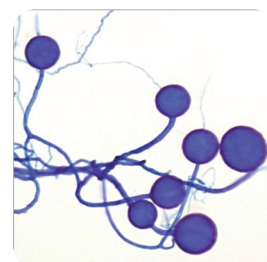
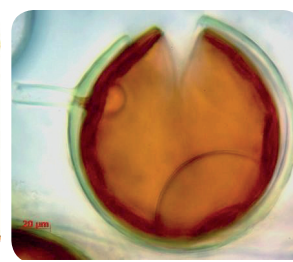
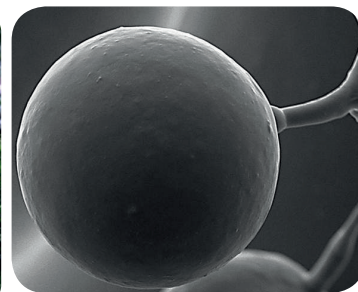
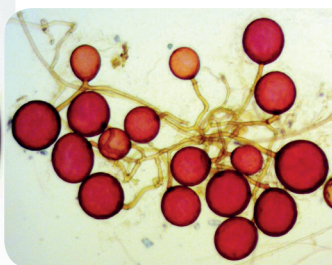
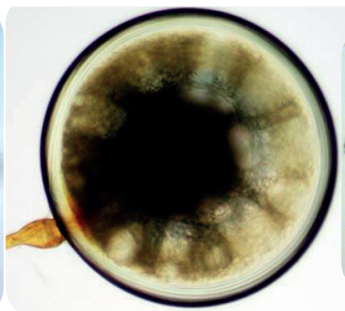
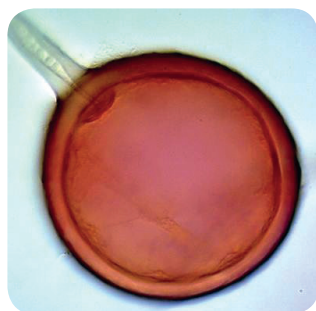


MYCORRHIZA NEWS

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RESEARCH FINDING PAPERS

Seasonal Colonization of Arbuscular Mycorrhiza in *Andrographis Paniculata* (Burm.f.) Nees

Kripamoy Chakraborty^{a*}, Jenifar Lushai^a, Aparajita Roy Das^b, Ajay Krishna Saha^b, and Panna Das^a

Introduction

Andrographis paniculata (Burm.f.) Nees is one of the extensively used medicinal plants and hence has the potential for export (Anandalwar and Vasantha 1989). Some of the attributes that make it such a unique herb include anticancer (Kumar, Sridevi, Kumar, *et al.* 2004), antihyperglycemic (Subramanian and Asmawi 2006), antimalarial (Misra, Guru, Katiyar, Srivastava, *et al.* 1992), antioxidant (Singh, Banerjee, and Rao 2001), antihepatitis (Sharma, Singh, Sehgal, *et al.* 1991), and anti-HIV activity (Yu, Chang, Su, *et al.* 2008).

From plant nutrition perspective, arbuscular mycorrhizal fungi (AM fungi) of Glomeromycota (Tedersoo, Sañchez-Ramírez, Kõljalg, *et al.* 2018) have the ability to create a specialized niche (McArthur and Knowles 1993; Tobar, Azcón, and Barea, 1994 a, b). Such symbiotic relation has many non-nutritional benefits such as improvement of plant growth and yield (Javaid, Iqbal, and Hafeez 1994; Cavagnaro, Jackson, Six, *et al.* 2006), enhancement of tolerance to various biotic (Khaosaad, García-Garrido, Steinkellner, *et al.* 2007) and abiotic stresses (Al-Garni 2006; Takeda, Kistner, Kosuta, *et al.* 2007). AM fungal morphology can be divided into three types: (i) *Arum*, (ii) *Paris*, and (iii) Intermediate (Dickson 2004). Morphological types of AM fungi have been examined in many plant taxa (Kubato and McGonigle 2005; Yamato and Iwasaki 2002; Muthukumar, Senthilkumar, Rajangam, *et al.* 2006; Muthukumar and Prakash 2009; Das Kayang

2010; Das, Saha, and Kayang 2013; Chakraborty, Sinha, Debnath, *et al.* 2016; Chakraborty, Talapatra, Roy Das, *et al.* 2019; Chakraborty, Banik, Debnath, *et al.* 2019).

Despite a moderate literature on the AM fungal colonization in *A. paniculata*, reports concerning structural features (within the root) and seasonal colonization is lacking. In this connection, the present study, carried out in Tripura, India is focused on the analysis of AM fungal colonization and composition associated with *A. paniculata*.

Materials and Methods

Study sites

For assessing AM fungal colonization and composition, root and soil samples of *A. paniculata* were collected during the dry season (early March) and wet rainy season (August) from two study sites of Suryamaninagar and Kanchancherra, Tripura. *A. paniculata* is an annual, branched, erect herbaceous plant, commonly found in hedgerows throughout the waste ground and road sides.

Root and soil sampling

The fine root samples of five randomly selected healthy and disease-free plants, distanced approximately 20 m away from each other were collected by uprooting. Utmost care was taken during root collection process. The task of identifying *A. paniculata* was difficult as the desired plant was surrounded by the robust

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composition of other herbs or shrubs. Root samples were first washed gently to remove the adhering soil and treated with formalin-acetic acid (FAA) solution before introducing to the laboratory for processing. The soil adhering to the roots and adjacent to roots was collected from each of the selected individual, mixed in marked zipped polythene bags and brought to the laboratory. The soil samples were divided into two equal halves. One half was stored at 4°C to assess the spore density and composition of AM fungi. The other half of the mixed soil was shade-dried and used for the assessment of soil physicochemical properties.

Analysis of rhizospheric soil

The pH and electrical conductivity (EC) were measured by using electronic digital pH and EC meter, respectively. The moisture content (MC) of the soil was determined by following Jackson (1967). The bulk density was determined by following Anderson and Ingram (1993). Estimation of soil organic carbon was done by following Anderson and Ingram (1993) and available soil phosphorus content was determined (Allen, Grimshaw, Parkinson, *et al.* 1974).

Assessment of AM fungal colonization

The root samples were washed several times in running tap water and cut into approximately 1 cm in size and cleaned with 10% NaOH at 90°C for 2 hours. This is followed by several rounds of washing of root samples with tap water. Then 2–3 drops of 2% hydrogen peroxide (H₂O₂) were added and slightly heated for additional cleaning. After this, the root segments were again washed with tap water and stained (Roy Das Talapatra, Chakraborty *et al.* 2015). After this, the root segments were mounted on lactoglycerol and observed under compound microscope (Olympus CX21i) with camera (SLIDE 500) for various AM fungal structures. The estimation of AM fungal colonization was done by magnified intersection method (McGonigle, Miller, Evans, *et al.* 1990).

Isolation and identification of AM fungal spores

Leaf litter and larger pebbles contained in the soil brought from the field were removed carefully. AM fungal spores were isolated by wet sieving and decanting method (Gerdeman and Nicolson 1963). The spores were then mounted on glass slides in polyvinyl-lactic acid glycerol and cautiously crushed under a dissecting microscope (Koske and Tessier 1983). All intact spores, free from parasitic attack, inhabiting the rhizosphere, were taken into consideration during the enumeration of spore numbers. Extracted spores were identified on the

basis of spore morphology, subcellular characters, and ornamentation in the spore wall. Spore characters were compared with the original descriptions.¹

Data analysis

Spore density (SD) was calculated in terms of number of spores in 50 g of soil samples. Mean and standard error of mean were also calculated. Duncan test was utilized to separate the mean colonization of AM fungi and soil physico-chemical properties using the software, *Statistica* 9.0.

Results

Soil properties

The rhizospheric soil physico-chemical properties of *A. paniculata* of both dry and wet seasons are presented in Table 1. At both the sites, between two seasons, significant difference in soil pH was observed. The EC differed considerably between two seasons in the soils of Suryamaninagar. Same trend was observed for MC difference between two seasons at both the study sites. In addition, bulk density of the soils from Suryamaninagar differed significantly between seasons. Soils of both the sites had shown noteworthy difference in available phosphorus and total nitrogen between the two seasons. Out of Suryamaninagar and Kanchancherra, notable organic carbon difference between two seasons was shown by soils of Kanchancherra.

AM fungal colonization

AM fungal colonization and composition and spore density is depicted in Table 2. AM fungal structures such as intercellular hyphae (Figure 1a), vesicles in the root cortex (Figure 1b and c), *Arum* type of AM morphology (Figure 1d and e), spores attached with roots (Figure 1f). These structures are mostly found in the root segments and are responsible for confirming the presence of AM fungi in the root segments of *A. paniculata*.

There is an appreciable difference in AM fungal colonization between two seasons of both the sites. AM fungal colonization and spore density were higher in wet season. The AM fungal species extracted from the rhizosphere of *A. paniculata* is depicted in Table 3. A total of six species of AM fungal spores were recovered from the rhizospheric soil inhabited by *A. paniculata*. Five and four species were isolated from the soils of Kanchancherra and Suryamaninagar, respectively. *Glomus multicaule*, *Rhizophagus clarus*, and *Rhizophagus diaphanus* were recovered from both the study sites.

¹ Details available at www.amf-phylogeny.com

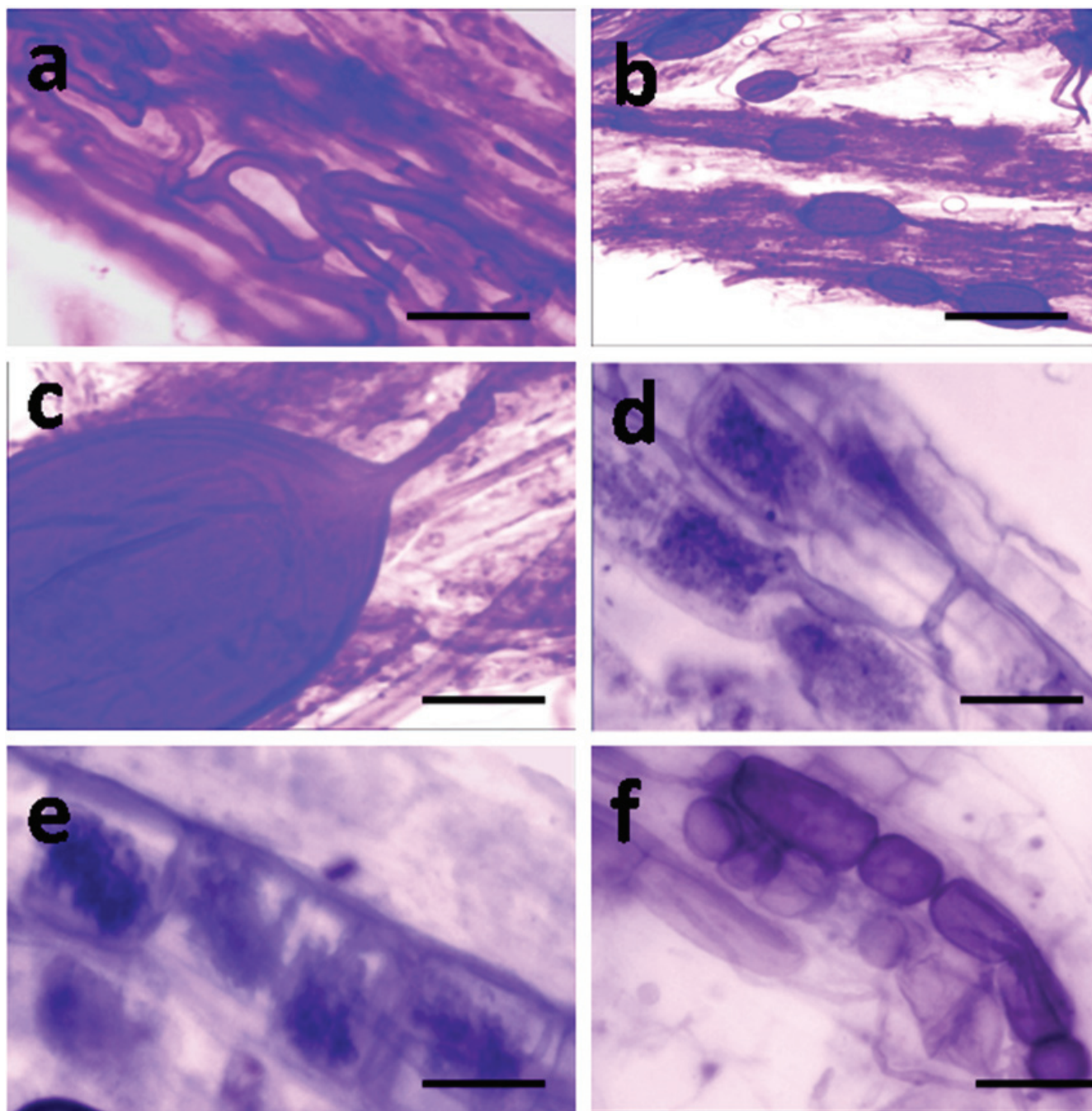


Figure 1 Light microscopic images of arbuscular mycorrhizal colonization in the roots of *Andrographis paniculata* (a): Hyphal coil in the epidermal layer of root, (b) and (c): Vesicles in the root cortex, (d) and (e): *Arum* type of AM fungal morphology in the cortical cells of root, and (f) Spores of AM fungi attached with roots. Scale bars (a, c, d, e, and f = 150 μ m, b = 200 μ m)

Discussion

On the basis of the knowledge gathered from the available resources, it can be concluded that this is the first attempt of the assessment of structural features and seasonal colonization by AM fungi associated with *A. paniculata* (Chiramel, Bagyaraj, and Patil 2006; Arpana and Bagyaraj 2007; Gupta, Chaturvedi, and Sharma 2009; Tejavathi, Anitha, Murthy, *et al.* 2011).

In the present assessment, AM fungal colonization varied significantly between the seasons. This seasonal variation in AM fungal colonization is mainly attributed to the additional nutrients' requirement for successful completion of the reproductive cycle (July–October) compared to the vegetative growth phase which is in agreement with the earlier findings (Javaid, Riaz, and Khan 2007). Literature survey

Table 1 Physico-chemical properties of rhizospheric soil of *Andrographis paniculata* from two seasons

Seasons	pH		EC (cS cm ⁻¹)		MC (%)		BD (g cm ⁻³)		AP(mg/g)		TN(kg/h)		OC (%)	
	S	K	S	K	S	K	S	K	S	K	S	K	S	K
Dry	6.39±0.01b	5.84±0.02b	24.33±2.03b	57±3.46a	7.37±0.24b	11.80±0.17b	1.38±0.01b	1.41±0.01a	43.13±2.05b	38.87±1.41b	69.45±1.16b	61.75±1.44b	0.82±0.01a	0.79±0.04b
Wet	6.72±0.02a	6.28±0.01a	21.33±1.45a	47±2.65a	11.13±0.34a	16.93±0.34a	1.34±0.02a	1.44±0.02a	22.13±0.75a	29.40±1.85a	72.77±2.84a	50.60±1.63a	0.88±0.02a	0.64±0.03a

Note Different alphabets differ significantly at $P<0.05$

AP: available phosphorus, BD: bulk density, EC: electrical conductivity, K: Kanchancherra; MC: moisture content, OC: organic carbon, S: Suryamaninagar, TN: total nitrogen

Table 2 Arbuscular mycorrhizal colonization and spore density of *Andrographis paniculata* during two seasons

Seasons	% RLA		% RLV		% RLH		SD/50 g soil	
	S	K	S	K	S	K	S	K
Dry	8.59±1.04b	11.16±1.14b	10.76±1.28b	14.30±1.13b	33.49±1.16b	46.80±1.56b	28.67±2.73b	36.67±2.60b
Wet	11.28±1.25a	15.44±1.32a	22.10±1.50a	22.10±1.50a	56.25±2.85a	66.60±2.07a	33.33±2.33a	47.33±2.60a

Note Different alphabets differ significantly at $P<0.05$

% RLA: percentage of root length arbuscules/arbusculate cells; % RLHL: percentage of root length hyphae/hyphal coil,

% RLV: percentage of root length vesicles, K: Kanchancherra, S: Suryamaninagar, SD: spore density

Table 3 Arbuscular mycorrhizal fungi isolated from the rhizosphere of *Andrographis paniculata*

AM fungi	Suryamaninagar		Kanchancherra	
	Dry	Wet	Dry	Wet
<i>Acaulospora cavernata</i>	-	-	-	+
<i>Funneliformis</i> sp.	+	+	-	-
<i>Glomus macrocarpum</i>	-	-	+	-
<i>Glomus multicaule</i>	+	-	-	+
<i>Rhizophagus clarus</i>	-	+	-	+
<i>Rhizophagus diaphanus</i>	+	-	+	-

Note + Presence; – Absence

concerning the role of AM fungi in plant reproduction pointed out that infection by AM fungi may result in increased reproduction in many plant species such as *Abutilon theophrasti* (Koide, Shumway, and Mabon 1994; Stanley, Koide, and Shumway 1993), wild and cultivated species of *Avena* (Koide, Li, Lewis, *et al.* 1988), *Glycine max* (Vejsadova, Siblikova, Gryndler, *et al.* 1993), *Triticum aestivum* (Karagiannidis and Hadjisavva-Zinoviadi 1998), and *Capsicum annuum* (Dodd, Krikun, and Haas 1983). This may be corresponding with the enhancement of potassium uptake in mycorrhizal-infected plants compared to non-mycorrhizal ones during that particular period (Dunne and Fitter 1989; McGonigle and Fitter 1988). The positive influence of AM fungi may be attributable with the increased tiller production in *Agropyron smithii* (Miller, Jarstfer, and Pillai, 1987) and tuber

production in *Solanum tuberosum* (Douds, Nagahashi, Reider, *et al.* 2007), possibly by altering host hormone balance (Miller, Jarstfer, and Pillai, 1987). Bryla and Koide (1990) reported that AM fungi also promote early flowering in AM fungi inoculated plants.

Plant roots harbor more than one AM fungi (Börstler, Renker, Kahmen, *et al.* 2006) and they are the key determinant in composition of the plant species in different habitats (van der Heijden, Boller, Wiemken, *et al.* 1998). AM fungi are dependent on season, soil type, nutrients, and spatial distribution of host species (Louis and Lim 1987; Harikumar and Bagyaraj 1988). In the rhizospheric soil, adhering and near to examined root samples, six AM fungal species belonging to the *Acaulospora*, *Glomus*, and *Rhizophagus* genera were extracted. *Glomus* was one of the most commonly occurring AM fungi in the soil of Tripura

(Chakraborty, Sinha, Debnath, *et al.* 2016; Sinha, Chakraborty, and Saha, 2016; Debnath, Sinha, Talapatra, *et al.* 2017; Chakraborty, Talapatra, Roy Das, *et al.* 2019; Chakraborty, Banik, Debnath, *et al.* 2019) and from India (Muthukumar and Udaiyan 2000; Bhattacharya and Bagyaraj 2002). The affluence of *Glomus* may be due to their high adaptability to varied soil conditions (Ho 1987).

Conclusion

The incidences of AM fungal colonization differ significantly during reproductive phase compared to vegetative growth phase underpin the positive impact of AM fungal colonization in plant reproduction. However, an extensive study under experimental conditions needs to be carried out before arriving at any concrete generalization. *A. paniculata* is an annual plant, having a single-reproductive season, can be applied as a test plant for assessment of the net effect of infection by AM fungi to reveal the exact role of native AM fungi inhabiting the same rhizosphere. These indispensable rhizospheric mycobiota may be used for the enhancement of plant growth, development and yield along with the increase in the production of pharmaceutically important compounds of medicinal plants.

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High-throughput Image-based Phenotyping for Studying Plant Responses to Arbuscular Mycorrhizal Fungi

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Arbuscular mycorrhizal fungi (AMF), as plant bio-stimulants, have been gaining prominence in agriculture because of their potential in improving nutrient uptake efficiency, tolerance to various stressors, and crop growth (Rouphael, Spichal, Panzarova, *et al.* 2018). Multiple benefits to plants by AMF include uptake of phosphorus and other poorly mobile nutrients (for example, N, S, K, Ca, Fe, Cu, Zn), increased soil aggregation and carbon sequestration, and stimulation of other organismal growth in the rhizosphere (Ingraffia, Amato, Frenda, *et al.* 2019; Battini, Grönlund, Agnolucci, *et al.* 2017). Responses to the mycorrhizal colonization may vary widely, depending on the host plant as well as the fungus. The aforementioned responses are positive for plant's growth, but there are a few negative responses exhibited by plants when exposed to AMF, for example, mycorrhizal growth depressions. These negative responses are gaining popularity amongst researchers/scientists engaged in AMF development. These responses can be observed in the form of phenotypic changes in plants. Plants respond to AMF and are colonized by them at different times and intensities. A better understanding of plant growth response to mycorrhizae can be achieved by collecting time series data of the plant phenotype. Such data sets can be laborious and costly to generate, as they usually rely on multiple harvests (Watts-Williams, Jewell, Brien, *et al.* 2019). An emerging advancement in obtaining such data is the use of image capture technology and open source analysis tools (Fahlgren, Gehan, and Baxter 2015). Plant phenotyping is an important tool in addressing and understanding plant environment interaction and its translation into application in crop management practices and effects of biostimulants (Pieruschka and Schurr 2019). Plant phenomics employs high-throughput image-based phenotyping of above-ground plant tissues (Marko, Brigila, Summerer, *et al.* 2018; Fahlgren, Gehan, and Baxter 2015). 'High-throughput' is a technological classification term that is relative to the effort associated with measurement (Fahlgren, Gehan, and Baxter 2015). Improvements in the specificity and throughput of phenotypic assessment at different biological levels such as phenomics, metabolomics, and genomics, are the main objectives of modern

phenotyping (Syta, Zivcak, Olsovska, *et al.* 2018). Modern phenotyping comprehensively assesses complex plant traits such as growth, development, tolerance, resistance to biotic and abiotic stresses, architecture, physiology and yield, through automated processes (Marko, Brigila, Summerer, *et al.* 2018; Fahlgren, Gehan, and Baxter 2015). Recent advances in this technology have enabled rapid worldwide development of high-throughput automated and semi-automated field and laboratory phenotyping platforms. The newly developed plant phenotyping platforms produce relatively large quantity of data than the initial platforms; hence need special systems for data management, access and storage, and also new statistical tools for deriving biologically significant signals from both experimental and environmental noise (Syta, Zivcak, Olsovska, *et al.* 2018).

High-throughput phenotyping platforms (HTPPs) are capable of accurate and non-destructive capturing of plant traits, both qualitatively and quantitatively, by imaging hundreds of plants per day (Marko, Brigila, Summerer, *et al.* 2018). This advancement permits time-series measurements that are necessary to follow the progression of growth and stress on individual plants. Phenotyping of whole shoots, as opposed to excised organs, allows for examination of architecture-dependent traits, such as tillering and flowering and architecture-independent traits such as biomass and colour. Also, eliminating destructive measurements increases the experimental capacity for genotypes, treatments, and biological replicates by reducing the required replicate sampling sets (Fahlgren, Gehan, and Baxter 2015). Examples of high-throughput platforms (HTPs) currently being used are growth chamber platforms (small-scale screening), greenhouse platforms (medium-scale screening), and field platforms (large-scale screening) (Rouphael, Spichal, Panzarova, *et al.* 2018). Greenhouse-based and growth-chamber phenotyping platforms have the advantage of increased experimental cycling and environmental control, but they are often defined by pot growth and a spectrum of environmental conditions that can be measured. Controlled environmental conditions are also well suited for the investigation of root phenotypes (Syta, Zivcak, Olsovska, *et al.* 2018). For

* Compiled from TERI Riza database
(TERI, Darbari Seth Block, India Habitat Centre, Lodhi Road, New Delhi – 110003, India)

targeting the scope of field experiments, unmanned aerial systems (UAS) offer a flexible alternative to ground-based phenotyping platforms, particularly for large-breeding nurseries and genetic studies with thousands of plots (Singh, Wang, Kumar *et al.* 2019). High-parameterized platforms that have been installed for phenotyping include semi-automatic evaluation of morphometric parameters using red–green–blue (RGB) image analysis, chlorophyll and fluorescence kinetic imaging and hyper spectral, thermal and infrared light imaging, positron emission tomography (PET), magnetic resonance imaging (MRI), computerized tomography (CT), and three-dimensional (3D) imaging. Photosynthetic parameters such as plant morphometry (using RGB systems), stomatal conductance (using IR thermal cameras), metabolomics of experimental plants at different stages of growth (using hyper-spectral imaging or HSI systems) can be evaluated as well (Syta, Zivcak, Olsovska, *et al.* 2018). A variety of cameras are available to capture signals from the visible and infrared spectrum of light. The use of diverse camera systems in HTPs results in images that require plant-centric trait extraction tools (for instance, tools available in Plant Image Analysis database). VIS (visible) cameras detect light in the visible range, from nearly 400 nm to 700 nm, and image-processing algorithms identify pixels that are plant derived and hence measure the morphological (shape, structure), geometric (length, area), and colour properties of the plants. It has been demonstrated that plant pixel area from a single-image stack can be used to calculate an approximate plant volume or total leaf area value that can accurately model fresh and dry weight, as well as above ground plant biomass. In addition, VIS imaging has also been used to measure dynamic processes like plant growth rates. The interaction of infrared light with plant tissue has several properties that make infrared analysis potentially useful for phenotyping. Infrared cameras that detect near-infrared (NIR) light are used for night imaging while those that detect short-wave infrared (SWIR) light are used for leaf water content. Thermal infrared (TIR) cameras detect long-wave infrared (LWIR) light which is emitted by leaves in a temperature-dependent intensity (Fahlgren, Gehan, and Baxter 2015). A disadvantage of VIS and NIR cameras is that specific wavelength information is lost in the output image. In contrast to this, state-of-the-art hyper spectral cameras detect hundreds of spectral bands with nanometer-level resolution between 350 nm and 2500 nm and thus are more suitable to detect plant stress (Fahlgren, Gehan, and Baxter 2015; Syta, Zivcak, Olsovska, *et al.* 2018). These systems are composed of controlled

watering and nutrient regimes regulated by automatic weighing systems and environmental controls in the imaging cabinet (in laboratory platforms) thereby ensuring precision. The control and programming of platform systems and data analysis is performed with sophisticated and user friendly software packages. Mass spectrometry-based imaging techniques (MALDI-MSI, DESI-MSI, MALDI-TOF, ESI-TOF) are also used as a part of HSI to provide knowledge of proteins and other metabolites in plant tissues (Syta, Zivcak, Olsovska, *et al.* 2018).

Watts-Williams, Jewell, Brien, *et al.* (2019) used HTP to explore growth responses (growth depression, in particular) of tomato, barley, and *Medicago truncatula* to *Rhizoglyphus irregularis* and zinc, thereby exploring the complexity of mycorrhizal responses. Another example involving the use of HTP facility is to analyse transgenic tomato plants, overexpressing *arginine decarboxylase 2* gene (a gene involved in polyamine biosynthetic pathway), for tolerance to abiotic stress and differences in water content as well as their ability to recover after drought stress (Marko, Brigila, Summerer, *et al.* 2018). Previous experiments utilizing HTP proved valuable for studies in variation of traits in chickpea, barley, wheat, and rice (Watts-Williams, Jewell, Brien, *et al.* 2019). *Arabidopsis thaliana*, a classical model plant in biology, has been studied using this technology. Currently, HTP technologies are gaining attention because of being able to accomplish many purposes such as for product screening, and development as efficient means to automated, non-destructive online monitoring of multiple morpho-physiological plant traits; of necessary time-series measurements for following the progression of growth, plant performance and stress responses of individual plants, at high resolution; for reduced cost, labour and time for analyses through automatization, remote sensing, improved data integration and experimental design (Rouphael, Spichal, Panzarova, *et al.* 2018). Further advancement of plant phenotyping could be made possible through developments in disciplines such as remote sensing, robotics, computer vision and artificial intelligence, to shorten processing time and enable real-time HSI monitoring. Also improvements in HSI methodology would meet important theoretical needs of plant physiology (for example, a standard spectrum database for the identification of biological compounds) (Syta, Zivcak, Olsovska, *et al.* 2018; Pieruschka and Schurr, 2019). It is, therefore, evident that such advanced techniques could help in the establishment of efficient protocols to study plant–fungal associations and can be further improved through experimentation.

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NEWS HIGHLIGHTS

Stowaway fungi hitch a ride with birds to be with their fungal partners

A new phytologist study says that researchers from Portugal provide first evidence that fungi hitch a ride with birds to be with their plant partners, thereby filling in a fundamental piece in understanding the global distribution of mycorrhizal fungi as well as the colonization of remote territories by plants and associated fungi.¹

Mapping the Wood Wide Web

The age-old subterranean social network of roots, fungi, and bacteria is now known as the ‘Wood Wide Web’. An international study, published in *Nature*, has produced the first global map of the mycorrhizal fungi networks. Using millions of direct observations of trees and their symbiotic associations on the ground, the researchers have built models from the bottom up to visualize these networks. “This study provides key information about who lives where and why”, says Dr Merlin Sheldrake, a Mycorrhizal Ecologist.²

Simple and sophisticated

It so turns out that AM Fungi are experts when it comes to dealing with resource inequality (like patchy phosphorus supply). They take advantage of their symbionts, by following the classic trading strategy

¹ Details available at www.eurekalert.org

² Details available at www.bbc.com

‘Buy low, sell high’. Using quantum dots to track phosphorus movements through fungal networks, the team of scientists from the Netherlands found out that resource inequality stimulated trade and the greater the disparity across its network, the more the fungus transferred phosphorus to the root.³

One among the reading list.....

‘Underland’, a delicious and absorbing work by the author Robert Macfarlane, describes the world that lies beneath our feet. The ‘Wood Wide Web’ is also a part of his search to illuminate the life underground.⁴

The new MycoApply Injector Endo

MycoApply Injector Endo is the latest addition to the MycoApply horticulture and turf line of products of Mycorrhizal Applications, Oregon. The concentrated powder formulation, on a soluble humic carrier, features four species of endomycorrhizal fungi: (i) *Glomus* (ii) intraradices, (iii) *G. mosseae*, and (iv) *G. etunicatum*. Developed for application via horticulture injection equipment, the drench can be applied to crops via boom spray, sprinkler systems, hand sprayers, etc.⁵

³ Details available at www.newscientist.com

⁴ Details available at www.ehn.org

⁵ Details available at www.greenhousemag.com



New Approaches and Techniques

A Novel Method for Anatomical Analysis of Edaphic Organisms

Plant root interactions with soil organisms have significant impacts on plant performance and yield. Organisms such as the arbuscular mycorrhizal fungi (AMF) have been associated with over 70%–80% of terrestrial vegetation and have been an interest of research for a long time. Visualization of how these organisms colonize root tissue plays a significant role in understanding how they affect root health and development. Laser ablation tomography (LAT) is an innovative imaging technology that fulfils the requirement for rapid, three-dimensional visualization of biological samples. This technique provides full colour scans of samples at spatial scales from 0.1 mm to 1 cm with micron-level resolution, hence, addressing a gap in sample throughput and scale that is unfulfilled by conventional microscopy techniques. The LAT system uses a pulsed UV laser source, from which the beam gets directed to the beam shaping optics and becomes an oscillating beam over a linear distance, thus creating a cutting sheet. The root sample is moved into the beam path on a motorized linear stage as the camera simultaneously images the exposed anatomy ablated by the beam. LAT enables the study of root anatomy and root organisms across a wide spectrum of plant species and edaphic organisms through the contrasting composition-specific autofluorescence spectra emitted from different tissue samples (plant and fungal), arthropods, bacteria, and nematodes. The spectral differentiation between tissues in roots and the colonizing organisms highlights the varied chemical composition (which is not visible under bright field conditions). LAT improves interpretation of root-organism interactions in

relatively large, opaque root segments. Due to its high-throughput imaging of root anatomy, LAT serves as an excellent tool for breeders and pathologists to conduct quantitative screens characterizing resistance to root pathogens. Deeper understanding of the relationships between root inhabiting biota can provide important insights into pest management and agricultural productivity. With significant opportunities to improve upon the present capabilities of LAT through modification of laser wavelengths, increased resolution and hyperspectral imaging technologies, many research applications remain for the employment of LAT.

Such technologies act as strengths when elaborating the mycorrhizal infection process and its establishment in the host plant. Further, they also give insight to understanding the ultra-structural details (layer-to-layer or wall-to-wall) that get be modified/ changed due to the symbiosis. Also, very little information on such technologies is found in the available literature and hence it becomes an important technology to be adopted and understood in-depth. A preliminary data has been made available by the authors (Strock, Schneider, Galindo-Castañeda, *et al.* 2019).

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RECENT REFERENCES

The latest additions to the network's database on mycorrhiza are published here for the members' information. The list consists of papers from the following journals:

- *AMB Express*
- *An International Journal of Plant Biology*
- *Applications in Plant Science*
- *Applied Soil Ecology*
- *Biotechnology Reports*
- *BMC Ecology*
- *Chemosphere*
- *Ecotoxicology and Environmental Safety*
- *Environmental Pollution*
- *Frontiers in Environmental Science*
- *Frontiers in Plant Sciences*
- *International Journal of Molecular Sciences*
- *Journal of Environmental Radioactivity*
- *Mycorrhiza*
- *Nature Communications*
- *Nature Plants*
- *Pest Management Science*
- *Planta*
- *Plant Biology (Stuttg)*
- *Plant, Cell and Environment*
- *Plant Science*
- *Scientific Reports*

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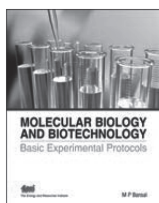
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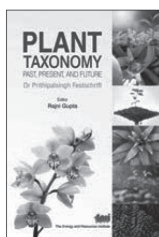


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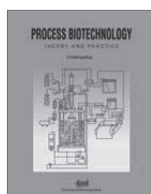


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E-mail: mycologycongress@insightsummits.com

Website: <https://www.asianmeetings.net/conferences/mycology>

Vienna, **Austria**
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14th International Conference on Microbial Interactions & Microbial Ecology

E-mail: microbialinteractions@brainstormingmeetings.com

Website: <https://microbialinteractions.expertconferences.org>

Tokyo, **Japan**
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Theme: A Sustainable Eco-friendly Agricultural Approach to Crop Improvement

E-mail: agriculture@conferenceint.com

Website: <https://agriculture.agriconferences.com/organizing-committee.php>

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E-mail: info@agroconference.com

Website: <https://agroconference.com>

Warsaw and Białowieża,
Poland
September 16–21, 2019

XVIII Congress of European Mycologists

E-mail: polskietowarzystwomykologiczne@gmail.com

Website: <https://xviiiicem.pl/>

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October 7–8, 2019

7th Global Summit on Plant Science

Email: agriculture@conferenceint.com

Website: <https://agriculture.agriconferences.com>

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6th International Conference on Mycology and Fungal Infections

E-mail: infections@pulsusmeet.net

Website: <https://fungalinfections.cmesociety.com>

Tsu, **Japan**
October 1–4, 2019

Asian Mycological Congress 2019

E-mail: amc2019officer@mycology-jp.org

Website: <http://amcfungi2019.com/index.html>

Milan, **Italy**
October 18–19, 2019

2nd European Plant Science Conference

Theme: Transforming Future of Plant Science

E-mail: plantscience@insightsummits.com

Website: <https://www.meetingsint.com/agri-aqua-conferences/plant-science>

Puducherry, **India**
November 7–9, 2019

National Conference on ‘Recent Advances in Biodiversity, Biology and Biotechnology of Fungi’ and 46th Annual Meeting of Mycological Society of India (MSI)

E-mail: sarmavv@yahoo.com; msi2019pu@gmail.com

Website: <http://fungiindia.co.in/images/2019/2019.pdf>

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