae for mutual benefits. *Trends in Plant Science* 23: 975–984.
- Field KJ, Pressel S. 2018. Unity in diversity: structural and functional insights into the ancient partnerships between plants and fungi. *New Phytologist* 220: 996–1011.
- Fitter AH, Heinemeyer A, Staddon PL. 2000. The impact of elevated CO₂ and global climate change on arbuscular mycorrhizas: a myco-centric approach. *New Phytologist* 147: 179–187.
- Hazard C, Johnson D. 2018. Does genotypic and species diversity of mycorrhizal plants and fungi affect ecosystem function? *New Phytologist* 220: 1122–1128.
- van der Heijden MG, Martin FM, Selosse MA, Sanders IR. 2015. Mycorrhizal ecology and evolution: the past, the present, and the future. *New Phytologist* 205: 1406–1423.
- Hempel S. 2018. Passengers and drivers of arbuscular mycorrhizal fungal communities at different scales. *New Phytologist* 220: 952–953.
- Hibbett DS, Ohman A, Kirk PM. 2009. Fungal ecology catches fire. *New Phytologist* 184: 279–282.
- Jiang S, Liu Y, Luo J, Qin M, Johnson NC, Öpik M, Vasar M, Chai Y, Zhou X, Mao L *et al.* 2018. Dynamics of arbuscular mycorrhizal fungal community structure and functioning along a nitrogen enrichment gradient in an alpine meadow ecosystem. *New Phytologist* 220: 1222–1235.
- Johnson D. 2018. Water, water everywhere . . . but how does it affect the functional diversity of ectomycorrhizal fungi? *New Phytologist* 220: 950–951.
- Kohler A, Kuo A, Nagy LG, Morin E, Barry KW, Buscot F, Canback B, Choi C, Cichocki N, Clum A *et al.* 2015. Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. *Nature Genetics* 47: 410–415.
- Köhler J, Yang N, Pena R, Raghavan V, Polle A, Meier IC. 2018. Ectomycorrhizal fungal diversity increases phosphorus uptake efficiency of European beech. *New Phytologist* 220: 1200–1210.
- Lanfranco L, Fiorilli V, Gutjahr C. 2018. Partner communication and role of nutrients in the arbuscular mycorrhizal symbiosis. *New Phytologist* 220: 1031–1046.
- Lekberg Y, Helgason T. 2018. *In situ* mycorrhizal function – knowledge gaps and future directions. *New Phytologist* 220: 957–962.
- Lekberg Y, Vasar M, Bullington LS, Sepp S-K, Antunes PM, Bunn R, Larkin BG, Öpik M. 2018. More bang for the buck? Can arbuscular mycorrhizal fungal communities be characterized adequately alongside other fungi using general fungal primers? *New Phytologist* 220: 971–976.
- Lofgren L, Nguyen NH, Kennedy PG. 2018. Ectomycorrhizal host specificity in a changing world: can legacy effects explain anomalous current associations? *New Phytologist* 220: 1273–1284.
- Martin F, Aerts A, Ahren D, Brun A, Danchin EGJ, Duchaussoy F, Gibon J, Kohler A, Lindquist E, Pereda V *et al.* 2008. The genome of *Laccaria bicolor* provides insights into mycorrhizal symbiosis. *Nature* 452: 88–92.
- Martin F, Kohler A, Murat C, Balestrini R, Coutinho PM, Jaillon O, Montanini B, Morin E, Noel B, Percudani R *et al.* 2010. Perigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. *Nature* 464: 1033–1038.
- Martin F, Uroz S, Barker D. 2017. Ancestral alliances: plant mutualistic symbioses with fungi and bacteria. *Science* 356: 819.
- Martino E, Morin E, Grelet G-A, Kuo A, Kohler A, Daghighino S, Barry KW, Cichocki N, Clum A, Dockter RB *et al.* 2018. Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. *New Phytologist* 217: 1213–1229.
- Mathieu S, Cusant L, Roux C, Corradi N. 2018. Arbuscular mycorrhizal fungi: intraspecific diversity and pangenomes. *New Phytologist* 220: 1129–1134.
- Nehls U, Plassard C. 2018. Nitrogen and phosphate metabolism in ectomycorrhizas. *New Phytologist* 220: 1047–1058.
- Neuenkamp L, Moora M, Öpik M, Davison J, Gerz M, Männistö M, Jairus T, Vasar M, Zobel M. 2018. The role of plant mycorrhizal type and status in modulating the relationship between plant and arbuscular mycorrhizal fungal communities. *New Phytologist* 220: 1236–1247.
- Pärtel M, Öpik M, Moora M, Tedersoo L, Szava-Kovats R, Rosendahl S, Rillig MC, Lekberg Y, Kreft H, Helgason T *et al.* 2017. Historical biome distribution and recent human disturbance shape the diversity of arbuscular mycorrhizal fungi. *New Phytologist* 216: 227–238.

- Pena R, Polle A. 2014. Attributing functions to ectomycorrhizal fungal identities in assemblages for nitrogen acquisition under stress. *ISME Journal* 8: 321–330.
- Perotto S, Daghino S, Martino E. 2018. Ericoid mycorrhizal fungi and their genomes: another side to the mycorrhizal symbiosis? *New Phytologist* 220: 1141–1147.
- Pither J, Pickles BJ, Simard SW, Ordóñez A, Williams JW. 2018. Below-ground biotic interactions moderated the postglacial range dynamics of trees. *New Phytologist* 220: 1148–1160.
- Plett KL. 2018. Fresh knowledge for an old relationship: new discoveries in molecular mycorrhizal research. *New Phytologist* 217: 26–28.
- Powell JR, Rillig MC. 2018. Biodiversity of arbuscular mycorrhizal fungi and ecosystem function. *New Phytologist* 220: 1059–1075.
- Rasmussen PU, Hugerth LW, Blanchet FG, Andersson AF, Lindahl BD, Tack AJM. 2018. Multiscale patterns and drivers of arbuscular mycorrhizal fungal communities in the roots and root-associated soil of a wild perennial herb. *New Phytologist* 220: 1248–1261.
- Rivero J, Álvarez D, Flors V, Azcón-Aguilar C, Pozo MJ. 2018. Root metabolic plasticity underlies functional diversity in mycorrhiza-enhanced stress tolerance in tomato. *New Phytologist* 220: 1322–1336.
- Ropars J, Toro KS, Noel J, Pelin A, Charron P, Farinelli L, Marton T, Krüger M, Fuchs J, Brachmann A *et al.* 2016. Evidence for the sexual origin of heterokaryosis in arbuscular mycorrhizal fungi. *Nature Microbiology* 1: 16033.
- Ryan MH, Graham JH. 2018. Little evidence that farmers should consider abundance or diversity of arbuscular mycorrhizal fungi when managing crops. *New Phytologist* 220: 1092–1107.
- Sanders IR. 2018. Sex, plasticity, and biologically significant variation in one Glomeromycotina species. *New Phytologist* 220: 968–970.
- Sawers RJH, Ramírez-Flores MR, Olalde-Portugal V, Paszkowski U. 2018. The impact of domestication and crop improvement on arbuscular mycorrhizal symbiosis in cereals: insights from genetics and genomics. *New Phytologist* 220: 1092–1107.
- Selosse M, Martin F. 2013. Mycorrhizas and *New Phytologist: une vraie histoire d'amour*. *New Phytologist* 200: 587–589.
- Storer K, Coggan A, Ineson P, Hodge A. 2018. Arbuscular mycorrhizal fungi reduce nitrous oxide emissions from N₂O hotspots. *New Phytologist* 220: 1285–1295.
- Strullu-Derrien C, Selosse M-A, Kenrick P, Martin FM. 2018. The origin and evolution of mycorrhizal symbioses: from palaeomycology to phylogenomics. *New Phytologist* 220: 1012–1030.
- Tisserant E, Malbreil M, Kuo A, Kohler A, Symeonidi A, Balestrini R, Charron P, Duensing N, Frei dit Frey NGianinazzi-Pearson, V *et al.* 2013. Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. *Proceedings of the National Academy of Sciences, USA* 110: 20117–20122.
- Van Geel M, Jacquemyn H, Plue J, Saar L, Kasari L, Peeters G, van Acker K, Honnay O, Ceulemans T. 2018. Abiotic rather than biotic filtering shapes the arbuscular mycorrhizal fungal communities of European seminatural grasslands. *New Phytologist* 220: 1262–1272.
- Waller LP, Felten J, Hiiesalu I, Vogt-Schilb H. 2018. Sharing resources for mutual benefit: crosstalk between disciplines deepens the understanding of mycorrhizal symbioses across scales. *New Phytologist* 217: 29–32.
- Willis KJ, ed. 2018. *State of the World's Fungi 2018*. Kew, London, UK: Royal Botanic Gardens.
- Zhang F, Anasontzis GE, Labourel A, Champion C, Haon M, Kempainen M, Commun C, Deveau A, Pardo A, Veneault-Fourrey C *et al.* 2018. The ectomycorrhizal basidiomycete *Laccaria bicolor* releases a secreted β -1,4 endoglucanase that plays a key role in symbiosis development. *New Phytologist* 220: 1309–1321.
- Zobel M. 2018. Eltonian niche width determines range expansion success in ectomycorrhizal conifers. *New Phytologist* 220: 947–949.

Key words: community, ecology, evolution, mycorrhizas, symbioses.



About *New Phytologist*

- *New Phytologist* is an electronic (online-only) journal owned by the New Phytologist Trust, a **not-for-profit organization** dedicated to the promotion of plant science, facilitating projects from symposia to free access for our Tansley reviews and Tansley insights.
- Regular papers, Letters, Research reviews, Rapid reports and both Modelling/Theory and Methods papers are encouraged. We are committed to rapid processing, from online submission through to publication 'as ready' via *Early View* – our average time to decision is <26 days. There are **no page or colour charges** and a PDF version will be provided for each article.
- The journal is available online at Wiley Online Library. Visit **www.newphytologist.com** to search the articles and register for table of contents email alerts.
- If you have any questions, do get in touch with Central Office (np-centraloffice@lancaster.ac.uk) or, if it is more convenient, our USA Office (np-usaoffice@lancaster.ac.uk)
- For submission instructions, subscription and all the latest information visit **www.newphytologist.com**