ISPP INTERNATIONAL SOCIETY FOR PLANT PATHOLOGY

PROMOTING WORLD-WIDE PLANT HEALTH AND FOOD SECURITY

INTERNATIONAL SOCIETY FOR PLANT PATHOLOGY

ISPP NEWSLETTER

ISSUE 54 (7) JULY 2024

Editor: Daniel Hüberli (**email**)

Join the ISPP **mail list**

IN THIS ISSUE:

Scientists find common genes defending coffee plants against devastating disease

A disease-surveillance network in Africa will accelerate detection and actions to prevent the spread of major rice diseases

Unlocking banana disease resistance: key enzymes identified for phytoalexin synthesis

Pioneering plant science research paves the way for deeper understanding of how the plant immune system functions

An inside look at how plants and mycorrhizal fungi cooperate

Fungal-mediated synthesis of silver nanoparticles: A novel strategy for plant disease management

Leaf surface microbiota transplantation confers resistance to coffee leaf rust in susceptible *Coffea arabica*

Current Vacancies

Acknowledgements

Coming Events

SCIENTISTS FIND COMMON GENES DEFENDING COFFEE PLANTS AGAINST DEVASTATING DISEASE

NANYANG TECHNOLOGICAL UNIVERSITY, SINGAPORE, NEWS, 15 APRIL 2024

Arabica coffee is the most economically important coffee globally and accounts for 60 per cent of coffee products worldwide. But the plants it hails from are vulnerable to a disease that, in the 1800s, devastated Sri Lanka's coffee empire. Now, an international team of researchers co-led by Nanyang Technological University, Singapore (NTU Singapore) has made a breakthrough that helps protect Arabica plants (*Coffea arabica*) against the fungal disease, coffee leaf rust.

Assistant Professor Jarkko Salojarvi, from NTU Singapore's School of Biological Sciences, co-led an international research team that mapped out the genomes of the Arabica plant (pictured) and two related coffee plants (Photo credit: NTU Singapore).

The other co-leads of the study, published in *Nature Genetics*, are based at the world's largest food and beverage company Nestlé, the Université de Montpellier in France and the University at Buffalo in the United States.

The scientists mapped out, in great detail, all the genetic material – or genomes – of Arabica and two related coffee plants. This allowed the team to identify a new combination of genes shared by the plants that are resistant to coffee leaf rust. With the data on the genomes, other useful traits in coffee plants can also be identified.

Discovering the resistance genes opens the way to better protect coffee lovers' daily fix and maintain their drink's high-quality taste, thereby supporting an industry employing millions of workers. According to the International Coffee Organisation, the livelihoods of 125 million people around the world depend on the coffee business.

Coffee leaf rust disease has wreaked havoc on coffee-producing nations and continues to wipe out coffee farms today. The United States Agency for International Development estimated that between 2012 and 2014, an outbreak of coffee leaf rust caused about US$1 billion (S$1.36 billion) in economic damages in Latin America.

Assistant Professor Jarkko Salojarvi from NTU's School of Biological Sciences, who co-led the research team, said: "The high-quality genome sequences of the three plant species, together with the candidate genetic sequences for coffee leaf rust resistance, form the cornerstone for breeding new varieties of Arabica plants that are more adaptable to change and more resistant to diseases caused by pathogens like fungi."

The project involved a large consortium of researchers and coffee breeders from Australia, Belgium, Brazil, Canada, China, Colombia, Finland, France, Germany, Indonesia, Italy, the Netherlands, South Africa, Spain, Switzerland, Uganda and the United States.

Dr Patrick Descombes, Senior Expert in Genomics at Nestlé Research, and one of the study's co-leads, said: "While other public references for Arabica do exist, the quality of our team's work is extremely high. We used state-of-the-art genomics approaches – including long and short reads high throughput sequencing – to create the most advanced, complete and continuous Arabica reference to date."

POOR GENETIC VARIABILITY

Arabica plants have low genetic diversity, which makes them susceptible to pests and diseases. The cultivated plants typically do not have the genetic trait that confers resistance to coffee leaf rust, which is caused by the *Hemileia vastatrix* fungi. The fungi form orange-yellow spots on the coffee plants' leaves, which eventually wither and fall. The loss of leaves lowers the quality and quantity of the plants' berries harvested for brewing coffee.

To prevent a potentially disastrous wipeout of Arabica plants worldwide by coffee leaf rust, the scientists studied the genomic origins and breeding history of the plant. They did so by mapping out the highly detailed genomic sequences of Arabica and two related coffee-producing plants, Robusta (*C. canephora*) and *C. eugenioides*, which are the modern-day ancestors of Arabica.

This was done using advanced techniques, namely PacBio high fidelity technology to sequence DNA with high accuracy, and high throughput chromosome conformation capture to create detailed 3D maps of how different DNA segments interact. The data for the genomes are publicly available.

The scientists' analysis suggested that the resistance to coffee leaf rust in Arabica may have been lost when Arabica plants became widely cultivated, as all cultivated Arabica coffee plants are derived from the same stock with very little genetic variability. However, a hybrid of Arabica and Robusta resistant to the disease was found on Timor island in 1927. Unfortunately, the resistance comes with a trade-off as the hybrid does not produce coffee that tastes as good as that from other Arabica plants. With no alternatives, the descendants of the Timor hybrid plant still form the basis of all coffee leaf rust resistant variants.

Previous research discovered some genes that potentially conferred resistance against leaf rust in different coffee plants. But without a map of the various coffee plants' genome, it was difficult to accurately identify these genes and hard to figure out if they were also found in other coffee plants, which would increase the chance that they coded for resistance. The gene identification process was also slow. However, with the new research mapping out the genomes of different coffee plants in great detail, identifying resistance genes will be faster and more accurate.

Using the plants' genome information, the researchers analysed the most common cultivated coffee varieties, representing about 95 per cent of the world's coffee production, and compared them with descendants of the Timor hybrid. This allowed them to find a region of DNA sequences common among different leaf rust resistant coffee plants, with a new combination of Robusta-based genes that may convey resistance in Arabica plants in general. Knowing the existence of these shared genes greatly increases the likelihood that these genetic sequences can indeed defend against leaf rust, and could allow breeders to select for them when growing new coffee varieties.

Through their analysis, the researchers also postulated that Arabica stemmed from a chance event 350,000 to 610,000 years ago when the Robusta and *C. eugenioides* plants were naturally cross-pollinated to create the first Arabica plants in the wild. This dating comes in between previous estimates, with an earlier one putting the chance event to as recently as 20,000 years ago, while others push it as far back as one million years ago. The researchers said the discrepancy of earlier figures could be due to historical changes in population sizes in the wild and cultivated plants, as well as the different sources and limited amount of data used.

The Arabica coffee plant (Photo credit: NTU Singapore).

By comparing the high-quality genomic sequences of Arabica with those of Robusta and *C. eugenioides*, the research team found that the three species are still highly similar genetically. This suggests that for future breeding programmes to ensure that Arabica plants have disease resistance, breeders can consider using other related coffee species, such as Robusta and *C. eugenioides*.

Using Arabica plants alone to breed for the resistance trait is problematic because the study found that even the wild varieties of Arabica, not just the cultivated ones, have very low genetic diversity, making it harder to breed for disease resistance.

"The low genetic diversity of both cultivated and wild modern Arabica plants is an obstacle for its breeding using the wild varieties of the plants. But close similarities found between Arabica, Robusta and *C. eugenioides* plants are likely to facilitate the introduction of interesting traits from the latter two into Arabica," said Asst Prof Salojarvi.

The highly detailed genomic sequences mapped for all three coffee plants also mean that other useful traits could be identified in future, such as resilience to drought, better crop yield and more aromatic coffee beans.

These traits can be identified with genetic markers, which can be used to predict the future performance of coffee seedlings, instead of waiting years for the plants to mature and bear berries to find out.

Since the leaf rust resistant hybrid from Timor does not produce coffee that is as good as that from the usual Arabica plants, the genome data compiled now provides a fast track for researchers to breed new disease-resistant plants that still retain the sublime, smooth and sweet taste of Arabica enjoyed by coffee lovers worldwide.

A DISEASE-SURVEILLANCE NETWORK IN AFRICA WILL ACCELERATE DETECTION AND ACTIONS TO PREVENT THE SPREAD OF MAJOR RICE DISEASES

INTERNATIONAL RICE RESEARCH INSTITUTE (IRRI) NEWS, 7 JUNE 2024

Rice diseases cause an annual yield loss of 30%, representing enough rice to feed over 70 million people. In Africa, where rice cultivation does not meet consumer demand, such losses are intolerable. Increasing rice trade between Asia, America, and Africa introduces new varieties and risks bringing rice pathogens to the continent. Furthermore, changing climates, including temperature, humidity, and heat variations, significantly impact disease occurrence, making previously disease-free areas more susceptible. Consequently, the dynamics of rice disease in Africa are vast, necessitating urgent surveillance and monitoring of pathogens.

Creating a surveillance network for rice diseases in Africa will enable the quicker detection of diseases and immediate actions to prevent their spread.

On 25-29 March, pathologists, and breeders from 20 African countries participated in a workshop conducted by the Africa Rice Center and CIRAD (Centre de coopération internationale en recherche agronomique pour le développement), with funding from CG-France, as a first step in constructing the network.

The event marked the beginning of a diagnostic and surveillance network aimed at sharing and empowering the technical capacities and cooperation among Africa's national plant protection organizations (NPPOs) and national agricultural research and extension systems (NARES) as well as initiatives from the Africa Rice Center, International Center for Tropical Agriculture (CIAT), IRRI, and French institutions, IRD (French National Research Institute for Sustainable Development) and CIRAD (Centre de coopération internationale en recherche agronomique pour le développement).

The participants identified the main network activities, including capacity building, regular disease surveillance, building national, regional, and international collaborations between NPPOs and NARES, and sharing protocols for diagnosis, surveillance, monitoring, and disease management.

The scientific exchanges between the CGIAR centers, French research institutions, NARS, and NPPOs will help develop an effective diagnostic and surveillance system to facilitate decision-making in the countries involved. Moreover, it will be the foundation for a robust regional network for monitoring and managing plant diseases.

In support of the network, scientists from IRRI provided updates on recent surveillance activities on rice blasts in Burundi, yellow mottle virus, and bacterial blight in Kenya.

Plant pathogens spread without borders. Therefore, conducting surveillance, diagnostics, and monitoring is crucial to detect their presence and severity. This allows for the implementation of management practices to prevent disease spread and reduce the impact on agricultural productivity.

Van Schepler-Luu, lead of the Plant Pathology and Host Plant Resistance Group at IRRI, presented the PathoTracer and the Biotic screening network (BioNET).

"PathoTracer is a global rice pathogen surveillance and monitoring platform that helps monitor the diversity and distribution of the different pathogen populations in a high throughput manner," said Dr. Schepler-Luu. "The information helps guide national rice breeding programs to prioritize genes that give rice plants resistance to certain diseases or determine varieties that would be effective against prevalent diseases in each rice-growing region."

BioNET is a global initiative to address plant diseases and pests. "With pathogens evolving faster than plants and the impact of climate change on disease and pest distribution," Dr. Schepler-Luu said. "BioNET will tackle these challenges through a global network of rice pathologists, entomologists, and breeders working on rice disease and pest surveillance and monitoring, disease and pest resistance gene discovery, and screening for disease and pest resistance rice."

UNLOCKING BANANA DISEASE RESISTANCE: KEY ENZYMES IDENTIFIED FOR PHYTOALEXIN SYNTHESIS

NANJING AGRICULTURAL UNIVERSITY THE ACADEMY OF SCIENCE, EUREK ALERT, 6JUNE 2024

A breakthrough in banana disease resistance was achieved with the identification of novel O-methyltransferases (OMTs) involved in the biosynthesis of phenylphenalenone phytoalexins. These compounds, found in wild bananas, hold promise for developing disease-resistant commercial cultivars. Researchers assembled a near-complete genome of *Musella lasiocarpa* and identified three novel OMTs that enhance the antifungal properties of these phytoalexins, providing a genetic resource for improving banana disease resistance through molecular breeding.

Bananas are a vital crop globally, but their yields are threatened by various diseases, particularly banana fusarium wilt caused by *Fusarium oxysporum*. Traditional control methods, including chemical pesticides, pose environmental risks and are not always effective. Wild banana relatives, which possess greater genetic diversity and higher concentrations of defense-related compounds, offer potential solutions. Based on these challenges, further research into the genetic mechanisms behind banana disease resistance is essential.

Researchers from the Jiangsu Key Laboratory for the Research and Utilization of Plant Resources and collaborators recently published a study (DOI:10.1093/hr/uhae042) in *Horticulture Research*. They assembled a nearly gapless genome of *Musella lasiocarpa*, a wild banana relative, to investigate the biosynthesis of phenylphenalenone (PhPN) phytoalexins. This study identified three novel O-methyltransferases (OMTs) involved in enhancing the antifungal properties of these compounds, paving the way for developing disease-resistant banana varieties.

The study focused on the biosynthesis pathway of PhPN phytoalexins, which are natural defense compounds in bananas. Using advanced genomic techniques, the team assembled a high-quality, nearly complete genome of Musella lasiocarpa. They integrated transcriptomic and metabolomic data to identify candidate genes involved in PhPN biosynthesis. Through phylogenetic analysis and in vitro enzymatic assays, three novel OMTs were characterized. These enzymes, Ml01G0494, Ml04G2958, and Ml08G0855, showed significant roles in the methylation modification of PhPNs, enhancing their antifungal activity against Fusarium oxysporum. Ml08G0855, in particular, was found to be a multifunctional enzyme targeting multiple hydroxyl groups in PhPN structures. The study also revealed that the methylation of PhPNs significantly boosts their antifungal properties, providing a potential genetic resource for improving disease resistance in bananas through molecular breeding.

Dr. Yu Chen, one of the corresponding authors, stated, "This research provides crucial insights into the genetic basis of disease resistance in bananas. By understanding and leveraging the biosynthetic pathways of phenylphenalenone phytoalexins, we can develop more resilient banana cultivars, ensuring better crop yields and sustainability in the face of increasing agricultural challenges."

The application of this research is twofold: it offers a direct application in banana breeding programs to enhance disease resistance through molecular techniques and provides a foundation for further studies into the role of phytoalexins in plant-pathogen interactions. The implications are far-reaching, potentially leading to the cultivation of hardier banana varieties that can withstand climate change-induced stress and reduce the environmental impact of disease management practices.

PIONEERING PLANT SCIENCE RESEARCH PAVES THE WAY FOR DEEPER UNDERSTANDING OF HOW THE PLANT IMMUNE SYSTEM FUNCTIONS

DONALD DANFORTH PLANT SCIENCE CENTER, 29 APRIL 2024

Researchers in the laboratory of Tessa Burch-Smith, PhD at the Danforth Plant Science Center and the University of Tennessee, Knoxville, are conducting pioneering work to discover how plants transmit information, important molecules and viruses between cells. In a recent study they demonstrated how plasmodesmata (PD) – structures that connect neighboring cells in leaves and other organs – are controlled by deposition of callose (a carbohydrate polymer) when plants are responding to infection. Their research compared different methods to rigorously quantify callose accumulation around the microscopic PD channels and paves the way for deeper understanding of how the plant immune system works. Results of their study were recently published in Comparing methods for detection and quantification of plasmodesmal callose in *Nicotiana benthamiana* leaves, in the journal *Molecular Plant Microbe Interactions*.

Callose, a polymer made of glucose molecules, is essential for regulating intercellular trafficking via plasmodesmata (PD). Pathogens manipulate PD-localised proteins to enable intercellular trafficking by removing callose at PD, or conversely by increasing callose accumulation at PD to limit intercellular trafficking during infection. Plant defense hormones like salicylic acid regulate PD-localised proteins to control PD and intercellular trafficking during immune defense responses such as systemic acquired resistance.

Measuring callose deposition at PD in plants has emerged as a popular way to assess likely trafficking of molecules between cells during plant immunity. Despite the popularity of this metric there is no standard for how these measurements should be made.

First Author Amie Sankoh, PhD, and her undergraduate colleague, Joseph Adjei, compared three commonly used methods for identifying and quantifying PD callose by aniline blue staining were evaluated to determine the most effective in the *Nicotiana benthamiana* leaf model. Both Amie and Joseph are Deaf and communicate primarily via American Sign Language.

Their results revealed that the most reliable method used aniline blue staining and fluorescent microscopy to measure callose deposition in fixed tissue. Manual or semi-automated workflows for image analysis were also compared and found to produce similar results although the semi-automated workflow produced a wider distribution of data points.

"We were surprised at how different the reliability of the different methods for detecting callose could be. We think this work will greatly improve consistency in experiments across labs," said Dr. Sankoh.

This study relied on the Advanced Bioimaging Laboratory at the Danforth Center. The team plans to use the identified protocol and analysis to investigate how callose levels at PD change over the course of infection with various hormones. Such studies could identify important times at which PD could be manipulated to disrupt the infection process and prevent plant disease.

AN INSIDE LOOK AT HOW PLANTS AND MYCORRHIZAL FUNGI COOPERATE

JOINT GENOME INSTITUTE NEWS, 8 APRIL 2024

For millions of years, underground fungi have lived in symbiosis with plant roots. Plants provide photosynthesised carbon, while fungi deliver water and nutrients. In order to do so, these organisms share space at cellular scale: fungi stretch a network of tendrils called arbuscules into a plant's root cells, and both organisms rearrange their cells around this structure to facilitate sharing.

Recently, researchers have been able to study both sides of this interaction up close, using RNA sequencing to understand gene expression: one of the first cross-kingdom spatially-resolved transcriptomics studies to date. This paper is the cover article for the April 2024 issue of *Nature Plants*.

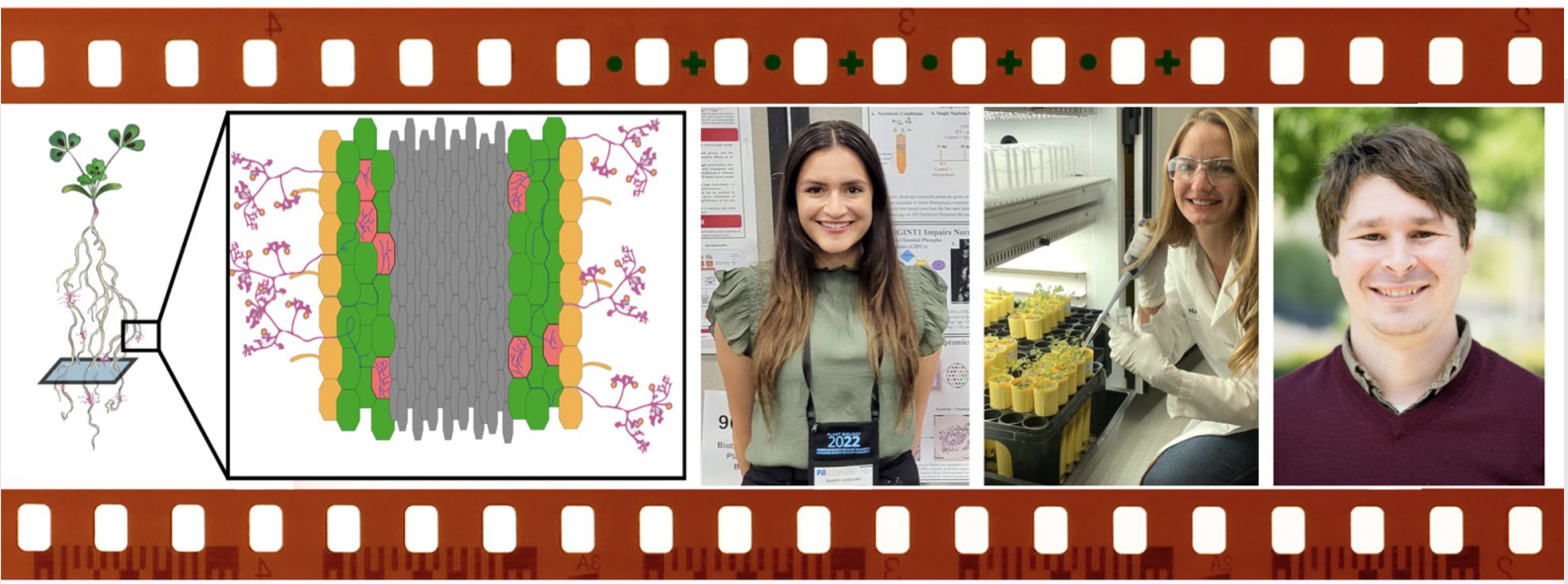
"We wanted to better understand the nature of this symbiosis at the cellular level — really understand how those two cell types [of two different organisms] are interacting with each other, without all the noise or other biological activity of the surrounding neighborhood," said Benjamin Cole, senior author of this work. Cole is a research scientist at the U.S. Department of Energy (DOE) Joint Genome Institute (JGI), a DOE Office of Science User Facility located at Lawrence Berkeley National Laboratory (Berkeley Lab).

Specific understanding of this symbiosis could offer improvements in multiple directions. On the fungi side, underground mycorrhizal networks can serve as a reservoir for carbon compounds that plants generate from carbon dioxide they take in. In this way, encouraging this symbiosis could improve the way soils store carbon from the atmosphere. For plants, boosting this relationship could improve biofuel feedstocks growing in nutrient-poor fields. "This is one interaction that allows plants to better survive in those environments," Karen Serrano said. She is first author of this paper and a graduate researcher at the Joint BioEnergy Institute (JBEI).

Cole led the work in collaboration with JBEI as part of the 2021 Laboratory Directed Research and Development (LDRD) program. Cole also received a DOE Early Career Research Program (ECRP) award in 2021, which aims in part to build off of this work. Former JGI postdoctoral scholar Margot Bezrutczyk collaborated extensively with Cole and Serrano to collect and analyze the single nuclei and spatial transcriptomics data this work leverages.

These experiments focused on two species at once: the model legume species Medicago truncatula and the mycorrhizal fungi Rhizophagus irregularis. To see how these organisms cooperate, this team applied R. irregularis spores directly to M. truncatula seedlings grown in a controlled environment chamber, so the fungus could colonize the plants' roots. Then, comparing with control seedlings which were not treated with fungi, they used multiple approaches to look at gene expression in both plant cells and fungal cells.

Using a technique called single nuclei RNA sequencing, the researchers identified different cell types within M. truncatula root cells, and profiled their gene expression. Then, the researchers used a technique called spatial transcriptomics, to generate maps of gene expression. This spatial transcriptomics technique allowed them to understand gene expression within circular capture areas roughly 55-microns in diameter — about the width of a human hair. At such resolution, this spatial transcriptomics data captured molecular information from both plant cells and fungal cells.



Left to right: Illustration of plant-fungal interactions; co-first authors Karen Serrano and Margot Bezrutczyk; senior author Benjamin Cole (Illustration by Thai Dao. K. Serrano courtesy of B.Cole; M. Bezrutczyk by B.Cole. B. Cole image by Thor Swift/Berkeley Lab. Filmstrip image by kstudio on Freepik.).

"Because this technology relies on just polyadenylated transcript capture — any RNA that is from eukaryotes — we were able to capture both plant and fungal transcripts," Serrano said. This team quantified the expression of over 12,000 fungal genes, in addition to associated plant genes.

All together, these data offer a granular view of both plant and fungal activity at different stages of this symbiosis. Within that activity, Serrano, Cole and their team found over 1,000 upregulated genes, 188 of which were shared with previous studies in the same system. With the right functional characterization, those genes could become dials for tuning this symbiosis. "Those are great candidates for genetic engineering. Our hope is that the community at large will follow that up," Serrano said.

This work focused on a relatively well-understood model system, so future directions will also include targeting biofuel feedstocks in similar studies. "We would like to look at arbuscular mycorrhizal symbiosis in other bioenergy grasses, like sorghum and switchgrass. We're optimizing systems now, so that we can get those working," Cole said.

FUNGAL-MEDIATED SYNTHESIS OF SILVER NANOPARTICLES: A NOVEL STRATEGY FOR PLANT DISEASE MANAGEMENT

A paper by Mansoor Ahmad Malik *et al.* titled "Fungal-mediated synthesis of silver nanoparticles: a novel strategy for plant disease management" was published on 28 June 2024 by *Front. Microbiol.* (Volume 15 - 2024). The abstract is as follows:-

Various traditional management techniques are employed to control plant diseases caused by bacteria and fungi. However, due to their drawbacks and adverse environmental effects, there is a shift toward employing more eco-friendly methods that are less harmful to the environment and human health. The main aim of the study was to biosynthesize silver Nanoparticles (AgNPs) from *Rhizoctonia solani* and *Cladosporium cladosporioides* using a green approach and to test the antimycotic activity of these biosynthesized AgNPs against a variety of pathogenic fungi. The characterization of samples was done by using UV–visible spectroscopy, SEM (scanning electron microscopy), FTIR (fourier transmission infrared spectroscopy), and XRD (X-ray diffractometry). During the study, the presence of strong plasmon absorbance bands at 420 and 450 nm confirmed the AgNPs biosynthesis by the fungi *R. solani* and *C. cladosporioides*. The biosynthesized AgNPs were 80–100 nm in size, asymmetrical in shape and became spherical to sub-spherical when aggregated. Assessment of the antifungal activity of the silver nanoparticles against various plant pathogenic fungi was carried out by agar well diffusion assay. Different concentration of AgNPs, 5 mg/mL 10 mg/mL and 15 mg/mL were tested to know the inhibitory effect of fungal plant pathogens viz. *Aspergillus flavus*, *Penicillium citrinum*, *Fusarium oxysporum*, *Fusarium metavorans*, and *Aspergillus aflatoxiformans*. However, 15 mg/mL concentration of the AgNPs showed excellent inhibitory activity against all tested fungal pathogens. Thus, the obtained results clearly suggest that silver nanoparticles may have important applications in controlling various plant diseases caused by fungi.

Read paper.

LEAF SURFACE MICROBIOTA TRANSPLANTATION CONFERS RESISTANCE TO COFFEE LEAF RUST IN SUSCEPTIBLE COFFEA ARABICA

A paper by Leandro Pio de Sousa and Jorge Maurício Costa Mondego titled "Leaf surface microbiota transplantation confers resistance to coffee leaf rust in susceptible *Coffea arabica*" was published on 10 April 2024 by *FEMS Microbiology Ecology* (vol. 100 (6), June 2024, fiae049). The abstract is as follows:-

Coffee leaf rust, caused by the fungus *Hemileia vastatrix*, has become a major concern for coffee-producing countries. Additionally, there has been an increase in the resistance of certain races of the fungus to fungicides and breeding cultivars, making producers use alternative control methods. In this work, we transplanted the leaf surface microbiota of rust-resistant coffee species (*Coffea racemosa* and *Coffea stenophylla*) to *Coffea arabica* and tested whether the new microbiota would be able to minimize the damage caused by *H. vastatrix*. It was seen that the transplant was successful in controlling rust, especially from *C. stenophylla*, but the protection depended on the concentration of the microbiota. Certain fungi, such as *Acrocalymma*, *Bipolaris*, *Didymella*, *Nigrospora*, *Setophaeosphaeria*, *Simplicillium*, *Stagonospora* and *Torula*, and bacteria, such as *Chryseobacterium*, *Sphingobium* and especially *Enterobacter*, had their populations increased and this may be related to the antagonism seen against *H. vastatrix*. Interestingly, the relative population of bacteria from genera *Pantoea*, *Methylobacterium* and *Sphingomonas* decreased after transplantation, suggesting a positive interaction between them and *H. vastatrix* development. Our findings may help to better understand the role of the microbiota in coffee leaf rust, as well as help to optimize the development of biocontrol agents.

Read paper.

CURRENT VACANCIES

Professor of Plant Disease Dynamics, The Department of Environmental Systems Science

(www.usys.ethz.ch) at ETH Zurich

The ideal candidate centers their research on the organismal biology of plant-pathogen interactions as related to global environmental problems (e.g., emerging and introduced plant diseases, biodiversity change) and solutions (e.g., ecosystem management, sustainable agriculture). Example topics include (but are not limited to): the drivers of emerging plant diseases (e.g., of agricultural crops, trees, and other plants of concern) and/or the ecological and evolutionary dynamics of plant-pathogen dynamics in species or ecosystems of interest (e.g., agricultural systems, forest ecosystems). Candidates applying integrative toolboxes, by combining field and greenhouse experiments or observations, mathematical modelling, and state-of-the-art tools (e.g., genomics, phenotyping, eDNA), would be a perfect fit for the position. The future professor is invited to take advantage of the opportunities for collaboration offered by the department, where environmental problems and the development of sustainable solutions are central motivators of research by all research groups.

Successful candidates must have established a strong research portfolio and leadership in the field and possess ample experience in teaching and mentoring. The future professor will be expected to teach undergraduate level courses (in German or English) and graduate level courses (in English) within the programs in Agricultural and Environmental Sciences. The hiring package includes base funding at a level commensurate with the appointment.

Closing date: 15 September 2024

More information on job and submit application online.

ACKNOWLEDGEMENTS

Thanks to Grahame Jackson, and Greg Johnson for contributions.

COMING EVENTS

XX International Plant Protection Congress
1 July – 5 July, 2024
Athens, Greece
Website: www.ippcathens2024.gr

Wild Plant Pathosystems 2024
7 July – 10 July, 2024
Kiel, Germany
Website: wildplantpath.net

International Conference on Plant Pathogenic Bacteria & Biocontrol 2024
7 July – 12 July, 2024
Virginia Tech, Blacksburg, Virginia, United States
Website: icppbbiocontrol2024.org

Triennial Conference of the European Association for Potato Research (EAPR)
7 July – 12 July, 2024
Oslo, Norway
Website: nibio.pameldingssystem.no/eapr2024

miCROPe 2024 conference - Microbe-assisted crop production – opportunities, challenges and needs
15 July – 18 July, 2024
Vienna, Austria
Website: www.micrope.org

Plant Health 2024
27 July – 31 July, 2024
Memphis, Tennessee, USA
Website:
www.apsnet.org/meetings/annual/Pages/default.aspx

Asian Conference on Plant Pathology 2024
3 August – 7 August, 2024
Changchun, Jilin, China
Website: acpp2024.tri-think.cn

12th International Mycological Congress
11 August – 15 August, 2024
Maastricht, Netherlands
Website: imc12.org

Australasian Soilborne Disease Symposium 2024
26 August – 29 August, 2024
Kingscliffe, New South Wales, Australia
Website: www.asds-apps.com/

11th IUFRO *Phytophthora* in Forests and Natural Ecosystems working party
8 September – 13 September, 2024
Bay of Islands (Paihia), New Zealand
Website: www.scienceevents.co.nz/iufro2024

International Phytobiomes Conference 2024
8 October – 10 October, 2024
St. Louis, MO, USA
Website: phytobiomesconference.org

Australasian plant virology workshop (APVW 2024)
29 October – 31 October, 2024
Gold Coast, Australia
Contact and Email: Fiona.Filardo@daf.qld.gov.au
Website: apvw-2024-.w.kamevents.currinda.com

9th ISHS International Postharvest Symposium
11 November – 15 November, 2024
Rotorua, New Zealand
Website: scienceevents.co.nz/postharvest2024

16th International *Trichoderma* & *Gliocladium* Workshop
12 November – 14 November, 2024
Lincoln University, Canterbury, New Zealand
Website: www.tg2024.org

International Symposium on Plant Pathogenic Sclerotiniaceae - BotryScleroMoni 2025. Joint meetings of XIX International *Botrytis* Symposium, XVII International *Sclerotinia* Workshop, and II International *Monilinia* Workshop
25 May – 30 May, 2025
Thessaloniki, Greece
Website: botryscleromoni.com

XVII Working Group "Biological and integrated control of plant pathogens." From single microbes to microbiome targeting One Health.
11 June – 14 June, 2025
University of Torino, Torino, Italy
Website: www.iobctorino2025.org

17th Congress of the Mediterranean Phytopathological Union - New phytopathology frontiers of research and education for plant health and food safety
7 July – 10 July, 2025
Ciheam-Bari, Italy
Contact and Email: Anna Maria D'Onghia,e-mail: mpu2025@iamb.it
Website: www.mpunion.org

13th International Workshop on Grapevine Trunk Diseases
21 July – 25 July, 2025
Ensenada, Baja California, México
Contact and Email: Rufina Hernández
13iwgtd@cicese.mx
Website (under construction): 13iwgtd.cicese.mx

14th Arab Congress of Plant Protection Sciences
3 November – 7 November, 2025
Algeria
Contact and Email: hou.boureghda@gmail.com
Website will be developed soon.

International Congress of Plant Pathology 2028
19 August – 25 August, 2028
Gold Coast, Queensland, Australia
Website: www.icpp2028.org

INTERNATIONAL SOCIETY FOR PLANT PATHOLOGY (ISPP)

WWW.ISPPWEB.ORG

The ISPP List is an e-mail list server which broadcasts messages and announcements to its subscribers. Its goal is to facilitate communication among members of the International Society for Plant Pathology and its Associated Societies. Advertised vacancies in plant pathology and ISPP Newsletter alerts are also sent to members of the ISPP List.

In accordance with the guidelines and recommendations established by the new EU General Data Protection Regulation 679/2016 (GDPR), the International Society for Plant Pathology has created a Privacy Information Notice containing all the information you need to know about how we collect, use and protect your personal data.

This policy explains when and why we collect personal information about our users, how we use it, the conditions under which we may disclose it to third parties, how we keep it safe and secure and your rights and choices in relation to your personal information.

Should you need further information please contact business.manager@issppweb.org

SUBSCRIBE OUR NEWSLETTER